

# "h2o"

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---

h2o-package

*H2O R Interface*

---

**Description**

This is a package for running H2O via its REST API from within R. To communicate with a H2O instance, the version of the R package must match the version of H2O. When connecting to a new H2O cluster, it is necessary to re-run the initializer.

**Details**

```

Package:  h2o
Type:    Package
Version:  3.32.1.6
Branch:   rel-zipf
Date:     Thu Aug 19 18:53:24 UTC 2021
License:  Apache License (== 2.0)
Depends:  R (>= 2.13.0), RCurl, jsonlite, statmod, tools, methods, utils

```

H2O is the scalable open source machine learning platform that offers parallelized implementations of many supervised and unsupervised machine learning algorithms such as Generalized Linear Models (GLM), Gradient Boosting Machines (including XGBoost), Random Forests, Deep Neural Networks (Deep Learning), Stacked Ensembles, Naive Bayes, Generalized Additive Models (GAM), Cox Proportional Hazards, K-Means, PCA, Word2Vec, as well as a fully automatic machine learning algorithm (H2O AutoML). As an example, to run GLM, call `h2o.glm` with the H2O parsed data and parameters (response variable, error distribution, etc.) as arguments.

This package enables the use of the H2O machine learning platform commands in R. To use H2O from R, you must start or connect to the "H2O cluster", the term we use to describe the backend H2O Java engine. To run H2O on your local machine, call `h2o.init` without any arguments, and H2O will be automatically launched at localhost:54321, where the IP is "127.0.0.1" and the port is 54321. If you have the H2O cluster running on a remote machine (e.g. AWS EC2), you must provide the IP and port of the remote machine as arguments to the `h2o.init` call.

Note that no actual data is stored in the R workspace; and no actual work is carried out by R. R only saves the named objects, which uniquely identify the data set, model, etc on the server. When the user makes a request, R queries the server via the REST API, which returns a JSON file with the relevant information that R then displays in the console.

**Author(s)**

Maintainer: Erin LeDell <erin@h2o.ai>

**References**

- [H2O.ai Homepage](#)
- [H2O User Guide](#)
- [H2O on GitHub](#)

---

```
.addParm
```

*TODO: No objects in this file are being used. Either remove file or use objects.*

---

**Description**

Append a <key,value> pair to a list.

**Usage**

```
.addParm(parms, k, v)
```

**Arguments**

<code>parms</code>	a list to add the <k,v> pair to
<code>k</code>	a key, typically the name of some algorithm parameter
<code>v</code>	a value, the value of the algorithm parameter

**Details**

Contained here are a set of helper methods that perform type checking on the value passed in.

---

`.check_for_ggplot2`     *Stop with a user friendly message if a user is missing the ggplot2 package or has an old version of it.*

---

**Description**

Stop with a user friendly message if a user is missing the ggplot2 package or has an old version of it.

**Usage**

```
.check_for_ggplot2(version = "3.0.0")
```

**Arguments**

<code>version</code>	minimal required ggplot2 version
----------------------	----------------------------------

---

`.collapse`     *Helper Collapse Function*

---

**Description**

Collapse a character vector into a ','-sep array of the form: [thing1,thing2,...]

**Usage**

```
.collapse(v)
```

**Arguments**

<code>v</code>	Character vector.
----------------	-------------------

---

`.consolidate_varimps`    *Consolidate variable importances*

---

**Description**

Consolidation works in the following way: 1. if varimp variable is in x => add it to consolidated\_varimps 2. for all remaining varimp variables: 1. find the longest prefix of varimp variable that is in x and add it to the consolidated varimp 2. if there was no match, throw an error 3. normalize the consolidated\_varimps so they sum up to 1

**Usage**

```
.consolidate_varimps(model)
```

**Arguments**

model                    H2OModel

**Value**

sorted named vector

---

`.create_leaderboard`    *Create a leaderboard like data frame for models*

---

**Description**

Create a leaderboard like data frame for models

**Usage**

```
.create_leaderboard(models_info, leaderboard_frame, top_n = 20)
```

**Arguments**

models\_info            H2OAutoML object or list of models  
 leaderboard\_frame     when provided with list of models, use this frame to calculate metrics  
 top\_n                   create leaderboard with just top\_n models

**Value**

a data.frame

---

.customized\_call      *A helper function that makes it easier to override/add params in a function call.*

---

**Description**

A helper function that makes it easier to override/add params in a function call.

**Usage**

```
.customized_call(fun, ..., overridable_defaults = NULL, overrides = NULL)
```

**Arguments**

fun                    Function to be called  
...                    Parameters that can't be overridden  
overridable\_defaults      List of parameters and values that can be overridden  
overrides                Parameters to add/override.

**Value**

result of fun

---

.find\_appropriate\_column\_name  
*Tries to match a fuzzy\_col\_name with a column name that exists in cols.*

---

**Description**

Tries to match a fuzzy\_col\_name with a column name that exists in cols.

**Usage**

```
.find_appropriate_column_name(fuzzy_col_name, cols)
```

**Arguments**

fuzzy\_col\_name    a name to be decoded  
cols                vector of columns that contain all possible column names, i.e., decode fuzzy\_col\_name must be in cols

**Value**

a correct column name

---

<code>.get_algorithm</code>	<i>Get the algorithm used by the model_or_model_id</i>
-----------------------------	--

---

**Description**

Get the algorithm used by the model\_or\_model\_id

**Usage**

```
.get_algorithm(model_or_model_id, treat_xrt_as_algorithm = FALSE)
```

**Arguments**

<code>model_or_model_id</code>	Model object or a string containing model id
<code>treat_xrt_as_algorithm</code>	Try to find out if a model is XRT and if so report it as xrt

**Value**

algorithm name

---

<code>.get_feature_count</code>	<i>Get feature count sorted by the count descending.</i>
---------------------------------	--

---

**Description**

Get feature count sorted by the count descending.

**Usage**

```
.get_feature_count(column)
```

**Arguments**

<code>column</code>	H2OFrame column
---------------------	-----------------

**Value**

named vector with feature counts

---

.get\_first\_of\_family *Get first of family models*

---

### Description

Get first of family models

### Usage

```
.get_first_of_family(models, all_stackedensembles = TRUE)
```

### Arguments

models           models or model ids  
all\_stackedensembles  
                  if TRUE, select all stacked ensembles

---

.h2o.doGET           *Just like doRawGET but fills in the default h2oRestApiVersion if none is provided*

---

### Description

Just like doRawGET but fills in the default h2oRestApiVersion if none is provided

### Usage

```
.h2o.doGET(h2oRestApiVersion, urlSuffix, parms, ...)
```

### Arguments

h2oRestApiVersion  
                  (Optional) A version number to prefix to the urlSuffix. If no version is provided, a default version is chosen for you.  
urlSuffix        The partial URL suffix to add to the calculated base URL for the instance  
parms           (Optional) Parameters to include in the request  
...              (Optional) Additional parameters.

### Value

A list object as described above

---

<code>.h2o.doPOST</code>	<i>Just like <code>doRawPOST</code> but fills in the default <code>h2oRestApiVersion</code> if none is provided</i>
--------------------------	---

---

**Description**

Just like `doRawPOST` but fills in the default `h2oRestApiVersion` if none is provided

**Usage**

```
.h2o.doPOST(h2oRestApiVersion, urlSuffix, parms, ...)
```

**Arguments**

<code>h2oRestApiVersion</code>	(Optional) A version number to prefix to the <code>urlSuffix</code> . If no version is provided, a default version is chosen for you.
<code>urlSuffix</code>	The partial URL suffix to add to the calculated base URL for the instance
<code>parms</code>	(Optional) Parameters to include in the request
<code>...</code>	(Optional) Additional parameters.

**Value**

A list object as described above

---

<code>.h2o.doRawGET</code>	<i>Perform a low-level HTTP GET operation on an H2O instance</i>
----------------------------	--

---

**Description**

Does not do any I/O level error checking. Caller must do its own validations. Does not modify the response payload in any way. Log the request and response if `h2o.startLogging()` has been called.

**Usage**

```
.h2o.doRawGET(
  conn = h2o.getConnection(),
  h2oRestApiVersion,
  urlSuffix,
  parms,
  ...
)
```



**Arguments**

conn	H2OConnection
h2oRestApiVersion	(Optional) A version number to prefix to the urlSuffix. If no version is provided, the version prefix is skipped.
urlSuffix	The partial URL suffix to add to the calculated base URL for the instance
parms	(Optional) Parameters to include in the request
...	(Optional) Additional parameters.

**Details**

The return value is a list as follows: \$url – Final calculated URL. \$postBody – The body of the POST request from client to server. \$curlError – TRUE if a socket-level error occurred. FALSE otherwise. \$curlErrorMessage – If curlError is TRUE a message about the error. \$statusCode – The HTTP status code. Usually 200 if the request succeeded. \$statusCodeMessage – A string describing the statusCode. \$payload – The raw response payload as a character vector.

**Value**

A list object as described above

---

.h2o.doRawPOST	<i>Perform a low-level HTTP POST operation on an H2O instance</i>
----------------	---

---

**Description**

Does not do any I/O level error checking. Caller must do its own validations. Does not modify the response payload in any way. Log the request and response if h2o.startLogging() has been called.

**Usage**

```
.h2o.doRawPOST(
  conn = h2o.getConnection(),
  h2oRestApiVersion,
  urlSuffix,
  parms,
  fileUploadInfo,
  ...
)
```

**Arguments**

conn	H2OConnection
h2oRestApiVersion	(Optional) A version number to prefix to the urlSuffix. If no version is provided, the version prefix is skipped.
urlSuffix	The partial URL suffix to add to the calculated base URL for the instance
parms	(Optional) Parameters to include in the request
fileUploadInfo	(Optional) Information to POST (NOTE: changes Content-type from XXX-www-url-encoded to multi-part). Use fileUpload(normalizePath("/path/to/file")).
...	(Optional) Additional parameters.

**Details**

The return value is a list as follows: \$url – Final calculated URL. \$postBody – The body of the POST request from client to server. \$curlError – TRUE if a socket-level error occurred. FALSE otherwise. \$curlErrorMessage – If curlError is TRUE a message about the error. \$statusCode – The HTTP status code. Usually 200 if the request succeeded. \$statusCodeMessage – A string describing the statusCode. \$payload – The raw response payload as a character vector.

**Value**

A list object as described above

---

.h2o.doSafeGET	<i>Perform a safe (i.e. error-checked) HTTP GET request to an H2O cluster.</i>
----------------	--

---

**Description**

This function validates that no CURL error occurred and that the HTTP response code is successful. If a failure occurred, then stop() is called with an error message. Since all necessary error checking is done inside this call, the valid payload is directly returned if the function successfully finishes without calling stop().

**Usage**

```
.h2o.doSafeGET(h2oRestApiVersion, urlSuffix, parms, ...)
```

**Arguments**

h2oRestApiVersion	(Optional) A version number to prefix to the urlSuffix. If no version is provided, a default version is chosen for you.
urlSuffix	The partial URL suffix to add to the calculated base URL for the instance
parms	(Optional) Parameters to include in the request
...	(Optional) Additional parameters.

**Value**

The raw response payload as a character vector

---

.h2o.doSafePOST	<i>Perform a safe (i.e. error-checked) HTTP POST request to an H2O cluster.</i>
-----------------	---

---

**Description**

This function validates that no CURL error occurred and that the HTTP response code is successful. If a failure occurred, then stop() is called with an error message. Since all necessary error checking is done inside this call, the valid payload is directly returned if the function successfully finishes without calling stop().

**Usage**

```
.h2o.doSafePOST(h2oRestApiVersion, urlSuffix, parms, fileUploadInfo, ...)
```

**Arguments**

h2oRestApiVersion	(Optional) A version number to prefix to the urlSuffix. If no version is provided, a default version is chosen for you.
urlSuffix	The partial URL suffix to add to the calculated base URL for the instance
parms	(Optional) Parameters to include in the request
fileUploadInfo	(Optional) Information to POST (NOTE: changes Content-type from XXX-www-url-encoded to multi-part). Use fileUpload(normalizePath("/path/to/file")).
...	(Optional) Additional parameters.

**Value**

The raw response payload as a character vector

---

.h2o.is_progress	<i>Check if Progress Bar is Enabled</i>
------------------	---

---

**Description**

Check if Progress Bar is Enabled

**Usage**

```
.h2o.is_progress()
```

---

.h2o.locate	<i>Locate a file given the pattern &lt;bucket&gt;/&lt;path/to/file&gt; e.g. h2o:::h2o.locate("smalldata/iris/iris22.csv") returns the absolute path to iris22.csv</i>
-------------	---

---

**Description**

Locate a file given the pattern <bucket>/<path/to/file> e.g. h2o:::h2o.locate("smalldata/iris/iris22.csv") returns the absolute path to iris22.csv

**Usage**

```
.h2o.locate(pathStub, root.parent = NULL)
```

**Arguments**

pathStub	relative path
root.parent	search root directory

---

.h2o.perfect_auc	<i>Internal function that calculates a precise AUC from given probabilities and actual responses.</i>
------------------	---

---

**Description**

Note: The underlying implementation is not distributed and can only handle limited size of data. For internal use only.

**Usage**

```
.h2o.perfect_auc(probs, acts)
```

**Arguments**

probs	An <a href="#">H2OFrame</a> holding vector of probabilities.
acts	An <a href="#">H2OFrame</a> holding vector of actuals.

---

.h2o.primitives	<i>Map of operations known to H2O</i>
-----------------	---------------------------------------

---

**Description**

Map of operations known to H2O

**Usage**

```
.h2o.primitives
```

**Format**

An object of class character of length 39.

---

.h2o.\_\_ALL\_CAPABILITIES

*Capabilities endpoints*

---

**Description**

Capabilities endpoints

**Usage**

.h2o.\_\_ALL\_CAPABILITIES

**Format**

An object of class character of length 1.

---

.h2o.\_\_checkConnectionHealth

*Check H2O Server Health*

---

**Description**

Warn if there are sick nodes.

**Usage**

.h2o.\_\_checkConnectionHealth()

---

.h2o.\_\_CREATE\_FRAME

*H2OFrame Manipulation*

---

**Description**

H2OFrame Manipulation

**Usage**

.h2o.\_\_CREATE\_FRAME

**Format**

An object of class character of length 1.

---

`.h2o.__DECRYPTION_SETUP`

*Decryption Endpoints*

---

**Description**

Decryption Endpoints

**Usage**

`.h2o.__DECRYPTION_SETUP`

**Format**

An object of class character of length 1.

---

`.h2o.__DKV`

*Removal Endpoints*

---

**Description**

Removal Endpoints

**Usage**

`.h2o.__DKV`

**Format**

An object of class character of length 1.

---

`.h2o.__EXPORT_FILES`

*Export Files Endpoint Generator*

---

**Description**

Export Files Endpoint Generator

**Usage**

`.h2o.__EXPORT_FILES(frame)`

**Arguments**

frame            H2OFrame

---

.h2o.\_\_FRAMES                      *Inspect/Summary Endpoints*

---

**Description**

Inspect/Summary Endpoints

**Usage**

.h2o.\_\_FRAMES

**Format**

An object of class character of length 1.

---

.h2o.\_\_IMPORT                      *Import/Export Endpoints*

---

**Description**

Import/Export Endpoints

**Usage**

.h2o.\_\_IMPORT

**Format**

An object of class character of length 1.

---

.h2o.\_\_JOBS                      *Administrative Endpoints*

---

**Description**

Administrative Endpoints

**Usage**

.h2o.\_\_JOBS

**Format**

An object of class character of length 1.





---

.h2o.\_\_MODEL\_METRICS *Model Metrics Endpoint*

---

**Description**

Model Metrics Endpoint

**Usage**

.h2o.\_\_MODEL\_METRICS(model, data)

**Arguments**

model	H2OModel.
data	H2OFrame.

---

.h2o.\_\_PARSE\_SETUP *Parse Endpoints*

---

**Description**

Parse Endpoints

**Usage**

.h2o.\_\_PARSE\_SETUP

**Format**

An object of class character of length 1.

---

.h2o.\_\_RAPIDS *Rapids Endpoint*

---

**Description**

Rapids Endpoint

**Usage**

.h2o.\_\_RAPIDS

**Format**

An object of class character of length 1.

---

*.h2o.\_\_REST\_API\_VERSION*

*H2O Package Constants*

---

### **Description**

The API endpoints for interacting with H2O via REST are named here.

### **Usage**

*.h2o.\_\_REST\_API\_VERSION*

### **Format**

An object of class integer of length 1.

### **Details**

Additionally, environment variables for the H2O package are named here. Endpoint Version

---

*.h2o.\_\_SEGMENT\_MODELS\_BUILDERS*

*Segment Models Builder Endpoint Generator*

---

### **Description**

Segment Models Builder Endpoint Generator

### **Usage**

*.h2o.\_\_SEGMENT\_MODELS\_BUILDERS(algo)*

### **Arguments**

*algo*                      Canonical identifier of H2O algorithm.

---

*.h2o.\_\_W2V\_SYNONYMS*      *Word2Vec Endpoints*

---

### **Description**

Word2Vec Endpoints

### **Usage**

*.h2o.\_\_W2V\_SYNONYMS*

### **Format**

An object of class character of length 1.

---

.has_varimp	<i>Has the model variable importance?</i>
-------------	---

---

**Description**

Has the model variable importance?

**Usage**

.has\_varimp(model)

**Arguments**

model                    model or a string containing model id

**Value**

boolean

---

.interpretable	<i>Is the model considered to be interpretable, i.e., simple enough.</i>
----------------	--

---

**Description**

Is the model considered to be interpretable, i.e., simple enough.

**Usage**

.interpretable(model)

**Arguments**

model                    model or a string containing model id

**Value**

boolean

---

<code>.is_h2o_model</code>	<i>Is the model an H2O model?</i>
----------------------------	-----------------------------------

---

**Description**

Is the model an H2O model?

**Usage**

```
.is_h2o_model(model)
```

**Arguments**

<code>model</code>	Either H2O model/model id => TRUE, or something else => FALSE
--------------------	---

**Value**

boolean

---

<code>.is_h2o_tree_model</code>	<i>Is the model a Tree-based H2O Model?</i>
---------------------------------	---

---

**Description**

Is the model a Tree-based H2O Model?

**Usage**

```
.is_h2o_tree_model(model)
```

**Arguments**

<code>model</code>	Either tree-based H2O model/model id => TRUE, or something else => FALSE
--------------------	--

**Value**

boolean

---

.is\_plotting\_to\_rnotebook  
*Check if we are plotting in to r notebook.*

---

**Description**

Check if we are plotting in to r notebook.

**Usage**

.is\_plotting\_to\_rnotebook()

**Value**

boolean

---

.leaderboard\_for\_row *Enhance leaderboard with per-model predictions.*

---

**Description**

Enhance leaderboard with per-model predictions.

**Usage**

.leaderboard\_for\_row(models\_info, newdata, row\_index, top\_n = 20)

**Arguments**

models_info	models_info object
newdata	H2OFrame
row_index	index of the inspected row
top_n	leaderboard will contain top_n models

**Value**

H2OFrame

---

.min_max	<i>Min-max normalization.</i>
----------	-------------------------------

---

**Description**

Min-max normalization.

**Usage**

```
.min_max(col)
```

**Arguments**

col	numeric vector
-----	----------------

**Value**

normalized numeric vector

---

.model_ids	<i>Get Model Ids</i>
------------	----------------------

---

**Description**

When provided with list of models it will extract model ids. When provided with model ids it won't change anything. Works for mixed list as well.

**Usage**

```
.model_ids(models)
```

**Arguments**

models	list or vector of models/model_ids
--------	------------------------------------

**Value**

a vector of model\_ids

---

.pkg.env

*The H2O Package Environment*

---

### **Description**

The H2O Package Environment

### **Usage**

.pkg.env

### **Format**

An object of class environment of length 4.

---

.plot\_varimp

*Plot variable importances with ggplot2*

---

### **Description**

Plot variable importances with ggplot2

### **Usage**

.plot\_varimp(model, top\_n = 10)

### **Arguments**

model	H2OModel
top_n	Plot just top_n features

### **Value**

list of variable importance, grouped variable importance, and variable importance plot

---

```
.process_models_or_automl
```

*Do basic validation and transform object to a "standardized" list containing models, and their properties such as x, y, whether it is a (multinomial) classification or not etc.*

---

### Description

Do basic validation and transform object to a "standardized" list containing models, and their properties such as x, y, whether it is a (multinomial) classification or not etc.

### Usage

```
.process_models_or_automl(  
  object,  
  newdata,  
  require_single_model = FALSE,  
  require_multiple_models = FALSE,  
  top_n_from_AutoML = NA,  
  only_with_varimp = FALSE,  
  best_of_family = FALSE,  
  require_newdata = TRUE  
)
```

### Arguments

object	Can be a single model/model_id, vector of model_id, list of models, H2OAutoML object
newdata	An H2OFrame with the same format as training frame
require_single_model	If true, make sure we were provided only one model
require_multiple_models	If true, make sure we were provided at least two models
top_n_from_AutoML	If set, don't return more than top_n models (applies only for AutoML object)
only_with_varimp	If TRUE, return only models that have variable importance
best_of_family	If TRUE, return only the best of family models; if FALSE return all models in object
require_newdata	If TRUE, require newdata to be specified; otherwise allow NULL instead, this can be used when there is no need to know if the problem is (multinomial) classification.

### Value

a list with the following names leader, is\_automl, models, is\_classification, is\_multinomial\_classification, x, y, model



---

.shorten\_model\_ids      *Shortens model ids if possible (iff there will be same amount of unique model\_ids as before)*

---

**Description**

Shortens model ids if possible (iff there will be same amount of unique model\_ids as before)

**Usage**

.shorten\_model\_ids(model\_ids)

**Arguments**

model\_ids      character vector

**Value**

character vector

---

.skip\_if\_not\_developer  
*H2O <-> R Communication and Utility Methods*

---

**Description**

Collected here are the various methods used by the h2o-R package to communicate with the H2O backend. There are methods for checking cluster health, polling, and inspecting objects in the H2O store.

**Usage**

.skip\_if\_not\_developer()

---

.uniformize      *Convert to quantiles when provided with numeric vector. When col is a factor vector assign uniformly value between 0 and 1 to each level.*

---

**Description**

Convert to quantiles when provided with numeric vector. When col is a factor vector assign uniformly value between 0 and 1 to each level.

**Usage**

.uniformize(col)

**Arguments**

col	vector
-----	--------

**Value**

vector with values between 0 and 1

---

.varimp	<i>Get variable importance in a standardized way.</i>
---------	---

---

**Description**

Get variable importance in a standardized way.

**Usage**

```
.varimp(model)
```

**Arguments**

model	H2OModel
-------	----------

**Value**

A named vector

---

.verify_dataxy	<i>Used to verify data, x, y and turn into the appropriate things</i>
----------------	---

---

**Description**

Used to verify data, x, y and turn into the appropriate things

**Usage**

```
.verify_dataxy(data, x, y, autoencoder = FALSE)
```

**Arguments**

data	H2OFrame
x	features
y	response
autoencoder	autoencoder flag

---

aaa

*Starting H2O For examples*

---

### Description

Starting H2O For examples

### Examples

```
## Not run:
if (Sys.info()['sysname'] == "Darwin" && Sys.info()['release'] == '13.4.0') {
  quit(save = "no")
} else {
  h2o.init(nthreads = 2)
}

## End(Not run)
```

---

apply

*Apply on H2O Datasets*

---

### Description

Method for apply on H2OFrame objects.

### Usage

```
apply(X, MARGIN, FUN, ...)
```

### Arguments

X	an H2OFrame object on which apply will operate.
MARGIN	the vector on which the function will be applied over, either 1 for rows or 2 for columns.
FUN	the function to be applied.
...	optional arguments to FUN.

### Value

Produces a new H2OFrame of the output of the applied function. The output is stored in H2O so that it can be used in subsequent H2O processes.

### See Also

[apply](#) for the base generic

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
summary(apply(iris_hf, 2, sum))

## End(Not run)
```

---

as.character.H2OFrame *Convert an H2OFrame to a String*

---

**Description**

Convert an H2OFrame to a String

**Usage**

```
## S3 method for class 'H2OFrame'
as.character(x, ...)
```

**Arguments**

x                    An H2OFrame object  
 ...                  Further arguments to be passed from or to other methods.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
pretrained <- as.h2o(data.frame(
  C1 = c("a", "b"), C2 = c(0, 1), C3 = c(1, 0), C4 = c(0.2, 0.8),
  stringsAsFactors = FALSE))
pretrained_w2v <- h2o.word2vec(pre_trained = pretrained, vec_size = 3)
words <- as.character(as.h2o(c("b", "a", "c", NA, "a")))
vecs <- h2o.transform(pretrained_w2v, words = words)

## End(Not run)
```

---

as.data.frame.H2OFrame

*Converts parsed H2O data into an R data frame*

---

**Description**

Downloads the H2O data and then scans it in to an R data frame.

**Usage**

```
## S3 method for class 'H2OFrame'  
as.data.frame(x, ...)
```

**Arguments**

x                    An H2OFrame object.  
...                  Further arguments to be passed down from other methods.

**Details**

Method as.data.frame.H2OFrame will use [fread](#) if data.table package is installed in required version.

**See Also**

[use.package](#)

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")  
prostate <- h2o.uploadFile(path = prostate_path)  
as.data.frame(prostate)  
  
## End(Not run)
```

---

as.data.frame.H2OSegmentModels

*Converts a collection of Segment Models to a data.frame*

---

**Description**

Converts a collection of Segment Models to a data.frame

**Usage**

```
## S3 method for class 'H2OSegmentModels'  
as.data.frame(x, ...)
```

**Arguments**

x                    Object of class [H2OSegmentModels](#).  
...                  Further arguments to be passed down from other methods.

**Value**

Returns data.frame with result of segment model training.

## Examples

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
models <- h2o.train_segments(algorithm = "gbm",
                             segment_columns = "Species",
                             x = c(1:3), y = 4,
                             training_frame = iris_hf,
                             ntrees = 5,
                             max_depth = 4)

as.data.frame(models)

## End(Not run)
```

---

as.factor

*Convert H2O Data to Factors*

---

## Description

Convert a column into a factor column.

## Usage

```
as.factor(x)
```

## Arguments

x                    a column from an H2OFrame data set.

## See Also

[as.factor](#).

## Examples

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
summary(prostate)

## End(Not run)
```

---

as.h2o	<i>Create H2OFrame</i>
--------	------------------------

---

## Description

Import R object to the H2O cluster.

## Usage

```
as.h2o(x, destination_frame = "", ...)  
  
## Default S3 method:  
as.h2o(x, destination_frame = "", ...)  
  
## S3 method for class 'H2OFrame'  
as.h2o(x, destination_frame = "", ...)  
  
## S3 method for class 'data.frame'  
as.h2o(x, destination_frame = "", use_datatable = TRUE, ...)  
  
## S3 method for class 'Matrix'  
as.h2o(x, destination_frame = "", use_datatable = TRUE, ...)
```

## Arguments

x	An R object.
destination_frame	A string with the desired name for the H2OFrame
...	arguments passed to method arguments.
use_datatable	allow usage of data.table

## Details

Method `as.h2o.data.frame` will use `fwrite` if `data.table` package is installed in required version.

To speedup execution time for large sparse matrices, use `h2o.datatable`. Make sure you have installed and imported `data.table` and `slam` packages. Turn on `h2o.datatable` by `options("h2o.use.data.table"=TRUE)`

## References

<https://www.h2o.ai/blog/fast-csv-writing-for-r/>

## See Also

[use.package](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
euro_hf <- as.h2o(euro)
letters_hf <- as.h2o(letters)
state_hf <- as.h2o(state.x77)
iris_hf_2 <- as.h2o(iris_hf)
stopifnot(is.h2o(iris_hf), dim(iris_hf) == dim(iris),
          is.h2o(euro_hf), dim(euro_hf) == c(length(euro), 1L),
          is.h2o(letters_hf), dim(letters_hf) == c(length(letters), 1L),
          is.h2o(state_hf), dim(state_hf) == dim(state.x77),
          is.h2o(iris_hf_2), dim(iris_hf_2) == dim(iris_hf))
if (requireNamespace("Matrix", quietly=TRUE)) {
  data <- rep(0, 100)
  data[(1:10) ^ 2] <- 1:10 * pi
  m <- matrix(data, ncol = 20, byrow = TRUE)
  m <- Matrix::Matrix(m, sparse = TRUE)
  m_hf <- as.h2o(m)
  stopifnot(is.h2o(m_hf), dim(m_hf) == dim(m))
}

## End(Not run)
```

---

as.matrix.H2OFrame      *Convert an H2OFrame to a matrix*

---

**Description**

Convert an H2OFrame to a matrix

**Usage**

```
## S3 method for class 'H2OFrame'
as.matrix(x, ...)
```

**Arguments**

x	An H2OFrame object
...	Further arguments to be passed down from other methods.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
describe <- h2o.describe(iris_hf)
mins = as.matrix(apply(iris_hf, 2, min))
print(mins)

## End(Not run)
```



---

as.numeric	<i>Convert H2O Data to Numeric</i>
------------	------------------------------------

---

**Description**

Converts an H2O column into a numeric value column.

**Usage**

```
as.numeric(x)
```

**Arguments**

x                    a column from an H2OFrame data set.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate[, 2] <- as.factor (prostate[, 2])
prostate[, 2] <- as.numeric(prostate[, 2])

## End(Not run)
```

---

as.vector.H2OFrame	<i>Convert an H2OFrame to a vector</i>
--------------------	--

---

**Description**

Convert an H2OFrame to a vector

**Usage**

```
## S3 method for class 'H2OFrame'
as.vector(x,mode)
```

**Arguments**

x                    An H2OFrame object  
mode                 Mode to coerce vector to

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
cor_R <- cor(as.matrix(iris[, 1]))
cor_h2o <- cor(iris_hf[, 1])
iris_R_cor <- cor(iris[, 1:4])
iris_H2O_cor <- as.data.frame(cor(iris_hf[, 1:4]))
h2o_vec <- as.vector(unlist(iris_H2O_cor))
r_vec <- as.vector(unlist(iris_R_cor))

## End(Not run)
```

---

australia	<i>Australia Coastal Data</i>
-----------	-------------------------------

---

**Description**

Temperature, soil moisture, runoff, and other environmental measurements from the Australia coast. The data is available from <https://cs.colby.edu/courses/S11/cs251/labs/lab07/AustraliaSubset.csv>.

**Format**

A data frame with 251 rows and 8 columns

---

colnames	<i>Returns the column names of an H2OFrame</i>
----------	--

---

**Description**

Returns the column names of an H2OFrame

**Usage**

```
colnames(x, do.NULL = TRUE, prefix = "col")
```

**Arguments**

x	An H2OFrame object.
do.NULL	logical. If FALSE and names are NULL, names are created.
prefix	for created names.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
colnames(iris_hf) # Returns "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"

## End(Not run)
```

---

dim.H2OFrame	<i>Returns the Dimensions of an H2OFrame</i>
--------------	--

---

**Description**

Returns the number of rows and columns for an H2OFrame object.

**Usage**

```
## S3 method for class 'H2OFrame'  
dim(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[dim](#) for the base R method.

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
iris_hf <- as.h2o(iris)  
dim(iris_hf)  
  
## End(Not run)
```

---

dimnames.H2OFrame	<i>Column names of an H2OFrame</i>
-------------------	------------------------------------

---

**Description**

Set column names of an H2O Frame

**Usage**

```
## S3 method for class 'H2OFrame'  
dimnames(x)
```

**Arguments**

x                    An H2OFrame

**Examples**

```
## Not run:
library(h2o)
h2o.init()

n <- 2000
# Generate variables V1, ... V10
X <- matrix(rnorm(10 * n), n, 10)
# y = +1 if sum_i x_{ij}^2 > chisq median on 10 df
y <- rep(-1, n)
y[apply(X*X, 1, sum) > qchisq(.5, 10)] <- 1
# Assign names to the columns of X:
dimnames(X)[[2]] <- c("V1", "V2", "V3", "V4", "V5", "V6", "V7", "V8", "V9", "V10")

## End(Not run)
```

---

```
feature_frequencies.H2OModel
```

*Retrieve the number of occurrences of each feature for given observations Available for GBM, Random Forest and Isolation Forest models.*

---

**Description**

Retrieve the number of occurrences of each feature for given observations Available for GBM, Random Forest and Isolation Forest models.

**Usage**

```
feature_frequencies.H2OModel(object, newdata, ...)
```

```
h2o.feature_frequencies(object, newdata, ...)
```

**Arguments**

object	a fitted <a href="#">H2OModel</a> object for which prediction is desired
newdata	An <a href="#">H2OFrame</a> object in which to look for variables with which to predict.
...	additional arguments to pass on.

**Value**

Returns an [H2OFrame](#) contain per-feature frequencies on the predict path for each input row.

**See Also**

[h2o.gbm](#) and [h2o.randomForest](#) for model generation in h2o.

---

generate_col_ind	<i>CHeck to see if the column names/indices entered is valid for the dataframe given. This is an internal function</i>
------------------	--

---

### Description

CHeck to see if the column names/indices entered is valid for the dataframe given. This is an internal function

### Usage

```
generate_col_ind(data, by)
```

### Arguments

data	The H2OFrame whose column names or indices are entered as a list
by	The column names/indices in a list.

---

get_seed.H2OModel	<i>Get the seed from H2OModel which was used during training. If a user does not set the seed parameter before training, the seed is auto-generated. It returns seed as the string if the value is bigger than the integer. For example, an autogenerated seed is always long so that the seed in R is a string.</i>
-------------------	--

---

### Description

Get the seed from H2OModel which was used during training. If a user does not set the seed parameter before training, the seed is autogenerated. It returns seed as the string if the value is bigger than the integer. For example, an autogenerated seed is always long so that the seed in R is a string.

### Usage

```
get_seed.H2OModel(object)
```

```
h2o.get_seed(object)
```

### Arguments

object	a fitted <a href="#">H2OModel</a> object.
--------	---

### Value

Returns seed to be used during training a model. Could be numeric or string.

## Examples

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
seed <- h2o.get_seed(prostate_gbm)

## End(Not run)
```

---

h2o.abs

*Compute the absolute value of x*

---

## Description

Compute the absolute value of x

## Usage

```
h2o.abs(x)
```

## Arguments

x                    An H2OFrame object.

## See Also

[MathFun](#) for the base R implementation, `abs()`.

## Examples

```
## Not run:
library(h2o)
h2o.init()
url <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/gbm_test/smtrees.csv"
smtrees_hf <- h2o.importFile(url)
smtrees_df <- read.csv(
  "https://s3.amazonaws.com/h2o-public-test-data/smalldata/gbm_test/smtrees.csv")
model <- h2o.gbm(x = c("girth", "height"), y = "vol", ntrees = 3, max_depth = 1,
  distribution = "gaussian", min_rows = 2, learn_rate = .1,
  training_frame = smtrees_hf)
pred <- as.data.frame(predict(model, newdata = smtrees_hf))
diff <- pred - smtrees_df[, 4]
diff_abs <- abs(diff)
print(diff_abs)

## End(Not run)
```

---

h2o.acos	<i>Compute the arc cosine of x</i>
----------	------------------------------------

---

**Description**

Compute the arc cosine of x

**Usage**

```
h2o.acos(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Trig](#) for the base R implementation, `acos()`.

**Examples**

```
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.acos(prostate[, 2])

## End(Not run)
```

---

h2o.aggregated_frame	<i>Retrieve an aggregated frame from an Aggregator model</i>
----------------------	--

---

**Description**

Retrieve an aggregated frame from the Aggregator model and use it to create a new frame.

**Usage**

```
h2o.aggregated_frame(model)
```

**Arguments**

model                an [H2OClusteringModel](#) corresponding from a `h2o.aggregator` call.

**Examples**

```

## Not run:
library(h2o)
h2o.init()
df <- h2o.createFrame(rows = 100,
                      cols = 5,
                      categorical_fraction = 0.6,
                      integer_fraction = 0,
                      binary_fraction = 0,
                      real_range = 100,
                      integer_range = 100,
                      missing_fraction = 0)

target_num_exemplars = 1000
rel_tol_num_exemplars = 0.5
encoding = "Eigen"
agg <- h2o.agggregator(training_frame = df,
                      target_num_exemplars = target_num_exemplars,
                      rel_tol_num_exemplars = rel_tol_num_exemplars,
                      categorical_encoding = encoding)

# Use the aggregated frame to create a new dataframe
new_df <- h2o.agggregated_frame(agg)

## End(Not run)

```

---

h2o.agggregator

*Build an Aggregated Frame*


---

**Description**

Builds an Aggregated Frame of an H2OFrame.

**Usage**

```

h2o.agggregator(
  training_frame,
  x,
  model_id = NULL,
  ignore_const_cols = TRUE,
  target_num_exemplars = 5000,
  rel_tol_num_exemplars = 0.5,
  transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"),
  categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
    "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
  save_mapping_frame = FALSE,
  num_iteration_without_new_exemplar = 500,
  export_checkpoints_dir = NULL
)

```

**Arguments**

`training_frame` Id of the training data frame.

`x` A vector containing the character names of the predictors in the model.



model_id	Destination id for this model; auto-generated if not specified.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
target_num_exemplars	Targeted number of exemplars Defaults to 5000.
rel_tol_num_exemplars	Relative tolerance for number of exemplars (e.g. 0.5 is +/- 50 percents) Defaults to 0.5.
transform	Transformation of training data Must be one of: "NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE". Defaults to NORMALIZE.
categorical_encoding	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.
save_mapping_frame	Logical. Whether to export the mapping of the aggregated frame Defaults to FALSE.
num_iteration_without_new_exemplar	The number of iterations to run before aggregator exits if the number of exemplars collected didn't change Defaults to 500.
export_checkpoints_dir	Automatically export generated models to this directory.

### Examples

```
## Not run:
library(h2o)
h2o.init()
df <- h2o.createFrame(rows = 100,
                      cols = 5,
                      categorical_fraction = 0.6,
                      integer_fraction = 0,
                      binary_fraction = 0,
                      real_range = 100,
                      integer_range = 100,
                      missing_fraction = 0)

target_num_exemplars = 1000
rel_tol_num_exemplars = 0.5
encoding = "Eigen"
agg <- h2o.aggregator(training_frame = df,
                      target_num_exemplars = target_num_exemplars,
                      rel_tol_num_exemplars = rel_tol_num_exemplars,
                      categorical_encoding = encoding)

## End(Not run)
```

**Description**

Retrieves the AIC value. If "train", "valid", and "xval" parameters are FALSE (default), then the training AIC value is returned. If more than one parameter is set to TRUE, then a named vector of AICs are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.aic(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> or <a href="#">H2OModelMetrics</a> .
train	Retrieve the training AIC
valid	Retrieve the validation AIC
xval	Retrieve the cross-validation AIC

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
p_sid <- h2o.runif(prostate)
prostate_train <- prostate[p_sid > .2,]
prostate_glm <- h2o.glm(x = 3:7, y = 2, training_frame = prostate_train)
aic_basic <- h2o.aic(prostate_glm)
print(aic_basic)

## End(Not run)
```

---

h2o.all

*Given a set of logical vectors, are all of the values true?*


---

**Description**

Given a set of logical vectors, are all of the values true?

**Usage**

```
h2o.all(x)
```

**Arguments**

x	An H2OFrame object.
---	---------------------

**See Also**

[all](#) for the base R implementation.

---

h2o.anomaly	<i>Anomaly Detection via H2O Deep Learning Model</i>
-------------	--

---

## Description

Detect anomalies in an H2O dataset using an H2O deep learning model with auto-encoding.

## Usage

```
h2o.anomaly(object, data, per_feature = FALSE)
```

## Arguments

object	An <a href="#">H2OAutoEncoderModel</a> object that represents the model to be used for anomaly detection.
data	An H2OFrame object.
per_feature	Whether to return the per-feature squared reconstruction error

## Value

Returns an H2OFrame object containing the reconstruction MSE or the per-feature squared error.

## See Also

[h2o.deeplearning](#) for making an H2OAutoEncoderModel.

## Examples

```
## Not run:
library(h2o)
h2o.init()
prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
prostate_dl = h2o.deeplearning(x = 3:9, training_frame = prostate, autoencoder = TRUE,
                             hidden = c(10, 10), epochs = 5)
prostate_anon = h2o.anomaly(prostate_dl, prostate)
head(prostate_anon)
prostate_anon_per_feature = h2o.anomaly(prostate_dl, prostate, per_feature = TRUE)
head(prostate_anon_per_feature)

## End(Not run)
```

---

h2o.any	<i>Given a set of logical vectors, is at least one of the values true?</i>
---------	--

---

**Description**

Given a set of logical vectors, is at least one of the values true?

**Usage**

```
h2o.any(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[all](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.any(iris[, 1] < 1000)

## End(Not run)
```

---

h2o.anyFactor	<i>Check H2OFrame columns for factors</i>
---------------	---

---

**Description**

Determines if any column of an H2OFrame object contains categorical data.

**Usage**

```
h2o.anyFactor(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

Returns a logical value indicating whether any of the columns in x are factors.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
h2o.anyFactor(iris_hf)

## End(Not run)
```

---

h2o.arrange	<i>Sorts an H2O frame by columns</i>
-------------	--------------------------------------

---

**Description**

Sorts H2OFrame by the columns specified. H2OFrame can contain String columns but should not sort on any String columns. Otherwise, an error will be thrown. To sort column c1 in descending order, do desc(c1). Returns a new H2OFrame, like dplyr::arrange.

**Usage**

```
h2o.arrange(x, ...)
```

**Arguments**

x	The H2OFrame input to be sorted.
...	The column names to sort by.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.arrange(iris, "species", "petal_len", "petal_wid")

## End(Not run)
```

---

h2o.ascharacter	<i>Convert H2O Data to Characters</i>
-----------------	---------------------------------------

---

**Description**

Convert H2O Data to Characters

**Usage**

```
h2o.ascharacter(x)
```

**Arguments**

x                    An H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.ascharacter(iris["species"])

## End(Not run)
```

---

h2o.asfactor	<i>Convert H2O Data to Factors</i>
--------------	------------------------------------

---

**Description**

Convert H2O Data to Factors

**Usage**

```
h2o.asfactor(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[factor](#) for the base R implementation, `as.factor()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
h2o.asfactor(cars["cylinders"])

## End(Not run)
```

---

h2o.asnumeric	<i>Convert H2O Data to Numerics</i>
---------------	-------------------------------------

---

**Description**

Convert H2O Data to Numerics

**Usage**

```
h2o.asnumeric(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[numeric](#) for the base R implementation, `as.numeric()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
h2o.asnumeric(cars)

## End(Not run)
```

---

h2o.assign	<i>Rename an H2O object.</i>
------------	------------------------------

---

**Description**

Makes a copy of the data frame and gives it the desired key.

**Usage**

```
h2o.assign(data, key)
```

**Arguments**

data                An H2OFrame object  
key                 The key to be associated with the H2O parsed data object

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
dim(cars)
split <- h2o.splitFrame(data = cars, ratios = 0.8)
train <- h2o.assign(split[[1]], key = "train")
test <- h2o.assign(split[[2]], key = "test")
dim(train)
dim(test)

## End(Not run)
```

---

h2o.as_date	<i>Convert between character representations and objects of Date class</i>
-------------	--

---

**Description**

Functions to convert between character representations and objects of class "Date" representing calendar dates.

**Usage**

```
h2o.as_date(x, format, ...)
```

**Arguments**

x	H2OFrame column of strings or factors to be converted
format	A character string indicating date pattern
...	Further arguments to be passed from or to other methods.

---

h2o.auc	<i>Retrieve the AUC</i>
---------	-------------------------

---

**Description**

Retrieves the AUC value from an [H2O Binomial Metrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training AUC value is returned. If more than one parameter is set to TRUE, then a named vector of AUCs are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.auc(object, train = FALSE, valid = FALSE, xval = FALSE)
```



**Arguments**

object	An <a href="#">H2OBinomialMetrics</a> or <a href="#">H2OMultinomialMetrics</a> object.
train	Retrieve the training AUC
valid	Retrieve the validation AUC
xval	Retrieve the cross-validation AUC

**See Also**

[h2o.giniCoef](#) for the Gini coefficient, [h2o.mse](#) for MSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating H2OModelMetrics objects.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.auc(perf)

## End(Not run)
```

---

h2o.aucpr

*Retrieve the AUCPR (Area Under Precision Recall Curve)*


---

**Description**

Retrieves the AUCPR value from an [H2OBinomialMetrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training AUCPR value is returned. If more than one parameter is set to TRUE, then a named vector of AUCPRs are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.aucpr(object, train = FALSE, valid = FALSE, xval = FALSE)
```

```
h2o.pr_auc(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OBinomialMetrics</a> object.
train	Retrieve the training aucpr
valid	Retrieve the validation aucpr
xval	Retrieve the cross-validation aucpr

**See Also**

[h2o.giniCoef](#) for the Gini coefficient, [h2o.mse](#) for MSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating H2OModelMetrics objects.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.aucpr(perf)

## End(Not run)
```

---

h2o.automl

*Automatic Machine Learning*


---

**Description**

The Automatic Machine Learning (AutoML) function automates the supervised machine learning model training process. The current version of AutoML trains and cross-validates the following algorithms (in the following order): three pre-specified XGBoost GBM (Gradient Boosting Machine) models, a fixed grid of GLMs, a default Random Forest (DRF), five pre-specified H2O GBMs, a near-default Deep Neural Net, an Extremely Randomized Forest (XRT), a random grid of XGBoost GBMs, a random grid of H2O GBMs, and a random grid of Deep Neural Nets. In some cases, there will not be enough time to complete all the algorithms, so some may be missing from the leaderboard. AutoML then trains two Stacked Ensemble models, one of all the models, and one of only the best models of each kind.

**Usage**

```
h2o.automl(
  x,
  y,
  training_frame,
  validation_frame = NULL,
  leaderboard_frame = NULL,
  blending_frame = NULL,
  nfolds = 5,
  fold_column = NULL,
  weights_column = NULL,
  balance_classes = FALSE,
  class_sampling_factors = NULL,
  max_after_balance_size = 5,
  max_runtime_secs = NULL,
  max_runtime_secs_per_model = NULL,
```

```

max_models = NULL,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
  "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error"),
stopping_tolerance = NULL,
stopping_rounds = 3,
seed = NULL,
project_name = NULL,
exclude_algos = NULL,
include_algos = NULL,
modeling_plan = NULL,
preprocessing = NULL,
exploitation_ratio = 0,
monotone_constraints = NULL,
keep_cross_validation_predictions = FALSE,
keep_cross_validation_models = FALSE,
keep_cross_validation_fold_assignment = FALSE,
sort_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC",
  "AUCPR", "mean_per_class_error"),
export_checkpoints_dir = NULL,
verbosity = "warn",
...
)

```

### Arguments

x	A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or index of the response variable in the model. For classification, the y column must be a factor, otherwise regression will be performed. Indexes are 1-based in R.
training_frame	Training frame (H2OFrame or ID).
validation_frame	Validation frame (H2OFrame or ID); Optional. This argument is ignored unless the user sets <code>nfolds = 0</code> . If cross-validation is turned off, then a validation frame can be specified and used for early stopping of individual models and early stopping of the grid searches. By default and when <code>nfolds &gt; 1</code> , cross-validation metrics will be used for early stopping and thus <code>validation_frame</code> will be ignored.
leaderboard_frame	Leaderboard frame (H2OFrame or ID); Optional. If provided, the Leaderboard will be scored using this data frame instead of using cross-validation metrics, which is the default.
blending_frame	Blending frame (H2OFrame or ID) used to train the the metalearning algorithm in Stacked Ensembles (instead of relying on cross-validated predicted values); Optional. When provided, it also is recommended to disable cross validation by setting <code>'nfolds=0'</code> and to provide a leaderboard frame for scoring purposes.
nfolds	Number of folds for k-fold cross-validation. Defaults to 5. Use 0 to disable cross-validation; this will also disable Stacked Ensemble (thus decreasing the overall model performance).
fold_column	Column with cross-validation fold index assignment per observation; used to override the default, randomized, 5-fold cross-validation scheme for individual models in the AutoML run.

<code>weights_column</code>	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed.
<code>balance_classes</code>	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
<code>class_sampling_factors</code>	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires <code>balance_classes</code> .
<code>max_after_balance_size</code>	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires <code>balance_classes</code> . Defaults to 5.0.
<code>max_runtime_secs</code>	This argument specifies the maximum time that the AutoML process will run for, prior to training the final Stacked Ensemble models. If neither <code>'max_runtime_secs'</code> nor <code>'max_models'</code> are specified by the user, then <code>'max_runtime_secs'</code> defaults to 3600 seconds (1 hour).
<code>max_runtime_secs_per_model</code>	Maximum runtime in seconds dedicated to each individual model training process. Use 0 to disable. Defaults to 0.
<code>max_models</code>	Maximum number of models to build in the AutoML process (does not include Stacked Ensembles). Defaults to NULL (no strict limit).
<code>stopping_metric</code>	Metric to use for early stopping ("AUTO" is logloss for classification, deviance for regression). Must be one of "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error". Defaults to "AUTO".
<code>stopping_tolerance</code>	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much). This value defaults to 0.001 if the dataset is at least 1 million rows; otherwise it defaults to a bigger value determined by the size of the dataset and the non-NA-rate. In that case, the value is computed as $1/\sqrt{nrows * non-NA-rate}$ .
<code>stopping_rounds</code>	Integer. Early stopping based on convergence of <code>stopping_metric</code> . Stop if simple moving average of length <code>k</code> of the <code>stopping_metric</code> does not improve for <code>k</code> ( <code>stopping_rounds</code> ) scoring events. Defaults to 3 and must be a non-zero integer. Use 0 to disable early stopping.
<code>seed</code>	Integer. Set a seed for reproducibility. AutoML can only guarantee reproducibility if <code>max_models</code> or early stopping is used because <code>max_runtime_secs</code> is resource limited, meaning that if the resources are not the same between runs, AutoML may be able to train more models on one run vs another.
<code>project_name</code>	Character string to identify an AutoML project. Defaults to NULL, which means a project name will be auto-generated.
<code>exclude_algos</code>	Vector of character strings naming the algorithms to skip during the model-building phase. An example use is <code>exclude_algos = c("GLM", "DeepLearning",</code>

	"DRF"), and the full list of options is: "DRF" (Random Forest and Extremely-Randomized Trees), "GLM", "XGBoost", "GBM", "DeepLearning" and "StackedEnsemble". Defaults to NULL, which means that all appropriate H2O algorithms will be used, if the search stopping criteria allow. Optional.
include_algos	Vector of character strings naming the algorithms to restrict to during the model-building phase. This can't be used in combination with exclude_algos param. Defaults to NULL, which means that all appropriate H2O algorithms will be used, if the search stopping criteria allow. Optional.
modeling_plan	List. The list of modeling steps to be used by the AutoML engine (they may not all get executed, depending on other constraints). Optional (Expert usage only).
preprocessing	List. The list of preprocessing steps to run. Only 'target_encoding' is currently supported.
exploitation_ratio	The budget ratio (between 0 and 1) dedicated to the exploitation (vs exploration) phase. By default, the exploitation phase is disabled (exploitation_ratio=0) as this is still experimental; to activate it, it is recommended to try a ratio around 0.1. Note that the current exploitation phase only tries to fine-tune the best XGBoost and the best GBM found during exploration.
monotone_constraints	List. A mapping representing monotonic constraints. Use +1 to enforce an increasing constraint and -1 to specify a decreasing constraint.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation predictions. This needs to be set to TRUE if running the same AutoML object for repeated runs because CV predictions are required to build additional Stacked Ensemble models in AutoML. This option defaults to FALSE.
keep_cross_validation_models	Logical. Whether to keep the cross-validated models. Keeping cross-validation models may consume significantly more memory in the H2O cluster. This option defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep fold assignments in the models. Deleting them will save memory in the H2O cluster. Defaults to FALSE.
sort_metric	Metric to sort the leaderboard by. For binomial classification choose between "AUC", "AUCPR", "logloss", "mean_per_class_error", "RMSE", "MSE". For regression choose between "mean_residual_deviance", "RMSE", "MSE", "MAE", and "RMSLE". For multinomial classification choose between "mean_per_class_error", "logloss", "RMSE", "MSE". Default is "AUTO". If set to "AUTO", then "AUC" will be used for binomial classification, "mean_per_class_error" for multinomial classification, and "mean_residual_deviance" for regression.
export_checkpoints_dir	(Optional) Path to a directory where every model will be stored in binary form.
verbosity	Verbosity of the backend messages printed during training; Optional. Must be one of NULL (live log disabled), "debug", "info", "warn". Defaults to "warn".
...	Additional (experimental) arguments to be passed through; Optional.

## Details

AutoML finds the best model, given a training frame and response, and returns an H2OAutoML object, which contains a leaderboard of all the models that were trained in the process, ranked by a default model performance metric.

**Value**

An [H2OAutoML](#) object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path, header = TRUE)
y <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 30)
lb <- h2o.get_leaderboard(aml)
head(lb)

## End(Not run)
```

---

h2o.betweenss	<i>Get the between cluster sum of squares</i>
---------------	---

---

**Description**

Get the between cluster sum of squares. If "train", "valid", and "xval" parameters are FALSE (default), then the training betweenss value is returned. If more than one parameter is set to TRUE, then a named vector of betweenss' are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.betweenss(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
train	Retrieve the training between cluster sum of squares
valid	Retrieve the validation between cluster sum of squares
xval	Retrieve the cross-validation between cluster sum of squares

**Examples**

```
## Not run:
library(h2o)
h2o.init()
fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
km <- h2o.kmeans(x = predictors, training_frame = fr, k = 3, nfolds = 3)
h2o.betweenss(km, train = TRUE)

## End(Not run)
```

---

h2o.biases	<i>Return the respective bias vector</i>
------------	--

---

**Description**

Return the respective bias vector

**Usage**

```
h2o.biases(object, vector_id = 1)
```

**Arguments**

object	An <a href="#">H2OModel</a> or <a href="#">H2OModelMetrics</a>
vector_id	An integer, ranging from 1 to number of layers + 1, that specifies the bias vector to return.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/chicago/chicagoCensus.csv"
census <- h2o.importFile(f)
census[, 1] <- as.factor(census[, 1])

dl_model <- h2o.deeplearning(x = c(1:3), y = 4, training_frame = census,
                             hidden = c(17, 191),
                             epochs = 1,
                             balance_classes = FALSE,
                             export_weights_and_biases = TRUE)
h2o.biases(dl_model, vector_id = 1)

## End(Not run)
```

---

h2o.bottomN	<i>H2O bottomN</i>
-------------	--------------------

---

**Description**

bottomN function will grab the bottom N percent of values of a column and return it in a H2OFrame. Extract the top N percent of values of a column and return it in a H2OFrame.

**Usage**

```
h2o.bottomN(x, column, nPercent)
```

**Arguments**

x	an H2OFrame
column	is a column name or column index to grab the top N percent value from
nPercent	is a bottom percentage value to grab

**Value**

An H2OFrame with 2 columns. The first column is the original row indices, second column contains the bottomN values

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f1 <- "https://s3.amazonaws.com/h2o-public-test-data/bigdata/laptop/jira/TopBottomNRep4.csv.zip"
f2 <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/jira/Bottom20Per.csv.zip"
data_Frame <- h2o.importFile(f1)
bottom_Answer <- h2o.importFile(f2)
nPercent <- c(1, 2, 3, 4)
frame_Names <- names(data_Frame)
nP <- nPercent[sample(1:length(nPercent), 1, replace = FALSE)]
col_Index <- sample(1:length(frame_Names), 1, replace = FALSE)
h2o.bottomN(data_Frame, frame_Names[col_Index], nP)

## End(Not run)
```

---

h2o.cbind

*Combine H2O Datasets by Columns*


---

**Description**

Takes a sequence of H2O data sets and combines them by column

**Usage**

```
h2o.cbind(...)
```

**Arguments**

... A sequence of H2OFrame arguments. All datasets must exist on the same H2O instance (IP and port) and contain the same number of rows.

**Value**

An H2OFrame object containing the combined ... arguments column-wise.

**See Also**

[cbind](#) for the base R method.



**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate_cbind <- h2o.cbind(prostate, prostate)
head(prostate_cbind)

## End(Not run)
```

---

h2o.ceiling	<i>Take a single numeric argument and return a numeric vector with the smallest integers</i>
-------------	--

---

**Description**

ceiling takes a single numeric argument *x* and returns a numeric vector containing the smallest integers not less than the corresponding elements of *x*.

**Usage**

```
h2o.ceiling(x)
```

**Arguments**

*x* An H2OFrame object.

**See Also**

[Round](#) for the base R implementation, `ceiling()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smалldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.ceiling(iris[, 1])

## End(Not run)
```

---

h2o.centers                    *Retrieve the Model Centers*

---

**Description**

Retrieve the Model Centers

**Usage**

```
h2o.centers(object)
```

**Arguments**

object                    An [H2OClusteringModel](#) object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")
h2o.ceiling(fr[, 1])

## End(Not run)
```

---

h2o.centersSTD                    *Retrieve the Model Centers STD*

---

**Description**

Retrieve the Model Centers STD

**Usage**

```
h2o.centersSTD(object)
```

**Arguments**

object                    An [H2OClusteringModel](#) object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
km <- h2o.kmeans(x = predictors, training_frame = fr, k = 3, nfolds = 3)
h2o.centersSTD(km)

## End(Not run)
```

---

h2o.centroid_stats	<i>Retrieve centroid statistics</i>
--------------------	-------------------------------------

---

**Description**

Retrieve the centroid statistics. If "train", "valid", and "xval" parameters are FALSE (default), then the training centroid stats value is returned. If more than one parameter is set to TRUE, then a named list of centroid stats data frames are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.centroid_stats(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
train	Retrieve the training centroid statistics
valid	Retrieve the validation centroid statistics
xval	Retrieve the cross-validation centroid statistics

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")  
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")  
km <- h2o.kmeans(x = predictors, training_frame = fr, k = 3, nfolds = 3)  
h2o.centroid_stats(km, train = TRUE)  
  
## End(Not run)
```

---

h2o.clearLog	<i>Delete All H2O R Logs</i>
--------------	------------------------------

---

**Description**

Clear all H2O R command and error response logs from the local disk. Used primarily for debugging purposes.

**Usage**

```
h2o.clearLog()
```

**See Also**

[h2o.startLogging](#), [h2o.stopLogging](#), [h2o.openLog](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
h2o.startLogging()
australia_path = system.file("extdata", "australia.csv", package = "h2o")
australia = h2o.importFile(path = australia_path)
h2o.stopLogging()
h2o.clearLog()

## End(Not run)
```

---

h2o.clusterInfo	<i>Print H2O cluster info</i>
-----------------	-------------------------------

---

**Description**

Print H2O cluster info

**Usage**

```
h2o.clusterInfo()
```

---

h2o.clusterIsUp	<i>Determine if an H2O cluster is up or not</i>
-----------------	---

---

**Description**

Determine if an H2O cluster is up or not

**Usage**

```
h2o.clusterIsUp(conn = h2o.getConnection())
```

**Arguments**

conn	H2OConnection object
------	----------------------

**Value**

TRUE if the cluster is up; FALSE otherwise

---

h2o.clusterStatus	<i>Return the status of the cluster</i>
-------------------	---

---

### Description

Retrieve information on the status of the cluster running H2O.

### Usage

```
h2o.clusterStatus()
```

### See Also

[H2OConnection](#), [h2o.init](#)

### Examples

```
## Not run:  
h2o.init()  
h2o.clusterStatus()  
  
## End(Not run)
```

---

h2o.cluster_sizes	<i>Retrieve the cluster sizes</i>
-------------------	-----------------------------------

---

### Description

Retrieve the cluster sizes. If "train", "valid", and "xval" parameters are FALSE (default), then the training cluster sizes value is returned. If more than one parameter is set to TRUE, then a named list of cluster size vectors are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.cluster_sizes(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

object	An <a href="#">H2OClusteringModel</a> object.
train	Retrieve the training cluster sizes
valid	Retrieve the validation cluster sizes
xval	Retrieve the cross-validation cluster sizes

## Examples

```
## Not run:
library(h2o)
h2o.init()
fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
km <- h2o.kmeans(x = predictors, training_frame = fr, k = 3, nfolds = 3)
h2o.cluster_sizes(km, train = TRUE)

## End(Not run)
```

---

h2o.coef	<i>Return the coefficients that can be applied to the non-standardized data.</i>
----------	--

---

## Description

Note: standardize = True by default. If set to False, then coef() returns the coefficients that are fit directly.

## Usage

```
h2o.coef(object)
```

## Arguments

object            an [H2OModel](#) object.

## Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "cylinders"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_glm <- h2o.glm(balance_classes = TRUE,
                   seed = 1234,
                   x = predictors,
                   y = response,
                   training_frame = train,
                   validation_frame = valid)

h2o.coef(cars_glm)

## End(Not run)
```

---

h2o.coef_norm	<i>Return coefficients fitted on the standardized data (requires standardize = True, which is on by default). These coefficients can be used to evaluate variable importance.</i>
---------------	---

---

**Description**

Return coefficients fitted on the standardized data (requires standardize = True, which is on by default). These coefficients can be used to evaluate variable importance.

**Usage**

```
h2o.coef_norm(object)
```

**Arguments**

object            an [H2OModel](#) object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "cylinders"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_glm <- h2o.glm(balance_classes = TRUE,
                   seed = 1234,
                   x = predictors,
                   y = response,
                   training_frame = train,
                   validation_frame = valid)

h2o.coef(cars_glm)

## End(Not run)
```

---

h2o.colnames	<i>Return column names of an H2OFrame</i>
--------------	---

---

**Description**

Return column names of an H2OFrame

**Usage**

```
h2o.colnames(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[colnames](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.colnames(frame)

## End(Not run)
```

---

h2o.columns\_by\_type     *Obtain a list of columns that are specified by 'coltype'*

---

**Description**

Obtain a list of columns that are specified by 'coltype'

**Usage**

```
h2o.columns_by_type(object, coltype = "numeric", ...)
```

**Arguments**

object	H2OFrame object
coltype	A character string indicating which column type to filter by. This must be one of the following: "numeric" - Numeric, but not categorical or time "categorical" - Integer, with a categorical/factor String mapping "string" - String column "time" - Long msec since the Unix Epoch - with a variety of display/parse options "uuid" - UUID "bad" - No none-NA rows (triple negative! all NAs or zero rows)
...	Ignored

**Value**

A list of column indices that correspond to "type"



**Examples**

```
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.columns_by_type(prostate, coltype = "numeric")

## End(Not run)
```

---

h2o.computeGram	<i>Compute weighted gram matrix.</i>
-----------------	--------------------------------------

---

**Description**

Compute weighted gram matrix.

**Usage**

```
h2o.computeGram(
  X,
  weights = "",
  use_all_factor_levels = FALSE,
  standardize = TRUE,
  skip_missing = FALSE
)
```

**Arguments**

X	an <a href="#">H2OModel</a> corresponding to H2O frame.
weights	character corresponding to name of weight vector in frame.
use_all_factor_levels	logical flag telling h2o whether or not to skip first level of categorical variables during one-hot encoding.
standardize	logical flag telling h2o whether or not to standardize data
skip_missing	logical flag telling h2o whether skip rows with missing data or impute them with mean

---

h2o.confusionMatrix	<i>Access H2O Confusion Matrices</i>
---------------------	--------------------------------------

---

**Description**

Retrieve either a single or many confusion matrices from H2O objects.

**Usage**

```

h2o.confusionMatrix(object, ...)

## S4 method for signature 'H2OModel'
h2o.confusionMatrix(object, newdata, valid = FALSE, ...)

## S4 method for signature 'H2OModelMetrics'
h2o.confusionMatrix(object, thresholds = NULL, metrics = NULL)

```

**Arguments**

object	Either an <a href="#">H2OModel</a> object or an <a href="#">H2OModelMetrics</a> object.
...	Extra arguments for extracting train or valid confusion matrices.
newdata	An H2OFrame object that can be scored on. Requires a valid response column.
valid	Retrieve the validation metric.
thresholds	(Optional) A value or a list of valid values between 0.0 and 1.0. This value is only used in the case of <a href="#">H2OBinomialMetrics</a> objects.
metrics	(Optional) A metric or a list of valid metrics ("min_per_class_accuracy", "absolute_mcc", "tnr", "fnr", "fpr", "tpr", "precision", "accuracy", "f0point5", "f2", "f1"). This value is only used in the case of <a href="#">H2OBinomialMetrics</a> objects.

**Details**

The [H2OModelMetrics](#) version of this function will only take [H2OBinomialMetrics](#) or [H2OMultinomialMetrics](#) objects. If no threshold is specified, all possible thresholds are selected.

**Value**

Calling this function on [H2OModel](#) objects returns a confusion matrix corresponding to the [predict](#) function. If used on an [H2OBinomialMetrics](#) object, returns a list of matrices corresponding to the number of thresholds specified.

**See Also**

[predict](#) for generating prediction frames, [h2o.performance](#) for creating [H2OModelMetrics](#).

**Examples**

```

## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
h2o.confusionMatrix(model, prostate)
# Generating a ModelMetrics object
perf <- h2o.performance(model, prostate)
h2o.confusionMatrix(perf)

## End(Not run)

```

---

h2o.connect	<i>Connect to a running H2O instance.</i>
-------------	---

---

### Description

Connect to a running H2O instance.

### Usage

```
h2o.connect(
  ip = "localhost",
  port = 54321,
  strict_version_check = TRUE,
  proxy = NA_character_,
  https = FALSE,
  cacert = NA_character_,
  insecure = FALSE,
  username = NA_character_,
  password = NA_character_,
  use_spnego = FALSE,
  cookies = NA_character_,
  context_path = NA_character_,
  config = NULL
)
```

### Arguments

ip	Object of class character representing the IP address of the server where H2O is running.
port	Object of class numeric representing the port number of the H2O server.
strict_version_check	(Optional) Setting this to FALSE is unsupported and should only be done when advised by technical support.
proxy	(Optional) A character string specifying the proxy path.
https	(Optional) Set this to TRUE to use https instead of http.
cacert	Path to a CA bundle file with root and intermediate certificates of trusted CAs.
insecure	(Optional) Set this to TRUE to disable SSL certificate checking.
username	(Optional) Username to login with.
password	(Optional) Password to login with.
use_spnego	(Optional) Set this to TRUE to enable SPNEGO authentication.
cookies	(Optional) Vector(or list) of cookies to add to request.
context_path	(Optional) The last part of connection URL: http://<ip>:<port>/<context_path>
config	(Optional) A list describing connection parameters. Using config makes h2o.connect ignore other parameters and collect named list members instead (see examples).

**Value**

an instance of H2OConnection object representing a connection to the running H2O instance.

**Examples**

```
## Not run:
library(h2o)
# Try to connect to a H2O instance running at http://localhost:54321/cluster_X
# If not found, start a local H2O instance from R with the default settings.
#h2o.connect(ip = "localhost", port = 54321, context_path = "cluster_X")
# Or
#config = list(ip = "localhost", port = 54321, context_path = "cluster_X")
#h2o.connect(config = config)

# Skip strict version check during connecting to the instance
#h2o.connect(config = c(strict_version_check = FALSE, config))

## End(Not run)
```

---

h2o.cor

*Correlation of columns.*


---

**Description**

Compute the correlation matrix of one or two H2OFrames.

**Usage**

```
h2o.cor(x, y = NULL, na.rm = FALSE, use, method = "Pearson")

cor(x, ...)
```

**Arguments**

x	An H2OFrame object.
y	NULL (default) or an H2OFrame. The default is equivalent to $y = x$ .
na.rm	logical. Should missing values be removed?
use	An optional character string indicating how to handle missing values. This must be one of the following: "everything" - outputs NaNs whenever one of its contributing observations is missing "all.obs" - presence of missing observations will throw an error "complete.obs" - discards missing values along with all observations in their rows so that only complete observations are used
method	str Method of correlation computation. Allowed values are: "Pearson" - Pearson's correlation coefficient "Spearman" - Spearman's correlation coefficient (Spearman's Rho) Defaults to "Pearson"
...	Further arguments to be passed down from other methods.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
cor(prostate$AGE)

## End(Not run)
```

---

h2o.cos

*Compute the cosine of x*

---

**Description**

Compute the cosine of x

**Usage**

```
h2o.cos(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Trig](#) for the base R implementation, `cos()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.cos(frame["C1"])

## End(Not run)
```

---

h2o.cosh	<i>Compute the hyperbolic cosine of x</i>
----------	---

---

**Description**

Compute the hyperbolic cosine of x

**Usage**

```
h2o.cosh(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Hyperbolic](#) for the base R implementation, `cosh()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.cosh(frame["C1"])

## End(Not run)
```

---

h2o.coxph	<i>Trains a Cox Proportional Hazards Model (CoxPH) on an H2O dataset</i>
-----------	--

---

**Description**

Trains a Cox Proportional Hazards Model (CoxPH) on an H2O dataset

**Usage**

```
h2o.coxph(
  x,
  event_column,
  training_frame,
  model_id = NULL,
  start_column = NULL,
  stop_column = NULL,
  weights_column = NULL,
```

```

offset_column = NULL,
stratify_by = NULL,
ties = c("efron", "breslow"),
init = 0,
lre_min = 9,
max_iterations = 20,
interactions = NULL,
interaction_pairs = NULL,
interactions_only = NULL,
use_all_factor_levels = FALSE,
export_checkpoints_dir = NULL,
single_node_mode = FALSE
)

```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except event_column, start_column and stop_column are used.
event_column	The name of binary data column in the training frame indicating the occurrence of an event.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
start_column	Start Time Column.
stop_column	Stop Time Column.
weights_column	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set weight = 0 for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with weight == 0.
offset_column	Offset column. This will be added to the combination of columns before applying the link function.
stratify_by	List of columns to use for stratification.
ties	Method for Handling Ties. Must be one of: "efron", "breslow". Defaults to efron.
init	Coefficient starting value. Defaults to 0.
lre_min	Minimum log-relative error. Defaults to 9.
max_iterations	Maximum number of iterations. Defaults to 20.
interactions	A list of predictor column indices to interact. All pairwise combinations will be computed for the list.
interaction_pairs	A list of pairwise (first order) column interactions.
interactions_only	A list of columns that should only be used to create interactions but should not itself participate in model training.

`use_all_factor_levels`  
 Logical. (Internal. For development only!) Indicates whether to use all factor levels. Defaults to FALSE.

`export_checkpoints_dir`  
 Automatically export generated models to this directory.

`single_node_mode`  
 Logical. Run on a single node to reduce the effect of network overhead (for smaller datasets) Defaults to FALSE.

### Examples

```

## Not run:
library(h2o)
h2o.init()

# Import the heart dataset
f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/coxph_test/heart.csv"
heart <- h2o.importFile(f)

# Set the predictor and response
predictor <- "age"
response <- "event"

# Train a Cox Proportional Hazards model
heart_coxph <- h2o.coxph(x = predictor, training_frame = heart,
                        event_column = "event",
                        start_column = "start",
                        stop_column = "stop")

## End(Not run)

```

---

h2o.createFrame

*Data H2OFrame Creation in H2O*

---

### Description

Creates a data frame in H2O with real-valued, categorical, integer, and binary columns specified by the user.

### Usage

```

h2o.createFrame(
  rows = 10000,
  cols = 10,
  randomize = TRUE,
  value = 0,
  real_range = 100,
  categorical_fraction = 0.2,
  factors = 100,
  integer_fraction = 0.2,
  integer_range = 100,
  binary_fraction = 0.1,
  binary_ones_fraction = 0.02,

```



```

    time_fraction = 0,
    string_fraction = 0,
    missing_fraction = 0.01,
    response_factors = 2,
    has_response = FALSE,
    seed,
    seed_for_column_types
  )

```

### Arguments

rows	The number of rows of data to generate.
cols	The number of columns of data to generate. Excludes the response column if <code>has_response = TRUE</code> .
randomize	A logical value indicating whether data values should be randomly generated. This must be <code>TRUE</code> if either <code>categorical_fraction</code> or <code>integer_fraction</code> is non-zero.
value	If <code>randomize = FALSE</code> , then all real-valued entries will be set to this value.
real_range	The range of randomly generated real values.
categorical_fraction	The fraction of total columns that are categorical.
factors	The number of (unique) factor levels in each categorical column.
integer_fraction	The fraction of total columns that are integer-valued.
integer_range	The range of randomly generated integer values.
binary_fraction	The fraction of total columns that are binary-valued.
binary_ones_fraction	The fraction of values in a binary column that are set to 1.
time_fraction	The fraction of randomly created date/time columns.
string_fraction	The fraction of randomly created string columns.
missing_fraction	The fraction of total entries in the data frame that are set to NA.
response_factors	If <code>has_response = TRUE</code> , then this is the number of factor levels in the response column.
has_response	A logical value indicating whether an additional response column should be prepended to the final H2O data frame. If set to <code>TRUE</code> , the total number of columns will be <code>cols+1</code> .
seed	A seed used to generate random values when <code>randomize = TRUE</code> .
seed_for_column_types	A seed used to generate random column types when <code>randomize = TRUE</code> .

### Value

Returns an H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
hf <- h2o.createFrame(rows = 1000, cols = 100, categorical_fraction = 0.1,
                      factors = 5, integer_fraction = 0.5, integer_range = 1,
                      has_response = TRUE)

head(hf)
summary(hf)

hf <- h2o.createFrame(rows = 100, cols = 10, randomize = FALSE, value = 5,
                      categorical_fraction = 0, integer_fraction = 0)

summary(hf)

## End(Not run)
```

---

```
h2o.cross_validation_fold_assignment
```

*Retrieve the cross-validation fold assignment*

---

**Description**

Retrieve the cross-validation fold assignment

**Usage**

```
h2o.cross_validation_fold_assignment(object)
```

**Arguments**

object            An [H2OModel](#) object.

**Value**

Returns a `H2OFrame`

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response, training_frame = train,
                   nfolds = 5, keep_cross_validation_fold_assignment = TRUE, seed = 1234)
h2o.cross_validation_fold_assignment(cars_gbm)

## End(Not run)
```

---

`h2o.cross_validation_holdout_predictions`*Retrieve the cross-validation holdout predictions*

---

**Description**

Retrieve the cross-validation holdout predictions

**Usage**

```
h2o.cross_validation_holdout_predictions(object)
```

**Arguments**

`object` An [H2OModel](#) object.

**Value**

Returns a `H2OFrame`

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response, training_frame = train,
  nfolds = 5, keep_cross_validation_predictions = TRUE, seed = 1234)
h2o.cross_validation_holdout_predictions(cars_gbm)

## End(Not run)
```

---

`h2o.cross_validation_models`*Retrieve the cross-validation models*

---

**Description**

Retrieve the cross-validation models

**Usage**

```
h2o.cross_validation_models(object)
```

**Arguments**

object            An [H2OModel](#) object.

**Value**

Returns a list of H2OModel objects

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response, training_frame = train,
                   nfolds = 5, keep_cross_validation_models = TRUE, seed = 1234)
h2o.cross_validation_models(cars_gbm)

## End(Not run)
```

---

h2o.cross\_validation\_predictions

*Retrieve the cross-validation predictions*

---

**Description**

Retrieve the cross-validation predictions

**Usage**

```
h2o.cross_validation_predictions(object)
```

**Arguments**

object            An [H2OModel](#) object.

**Value**

Returns a list of H2OFrame objects

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response, training_frame = train,
                   nfolds = 5, keep_cross_validation_predictions = TRUE, seed = 1234)
h2o.cross_validation_predictions(cars_gbm)

## End(Not run)
```

---

h2o.cummax

*Return the cumulative max over a column or across a row*


---

**Description**

Return the cumulative max over a column or across a row

**Usage**

```
h2o.cummax(x, axis = 0)
```

**Arguments**

**x** An H2OFrame object.

**axis** An int that indicates whether to do down a column (0) or across a row (1).

**See Also**

[cumsum](#) for the base R implementation, `cummax()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                         categorical_fraction = 0.0,
                         missing_fraction = 0.7,
                         seed = 123)

h2o.cummax(frame, 1)

## End(Not run)
```

---

h2o.cummin	<i>Return the cumulative min over a column or across a row</i>
------------	--

---

**Description**

Return the cumulative min over a column or across a row

**Usage**

```
h2o.cummin(x, axis = 0)
```

**Arguments**

x	An H2OFrame object.
axis	An int that indicates whether to do down a column (0) or across a row (1).

**See Also**

[cumsum](#) for the base R implementation, `cummin()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.cummin(frame, 1)

## End(Not run)
```

---

h2o.cumprod	<i>Return the cumulative product over a column or across a row</i>
-------------	--

---

**Description**

Return the cumulative product over a column or across a row

**Usage**

```
h2o.cumprod(x, axis = 0)
```

**Arguments**

x	An H2OFrame object.
axis	An int that indicates whether to do down a column (0) or across a row (1).

**See Also**

[cumsum](#) for the base R implementation, `cumprod()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.cumprod(frame, 1)

## End(Not run)
```

---

h2o.cumsum

*Return the cumulative sum over a column or across a row*

---

**Description**

Return the cumulative sum over a column or across a row

**Usage**

```
h2o.cumsum(x, axis = 0)
```

**Arguments**

`x` An H2OFrame object.

`axis` An int that indicates whether to do down a column (0) or across a row (1).

**See Also**

[cumsum](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.cumsum(frame, 1)

## End(Not run)
```

h2o.cut

*Cut H2O Numeric Data to Factor***Description**

Divides the range of the H2O data into intervals and codes the values according to which interval they fall in. The leftmost interval corresponds to the level one, the next is level two, etc.

**Usage**

```
h2o.cut(
  x,
  breaks,
  labels = NULL,
  include.lowest = FALSE,
  right = TRUE,
  dig.lab = 3,
  ...
)

## S3 method for class 'H2OFrame'
cut(
  x,
  breaks,
  labels = NULL,
  include.lowest = FALSE,
  right = TRUE,
  dig.lab = 3,
  ...
)
```

**Arguments**

x	An H2OFrame object with a single numeric column.
breaks	A numeric vector of two or more unique cut points.
labels	Labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation.
include.lowest	Logical, indicating if an 'x[i]' equal to the lowest (or highest, for right = FALSE) 'breaks' value should be included
right	Logical, indicating if the intervals should be closed on the right (opened on the left) or vice versa.
dig.lab	Integer which is used when labels are not given, determines the number of digits used in formatting the break numbers.
...	Further arguments passed to or from other methods.

**Value**

Returns an H2OFrame object containing the factored data with intervals as levels.



**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
summary(iris_hf)

# Cut sepal length column into intervals determined by min/max/quantiles
sepal_len_cut <- cut(iris_hf$Sepal.Length, c(4.2, 4.8, 5.8, 6, 8))
head(sepal_len_cut)
summary(sepal_len_cut)

## End(Not run)
```

---

h2o.day

*Convert Milliseconds to Day of Month in H2O Datasets*

---

**Description**

Converts the entries of an H2OFrame object from milliseconds to days of the month (on a 1 to 31 scale).

**Usage**

```
h2o.day(x)

day(x)

## S3 method for class 'H2OFrame'
day(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

An H2OFrame object containing the entries of x converted to days of the month.

**See Also**

[h2o.month](#)

---

h2o.dayOfWeek	<i>Convert Milliseconds to Day of Week in H2O Datasets</i>
---------------	--

---

**Description**

Converts the entries of an H2OFrame object from milliseconds to days of the week (on a 0 to 6 scale).

**Usage**

```
h2o.dayOfWeek(x)

dayOfWeek(x)

## S3 method for class 'H2OFrame'
dayOfWeek(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

An H2OFrame object containing the entries of x converted to days of the week.

**See Also**

[h2o.day](#), [h2o.month](#)

---

h2o.dct	<i>Compute DCT of an H2OFrame</i>
---------	-----------------------------------

---

**Description**

Compute the Discrete Cosine Transform of every row in the H2OFrame

**Usage**

```
h2o.dct(data, destination_frame, dimensions, inverse = FALSE)
```

**Arguments**

data	An H2OFrame object representing the dataset to transform
destination_frame	A frame ID for the result
dimensions	An array containing the 3 integer values for height, width, depth of each sample. The product of HxWxD must total up to less than the number of columns. For 1D, use c(L,1,1), for 2D, use C(N,M,1).
inverse	Whether to perform the inverse transform

**Value**

Returns an H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
df <- h2o.createFrame(rows = 1000, cols = 8 * 16 * 24,
                      categorical_fraction = 0, integer_fraction = 0, missing_fraction = 0)
df1 <- h2o.dct(data = df, dimensions = c(8 * 16 * 24, 1, 1))
df2 <- h2o.dct(data = df1, dimensions = c(8 * 16 * 24, 1, 1), inverse = TRUE)
max(abs(df1 - df2))

df1 <- h2o.dct(data = df, dimensions = c(8 * 16, 24, 1))
df2 <- h2o.dct(data = df1, dimensions = c(8 * 16, 24, 1), inverse = TRUE)
max(abs(df1 - df2))

df1 <- h2o.dct(data = df, dimensions = c(8, 16, 24))
df2 <- h2o.dct(data = df1, dimensions = c(8, 16, 24), inverse = TRUE)
max(abs(df1 - df2))

## End(Not run)
```

---

h2o.ddply

*Split H2O Dataset, Apply Function, and Return Results*


---

**Description**

For each subset of an H2O data set, apply a user-specified function, then combine the results. This is an experimental feature based on `plyr::ddply`.

**Usage**

```
h2o.ddply(X, .variables, FUN, ..., .progress = "none")
```

**Arguments**

X	An H2OFrame object to be processed.
.variables	Variables to split X by, either the indices or names of a set of columns.
FUN	Function to apply to each subset grouping.
...	Additional arguments passed on to FUN.
.progress	Name of the progress bar to use. #TODO: (Currently unimplemented)

**Value**

Returns an H2OFrame object containing the results from the split/apply operation, arranged

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import iris dataset to H2O
iris_hf <- as.h2o(iris)
# Add function taking mean of Sepal.Length column
fun <- function(df) { sum(df[, 1], na.rm = TRUE) / nrow(df) }
# Apply function to groups by flower specie
# uses h2o's ddply, since iris_hf is an H2OFrame object
res <- h2o.ddply(iris_hf, "Species", fun)
head(res)

## End(Not run)
```

---

h2o.decryptionSetup    *Setup a Decryption Tool*

---

**Description**

If your source file is encrypted - setup a Decryption Tool and then provide the reference (result of this function) to the import functions.

**Usage**

```
h2o.decryptionSetup(
  keystore,
  keystore_type = "JCEKS",
  key_alias = NA_character_,
  password = NA_character_,
  decrypt_tool = "",
  decrypt_impl = "water.parser.GenericDecryptionTool",
  cipher_spec = NA_character_
)
```

**Arguments**

keystore	An H2OFrame object referencing a loaded Java Keystore (see example).
keystore_type	(Optional) Specification of Keystore type, defaults to JCEKS.
key_alias	Which key from the keystore to use for decryption.
password	Password to the keystore and the key.
decrypt_tool	(Optional) Name of the decryption tool.
decrypt_impl	(Optional) Java class name implementing the Decryption Tool.
cipher_spec	Specification of a cipher (eg.: AES/ECB/PKCS5Padding).

**See Also**

[h2o.importFile](#), [h2o.parseSetup](#)



```

prostate_deepfeatures_layer1 = h2o.deepfeatures(prostate_dl, prostate, layer = 1)
prostate_deepfeatures_layer2 = h2o.deepfeatures(prostate_dl, prostate, layer = 2)
head(prostate_deepfeatures_layer1)
head(prostate_deepfeatures_layer2)

## End(Not run)

```

---

h2o.deeplearning

*Build a Deep Neural Network model using CPUs*


---

## Description

Builds a feed-forward multilayer artificial neural network on an H2OFrame.

## Usage

```

h2o.deeplearning(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
  fold_column = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  weights_column = NULL,
  offset_column = NULL,
  balance_classes = FALSE,
  class_sampling_factors = NULL,
  max_after_balance_size = 5,
  checkpoint = NULL,
  pretrained_autoencoder = NULL,
  overwrite_with_best_model = TRUE,
  use_all_factor_levels = TRUE,
  standardize = TRUE,
  activation = c("Tanh", "TanhWithDropout", "Rectifier", "RectifierWithDropout",
    "Maxout", "MaxoutWithDropout"),
  hidden = c(200, 200),
  epochs = 10,
  train_samples_per_iteration = -2,
  target_ratio_comm_to_comp = 0.05,
  seed = -1,
  adaptive_rate = TRUE,
  rho = 0.99,
  epsilon = 1e-08,

```

```
rate = 0.005,
rate_annealing = 1e-06,
rate_decay = 1,
momentum_start = 0,
momentum_ramp = 1e+06,
momentum_stable = 0,
nesterov_accelerated_gradient = TRUE,
input_dropout_ratio = 0,
hidden_dropout_ratios = NULL,
l1 = 0,
l2 = 0,
max_w2 = 3.4028235e+38,
initial_weight_distribution = c("UniformAdaptive", "Uniform", "Normal"),
initial_weight_scale = 1,
initial_weights = NULL,
initial_biases = NULL,
loss = c("Automatic", "CrossEntropy", "Quadratic", "Huber", "Absolute", "Quantile"),
distribution = c("AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma",
  "tweedie", "laplace", "quantile", "huber"),
quantile_alpha = 0.5,
tweedie_power = 1.5,
huber_alpha = 0.9,
score_interval = 5,
score_training_samples = 10000,
score_validation_samples = 0,
score_duty_cycle = 0.1,
classification_stop = 0,
regression_stop = 1e-06,
stopping_rounds = 5,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
  "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error",
  "custom", "custom_increasing"),
stopping_tolerance = 0,
max_runtime_secs = 0,
score_validation_sampling = c("Uniform", "Stratified"),
diagnostics = TRUE,
fast_mode = TRUE,
force_load_balance = TRUE,
variable_importances = TRUE,
replicate_training_data = TRUE,
single_node_mode = FALSE,
shuffle_training_data = FALSE,
missing_values_handling = c("MeanImputation", "Skip"),
quiet_mode = FALSE,
autoencoder = FALSE,
sparse = FALSE,
col_major = FALSE,
average_activation = 0,
sparsity_beta = 0,
max_categorical_features = 2147483647,
reproducible = FALSE,
export_weights_and_biases = FALSE,
```

```

mini_batch_size = 1,
categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
  "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
elastic_averaging = FALSE,
elastic_averaging_moving_rate = 0.9,
elastic_averaging_regularization = 0.001,
export_checkpoints_dir = NULL,
auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
  "WEIGHTED_OVO"),
verbose = FALSE
)

```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
nfolds	Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
keep_cross_validation_models	Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
weights_column	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase



the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set weight = 0 for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with weight == 0.

offset_column	Offset column. This will be added to the combination of columns before applying the link function.
balance_classes	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
class_sampling_factors	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires balance_classes.
max_after_balance_size	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires balance_classes. Defaults to 5.0.
checkpoint	Model checkpoint to resume training with.
pretrained_autoencoder	Pretrained autoencoder model to initialize this model with.
overwrite_with_best_model	Logical. If enabled, override the final model with the best model found during training. Defaults to TRUE.
use_all_factor_levels	Logical. Use all factor levels of categorical variables. Otherwise, the first factor level is omitted (without loss of accuracy). Useful for variable importances and auto-enabled for autoencoder. Defaults to TRUE.
standardize	Logical. If enabled, automatically standardize the data. If disabled, the user must provide properly scaled input data. Defaults to TRUE.
activation	Activation function. Must be one of: "Tanh", "TanhWithDropout", "Rectifier", "RectifierWithDropout", "Maxout", "MaxoutWithDropout". Defaults to Rectifier.
hidden	Hidden layer sizes (e.g. [100, 100]). Defaults to c(200, 200).
epochs	How many times the dataset should be iterated (streamed), can be fractional. Defaults to 10.
train_samples_per_iteration	Number of training samples (globally) per MapReduce iteration. Special values are 0: one epoch, -1: all available data (e.g., replicated training data), -2: automatic. Defaults to -2.
target_ratio_comm_to_comp	Target ratio of communication overhead to computation. Only for multi-node operation and train_samples_per_iteration = -2 (auto-tuning). Defaults to 0.05.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Note: only reproducible when running single threaded. Defaults to -1 (time-based random number).
adaptive_rate	Logical. Adaptive learning rate. Defaults to TRUE.
rho	Adaptive learning rate time decay factor (similarity to prior updates). Defaults to 0.99.

epsilon	Adaptive learning rate smoothing factor (to avoid divisions by zero and allow progress). Defaults to 1e-08.
rate	Learning rate (higher => less stable, lower => slower convergence). Defaults to 0.005.
rate_annealing	Learning rate annealing: $\text{rate} / (1 + \text{rate\_annealing} * \text{samples})$ . Defaults to 1e-06.
rate_decay	Learning rate decay factor between layers (N-th layer: $\text{rate} * \text{rate\_decay} ^ (n - 1)$ ). Defaults to 1.
momentum_start	Initial momentum at the beginning of training (try 0.5). Defaults to 0.
momentum_ramp	Number of training samples for which momentum increases. Defaults to 1000000.
momentum_stable	Final momentum after the ramp is over (try 0.99). Defaults to 0.
nesterov_accelerated_gradient	Logical. Use Nesterov accelerated gradient (recommended). Defaults to TRUE.
input_dropout_ratio	Input layer dropout ratio (can improve generalization, try 0.1 or 0.2). Defaults to 0.
hidden_dropout_ratios	Hidden layer dropout ratios (can improve generalization), specify one value per hidden layer, defaults to 0.5.
l1	L1 regularization (can add stability and improve generalization, causes many weights to become 0). Defaults to 0.
l2	L2 regularization (can add stability and improve generalization, causes many weights to be small). Defaults to 0.
max_w2	Constraint for squared sum of incoming weights per unit (e.g. for Rectifier). Defaults to 3.4028235e+38.
initial_weight_distribution	Initial weight distribution. Must be one of: "UniformAdaptive", "Uniform", "Normal". Defaults to UniformAdaptive.
initial_weight_scale	Uniform: -value...value, Normal: stddev. Defaults to 1.
initial_weights	A list of H2OFrame ids to initialize the weight matrices of this model with.
initial_biases	A list of H2OFrame ids to initialize the bias vectors of this model with.
loss	Loss function. Must be one of: "Automatic", "CrossEntropy", "Quadratic", "Huber", "Absolute", "Quantile". Defaults to Automatic.
distribution	Distribution function Must be one of: "AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber". Defaults to AUTO.
quantile_alpha	Desired quantile for Quantile regression, must be between 0 and 1. Defaults to 0.5.
tweedie_power	Tweedie power for Tweedie regression, must be between 1 and 2. Defaults to 1.5.
huber_alpha	Desired quantile for Huber/M-regression (threshold between quadratic and linear loss, must be between 0 and 1). Defaults to 0.9.
score_interval	Shortest time interval (in seconds) between model scoring. Defaults to 5.

score_training_samples	Number of training set samples for scoring (0 for all). Defaults to 10000.
score_validation_samples	Number of validation set samples for scoring (0 for all). Defaults to 0.
score_duty_cycle	Maximum duty cycle fraction for scoring (lower: more training, higher: more scoring). Defaults to 0.1.
classification_stop	Stopping criterion for classification error fraction on training data (-1 to disable). Defaults to 0.
regression_stop	Stopping criterion for regression error (MSE) on training data (-1 to disable). Defaults to 1e-06.
stopping_rounds	Early stopping based on convergence of stopping_metric. Stop if simple moving average of length k of the stopping_metric does not improve for k:=stopping_rounds scoring events (0 to disable) Defaults to 5.
stopping_metric	Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
stopping_tolerance	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.
max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
score_validation_sampling	Method used to sample validation dataset for scoring. Must be one of: "Uniform", "Stratified". Defaults to Uniform.
diagnostics	Logical. Enable diagnostics for hidden layers. Defaults to TRUE.
fast_mode	Logical. Enable fast mode (minor approximation in back-propagation). Defaults to TRUE.
force_load_balance	Logical. Force extra load balancing to increase training speed for small datasets (to keep all cores busy). Defaults to TRUE.
variable_importances	Logical. Compute variable importances for input features (Gedeon method) - can be slow for large networks. Defaults to TRUE.
replicate_training_data	Logical. Replicate the entire training dataset onto every node for faster training on small datasets. Defaults to TRUE.
single_node_mode	Logical. Run on a single node for fine-tuning of model parameters. Defaults to FALSE.
shuffle_training_data	Logical. Enable shuffling of training data (recommended if training data is replicated and train_samples_per_iteration is close to #nodes x #rows, or if using balance_classes). Defaults to FALSE.

missing_values_handling	Handling of missing values. Either MeanImputation or Skip. Must be one of: "MeanImputation", "Skip". Defaults to MeanImputation.
quiet_mode	Logical. Enable quiet mode for less output to standard output. Defaults to FALSE.
autoencoder	Logical. Auto-Encoder. Defaults to FALSE.
sparse	Logical. Sparse data handling (more efficient for data with lots of 0 values). Defaults to FALSE.
col_major	Logical. #DEPRECATED Use a column major weight matrix for input layer. Can speed up forward propagation, but might slow down backpropagation. Defaults to FALSE.
average_activation	Average activation for sparse auto-encoder. #Experimental Defaults to 0.
sparsity_beta	Sparsity regularization. #Experimental Defaults to 0.
max_categorical_features	Max. number of categorical features, enforced via hashing. #Experimental Defaults to 2147483647.
reproducible	Logical. Force reproducibility on small data (will be slow - only uses 1 thread). Defaults to FALSE.
export_weights_and_biases	Logical. Whether to export Neural Network weights and biases to H2O Frames. Defaults to FALSE.
mini_batch_size	Mini-batch size (smaller leads to better fit, larger can speed up and generalize better). Defaults to 1.
categorical_encoding	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited". Defaults to AUTO.
elastic_averaging	Logical. Elastic averaging between compute nodes can improve distributed model convergence. #Experimental Defaults to FALSE.
elastic_averaging_moving_rate	Elastic averaging moving rate (only if elastic averaging is enabled). Defaults to 0.9.
elastic_averaging_regularization	Elastic averaging regularization strength (only if elastic averaging is enabled). Defaults to 0.001.
export_checkpoints_dir	Automatically export generated models to this directory.
auc_type	Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO", "WEIGHTED_OVO". Defaults to AUTO.
verbose	Logical. Print scoring history to the console (Metrics per epoch). Defaults to FALSE.

**See Also**

[predict.H2OModel](#) for prediction

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_dl <- h2o.deeplearning(x = 1:4, y = 5, training_frame = iris_hf, seed=123456)

# now make a prediction
predictions <- h2o.predict(iris_dl, iris_hf)

## End(Not run)
```

---

h2o.describe

*H2O Description of A Dataset*

---

**Description**

Reports the "Flow" style summary rollups on an instance of H2OFrame. Includes information about column types, mins/maxs/missing/zero counts/stds/number of levels

**Usage**

```
h2o.describe(frame)
```

**Arguments**

frame            An H2OFrame object.

**Value**

A table with the Frame stats.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path)
h2o.describe(prostate)

## End(Not run)
```

---

h2o.diff1ag1	<i>Conduct a lag 1 transform on a numeric H2OFrame column</i>
--------------	---

---

**Description**

Conduct a lag 1 transform on a numeric H2OFrame column

**Usage**

```
h2o.diff1ag1(object)
```

**Arguments**

object            H2OFrame object

**Value**

Returns an H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "cylinders"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response, training_frame = train,
  validation_frame = valid, nfolds = 5, seed = 1234)
h2o.diff1ag1(cars["cylinders"])

## End(Not run)
```

---

h2o.dim	<i>Returns the number of rows and columns for an H2OFrame object.</i>
---------	---

---

**Description**

Returns the number of rows and columns for an H2OFrame object.

**Usage**

```
h2o.dim(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[dim](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
h2o.dim(cars)

## End(Not run)
```

---

h2o.dimnames	<i>Column names of an H2OFrame</i>
--------------	------------------------------------

---

**Description**

Column names of an H2OFrame

**Usage**

```
h2o.dimnames(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[dimnames](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
h2o.dimnames(cars)

## End(Not run)
```

---

h2o.distance	<i>Compute a pairwise distance measure between all rows of two numeric H2OFrames.</i>
--------------	---

---

**Description**

Compute a pairwise distance measure between all rows of two numeric H2OFrames.

**Usage**

```
h2o.distance(x, y, measure)
```

**Arguments**

x	An H2OFrame object (large, references).
y	An H2OFrame object (small, queries).
measure	An optional string indicating what distance measure to use. Must be one of: "l1" - Absolute distance (L1-norm, >=0) "l2" - Euclidean distance (L2-norm, >=0) "cosine" - Cosine similarity (-1...1) "cosine_sq" - Squared Cosine similarity (0...1)

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.distance(prostate[11:30, ], prostate[1:10, ], "cosine")

## End(Not run)
```

---

h2o.downloadAllLogs	<i>Download H2O Log Files to Disk</i>
---------------------	---------------------------------------

---

**Description**

h2o.downloadAllLogs downloads all H2O log files to local disk in .zip format. Generally used for debugging purposes.

**Usage**

```
h2o.downloadAllLogs(dirname = ".", filename = NULL)
```

**Arguments**

dirname	(Optional) A character string indicating the directory that the log file should be saved in.
filename	(Optional) A character string indicating the name that the log file should be saved to. Note that the saved format is .zip, so the file name must include the .zip extension.



**Examples**

```
## Not run:
h2o.downloadAllLogs(dirname='./your_directory_name/', filename = 'autoh2o_log.zip')

## End(Not run)
```

---

h2o.downloadCSV	<i>Download H2O Data to Disk</i>
-----------------	----------------------------------

---

**Description**

Download an H2O data set to a CSV file on the local disk

**Usage**

```
h2o.downloadCSV(data, filename)
```

**Arguments**

data	an H2OFrame object to be downloaded.
filename	A string indicating the name that the CSV file should be should be saved to.

**Warning**

Files located on the H2O server may be very large! Make sure you have enough hard drive space to accomodate the entire file.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)

file_path <- paste(getwd(), "my_iris_file.csv", sep = .Platform$file.sep)
h2o.downloadCSV(iris_hf, file_path)
file.info(file_path)
file.remove(file_path)

## End(Not run)
```

---

h2o.download_model	<i>Download the model in binary format. The owner of the file saved is the user by which python session was executed.</i>
--------------------	---

---

### Description

Download the model in binary format. The owner of the file saved is the user by which python session was executed.

### Usage

```
h2o.download_model(
  model,
  path = NULL,
  export_cross_validation_predictions = FALSE
)
```

### Arguments

model	An H2OModel
path	The path where binary file should be downloaded. Downloaded to current directory by default.
export_cross_validation_predictions	A boolean flag indicating whether the download model should be saved with CV Holdout Frame predictions. Default is not to export the predictions.

### Examples

```
## Not run:
library(h2o)
h <- h2o.init()
fr <- as.h2o(iris)
my_model <- h2o.gbm(x = 1:4, y = 5, training_frame = fr)
h2o.download_model(my_model) # save to the current working directory

## End(Not run)
```

---

h2o.download_mojo	<i>Download the model in MOJO format.</i>
-------------------	---

---

### Description

Download the model in MOJO format.

**Usage**

```
h2o.download_mojo(
  model,
  path = getwd(),
  get_genmodel_jar = FALSE,
  genmodel_name = "",
  genmodel_path = ""
)
```

**Arguments**

model	An H2OModel
path	The path where MOJO file should be saved. Saved to current directory by default.
get_genmodel_jar	If TRUE, then also download h2o-genmodel.jar and store it in either in the same folder
genmodel_name	Custom name of genmodel jar.
genmodel_path	Path to store h2o-genmodel.jar. If left blank and “get_genmodel_jar“ is TRUE, then the h2o-genmodel.jar

**Value**

Name of the MOJO file written to the path.

**Examples**

```
## Not run:
library(h2o)
h <- h2o.init()
fr <- as.h2o(iris)
my_model <- h2o.gbm(x = 1:4, y = 5, training_frame = fr)
h2o.download_mojo(my_model) # save to the current working directory

## End(Not run)
```

---

h2o.download_pojo	<i>Download the Scoring POJO (Plain Old Java Object) of an H2O Model</i>
-------------------	--

---

**Description**

Download the Scoring POJO (Plain Old Java Object) of an H2O Model

**Usage**

```
h2o.download_pojo(
  model,
  path = NULL,
  getjar = NULL,
  get_jar = TRUE,
  jar_name = ""
)
```

**Arguments**

model	An H2OModel
path	The path to the directory to store the POJO (no trailing slash). If NULL, then print to to console. The file name will be a compilable java file name.
get_jar	(DEPRECATED) Whether to also download the h2o-genmodel.jar file needed to compile the POJO. This argument is now called 'get_jar'.
get_jar	Whether to also download the h2o-genmodel.jar file needed to compile the POJO
jar_name	Custom name of genmodel jar.

**Value**

If path is NULL, then pretty print the POJO to the console. Otherwise save it to the specified directory and return POJO file name.

**Examples**

```
## Not run:
library(h2o)
h <- h2o.init()
fr <- as.h2o(iris)
my_model <- h2o.gbm(x = 1:4, y = 5, training_frame = fr)

h2o.download_pojo(my_model) # print the model to screen
# h2o.download_pojo(my_model, getwd()) # save the POJO and jar file to the current working
#                                     directory, NOT RUN
# h2o.download_pojo(my_model, getwd(), get_jar = FALSE ) # save only the POJO to the current
#                                                         working directory, NOT RUN
h2o.download_pojo(my_model, getwd()) # save to the current working directory

## End(Not run)
```

---

h2o.drop\_duplicates    *Drops duplicated rows.*

---

**Description**

Drops duplicated rows across specified columns.

**Usage**

```
h2o.drop_duplicates(frame, columns, keep = "first")
```

**Arguments**

frame	An H2OFrame object to drop duplicates on.
columns	Columns to compare during the duplicate detection process.
keep	Which rows to keep. The "first" value (default) keeps the first row and deletes the rest. The "last" keeps the last row.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

data <- as.h2o(iris)
deduplicated_data <- h2o.drop_duplicates(data, c("Species", "Sepal.Length"), keep = "first")

## End(Not run)
```

---

h2o.entropy	<i>Shannon entropy</i>
-------------	------------------------

---

**Description**

Return the Shannon entropy of a string column. If the string is empty, the entropy is 0.

**Usage**

```
h2o.entropy(x)
```

**Arguments**

x                    The column on which to calculate the entropy.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
buys <- as.h2o(c("no", "no", "yes", "yes", "yes", "no", "yes", "no", "yes", "yes", "no"))
buys_entropy <- h2o.entropy(buys)

## End(Not run)
```

---

h2o.exp	<i>Compute the exponential function of x</i>
---------	--

---

**Description**

Compute the exponential function of x

**Usage**

```
h2o.exp(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Log](#) for the base R implementation, `exp()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.exp(frame["C1"])

## End(Not run)
```

---

h2o.explain

*Generate Model Explanations*


---

**Description**

The H2O Explainability Interface is a convenient wrapper to a number of explainability methods and visualizations in H2O. The function can be applied to a single model or group of models and returns a list of explanations, which are individual units of explanation such as a partial dependence plot or a variable importance plot. Most of the explanations are visual (ggplot plots). These plots can also be created by individual utility functions as well.

**Usage**

```
h2o.explain(
  object,
  newdata,
  columns = NULL,
  top_n_features = 5,
  include_explanations = "ALL",
  exclude_explanations = NULL,
  plot_overrides = NULL
)
```

**Arguments**

object	One of the following: an H2O model, a list of H2O models, an H2OAutoML object or an H2OAutoML Leaderboard slice.
newdata	An H2OFrame.
columns	A vector of column names or column indices to create plots with. If specified parameter <code>top_n_features</code> will be ignored.
top_n_features	An integer specifying the number of columns to use, ranked by variable importance (where applicable).

```

include_explanations
    If specified, return only the specified model explanations. (Mutually exclusive
    with exclude_explanations)
exclude_explanations
    Exclude specified model explanations.
plot_overrides
    Overrides for individual model explanations, e.g. list(shap_summary_plot = list(columns = 50

```

**Value**

List of outputs with class "H2OExplanation"

**Examples**

```

## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
aml <- h2o.automl(y = response,
                 training_frame = train,
                 max_models = 10,
                 seed = 1)

# Create the explanation for whole H2OAutoML object
exa <- h2o.explain(aml, test)
print(exa)

# Create the explanation for the leader model
exm <- h2o.explain(aml@leader, test)
print(exm)

## End(Not run)

```

---

h2o.explain\_row

*Generate Model Explanations for a single row*


---

**Description**

Explain the behavior of a model or group of models with respect to a single row of data. The function returns a list of explanations, which are individual units of explanation such as a partial dependence plot or a variable importance plot. Most of the explanations are visual (ggplot plots). These plots can also be created by individual utility functions as well.

**Usage**

```
h2o.explain_row(
  object,
  newdata,
  row_index,
  columns = NULL,
  top_n_features = 5,
  include_explanations = "ALL",
  exclude_explanations = NULL,
  plot_overrides = NULL
)
```

**Arguments**

object	One of the following: an H2O model, a list of H2O models, an H2OAutoML object or an H2OAutoML Leaderboard slice.
newdata	An H2OFrame.
row_index	A row index of the instance to explain.
columns	A vector of column names or column indices to create plots with. If specified parameter top_n_features will be ignored.
top_n_features	An integer specifying the number of columns to use, ranked by variable importance (where applicable).
include_explanations	If specified, return only the specified model explanations. (Mutually exclusive with exclude_explanations)
exclude_explanations	Exclude specified model explanations.
plot_overrides	Overrides for individual model explanations, e.g., list(shap_explain_row = list(columns = 5))

**Value**

List of outputs with class "H2OExplanation"

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
```



```

aml <- h2o.automl(y = response,
                 training_frame = train,
                 max_models = 10,
                 seed = 1)

# Create the explanation for whole H2OAutoML object
exa <- h2o.explain_row(aml, test, row_index = 1)
print(exa)

# Create the explanation for the leader model
exm <- h2o.explain_row(aml@leader, test, row_index = 1)
print(exm)

## End(Not run)

```

---

h2o.exportFile	<i>Export an H2O Data Frame (H2OFrame) to a File or to a collection of Files.</i>
----------------	---

---

### Description

Exports an H2OFrame (which can be either VA or FV) to a file. This file may be on the H2O instace's local filesystem, or to HDFS (preface the path with hdfs://) or to S3N (preface the path with s3n://).

### Usage

```

h2o.exportFile(
  data,
  path,
  force = FALSE,
  sep = ",",
  compression = NULL,
  parts = 1,
  header = TRUE,
  quote_header = TRUE
)

```

### Arguments

data	An H2OFrame object.
path	The path to write the file to. Must include the directory and also filename if exporting to a single file. May be prefaced with hdfs:// or s3n://. Each row of data appears as line of the file.
force	logical, indicates how to deal with files that already exist.
sep	The field separator character. Values on each line of the file will be separated by this character (default ",").
compression	How to compress the exported dataset (default none; gzip, bzip2 and snappy available)

parts	integer, number of part files to export to. Default is to write to a single file. Large data can be exported to multiple 'part' files, where each part file contains subset of the data. User can specify the maximum number of part files or use value -1 to indicate that H2O should itself determine the optimal number of files. Parameter path will be considered to be a path to a directory if export to multiple part files is desired. Part files conform to naming scheme 'part-m-?????'.
header	logical, indicates whether to write the header line. Default is to include the header in the output file.
quote_header	logical, indicates whether column names should be quoted. Default is to use quotes.

### Details

In the case of existing files `force = TRUE` will overwrite the file. Otherwise, the operation will fail.

### Examples

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)

# These aren't real paths
# h2o.exportFile(iris_hf, path = "/path/on/h2o/server/filesystem/iris.csv")
# h2o.exportFile(iris_hf, path = "hdfs://path/in/hdfs/iris.csv")
# h2o.exportFile(iris_hf, path = "s3n://path/in/s3/iris.csv")

## End(Not run)
```

---

h2o.exportHDFS

*Export a Model to HDFS*

---

### Description

Exports an [H2OModel](#) to HDFS.

### Usage

```
h2o.exportHDFS(object, path, force = FALSE)
```

### Arguments

object	an <a href="#">H2OModel</a> class object.
path	The path to write the model to. Must include the directory and filename.
force	logical, indicates how to deal with files that already exist.

**Examples**

```
## Not run:
library(h2o)
h2o.init

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/iris/iris_train.csv"
train <- h2o.importFile(f)
h2o.exportHDFS(train, path = " ", force = FALSE)

## End(Not run)
```

---

h2o.feature\_interaction

*Feature interactions and importance, leaf statistics and split value histograms in a tabular form. Available for XGBoost and GBM.*

---

**Description**

Metrics: Gain - Total gain of each feature or feature interaction. FScore - Amount of possible splits taken on a feature or feature interaction. wFScore - Amount of possible splits taken on a feature or feature interaction weighed by the probability of the splits to take place. Average wFScore - wFScore divided by FScore. Average Gain - Gain divided by FScore. Expected Gain - Total gain of each feature or feature interaction weighed by the probability to gather the gain. Average Tree Index Average Tree Depth

**Usage**

```
h2o.feature_interaction(
  model,
  max_interaction_depth = 100,
  max_tree_depth = 100,
  max_deepening = -1
)
```

**Arguments**

`model` A trained xgboost model.

`max_interaction_depth` Upper bound for extracted feature interactions depth. Defaults to 100.

`max_tree_depth` Upper bound for tree depth. Defaults to 100.

`max_deepening` Upper bound for interaction start deepening (zero deepening => interactions starting at root only). Defaults to -1.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
boston <- h2o.importFile(
  "https://s3.amazonaws.com/h2o-public-test-data/smalldata/gbm_test/BostonHousing.csv",
  destination_frame="boston"
```

```

    )
  boston_xgb <- h2o.xgboost(training_frame = boston, y = "medv", seed = 1234)
  feature_interactions <- h2o.feature_interaction(boston_xgb)

  ## End(Not run)

```

---

h2o.fillna	<i>fillNA</i>
------------	---------------

---

### Description

Fill NA's in a sequential manner up to a specified limit

### Usage

```
h2o.fillna(x, method = "forward", axis = 1, maxlen = 1L)
```

### Arguments

x	an H2OFrame
method	A String: "forward" or "backward"
axis	An Integer 1 for row-wise fill (default), 2 for column-wise fill
maxlen	An Integer for maximum number of consecutive NA's to fill

### Value

An H2OFrame after filling missing values

### Examples

```

## Not run:
library(h2o)
h2o.init()

frame_with_nas <- h2o.createFrame(rows = 6, cols = 2,
                                categorical_fraction = 0.0,
                                missing_fraction = 0.7,
                                seed = 123)
frame <- h2o.fillna(frame_with_nas, "forward", axis = 1, maxlen = 2L)

## End(Not run)

```

---

h2o.filterNACols	<i>Filter NA Columns</i>
------------------	--------------------------

---

**Description**

Filter NA Columns

**Usage**

```
h2o.filterNACols(data, frac = 0.2)
```

**Arguments**

data	A dataset to filter on.
frac	The threshold of NAs to allow per column (columns $\geq$ this threshold are filtered)

**Value**

Returns a numeric vector of indexes that pertain to non-NA columns

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
frame <- h2o.createFrame(rows = 6, cols = 2,  
                        categorical_fraction = 0.0,  
                        missing_fraction = 0.7,  
                        seed = 123)  
h2o.filterNACols(frame, frac = 0.5)  
h2o.filterNACols(frame, frac = 0.6)  
  
## End(Not run)
```

---

h2o.findSynonyms	<i>Find synonyms using a word2vec model.</i>
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---

**Description**

Find synonyms using a word2vec model.

**Usage**

```
h2o.findSynonyms(word2vec, word, count = 20)
```

**Arguments**

word2vec	A word2vec model.
word	A single word to find synonyms for.
count	The top 'count' synonyms will be returned.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

job_titles <- h2o.importFile(
  "https://s3.amazonaws.com/h2o-public-test-data/smalldata/craigslistJobTitles.csv",
  col.names = c("category", "jobtitle"), col.types = c("String", "String"), header = TRUE
)
words <- h2o.tokenize(job_titles, " ")
vec <- h2o.word2vec(training_frame = words)
h2o.findSynonyms(vec, "teacher", count = 20)

## End(Not run)
```

---

```
h2o.find_row_by_threshold
```

*Find the threshold, give the max metric. No duplicate thresholds allowed*

---

**Description**

Find the threshold, give the max metric. No duplicate thresholds allowed

**Usage**

```
h2o.find_row_by_threshold(object, threshold)
```

**Arguments**

object	H2OBinomialMetrics
threshold	number between 0 and 1

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response,
  training_frame = train, validation_frame = valid,
  build_tree_one_node = TRUE, seed = 1234)
perf <- h2o.performance(cars_gbm, cars)
h2o.find_row_by_threshold(perf, 0.5)

## End(Not run)
```

---

```
h2o.find_threshold_by_max_metric
      Find the threshold, give the max metric
```

---

**Description**

Find the threshold, give the max metric

**Usage**

```
h2o.find_threshold_by_max_metric(object, metric)
```

**Arguments**

object	H2OBinomialMetrics
metric	"F1," for example

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response,
                   training_frame = train, validation_frame = valid,
                   build_tree_one_node = TRUE, seed = 1234)
perf <- h2o.performance(cars_gbm, cars)
h2o.find_threshold_by_max_metric(perf, "fnr")

## End(Not run)
```

---

```
h2o.floor
      Take a single numeric argument and return a numeric vector with the largest integers
```

---

**Description**

floor takes a single numeric argument x and returns a numeric vector containing the largest integers not greater than the corresponding elements of x.

**Usage**

```
h2o.floor(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Round](#) for the base R implementation, `floor()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.floor(frame["C2"])

## End(Not run)
```

---

h2o.flow	<i>Open H2O Flow</i>
----------	----------------------

---

**Description**

Open H2O Flow in your browser

**Usage**

```
h2o.flow()
```

---

h2o.gainsLift	<i>Access H2O Gains/Lift Tables</i>
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---

**Description**

Retrieve either a single or many Gains/Lift tables from H2O objects.

**Usage**

```
h2o.gainsLift(object, ...)
```

## S4 method for signature 'H2OModel'

```
h2o.gainsLift(object, newdata, valid = FALSE, xval = FALSE, ...)
```

## S4 method for signature 'H2OModelMetrics'

```
h2o.gainsLift(object)
```



**Arguments**

object	Either an <a href="#">H2OModel</a> object or an <a href="#">H2OModelMetrics</a> object.
...	further arguments to be passed to/from this method.
newdata	An H2OFrame object that can be scored on. Requires a valid response column.
valid	Retrieve the validation metric.
xval	Retrieve the cross-validation metric.

**Details**

The [H2OModelMetrics](#) version of this function will only take [H2OBinomialMetrics](#) objects.

**Value**

Calling this function on [H2OModel](#) objects returns a Gains/Lift table corresponding to the [predict](#) function.

**See Also**

[predict](#) for generating prediction frames, [h2o.performance](#) for creating [H2OModelMetrics](#).

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, distribution = "bernoulli",
                training_frame = prostate, validation_frame = prostate, nfolds = 3)
h2o.gainsLift(model)                ## extract training metrics
h2o.gainsLift(model, valid = TRUE) ## extract validation metrics (here: the same)
h2o.gainsLift(model, xval = TRUE)  ## extract cross-validation metrics
h2o.gainsLift(model, newdata = prostate) ## score on new data (here: the same)
# Generating a ModelMetrics object
perf <- h2o.performance(model, prostate)
h2o.gainsLift(perf)                ## extract from existing metrics object

## End(Not run)
```

---

h2o.gam

*Fit a General Additive Model*


---

**Description**

Creates a generalized additive model, specified by a response variable, a set of predictors, and a description of the error distribution.

**Usage**

```

h2o.gam(
  x,
  y,
  training_frame,
  gam_columns,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,
  seed = -1,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
  fold_column = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  offset_column = NULL,
  weights_column = NULL,
  family = c("AUTO", "gaussian", "binomial", "quasibinomial", "ordinal", "multinomial",
    "poisson", "gamma", "tweedie", "negativebinomial", "fractionalbinomial"),
  tweedie_variance_power = 0,
  tweedie_link_power = 0,
  theta = 0,
  solver = c("AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE",
    "COORDINATE_DESCENT", "GRADIENT_DESCENT_LH", "GRADIENT_DESCENT_SQERR"),
  alpha = NULL,
  lambda = NULL,
  lambda_search = FALSE,
  early_stopping = TRUE,
  nlambdas = -1,
  standardize = FALSE,
  missing_values_handling = c("MeanImputation", "Skip", "PlugValues"),
  plug_values = NULL,
  compute_p_values = FALSE,
  remove_collinear_columns = FALSE,
  intercept = TRUE,
  non_negative = FALSE,
  max_iterations = -1,
  objective_epsilon = -1,
  beta_epsilon = 1e-04,
  gradient_epsilon = -1,
  link = c("family_default", "identity", "logit", "log", "inverse", "tweedie",
    "ologit"),
  startval = NULL,
  prior = -1,
  cold_start = FALSE,
  lambda_min_ratio = -1,
  beta_constraints = NULL,
  max_active_predictors = -1,
  interactions = NULL,
  interaction_pairs = NULL,

```

```

obj_reg = -1,
export_checkpoints_dir = NULL,
stopping_rounds = 0,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
  "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error",
  "custom", "custom_increasing"),
stopping_tolerance = 0.001,
balance_classes = FALSE,
class_sampling_factors = NULL,
max_after_balance_size = 5,
max_runtime_secs = 0,
custom_metric_func = NULL,
num_knots = NULL,
knot_ids = NULL,
standardize_tp_gam_cols = FALSE,
scale_tp_penalty_mat = FALSE,
bs = NULL,
scale = NULL,
keep_gam_cols = FALSE,
auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
  "WEIGHTED_OVO")
)

```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
gam_columns	Arrays of predictor column names for gam for smoothers using single or multiple predictors like 'c1','c2','c3','c4',...
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
nfolds	Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
keep_cross_validation_models	Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.

fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
offset_column	Offset column. This will be added to the combination of columns before applying the link function.
weights_column	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set weight = 0 for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with weight == 0.
family	Family. Use binomial for classification with logistic regression, others are for regression problems. Must be one of: "AUTO", "gaussian", "binomial", "quasi-binomial", "ordinal", "multinomial", "poisson", "gamma", "tweedie", "negative-binomial", "fractionalbinomial". Defaults to AUTO.
tweedie_variance_power	Tweedie variance power Defaults to 0.
tweedie_link_power	Tweedie link power Defaults to 0.
theta	Theta Defaults to 0.
solver	AUTO will set the solver based on given data and the other parameters. IRLSM is fast on problems with small number of predictors and for lambda-search with L1 penalty, L_BFGS scales better for datasets with many columns. Must be one of: "AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE", "COORDINATE_DESCENT", "GRADIENT_DESCENT_LH", "GRADIENT_DESCENT_SQERR". Defaults to AUTO.
alpha	Distribution of regularization between the L1 (Lasso) and L2 (Ridge) penalties. A value of 1 for alpha represents Lasso regression, a value of 0 produces Ridge regression, and anything in between specifies the amount of mixing between the two. Default value of alpha is 0 when SOLVER = 'L-BFGS'; 0.5 otherwise.
lambda	Regularization strength
lambda_search	Logical. Use lambda search starting at lambda max, given lambda is then interpreted as lambda min Defaults to FALSE.
early_stopping	Logical. Stop early when there is no more relative improvement on train or validation (if provided) Defaults to TRUE.
nlambda	Number of lambdas to be used in a search. Default indicates: If alpha is zero, with lambda search set to True, the value of nlambda is set to 30 (fewer lambdas are needed for ridge regression) otherwise it is set to 100. Defaults to -1.

standardize	Logical. Standardize numeric columns to have zero mean and unit variance Defaults to FALSE.
missing_values_handling	Handling of missing values. Either MeanImputation, Skip or PlugValues. Must be one of: "MeanImputation", "Skip", "PlugValues". Defaults to MeanImputation.
plug_values	Plug Values (a single row frame containing values that will be used to impute missing values of the training/validation frame, use with conjunction missing_values_handling = PlugValues)
compute_p_values	Logical. Request p-values computation, p-values work only with IRLSM solver and no regularization Defaults to FALSE.
remove_collinear_columns	Logical. In case of linearly dependent columns, remove some of the dependent columns Defaults to FALSE.
intercept	Logical. Include constant term in the model Defaults to TRUE.
non_negative	Logical. Restrict coefficients (not intercept) to be non-negative Defaults to FALSE.
max_iterations	Maximum number of iterations Defaults to -1.
objective_epsilon	Converge if objective value changes less than this. Default indicates: If lambda_search is set to True the value of objective_epsilon is set to .0001. If the lambda_search is set to False and lambda is equal to zero, the value of objective_epsilon is set to .000001, for any other value of lambda the default value of objective_epsilon is set to .0001. Defaults to -1.
beta_epsilon	Converge if beta changes less (using L-infinity norm) than beta esilon, ONLY applies to IRLSM solver Defaults to 0.0001.
gradient_epsilon	Converge if objective changes less (using L-infinity norm) than this, ONLY applies to L-BFGS solver. Default indicates: If lambda_search is set to False and lambda is equal to zero, the default value of gradient_epsilon is equal to .000001, otherwise the default value is .0001. If lambda_search is set to True, the conditional values above are 1E-8 and 1E-6 respectively. Defaults to -1.
link	Link function. Must be one of: "family_default", "identity", "logit", "log", "inverse", "tweedie", "ologit". Defaults to family_default.
startval	double array to initialize coefficients for GAM.
prior	Prior probability for y==1. To be used only for logistic regression iff the data has been sampled and the mean of response does not reflect reality. Defaults to -1.
cold_start	Logical. Only applicable to multiple alpha/lambda values when calling GLM from GAM. If false, build the next model for next set of alpha/lambda values starting from the values provided by current model. If true will start GLM model from scratch. Defaults to FALSE.
lambda_min_ratio	Minimum lambda used in lambda search, specified as a ratio of lambda_max (the smallest lambda that drives all coefficients to zero). Default indicates: if the number of observations is greater than the number of variables, then lambda_min_ratio is set to 0.0001; if the number of observations is less than the number of variables, then lambda_min_ratio is set to 0.01. Defaults to -1.

<code>beta_constraints</code>	Beta constraints
<code>max_active_predictors</code>	Maximum number of active predictors during computation. Use as a stopping criterion to prevent expensive model building with many predictors. Default indicates: If the IRLSM solver is used, the value of <code>max_active_predictors</code> is set to 5000 otherwise it is set to 100000000. Defaults to -1.
<code>interactions</code>	A list of predictor column indices to interact. All pairwise combinations will be computed for the list.
<code>interaction_pairs</code>	A list of pairwise (first order) column interactions.
<code>obj_reg</code>	Likelihood divider in objective value computation, default is 1/nobs Defaults to -1.
<code>export_checkpoints_dir</code>	Automatically export generated models to this directory.
<code>stopping_rounds</code>	Early stopping based on convergence of <code>stopping_metric</code> . Stop if simple moving average of length <code>k</code> of the <code>stopping_metric</code> does not improve for <code>k:=stopping_rounds</code> scoring events (0 to disable) Defaults to 0.
<code>stopping_metric</code>	Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and <code>anomaly_score</code> for Isolation Forest). Note that <code>custom</code> and <code>custom_increasing</code> can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
<code>stopping_tolerance</code>	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
<code>balance_classes</code>	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
<code>class_sampling_factors</code>	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires <code>balance_classes</code> .
<code>max_after_balance_size</code>	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires <code>balance_classes</code> . Defaults to 5.0.
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>custom_metric_func</code>	Reference to custom evaluation function, format: 'language:keyName=funcName'
<code>num_knots</code>	Number of knots for gam predictors
<code>knot_ids</code>	String arrays storing frame keys of knots. One for each gam column set specified in <code>gam_columns</code>
<code>standardize_tp_gam_cols</code>	Logical. standardize tp (thin plate) predictor columns Defaults to FALSE.

scale_tp_penalty_mat	Logical. Scale penalty matrix for tp (thin plate) smoothers as in R Defaults to FALSE.
bs	Basis function type for each gam predictors, 0 for cr, 1 for thin plate regression with knots, 2 for thin plate regression with SVD. If specified, must be the same size as gam_columns
scale	Smoothing parameter for gam predictors. If specified, must be of the same length as gam_columns
keep_gam_cols	Logical. Save keys of model matrix Defaults to FALSE.
auc_type	Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO", "WEIGHTED_OVO". Defaults to AUTO.

### Examples

```
## Not run:
h2o.init()

# Run GAM of CAPSULE ~ AGE + RACE + PSA + DCAPS
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
h2o.gam(y = "CAPSULE", x = c("RACE"), gam_columns = c("PSA"),
        training_frame = prostate, family = "binomial")

## End(Not run)
```

---

h2o.gbm

*Build gradient boosted classification or regression trees*


---

### Description

Builds gradient boosted classification trees and gradient boosted regression trees on a parsed data set. The default distribution function will guess the model type based on the response column type. In order to run properly, the response column must be an numeric for "gaussian" or an enum for "bernoulli" or "multinomial".

### Usage

```
h2o.gbm(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  score_each_iteration = FALSE,
  score_tree_interval = 0,
```

```

fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
fold_column = NULL,
ignore_const_cols = TRUE,
offset_column = NULL,
weights_column = NULL,
balance_classes = FALSE,
class_sampling_factors = NULL,
max_after_balance_size = 5,
ntrees = 50,
max_depth = 5,
min_rows = 10,
nbins = 20,
nbins_top_level = 1024,
nbins_cats = 1024,
r2_stopping = Inf,
stopping_rounds = 0,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
  "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error",
  "custom", "custom_increasing"),
stopping_tolerance = 0.001,
max_runtime_secs = 0,
seed = -1,
build_tree_one_node = FALSE,
learn_rate = 0.1,
learn_rate_annealing = 1,
distribution = c("AUTO", "bernoulli", "quasibinomial", "multinomial", "gaussian",
  "poisson", "gamma", "tweedie", "laplace", "quantile", "huber", "custom"),
quantile_alpha = 0.5,
tweedie_power = 1.5,
huber_alpha = 0.9,
checkpoint = NULL,
sample_rate = 1,
sample_rate_per_class = NULL,
col_sample_rate = 1,
col_sample_rate_change_per_level = 1,
col_sample_rate_per_tree = 1,
min_split_improvement = 1e-05,
histogram_type = c("AUTO", "UniformAdaptive", "Random", "QuantilesGlobal",
  "RoundRobin"),
max_abs_leafnode_pred = Inf,
pred_noise_bandwidth = 0,
categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
  "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
calibrate_model = FALSE,
calibration_frame = NULL,
custom_metric_func = NULL,
custom_distribution_func = NULL,
export_checkpoints_dir = NULL,
monotone_constraints = NULL,
check_constant_response = TRUE,
gainlift_bins = -1,
auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",

```



```

    "WEIGHTED_OVO"),
  verbose = FALSE
)

```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
nfolds	Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
keep_cross_validation_models	Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
score_tree_interval	Score the model after every so many trees. Disabled if set to 0. Defaults to 0.
fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
offset_column	Offset column. This will be added to the combination of columns before applying the link function.
weights_column	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set weight = 0 for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with weight == 0.

<code>balance_classes</code>	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
<code>class_sampling_factors</code>	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires <code>balance_classes</code> .
<code>max_after_balance_size</code>	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires <code>balance_classes</code> . Defaults to 5.0.
<code>ntrees</code>	Number of trees. Defaults to 50.
<code>max_depth</code>	Maximum tree depth (0 for unlimited). Defaults to 5.
<code>min_rows</code>	Fewest allowed (weighted) observations in a leaf. Defaults to 10.
<code>nbins</code>	For numerical columns (real/int), build a histogram of (at least) this many bins, then split at the best point Defaults to 20.
<code>nbins_top_level</code>	For numerical columns (real/int), build a histogram of (at most) this many bins at the root level, then decrease by factor of two per level Defaults to 1024.
<code>nbins_cats</code>	For categorical columns (factors), build a histogram of this many bins, then split at the best point. Higher values can lead to more overfitting. Defaults to 1024.
<code>r2_stopping</code>	<code>r2_stopping</code> is no longer supported and will be ignored if set - please use <code>stopping_rounds</code> , <code>stopping_metric</code> and <code>stopping_tolerance</code> instead. Previous version of H2O would stop making trees when the $R^2$ metric equals or exceeds this Defaults to $1.797693135e+308$ .
<code>stopping_rounds</code>	Early stopping based on convergence of <code>stopping_metric</code> . Stop if simple moving average of length <code>k</code> of the <code>stopping_metric</code> does not improve for <code>k:=stopping_rounds</code> scoring events (0 to disable) Defaults to 0.
<code>stopping_metric</code>	Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and <code>anomaly_score</code> for Isolation Forest). Note that custom and <code>custom_increasing</code> can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
<code>stopping_tolerance</code>	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>seed</code>	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
<code>build_tree_one_node</code>	Logical. Run on one node only; no network overhead but fewer cpus used. Suitable for small datasets. Defaults to FALSE.
<code>learn_rate</code>	Learning rate (from 0.0 to 1.0) Defaults to 0.1.

learn_rate_annealing	Scale the learning rate by this factor after each tree (e.g., 0.99 or 0.999) Defaults to 1.
distribution	Distribution function Must be one of: "AUTO", "bernoulli", "quasibinomial", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber", "custom". Defaults to AUTO.
quantile_alpha	Desired quantile for Quantile regression, must be between 0 and 1. Defaults to 0.5.
tweedie_power	Tweedie power for Tweedie regression, must be between 1 and 2. Defaults to 1.5.
huber_alpha	Desired quantile for Huber/M-regression (threshold between quadratic and linear loss, must be between 0 and 1). Defaults to 0.9.
checkpoint	Model checkpoint to resume training with.
sample_rate	Row sample rate per tree (from 0.0 to 1.0) Defaults to 1.
sample_rate_per_class	A list of row sample rates per class (relative fraction for each class, from 0.0 to 1.0), for each tree
col_sample_rate	Column sample rate (from 0.0 to 1.0) Defaults to 1.
col_sample_rate_change_per_level	Relative change of the column sampling rate for every level (must be > 0.0 and <= 2.0) Defaults to 1.
col_sample_rate_per_tree	Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.
min_split_improvement	Minimum relative improvement in squared error reduction for a split to happen Defaults to 1e-05.
histogram_type	What type of histogram to use for finding optimal split points Must be one of: "AUTO", "UniformAdaptive", "Random", "QuantilesGlobal", "RoundRobin". Defaults to AUTO.
max_abs_leafnode_pred	Maximum absolute value of a leaf node prediction Defaults to 1.797693135e+308.
pred_noise_bandwidth	Bandwidth (sigma) of Gaussian multiplicative noise $\sim N(1, \text{sigma})$ for tree node predictions Defaults to 0.
categorical_encoding	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.
calibrate_model	Logical. Use Platt Scaling to calculate calibrated class probabilities. Calibration can provide more accurate estimates of class probabilities. Defaults to FALSE.
calibration_frame	Calibration frame for Platt Scaling
custom_metric_func	Reference to custom evaluation function, format: 'language:keyName=funcName'
custom_distribution_func	Reference to custom distribution, format: 'language:keyName=funcName'

export_checkpoints_dir	Automatically export generated models to this directory.
monotone_constraints	A mapping representing monotonic constraints. Use +1 to enforce an increasing constraint and -1 to specify a decreasing constraint.
check_constant_response	Logical. Check if response column is constant. If enabled, then an exception is thrown if the response column is a constant value. If disabled, then model will train regardless of the response column being a constant value or not. Defaults to TRUE.
gainslift_bins	Gains/Lift table number of bins. 0 means disabled.. Default value -1 means automatic binning. Defaults to -1.
auc_type	Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO", "WEIGHTED_OVO". Defaults to AUTO.
verbose	Logical. Print scoring history to the console (Metrics per tree). Defaults to FALSE.

### See Also

[predict.H2OModel](#) for prediction

### Examples

```
## Not run:
library(h2o)
h2o.init()

# Run regression GBM on australia data
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
independent <- c("premax", "salmx", "minairtemp", "maxairtemp", "maxsst",
                "maxsoilmoist", "Max_czcs")
dependent <- "runoffnew"
h2o.gbm(y = dependent, x = independent, training_frame = australia,
        ntrees = 3, max_depth = 3, min_rows = 2)

## End(Not run)
```

---

h2o.generic	<i>Imports a generic model into H2O. Such model can be used then used for scoring and obtaining additional information about the model. The imported model has to be supported by H2O.</i>
-------------	--

---

### Description

Imports a generic model into H2O. Such model can be used then used for scoring and obtaining additional information about the model. The imported model has to be supported by H2O.

### Usage

```
h2o.generic(model_id = NULL, model_key = NULL, path = NULL)
```

**Arguments**

model_id	Destination id for this model; auto-generated if not specified.
model_key	Key to the self-contained model archive already uploaded to H2O.
path	Path to file with self-contained model archive.

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()

# generic_model <- h2o.genericModel("/path/to/model.zip")
# predictions <- h2o.predict(generic_model, dataset)

## End(Not run)
```

---

h2o.genericModel	<i>Imports a model under given path, creating a Generic model with it.</i>
------------------	--

---

**Description**

Usage example: `generic_model <- h2o.genericModel(model_file_path = "/path/to/mojo.zip")` `predictions <- h2o.predict(generic_model, dataset)`

**Usage**

```
h2o.genericModel(mojo_file_path)
```

**Arguments**

mojo\_file\_path Filesystem path to the model imported

**Value**

Returns H2O Generic Model based on given embedded model

**Examples**

```
## Not run:

# Import default Iris dataset as H2O frame
data <- as.h2o(iris)

# Train a very simple GBM model
features <- c("Sepal.Length", "Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
original_model <- h2o.gbm(x = features, y = "Species", training_frame = data)

# Download the trained GBM model as MOJO (temporary directory used in this example)
mojo_original_name <- h2o.download_mojo(model = original_model, path = tempdir())
mojo_original_path <- paste0(tempdir(), "/", mojo_original_name)

# Import the MOJO as Generic model
generic_model <- h2o.genericModel(mojo_original_path)
```

```
# Perform scoring with the generic model
generic_model_predictions <- h2o.predict(generic_model, data)

## End(Not run)
```

---

h2o.getAlphaBest      *Extract best alpha value found from glm model.*

---

### Description

This function allows setting betas of an existing glm model.

### Usage

```
h2o.getAlphaBest(model)
```

### Arguments

model                  an [H2OModel](#) corresponding from a h2o.glm call.

---

h2o.getConnection      *Retrieve an H2O Connection*

---

### Description

Attempt to recover an h2o connection.

### Usage

```
h2o.getConnection()
```

### Value

Returns an [H2OConnection](#) object.

---

h2o.getFrame	<i>Get an R Reference to an H2O Dataset, that will NOT be GC'd by default</i>
--------------	---

---

### Description

Get the reference to a frame with the given id in the H2O instance.

### Usage

```
h2o.getFrame(id)
```

### Arguments

id                    A string indicating the unique frame of the dataset to retrieve.

### Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
train <- h2o.importFile(f)
y <- "species"
x <- setdiff(names(train), y)
train[, y] <- as.factor(train[, y])
nfolds <- 5
num_base_models <- 2
my_gbm <- h2o.gbm(x = x, y = y, training_frame = train,
                 distribution = "multinomial", ntrees = 10,
                 max_depth = 3, min_rows = 2, learn_rate = 0.2,
                 nfolds = nfolds, fold_assignment = "Modulo",
                 keep_cross_validation_predictions = TRUE, seed = 1)
my_rf <- h2o.randomForest(x = x, y = y, training_frame = train,
                        ntrees = 50, nfolds = nfolds, fold_assignment = "Modulo",
                        keep_cross_validation_predictions = TRUE, seed = 1)
stack <- h2o.stackedEnsemble(x = x, y = y, training_frame = train,
                           model_id = "my_ensemble_l1",
                           base_models = list(my_gbm@model_id, my_rf@model_id),
                           keep_levelone_frame = TRUE)
h2o.getFrame(stack@model$levelone_frame_id$name)

## End(Not run)
```

---

h2o.getGLMFullRegularizationPath

*Extract full regularization path from a GLM model*

---

**Description**

Extract the full regularization path from a GLM model (assuming it was run with the lambda search option).

**Usage**

```
h2o.getGLMFullRegularizationPath(model)
```

**Arguments**

model                    an [H2OModel](#) corresponding from a `h2o.glm` call.

---

h2o.getGrid	<i>Get a grid object from H2O distributed K/V store.</i>
-------------	--

---

**Description**

Note that if neither cross-validation nor a validation frame is used in the grid search, then the training metrics will display in the "get grid" output. If a validation frame is passed to the grid, and `nfolds = 0`, then the validation metrics will display. However, if `nfolds > 1`, then cross-validation metrics will display even if a validation frame is provided.

**Usage**

```
h2o.getGrid(grid_id, sort_by, decreasing, verbose = FALSE)
```

**Arguments**

grid_id	ID of existing grid object to fetch
sort_by	Sort the models in the grid space by a metric. Choices are "logloss", "residual_deviance", "mse", "auc", "accuracy", "precision", "recall", "f1", etc.
decreasing	Specify whether sort order should be decreasing
verbose	Controls verbosity of the output, if enabled prints out error messages for failed models (default: FALSE)

**Examples**

```
## Not run:
library(h2o)
library(jsonlite)
h2o.init()
iris_hf <- as.h2o(iris)
h2o.grid("gbm", grid_id = "gbm_grid_id", x = c(1:4), y = 5,
        training_frame = iris_hf, hyper_params = list(ntrees = c(1, 2, 3)))
grid <- h2o.getGrid("gbm_grid_id")
# Get grid summary
summary(grid)
# Fetch grid models
model_ids <- grid@model_ids
models <- lapply(model_ids, function(id) { h2o.getModel(id)})

## End(Not run)
```



---

h2o.getId	<i>Get back-end distributed key/value store id from an H2OFrame.</i>
-----------	--

---

**Description**

Get back-end distributed key/value store id from an H2OFrame.

**Usage**

```
h2o.getId(x)
```

**Arguments**

x	An H2OFrame
---	-------------

**Value**

The id of the H2OFrame

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.getId(iris)

## End(Not run)
```

---

h2o.getLambdaBest	<i>Extract best lambda value found from glm model.</i>
-------------------	--

---

**Description**

This function allows setting betas of an existing glm model.

**Usage**

```
h2o.getLambdaBest(model)
```

**Arguments**

model	an <a href="#">H2OModel</a> corresponding from a h2o.glm call.
-------	--

---

h2o.getLambdaMax	<i>Extract the maximum lambda value used during lambda search from glm model.</i>
------------------	---

---

**Description**

This function allows setting betas of an existing glm model.

**Usage**

```
h2o.getLambdaMax(model)
```

**Arguments**

model	an <a href="#">H2OModel</a> corresponding from a h2o.glm call.
-------	--

---

h2o.getLambdaMin	<i>Extract the minimum lambda value calculated during lambda search from glm model. Note that due to early stop, this minimum lambda value may not be used in the actual lambda search.</i>
------------------	---

---

**Description**

This function allows setting betas of an existing glm model.

**Usage**

```
h2o.getLambdaMin(model)
```

**Arguments**

model	an <a href="#">H2OModel</a> corresponding from a h2o.glm call.
-------	--

---

h2o.getModel	<i>Get an R reference to an H2O model</i>
--------------	---

---

**Description**

Returns a reference to an existing model in the H2O instance.

**Usage**

```
h2o.getModel(model_id)
```

**Arguments**

model_id	A string indicating the unique model_id of the model to retrieve.
----------	---

**Value**

Returns an object that is a subclass of [H2OModel](#).

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
model_id <- h2o.gbm(x = 1:4, y = 5, training_frame = iris_hf)@model_id
model_retrieved <- h2o.getModel(model_id)

## End(Not run)
```

---

h2o.getModelTree	<i>Fetches a single tree of a H2O model. This function is intended to be used on Gradient Boosting Machine models or Distributed Random Forest models.</i>
------------------	--

---

**Description**

Fetches a single tree of a H2O model. This function is intended to be used on Gradient Boosting Machine models or Distributed Random Forest models.

**Usage**

```
h2o.getModelTree(model, tree_number, tree_class = NA)
```

**Arguments**

model	Model with trees
tree_number	Number of the tree in the model to fetch, starting with 1
tree_class	Name of the class of the tree (if applicable). This value is ignored for regression and binomial response column, as there is only one tree built. As there is exactly one class per categorical level, name of tree's class equals to the corresponding categorical level of response column.

**Value**

Returns an H2OTree object with detailed information about a tree.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smалldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
gbm_model <- h2o.gbm(y = "species", training_frame = iris)
tree <- h2o.getModelTree(gbm_model, 1, "Iris-setosa")

## End(Not run)
```

---

h2o.getTimezone	<i>Get the Time Zone on the H2O cluster Returns a string</i>
-----------------	--

---

**Description**

Get the Time Zone on the H2O cluster Returns a string

**Usage**

```
h2o.getTimezone()
```

---

h2o.getTypes	<i>Get the types-per-column</i>
--------------	---------------------------------

---

**Description**

Get the types-per-column

**Usage**

```
h2o.getTypes(x)
```

**Arguments**

x	An H2OFrame
---	-------------

**Value**

A list of types per column

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smалldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.getTypes(iris)

## End(Not run)
```

---

h2o.getVersion	<i>Get h2o version</i>
----------------	------------------------

---

**Description**

Get h2o version

**Usage**

```
h2o.getVersion()
```

---

h2o.get_automl	<i>Get an R object that is a subclass of <a href="#">H2OAutoML</a></i>
----------------	--

---

**Description**

Get an R object that is a subclass of [H2OAutoML](#)

**Usage**

```
h2o.get_automl(project_name)
```

```
h2o.getAutoML(project_name)
```

**Arguments**

project\_name    A string indicating the project\_name of the automl instance to retrieve.

**Value**

Returns an object that is a subclass of [H2OAutoML](#).

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path, header = TRUE)
y <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification
aml <- h2o.automl(y = y, training_frame = prostate,
                max_runtime_secs = 30, project_name = "prostate")
aml2 <- h2o.get_automl("prostate")

## End(Not run)
```

---

h2o.get_best_model	<i>Get best model of a given family/algorithm for a given criterion from an AutoML object.</i>
--------------------	--

---

**Description**

Get best model of a given family/algorithm for a given criterion from an AutoML object.

**Usage**

```
h2o.get_best_model(
  object,
  algorithm = c("any", "basemodel", "deeplearning", "drf", "gbm", "glm",
               "stackedensemble", "xgboost"),
  criterion = c("AUTO", "AUC", "AUCPR", "logloss", "MAE", "mean_per_class_error",
               "deviance", "MSE", "predict_time_per_row_ms", "RMSE", "RMSLE", "training_time_ms")
)
```

**Arguments**

object	H2OAutoML object
algorithm	One of "any", "basemodel", "deeplearning", "drf", "gbm", "glm", "stackedensemble", "xgboost"
criterion	<p>Criterion can be one of the metrics reported in the leaderboard. If set to NULL, the same ordering as in the leaderboard will be used. Available criteria:</p> <ul style="list-style-type: none"> <li>• Regression metrics: deviance, RMSE, MSE, MAE, RMSLE</li> <li>• Binomial metrics: AUC, logloss, AUCPR, mean_per_class_error, RMSE, MSE</li> <li>• Multinomial metrics: mean_per_class_error, logloss, RMSE, MSE</li> </ul> <p>The following additional leaderboard information can be also used as a criterion:</p> <ul style="list-style-type: none"> <li>• 'training_time_ms': column providing the training time of each model in milliseconds (doesn't include the training of cross validation models).</li> <li>• 'predict_time_per_row_ms': column providing the average prediction time by the model for a single row.</li> </ul>

**Value**

An H2OModel or NULL if no model of a given family is present

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path, header = TRUE)
y <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 30)
gbm <- h2o.get_best_model(aml, "gbm")

## End(Not run)
```

---

h2o.get\_leaderboard     *Retrieve the leaderboard from the AutoML instance.*

---

**Description**

Contrary to the default leaderboard attached to the automl instance, this one can return columns other than the metrics.

**Usage**

```
h2o.get_leaderboard(object, extra_columns = NULL)
```

**Arguments**

- |               |   |
|---------------|---|
| object        | The object for which to return the leaderboard. Currently, only H2OAutoML instances are supported.  |
| extra_columns | A string or a list of string specifying which optional columns should be added to the leaderboard. Defaults to None. Currently supported extensions are: <ul style="list-style-type: none"> <li>• 'ALL': adds all columns below.</li> <li>• 'training_time_ms': column providing the training time of each model in milliseconds (doesn't include the training of cross validation models).</li> <li>• 'predict_time_per_row_ms': column providing the average prediction time by the model for a single row.</li> <li>• 'algo': column providing the algorithm name for each model.</li> </ul> |

**Value**

An H2OFrame representing the leaderboard.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path, header = TRUE)
y <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 30)
lb <- h2o.get_leaderboard(aml)
head(lb)

## End(Not run)
```

---

`h2o.get_ntrees_actual` *Retrieve actual number of trees for tree algorithms*

---

**Description**

Retrieve actual number of trees for tree algorithms

**Usage**

```
h2o.get_ntrees_actual(object)
```

**Arguments**

object	An <a href="#">H2OModel</a> object.
--------	-------------------------------------

---

```
h2o.get_segment_models
```

*Retrieves an instance of [H2OSegmentModels](#) for a given id.*

---

### Description

Retrieves an instance of [H2OSegmentModels](#) for a given id.

### Usage

```
h2o.get_segment_models(segment_models_id)
```

### Arguments

```
segment_models_id
```

A string indicating the unique segment\_models\_id

### Value

Returns an object that is a subclass of [H2OSegmentModels](#).

### Examples

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
h2o.train_segments(algorithm = "gbm",
                  segment_columns = "Species", segment_models_id="models_by_species",
                  x = c(1:3), y = 4, training_frame = iris_hf, ntrees = 5, max_depth = 4)
models <- h2o.get_segment_models("models_by_species")
as.data.frame(models)

## End(Not run)
```

---

```
h2o.giniCoef
```

*Retrieve the GINI Coefficient*

---

### Description

Retrieves the GINI coefficient from an [H2OBinomialMetrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training GINIvalue is returned. If more than one parameter is set to TRUE, then a named vector of GINIs are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.giniCoef(object, train = FALSE, valid = FALSE, xval = FALSE)
```



**Arguments**

object	an <a href="#">H2OBinomialMetrics</a> object.
train	Retrieve the training GINI Coefficient
valid	Retrieve the validation GINI Coefficient
xval	Retrieve the cross-validation GINI Coefficient

**See Also**

[h2o.auc](#) for AUC, [h2o.giniCoef](#) for the GINI coefficient, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating H2OModelMetrics objects.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.giniCoef(perf)

## End(Not run)
```

---

h2o.glm

*Fit a generalized linear model*


---

**Description**

Fits a generalized linear model, specified by a response variable, a set of predictors, and a description of the error distribution.

**Usage**

```
h2o.glm(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,
  checkpoint = NULL,
  export_checkpoints_dir = NULL,
  seed = -1,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
```

```

fold_column = NULL,
random_columns = NULL,
ignore_const_cols = TRUE,
score_each_iteration = FALSE,
score_iteration_interval = -1,
offset_column = NULL,
weights_column = NULL,
family = c("AUTO", "gaussian", "binomial", "fractionalbinomial", "quasibinomial",
  "ordinal", "multinomial", "poisson", "gamma", "tweedie", "negativebinomial"),
rand_family = c("[gaussian]"),
tweedie_variance_power = 0,
tweedie_link_power = 1,
theta = 1e-10,
solver = c("AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE",
  "COORDINATE_DESCENT", "GRADIENT_DESCENT_LH", "GRADIENT_DESCENT_SQERR"),
alpha = NULL,
lambda = NULL,
lambda_search = FALSE,
early_stopping = TRUE,
nlambdas = -1,
standardize = TRUE,
missing_values_handling = c("MeanImputation", "Skip", "PlugValues"),
plug_values = NULL,
compute_p_values = FALSE,
remove_collinear_columns = FALSE,
intercept = TRUE,
non_negative = FALSE,
max_iterations = -1,
objective_epsilon = -1,
beta_epsilon = 1e-04,
gradient_epsilon = -1,
link = c("family_default", "identity", "logit", "log", "inverse", "tweedie",
  "ologit"),
rand_link = c("[identity]", "[family_default]"),
startval = NULL,
calc_like = FALSE,
HGLM = FALSE,
prior = -1,
cold_start = FALSE,
lambda_min_ratio = -1,
beta_constraints = NULL,
max_active_predictors = -1,
interactions = NULL,
interaction_pairs = NULL,
obj_reg = -1,
stopping_rounds = 0,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
  "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error",
  "custom", "custom_increasing"),
stopping_tolerance = 0.001,
balance_classes = FALSE,
class_sampling_factors = NULL,

```

```

    max_after_balance_size = 5,
    max_runtime_secs = 0,
    custom_metric_func = NULL,
    generate_scoring_history = FALSE,
    auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
                "WEIGHTED_OVO")
  )

```

### Arguments

**x** (Optional) A vector containing the names or indices of the predictor variables to use in building the model. If **x** is missing, then all columns except **y** are used.

**y** The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.

**training\_frame** Id of the training data frame.

**model\_id** Destination id for this model; auto-generated if not specified.

**validation\_frame** Id of the validation data frame.

**nfolds** Number of folds for K-fold cross-validation (0 to disable or  $\geq 2$ ). Defaults to 0.

**checkpoint** Model checkpoint to resume training with.

**export\_checkpoints\_dir** Automatically export generated models to this directory.

**seed** Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).

**keep\_cross\_validation\_models** Logical. Whether to keep the cross-validation models. Defaults to TRUE.

**keep\_cross\_validation\_predictions** Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.

**keep\_cross\_validation\_fold\_assignment** Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.

**fold\_assignment** Cross-validation fold assignment scheme, if **fold\_column** is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.

**fold\_column** Column with cross-validation fold index assignment per observation.

**random\_columns** random columns indices for HGLM.

**ignore\_const\_cols** Logical. Ignore constant columns. Defaults to TRUE.

**score\_each\_iteration** Logical. Whether to score during each iteration of model training. Defaults to FALSE.

score_iteration_interval	Perform scoring for every score_iteration_interval iterations Defaults to -1.
offset_column	Offset column. This will be added to the combination of columns before applying the link function.
weights_column	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set weight = 0 for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with weight == 0.
family	Family. Use binomial for classification with logistic regression, others are for regression problems. Must be one of: "AUTO", "gaussian", "binomial", "fractionalbinomial", "quasibinomial", "ordinal", "multinomial", "poisson", "gamma", "tweedie", "negativebinomial". Defaults to AUTO.
rand_family	Random Component Family array. One for each random component. Only support gaussian for now. Must be one of: "[gaussian]".
tweedie_variance_power	Tweedie variance power Defaults to 0.
tweedie_link_power	Tweedie link power Defaults to 1.
theta	Theta Defaults to 1e-10.
solver	AUTO will set the solver based on given data and the other parameters. IRLSM is fast on problems with small number of predictors and for lambda-search with L1 penalty, L_BFGS scales better for datasets with many columns. Must be one of: "AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE", "COORDINATE_DESCENT", "GRADIENT_DESCENT_LH", "GRADIENT_DESCENT_SQERR". Defaults to AUTO.
alpha	Distribution of regularization between the L1 (Lasso) and L2 (Ridge) penalties. A value of 1 for alpha represents Lasso regression, a value of 0 produces Ridge regression, and anything in between specifies the amount of mixing between the two. Default value of alpha is 0 when SOLVER = 'L-BFGS'; 0.5 otherwise.
lambda	Regularization strength
lambda_search	Logical. Use lambda search starting at lambda max, given lambda is then interpreted as lambda min Defaults to FALSE.
early_stopping	Logical. Stop early when there is no more relative improvement on train or validation (if provided) Defaults to TRUE.
nlambdas	Number of lambdas to be used in a search. Default indicates: If alpha is zero, with lambda search set to True, the value of nlambdas is set to 30 (fewer lambdas are needed for ridge regression) otherwise it is set to 100. Defaults to -1.
standardize	Logical. Standardize numeric columns to have zero mean and unit variance Defaults to TRUE.
missing_values_handling	Handling of missing values. Either MeanImputation, Skip or PlugValues. Must be one of: "MeanImputation", "Skip", "PlugValues". Defaults to MeanImputation.

plug_values	Plug Values (a single row frame containing values that will be used to impute missing values of the training/validation frame, use with conjunction missing_values_handling = PlugValues)
compute_p_values	Logical. Request p-values computation, p-values work only with IRLSM solver and no regularization Defaults to FALSE.
remove_collinear_columns	Logical. In case of linearly dependent columns, remove some of the dependent columns Defaults to FALSE.
intercept	Logical. Include constant term in the model Defaults to TRUE.
non_negative	Logical. Restrict coefficients (not intercept) to be non-negative Defaults to FALSE.
max_iterations	Maximum number of iterations Defaults to -1.
objective_epsilon	Converge if objective value changes less than this. Default indicates: If lambda_search is set to True the value of objective_epsilon is set to .0001. If the lambda_search is set to False and lambda is equal to zero, the value of objective_epsilon is set to .000001, for any other value of lambda the default value of objective_epsilon is set to .0001. Defaults to -1.
beta_epsilon	Converge if beta changes less (using L-infinity norm) than beta esilon, ONLY applies to IRLSM solver Defaults to 0.0001.
gradient_epsilon	Converge if objective changes less (using L-infinity norm) than this, ONLY applies to L-BFGS solver. Default indicates: If lambda_search is set to False and lambda is equal to zero, the default value of gradient_epsilon is equal to .000001, otherwise the default value is .0001. If lambda_search is set to True, the conditional values above are 1E-8 and 1E-6 respectively. Defaults to -1.
link	Link function. Must be one of: "family_default", "identity", "logit", "log", "inverse", "tweedie", "ologit". Defaults to family_default.
rand_link	Link function array for random component in HGLM. Must be one of: "[identity]", "[family_default]".
startval	double array to initialize fixed and random coefficients for HGLM, coefficients for GLM.
calc_like	Logical. if true, will return likelihood function value for HGLM. Defaults to FALSE.
HGLM	Logical. If set to true, will return HGLM model. Otherwise, normal GLM model will be returned Defaults to FALSE.
prior	Prior probability for y==1. To be used only for logistic regression iff the data has been sampled and the mean of response does not reflect reality. Defaults to -1.
cold_start	Logical. Only applicable to multiple alpha/lambda values. If false, build the next model for next set of alpha/lambda values starting from the values provided by current model. If true will start GLM model from scratch. Defaults to FALSE.
lambda_min_ratio	Minimum lambda used in lambda search, specified as a ratio of lambda_max (the smallest lambda that drives all coefficients to zero). Default indicates: if the number of observations is greater than the number of variables, then lambda_min_ratio is set to 0.0001; if the number of observations is less than the number of variables, then lambda_min_ratio is set to 0.01. Defaults to -1.

<code>beta_constraints</code>	Beta constraints
<code>max_active_predictors</code>	Maximum number of active predictors during computation. Use as a stopping criterion to prevent expensive model building with many predictors. Default indicates: If the IRLSM solver is used, the value of <code>max_active_predictors</code> is set to 5000 otherwise it is set to 100000000. Defaults to -1.
<code>interactions</code>	A list of predictor column indices to interact. All pairwise combinations will be computed for the list.
<code>interaction_pairs</code>	A list of pairwise (first order) column interactions.
<code>obj_reg</code>	Likelihood divider in objective value computation, default is 1/nobs Defaults to -1.
<code>stopping_rounds</code>	Early stopping based on convergence of <code>stopping_metric</code> . Stop if simple moving average of length <code>k</code> of the <code>stopping_metric</code> does not improve for <code>k:=stopping_rounds</code> scoring events (0 to disable) Defaults to 0.
<code>stopping_metric</code>	Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and <code>anomaly_score</code> for Isolation Forest). Note that <code>custom</code> and <code>custom_increasing</code> can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
<code>stopping_tolerance</code>	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
<code>balance_classes</code>	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
<code>class_sampling_factors</code>	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires <code>balance_classes</code> .
<code>max_after_balance_size</code>	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires <code>balance_classes</code> . Defaults to 5.0.
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>custom_metric_func</code>	Reference to custom evaluation function, format: 'language:keyName=funcName'
<code>generate_scoring_history</code>	Logical. If set to true, will generate scoring history for GLM. This may significantly slow down the algo. Defaults to FALSE.
<code>auc_type</code>	Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO", "WEIGHTED_OVO". Defaults to AUTO.

**Value**

A subclass of `H2OModel` is returned. The specific subclass depends on the machine learning task at hand (if it's binomial classification, then an `H2OBinomialModel` is returned, if it's regression then a `H2ORegressionModel` is returned). The default print-out of the models is shown, but further GLM-specific information can be queried out of the object. To access these various items, please refer to the `seealso` section below. Upon completion of the GLM, the resulting object has coefficients, normalized coefficients, residual/null deviance, aic, and a host of model metrics including MSE, AUC (for logistic regression), degrees of freedom, and confusion matrices. Please refer to the more in-depth GLM documentation available here: <https://h2o-release.s3.amazonaws.com/h2o-dev/rel-shannon/2/docs-website/h2o-docs/index.html#Data+Science+Algorithms-GLM>

**See Also**

`predict.H2OModel` for prediction, `h2o.mse`, `h2o.auc`, `h2o.confusionMatrix`, `h2o.performance`, `h2o.giniCoef`, `h2o.logloss`, `h2o.varimp`, `h2o.scoreHistory`

**Examples**

```
## Not run:
h2o.init()

# Run GLM of CAPSULE ~ AGE + RACE + PSA + DCAPS
prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"), training_frame = prostate,
        family = "binomial", nfolds = 0, alpha = 0.5, lambda_search = FALSE)

# Run GLM of VOL ~ CAPSULE + AGE + RACE + PSA + GLEASON
predictors = setdiff(colnames(prostate), c("ID", "DPROS", "DCAPS", "VOL"))
h2o.glm(y = "VOL", x = predictors, training_frame = prostate, family = "gaussian",
        nfolds = 0, alpha = 0.1, lambda_search = FALSE)

# GLM variable importance
# Also see:
# https://github.com/h2oai/h2o/blob/master/R/tests/testdir_demos/runit_demo_VI_all_algos.R
bank = h2o.importFile(
  path="https://s3.amazonaws.com/h2o-public-test-data/smalldata/demos/bank-additional-full.csv"
)
predictors = 1:20
target = "y"
glm = h2o.glm(x = predictors,
              y = target,
              training_frame = bank,
              family = "binomial",
              standardize = TRUE,
              lambda_search = TRUE)
h2o.std_coef_plot(glm, num_of_features = 20)

## End(Not run)
```

h2o.glm

*Generalized low rank decomposition of an H2O data frame***Description**

Builds a generalized low rank decomposition of an H2O data frame

**Usage**

```

h2o.glm(
  training_frame,
  cols = NULL,
  model_id = NULL,
  validation_frame = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  representation_name = NULL,
  loading_name = NULL,
  transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"),
  k = 1,
  loss = c("Quadratic", "Absolute", "Huber", "Poisson", "Hinge", "Logistic",
    "Periodic"),
  loss_by_col = c("Quadratic", "Absolute", "Huber", "Poisson", "Hinge", "Logistic",
    "Periodic", "Categorical", "Ordinal"),
  loss_by_col_idx = NULL,
  multi_loss = c("Categorical", "Ordinal"),
  period = 1,
  regularization_x = c("None", "Quadratic", "L2", "L1", "NonNegative", "OneSparse",
    "UnitOneSparse", "Simplex"),
  regularization_y = c("None", "Quadratic", "L2", "L1", "NonNegative", "OneSparse",
    "UnitOneSparse", "Simplex"),
  gamma_x = 0,
  gamma_y = 0,
  max_iterations = 1000,
  max_updates = 2000,
  init_step_size = 1,
  min_step_size = 1e-04,
  seed = -1,
  init = c("Random", "SVD", "PlusPlus", "User"),
  svd_method = c("GramSVD", "Power", "Randomized"),
  user_y = NULL,
  user_x = NULL,
  expand_user_y = TRUE,
  impute_original = FALSE,
  recover_svd = FALSE,
  max_runtime_secs = 0,
  export_checkpoints_dir = NULL
)

```

**Arguments**

`training_frame` Id of the training data frame.



cols	(Optional) A vector containing the data columns on which k-means operates.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
representation_name	Frame key to save resulting X
loading_name	[Deprecated] Use representation_name instead. Frame key to save resulting X.
transform	Transformation of training data Must be one of: "NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE". Defaults to NONE.
k	Rank of matrix approximation Defaults to 1.
loss	Numeric loss function Must be one of: "Quadratic", "Absolute", "Huber", "Poisson", "Hinge", "Logistic", "Periodic". Defaults to Quadratic.
loss_by_col	Loss function by column (override) Must be one of: "Quadratic", "Absolute", "Huber", "Poisson", "Hinge", "Logistic", "Periodic", "Categorical", "Ordinal".
loss_by_col_idx	Loss function by column index (override)
multi_loss	Categorical loss function Must be one of: "Categorical", "Ordinal". Defaults to Categorical.
period	Length of period (only used with periodic loss function) Defaults to 1.
regularization_x	Regularization function for X matrix Must be one of: "None", "Quadratic", "L2", "L1", "NonNegative", "OneSparse", "UnitOneSparse", "Simplex". Defaults to None.
regularization_y	Regularization function for Y matrix Must be one of: "None", "Quadratic", "L2", "L1", "NonNegative", "OneSparse", "UnitOneSparse", "Simplex". Defaults to None.
gamma_x	Regularization weight on X matrix Defaults to 0.
gamma_y	Regularization weight on Y matrix Defaults to 0.
max_iterations	Maximum number of iterations Defaults to 1000.
max_updates	Maximum number of updates, defaults to 2*max_iterations Defaults to 2000.
init_step_size	Initial step size Defaults to 1.
min_step_size	Minimum step size Defaults to 0.0001.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
init	Initialization mode Must be one of: "Random", "SVD", "PlusPlus", "User". Defaults to PlusPlus.
svd_method	Method for computing SVD during initialization (Caution: Randomized is currently experimental and unstable) Must be one of: "GramSVD", "Power", "Randomized". Defaults to Randomized.

user_y	User-specified initial Y
user_x	User-specified initial X
expand_user_y	Logical. Expand categorical columns in user-specified initial Y Defaults to TRUE.
impute_original	Logical. Reconstruct original training data by reversing transform Defaults to FALSE.
recover_svd	Logical. Recover singular values and eigenvectors of XY Defaults to FALSE.
max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
export_checkpoints_dir	Automatically export generated models to this directory.

**Value**

an object of class [H2ODimReductionModel](#).

**References**

M. Udell, C. Horn, R. Zadeh, S. Boyd (2014). Generalized Low Rank Models[<https://arxiv.org/abs/1410.0342>]. Unpublished manuscript, Stanford Electrical Engineering Department. N. Halko, P.G. Martinsson, J.A. Tropp. Finding structure with randomness: Probabilistic algorithms for constructing approximate matrix decompositions[<https://arxiv.org/abs/0909.4061>]. SIAM Rev., Survey and Review section, Vol. 53, num. 2, pp. 217-288, June 2011.

**See Also**

[h2o.kmeans](#), [h2o.svd](#), [h2o.prcomp](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
h2o.glm(training_frame = australia, k = 5, loss = "Quadratic", regularization_x = "L1",
        gamma_x = 0.5, gamma_y = 0, max_iterations = 1000)

## End(Not run)
```

---

h2o.grep

*Search for matches to an argument pattern*

---

**Description**

Searches for matches to argument ‘pattern’ within each element of a string column.

## Usage

```
h2o.grep(  
  pattern,  
  x,  
  ignore.case = FALSE,  
  invert = FALSE,  
  output.logical = FALSE  
)
```

## Arguments

pattern	A character string containing a regular expression.
x	An H2O frame that wraps a single string column.
ignore.case	If TRUE case is ignored during matching.
invert	Identify elements that do not match the pattern.
output.logical	If TRUE returns logical vector of indicators instead of list of matching positions

## Details

This function has similar semantics as R's native `grep` function and it supports a subset of its parameters. Default behavior is to return indices of the elements matching the pattern. Parameter 'output.logical' can be used to return a logical vector indicating if the element matches the pattern (1) or not (0).

## Value

H2OFrame holding the matching positions or a logical vector if 'output.logical' is enabled.

## Examples

```
## Not run:  
library(h2o)  
h2o.init()  
addresses <- as.h2o(c("2307", "Leghorn St", "Mountain View", "CA", "94043"))  
zip_codes <- addresses[h2o.grep("[0-9]{5}", addresses, output.logical = TRUE),]  
  
## End(Not run)
```

---

h2o.grid

*H2O Grid Support*

---

## Description

Provides a set of functions to launch a grid search and get its results.

**Usage**

```

h2o.grid(
  algorithm,
  grid_id,
  x,
  y,
  training_frame,
  ...,
  hyper_params = list(),
  is_supervised = NULL,
  do_hyper_params_check = FALSE,
  search_criteria = NULL,
  export_checkpoints_dir = NULL,
  recovery_dir = NULL,
  parallelism = 1
)

```

**Arguments**

algorithm	Name of algorithm to use in grid search (gbm, randomForest, kmeans, glm, deeplearning, naivebayes, pca).
grid_id	(Optional) ID for resulting grid search. If it is not specified then it is autogenerated.
x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
...	arguments describing parameters to use with algorithm (i.e., x, y, training_frame). Look at the specific algorithm - h2o.gbm, h2o.glm, h2o.kmeans, h2o.deepLearning - for available parameters.
hyper_params	List of lists of hyper parameters (i.e., list(ntrees=c(1,2), max_depth=c(5,7))).
is_supervised	(Optional) If specified then override the default heuristic which decides if the given algorithm name and parameters specify a supervised or unsupervised algorithm.
do_hyper_params_check	Perform client check for specified hyper parameters. It can be time expensive for large hyper space.
search_criteria	(Optional) List of control parameters for smarter hyperparameter search. The list can include values for: strategy, max_models, max_runtime_secs, stopping_metric, stopping_tolerance, stopping_rounds and seed. The default strategy 'Cartesian' covers the entire space of hyperparameter combinations. If you want to use cartesian grid search, you can leave the search_criteria argument unspecified. Specify the "RandomDiscrete" strategy to get random search of all the combinations of your hyperparameters with three ways of specifying when to

stop the search: max number of models, max time, and metric-based early stopping (e.g., stop if MSE has not improved by 0.0001 over the 5 best models). Examples below: `list(strategy = "RandomDiscrete", max_runtime_secs = 600, max_models = 42)` or `list(strategy = "RandomDiscrete", max_models = 42, max_runtime_secs = 28800)` or `list(strategy = "RandomDiscrete", stopping_metric = "AUTO", stopping_tolerance = 0.0001)` or `list(strategy = "RandomDiscrete", stopping_metric = "misclassification", stopping_tolerance = 0.0001)`

`export_checkpoints_dir` Directory to automatically export grid and its models to.

`recovery_dir` When specified the grid and all necessary data (frames, models) will be saved to this directory (use HDFS or other distributed file-system). Should the cluster crash during training, the grid can be reloaded from this directory via `h2o.loadGrid` and training can be resumed

`parallelism` Level of Parallelism during grid model building. 1 = sequential building (default). Use the value of 0 for adaptive parallelism - decided by H2O. Any number > 1 sets the exact number of models built in parallel.

### Details

Launch grid search with given algorithm and parameters.

### Examples

```
## Not run:
library(h2o)
library(jsonlite)
h2o.init()
iris_hf <- as.h2o(iris)
grid <- h2o.grid("gbm", x = c(1:4), y = 5, training_frame = iris_hf,
               hyper_params = list(ntrees = c(1, 2, 3)))
# Get grid summary
summary(grid)
# Fetch grid models
model_ids <- grid@model_ids
models <- lapply(model_ids, function(id) { h2o.getModel(id)})

## End(Not run)
```

---

h2o.group\_by

*Group and Apply by Column*

---

### Description

Performs a group by and apply similar to `ddply`.

### Usage

```
h2o.group_by(
  data,
  by,
  ...,
  gb.control = list(na.methods = NULL, col.names = NULL)
)
```

**Arguments**

<code>data</code>	an H2OFrame object.
<code>by</code>	a list of column names
<code>...</code>	any supported aggregate function. See <a href="#">Details</a> : for more help.
<code>gb.control</code>	a list of how to handle NA values in the dataset as well as how to name output columns. The method is specified using the <code>rm.method</code> argument. See <a href="#">Details</a> : for more help.

**Details**

In the case of `na.methods` within `gb.control`, there are three possible settings. "all" will include NAs in computation of functions. "rm" will completely remove all NA fields. "ignore" will remove NAs from the numerator but keep the rows for computational purposes. If a list smaller than the number of columns groups is supplied, the list will be padded by "ignore".

Note that to specify a list of column names in the `gb.control` list, you must add the `col.names` argument. Similar to `na.methods`, `col.names` will pad the list with the default column names if the length is less than the number of columns groups supplied.

Supported functions include `nrow`. This function is required and accepts a string for the name of the generated column. Other supported aggregate functions accept `col` and `na` arguments for specifying columns and the handling of NAs ("all", "ignore", and GroupBy object; `max` calculates the maximum of each column specified in `col` for each group of a GroupBy object; `mean` calculates the mean of each column specified in `col` for each group of a GroupBy object; `min` calculates the minimum of each column specified in `col` for each group of a GroupBy object; `mode` calculates the mode of each column specified in `col` for each group of a GroupBy object; `sd` calculates the standard deviation of each column specified in `col` for each group of a GroupBy object; `ss` calculates the sum of squares of each column specified in `col` for each group of a GroupBy object; `sum` calculates the sum of each column specified in `col` for each group of a GroupBy object; and `var` calculates the variance of each column specified in `col` for each group of a GroupBy object. If an aggregate is provided without a value (for example, as `max` in `sum(col="X1", na="all").mean(col="X5", na="all").max()`), then it is assumed that the aggregation should apply to all columns except the GroupBy columns. However, operations will not be performed on String columns. They will be skipped. Note again that `nrow` is required and cannot be empty.

**Value**

Returns a new H2OFrame object with columns equivalent to the number of groups created

**Examples**

```
## Not run:
library(h2o)
h2o.init()
df <- h2o.importFile(paste("https://s3.amazonaws.com/h2o-public-test-data",
                          "/smalldata/prostate/prostate.csv",
                          sep=""))
h2o.group_by(data = df, by = "RACE", nrow("VOL"))

## End(Not run)
```

---

h2o.gsub	<i>String Global Substitute</i>
----------	---------------------------------

---

**Description**

Creates a copy of the target column in which each string has all occurrence of the regex pattern replaced with the replacement substring.

**Usage**

```
h2o.gsub(pattern, replacement, x, ignore.case = FALSE)
```

**Arguments**

pattern	The pattern to replace.
replacement	The replacement pattern.
x	The column on which to operate.
ignore.case	Case sensitive or not

**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_gsub <- as.h2o("r tutorial")
sub_string <- h2o.gsub("r ", "H2O ", string_to_gsub)

## End(Not run)
```

---

h2o.h	<i>Calculates Friedman and Popescu's H statistics, in order to test for the presence of an interaction between specified variables in h2o gbm and xgb models. H varies from 0 to 1. It will have a value of 0 if the model exhibits no interaction between specified variables and a correspondingly larger value for a stronger interaction effect between them. NaN is returned if a computation is spoiled by weak main effects and rounding errors.</i>
-------	---

---

**Description**

See Jerome H. Friedman and Bogdan E. Popescu, 2008, "Predictive learning via rule ensembles", \*Ann. Appl. Stat.\* \*\*2\*\*::916-954, [http://projecteuclid.org/download/pdfview\\_1/euclid.aos/1223908046](http://projecteuclid.org/download/pdfview_1/euclid.aos/1223908046), s. 8.1.

**Usage**

```
h2o.h(model, frame, variables)
```

**Arguments**

model	A trained gradient-boosting model.
frame	A frame that current model has been fitted to.
variables	Variables of the interest.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate.hex <- h2o.importFile(
  "https://s3.amazonaws.com/h2o-public-test-data/smalldata/logreg/prostate.csv",
  destination_frame="prostate.hex"
)
prostate.hex$CAPSULE <- as.factor(prostate.hex$CAPSULE)
prostate.hex$RACE <- as.factor(prostate.hex$RACE)
prostate.h2o <- h2o.gbm(x = 3:9, y = "CAPSULE", training_frame = prostate.hex,
  distribution = "bernoulli", ntrees = 100, max_depth = 5, min_rows = 10, learn_rate = 0.1)
h_val <- h2o.h(prostate.h2o, prostate.hex, c('DPROS', 'DCAPS'))

## End(Not run)
```

---

h2o.head

*Return the Head or Tail of an H2O Dataset.*


---

**Description**

Returns the first or last rows of an H2OFrame object.

**Usage**

```
h2o.head(x, n = 6L, m = 200L, ...)

## S3 method for class 'H2OFrame'
head(x, n = 6L, m = 200L, ...)

h2o.tail(x, n = 6L, m = 200L, ...)

## S3 method for class 'H2OFrame'
tail(x, n = 6L, m = 200L, ...)
```

**Arguments**

x	An H2OFrame object.
n	(Optional) A single integer. If positive, number of rows in x to return. If negative, all but the n first/last number of rows in x.
m	(Optional) A single integer. If positive, number of columns in x to return. If negative, all but the m first/last number of columns in x.
...	Ignored.



**Value**

An H2OFrame containing the first or last n rows and m columns of an H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init(ip <- "localhost", port = 54321, startH2O = TRUE)
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
# Return the first 10 rows and 6 columns
h2o.head(australia, n = 10L, m = 6L)
# Return the last 10 rows and 6 columns
h2o.tail(australia, n = 10L, m = 6L)

# For Jupyter notebook with an R kernel,
# view all rows of a data frame
options(repr.matrix.max.rows = 600, repr.matrix.max.cols = 200)

## End(Not run)
```

---

h2o.HGLMMetrics	<i>Retrieve HGLM ModelMetrics</i>
-----------------	-----------------------------------

---

**Description**

Retrieve HGLM ModelMetrics

**Usage**

```
h2o.HGLMMetrics(object)
```

**Arguments**

object            an H2OModel object or H2OModelMetrics.

---

h2o.hist	<i>Compute A Histogram</i>
----------	----------------------------

---

**Description**

Compute a histogram over a numeric column. If breaks=="FD", the MAD is used over the IQR in computing bin width. Note that we do not beautify the breakpoints as R does.

**Usage**

```
h2o.hist(x, breaks = "Sturges", plot = TRUE)
```

**Arguments**

x	A single numeric column from an H2OFrame.
breaks	Can be one of the following: A string: "Sturges", "Rice", "sqrt", "Doane", "FD", "Scott" A single number for the number of breaks splitting the range of the vec into number of breaks bins of equal width A vector of numbers giving the split points, e.g., c(-50,213.2123,9324834)
plot	A logical value indicating whether or not a plot should be generated (default is TRUE).

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.asnumeric(iris["petal_len"])
h2o.hist(iris["petal_len"], breaks = "Sturges", plot = TRUE)

## End(Not run)
```

---

h2o.hit\_ratio\_table    *Retrieve the Hit Ratios*

---

**Description**

If "train", "valid", and "xval" parameters are FALSE (default), then the training Hit Ratios value is returned. If more than one parameter is set to TRUE, then a named list of Hit Ratio tables are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.hit_ratio_table(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> object.
train	Retrieve the training Hit Ratio
valid	Retrieve the validation Hit Ratio
xval	Retrieve the cross-validation Hit Ratio

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smldata/iris/iris_wheader.csv"
iris <- h2o.importFile(f)
iris_split <- h2o.splitFrame(data = iris, ratios = 0.8, seed = 1234)
```

```
train <- iris_split[[1]]
valid <- iris_split[[2]]

iris_xgb <- h2o.xgboost(x = 1:4, y = 5, training_frame = train, validation_frame = valid)
hrt_iris <- h2o.hit_ratio_table(iris_xgb, valid = TRUE)
hrt_iris

## End(Not run)
```

---

h2o.hour

*Convert Milliseconds to Hour of Day in H2O Datasets*

---

### Description

Converts the entries of an H2OFrame object from milliseconds to hours of the day (on a 0 to 23 scale).

### Usage

```
h2o.hour(x)
```

```
hour(x)
```

```
## S3 method for class 'H2OFrame'
```

```
hour(x)
```

### Arguments

x                    An H2OFrame object.

### Value

An H2OFrame object containing the entries of x converted to hours of the day.

### See Also

[h2o.day](#)

---

h2o.ice\_plot

*Plot Individual Conditional Expectation (ICE) for each decile*

---

### Description

Individual Conditional Expectation (ICE) plot gives a graphical depiction of the marginal effect of a variable on the response. ICE plots are similar to partial dependence plots (PDP); PDP shows the average effect of a feature while ICE plot shows the effect for a single instance. This function will plot the effect for each decile. In contrast to the PDP, ICE plots can provide more insight, especially when there is stronger feature interaction.

**Usage**

```
h2o.ice_plot(model, newdata, column, target = NULL, max_levels = 30)
```

**Arguments**

model	An H2OModel.
newdata	An H2OFrame.
column	A feature column name to inspect.
target	If multinomial, plot PDP just for target category. Character string.
max_levels	An integer specifying the maximum number of factor levels to show. Defaults to 30.

**Value**

A ggplot2 object

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
gbm <- h2o.gbm(y = response,
               training_frame = train)

# Create the individual conditional expectations plot
ice <- h2o.ice_plot(gbm, test, column = "alcohol")
print(ice)

## End(Not run)
```

---

h2o.ifelse

*H2O Apply Conditional Statement*


---

**Description**

Applies conditional statements to numeric vectors in H2O parsed data objects when the data are numeric.

**Usage**

```
h2o.ifelse(test, yes, no)
```

```
ifelse(test, yes, no)
```

**Arguments**

test	A logical description of the condition to be met (>, <, =, etc...)
yes	The value to return if the condition is TRUE.
no	The value to return if the condition is FALSE.

**Details**

Both numeric and categorical values can be tested. However when returning a yes and no condition both conditions must be either both categorical or numeric.

**Value**

Returns a vector of new values matching the conditions stated in the ifelse call.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.importFile(path = australia_path)
australia[, 9] <- ifelse(australia[, 3] < 279.9, 1, 0)
summary(australia)

## End(Not run)
```

---

h2o.importFile

*Import Files into H2O*

---

**Description**

Imports files into an H2O cluster. The default behavior is to pass-through to the parse phase automatically.

**Usage**

```
h2o.importFile(
  path,
  destination_frame = "",
  parse = TRUE,
  header = NA,
  sep = "",
  col.names = NULL,
  col.types = NULL,
  na.strings = NULL,
```

```
    decrypt_tool = NULL,  
    skipped_columns = NULL,  
    custom_non_data_line_markers = NULL,  
    partition_by = NULL,  
    quotechar = NULL,  
    escapechar = ""  
  )
```

```
h2o.importFolder(  
  path,  
  pattern = "",  
  destination_frame = "",  
  parse = TRUE,  
  header = NA,  
  sep = "",  
  col.names = NULL,  
  col.types = NULL,  
  na.strings = NULL,  
  decrypt_tool = NULL,  
  skipped_columns = NULL,  
  custom_non_data_line_markers = NULL,  
  partition_by = NULL,  
  quotechar = NULL,  
  escapechar = "\\\"  
)
```

```
h2o.importHDFS(  
  path,  
  pattern = "",  
  destination_frame = "",  
  parse = TRUE,  
  header = NA,  
  sep = "",  
  col.names = NULL,  
  na.strings = NULL  
)
```

```
h2o.uploadFile(  
  path,  
  destination_frame = "",  
  parse = TRUE,  
  header = NA,  
  sep = "",  
  col.names = NULL,  
  col.types = NULL,  
  na.strings = NULL,  
  progressBar = FALSE,  
  parse_type = NULL,  
  decrypt_tool = NULL,  
  skipped_columns = NULL,  
  quotechar = NULL,  
  escapechar = "\\\"
```

)

**Arguments**

path	The complete URL or normalized file path of the file to be imported. Each row of data appears as one line of the file.
destination_frame	(Optional) The unique hex key assigned to the imported file. If none is given, a key will automatically be generated based on the URL path.
parse	(Optional) A logical value indicating whether the file should be parsed after import, for details see <a href="#">h2o.parseRaw</a> .
header	(Optional) A logical value indicating whether the first line of the file contains column headers. If left empty, the parser will try to automatically detect this.
sep	(Optional) The field separator character. Values on each line of the file are separated by this character. If sep = "", the parser will automatically detect the separator.
col.names	(Optional) An H2OFrame object containing a single delimited line with the column names for the file.
col.types	(Optional) A vector to specify whether columns should be forced to a certain type upon import parsing.
na.strings	(Optional) H2O will interpret these strings as missing.
decrypt_tool	(Optional) Specify a Decryption Tool (key-reference acquired by calling <a href="#">h2o.decryptionSetup</a> .
skipped_columns	a list of column indices to be skipped during parsing.
custom_non_data_line_markers	(Optional) If a line in imported file starts with any character in given string it will NOT be imported. Empty string means all lines are imported, NULL means that default behaviour for given format will be used
partition_by	names of the columns the persisted dataset has been partitioned by.
quotechar	A hint for the parser which character to expect as quoting character. None (default) means autodetection.
escapechar	(Optional) One ASCII character used to escape other characters.
pattern	(Optional) Character string containing a regular expression to match file(s) in the folder.
progressBar	(Optional) When FALSE, tell H2O parse call to block synchronously instead of polling. This can be faster for small datasets but loses the progress bar.
parse_type	(Optional) Specify which parser type H2O will use. Valid types are "ARFF", "XLS", "CSV", "SVMLight"

**Details**

`h2o.importFile` is a parallelized reader and pulls information from the server from a location specified by the client. The path is a server-side path. This is a fast, scalable, highly optimized way to read data. H2O pulls the data from a data store and initiates the data transfer as a read operation.

Unlike the import function, which is a parallelized reader, `h2o.uploadFile` is a push from the client to the server. The specified path must be a client-side path. This is not scalable and is only intended for smaller data sizes. The client pushes the data from a local filesystem (for example, on

your machine where R is running) to H2O. For big-data operations, you don't want the data stored on or flowing through the client.

`h2o.importFolder` imports an entire directory of files. If the given path is relative, then it will be relative to the start location of the H2O instance. The default behavior is to pass-through to the parse phase automatically.

`h2o.importHDFS` is deprecated. Instead, use `h2o.importFile`.

### See Also

[h2o.import\\_sql\\_select](#), [h2o.import\\_sql\\_table](#), [h2o.parseRaw](#)

### Examples

```
## Not run:
h2o.init(ip = "localhost", port = 54321, startH2O = TRUE)
prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
class(prostate)
summary(prostate)

#Import files with a certain regex pattern by utilizing h2o.importFolder()
#In this example we import all .csv files in the directory prostate_folder
prostate_path = system.file("extdata", "prostate_folder", package = "h2o")
prostate_pattern = h2o.importFolder(path = prostate_path, pattern = ".*.csv")
class(prostate_pattern)
summary(prostate_pattern)

## End(Not run)
```

---

`h2o.import_hive_table` *Import Hive Table into H2O*

---

### Description

Import Hive table to H2OFrame in memory. Make sure to start H2O with Hive on classpath. Uses `hive-site.xml` on classpath to connect to Hive. When database is specified as jdbc URL uses Hive JDBC driver to obtain table metadata. then uses direct HDFS access to import data.

### Usage

```
h2o.import_hive_table(
  database,
  table,
  partitions = NULL,
  allow_multi_format = FALSE
)
```

### Arguments

<code>database</code>	Name of Hive database (default database will be used by default), can be also a JDBC URL
<code>table</code>	name of Hive table to import



`partitions` a list of lists of strings - partition key column values of partitions you want to import.

`allow_multi_format` enable import of partitioned tables with different storage formats used. WARNING: this may fail on out-of-memory for tables with a large number of small partitions.

### Details

For example, `my_citibike_data = h2o.import_hive_table("default", "citibike20k", partitions = list(c("2017", "01"), c("2017", "02")))` `my_citibike_data = h2o.import_hive_table("jdbc:hive2://hive-server:10000/default", "citibike20k", allow_multi_format = TRUE)`

---

`h2o.import_mojo` *Imports a MOJO under given path, creating a Generic model with it.*

---

### Description

Usage example: `mojo_model <- h2o.import_mojo(model_file_path = "/path/to/mojo.zip")` `predictions <- h2o.predict(mojo_model, dataset)`

### Usage

```
h2o.import_mojo(mojo_file_path)
```

### Arguments

`mojo_file_path` Filesystem path to the model imported

### Value

Returns H2O Generic Model embedding given MOJO model

### Examples

```
## Not run:

# Import default Iris dataset as H2O frame
data <- as.h2o(iris)

# Train a very simple GBM model
features <- c("Sepal.Length", "Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
original_model <- h2o.gbm(x = features, y = "Species", training_frame = data)

# Download the trained GBM model as MOJO (temporary directory used in this example)
mojo_original_path <- h2o.save_mojo(original_model, path = tempdir())

# Import the MOJO and obtain a Generic model
mojo_model <- h2o.import_mojo(mojo_original_path)

# Perform scoring with the generic model
predictions <- h2o.predict(mojo_model, data)

## End(Not run)
```

---

h2o.import\_sql\_select *Import SQL table that is result of SELECT SQL query into H2O*

---

### Description

Creates a temporary SQL table from the specified sql\_query. Runs multiple SELECT SQL queries on the temporary table concurrently for parallel ingestion, then drops the table. Be sure to start the h2o.jar in the terminal with your downloaded JDBC driver in the classpath: 'java -cp <path\_to\_h2o\_jar>:<path\_to\_jdbc\_driver>:water.H2OApp' Also see h2o.import\_sql\_table. Currently supported SQL databases are MySQL, PostgreSQL, MariaDB, Hive, Oracle and Microsoft SQL Server.

### Usage

```
h2o.import_sql_select(
  connection_url,
  select_query,
  username,
  password,
  use_temp_table = NULL,
  temp_table_name = NULL,
  optimize = NULL,
  fetch_mode = NULL
)
```

### Arguments

connection_url	URL of the SQL database connection as specified by the Java Database Connectivity (JDBC) Driver. For example, "jdbc:mysql://localhost:3306/menagerie?&useSSL=false"
select_query	SQL query starting with 'SELECT' that returns rows from one or more database tables.
username	Username for SQL server
password	Password for SQL server
use_temp_table	Whether a temporary table should be created from select_query
temp_table_name	Name of temporary table to be created from select_query
optimize	(Optional) Optimize import of SQL table for faster imports. Experimental. Default is true.
fetch_mode	(Optional) Set to DISTRIBUTED to enable distributed import. Set to SINGLE to force a sequential read from the database Can be used for databases that do not support OFFSET-like clauses in SQL statements.

### Details

```
For example, my_sql_conn_url <- "jdbc:mysql://172.16.2.178:3306/ingestSQL?&useSSL=false"
select_query <- "SELECT bikeid from citibike20k" username <- "root" password <- "abc123"
my_citibike_data <- h2o.import_sql_select(my_sql_conn_url, select_query, username, password)
```

---

 h2o.import\_sql\_table *Import SQL Table into H2O*


---

### Description

Imports SQL table into an H2O cluster. Assumes that the SQL table is not being updated and is stable. Runs multiple SELECT SQL queries concurrently for parallel ingestion. Be sure to start the h2o.jar in the terminal with your downloaded JDBC driver in the classpath: 'java -cp <path\_to\_h2o\_jar>:<path\_to\_jdbc\_driver\_jar> water.H2OApp' Also see h2o.import\_sql\_select. Currently supported SQL databases are MySQL, PostgreSQL, MariaDB, Hive, Oracle and Microsoft SQL Server.

### Usage

```
h2o.import_sql_table(
  connection_url,
  table,
  username,
  password,
  columns = NULL,
  optimize = NULL,
  fetch_mode = NULL
)
```

### Arguments

connection_url	URL of the SQL database connection as specified by the Java Database Connectivity (JDBC) Driver. For example, "jdbc:mysql://localhost:3306/menagerie?&useSSL=false"
table	Name of SQL table
username	Username for SQL server
password	Password for SQL server
columns	(Optional) Character vector of column names to import from SQL table. Default is to import all columns.
optimize	(Optional) Optimize import of SQL table for faster imports. Default is true. Ignored - use fetch_mode instead.
fetch_mode	(Optional) Set to DISTRIBUTED to enable distributed import. Set to SINGLE to force a sequential read from the database Can be used for databases that do not support OFFSET-like clauses in SQL statements.

### Details

For example, my\_sql\_conn\_url <- "jdbc:mysql://172.16.2.178:3306/ingestSQL?&useSSL=false"  
 table <- "citibike20k" username <- "root" password <- "abc123" my\_citibike\_data <- h2o.import\_sql\_table(my\_sql\_conn\_url, table, username, password)

h2o.impute

*Basic Imputation of H2O Vectors***Description**

Perform inplace imputation by filling missing values with aggregates computed on the "na.rm'd" vector. Additionally, it's possible to perform imputation based on groupings of columns from within data; these columns can be passed by index or name to the `by` parameter. If a factor column is supplied, then the method must be "mode".

**Usage**

```
h2o.impute(
  data,
  column = 0,
  method = c("mean", "median", "mode"),
  combine_method = c("interpolate", "average", "lo", "hi"),
  by = NULL,
  groupByFrame = NULL,
  values = NULL
)
```

**Arguments**

<code>data</code>	The dataset containing the column to impute.
<code>column</code>	A specific column to impute, default of 0 means impute the whole frame.
<code>method</code>	"mean" replaces NAs with the column mean; "median" replaces NAs with the column median; "mode" replaces with the most common factor (for factor columns only);
<code>combine_method</code>	If method is "median", then choose how to combine quantiles on even sample sizes. This parameter is ignored in all other cases.
<code>by</code>	group by columns
<code>groupByFrame</code>	Impute the column <code>col</code> with this pre-computed grouped frame.
<code>values</code>	A vector of impute values (one per column). NaN indicates to skip the column

**Details**

The default method is selected based on the type of the column to impute. If the column is numeric then "mean" is selected; if it is categorical, then "mode" is selected. Other column types (e.g. String, Time, UUID) are not supported.

**Value**

an H2OFrame with imputed values

**Examples**

```
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
iris_hf[sample(nrow(iris_hf), 40), 5] <- NA # randomly replace 50 values with NA
# impute with a group by
iris_hf <- h2o.impute(iris_hf, "Species", "mode", by = c("Sepal.Length", "Sepal.Width"))

## End(Not run)
```

---

h2o.init	<i>Initialize and Connect to H2O</i>
----------	--------------------------------------

---

**Description**

Attempts to start and/or connect to and H2O instance.

**Usage**

```
h2o.init(
  ip = "localhost",
  port = 54321,
  name = NA_character_,
  startH2O = TRUE,
  forceDL = FALSE,
  enable_assertions = TRUE,
  license = NULL,
  nthreads = -1,
  max_mem_size = NULL,
  min_mem_size = NULL,
  ice_root = tempdir(),
  log_dir = NA_character_,
  log_level = NA_character_,
  strict_version_check = TRUE,
  proxy = NA_character_,
  https = FALSE,
  cacert = NA_character_,
  insecure = FALSE,
  username = NA_character_,
  password = NA_character_,
  use_spnego = FALSE,
  cookies = NA_character_,
  context_path = NA_character_,
  ignore_config = FALSE,
  extra_classpath = NULL,
  jvm_custom_args = NULL,
  bind_to_localhost = TRUE
)
```

**Arguments**

ip	Object of class character representing the IP address of the server where H2O is running.
port	Object of class numeric representing the port number of the H2O server.
name	(Optional) A character string representing the H2O cluster name.
startH2O	(Optional) A logical value indicating whether to try to start H2O from R if no connection with H2O is detected. This is only possible if ip = "localhost" or ip = "127.0.0.1". If an existing connection is detected, R does not start H2O.
forceDL	(Optional) A logical value indicating whether to force download of the H2O executable. Defaults to FALSE, so the executable will only be downloaded if it does not already exist in the h2o R library resources directory h2o/java/h2o.jar. This value is only used when R starts H2O.
enable_assertions	(Optional) A logical value indicating whether H2O should be launched with assertions enabled. Used mainly for error checking and debugging purposes. This value is only used when R starts H2O.
license	(Optional) A character string value specifying the full path of the license file. This value is only used when R starts H2O.
nthreads	(Optional) Number of threads in the thread pool. This relates very closely to the number of CPUs used. -1 means use all CPUs on the host (Default). A positive integer specifies the number of CPUs directly. This value is only used when R starts H2O.
max_mem_size	(Optional) A character string specifying the maximum size, in bytes, of the memory allocation pool to H2O. This value must be a multiple of 1024 greater than 2MB. Append the letter m or M to indicate megabytes, or g or G to indicate gigabytes. This value is only used when R starts H2O. If max_mem_size is not defined, then the amount of memory that H2O allocates will be determined by the default memory of Java Virtual Machine. This amount is dependent on the Java version, but it will generally be 25 percent of the machine's physical memory.
min_mem_size	(Optional) A character string specifying the minimum size, in bytes, of the memory allocation pool to H2O. This value must be a multiple of 1024 greater than 2MB. Append the letter m or M to indicate megabytes, or g or G to indicate gigabytes. This value is only used when R starts H2O.
ice_root	(Optional) A directory to handle object spillage. The default varies by OS.
log_dir	(Optional) A directory where H2O server logs are stored. The default varies by OS.
log_level	(Optional) The level of logging of H2O server. The default is INFO.
strict_version_check	(Optional) Setting this to FALSE is unsupported and should only be done when advised by technical support.
proxy	(Optional) A character string specifying the proxy path.
https	(Optional) Set this to TRUE to use https instead of http.
cacert	(Optional) Path to a CA bundle file with root and intermediate certificates of trusted CAs.
insecure	(Optional) Set this to TRUE to disable SSL certificate checking.

username	(Optional) Username to login with.
password	(Optional) Password to login with.
use_spnego	(Optional) Set this to TRUE to enable SPNEGO authentication.
cookies	(Optional) Vector(or list) of cookies to add to request.
context_path	(Optional) The last part of connection URL: http://<ip>:<port>/<context_path>
ignore_config	(Optional) A logical value indicating whether a search for a .h2oconfig file should be conducted or not. Default value is FALSE.
extra_classpath	(Optional) A vector of paths to libraries to be added to the Java classpath when H2O is started from R.
jvm_custom_args	(Optional) A character list of custom arguments for the JVM where new H2O instance is going to run, if started. Ignored when connecting to an existing instance.
bind_to_localhost	(Optional) A logical flag indicating whether access to the H2O instance should be restricted to the local machine (default) or if it can be reached from other computers on the network. Only applicable when H2O is started from R.

### Details

By default, this method first checks if an H2O instance is connectible. If it cannot connect and `start = TRUE` with `ip = "localhost"`, it will attempt to start an instance of H2O at `localhost:54321`. If an open ip and port of your choice are passed in, then this method will attempt to start an H2O instance at that specified ip port.

When initializing H2O locally, this method searches for `h2o.jar` in the R library resources (`system.file("java", "h2o.` and if the file does not exist, it will automatically attempt to download the correct version from Amazon S3. The user must have Internet access for this process to be successful.

Once connected, the method checks to see if the local H2O R package version matches the version of H2O running on the server. If there is a mismatch and the user indicates she wishes to upgrade, it will remove the local H2O R package and download/install the H2O R package from the server.

### Value

this method will load it and return a `H2OConnection` object containing the IP address and port number of the H2O server.

### Note

Users may wish to manually upgrade their package (rather than waiting until being prompted), which requires that they fully uninstall and reinstall the H2O package, and the H2O client package. You must unload packages running in the environment before upgrading. It's recommended that users restart R or R studio after upgrading

### See Also

[H2O R package documentation](#) for more details. [h2o.shutdown](#) for shutting down from R.

**Examples**

```
## Not run:
# Try to connect to a local H2O instance that is already running.
# If not found, start a local H2O instance from R with the default settings.
h2o.init()

# Try to connect to a local H2O instance.
# If not found, raise an error.
h2o.init(startH2O = FALSE)

# Try to connect to a local H2O instance that is already running.
# If not found, start a local H2O instance from R with 5 gigabytes of memory.
h2o.init(max_mem_size = "5g")

# Try to connect to a local H2O instance that is already running.
# If not found, start a local H2O instance from R that uses 5 gigabytes of memory.
h2o.init(max_mem_size = "5g")

## End(Not run)
```

---

```
h2o.insertMissingValues
```

*Insert Missing Values into an H2OFrame*

---

**Description**

Randomly replaces a user-specified fraction of entries in an H2O dataset with missing values.

**Usage**

```
h2o.insertMissingValues(data, fraction = 0.1, seed = -1)
```

**Arguments**

data	An H2OFrame object representing the dataset.
fraction	A number between 0 and 1 indicating the fraction of entries to replace with missing.
seed	A random number used to select which entries to replace with missing values. Default of seed = -1 will automatically generate a seed in H2O.

**Value**

Returns an H2OFrame object.

**WARNING**

This will modify the original dataset. Unless this is intended, this function should only be called on a subset of the original.



**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
summary(iris_hf)

iris_miss <- h2o.insertMissingValues(iris_hf, fraction = 0.25)
head(iris_miss)
summary(iris_miss)

## End(Not run)
```

---

h2o.interaction

*Categorical Interaction Feature Creation in H2O*


---

**Description**

Creates a data frame in H2O with n-th order interaction features between categorical columns, as specified by the user.

**Usage**

```
h2o.interaction(
  data,
  destination_frame,
  factors,
  pairwise,
  max_factors,
  min_occurrence
)
```

**Arguments**

data	An H2OFrame object containing the categorical columns.
destination_frame	A string indicating the destination key. If empty, this will be auto-generated by H2O.
factors	Factor columns (either indices or column names).
pairwise	Whether to create pairwise interactions between factors (otherwise create one higher-order interaction). Only applicable if there are 3 or more factors.
max_factors	Max. number of factor levels in pair-wise interaction terms (if enforced, one extra catch-all factor will be made)
min_occurrence	Min. occurrence threshold for factor levels in pair-wise interaction terms

**Value**

Returns an H2OFrame object.

**Examples**

```

## Not run:
library(h2o)
h2o.init()

# Create some random data
my_frame <- h2o.createFrame(rows = 20, cols = 5,
                           seed = -12301283, randomize = TRUE, value = 0,
                           categorical_fraction = 0.8, factors = 10, real_range = 1,
                           integer_fraction = 0.2, integer_range = 10,
                           binary_fraction = 0, binary_ones_fraction = 0.5,
                           missing_fraction = 0.2,
                           response_factors = 1)

# Turn integer column into a categorical
my_frame[,5] <- as.factor(my_frame[,5])
head(my_frame, 20)

# Create pairwise interactions
pairwise <- h2o.interaction(my_frame,
                           factors = list(c(1, 2), c("C2", "C3", "C4")),
                           pairwise = TRUE, max_factors = 10, min_occurrence = 1)

head(pairwise, 20)
h2o.levels(pairwise, 2)

# Create 5-th order interaction
higherorder <- h2o.interaction(my_frame, factors = c(1, 2, 3, 4, 5),
                              pairwise = FALSE, max_factors = 10000, min_occurrence = 1)

head(higherorder, 20)

# Limit the number of factors of the "categoricalized" integer column
# to at most 3 factors, and only if they occur at least twice
head(my_frame[,5], 20)
trim_integer_levels <- h2o.interaction(my_frame, factors = "C5", pairwise = FALSE, max_factors = 3,
                                       min_occurrence = 2)

head(trim_integer_levels, 20)

# Put all together
my_frame <- h2o.cbind(my_frame, pairwise, higherorder, trim_integer_levels)
my_frame
head(my_frame, 20)
summary(my_frame)

## End(Not run)

```

---

h2o.isax

*iSAX*


---

**Description**

Compute the iSAX index for a DataFrame which is assumed to be numeric time series data

**Usage**

```
h2o.isax(x, num_words, max_cardinality, optimize_card = FALSE)
```

**Arguments**

x	an H2OFrame
num_words	Number of iSAX words for the timeseries. ie granularity along the time series
max_cardinality	Maximum cardinality of the iSAX word. Each word can have less than the max
optimize_card	An optimization flag that will find the max cardinality regardless of what is passed in for max_cardinality.

**Value**

An H2OFrame with the name of time series, string representation of iSAX word, followed by binary representation

**References**

[https://www.cs.ucr.edu/~eamonn/iSAX\\_2.0.pdf](https://www.cs.ucr.edu/~eamonn/iSAX_2.0.pdf)  
<https://www.cs.ucr.edu/~eamonn/SAX.pdf>

**Examples**

```
## Not run:
library(h2o)
h2o.init()
df <- h2o.createFrame(rows = 1, cols = 256, randomize = TRUE, value = 0,
                      real_range = 100, categorical_fraction = 0, factors = 0,
                      integer_fraction = 0, integer_range = 100, binary_fraction = 0,
                      binary_ones_fraction = 0, time_fraction = 0, string_fraction = 0,
                      missing_fraction = 0, has_response = FALSE, seed = 123)
df2 <- h2o.cumsum(df, axis = 1)
h2o.isax(df2, num_words = 10, max_cardinality = 10)

## End(Not run)
```

---

h2o.ischaracter	<i>Check if character</i>
-----------------	---------------------------

---

**Description**

Check if character

**Usage**

```
h2o.ischaracter(x)
```

**Arguments**

x	An H2OFrame object.
---	---------------------

**See Also**

[character](#) for the base R implementation, `is.character()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/iris/iris_wheader.csv"
iris <- h2o.importFile(f)
iris_char <- h2o.ascharacter(iris["class"])
h2o.ischaracter(iris_char)

## End(Not run)
```

---

h2o.isfactor	<i>Check if factor</i>
--------------	------------------------

---

**Description**

Check if factor

**Usage**

```
h2o.isfactor(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[factor](#) for the base R implementation, `is.factor()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
h2o.isfactor(cars["economy_20mpg"])

## End(Not run)
```

---

h2o.isnumeric	<i>Check if numeric</i>
---------------	-------------------------

---

**Description**

Check if numeric

**Usage**

```
h2o.isnumeric(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[numeric](#) for the base R implementation, `is.numeric()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/iris/iris_wheader.csv"
iris <- h2o.importFile(f)
h2o.isnumeric(iris["sepal_len"])

## End(Not run)
```

---

h2o.isolationForest	<i>Trains an Isolation Forest model</i>
---------------------	---

---

**Description**

Trains an Isolation Forest model

**Usage**

```
h2o.isolationForest(
  training_frame,
  x,
  model_id = NULL,
  score_each_iteration = FALSE,
  score_tree_interval = 0,
  ignore_const_cols = TRUE,
  ntrees = 50,
  max_depth = 8,
  min_rows = 1,
  max_runtime_secs = 0,
```

```

seed = -1,
build_tree_one_node = FALSE,
mtries = -1,
sample_size = 256,
sample_rate = -1,
col_sample_rate_change_per_level = 1,
col_sample_rate_per_tree = 1,
categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
  "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
stopping_rounds = 0,
stopping_metric = c("AUTO", "anomaly_score"),
stopping_tolerance = 0.01,
export_checkpoints_dir = NULL,
contamination = -1,
validation_frame = NULL,
validation_response_column = NULL
)

```

### Arguments

`training_frame` Id of the training data frame.

`x` A vector containing the character names of the predictors in the model.

`model_id` Destination id for this model; auto-generated if not specified.

`score_each_iteration` Logical. Whether to score during each iteration of model training. Defaults to FALSE.

`score_tree_interval` Score the model after every so many trees. Disabled if set to 0. Defaults to 0.

`ignore_const_cols` Logical. Ignore constant columns. Defaults to TRUE.

`ntrees` Number of trees. Defaults to 50.

`max_depth` Maximum tree depth (0 for unlimited). Defaults to 8.

`min_rows` Fewest allowed (weighted) observations in a leaf. Defaults to 1.

`max_runtime_secs` Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

`seed` Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).

`build_tree_one_node` Logical. Run on one node only; no network overhead but fewer cpus used. Suitable for small datasets. Defaults to FALSE.

`mtries` Number of variables randomly sampled as candidates at each split. If set to -1, defaults (number of predictors)/3. Defaults to -1.

`sample_size` Number of randomly sampled observations used to train each Isolation Forest tree. Only one of parameters `sample_size` and `sample_rate` should be defined. If `sample_rate` is defined, `sample_size` will be ignored. Defaults to 256.

`sample_rate` Rate of randomly sampled observations used to train each Isolation Forest tree. Needs to be in range from 0.0 to 1.0. If set to -1, `sample_rate` is disabled and `sample_size` will be used instead. Defaults to -1.

`col_sample_rate_change_per_level`  
Relative change of the column sampling rate for every level (must be  $> 0.0$  and  $\leq 2.0$ ) Defaults to 1.

`col_sample_rate_per_tree`  
Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.

`categorical_encoding`  
Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.

`stopping_rounds`  
Early stopping based on convergence of `stopping_metric`. Stop if simple moving average of length `k` of the `stopping_metric` does not improve for `k:=stopping_rounds` scoring events (0 to disable) Defaults to 0.

`stopping_metric`  
Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and `anomaly_score` for Isolation Forest). Note that `custom` and `custom_increasing` can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "anomaly\_score". Defaults to AUTO.

`stopping_tolerance`  
Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.01.

`export_checkpoints_dir`  
Automatically export generated models to this directory.

`contamination` Contamination ratio - the proportion of anomalies in the input dataset. If undefined (-1) the predict function will not mark observations as anomalies and only anomaly score will be returned. Defaults to -1 (undefined). Defaults to -1.

`validation_frame`  
Id of the validation data frame.

`validation_response_column`  
(experimental) Name of the response column in the validation frame. Response column should be binary and indicate not anomaly/anomaly.

## Examples

```
## Not run:
library(h2o)
h2o.init()

# Import the cars dataset
f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)

# Set the predictors
predictors <- c("displacement", "power", "weight", "acceleration", "year")

# Train the IF model
cars_if <- h2o.isolationForest(x = predictors, training_frame = cars,
                              seed = 1234, stopping_metric = "anomaly_score",
                              stopping_rounds = 3, stopping_tolerance = 0.1)

## End(Not run)
```

---

h2o.is_client	<i>Check Client Mode Connection</i>
---------------	-------------------------------------

---

**Description**

Check Client Mode Connection

**Usage**

```
h2o.is_client()
```

---

h2o.keyof	<i>Method on Keyed objects allowing to obtain their key.</i>
-----------	--

---

**Description**

Method on Keyed objects allowing to obtain their key.

**Usage**

```
h2o.keyof(object)

## S4 method for signature 'Keyed'
h2o.keyof(object)

## S4 method for signature 'H2OModel'
h2o.keyof(object)

## S4 method for signature 'H2OGrid'
h2o.keyof(object)

## S4 method for signature 'H2OFrame'
h2o.keyof(object)

## S4 method for signature 'H2OAutoML'
h2o.keyof(object)
```

**Arguments**

object	A Keyed object
--------	----------------

**Value**

the string key holding the persistent object.



---

h2o.kfold_column	<i>Produce a k-fold column vector.</i>
------------------	--

---

**Description**

Create a k-fold vector useful for H2O algorithms that take a `fold_assignments` argument.

**Usage**

```
h2o.kfold_column(data, nfolds, seed = -1)
```

**Arguments**

data	A dataframe against which to create the fold column.
nfolds	The number of desired folds.
seed	A random seed, -1 indicates that H2O will choose one.

**Value**

Returns an H2OFrame object with fold assignments.

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/iris/iris_wheader.csv"  
iris <- h2o.importFile(f)  
kfold <- h2o.kfold_column(iris, nfolds = 5, seed = 1234)  
  
## End(Not run)
```

---

h2o.killMinus3	<i>Dump the stack into the JVM's stdout.</i>
----------------	--

---

**Description**

A poor man's profiler, but effective.

**Usage**

```
h2o.killMinus3()
```

h2o.kmeans

*Performs k-means clustering on an H2O dataset***Description**

Performs k-means clustering on an H2O dataset

**Usage**

```
h2o.kmeans(
  training_frame,
  x,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
  fold_column = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  k = 1,
  estimate_k = FALSE,
  user_points = NULL,
  max_iterations = 10,
  standardize = TRUE,
  seed = -1,
  init = c("Random", "PlusPlus", "Furthest", "User"),
  max_runtime_secs = 0,
  categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
    "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
  export_checkpoints_dir = NULL,
  cluster_size_constraints = NULL
)
```

**Arguments**

`training_frame` Id of the training data frame.

`x` A vector containing the character names of the predictors in the model.

`model_id` Destination id for this model; auto-generated if not specified.

`validation_frame` Id of the validation data frame.

`nfolds` Number of folds for K-fold cross-validation (0 to disable or  $\geq 2$ ). Defaults to 0.

`keep_cross_validation_models` Logical. Whether to keep the cross-validation models. Defaults to TRUE.

`keep_cross_validation_predictions` Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.

keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
k	The max. number of clusters. If estimate_k is disabled, the model will find k centroids, otherwise it will find up to k centroids. Defaults to 1.
estimate_k	Logical. Whether to estimate the number of clusters (<=k) iteratively and deterministically. Defaults to FALSE.
user_points	This option allows you to specify a dataframe, where each row represents an initial cluster center. The user-specified points must have the same number of columns as the training observations. The number of rows must equal the number of clusters
max_iterations	Maximum training iterations (if estimate_k is enabled, then this is for each inner Lloyds iteration) Defaults to 10.
standardize	Logical. Standardize columns before computing distances Defaults to TRUE.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
init	Initialization mode Must be one of: "Random", "PlusPlus", "Furthest", "User". Defaults to Furthest.
max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
categorical_encoding	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.
export_checkpoints_dir	Automatically export generated models to this directory.
cluster_size_constraints	An array specifying the minimum number of points that should be in each cluster. The length of the constraints array has to be the same as the number of clusters.

**Value**

an object of class [H2OClusteringModel](#).

**See Also**

[h2o.cluster\\_sizes](#), [h2o.totss](#), [h2o.num\\_iterations](#), [h2o.betweenss](#), [h2o.tot\\_withinss](#), [h2o.withinss](#), [h2o.centersSTD](#), [h2o.centers](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.kmeans(training_frame = prostate, k = 10, x = c("AGE", "RACE", "VOL", "GLEASON"))

## End(Not run)
```

---

h2o.kolmogorov\_smirnov

*Kolmogorov-Smirnov metric for binomial models*

---

**Description**

Retrieves a Kolmogorov-Smirnov metric for given binomial model. The number returned is in range between 0 and 1. K-S metric represents the degree of separation between the positive (1) and negative (0) cumulative distribution functions. Detailed metrics per each group are to be found in the gains-lift table.

**Usage**

```
h2o.kolmogorov_smirnov(object)

## S4 method for signature 'H2OModelMetrics'
h2o.kolmogorov_smirnov(object)

## S4 method for signature 'H2OModel'
h2o.kolmogorov_smirnov(object)
```

**Arguments**

object            Either an [H2OModel](#) object or an [H2OModelMetrics](#) object.

**Details**

The [H2OModelMetrics](#) version of this function will only take [H2OBinomialMetrics](#) objects.

**Value**

Kolmogorov-Smirnov metric, a number between 0 and 1.

**See Also**

[h2o.gainsLift](#) to see detailed K-S metrics per group

**Examples**

```
## Not run:
library(h2o)
h2o.init()
data <- h2o.importFile(
  path = "https://s3.amazonaws.com/h2o-public-test-data/smalldata/airlines/allyears2k_headers.zip")
model <- h2o.gbm(x = c("Origin", "Distance"), y = "IsDepDelayed",
  training_frame = data, ntrees = 1)
h2o.kolmogorov_smirnov(model)

## End(Not run)
```

---

h2o.kurtosis	<i>Kurtosis of a column</i>
--------------	-----------------------------

---

**Description**

Obtain the kurtosis of a column of a parsed H2O data object.

**Usage**

```
h2o.kurtosis(x, ..., na.rm = TRUE)

kurtosis.H2OFrame(x, ..., na.rm = TRUE)
```

**Arguments**

x	An H2OFrame object.
...	Further arguments to be passed from or to other methods.
na.rm	A logical value indicating whether NA or missing values should be stripped before the computation.

**Value**

Returns a list containing the kurtosis for each column (NaN for non-numeric columns).

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.kurtosis(prostate$AGE)

## End(Not run)
```

---

```
h2o.learning_curve_plot
```

*Learning Curve Plot*

---

### Description

Create learning curve plot for an H2O Model. Learning curves show error metric dependence on learning progress, e.g., RMSE vs number of trees trained so far in GBM. There can be up to 4 curves showing Training, Validation, Training on CV Models, and Cross-validation error.

### Usage

```
h2o.learning_curve_plot(
  model,
  metric = c("AUTO", "auc", "aucpr", "mae", "rmse", "anomaly_score", "convergence",
            "custom", "custom_increasing", "deviance", "lift_top_group", "logloss",
            "misclassification", "negative_log_likelihood", "objective", "sumetaieta02"),
  cv_ribbon = NULL,
  cv_lines = NULL
)
```

### Arguments

<code>model</code>	an H2O model
<code>metric</code>	Metric to be used for the learning curve plot. These should mostly correspond with stopping metric.
<code>cv_ribbon</code>	if True, plot the CV mean as a and CV standard deviation as a ribbon around the mean, if NULL, it will attempt to automatically determine if this is suitable visualisation
<code>cv_lines</code>	if True, plot scoring history for individual CV models, if NULL, it will attempt to automatically determine if this is suitable visualisation

### Value

A ggplot2 object

### Examples

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
```

```

train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
gbm <- h2o.gbm(y = response,
               training_frame = train)

# Create the learning curve plot
learning_curve <- h2o.learning_curve_plot(gbm)
print(learning_curve)

## End(Not run)

```

---

h2o.levels	<i>Return the levels from the column requested column.</i>
------------	--

---

### Description

Return the levels from the column requested column.

### Usage

```
h2o.levels(x, i)
```

### Arguments

x	An H2OFrame object.
i	Optional, the index of the column whose domain is to be returned.

### See Also

[levels](#) for the base R method.

### Examples

```

## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
h2o.levels(iris_hf, 5) # returns "setosa" "versicolor" "virginica"

## End(Not run)

```

---

h2o.listTimezones	<i>List all of the Time Zones Acceptable by the H2O cluster.</i>
-------------------	--

---

### Description

List all of the Time Zones Acceptable by the H2O cluster.

### Usage

```
h2o.listTimezones()
```

h2o.list\_all\_extensions

*List all H2O registered extensions*

---

**Description**

List all H2O registered extensions

**Usage**

h2o.list\_all\_extensions()

---

h2o.list\_api\_extensions

*List registered API extensions*

---

**Description**

List registered API extensions

**Usage**

h2o.list\_api\_extensions()

---

h2o.list\_core\_extensions

*List registered core extensions*

---

**Description**

List registered core extensions

**Usage**

h2o.list\_core\_extensions()

---

h2o.list\_jobs

*Return list of jobs performed by the H2O cluster*

---

**Description**

Return list of jobs performed by the H2O cluster

**Usage**

h2o.list\_jobs()



---

h2o.list_models	<i>Get an list of all model ids present in the cluster</i>
-----------------	--

---

**Description**

Get an list of all model ids present in the cluster

**Usage**

```
h2o.list_models()
```

**Value**

Returns a vector of model ids.

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
iris_hf <- as.h2o(iris)  
model_id <- h2o.gbm(x = 1:4, y = 5, training_frame = iris_hf)@model_id  
model_id_list <- h2o.list_models()  
  
## End(Not run)
```

---

h2o.loadGrid	<i>Loads previously saved grid with all it's models from the same folder</i>
--------------	--

---

**Description**

Returns a reference to the loaded Grid.

**Usage**

```
h2o.loadGrid(grid_path, load_params_references = FALSE)
```

**Arguments**

grid_path	A character string containing the path to the file with the grid saved.
load_params_references	A logical which if true will attempt to reload saved objects referenced by grid parameters (e.g. training frame, calibration frame), will fail if grid was saved without referenced objects.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris <- as.h2o(iris)

ntrees_opts = c(1, 5)
learn_rate_opts = c(0.1, 0.01)
size_of_hyper_space = length(ntrees_opts) * length(learn_rate_opts)

hyper_parameters = list(ntrees = ntrees_opts, learn_rate = learn_rate_opts)
# Tempdir is chosen arbitrarily. May be any valid folder on an H2O-supported filesystem.
baseline_grid <- h2o.grid("gbm", grid_id="gbm_grid_test", x=1:4, y=5, training_frame=iris,
hyper_params = hyper_parameters, export_checkpoints_dir = tempdir())
# Remove everything from the cluster or restart it
h2o.removeAll()
grid <- h2o.loadGrid(paste0(tempdir(),"/",baseline_grid@grid_id))

## End(Not run)
```

---

h2o.loadModel

*Load H2O Model from HDFS or Local Disk*


---

**Description**

Load a saved H2O model from disk. (Note that ensemble binary models can now be loaded using this method.)

**Usage**

```
h2o.loadModel(path)
```

**Arguments**

path                    The path of the H2O Model to be imported.

**Value**

Returns a [H2OModel](#) object of the class corresponding to the type of model loaded.

**See Also**

[h2o.saveModel](#), [H2OModel](#)

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
# prostate = h2o.importFile(path = prostate_path)
# prostate_glm = h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
```

```
# training_frame = prostate, family = "binomial", alpha = 0.5)
# glmmodel_path = h2o.saveModel(prostate_glm, dir = "/Users/UserName/Desktop")
# glmmodel_load = h2o.loadModel(glmmodel_path)

## End(Not run)
```

---

h2o.load_frame	<i>Load frame previously stored in H2O's native format.</i>
----------------	---

---

### Description

Load frame previously stored in H2O's native format.

### Usage

```
h2o.load_frame(frame_id, dir, force = TRUE)
```

### Arguments

frame_id	the frame ID of the original frame
dir	a filesystem location where to look for frame data
force	logical. overwrite an already existing frame (defaults to true)

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
h2o.save_frame(prostate, "/tmp/prostate")
prostate.key <- h2o.getId(prostate)
h2o.rm(prostate)
prostate <- h2o.load_frame(prostate.key, "/tmp/prostate")

## End(Not run)
```

---

h2o.log	<i>Compute the logarithm of x</i>
---------	-----------------------------------

---

### Description

Compute the logarithm of x

### Usage

```
h2o.log(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Log](#) for the base R implementation, `log`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.log(frame)

## End(Not run)
```

---

h2o.log10	<i>Compute the log10 of x</i>
-----------	-------------------------------

---

**Description**

Compute the log10 of x

**Usage**

```
h2o.log10(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Log](#) for the base R implementation, `log10()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.log10(frame)

## End(Not run)
```

---

h2o.log1p	<i>Compute the log1p of x</i>
-----------	-------------------------------

---

**Description**

Compute the log1p of x

**Usage**

```
h2o.log1p(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Log](#) for the base R implementation, `log1p()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                        categorical_fraction = 0.0,
                        missing_fraction = 0.7,
                        seed = 123)

h2o.log1p(frame)

## End(Not run)
```

---

h2o.log2	<i>Compute the log2 of x</i>
----------	------------------------------

---

**Description**

Compute the log2 of x

**Usage**

```
h2o.log2(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Log](#) for the base R implementation, `log2()`

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.log2(frame)

## End(Not run)
```

---

h2o.logAndEcho	<i>Log a message on the server-side logs</i>
----------------	--

---

**Description**

This is helpful when running several pieces of work one after the other on a single H2O cluster and you want to make a notation in the H2O server side log where one piece of work ends and the next piece of work begins.

**Usage**

```
h2o.logAndEcho(message)
```

**Arguments**

message	A character string with the message to write to the log.
---------	--

**Details**

h2o.logAndEcho sends a message to H2O for logging. Generally used for debugging purposes.

---

h2o.logloss	<i>Retrieve the Log Loss Value</i>
-------------	------------------------------------

---

**Description**

Retrieves the log loss output for a [H2OBinomialMetrics](#) or [H2OMultinomialMetrics](#) object. If "train", "valid", and "xval" parameters are FALSE (default), then the training Log Loss value is returned. If more than one parameter is set to TRUE, then a named vector of Log Losses are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.logloss(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	a <a href="#">H2OModelMetrics</a> object of the correct type.
train	Retrieve the training Log Loss
valid	Retrieve the validation Log Loss
xval	Retrieve the cross-validation Log Loss

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_splits <- h2o.splitFrame(data = cars, ratios = .8, seed = 1234)
train <- cars_splits[[1]]
valid <- cars_splits[[2]]
car_drf <- h2o.randomForest(x = predictors,
                           y = response,
                           training_frame = train,
                           validation_frame = valid)
h2o.logloss(car_drf, train = TRUE, valid = TRUE)

## End(Not run)
```

h2o.ls

*List Keys on an H2O Cluster***Description**

Accesses a list of object keys in the running instance of H2O.

**Usage**

```
h2o.ls()
```

**Value**

Returns a list of hex keys in the current H2O instance.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.ls()

## End(Not run)
```

---

h2o.lstrip	<i>Strip set from left</i>
------------	----------------------------

---

### Description

Return a copy of the target column with leading characters removed. The set argument is a string specifying the set of characters to be removed. If omitted, the set argument defaults to removing whitespace.

### Usage

```
h2o.lstrip(x, set = " ")
```

### Arguments

x	The column whose strings should be lstrip-ed.
set	string of characters to be removed

### Examples

```
## Not run:
library(h2o)
h2o.init()
string_to_lstrip <- as.h2o("1234567890")
lstrip_string <- h2o.lstrip(string_to_lstrip, "123") #Remove "123"

## End(Not run)
```

---

h2o.mae	<i>Retrieve the Mean Absolute Error Value</i>
---------	---

---

### Description

Retrieves the mean absolute error (MAE) value from an H2O model. If "train", "valid", and "xval" parameters are FALSE (default), then the training MAE value is returned. If more than one parameter is set to TRUE, then a named vector of MAEs are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.mae(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

object	An <a href="#">H2OModel</a> object.
train	Retrieve the training MAE
valid	Retrieve the validation set MAE if a validation set was passed in during model build time.
xval	Retrieve the cross-validation MAE



**Examples**

```
## Not run:
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.deeplearning(x = 2:5, y = 1, training_frame = fr)

h2o.mae(m)

## End(Not run)
```

---

h2o.makeGLMModel	<i>Set betas of an existing H2O GLM Model</i>
------------------	---

---

**Description**

This function allows setting betas of an existing glm model.

**Usage**

```
h2o.makeGLMModel(model, beta)
```

**Arguments**

model	an <a href="#">H2OModel</a> corresponding from a h2o.glm call.
beta	a new set of betas (a named vector)

---

h2o.make_metrics	<i>Create Model Metrics from predicted and actual values in H2O</i>
------------------	---

---

**Description**

Given predicted values (target for regression, class-1 probabilities or binomial or per-class probabilities for multinomial), compute a model metrics object

**Usage**

```
h2o.make_metrics(
  predicted,
  actuals,
  domain = NULL,
  distribution = NULL,
  weights = NULL,
  auc_type = "NONE"
)
```

**Arguments**

predicted	An H2OFrame containing predictions
actuals	An H2OFrame containing actual values
domain	Vector with response factors for classification.
distribution	Distribution for regression.
weights	(optional) An H2OFrame containing observation weights.
auc_type	(optional) For multinomial classification you have to specify which type of aggregated AUC/AUCPR will be used to calculate this metric.

**Value**

Returns an object of the [H2OModelMetrics](#) subclass.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
pred <- h2o.predict(prostate_gbm, prostate)[, 3] ## class-1 probability
h2o.make_metrics(pred, prostate$CAPSULE)

## End(Not run)
```

---

h2o.match

*Value Matching in H2O*


---

**Description**

match and %in% return values similar to the base R generic functions.

**Usage**

```
h2o.match(x, table, nomatch = 0, incomparables = NULL)

match.H2OFrame(x, table, nomatch = 0, incomparables = NULL)

x %in% table
```

**Arguments**

x	a categorical vector from an H2OFrame object with values to be matched.
table	an R object to match x against.
nomatch	the value to be returned in the case when no match is found.
incomparables	a vector of values that cannot be matched. Any value in x matching a value in this vector is assigned the nomatch value.

**Value**

Returns a vector of the positions of (first) matches of its first argument in its second

**See Also**

[match](#) for base R implementation.

**Examples**

```
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
h2o.match(iris_hf[, 5], c("setosa", "versicolor"))

## End(Not run)
```

---

h2o.max

*Returns the maxima of the input values.*

---

**Description**

Returns the maxima of the input values.

**Usage**

```
h2o.max(x, na.rm = FALSE)
```

**Arguments**

x	An H2OFrame object.
na.rm	logical, indicating whether missing values should be removed.

**See Also**

[Extremes](#) for the base R implementation, `max()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.max(iris["petal_len"], na.rm = TRUE)

## End(Not run)
```

---

h2o.mean	<i>Compute the frame's mean by-column (or by-row).</i>
----------	--

---

### Description

Compute the frame's mean by-column (or by-row).

### Usage

```
h2o.mean(x, na.rm = FALSE, axis = 0, return_frame = FALSE, ...)
```

```
## S3 method for class 'H2OFrame'
```

```
mean(x, na.rm = FALSE, axis = 0, return_frame = FALSE, ...)
```

### Arguments

x	An H2OFrame object.
na.rm	logical. Indicate whether missing values should be removed.
axis	integer. Indicate whether to calculate the mean down a column (0) or across a row (1). NOTE: This is only applied when return_frame is set to TRUE. Otherwise, this parameter is ignored.
return_frame	logical. Indicate whether to return an H2O frame or a list. Default is FALSE (returns a list).
...	Further arguments to be passed from or to other methods.

### Value

Returns a list containing the mean for each column (NaN for non-numeric columns) if return\_frame is set to FALSE. If return\_frame is set to TRUE, then it will return an H2O frame with means per column or row (depends on axis argument).

### See Also

[Round](#) for base R implementation, [mean\(\)](#) and [colSums](#) for the base R implementation, [colMeans\(\)](#).

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
# Default behavior. Will return list of means per column.
h2o.mean(prostate$AGE)
# return_frame set to TRUE. This will return an H2O Frame
# with mean per row or column (depends on axis argument)
h2o.mean(prostate, na.rm = TRUE, axis = 1, return_frame = TRUE)

## End(Not run)
```

---

`h2o.mean_per_class_error`*Retrieve the mean per class error*

---

### Description

Retrieves the mean per class error from an [H2OBinomialMetrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training mean per class error value is returned. If more than one parameter is set to TRUE, then a named vector of mean per class errors are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.mean_per_class_error(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

object	An <a href="#">H2OBinomialMetrics</a> object.
train	Retrieve the training mean per class error
valid	Retrieve the validation mean per class error
xval	Retrieve the cross-validation mean per class error

### See Also

[h2o.mse](#) for MSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating H2OModelMetrics objects.

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.mean_per_class_error(perf)
h2o.mean_per_class_error(model, train=TRUE)

## End(Not run)
```

---

 h2o.mean\_residual\_deviance

*Retrieve the Mean Residual Deviance value*


---

### Description

Retrieves the Mean Residual Deviance value from an H2O model. If "train", "valid", and "xval" parameters are FALSE (default), then the training Mean Residual Deviance value is returned. If more than one parameter is set to TRUE, then a named vector of Mean Residual Deviances are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.mean_residual_deviance(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

object	An <a href="#">H2OModel</a> object.
train	Retrieve the training Mean Residual Deviance
valid	Retrieve the validation Mean Residual Deviance
xval	Retrieve the cross-validation Mean Residual Deviance

### Examples

```
## Not run:
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.deeplearning(x = 2:5, y = 1, training_frame = fr)

h2o.mean_residual_deviance(m)

## End(Not run)
```

---

 h2o.median

*H2O Median*


---

### Description

Compute the median of an H2OFrame.

### Usage

```
h2o.median(x, na.rm = TRUE)

## S3 method for class 'H2OFrame'
median(x, na.rm = TRUE)
```

**Arguments**

x                    An H2OFrame object.  
na.rm                a logical, indicating whether na's are omitted.

**Value**

Returns a list containing the median for each column (NaN for non-numeric columns)

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.median(prostate)

## End(Not run)
```

---

h2o.melt	<i>Converts a frame to key-value representation while optionally skipping NA values. Inverse operation to h2o.pivot.</i>
----------	--

---

**Description**

Pivot the frame designated by the three columns: index, column, and value. Index and column should be of type enum, int, or time. For cases of multiple indexes for a column label, the aggregation method is to pick the first occurrence in the data frame

**Usage**

```
h2o.melt(
  x,
  id_vars,
  value_vars = NULL,
  var_name = "variable",
  value_name = "value",
  skipna = FALSE
)
```

**Arguments**

x                    an H2OFrame  
id\_vars              the columns used as identifiers  
value\_vars           what columns will be converted to key-value pairs (optional, if not specified complement to id\_vars will be used)  
var\_name             name of the key-column (default: "variable")  
value\_name           name of the value-column (default: "value")  
skipna                if enabled, do not include NAs in the result (default: FALSE)

**Value**

an unpivoted H2OFrame

---

h2o.merge

*Merge Two H2O Data Frames*

---

**Description**

Merges two H2OFrame objects with the same arguments and meanings as merge() in base R. However, we do not support all=TRUE, all.x=TRUE and all.y=TRUE. The default method is auto and it will default to the radix method. The radix method will return the correct merge result regardless of duplicated rows in the right frame. In addition, the radix method can perform merge even if you have string columns in your frames. If there are duplicated rows in your right frame, they will not be included if you use the hash method. The hash method cannot perform merge if you have string columns in your left frame. Hence, we consider the radix method superior to the hash method and is the default method to use.

**Usage**

```
h2o.merge(
  x,
  y,
  by = intersect(names(x), names(y)),
  by.x = by,
  by.y = by,
  all = FALSE,
  all.x = all,
  all.y = all,
  method = "auto"
)
```

**Arguments**

x, y	H2OFrame objects
by	columns used for merging by default the common names
by.x	x columns used for merging by name or number
by.y	y columns used for merging by name or number
all	TRUE includes all rows in x and all rows in y even if there is no match to the other
all.x	If all.x is true, all rows in the x will be included, even if there is no matching row in y, and vice-versa for all.y.
all.y	see all.x
method	auto(default), radix, hash



**Examples**

```
## Not run:
library(h2o)
h2o.init()
left <- data.frame(fruit = c('apple', 'orange', 'banana', 'lemon', 'strawberry', 'blueberry'),
  color <- c('red', 'orange', 'yellow', 'yellow', 'red', 'blue'))
right <- data.frame(fruit = c('apple', 'orange', 'banana', 'lemon', 'strawberry', 'watermelon'),
  citrus <- c(FALSE, TRUE, FALSE, TRUE, FALSE, FALSE))
left_hf <- as.h2o(left)
right_hf <- as.h2o(right)
merged <- h2o.merge(left_hf, right_hf, all.x = TRUE)

## End(Not run)
```

---

h2o.metric

*H2O Model Metric Accessor Functions*

---

**Description**

A series of functions that retrieve model metric details.

**Usage**

```
h2o.metric(object, thresholds, metric, transform = NULL)
```

```
h2o.F0point5(object, thresholds)
```

```
h2o.F1(object, thresholds)
```

```
h2o.F2(object, thresholds)
```

```
h2o.accuracy(object, thresholds)
```

```
h2o.error(object, thresholds)
```

```
h2o.maxPerClassError(object, thresholds)
```

```
h2o.mean_per_class_accuracy(object, thresholds)
```

```
h2o.mcc(object, thresholds)
```

```
h2o.precision(object, thresholds)
```

```
h2o.tpr(object, thresholds)
```

```
h2o.fpr(object, thresholds)
```

```
h2o.fnr(object, thresholds)
```

```
h2o.tnr(object, thresholds)
```

```
h2o.recall(object, thresholds)
```

```
h2o.sensitivity(object, thresholds)
```

```
h2o.fallout(object, thresholds)
```

```
h2o.missrate(object, thresholds)
```

```
h2o.specificity(object, thresholds)
```

### Arguments

object	An <a href="#">H2OModelMetrics</a> object of the correct type.
thresholds	(Optional) A value or a list of values between 0.0 and 1.0. If not set, then all thresholds will be returned. If "max", then the threshold maximizing the metric will be used.
metric	(Optional) the metric to retrieve. If not set, then all metrics will be returned.
transform	(Optional) a list describing a transformer for the given metric, if any. e.g. transform=list(op=foo_fn, name="foo") will rename the given metric to "foo" and apply function foo_fn to the metric values.

### Details

Many of these functions have an optional thresholds parameter. Currently only increments of 0.1 are allowed. If not specified, the functions will return all possible values. Otherwise, the function will return the value for the indicated threshold.

Currently, these functions are only supported by [H2OBinomialMetrics](#) objects.

### Value

Returns either a single value, or a list of values.

### See Also

[h2o.auc](#) for AUC, [h2o.giniCoef](#) for the GINI coefficient, and [h2o.mse](#) for MSE. See [h2o.performance](#) for creating [H2OModelMetrics](#) objects.

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate$CAPSULE <- as.factor(prostate$CAPSULE)
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.F1(perf)

## End(Not run)
```

---

h2o.min	<i>Returns the minima of the input values.</i>
---------	--

---

**Description**

Returns the minima of the input values.

**Usage**

```
h2o.min(x, na.rm = FALSE)
```

**Arguments**

x	An H2OFrame object.
na.rm	logical. indicating whether missing values should be removed.

**See Also**

[Extremes](#) for the base R implementation, `min()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.min(iris["sepal_len"], na.rm = TRUE)

## End(Not run)
```

---

h2o.mktime	<i>Compute msec since the Unix Epoch</i>
------------	--

---

**Description**

Compute msec since the Unix Epoch

**Usage**

```
h2o.mktime(
  year = 1970,
  month = 0,
  day = 0,
  hour = 0,
  minute = 0,
  second = 0,
  msec = 0
)
```

**Arguments**

year	Defaults to 1970
month	zero based (months are 0 to 11)
day	zero based (days are 0 to 30)
hour	hour
minute	minute
second	second
msec	msec

**Examples**

```
## Not run:
library(h2o)
h2o.init()

x = as.h2o(c(2018, 3, 2, 6, 32, 0, 0))
h2o.mkttime(x)

## End(Not run)
```

---

```
h2o.model_correlation_heatmap
```

*Model Prediction Correlation Heatmap*

---

**Description**

This plot shows the correlation between the predictions of the models. For classification, frequency of identical predictions is used. By default, models are ordered by their similarity (as computed by hierarchical clustering).

**Usage**

```
h2o.model_correlation_heatmap(
  object,
  newdata,
  top_n = 20,
  cluster_models = TRUE,
  triangular = TRUE
)
```

**Arguments**

object	An H2OAutoML object or list of H2O models.
newdata	An H2O Frame. Predictions from the models will be generated using this frame, so this should be a holdout set.
top_n	Integer specifying the number models shown in the heatmap (used only with an AutoML object, and based on the leaderboard ranking. Defaults to 20.
cluster_models	Logical. Order models based on their similarity. Defaults to TRUE.
triangular	Print just the lower triangular part of correlation matrix. Defaults to TRUE.

**Value**

A ggplot2 object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
aml <- h2o.automl(y = response,
                 training_frame = train,
                 max_models = 10,
                 seed = 1)

# Create the model correlation heatmap
model_correlation_heatmap <- h2o.model_correlation_heatmap(aml, test)
print(model_correlation_heatmap)

## End(Not run)
```

---

h2o.mojo\_predict\_csv *H2O Prediction from R without having H2O running*

---

**Description**

Provides the method `h2o.mojo_predict_csv` with which you can predict a MOJO model from R.

**Usage**

```
h2o.mojo_predict_csv(
  input_csv_path,
  mojo_zip_path,
  output_csv_path = NULL,
  genmodel_jar_path = NULL,
  classpath = NULL,
  java_options = NULL,
  verbose = F,
  setInvNumNA = F
)
```

**Arguments**

input_csv_path	Path to input CSV file.
mojo_zip_path	Path to MOJO zip downloaded from H2O.
output_csv_path	Optional, path to the output CSV file with computed predictions. If NULL (default), then predictions will be saved as prediction.csv in the same folder as the MOJO zip.
genmodel_jar_path	Optional, path to genmodel jar file. If NULL (default) then the h2o-genmodel.jar in the same folder as the MOJO zip will be used.
classpath	Optional, specifies custom user defined classpath which will be used when scoring. If NULL (default) then the default classpath for this MOJO model will be used.
java_options	Optional, custom user defined options for Java. By default '-Xmx4g -XX:ReservedCodeCacheSize=2' is used.
verbose	Optional, if TRUE, then additional debug information will be printed. FALSE by default.
setInvNumNA	Optional, if TRUE, then then for an string that cannot be parsed into a number an N/A value will be produced, if false the command will fail. FALSE by default.

**Value**

Returns a data.frame containing computed predictions

---

h2o.mojo\_predict\_df     *H2O Prediction from R without having H2O running*

---

**Description**

Provides the method h2o.mojo\_predict\_df with which you can predict a MOJO model from R.

**Usage**

```
h2o.mojo_predict_df(
  frame,
  mojo_zip_path,
  genmodel_jar_path = NULL,
  classpath = NULL,
  java_options = NULL,
  verbose = F,
  setInvNumNA = F
)
```

**Arguments**

frame	data.frame to score.
mojo_zip_path	Path to MOJO zip downloaded from H2O.

genmodel_jar_path	Optional, path to genmodel jar file. If NULL (default) then the h2o-genmodel.jar in the same folder as the MOJO zip will be used.
classpath	Optional, specifies custom user defined classpath which will be used when scoring. If NULL (default) then the default classpath for this MOJO model will be used.
java_options	Optional, custom user defined options for Java. By default '-Xmx4g -XX:ReservedCodeCacheSize=2' is used.
verbose	Optional, if TRUE, then additional debug information will be printed. FALSE by default.
setInvNumNA	Optional, if TRUE, then then for an string that cannot be parsed into a number an N/A value will be produced, if false the command will fail. FALSE by default.

**Value**

Returns a data.frame containing computed predictions

---

h2o.month

*Convert Milliseconds to Months in H2O Datasets*

---

**Description**

Converts the entries of an H2OFrame object from milliseconds to months (on a 1 to 12 scale).

**Usage**

```
h2o.month(x)

month(x)

## S3 method for class 'H2OFrame'
month(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

An H2OFrame object containing the entries of x converted to months of the year.

**See Also**

[h2o.year](#)

h2o.mse

*Retrieves Mean Squared Error Value***Description**

Retrieves the mean squared error value from an [H2OModelMetrics](#) object. If "train", "valid", and "xval" parameters are FALSE (default), then the training MSE value is returned. If more than one parameter is set to TRUE, then a named vector of MSEs are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.mse(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModelMetrics</a> object of the correct type.
train	Retrieve the training MSE
valid	Retrieve the validation MSE
xval	Retrieve the cross-validation MSE

**Details**

This function only supports [H2OBinomialMetrics](#), [H2OMultinomialMetrics](#), and [H2ORegressionMetrics](#) objects.

**See Also**

[h2o.auc](#) for AUC, [h2o.mse](#) for MSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating [H2OModelMetrics](#) objects.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.mse(perf)

## End(Not run)
```



---

`h2o.multinomial_aucpr_table`

*Retrieve the all PR AUC values in a table (One to Rest, One to One, macro and weighted average) for multinomial classification.*

---

### Description

Retrieves the PR AUC table from an [H2OMultinomialMetrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training PR AUC table is returned. If more than one parameter is set to TRUE, then a named vector of PR AUC tables are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.multinomial_aucpr_table(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

<code>object</code>	An <a href="#">H2OMultinomialMetrics</a> object.
<code>train</code>	Retrieve the training PR AUC table
<code>valid</code>	Retrieve the validation PR AUC table
<code>xval</code>	Retrieve the cross-validation PR AUC table

### See Also

[h2o.giniCoef](#) for the Gini coefficient, [h2o.mse](#) for MSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating H2OModelMetrics objects.

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.multinomial_aucpr_table(perf)

## End(Not run)
```

---

h2o.multinomial\_auc\_table

*Retrieve the all AUC values in a table (One to Rest, One to One, macro and weighted average) for multinomial classification.*

---

### Description

Retrieves the AUC table from an [H2OMultinomialMetrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training AUC table is returned. If more than one parameter is set to TRUE, then a named vector of AUC tables are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.multinomial_auc_table(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

object	An <a href="#">H2OMultinomialMetrics</a> object.
train	Retrieve the training AUC table
valid	Retrieve the validation AUC table
xval	Retrieve the cross-validation AUC table

### See Also

[h2o.giniCoef](#) for the Gini coefficient, [h2o.mse](#) for MSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating H2OModelMetrics objects.

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.multinomial_auc_table(perf)

## End(Not run)
```

---

h2o.nacnt	<i>Count of NAs per column</i>
-----------	--------------------------------

---

**Description**

Gives the count of NAs per column.

**Usage**

```
h2o.nacnt(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

Returns a list containing the count of NAs per column

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
h2o.nacnt(iris_hf) # should return all 0s
h2o.insertMissingValues(iris_hf)
h2o.nacnt(iris_hf)

## End(Not run)
```

---

h2o.naiveBayes	<i>Compute naive Bayes probabilities on an H2O dataset.</i>
----------------	---

---

**Description**

The naive Bayes classifier assumes independence between predictor variables conditional on the response, and a Gaussian distribution of numeric predictors with mean and standard deviation computed from the training dataset. When building a naive Bayes classifier, every row in the training dataset that contains at least one NA will be skipped completely. If the test dataset has missing values, then those predictors are omitted in the probability calculation during prediction.

**Usage**

```

h2o.naiveBayes(
  x,
  y,
  training_frame,
  model_id = NULL,
  nfolds = 0,
  seed = -1,
  fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
  fold_column = NULL,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  validation_frame = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  balance_classes = FALSE,
  class_sampling_factors = NULL,
  max_after_balance_size = 5,
  laplace = 0,
  threshold = 0.001,
  min_sdev = 0.001,
  eps = 0,
  eps_sdev = 0,
  min_prob = 0.001,
  eps_prob = 0,
  compute_metrics = TRUE,
  max_runtime_secs = 0,
  export_checkpoints_dir = NULL,
  gainslift_bins = -1,
  auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
    "WEIGHTED_OVO")
)

```

**Arguments**

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
nfolds	Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).

fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.
keep_cross_validation_models	Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
validation_frame	Id of the validation data frame.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
balance_classes	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
class_sampling_factors	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires balance_classes.
max_after_balance_size	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires balance_classes. Defaults to 5.0.
laplace	Laplace smoothing parameter Defaults to 0.
threshold	This argument is deprecated, use 'min_sdev' instead. The minimum standard deviation to use for observations without enough data. Must be at least 1e-10.
min_sdev	The minimum standard deviation to use for observations without enough data. Must be at least 1e-10.
eps	This argument is deprecated, use 'eps_sdev' instead. A threshold cutoff to deal with numeric instability, must be positive.
eps_sdev	A threshold cutoff to deal with numeric instability, must be positive.
min_prob	Min. probability to use for observations with not enough data.
eps_prob	Cutoff below which probability is replaced with min_prob.
compute_metrics	Logical. Compute metrics on training data Defaults to TRUE.
max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
export_checkpoints_dir	Automatically export generated models to this directory.

`gainslift_bins` Gains/Lift table number of bins. 0 means disabled.. Default value -1 means automatic binning. Defaults to -1.

`auc_type` Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO\_OVR", "WEIGHTED\_OVR", "MACRO\_OVO", "WEIGHTED\_OVO". Defaults to AUTO.

### Value

an object of class `H2OBinomialModel` if the response has two categorical levels, and `H2OMultinomialModel` otherwise.

### Examples

```
## Not run:
h2o.init()
votes_path <- system.file("extdata", "housevotes.csv", package = "h2o")
votes <- h2o.uploadFile(path = votes_path, header = TRUE)
h2o.naiveBayes(x = 2:17, y = 1, training_frame = votes, laplace = 3)

## End(Not run)
```

---

`h2o.names`

*Column names of an H2OFrame*

---

### Description

Column names of an H2OFrame

### Usage

```
h2o.names(x)
```

### Arguments

`x` An H2OFrame object.

### See Also

[names](#) for the base R implementation.

### Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smалldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.names(iris)

## End(Not run)
```

---

h2o.na_omit	<i>Remove Rows With NAs</i>
-------------	-----------------------------

---

**Description**

Remove Rows With NAs

**Usage**

```
h2o.na_omit(object, ...)
```

**Arguments**

object	H2OFrame object
...	Ignored

**Value**

Returns an H2OFrame object containing non-NA rows.

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
frame <- h2o.createFrame(rows = 6, cols = 2,  
                          categorical_fraction = 0.0,  
                          missing_fraction = 0.7,  
                          seed = 123)  
  
h2o.na_omit(frame)  
  
## End(Not run)
```

---

h2o.nchar	<i>String length</i>
-----------	----------------------

---

**Description**

String length

**Usage**

```
h2o.nchar(x)
```

**Arguments**

x	The column whose string lengths will be returned.
---	---

**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_nchar <- as.h2o("r tutorial")
nchar_string <- h2o.nchar(string_to_nchar)

## End(Not run)
```

---

h2o.ncol

*Return the number of columns present in x.*


---

**Description**

Return the number of columns present in x.

**Usage**

```
h2o.ncol(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[nrow](#) for the base R implementation, `ncol()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.ncol(iris)

## End(Not run)
```

---

h2o.networkTest

*View Network Traffic Speed*


---

**Description**

View speed with various file sizes.

**Usage**

```
h2o.networkTest()
```



**Value**

Returns a table listing the network speed for 1B, 10KB, and 10MB.

---

h2o.nlevels	<i>Get the number of factor levels for this frame.</i>
-------------	--

---

**Description**

Get the number of factor levels for this frame.

**Usage**

```
h2o.nlevels(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[nlevels](#) for the base R method.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
h2o.nlevels(cars)

## End(Not run)
```

---

h2o.no_progress	<i>Disable Progress Bar</i>
-----------------	-----------------------------

---

**Description**

Disable Progress Bar

**Usage**

```
h2o.no_progress()
```

**Examples**

```
## Not run:
library(h2o)
h2o.init()
h2o.no_progress()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smалldata/iris/iris_wheader.csv"
iris <- h2o.importFile(f)
iris["class"] <- as.factor(iris["class"])
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
splits <- h2o.splitFrame(iris, ratios = 0.8, seed = 1234)
train <- splits[[1]]
valid <- splits[[2]]

iris_km <- h2o.kmeans(x = predictors,
                     training_frame = train,
                     validation_frame = valid,
                     k = 10, estimate_k = TRUE,
                     standardize = FALSE, seed = 1234)

## End(Not run)
```

---

h2o.nrow

*Return the number of rows present in x.*


---

**Description**

Return the number of rows present in x.

**Usage**

```
h2o.nrow(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[nrow](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smалldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
h2o.nrow(cars)

## End(Not run)
```

---

h2o.null_deviance	<i>Retrieve the null deviance</i>
-------------------	-----------------------------------

---

### Description

If "train", "valid", and "xval" parameters are FALSE (default), then the training null deviance value is returned. If more than one parameter is set to TRUE, then a named vector of null deviances are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.null_deviance(object, train = FALSE, valid = FALSE, xval = FALSE)
```

### Arguments

object	An <a href="#">H2OModel</a> or <a href="#">H2OModelMetrics</a>
train	Retrieve the training null deviance
valid	Retrieve the validation null deviance
xval	Retrieve the cross-validation null deviance

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
  training_frame = prostate, family = "binomial", nfolds = 0,
  alpha = 0.5, lambda_search = FALSE)
h2o.null_deviance(prostate_glm, train = TRUE)

## End(Not run)
```

---

h2o.null_dof	<i>Retrieve the null degrees of freedom</i>
--------------	---

---

### Description

If "train", "valid", and "xval" parameters are FALSE (default), then the training null degrees of freedom value is returned. If more than one parameter is set to TRUE, then a named vector of null degrees of freedom are returned, where the names are "train", "valid" or "xval".

### Usage

```
h2o.null_dof(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> or <a href="#">H2OModelMetrics</a>
train	Retrieve the training null degrees of freedom
valid	Retrieve the validation null degrees of freedom
xval	Retrieve the cross-validation null degrees of freedom

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
  training_frame = prostate, family = "binomial", nfolds = 0,
  alpha = 0.5, lambda_search = FALSE)
h2o.null_dof(prostate_glm, train = TRUE)

## End(Not run)
```

---

h2o.num_iterations	<i>Retrieve the number of iterations.</i>
--------------------	---

---

**Description**

Retrieve the number of iterations.

**Usage**

```
h2o.num_iterations(object)
```

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
--------	---

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
  training_frame = prostate, family = "binomial",
  nfolds = 0, alpha = 0.5, lambda_search = FALSE)
h2o.num_iterations(prostate_glm)

## End(Not run)
```

---

 h2o.num\_valid\_substrings

*Count of substrings >= 2 chars that are contained in file*


---

### Description

Find the count of all possible substrings >= 2 chars that are contained in the specified line-separated text file.

### Usage

```
h2o.num_valid_substrings(x, path)
```

### Arguments

x	The column on which to calculate the number of valid substrings.
path	Path to text file containing line-separated strings to be referenced.

---

h2o.openLog

*View H2O R Logs*


---

### Description

Open existing logs of H2O R POST commands and error responses on local disk. Used primarily for debugging purposes.

### Usage

```
h2o.openLog(type)
```

### Arguments

type	Currently unimplemented.
------	--------------------------

### See Also

[h2o.startLogging](#), [h2o.stopLogging](#), [h2o.clearLog](#)

### Examples

```
## Not run:
h2o.init()

h2o.startLogging()
australia_path = system.file("extdata", "australia.csv", package = "h2o")
australia = h2o.importFile(path = australia_path)
h2o.stopLogging()

# Not run to avoid windows being opened during R CMD check
# h2o.openLog("Command")
# h2o.openLog("Error")

## End(Not run)
```

---

h2o.parseRaw

*H2O Data Parsing*


---

### Description

The second phase in the data ingestion step.

### Usage

```
h2o.parseRaw(
  data,
  pattern = "",
  destination_frame = "",
  header = NA,
  sep = "",
  col.names = NULL,
  col.types = NULL,
  na.strings = NULL,
  blocking = FALSE,
  parse_type = NULL,
  chunk_size = NULL,
  decrypt_tool = NULL,
  skipped_columns = NULL,
  custom_non_data_line_markers = NULL,
  partition_by = NULL,
  quotechar = NULL,
  escapechar = ""
)
```

### Arguments

data	An H2OFrame object to be parsed.
pattern	(Optional) Character string containing a regular expression to match file(s) in the folder.
destination_frame	(Optional) The hex key assigned to the parsed file.
header	(Optional) A logical value indicating whether the first row is the column header. If missing, H2O will automatically try to detect the presence of a header.
sep	(Optional) The field separator character. Values on each line of the file are separated by this character. If sep = "", the parser will automatically detect the separator.
col.names	(Optional) An H2OFrame object containing a single delimited line with the column names for the file. If skipped_columns are specified, only list column names of columns that are not skipped.
col.types	(Optional) A vector specifying the types to attempt to force over columns. If skipped_columns are specified, only list column types of columns that are not skipped.
na.strings	(Optional) H2O will interpret these strings as missing.

blocking	(Optional) Tell H2O parse call to block synchronously instead of polling. This can be faster for small datasets but loses the progress bar.
parse_type	(Optional) Specify which parser type H2O will use. Valid types are "ARFF", "XLS", "CSV", "SVMLight"
chunk_size	size of chunk of (input) data in bytes
decrypt_tool	(Optional) Specify a Decryption Tool (key-reference acquired by calling <a href="#">h2o.decryptSetup</a> .
skipped_columns	a list of column indices to be excluded from parsing
custom_non_data_line_markers	(Optional) If a line in imported file starts with any character in given string it will NOT be imported. Empty string means all lines are imported, NULL means that default behaviour for given format will be used
partition_by	(Optional) Names of the columns the persisted dataset has been partitioned by.
quotechar	A hint for the parser which character to expect as quoting character. None (default) means autodetection.
escapechar	(Optional) One ASCII character used to escape other characters.

### Details

Parse the Raw Data produced by the import phase.

### See Also

[h2o.importFile](#), [h2o.parseSetup](#)

---

h2o.parseSetup	<i>Get a parse setup back for the staged data.</i>
----------------	--

---

### Description

Get a parse setup back for the staged data.

### Usage

```
h2o.parseSetup(
  data,
  pattern = "",
  destination_frame = "",
  header = NA,
  sep = "",
  col.names = NULL,
  col.types = NULL,
  na.strings = NULL,
  parse_type = NULL,
  chunk_size = NULL,
  decrypt_tool = NULL,
  skipped_columns = NULL,
  custom_non_data_line_markers = NULL,
  partition_by = NULL,
  single_quotes = FALSE,
  escapechar = ""
)
```

**Arguments**

data	An H2OFrame object to be parsed.
pattern	(Optional) Character string containing a regular expression to match file(s) in the folder.
destination_frame	(Optional) The hex key assigned to the parsed file.
header	(Optional) A logical value indicating whether the first row is the column header. If missing, H2O will automatically try to detect the presence of a header.
sep	(Optional) The field separator character. Values on each line of the file are separated by this character. If sep = "", the parser will automatically detect the separator.
col.names	(Optional) An H2OFrame object containing a single delimited line with the column names for the file. If skipped_columns are specified, only list column names of columns that are not skipped.
col.types	(Optional) A vector specifying the types to attempt to force over columns. If skipped_columns are specified, only list column types of columns that are not skipped.
na.strings	(Optional) H2O will interpret these strings as missing.
parse_type	(Optional) Specify which parser type H2O will use. Valid types are "ARFF", "XLS", "CSV", "SVMLight"
chunk_size	size of chunk of (input) data in bytes
decrypt_tool	(Optional) Specify a Decryption Tool (key-reference acquired by calling <a href="#">h2o.decryptionSetup</a> ).
skipped_columns	a list of column indices to be excluded from parsing
custom_non_data_line_markers	(Optional) If a line in imported file starts with any character in given string it will NOT be imported. Empty string means all lines are imported, NULL means that default behaviour for given format will be used
partition_by	(Optional) Names of the columns the persisted dataset has been partitioned by.
single_quotes	If set to true, the parser expects single quotes. False for double quotes (default).
escapechar	(Optional) One ASCII character used to escape other characters.

**See Also**

[h2o.parseRaw](#)

---

h2o.partialPlot

*Partial Dependence Plots*

---

**Description**

Partial dependence plot gives a graphical depiction of the marginal effect of a variable on the response. The effect of a variable is measured in change in the mean response. Note: Unlike random-Forest's partialPlot when plotting partial dependence the mean response (probabilities) is returned rather than the mean of the log class probability.



**Usage**

```

h2o.partialPlot(
  object,
  data,
  cols,
  destination_key,
  nbins = 20,
  plot = TRUE,
  plot_stddev = TRUE,
  weight_column = -1,
  include_na = FALSE,
  user_splits = NULL,
  col_pairs_2dpp = NULL,
  save_to = NULL,
  row_index = -1,
  targets = NULL
)

```

**Arguments**

object	An <a href="#">H2OModel</a> object.
data	An <a href="#">H2OFrame</a> object used for scoring and constructing the plot.
cols	Feature(s) for which partial dependence will be calculated.
destination_key	An key reference to the created partial dependence tables in H2O.
nbins	Number of bins used. For categorical columns make sure the number of bins exceeds the level count. If you enable <code>add_missing_NA</code> , the returned length will be <code>nbins+1</code> .
plot	A logical specifying whether to plot partial dependence table.
plot_stddev	A logical specifying whether to add std err to partial dependence plot.
weight_column	A string denoting which column of data should be used as the weight column.
include_na	A logical specifying whether missing value should be included in the Feature values.
user_splits	A two-level nested list containing user defined split points for pdp plots for each column. If there are two columns using user defined split points, there should be two lists in the nested list. Inside each list, the first element is the column name followed by values defined by the user.
col_pairs_2dpp	A two-level nested list like this: <code>col_pairs_2dpp = list(c("col1_name", "col2_name"), c("col1_name", "col3_name"), ...)</code> where a 2D partial plots will be generated for <code>col1_name</code> , <code>col2_name</code> pair, for <code>col1_name</code> , <code>col3_name</code> pair and whatever other pairs that are specified in the nested list.
save_to	Fully qualified prefix of the image files the resulting plots should be saved to, e.g. <code>"/home/user/pdp"</code> . Plots for each feature are saved separately in PNG format, each file receives a suffix equal to the corresponding feature name, e.g. <code>"/home/user/pdp_AGE.png"</code> . If the files already exists, they will be overridden. Files are only saves if <code>plot = TRUE</code> (default).
row_index	Row for which partial dependence will be calculated instead of the whole input frame.
targets	Target classes for multinomial model.

**Value**

Plot and list of calculated mean response tables for each feature requested.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate[, "CAPSULE"] <- as.factor(prostate[, "CAPSULE"])
prostate[, "RACE"] <- as.factor(prostate[, "RACE"])
prostate_gbm <- h2o.gbm(x = c("AGE", "RACE"),
  y = "CAPSULE",
  training_frame = prostate,
  ntrees = 10,
  max_depth = 5,
  learn_rate = 0.1)
h2o.partialPlot(object = prostate_gbm, data = prostate, cols = c("AGE", "RACE"))

iris_hex <- as.h2o(iris)
iris_gbm <- h2o.gbm(x = c(1:4), y = 5, training_frame = iris_hex)

# one target class
h2o.partialPlot(object = iris_gbm, data = iris_hex, cols="Petal.Length", targets=c("setosa"))
# three target classes
h2o.partialPlot(object = iris_gbm, data = iris_hex, cols="Petal.Length",
  targets=c("setosa", "virginica", "versicolor"))

## End(Not run)
```

---

h2o.pd\_multi\_plot

*Plot partial dependencies for a variable across multiple models*


---

**Description**

Partial dependence plot (PDP) gives a graphical depiction of the marginal effect of a variable on the response. The effect of a variable is measured in change in the mean response. PDP assumes independence between the feature for which is the PDP computed and the rest.

**Usage**

```
h2o.pd_multi_plot(
  object,
  newdata,
  column,
  best_of_family = TRUE,
  target = NULL,
  row_index = NULL,
  max_levels = 30
)
```

**Arguments**

object	Either a list of H2O models/model_ids or an H2OAutoML object.
newdata	An H2OFrame.
column	A feature column name to inspect. Character string.
best_of_family	If TRUE, plot only the best model of each algorithm family; if FALSE, plot all models. Defaults to TRUE.
target	If multinomial, plot PDP just for target category.
row_index	Optional. Calculate Individual Conditional Expectation (ICE) for row, row_index. Integer.
max_levels	An integer specifying the maximum number of factor levels to show. Defaults to 30.

**Value**

A ggplot2 object

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
aml <- h2o.automl(y = response,
                 training_frame = train,
                 max_models = 10,
                 seed = 1)

# Create the partial dependence plot
pdp <- h2o.pd_multi_plot(aml, test, column = "alcohol")
print(pdp)

## End(Not run)
```

---

h2o.pd_plot	<i>Plot partial dependence for a variable</i>
-------------	---

---

### Description

Partial dependence plot (PDP) gives a graphical depiction of the marginal effect of a variable on the response. The effect of a variable is measured in change in the mean response. PDP assumes independence between the feature for which is the PDP computed and the rest.

### Usage

```
h2o.pd_plot(
  object,
  newdata,
  column,
  target = NULL,
  row_index = NULL,
  max_levels = 30
)
```

### Arguments

object	An H2O model.
newdata	An H2OFrame. Used to generate predictions used in Partial Dependence calculations.
column	A feature column name to inspect. Character string.
target	If multinomial, plot PDP just for target category. Character string.
row_index	Optional. Calculate Individual Conditional Expectation (ICE) for row, row_index. Integer.
max_levels	An integer specifying the maximum number of factor levels to show. Defaults to 30.

### Value

A ggplot2 object

### Examples

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
```

```

train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
gbm <- h2o.gbm(y = response,
               training_frame = train)

# Create the partial dependence plot
pdp <- h2o.pd_plot(gbm, test, column = "alcohol")
print(pdp)

## End(Not run)

```

---

h2o.performance

*Model Performance Metrics in H2O*


---

## Description

Given a trained h2o model, compute its performance on the given dataset. However, if the dataset does not contain the response/target column, no performance will be returned. Instead, a warning message will be printed.

## Usage

```

h2o.performance(
  model,
  newdata = NULL,
  train = FALSE,
  valid = FALSE,
  xval = FALSE,
  data = NULL,
  auc_type = "NONE"
)

```

## Arguments

model	An <a href="#">H2OModel</a> object
newdata	An <a href="#">H2OFrame</a> . The model will make predictions on this dataset, and subsequently score them. The dataset should match the dataset that was used to train the model, in terms of column names, types, and dimensions. If newdata is passed in, then train, valid, and xval are ignored.
train	A logical value indicating whether to return the training metrics (constructed during training).  Note: when the trained h2o model uses <code>balance_classes</code> , the training metrics constructed during training will be from the balanced training dataset. For more information visit: <a href="https://0xdata.atlassian.net/browse/TN-9">https://0xdata.atlassian.net/browse/TN-9</a>
valid	A logical value indicating whether to return the validation metrics (constructed during training).
xval	A logical value indicating whether to return the cross-validation metrics (constructed during training).

data (DEPRECATED) An H2OFrame. This argument is now called 'newdata'.

auc\_type For multinomila model only. Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO\_OVR", "WEIGHTED\_OVR", "MACRO\_OVO", "WEIGHTED\_OVO". Default is "NONE"

### Value

Returns an object of the [H2OModelMetrics](#) subclass.

### Examples

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
h2o.performance(model = prostate_gbm, newdata=prostate)

## If model uses balance_classes
## the results from train = TRUE will not match the results from newdata = prostate
prostate_gbm_balanced <- h2o.gbm(3:9, "CAPSULE", prostate, balance_classes = TRUE)
h2o.performance(model = prostate_gbm_balanced, newdata = prostate)
h2o.performance(model = prostate_gbm_balanced, train = TRUE)

## End(Not run)
```

---

h2o.pivot

*Pivot a frame*

---

### Description

Pivot the frame designated by the three columns: index, column, and value. Index and column should be of type enum, int, or time. For cases of multiple indexes for a column label, the aggregation method is to pick the first occurrence in the data frame

### Usage

```
h2o.pivot(x, index, column, value)
```

### Arguments

x	an H2OFrame
index	the column where pivoted rows should be aligned on
column	the column to pivot
value	values of the pivoted table

### Value

An H2OFrame with columns from the columns arg, aligned on the index arg, with values from values arg

**Examples**

```
## Not run:
library(h2o)
h2o.init()

df = h2o.createFrame(rows = 1000, cols = 3, factors = 10, integer_fraction = 1.0/3,
                    categorical_fraction = 1.0/3, missing_fraction = 0.0, seed = 123)
df$C3 = h2o.abs(df$C3)
h2o.pivot(df, index="C3", column="C2", value="C1")

## End(Not run)
```

---

h2o.prcomp

*Principal component analysis of an H2O data frame*


---

**Description**

Principal components analysis of an H2O data frame using the power method to calculate the singular value decomposition of the Gram matrix.

**Usage**

```
h2o.prcomp(
  training_frame,
  x,
  model_id = NULL,
  validation_frame = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"),
  pca_method = c("GramSVD", "Power", "Randomized", "GLRM"),
  pca_impl = c("MTJ_EVD_DENSEMATRIX", "MTJ_EVD_SYMMMATRIX", "MTJ_SVD_DENSEMATRIX",
              "JAMA"),
  k = 1,
  max_iterations = 1000,
  use_all_factor_levels = FALSE,
  compute_metrics = TRUE,
  impute_missing = FALSE,
  seed = -1,
  max_runtime_secs = 0,
  export_checkpoints_dir = NULL
)
```

**Arguments**

`training_frame` Id of the training data frame.

`x` A vector containing the character names of the predictors in the model.

`model_id` Destination id for this model; auto-generated if not specified.

`validation_frame` Id of the validation data frame.

<code>ignore_const_cols</code>	Logical. Ignore constant columns. Defaults to TRUE.
<code>score_each_iteration</code>	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
<code>transform</code>	Transformation of training data Must be one of: "NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE". Defaults to NONE.
<code>pca_method</code>	Specify the algorithm to use for computing the principal components: GramSVD - uses a distributed computation of the Gram matrix, followed by a local SVD; Power - computes the SVD using the power iteration method (experimental); Randomized - uses randomized subspace iteration method; GLRM - fits a generalized low-rank model with L2 loss function and no regularization and solves for the SVD using local matrix algebra (experimental) Must be one of: "GramSVD", "Power", "Randomized", "GLRM". Defaults to GramSVD.
<code>pca_impl</code>	Specify the implementation to use for computing PCA (via SVD or EVD): MTJ_EVD_DENSEMATRIX - eigenvalue decompositions for dense matrix using MTJ; MTJ_EVD_SYMMMATRIX - eigenvalue decompositions for symmetric matrix using MTJ; MTJ_SVD_DENSEMATRIX - singular-value decompositions for dense matrix using MTJ; JAMA - eigenvalue decompositions for dense matrix using JAMA. References: JAMA - <a href="http://math.nist.gov/javanumerics/jama/">http://math.nist.gov/javanumerics/jama/</a> ; MTJ - <a href="https://github.com/fommil/matrix-toolkits-java/">https://github.com/fommil/matrix-toolkits-java/</a> Must be one of: "MTJ_EVD_DENSEMATRIX", "MTJ_EVD_SYMMMATRIX", "MTJ_SVD_DENSEMATRIX", "JAMA".
<code>k</code>	Rank of matrix approximation Defaults to 1.
<code>max_iterations</code>	Maximum training iterations Defaults to 1000.
<code>use_all_factor_levels</code>	Logical. Whether first factor level is included in each categorical expansion Defaults to FALSE.
<code>compute_metrics</code>	Logical. Whether to compute metrics on the training data Defaults to TRUE.
<code>impute_missing</code>	Logical. Whether to impute missing entries with the column mean Defaults to FALSE.
<code>seed</code>	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>export_checkpoints_dir</code>	Automatically export generated models to this directory.

**Value**

an object of class [H2ODimReductionModel](#).

**References**

N. Halko, P.G. Martinsson, J.A. Tropp. Finding structure with randomness: Probabilistic algorithms for constructing approximate matrix decompositions[<http://arxiv.org/abs/0909.4061>]. SIAM Rev., Survey and Review section, Vol. 53, num. 2, pp. 217-288, June 2011.



**See Also**

[h2o.svd](#), [h2o.glm](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
h2o.prcomp(training_frame = australia, k = 8, transform = "STANDARDIZE")

## End(Not run)
```

---

h2o.predict	<i>Predict on an H2O Model</i>
-------------	--------------------------------

---

**Description**

Predict on an H2O Model

**Usage**

```
h2o.predict(object, newdata, ...)
```

**Arguments**

object	a fitted model object for which prediction is desired.
newdata	An H2OFrame object in which to look for variables with which to predict.
...	additional arguments to pass on.

**Value**

Returns an H2OFrame object with probabilities and default predictions.

---

h2o.predict_json	<i>H2O Prediction from R without having H2O running</i>
------------------	---

---

**Description**

Provides the method h2o.predict with which you can predict a MOJO or POJO Jar model from R.

**Usage**

```
h2o.predict_json(model, json, genmodelpath, labels, classpath, javaoptions)
```

**Arguments**

model	String with file name of MOJO or POJO Jar
json	JSON String with inputs to model
genmodelpath	(Optional) path name to h2o-genmodel.jar, if not set defaults to same dir as MOJO
labels	(Optional) if TRUE then show output labels in result
classpath	(Optional) Extra items for the class path of where to look for Java classes, e.g., h2o-genmodel.jar
javaoptions	(Optional) Java options string, default if "-Xmx4g"

**Value**

Returns an object with the prediction result

**Examples**

```
## Not run:
library(h2o)
h2o.predict_json('~/GBM_model_python_1473313897851_6.zip', '{"C7":1}')
h2o.predict_json('~/GBM_model_python_1473313897851_6.zip', '{"C7":1}', c(".", "lib"))

## End(Not run)
```

---

h2o.print

*Print An H2OFrame*

---

**Description**

Print An H2OFrame

**Usage**

```
h2o.print(x, n = 6L)
```

**Arguments**

x	An H2OFrame object
n	An (Optional) A single integer. If positive, number of rows in x to return. If negative, all but the n first/last number of rows in x. Anything bigger than 20 rows will require asking the server (first 20 rows are cached on the client).

**Examples**

```
## Not run:
library()
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smалldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.print(iris["species"], n = 15)

## End(Not run)
```

---

h2o.prod	<i>Return the product of all the values present in its arguments.</i>
----------	---

---

**Description**

Return the product of all the values present in its arguments.

**Usage**

```
h2o.prod(x)
```

**Arguments**

x	An H2OFrame object.
---	---------------------

**See Also**

[prod](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.prod(iris["petal_len"])

## End(Not run)
```

---

h2o.proj_archetypes	<i>Convert Archetypes to Features from H2O GLRM Model</i>
---------------------	---

---

**Description**

Project each archetype in an H2O GLRM model into the corresponding feature space from the H2O training frame.

**Usage**

```
h2o.proj_archetypes(object, data, reverse_transform = FALSE)
```

**Arguments**

object	An <a href="#">H2ODimReductionModel</a> object that represents the model containing archetypes to be projected.
data	An H2OFrame object representing the training data for the H2O GLRM model.
reverse_transform	(Optional) A logical value indicating whether to reverse the transformation from model-building by re-scaling columns and adding back the offset to each column of the projected archetypes.

**Value**

Returns an H2OFrame object containing the projection of the archetypes down into the original feature space, where each row is one archetype.

**See Also**

[h2o.glm](#) for making an H2ODimReductionModel.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_glm <- h2o.glm(training_frame = iris_hf, k = 4, loss = "Quadratic",
                   multi_loss = "Categorical", max_iterations = 1000)
iris_parch <- h2o.proj_archetypes(iris_glm, iris_hf)
head(iris_parch)

## End(Not run)
```

---

h2o.psvm

*Trains a Support Vector Machine model on an H2O dataset*


---

**Description**

Alpha version. Supports only binomial classification problems.

**Usage**

```
h2o.psvm(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  ignore_const_cols = TRUE,
  hyper_param = 1,
  kernel_type = c("gaussian"),
  gamma = -1,
  rank_ratio = -1,
  positive_weight = 1,
  negative_weight = 1,
  disable_training_metrics = TRUE,
  sv_threshold = 1e-04,
  fact_threshold = 1e-05,
  feasible_threshold = 0.001,
  surrogate_gap_threshold = 0.001,
  mu_factor = 10,
  max_iterations = 200,
  seed = -1
)
```

**Arguments**

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a binary categorical/factor variable or a numeric variable with values -1/1 (for compatibility with SVMlight format).
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
hyper_param	Penalty parameter C of the error term Defaults to 1.
kernel_type	Type of used kernel Must be one of: "gaussian". Defaults to gaussian.
gamma	Coefficient of the kernel (currently RBF gamma for gaussian kernel, -1 means $1/\#features$ ) Defaults to -1.
rank_ratio	Desired rank of the ICF matrix expressed as an ration of number of input rows (-1 means use $\sqrt{\#rows}$ ). Defaults to -1.
positive_weight	Weight of positive (+1) class of observations Defaults to 1.
negative_weight	Weight of positive (-1) class of observations Defaults to 1.
disable_training_metrics	Logical. Disable calculating training metrics (expensive on large datasets) Defaults to TRUE.
sv_threshold	Threshold for accepting a candidate observation into the set of support vectors Defaults to 0.0001.
fact_threshold	Convergence threshold of the Incomplete Cholesky Factorization (ICF) Defaults to $1e-05$ .
feasible_threshold	Convergence threshold for primal-dual residuals in the IPM iteration Defaults to 0.001.
surrogate_gap_threshold	Feasibility criterion of the surrogate duality gap (eta) Defaults to 0.001.
mu_factor	Increasing factor mu Defaults to 10.
max_iterations	Maximum number of iteration of the algorithm Defaults to 200.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the splice dataset
f <- "https://s3.amazonaws.com/h2o-public-test-data/smалldata/splice/splice.svm"
```

```
splice <- h2o.importFile(f)

# Train the Support Vector Machine model
svm_model <- h2o.psvm(gamma = 0.01, rank_ratio = 0.1,
                     y = "C1", training_frame = splice,
                     disable_training_metrics = FALSE)

## End(Not run)
```

---

h2o.quantile

*Quantiles of H2O Frames.*


---

## Description

Obtain and display quantiles for H2O parsed data.

## Usage

```
h2o.quantile(
  x,
  probs = c(0.001, 0.01, 0.1, 0.25, 0.333, 0.5, 0.667, 0.75, 0.9, 0.99, 0.999),
  combine_method = c("interpolate", "average", "avg", "low", "high"),
  weights_column = NULL,
  ...
)

## S3 method for class 'H2OFrame'
quantile(
  x,
  probs = c(0.001, 0.01, 0.1, 0.25, 0.333, 0.5, 0.667, 0.75, 0.9, 0.99, 0.999),
  combine_method = c("interpolate", "average", "avg", "low", "high"),
  weights_column = NULL,
  ...
)
```

## Arguments

x	An H2OFrame object with a single numeric column.
probs	Numeric vector of probabilities with values in [0,1].
combine_method	How to combine quantiles for even sample sizes. Default is to do linear interpolation. E.g., If method is "lo", then it will take the lo value of the quantile. Abbreviations for average, low, and high are acceptable (avg, lo, hi).
weights_column	(Optional) String name of the observation weights column in x or an H2OFrame object with a single numeric column of observation weights.
...	Further arguments passed to or from other methods.

## Details

quantile.H2OFrame, a method for the [quantile](#) generic. Obtain and return quantiles for an H2OFrame object.

**Value**

A vector describing the percentiles at the given cutoffs for the H2OFrame object.

**Examples**

```
## Not run:
# Request quantiles for an H2O parsed data set:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
# Request quantiles for a subset of columns in an H2O parsed data set
quantile(prostate[, 3])
for(i in 1:ncol(prostate))
  quantile(prostate[, i])

## End(Not run)
```

---

h2o.r2

*Retrieve the R2 value*


---

**Description**

Retrieves the R2 value from an H2O model. Will return  $R^2$  for GLM Models and will return NaN otherwise. If "train", "valid", and "xval" parameters are FALSE (default), then the training R2 value is returned. If more than one parameter is set to TRUE, then a named vector of R2s are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.r2(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> object.
train	Retrieve the training R2
valid	Retrieve the validation set R2 if a validation set was passed in during model build time.
xval	Retrieve the cross-validation R2

**Examples**

```
## Not run:
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.glm(x = 2:5, y = 1, training_frame = fr)

h2o.r2(m)

## End(Not run)
```

---

h2o.randomForest	<i>Build a Random Forest model</i>
------------------	------------------------------------

---

### Description

Builds a Random Forest model on an H2OFrame.

### Usage

```
h2o.randomForest(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,
  keep_cross_validation_models = TRUE,
  keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE,
  score_each_iteration = FALSE,
  score_tree_interval = 0,
  fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
  fold_column = NULL,
  ignore_const_cols = TRUE,
  offset_column = NULL,
  weights_column = NULL,
  balance_classes = FALSE,
  class_sampling_factors = NULL,
  max_after_balance_size = 5,
  ntrees = 50,
  max_depth = 20,
  min_rows = 1,
  nbins = 20,
  nbins_top_level = 1024,
  nbins_cats = 1024,
  r2_stopping = Inf,
  stopping_rounds = 0,
  stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
    "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error",
    "custom", "custom_increasing"),
  stopping_tolerance = 0.001,
  max_runtime_secs = 0,
  seed = -1,
  build_tree_one_node = FALSE,
  mtries = -1,
  sample_rate = 0.632,
  sample_rate_per_class = NULL,
  binomial_double_trees = FALSE,
  checkpoint = NULL,
  col_sample_rate_change_per_level = 1,
  col_sample_rate_per_tree = 1,
```



```

min_split_improvement = 1e-05,
histogram_type = c("AUTO", "UniformAdaptive", "Random", "QuantilesGlobal",
  "RoundRobin"),
categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
  "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
calibrate_model = FALSE,
calibration_frame = NULL,
distribution = c("AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma",
  "tweedie", "laplace", "quantile", "huber"),
custom_metric_func = NULL,
export_checkpoints_dir = NULL,
check_constant_response = TRUE,
gainslift_bins = -1,
auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
  "WEIGHTED_OVO"),
verbose = FALSE
)

```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
nfolds	Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
keep_cross_validation_models	Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
score_tree_interval	Score the model after every so many trees. Disabled if set to 0. Defaults to 0.
fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.

<code>ignore_const_cols</code>	Logical. Ignore constant columns. Defaults to TRUE.
<code>offset_column</code>	Offset column. This argument is deprecated and has no use for Random Forest.
<code>weights_column</code>	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set <code>weight = 0</code> for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with <code>weight == 0</code> .
<code>balance_classes</code>	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
<code>class_sampling_factors</code>	Desired over/under-sampling ratios per class (in lexicographic order). If not specified, sampling factors will be automatically computed to obtain class balance during training. Requires <code>balance_classes</code> .
<code>max_after_balance_size</code>	Maximum relative size of the training data after balancing class counts (can be less than 1.0). Requires <code>balance_classes</code> . Defaults to 5.0.
<code>ntrees</code>	Number of trees. Defaults to 50.
<code>max_depth</code>	Maximum tree depth (0 for unlimited). Defaults to 20.
<code>min_rows</code>	Fewest allowed (weighted) observations in a leaf. Defaults to 1.
<code>nbins</code>	For numerical columns (real/int), build a histogram of (at least) this many bins, then split at the best point Defaults to 20.
<code>nbins_top_level</code>	For numerical columns (real/int), build a histogram of (at most) this many bins at the root level, then decrease by factor of two per level Defaults to 1024.
<code>nbins_cats</code>	For categorical columns (factors), build a histogram of this many bins, then split at the best point. Higher values can lead to more overfitting. Defaults to 1024.
<code>r2_stopping</code>	<code>r2_stopping</code> is no longer supported and will be ignored if set - please use <code>stopping_rounds</code> , <code>stopping_metric</code> and <code>stopping_tolerance</code> instead. Previous version of H2O would stop making trees when the $R^2$ metric equals or exceeds this Defaults to $1.797693135e+308$ .
<code>stopping_rounds</code>	Early stopping based on convergence of <code>stopping_metric</code> . Stop if simple moving average of length <code>k</code> of the <code>stopping_metric</code> does not improve for <code>k:=stopping_rounds</code> scoring events (0 to disable) Defaults to 0.
<code>stopping_metric</code>	Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and <code>anomaly_score</code> for Isolation Forest). Note that <code>custom</code> and <code>custom_increasing</code> can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
<code>stopping_tolerance</code>	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.

max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
build_tree_one_node	Logical. Run on one node only; no network overhead but fewer cpus used. Suitable for small datasets. Defaults to FALSE.
mtries	Number of variables randomly sampled as candidates at each split. If set to -1, defaults to sqrt(p) for classification and p/3 for regression (where p is the # of predictors Defaults to -1.
sample_rate	Row sample rate per tree (from 0.0 to 1.0) Defaults to 0.632.
sample_rate_per_class	A list of row sample rates per class (relative fraction for each class, from 0.0 to 1.0), for each tree
binomial_double_trees	Logical. For binary classification: Build 2x as many trees (one per class) - can lead to higher accuracy. Defaults to FALSE.
checkpoint	Model checkpoint to resume training with.
col_sample_rate_change_per_level	Relative change of the column sampling rate for every level (must be > 0.0 and <= 2.0) Defaults to 1.
col_sample_rate_per_tree	Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.
min_split_improvement	Minimum relative improvement in squared error reduction for a split to happen Defaults to 1e-05.
histogram_type	What type of histogram to use for finding optimal split points Must be one of: "AUTO", "UniformAdaptive", "Random", "QuantilesGlobal", "RoundRobin". Defaults to AUTO.
categorical_encoding	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.
calibrate_model	Logical. Use Platt Scaling to calculate calibrated class probabilities. Calibration can provide more accurate estimates of class probabilities. Defaults to FALSE.
calibration_frame	Calibration frame for Platt Scaling
distribution	Distribution. This argument is deprecated and has no use for Random Forest.
custom_metric_func	Reference to custom evaluation function, format: 'language:keyName=funcName'
export_checkpoints_dir	Automatically export generated models to this directory.
check_constant_response	Logical. Check if response column is constant. If enabled, then an exception is thrown if the response column is a constant value.If disabled, then model will train regardless of the response column being a constant value or not. Defaults to TRUE.

gainslift_bins	Gains/Lift table number of bins. 0 means disabled.. Default value -1 means automatic binning. Defaults to -1.
auc_type	Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO", "WEIGHTED_OVO". Defaults to AUTO.
verbose	Logical. Print scoring history to the console (Metrics per tree). Defaults to FALSE.

**Value**

Creates a [H2OModel](#) object of the right type.

**See Also**

[predict.H2OModel](#) for prediction

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the cars dataset
f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)

# Set predictors and response; set response as a factor
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"

# Train the DRF model
cars_drf <- h2o.randomForest(x = predictors, y = response,
                             training_frame = cars, nfolds = 5,
                             seed = 1234)

## End(Not run)
```

---

h2o.range

*Returns a vector containing the minimum and maximum of all the given arguments.*

---

**Description**

Returns a vector containing the minimum and maximum of all the given arguments.

**Usage**

```
h2o.range(x, na.rm = FALSE, finite = FALSE)
```

**Arguments**

x	An H2OFrame object.
na.rm	logical. indicating whether missing values should be removed.
finite	logical. indicating if all non-finite elements should be omitted.

**See Also**

[range](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.range(iris["petal_len"], na.rm = TRUE, finite = TRUE)

## End(Not run)
```

---

**h2o.rank\_within\_group\_by**

*This function will add a new column rank where the ranking is produced as follows: 1. sorts the H2OFrame by columns sorted in by columns specified in group\_by\_cols and sort\_cols in the directions specified by the ascending for the sort\_cols. The sort directions for the group\_by\_cols are ascending only. 2. A new rank column is added to the frame which will contain a rank assignment performed next. The user can choose to assign a name to this new column. The default name is New\_Rank\_column. 3. For each groupby groups, a rank is assigned to the row starting from 1, 2, ... to the end of that group. 4. If sort\_cols\_sorted is TRUE, a final sort on the frame will be performed frame according to the sort\_cols and the sort directions in ascending. If sort\_cols\_sorted is FALSE (by default), the frame from step 3 will be returned as is with no extra sort. This may provide a small speedup if desired.*

---

**Description**

This function will add a new column rank where the ranking is produced as follows: 1. sorts the H2OFrame by columns sorted in by columns specified in group\_by\_cols and sort\_cols in the directions specified by the ascending for the sort\_cols. The sort directions for the group\_by\_cols are ascending only. 2. A new rank column is added to the frame which will contain a rank assignment performed next. The user can choose to assign a name to this new column. The default name is New\_Rank\_column. 3. For each groupby groups, a rank is assigned to the row starting from 1, 2, ... to the end of that group. 4. If sort\_cols\_sorted is TRUE, a final sort on the frame will be performed frame according to the sort\_cols and the sort directions in ascending. If sort\_cols\_sorted is FALSE (by default), the frame from step 3 will be returned as is with no extra sort. This may provide a small speedup if desired.

**Usage**

```
h2o.rank_within_group_by(
  x,
  group_by_cols,
  sort_cols,
```

```

ascending = NULL,
new_col_name = "New_Rank_column",
sort_cols_sorted = FALSE
)

```

### Arguments

**x** The H2OFrame input to be sorted.

**group\_by\_cols** a list of column names or indices to form the groupby groups

**sort\_cols** a list of column names or indices for sorting

**ascending** a list of Boolean to determine if ascending sort (set to TRUE) is needed for each column in `sort_cols` (optional). Default is ascending sort for all. To perform descending sort, set value to FALSE

**new\_col\_name** new column name for the newly added rank column if specified (optional). Default name is `New_Rank_column`.

**sort\_cols\_sorted** Boolean to determine if the final returned frame is to be sorted according to the `sort_cols` and sort directions in ascending. Default is FALSE.

The following example is generated by Nidhi Mehta.

If the input frame is train:

```

ID Group_by_column num data Column_to_arrange_by num_1 fdata 12 1 2941.552
1 3 -3177.9077 1 12 1 2941.552 1 5 -13311.8247 1 12 2 -22722.174 1 3 -
3177.9077 1 12 2 -22722.174 1 5 -13311.8247 1 13 3 -12776.884 1 5 -18421.6171
0 13 3 -12776.884 1 4 28080.1607 0 13 1 -6049.830 1 5 -18421.6171 0 13 1 -
6049.830 1 4 28080.1607 0 15 3 -16995.346 1 1 -9781.6373 0 16 1 -10003.593
0 3 -61284.6900 0 16 3 26052.495 1 3 -61284.6900 0 16 3 -22905.288 0 3 -
61284.6900 0 17 2 -13465.496 1 2 12094.4851 1 17 2 -13465.496 1 3 -11772.1338
1 17 2 -13465.496 1 3 -415.1114 0 17 2 -3329.619 1 2 12094.4851 1 17 2 -
3329.619 1 3 -11772.1338 1 17 2 -3329.619 1 3 -415.1114 0

```

If the following commands are issued: `rankedF1 <- h2o.rank_within_group_by(train, c("Group_by_column"), c("Column_to_arrange_by"), c(TRUE))` `h2o.summary(rankedF1)`

The returned frame `rankedF1` will look like this: `ID Group_by_column num fdata Column_to_arrange_by num_1 fdata.1 New_Rank_column 12 1 2941.552 1 3 -3177.9077 1 1 16 1 -10003.593 0 3 -61284.6900 0 2 13 1 -6049.830 0 4 28080.1607 0 3 12 1 2941.552 1 5 -13311.8247 1 4 13 1 -6049.830 0 5 -18421.6171 0 5 17 2 -13465.496 0 2 12094.4851 1 1 17 2 -3329.619 0 2 12094.4851 1 2 12 2 -22722.174 1 3 -3177.9077 1 3 17 2 -13465.496 0 3 -11772.1338 1 4 17 2 -13465.496 0 3 -415.1114 0 5 17 2 -3329.619 0 3 -11772.1338 1 6 17 2 -3329.619 0 3 -415.1114 0 7 12 2 -22722.174 1 5 -13311.8247 1 8 15 3 -16995.346 1 1 -9781.6373 0 1 16 3 26052.495 0 3 -61284.6900 0 2 16 3 -22905.288 1 3 -61284.6900 0 3 13 3 -12776.884 1 4 28080.1607 0 4 13 3 -12776.884 1 5 -18421.6171 0 5`

If the following commands are issued: `rankedF1 <- h2o.rank_within_group_by(train, c("Group_by_column"), c("Column_to_arrange_by"), c(TRUE), sort_cols_sorted=TRUE)` `h2o.summary(rankedF1)`

The returned frame will be sorted according to `sortCols` and hence look like this instead: `ID Group_by_column num fdata Column_to_arrange_by num_1 fdata.1 New_Rank_column 15 3 -16995.346 1 1 -9781.6373 0 1 17 2 -13465.496 0 2 12094.4851 1 1 17 2 -3329.619 0 2 12094.4851 1 2 12 1 2941.552 1 3`

```
-3177.9077 1 1 12 2 -22722.174 1 3 -3177.9077 1 3 16 1 -10003.593 0 3 -
61284.6900 0 2 16 3 26052.495 0 3 -61284.6900 0 2 16 3 -22905.288 1 3 -
61284.6900 0 3 17 2 -13465.496 0 3 -11772.1338 1 4 17 2 -13465.496 0 3 -
415.1114 0 5 17 2 -3329.619 0 3 -11772.1338 1 6 17 2 -3329.619 0 3 -415.1114
0 7 13 3 -12776.884 1 4 28080.1607 0 4 13 1 -6049.830 0 4 28080.1607 0 3
12 1 2941.552 1 5 -13311.8247 1 4 12 2 -22722.174 1 5 -13311.8247 1 8 13 3
-12776.884 1 5 -18421.6171 0 5 13 1 -6049.830 0 5 -18421.6171 0 5
```

## Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/airlines/allyears2k_headers.zip"
air <- h2o.importFile(f)
group_cols <- c("Distance")
sort_cols <- c("IsArrDelayed", "IsDepDelayed")
sort_directions <- c(TRUE, FALSE)
h2o.rank_within_group_by(x = air, group_by_cols = group_cols,
                          sort_cols = sort_cols,
                          ascending = sort_directions,
                          new_col_name = "New_Rank",
                          sort_cols_sorted = TRUE)

## End(Not run)
```

---

h2o.rapids

*Execute a Rapids expression.*

---

## Description

Execute a Rapids expression.

## Usage

```
h2o.rapids(expr)
```

## Arguments

expr            The rapids expression (ascii string)

## Examples

```
## Not run:
h2o.rapids('(setproperty "sys.ai.h2o.algos.evaluate_auto_model_parameters" "true")')

## End(Not run)
```

---

`h2o.rbind`*Combine H2O Datasets by Rows*

---

**Description**

Takes a sequence of H2O data sets and combines them by rows

**Usage**

```
h2o.rbind(...)
```

**Arguments**

... A sequence of H2OFrame arguments. All datasets must exist on the same H2O instance (IP and port) and contain the same number and types of columns.

**Value**

An H2OFrame object containing the combined ... arguments row-wise.

**See Also**

[cbind](#) for the base R method, `rbind()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate_rbind <- h2o.rbind(prostate, prostate)
head(prostate_rbind)
dim(prostate)
dim(prostate_rbind)

## End(Not run)
```

---

`h2o.reconstruct`*Reconstruct Training Data via H2O GLRM Model*

---

**Description**

Reconstruct the training data and impute missing values from the H2O GLRM model by computing the matrix product of X and Y, and transforming back to the original feature space by minimizing each column's loss function.

**Usage**

```
h2o.reconstruct(object, data, reverse_transform = FALSE)
```



**Arguments**

object	An <a href="#">H2ODimReductionModel</a> object that represents the model to be used for reconstruction.
data	An H2OFrame object representing the training data for the H2O GLRM model. Used to set the domain of each column in the reconstructed frame.
reverse_transform	(Optional) A logical value indicating whether to reverse the transformation from model-building by re-scaling columns and adding back the offset to each column of the reconstructed frame.

**Value**

Returns an H2OFrame object containing the approximate reconstruction of the training data;

**See Also**

[h2o.glm](#) for making an H2ODimReductionModel.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_glm <- h2o.glm(training_frame = iris_hf, k = 4, transform = "STANDARDIZE",
                   loss = "Quadratic", multi_loss = "Categorical", max_iterations = 1000)
iris_rec <- h2o.reconstruct(iris_glm, iris_hf, reverse_transform = TRUE)
head(iris_rec)

## End(Not run)
```

---

h2o.relevel

*Reorders levels of an H2O factor, similarly to standard R's relevel.*


---

**Description**

The levels of a factor are reordered so that the reference level is at level 0, remaining levels are moved down as needed.

**Usage**

```
h2o.relevel(x, y)
```

**Arguments**

x	factor column in h2o frame
y	reference level (string)

**Value**

new reordered factor column

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Convert iris dataset to an H2OFrame
iris_hf <- as.h2o(iris)
# Look at current ordering of the Species column levels
h2o.levels(iris_hf["Species"])
# "setosa"      "versicolor" "virginica"
# Change the reference level to "virginica"
iris_hf["Species"] <- h2o.relevel(x = iris_hf["Species"], y = "virginica")
# Observe new ordering
h2o.levels(iris_hf["Species"])
# "virginica" "setosa"      "versicolor"

## End(Not run)
```

---

h2o.removeAll

*Remove All Objects on the H2O Cluster*


---

**Description**

Removes the data from the h2o cluster, but does not remove the local references. Retains models, frames and vectors specified in `retained_elements` argument. Retained elements must be instances/ids of models and frames only. For models retained, training and validation frames are retained as well. Cross validation models of a retained model are NOT retained automatically, those must be specified explicitly.

**Usage**

```
h2o.removeAll(timeout_secs = 0, retained_elements = c())
```

**Arguments**

`timeout_secs` Timeout in seconds. Default is no timeout.

`retained_elements`

Instances or ids of models and frames to be retained. Combination of instances and ids in the same list is also a valid input.

**See Also**

[h2o.rm](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.ls()
h2o.removeAll()
```

```
h2o.ls()
## End(Not run)
```

---

h2o.removeVecs	<i>Delete Columns from an H2OFrame</i>
----------------	--

---

### Description

Delete the specified columns from the H2OFrame. Returns an H2OFrame without the specified columns.

### Usage

```
h2o.removeVecs(data, cols)
```

### Arguments

data	The H2OFrame.
cols	The columns to remove.

---

h2o.rep_len	<i>Replicate Elements of Vectors or Lists into H2O</i>
-------------	--

---

### Description

h2o.rep\_len performs just as rep does. It replicates the values in x in the H2O backend.

### Usage

```
h2o.rep_len(x, length.out)
```

### Arguments

x	an H2O frame
length.out	non negative integer. The desired length of the output vector.

### Value

Creates an H2OFrame of the same type as x

### Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_train.csv"
iris <- h2o.importFile(f)
h2o.rep_len(iris, length.out = 3)

## End(Not run)
```

---

h2o.reset\_threshold     *Reset model threshold and return old threshold value.*

---

### Description

Reset model threshold and return old threshold value.

### Usage

```
h2o.reset_threshold(object, threshold)
```

### Arguments

object             An [H2OModel](#) object.  
 threshold         A threshold value from 0 to 1 included.

### Value

Returns the previous threshold used in the model.

### Examples

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
  training_frame = prostate, family = "binomial",
  nfolds = 0, alpha = 0.5, lambda_search = FALSE)
old_threshold <- h2o.reset_threshold(prostate_glm, 0.9)

## End(Not run)
```

---

h2o.residual\_analysis\_plot  
                           *Residual Analysis*

---

### Description

Do Residual Analysis and plot the fitted values vs residuals on a test dataset. Ideally, residuals should be randomly distributed. Patterns in this plot can indicate potential problems with the model selection, e.g., using simpler model than necessary, not accounting for heteroscedasticity, autocorrelation, etc. If you notice "striped" lines of residuals, that is just an indication that your response variable was integer valued instead of real valued.

### Usage

```
h2o.residual_analysis_plot(model, newdata)
```

**Arguments**

model            An H2OModel.  
newdata          An H2OFrame. Used to calculate residuals.

**Value**

A ggplot2 object

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
# Import the wine dataset into H2O:  
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"  
df <- h2o.importFile(f)  
  
# Set the response  
response <- "quality"  
  
# Split the dataset into a train and test set:  
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)  
train <- splits[[1]]  
test <- splits[[2]]  
  
# Build and train the model:  
gbm <- h2o.gbm(y = response,  
              training_frame = train)  
  
# Create the residual analysis plot  
residual_analysis_plot <- h2o.residual_analysis_plot(gbm, test)  
print(residual_analysis_plot)  
  
## End(Not run)
```

---

h2o.residual\_deviance *Retrieve the residual deviance*

---

**Description**

If "train", "valid", and "xval" parameters are FALSE (default), then the training residual deviance value is returned. If more than one parameter is set to TRUE, then a named vector of residual deviances are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.residual_deviance(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> or <a href="#">H2OModelMetrics</a>
train	Retrieve the training residual deviance
valid	Retrieve the validation residual deviance
xval	Retrieve the cross-validation residual deviance

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
  training_frame = prostate, family = "binomial",
  nfolds = 0, alpha = 0.5, lambda_search = FALSE)
h2o.residual_deviance(prostate_glm, train = TRUE)

## End(Not run)
```

---

h2o.residual_dof	<i>Retrieve the residual degrees of freedom</i>
------------------	---

---

**Description**

If "train", "valid", and "xval" parameters are FALSE (default), then the training residual degrees of freedom value is returned. If more than one parameter is set to TRUE, then a named vector of residual degrees of freedom are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.residual_dof(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> or <a href="#">H2OModelMetrics</a>
train	Retrieve the training residual degrees of freedom
valid	Retrieve the validation residual degrees of freedom
xval	Retrieve the cross-validation residual degrees of freedom

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
```

```

prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
  training_frame = prostate, family = "binomial",
  nfolds = 0, alpha = 0.5, lambda_search = FALSE)
h2o.residual_dof(prostate_glm, train = TRUE)

## End(Not run)

```

---

h2o.resume	<i>Triggers auto-recovery resume - this will look into configured recovery dir and resume and tasks that were interrupted by unexpected cluster stopping.</i>
------------	---

---

### Description

Triggers auto-recovery resume - this will look into configured recovery dir and resume and tasks that were interrupted by unexpected cluster stopping.

### Usage

```
h2o.resume(recovery_dir = NULL)
```

### Arguments

recovery_dir	A character path to where cluster recovery data is stored, if blank, will use cluster's configuration.
--------------	--

---

h2o.resumeGrid	<i>Resume previously stopped grid training.</i>
----------------	---

---

### Description

Resume previously stopped grid training.

### Usage

```
h2o.resumeGrid(grid_id, recovery_dir = NULL, ...)
```

### Arguments

grid_id	ID of existing grid search
recovery_dir	When specified the grid and all necessary data (frames, models) will be saved to this directory (use HDFS or other distributed file-system). Should the cluster crash during training, the grid can be reloaded from this directory via <code>h2o.loadGrid</code> and training can be resumed
...	Additional parameters to modify the resumed Grid.

---

`h2o.rm`*Delete Objects In H2O*

---

**Description**

Remove the h2o Big Data object(s) having the key name(s) from ids.

**Usage**

```
h2o.rm(ids, cascade = TRUE)
```

**Arguments**

<code>ids</code>	The object or hex key associated with the object to be removed or a vector/list of those things.
<code>cascade</code>	Boolean, if set to TRUE (default), the object dependencies (e.g. submodels) are also removed.

**See Also**

[h2o.assign](#), [h2o.ls](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris <- as.h2o(iris)
model <- h2o.glm(1:4,5,training = iris, family = "multinomial")
h2o.rm(iris)

## End(Not run)
```

---

`h2o.rmse`*Retrieves Root Mean Squared Error Value*

---

**Description**

Retrieves the root mean squared error value from an [H2OModelMetrics](#) object. If "train", "valid", and "xval" parameters are FALSE (default), then the training RMSE value is returned. If more than one parameter is set to TRUE, then a named vector of RMSEs are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.rmse(object, train = FALSE, valid = FALSE, xval = FALSE)
```



**Arguments**

object	An <a href="#">H2OModelMetrics</a> object of the correct type.
train	Retrieve the training RMSE
valid	Retrieve the validation RMSE
xval	Retrieve the cross-validation RMSE

**Details**

This function only supports [H2OBinomialMetrics](#), [H2OMultinomialMetrics](#), and [H2ORegressionMetrics](#) objects.

**See Also**

[h2o.auc](#) for AUC, [h2o.mse](#) for RMSE, and [h2o.metric](#) for the various threshold metrics. See [h2o.performance](#) for creating [H2OModelMetrics](#) objects.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)

prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.rmse(perf)

## End(Not run)
```

---

h2o.rmsle

*Retrieve the Root Mean Squared Log Error*


---

**Description**

Retrieves the root mean squared log error (RMSLE) value from an H2O model. If "train", "valid", and "xval" parameters are FALSE (default), then the training rmsle value is returned. If more than one parameter is set to TRUE, then a named vector of rmsles are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.rmsle(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OModel</a> object.
train	Retrieve the training rmsle
valid	Retrieve the validation set rmsle if a validation set was passed in during model build time.
xval	Retrieve the cross-validation rmsle

**Examples**

```
## Not run:
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.deeplearning(x = 2:5, y = 1, training_frame = fr)

h2o.rmsle(m)

## End(Not run)
```

---

h2o.round

*Round doubles/floats to the given number of decimal places.*

---

**Description**

Round doubles/floats to the given number of decimal places.

**Usage**

```
h2o.round(x, digits = 0)

round(x, digits = 0)
```

**Arguments**

x	An H2OFrame object.
digits	Number of decimal places to round doubles/floats. Rounding to a negative number of decimal places is

**See Also**

[Round](#) for the base R implementation, `round()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/coxph_test/heart.csv"
heart <- h2o.importFile(f)

h2o.round(heart["age"], digits = 3)

## End(Not run)
```

---

h2o.rstrip	<i>Strip set from right</i>
------------	-----------------------------

---

### Description

Return a copy of the target column with trailing characters removed. The set argument is a string specifying the set of characters to be removed. If omitted, the set argument defaults to removing whitespace.

### Usage

```
h2o.rstrip(x, set = " ")
```

### Arguments

x	The column whose strings should be rstrip-ed.
set	string of characters to be removed

### Examples

```
## Not run:
library(h2o)
h2o.init()
string_to_rstrip <- as.h2o("1234567890")
rstrip_string <- h2o.rstrip(string_to_rstrip, "890") #Remove "890"

## End(Not run)
```

---

h2o.rulefit	<i>Build a RuleFit Model</i>
-------------	------------------------------

---

### Description

Builds a Distributed RuleFit model on a parsed dataset, for regression or classification.

### Usage

```
h2o.rulefit(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  seed = -1,
  algorithm = c("AUTO", "DRF", "GBM"),
  min_rule_length = 3,
  max_rule_length = 3,
  max_num_rules = -1,
  model_type = c("rules_and_linear", "rules", "linear"),
  weights_column = NULL,
```

```
distribution = c("AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma",
  "tweedie", "laplace", "quantile", "huber"),
rule_generation_ntrees = 50
)
```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
algorithm	The algorithm to use to generate rules. Must be one of: "AUTO", "DRF", "GBM". Defaults to AUTO.
min_rule_length	Minimum length of rules. Defaults to 3.
max_rule_length	Maximum length of rules. Defaults to 3.
max_num_rules	The maximum number of rules to return. defaults to -1 which means the number of rules is selected by diminishing returns in model deviance. Defaults to -1.
model_type	Specifies type of base learners in the ensemble. Must be one of: "rules_and_linear", "rules", "linear". Defaults to rules_and_linear.
weights_column	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set weight = 0 for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with weight == 0.
distribution	Distribution function Must be one of: "AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber". Defaults to AUTO.
rule_generation_ntrees	specifies the number of trees to build in the tree model. Defaults to 50. Defaults to 50.

### Examples

```
## Not run:
library(h2o)
```

```

h2o.init()

# Import the titanic dataset:
f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/gbm_test/titanic.csv"
coltypes <- list(by.col.name = c("pclass", "survived"), types=c("Enum", "Enum"))
df <- h2o.importFile(f, col.types = coltypes)

# Split the dataset into train and test
splits <- h2o.splitFrame(data = df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Set the predictors and response; set the factors:
response <- "survived"
predictors <- c("age", "sibsp", "parch", "fare", "sex", "pclass")

# Build and train the model:
rfit <- h2o.rulefit(y = response,
                  x = predictors,
                  training_frame = train,
                  max_rule_length = 10,
                  max_num_rules = 100,
                  seed = 1)

# Retrieve the rule importance:
print(rfit@model$rule_importance)

# Predict on the test data:
h2o.predict(rfit, newdata = test)

## End(Not run)

```

---

h2o.runif

*Produce a Vector of Random Uniform Numbers*


---

### Description

Creates a vector of random uniform numbers equal in length to the length of the specified H2O dataset.

### Usage

```
h2o.runif(x, seed = -1)
```

### Arguments

x	An H2OFrame object.
seed	A random seed used to generate draws from the uniform distribution.

### Value

A vector of random, uniformly distributed numbers. The elements are between 0 and 1.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path)
s <- h2o.runif(prostate)
summary(s)

prostate_train <- prostate[s <= 0.8,]
prostate_test <- prostate[s > 0.8,]
nrow(prostate_train) + nrow(prostate_test)

## End(Not run)
```

---

h2o.saveGrid	<i>Saves an existing Grid of models into a given folder.</i>
--------------	--

---

**Description**

Returns a reference to the saved Grid.

**Usage**

```
h2o.saveGrid(
  grid_directory,
  grid_id,
  save_params_references = FALSE,
  export_cross_validation_predictions = FALSE
)
```

**Arguments**

**grid\_directory** A character string containing the path to the folder for the grid to be saved to.

**grid\_id** A character string with identification of the grid to be saved.

**save\_params\_references**  
A logical indicating if objects referenced by grid parameters (e.g. training frame, calibration frame) should also be saved.

**export\_cross\_validation\_predictions**  
A logical indicating whether exported model artifacts should also include CV holdout Frame predictions.

**Value**

Returns an object that is a subclass of [H2OGrid](#).

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris <- as.h2o(iris)

ntrees_opts = c(1, 5)
learn_rate_opts = c(0.1, 0.01)
size_of_hyper_space = length(ntrees_opts) * length(learn_rate_opts)

hyper_parameters = list(ntrees = ntrees_opts, learn_rate = learn_rate_opts)
# Tempdir is chosen arbitrarily. May be any valid folder on an H2O-supported filesystem.
baseline_grid <- h2o.grid(algorithm = "gbm",
  grid_id = "gbm_grid_test",
  x = 1:4,
  y = 5,
  training_frame = iris,
  hyper_params = hyper_parameters)

grid_path <- h2o.saveGrid(grid_directory = tempdir(), grid_id = baseline_grid@grid_id)
# Remove everything from the cluster or restart it
h2o.removeAll()
grid <- h2o.loadGrid(grid_path)

## End(Not run)
```

---

h2o.saveModel

*Save an H2O Model Object to Disk*


---

**Description**

Save an [H2OModel](#) to disk. (Note that ensemble binary models can be saved.)

**Usage**

```
h2o.saveModel(
  object,
  path = "",
  force = FALSE,
  export_cross_validation_predictions = FALSE
)
```

**Arguments**

object	an <a href="#">H2OModel</a> object.
path	string indicating the directory the model will be written to.
force	logical, indicates how to deal with files that already exist.
export_cross_validation_predictions	logical, indicates whether the exported model artifacts should also include CV Holdout Frame predictions. Default is not to export the predictions.

**Details**

In the case of existing files `force = TRUE` will overwrite the file. Otherwise, the operation will fail.  
The owner of the file saved is the user by which H2O cluster was executed.

**See Also**

[h2o.loadModel](#) for loading a model to H2O from disk

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.importFile(path = paste("https://raw.githubusercontent.com",
#   "h2oai/h2o-2/master/smalldata/logreg/prostate.csv", sep = "/"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#   training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.saveModel(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)

## End(Not run)
```

---

`h2o.saveModelDetails` *Save an H2O Model Details*

---

**Description**

Save Model Details of an H2O Model in JSON Format

**Usage**

```
h2o.saveModelDetails(object, path = "", force = FALSE)
```

**Arguments**

<code>object</code>	an <a href="#">H2OModel</a> object.
<code>path</code>	string indicating the directory the model details will be written to.
<code>force</code>	logical, indicates how to deal with files that already exist.

**Details**

Model Details will download as a JSON file. In the case of existing files `force = TRUE` will overwrite the file. Otherwise, the operation will fail.

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.uploadFile(path = system.file("extdata", "prostate.csv", package = "h2o"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#   training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.saveModelDetails(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)

## End(Not run)
```



---

h2o.saveMojo	<i>Deprecated - use h2o.save_mojo instead. Save an H2O Model Object as Mojo to Disk</i>
--------------	---

---

**Description**

Save an MOJO (Model Object, Optimized) to disk.

**Usage**

```
h2o.saveMojo(object, path = "", force = FALSE)
```

**Arguments**

object	an <a href="#">H2OModel</a> object.
path	string indicating the directory the model will be written to.
force	logical, indicates how to deal with files that already exist.

**Details**

MOJO will download as a zip file. In the case of existing files `force = TRUE` will overwrite the file. Otherwise, the operation will fail.

**See Also**

[h2o.saveModel](#) for saving a model to disk as a binary object.

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.uploadFile(path = system.file("extdata", "prostate.csv", package="h2o"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#                       training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.saveMojo(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)

## End(Not run)
```

---

h2o.save_frame	<i>Store frame data in H2O's native format.</i>
----------------	---

---

**Description**

Store frame data in H2O's native format.

**Usage**

```
h2o.save_frame(x, dir, force = TRUE)
```

**Arguments**

x	An H2OFrame object
dir	a filesystem location where to write frame data (hdfs, nfs)
force	logical. overwrite already existing files (defaults to true)

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
h2o.save_frame(prostate, "/tmp/prostate")

## End(Not run)
```

---

h2o.save_mojo	<i>Save an H2O Model Object as Mojo to Disk</i>
---------------	---

---

**Description**

Save an MOJO (Model Object, Optimized) to disk.

**Usage**

```
h2o.save_mojo(object, path = "", force = FALSE)
```

**Arguments**

object	an <a href="#">H2OModel</a> object.
path	string indicating the directory the model will be written to.
force	logical, indicates how to deal with files that already exist.

**Details**

MOJO will download as a zip file. In the case of existing files `force = TRUE` will overwrite the file. Otherwise, the operation will fail.

**See Also**

[h2o.saveModel](#) for saving a model to disk as a binary object.

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.uploadFile(path = system.file("extdata", "prostate.csv", package="h2o"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#                       training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.save_mojo(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)

## End(Not run)
```

---

h2o.save_to_hive	<i>Save contents of this data frame into a Hive table</i>
------------------	---

---

**Description**

For example, `h2o.save_to_hive(data_frame, "jdbc:hive2://host:10000/database", "table_name")` `h2o.save_to_hive(data_f`  
`"jdbc:hive2://host:10000/", "database.table_name", format = "parquet")`

**Usage**

```
h2o.save_to_hive(
  data,
  jdbc_url,
  table_name,
  format = "csv",
  table_path = NULL,
  tmp_path = NULL
)
```

**Arguments**

<code>data</code>	A H2O Frame object to be saved.
<code>jdbc_url</code>	Hive JDBC connection URL.
<code>table_name</code>	Table name into which to store the data. The table must not exist as it will be created
<code>format</code>	Storage format of created Hive table. (default csv, can be csv or parquet)
<code>table_path</code>	If specified, the table will be created as an external table and this is where the data
<code>tmp_path</code>	Path where to store temporary data.

---

h2o.scale

*Scaling and Centering of an H2OFrame*


---

**Description**

Centers and/or scales the columns of an H2O dataset.

**Usage**

```
h2o.scale(x, center = TRUE, scale = TRUE, inplace = FALSE)
```

**Arguments**

x	An H2OFrame object.
center	either a logical value or numeric vector of length equal to the number of columns of x.
scale	either a logical value or numeric vector of length equal to the number of columns of x.
inplace	a logical values indicating whether directly overwrite original data (disabled by default). Exposed for backwards compatibility (prior versions of this functions were always doing an inplace update).

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
summary(iris_hf)

# Scale and center all the numeric columns in iris data set
iris_scaled <- h2o.scale(iris_hf[, 1:4])

## End(Not run)
```

---

h2o.scoreHistory

*Retrieve Model Score History*


---

**Description**

Retrieve Model Score History

**Usage**

```
h2o.scoreHistory(object)
```

**Arguments**

object	An <a href="#">H2OModel</a> object.
--------	-------------------------------------

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
cars["economy_20mpg"] <- as.factor(cars["economy_20mpg"])
predictors <- c("displacement", "power", "weight", "acceleration", "year")
response <- "economy_20mpg"
cars_split <- h2o.splitFrame(data = cars, ratios = 0.8, seed = 1234)
train <- cars_split[[1]]
valid <- cars_split[[2]]
cars_gbm <- h2o.gbm(x = predictors, y = response,
                   training_frame = train,
                   validation_frame = valid,
                   seed = 1234)
h2o.scoreHistory(cars_gbm)

## End(Not run)
```

---

h2o.scoreHistoryGAM	<i>Retrieve GLM Model Score History buried in GAM model</i>
---------------------	---

---

**Description**

Retrieve GLM Model Score History buried in GAM model

**Usage**

```
h2o.scoreHistoryGAM(object)
```

**Arguments**

object	An <a href="#">H2OModel</a> object.
--------	-------------------------------------

---

h2o.screepLOT	<i>Scree Plot</i>
---------------	-------------------

---

**Description**

Scree Plot

**Usage**

```
h2o.screepLOT(model, type = c("barplot", "lines"))
```

**Arguments**

model	A PCA model
type	Type of the plot. Either "barplot" or "lines".

---

h2o.sd	<i>Standard Deviation of a column of data.</i>
--------	--

---

**Description**

Obtain the standard deviation of a column of data.

**Usage**

```
h2o.sd(x, na.rm = FALSE)
```

```
sd(x, na.rm = FALSE)
```

**Arguments**

x	An H2OFrame object.
na.rm	logical. Should missing values be removed?

**See Also**

[h2o.var](#) for variance, and [sd](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
sd(prostate$AGE)

## End(Not run)
```

---

h2o.sdev	<i>Retrieve the standard deviations of principal components</i>
----------	---

---

**Description**

Retrieve the standard deviations of principal components

**Usage**

```
h2o.sdev(object)
```

**Arguments**

object	An <a href="#">H2ODimReductionModel</a> object.
--------	---

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
predictors <- c("displacement", "power", "weight", "acceleration", "year")
cars_pca <- h2o.prcomp(cars, transform = "STANDARDIZE",
                     k = 3, x = predictors, seed = 12345)
h2o.sdev(cars_pca)

## End(Not run)
```

---

h2o.setLevels

*Set Levels of H2O Factor Column*


---

**Description**

Works on a single categorical vector. New domains must be aligned with the old domains. This call has **SIDE EFFECTS** and mutates the column in place (change of the levels will also affect all the frames that are referencing this column). If you want to make a copy of the column instead, use parameter `in.place = FALSE`.

**Usage**

```
h2o.setLevels(x, levels, in.place = TRUE)
```

**Arguments**

x	A single categorical column.
levels	A character vector specifying the new levels. The number of new levels must match the number of old levels.
in.place	Indicates whether new domain will be directly applied to the column (in place change) or if a copy of the column will be created with the given domain levels.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
new_levels <- c("setosa", "versicolor", "caroliniana")
iris_hf$Species <- h2o.setLevels(iris_hf$Species, new_levels, in.place = FALSE)
h2o.levels(iris_hf$Species)

## End(Not run)
```

---

h2o.setTimezone      *Set the Time Zone on the H2O cluster*

---

### Description

Set the Time Zone on the H2O cluster

### Usage

```
h2o.setTimezone(tz)
```

### Arguments

tz                      The desired timezone.

### Examples

```
## Not run:
library(h2o)
h2o.init()

h2o.setTimezone("America/Juneau")
h2o.getTimezone()

## End(Not run)
```

---

h2o.set\_s3\_credentials      *Creates a new Amazon S3 client internally with specified credentials.*

---

### Description

There are no validations done to the credentials. Incorrect credentials are thus revealed with first S3 import call.

### Usage

```
h2o.set_s3_credentials(secretKeyId, secretAccessKey, sessionToken = NULL)
```

### Arguments

secretKeyId      Amazon S3 Secret Key ID (provided by Amazon)

secretAccessKey      Amazon S3 Secret Access Key (provided by Amazon)

sessionToken      Amazon Session Token (optional, only when using AWS Temporary Credentials)



---

 h2o.shap\_explain\_row\_plot

*SHAP Local Explanation*


---

### Description

SHAP explanation shows contribution of features for a given instance. The sum of the feature contributions and the bias term is equal to the raw prediction of the model, i.e., prediction before applying inverse link function. H2O implements TreeSHAP which when the features are correlated, can increase contribution of a feature that had no influence on the prediction.

### Usage

```
h2o.shap_explain_row_plot(
  model,
  newdata,
  row_index,
  columns = NULL,
  top_n_features = 10,
  plot_type = c("barplot", "breakdown"),
  contribution_type = c("both", "positive", "negative")
)
```

### Arguments

model	An H2O tree-based model. This includes Random Forest, GBM and XGboost only. Must be a binary classification or regression model.
newdata	An H2O Frame, used to determine feature contributions.
row_index	Instance row index.
columns	List of columns or list of indices of columns to show. If specified, then the top_n_features parameter will be ignored.
top_n_features	Integer specifying the maximum number of columns to show (ranked by their contributions). When plot_type = "barplot", then top_n_features features will be chosen for each contribution_type.
plot_type	Either "barplot" or "breakdown". Defaults to "barplot".
contribution_type	When plot_type == "barplot", plot one of "negative", "positive", or "both" contributions. Defaults to "both".

### Value

A ggplot2 object.

### Examples

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
```

```
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
gbm <- h2o.gbm(y = response,
               training_frame = train)

# Create the SHAP row explanation plot
shap_explain_row_plot <- h2o.shap_explain_row_plot(gbm, test, row_index = 1)
print(shap_explain_row_plot)

## End(Not run)
```

---

h2o.shap\_summary\_plot *SHAP Summary Plot*

---

## Description

SHAP summary plot shows the contribution of the features for each instance (row of data). The sum of the feature contributions and the bias term is equal to the raw prediction of the model, i.e., prediction before applying inverse link function.

## Usage

```
h2o.shap_summary_plot(
  model,
  newdata,
  columns = NULL,
  top_n_features = 20,
  sample_size = 1000
)
```

## Arguments

model	An H2O tree-based model. This includes Random Forest, GBM and XGboost only. Must be a binary classification or regression model.
newdata	An H2O Frame, used to determine feature contributions.
columns	List of columns or list of indices of columns to show. If specified, then the top_n_features parameter will be ignored.
top_n_features	Integer specifying the maximum number of columns to show (ranked by variable importance).
sample_size	Integer specifying the maximum number of observations to be plotted.

**Value**

A ggplot2 object

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
gbm <- h2o.gbm(y = response,
               training_frame = train)

# Create the SHAP summary plot
shap_summary_plot <- h2o.shap_summary_plot(gbm, test)
print(shap_summary_plot)

## End(Not run)
```

---

h2o.show\_progress      *Enable Progress Bar*

---

**Description**

Enable Progress Bar

**Usage**

```
h2o.show_progress()
```

**Examples**

```
## Not run:
library(h2o)
h2o.init()
h2o.no_progress()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_wheader.csv"
iris <- h2o.importFile(f)
iris["class"] <- as.factor(iris["class"])
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
splits <- h2o.splitFrame(iris, ratios = 0.8, seed = 1234)
```

```
train <- splits[[1]]
valid <- splits[[2]]
h2o.show_progress()

iris_km <- h2o.kmeans(x = predictors,
                     training_frame = train,
                     validation_frame = valid,
                     k = 10, estimate_k = TRUE,
                     standardize = FALSE, seed = 1234)

## End(Not run)
```

---

h2o.shutdown

*Shut Down H2O Instance*

---

### Description

Shut down the specified instance. All data will be lost.

### Usage

```
h2o.shutdown(prompt = TRUE)
```

### Arguments

prompt	A logical value indicating whether to prompt the user before shutting down the H2O server.
--------	--

### Details

This method checks if H2O is running at the specified IP address and port, and if it is, shuts down that H2O instance.

### WARNING

All data, models, and other values stored on the server will be lost! Only call this function if you and all other clients connected to the H2O server are finished and have saved your work.

### Note

Users must call `h2o.shutdown` explicitly in order to shut down the local H2O instance started by R. If R is closed before H2O, then an attempt will be made to automatically shut down H2O. This only applies to local instances started with `h2o.init`, not remote H2O servers.

### See Also

[h2o.init](#)

**Examples**

```
# Don't run automatically to prevent accidentally shutting down a cluster
## Not run:
library(h2o)
h2o.init()
h2o.shutdown()

## End(Not run)
```

---

h2o.signif

*Round doubles/floats to the given number of significant digits.*

---

**Description**

Round doubles/floats to the given number of significant digits.

**Usage**

```
h2o.signif(x, digits = 6)

signif(x, digits = 6)
```

**Arguments**

x	An H2OFrame object.
digits	Number of significant digits to round doubles/floats.

**See Also**

[Round](#) for the base R implementation, `signif()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/coxph_test/heart.csv"
heart <- h2o.importFile(f)

h2o.signif(heart["age"], digits = 3)

## End(Not run)
```

---

h2o.sin	<i>Compute the sine of x</i>
---------	------------------------------

---

**Description**

Compute the sine of x

**Usage**

```
h2o.sin(x)
```

**Arguments**

x	An H2OFrame object.
---	---------------------

**See Also**

[Trig](#) for the base R implementation, `sin()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.sin(frame)

## End(Not run)
```

---

h2o.skewness	<i>Skewness of a column</i>
--------------	-----------------------------

---

**Description**

Obtain the skewness of a column of a parsed H2O data object.

**Usage**

```
h2o.skewness(x, ..., na.rm = TRUE)

skewness.H2OFrame(x, ..., na.rm = TRUE)
```

**Arguments**

x	An H2OFrame object.
...	Further arguments to be passed from or to other methods.
na.rm	A logical value indicating whether NA or missing values should be stripped before the computation.

**Value**

Returns a list containing the skewness for each column (NaN for non-numeric columns).

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.skewness(prostate$AGE)

## End(Not run)
```

---

h2o.splitFrame

*Split an H2O Data Set*


---

**Description**

Split an existing H2O data set according to user-specified ratios. The number of subsets is always 1 more than the number of given ratios. Note that this does not give an exact split. H2O is designed to be efficient on big data using a probabilistic splitting method rather than an exact split. For example, when specifying a split of 0.75/0.25, H2O will produce a test/train split with an expected value of 0.75/0.25 rather than exactly 0.75/0.25. On small datasets, the sizes of the resulting splits will deviate from the expected value more than on big data, where they will be very close to exact.

**Usage**

```
h2o.splitFrame(data, ratios = 0.75, destination_frames, seed = -1)
```

**Arguments**

data	An H2OFrame object, to be split.
ratios	A numeric value or array indicating the ratio of total rows contained in each split. Must total up to less than 1. e.g. c(0.8) for 80/20 split.
destination_frames	An array of frame IDs equal to the number of values specified in the ratios array, plus one.
seed	Random seed.

**Value**

Returns a list of split H2OFrames

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_split <- h2o.splitFrame(iris_hf, ratios = c(0.2, 0.5))
head(iris_split[[1]])
summary(iris_split[[1]])

## End(Not run)
```

---

h2o.sqrt

*Compute the square root of x*

---

**Description**

Compute the square root of x

**Usage**

```
h2o.sqrt(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[MathFun](#) for the base R implementation, `sqrt()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                        categorical_fraction = 0.0,
                        missing_fraction = 0.7,
                        seed = 123)

h2o.sqrt(frame)

## End(Not run)
```



---

h2o.stackedEnsemble     *Builds a Stacked Ensemble*

---

### Description

Build a stacked ensemble (aka. Super Learner) using the H2O base learning algorithms specified by the user.

### Usage

```
h2o.stackedEnsemble(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  blending_frame = NULL,
  base_models = list(),
  metalearner_algorithm = c("AUTO", "deeplearning", "drf", "gbm", "glm", "naivebayes",
    "xgboost"),
  metalearner_nfolds = 0,
  metalearner_fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
  metalearner_fold_column = NULL,
  metalearner_params = NULL,
  metalearner_transform = c("NONE", "Logit"),
  max_runtime_secs = 0,
  weights_column = NULL,
  offset_column = NULL,
  seed = -1,
  score_training_samples = 10000,
  keep_levelone_frame = FALSE,
  export_checkpoints_dir = NULL,
  auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
    "WEIGHTED_OVO")
)
```

### Arguments

x	(Optional). A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used. Training frame is used only to compute ensemble training metrics.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.

<code>blending_frame</code>	Frame used to compute the predictions that serve as the training frame for the metalearner (triggers blending mode if provided)
<code>base_models</code>	List of models or grids (or their ids) to ensemble/stack together. Grids are expanded to individual models. If not using blending frame, then models must have been cross-validated using <code>nfolds &gt; 1</code> , and folds must be identical across models.
<code>metalearner_algorithm</code>	Type of algorithm to use as the metalearner. Options include 'AUTO' (GLM with non negative weights; if <code>validation_frame</code> is present, a lambda search is performed), 'deplearning' (Deep Learning with default parameters), 'drf' (Random Forest with default parameters), 'gbm' (GBM with default parameters), 'glm' (GLM with default parameters), 'naivebayes' (NaiveBayes with default parameters), or 'xgboost' (if available, XGBoost with default parameters). Must be one of: "AUTO", "deplearning", "drf", "gbm", "glm", "naivebayes", "xgboost". Defaults to AUTO.
<code>metalearner_nfolds</code>	Number of folds for K-fold cross-validation of the metalearner algorithm (0 to disable or $\geq 2$ ). Defaults to 0.
<code>metalearner_fold_assignment</code>	Cross-validation fold assignment scheme for metalearner cross-validation. Defaults to AUTO (which is currently set to Random). The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified".
<code>metalearner_fold_column</code>	Column with cross-validation fold index assignment per observation for cross-validation of the metalearner.
<code>metalearner_params</code>	Parameters for metalearner algorithm
<code>metalearner_transform</code>	Transformation used for the level one frame. Must be one of: "NONE", "Logit". Defaults to NONE.
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>weights_column</code>	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set <code>weight = 0</code> for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with <code>weight == 0</code> .
<code>offset_column</code>	Offset column. This will be added to the combination of columns before applying the link function.
<code>seed</code>	Seed for random numbers; passed through to the metalearner algorithm. Defaults to -1 (time-based random number).
<code>score_training_samples</code>	Specify the number of training set samples for scoring. The value must be $\geq 0$ . To use all training samples, enter 0. Defaults to 10000.

keep\_levelone\_frame  
 Logical. Keep level one frame used for metalearner training. Defaults to FALSE.

export\_checkpoints\_dir  
 Automatically export generated models to this directory.

auc\_type  
 Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO\_OVR", "WEIGHTED\_OVR", "MACRO\_OVO", "WEIGHTED\_OVO". Defaults to AUTO.

## Examples

```
## Not run:
library(h2o)
h2o.init()

# Import a sample binary outcome train/test set
train <- h2o.importFile("https://s3.amazonaws.com/erin-data/higgs/higgs_train_10k.csv")
test <- h2o.importFile("https://s3.amazonaws.com/erin-data/higgs/higgs_test_5k.csv")

# Identify predictors and response
y <- "response"
x <- setdiff(names(train), y)

# For binary classification, response should be a factor
train[, y] <- as.factor(train[, y])
test[, y] <- as.factor(test[, y])

# Number of CV folds
nfolds <- 5

# Train & Cross-validate a GBM
my_gbm <- h2o.gbm(x = x,
  y = y,
  training_frame = train,
  distribution = "bernoulli",
  ntrees = 10,
  max_depth = 3,
  min_rows = 2,
  learn_rate = 0.2,
  nfolds = nfolds,
  fold_assignment = "Modulo",
  keep_cross_validation_predictions = TRUE,
  seed = 1)

# Train & Cross-validate a RF
my_rf <- h2o.randomForest(x = x,
  y = y,
  training_frame = train,
  ntrees = 50,
  nfolds = nfolds,
  fold_assignment = "Modulo",
  keep_cross_validation_predictions = TRUE,
  seed = 1)

# Train a stacked ensemble using the GBM and RF above
ensemble <- h2o.stackedEnsemble(x = x,
  y = y,
  training_frame = train,
```

```

model_id = "my_ensemble_binomial",
base_models = list(my_gbm, my_rf))

## End(Not run)

```

---

h2o.startLogging      *Start Writing H2O R Logs*

---

### Description

Begin logging H2o R POST commands and error responses to local disk. Used primarily for debugging purposes.

### Usage

```
h2o.startLogging(file)
```

### Arguments

file                    a character string name for the file, automatically generated

### See Also

[h2o.stopLogging](#), [h2o.clearLog](#),                    [h2o.openLog](#)

### Examples

```

## Not run:
library(h2o)
h2o.init()
h2o.startLogging()
australia_path = system.file("extdata", "australia.csv", package = "h2o")
australia = h2o.importFile(path = australia_path)
h2o.stopLogging()

## End(Not run)

```

---

h2o.std\_coef\_plot      *Plot Standardized Coefficient Magnitudes*

---

### Description

Plot a GLM model's standardized coefficient magnitudes.

### Usage

```
h2o.std_coef_plot(model, num_of_features = NULL)
```

**Arguments**

model                    A trained generalized linear model  
num\_of\_features           The number of features to be shown in the plot

**See Also**

[h2o.varimp\\_plot](#) for variable importances plot of random forest, GBM, deep learning.

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
  
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")  
prostate <- h2o.importFile(prostate_path)  
prostate[, 2] <- as.factor(prostate[, 2])  
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),  
                      training_frame = prostate, family = "binomial",  
                      nfold = 0, alpha = 0.5, lambda_search = FALSE)  
h2o.std_coef_plot(prostate_glm)  
  
## End(Not run)
```

---

h2o.stopLogging                    *Stop Writing H2O R Logs*

---

**Description**

Halt logging of H2O R POST commands and error responses to local disk. Used primarily for debugging purposes.

**Usage**

```
h2o.stopLogging()
```

**See Also**

[h2o.startLogging](#), [h2o.clearLog](#),                    [h2o.openLog](#)

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
h2o.startLogging()  
australia_path = system.file("extdata", "australia.csv", package = "h2o")  
australia = h2o.importFile(path = australia_path)  
h2o.stopLogging()  
  
## End(Not run)
```

---

h2o.str	<i>Display the structure of an H2OFrame object</i>
---------	--

---

**Description**

Display the structure of an H2OFrame object

**Usage**

```
h2o.str(object, ..., cols = FALSE)
```

**Arguments**

object	An H2OFrame.
...	Further arguments to be passed from or to other methods.
cols	Print the per-column str for the H2OFrame

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
  categorical_fraction = 0.0,
  missing_fraction = 0.7,
  seed = 123)
h2o.str(frame, cols = FALSE)

## End(Not run)
```

---

h2o.stringdist	<i>Compute element-wise string distances between two H2OFrames</i>
----------------	--

---

**Description**

Compute element-wise string distances between two H2OFrames. Both frames need to have the same shape (N x M) and only contain string/factor columns. Return a matrix (H2OFrame) of shape N x M.

**Usage**

```
h2o.stringdist(
  x,
  y,
  method = c("lv", "lcs", "qgram", "jaccard", "jw", "soundex"),
  compare_empty = TRUE
)
```

**Arguments**

x	An H2OFrame
y	A comparison H2OFrame
method	A string identifier indicating what string distance measure to use. Must be one of: "lv" - Levenshtein distance "lcs" - Longest common substring distance "qgram" - q-gram distance "jaccard" - Jaccard distance between q-gram profiles "jw" - Jaro, or Jaro-Winker distance "soundex" - Distance based on soundex encoding
compare_empty	if set to FALSE, empty strings will be handled as NaNs

**Examples**

```
## Not run:
h2o.init()
x <- as.h2o(c("Martha", "Dwayne", "Dixon"))
y <- as.character(as.h2o(c("Marhta", "Duane", "Dicksonx")))
h2o.stringdist(x, y, method = "jw")

## End(Not run)
```

---

h2o.strsplit	<i>String Split</i>
--------------	---------------------

---

**Description**

String Split

**Usage**

```
h2o.strsplit(x, split)
```

**Arguments**

x	The column whose strings must be split.
split	The pattern to split on.

**Value**

An H2OFrame where each column is the outcome of the string split.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_split <- as.h2o("Split at every character.")
split_string <- h2o.strsplit(string_to_split, "")

## End(Not run)
```

---

h2o.sub	<i>String Substitute</i>
---------	--------------------------

---

### Description

Creates a copy of the target column in which each string has the first occurrence of the regex pattern replaced with the replacement substring.

### Usage

```
h2o.sub(pattern, replacement, x, ignore.case = FALSE)
```

### Arguments

pattern	The pattern to replace.
replacement	The replacement pattern.
x	The column on which to operate.
ignore.case	Case sensitive or not

### Examples

```
## Not run:
library(h2o)
h2o.init()
string_to_sub <- as.h2o("r tutorial")
sub_string <- h2o.sub("r ", "H2O ", string_to_sub)

## End(Not run)
```

---

h2o.substring	<i>Substring</i>
---------------	------------------

---

### Description

Returns a copy of the target column that is a substring at the specified start and stop indices, inclusive. If the stop index is not specified, then the substring extends to the end of the original string. If start is longer than the number of characters in the original string, or is greater than stop, an empty string is returned. Negative start is coerced to 0.

### Usage

```
h2o.substring(x, start, stop = "[ ]")
```

```
h2o.substr(x, start, stop = "[ ]")
```

### Arguments

x	The column on which to operate.
start	The index of the first element to be included in the substring.
stop	Optional, The index of the last element to be included in the substring.



**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_substring <- as.h2o("1234567890")
substr <- h2o.substring(string_to_substring, 2) #Get substring from second index onwards

## End(Not run)
```

---

h2o.sum

---

*Compute the frame's sum by-column (or by-row).*


---

**Description**

Compute the frame's sum by-column (or by-row).

**Usage**

```
h2o.sum(x, na.rm = FALSE, axis = 0, return_frame = FALSE)
```

**Arguments**

x	An H2OFrame object.
na.rm	logical. indicating whether missing values should be removed.
axis	An int that indicates whether to do down a column (0) or across a row (1). For row or column sums, the return_frame parameter must be TRUE.
return_frame	A boolean that indicates whether to return an H2O frame or one single aggregated value. Default is FALSE.

**See Also**

[sum](#) for the base R implementation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                        categorical_fraction = 0.0,
                        missing_fraction = 0.7,
                        seed = 123)
h2o.sum(frame["C1"], na.rm = TRUE, axis = 0, return_frame = TRUE)

## End(Not run)
```

---

h2o.summary

*Summarizes the columns of an H2OFrame.*


---

### Description

A method for the `summary` generic. Summarizes the columns of an H2O data frame or subset of columns and rows using vector notation (e.g. `dataset[row, col]`).

### Usage

```
h2o.summary(object, factors = 6L, exact_quantiles = FALSE, ...)
```

```
## S3 method for class 'H2OFrame'
summary(object, factors, exact_quantiles, ...)
```

### Arguments

<code>object</code>	An H2OFrame object.
<code>factors</code>	The number of factors to return in the summary. Default is the top 6.
<code>exact_quantiles</code>	Compute exact quantiles or use approximation. Default is to use approximation.
<code>...</code>	Further arguments passed to or from other methods.

### Details

By default it uses approximated version of quantiles computation, however, user can modify this behavior by setting up `exact_quantiles` argument to true.

### Value

A table displaying the minimum, 1st quartile, median, mean, 3rd quartile and maximum for each numeric column, and the levels and category counts of the levels in each categorical column.

### Examples

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path)
summary(prostate)
summary(prostate$GLEASON)
summary(prostate[, 4:6])
summary(prostate, exact_quantiles = TRUE)

## End(Not run)
```

---

h2o.svd	<i>Singular value decomposition of an H2O data frame using the power method</i>
---------	---

---

### Description

Singular value decomposition of an H2O data frame using the power method

### Usage

```
h2o.svd(
  training_frame,
  x,
  destination_key,
  model_id = NULL,
  validation_frame = NULL,
  ignore_const_cols = TRUE,
  score_each_iteration = FALSE,
  transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"),
  svd_method = c("GramSVD", "Power", "Randomized"),
  nv = 1,
  max_iterations = 1000,
  seed = -1,
  keep_u = TRUE,
  u_name = NULL,
  use_all_factor_levels = TRUE,
  max_runtime_secs = 0,
  export_checkpoints_dir = NULL
)
```

### Arguments

training_frame	Id of the training data frame.
x	A vector containing the character names of the predictors in the model.
destination_key	(Optional) The unique key assigned to the resulting model. Automatically generated if none is provided.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
ignore_const_cols	Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
transform	Transformation of training data Must be one of: "NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE". Defaults to NONE.
svd_method	Method for computing SVD (Caution: Randomized is currently experimental and unstable) Must be one of: "GramSVD", "Power", "Randomized". Defaults to GramSVD.

nv	Number of right singular vectors Defaults to 1.
max_iterations	Maximum iterations Defaults to 1000.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
keep_u	Logical. Save left singular vectors? Defaults to TRUE.
u_name	Frame key to save left singular vectors
use_all_factor_levels	Logical. Whether first factor level is included in each categorical expansion Defaults to TRUE.
max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
export_checkpoints_dir	Automatically export generated models to this directory.

**Value**

an object of class [H2ODimReductionModel](#).

**References**

N. Halko, P.G. Martinsson, J.A. Tropp. Finding structure with randomness: Probabilistic algorithms for constructing approximate matrix decompositions[<https://arxiv.org/abs/0909.4061>]. SIAM Rev., Survey and Review section, Vol. 53, num. 2, pp. 217-288, June 2011.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
h2o.svd(training_frame = australia, nv = 8)

## End(Not run)
```

---

h2o.table

*Cross Tabulation and Table Creation in H2O*


---

**Description**

Uses the cross-classifying factors to build a table of counts at each combination of factor levels.

**Usage**

```
h2o.table(x, y = NULL, dense = TRUE)
```

```
table.H2OFrame(x, y = NULL, dense = TRUE)
```

**Arguments**

x	An H2OFrame object with at most two columns.
y	An H2OFrame similar to x, or NULL.
dense	A logical for dense representation, which lists only non-zero counts, 1 combination per row. Set to FALSE to expand counts across all combinations.

**Value**

Returns a tabulated H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
summary(prostate)

# Counts of the ages of all patients
head(h2o.table(prostate[, 3]))
h2o.table(prostate[, 3])

# Two-way table of ages (rows) and race (cols) of all patients
head(h2o.table(prostate[, c(3, 4)]))
h2o.table(prostate[, c(3, 4)])

## End(Not run)
```

---

h2o.tabulate

*Tabulation between Two Columns of an H2OFrame*


---

**Description**

Simple Co-Occurrence based tabulation of X vs Y, where X and Y are two Vecs in a given dataset. Uses histogram of given resolution in X and Y. Handles numerical/categorical data and missing values. Supports observation weights.

**Usage**

```
h2o.tabulate(data, x, y, weights_column = NULL, nbins_x = 50, nbins_y = 50)
```

**Arguments**

data	An H2OFrame object.
x	predictor column
y	response column
weights_column	(optional) observation weights column
nbins_x	number of bins for predictor column
nbins_y	number of bins for response column

**Value**

Returns two TwoDimTables of 3 columns each count\_table: X Y counts response\_table: X meanY counts

**Examples**

```
## Not run:
library(h2o)
h2o.init()
df <- as.h2o(iris)
tab <- h2o.tabulate(data = df, x = "Sepal.Length", y = "Petal.Width",
  weights_column = NULL, nbins_x = 10, nbins_y = 10)
plot(tab)

## End(Not run)
```

---

h2o.tan

*Compute the tangent of x*

---

**Description**

Compute the tangent of x

**Usage**

```
h2o.tan(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Trig](#) for the base R implementation, tan().

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
  categorical_fraction = 0.0,
  missing_fraction = 0.7,
  seed = 123)

h2o.tan(frame)

## End(Not run)
```

---

h2o.tanh	<i>Compute the hyperbolic tangent of x</i>
----------	--

---

**Description**

Compute the hyperbolic tangent of x

**Usage**

```
h2o.tanh(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[Hyperbolic](#) for the base R implementation, `tanh()`.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

h2o.tanh(frame)

## End(Not run)
```

---

h2o.targetencoder	<i>Transformation of a categorical variable with a mean value of the target variable</i>
-------------------	--

---

**Description**

Transformation of a categorical variable with a mean value of the target variable

**Usage**

```
h2o.targetencoder(
  x,
  y,
  training_frame,
  model_id = NULL,
  fold_column = NULL,
  columns_to_encode = NULL,
  keep_original_categorical_columns = TRUE,
```

```

blending = FALSE,
inflection_point = 10,
smoothing = 20,
data_leakage_handling = c("leave_one_out", "k_fold", "none", "LeaveOneOut", "KFold",
  "None"),
noise = 0.01,
seed = -1,
...
)

```

### Arguments

<code>x</code>	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If <code>x</code> is missing, then all columns except <code>y</code> are used.
<code>y</code>	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
<code>training_frame</code>	Id of the training data frame.
<code>model_id</code>	Destination id for this model; auto-generated if not specified.
<code>fold_column</code>	Column with cross-validation fold index assignment per observation.
<code>columns_to_encode</code>	List of categorical columns or groups of categorical columns to encode. When groups of columns are specified, each group is encoded as a single column (interactions are created internally).
<code>keep_original_categorical_columns</code>	Logical. If true, the original non-encoded categorical features will remain in the result frame. Defaults to TRUE.
<code>blending</code>	Logical. If true, enables blending of posterior probabilities (computed for a given categorical value) with prior probabilities (computed on the entire set). This allows to mitigate the effect of categorical values with small cardinality. The blending effect can be tuned using the ‘ <code>inflection_point</code> ’ and ‘ <code>smoothing</code> ’ parameters. Defaults to FALSE.
<code>inflection_point</code>	Inflection point of the sigmoid used to blend probabilities (see ‘ <code>blending</code> ’ parameter). For a given categorical value, if it appears less than ‘ <code>inflection_point</code> ’ in a data sample, then the influence of the posterior probability will be smaller than the prior. Defaults to 10.
<code>smoothing</code>	Smoothing factor corresponds to the inverse of the slope at the inflection point on the sigmoid used to blend probabilities (see ‘ <code>blending</code> ’ parameter). If smoothing tends towards 0, then the sigmoid used for blending turns into a Heaviside step function. Defaults to 20.
<code>data_leakage_handling</code>	Data leakage handling strategy used to generate the encoding. Supported options are: 1) "none" (default) - no holdout, using the entire training frame. 2) "leave_one_out" - current row's response value is subtracted from the per-level frequencies pre-calculated on the entire training frame. 3) "k_fold" - encodings for a fold are generated based on out-of-fold data. Must be one of: "leave_one_out", "k_fold", "none", "LeaveOneOut", "KFold", "None". Defaults to None.



noise	The amount of noise to add to the encoded column. Use 0 to disable noise, and -1 (=AUTO) to let the algorithm determine a reasonable amount of noise. Defaults to 0.01.
seed	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
...	Mainly used for backwards compatibility, to allow deprecated parameters.

### Examples

```
## Not run:
library(h2o)
h2o.init()
#Import the titanic dataset
f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/gbm_test/titanic.csv"
titanic <- h2o.importFile(f)

# Set response as a factor
response <- "survived"
titanic[response] <- as.factor(titanic[response])

# Split the dataset into train and test
splits <- h2o.splitFrame(data = titanic, ratios = .8, seed = 1234)
train <- splits[[1]]
test <- splits[[2]]

# Choose which columns to encode
encode_columns <- c("home.dest", "cabin", "embarked")

# Train a TE model
te_model <- h2o.targetencoder(x = encode_columns,
                             y = response,
                             training_frame = train,
                             fold_column = "pclass",
                             data_leakage_handling = "KFold")

# New target encoded train and test sets
train_te <- h2o.transform(te_model, train)
test_te <- h2o.transform(te_model, test)

## End(Not run)
```

---

h2o.target\_encode\_apply

*Apply Target Encoding Map to Frame*

---

### Description

Applies a target encoding map to an H2OFrame object. Computing target encoding for high cardinality categorical columns can improve performance of supervised learning models. A Target Encoding tutorial is available here: [https://github.com/h2oai/h2o-tutorials/blob/master/best-practices/categorical-predictors/target\\_encoding.md](https://github.com/h2oai/h2o-tutorials/blob/master/best-practices/categorical-predictors/target_encoding.md).

**Usage**

```
h2o.target_encode_apply(
  data,
  x,
  y,
  target_encode_map,
  holdout_type,
  fold_column = NULL,
  blended_avg = TRUE,
  noise_level = NULL,
  seed = -1
)
```

**Arguments**

data	An H2OFrame object with which to apply the target encoding map.
x	A list containing the names or indices of the variables to encode. A target encoding column will be created for each element in the list. Items in the list can be multiple columns. For example, if <code>x = list(c("A"), c("B", "C"))</code> , then the resulting frame will have a target encoding column for A and a target encoding column for B & C (in this case, we group by two columns).
y	The name or column index of the response variable in the data. The response variable can be either numeric or binary.
target_encode_map	A list of H2OFrame objects that is the results of the <a href="#">h2o.target_encode_create</a> function.
holdout_type	The holdout type used. Must be one of: "LeaveOneOut", "KFold", "None".
fold_column	(Optional) The name or column index of the fold column in the data. Defaults to NULL (no 'fold_column'). Only required if 'holdout_type' = "KFold".
blended_avg	Logical. (Optional) Whether to perform blended average.
noise_level	(Optional) The amount of random noise added to the target encoding. This helps prevent overfitting. Defaults to 0.01 * range of y.
seed	(Optional) A random seed used to generate draws from the uniform distribution for random noise. Defaults to -1.

**Value**

Returns an H2OFrame object containing the target encoding per record.

**See Also**

[h2o.target\\_encode\\_create](#) for creating the target encoding map

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Get Target Encoding Frame on bank-additional-full data with numeric `y`
data <- h2o.importFile(
```

```

path = "https://s3.amazonaws.com/h2o-public-test-data/smalldata/demos/bank-additional-full.csv")
splits <- h2o.splitFrame(data, seed = 1234)
train <- splits[[1]]
test <- splits[[2]]
mapping <- h2o.target_encode_create(data = train, x = list(c("job"), c("job", "marital")),
                                   y = "age")

# Apply mapping to the training dataset
train_encode <- h2o.target_encode_apply(data = train, x = list(c("job"), c("job", "marital")),
                                       y = "age", mapping, holdout_type = "LeaveOneOut")

# Apply mapping to a test dataset
test_encode <- h2o.target_encode_apply(data = test, x = list(c("job"), c("job", "marital")),
                                       y = "age", target_encode_map = mapping,
                                       holdout_type = "None")

## End(Not run)

```

---

h2o.target\_encode\_create  
*Create Target Encoding Map*

---

## Description

Creates a target encoding map based on group-by columns ('x') and a numeric or binary target column ('y'). Computing target encoding for high cardinality categorical columns can improve performance of supervised learning models. A Target Encoding tutorial is available here: [https://github.com/h2oai/h2o-tutorials/blob/master/best-practices/categorical-predictors/target\\_encoding.md](https://github.com/h2oai/h2o-tutorials/blob/master/best-practices/categorical-predictors/target_encoding.md).

## Usage

```
h2o.target_encode_create(data, x, y, fold_column = NULL)
```

## Arguments

data	An H2OFrame object with which to create the target encoding map.
x	A list containing the names or indices of the variables to encode. A target encoding map will be created for each element in the list. Items in the list can be multiple columns. For example, if 'x = list(c("A"), c("B", "C"))', then there will be one mapping frame for A and one mapping frame for B & C (in this case, we group by two columns).
y	The name or column index of the response variable in the data. The response variable can be either numeric or binary.
fold_column	(Optional) The name or column index of the fold column in the data. Defaults to NULL (no 'fold_column').

## Value

Returns a list of H2OFrame objects containing the target encoding mapping for each column in 'x'.

**See Also**

[h2o.target\\_encode\\_apply](#) for applying the target encoding mapping to a frame.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Get Target Encoding Map on bank-additional-full data with numeric response
data <- h2o.importFile(
  path = "https://s3.amazonaws.com/h2o-public-test-data/smalldata/demos/bank-additional-full.csv")
mapping_age <- h2o.target_encode_create(data = data, x = list(c("job"), c("job", "marital")),
  y = "age")

head(mapping_age)

# Get Target Encoding Map on bank-additional-full data with binary response
mapping_y <- h2o.target_encode_create(data = data, x = list(c("job"), c("job", "marital")),
  y = "y")

head(mapping_y)

## End(Not run)
```

---

h2o.tf\_idf

*Computes TF-IDF values for each word in given documents.*


---

**Description**

Computes TF-IDF values for each word in given documents.

**Usage**

```
h2o.tf_idf(
  frame,
  document_id_col,
  text_col,
  preprocess = TRUE,
  case_sensitive = TRUE
)
```

**Arguments**

frame	documents or words frame for which TF-IDF values should be computed.
document_id_col	index or name of a column containing document IDs.
text_col	index or name of a column containing documents if ‘preprocess = TRUE’ or words if ‘preprocess = FALSE’.
preprocess	whether input text data should be pre-processed. Defaults to ‘TRUE’.
case_sensitive	whether input data should be treated as case sensitive. Defaults to ‘TRUE’.

**Value**

resulting frame with TF-IDF values. Row format: documentID, word, TF, IDF, TF-IDF

---

h2o.toFrame	<i>Convert a word2vec model into an H2OFrame</i>
-------------	--

---

**Description**

Converts a given word2vec model into an H2OFrame. The frame represents learned word embeddings

**Usage**

```
h2o.toFrame(word2vec)
```

**Arguments**

word2vec            A word2vec model.

**Examples**

```
## Not run:
h2o.init()

# Build a dummy word2vec model
data <- as.character(as.h2o(c("a", "b", "a")))
w2v_model <- h2o.word2vec(data, sent_sample_rate = 0, min_word_freq = 0, epochs = 1, vec_size = 2)

# Transform words to vectors and return average vector for each sentence
h2o.toFrame(w2v_model) # -> Frame made of 2 rows and 2 columns

## End(Not run)
```

---

h2o.tokenize	<i>Tokenize String</i>
--------------	------------------------

---

**Description**

h2o.tokenize is similar to h2o.strsplit, the difference between them is that h2o.tokenize will store the tokenized text into a single column making it easier for additional processing (filtering stop words, word2vec algo, ...).

**Usage**

```
h2o.tokenize(x, split)
```

**Arguments**

x                    The column or columns whose strings to tokenize.  
split                The regular expression to split on.

**Value**

An H2OFrame with a single column representing the tokenized Strings. Original rows of the input DF are separated by NA.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_tokenize <- as.h2o("Split at every character and tokenize.")
tokenize_string <- h2o.tokenize(as.character(string_to_tokenize), "")

## End(Not run)
```

---

h2o.tolower	<i>Convert strings to lowercase</i>
-------------	-------------------------------------

---

**Description**

Convert strings to lowercase

**Usage**

```
h2o.tolower(x)
```

**Arguments**

x                    An H2OFrame object whose strings should be lower cased

**Value**

An H2OFrame with all entries in lowercase format

**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_lower <- as.h2o("ABCDE")
lowered_string <- h2o.tolower(string_to_lower)

## End(Not run)
```

---

h2o.topN	<i>H2O topN</i>
----------	-----------------

---

**Description**

Extract the top N percent of values of a column and return it in a H2OFrame.

**Usage**

```
h2o.topN(x, column, nPercent)
```

**Arguments**

x	an H2OFrame
column	is a column name or column index to grab the top N percent value from
nPercent	is a top percentage value to grab

**Value**

An H2OFrame with 2 columns. The first column is the original row indices, second column contains the topN values

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/bigdata/laptop/jira/TopBottomNRep4.csv.zip"
dataset <- h2o.importFile(f)
frameNames <- names(dataset)
nPercent <- c(1, 2, 3, 4)
nP <- nPercent[sample(1:length(nPercent), 1, replace = FALSE)]
colIndex <- sample(1:length(frameNames), 1, replace = FALSE)
h2o.topN(dataset, frameNames[colIndex], nP)

## End(Not run)
```

---

h2o.totss	<i>Get the total sum of squares.</i>
-----------	--------------------------------------

---

**Description**

If "train", "valid", and "xval" parameters are FALSE (default), then the training totss value is returned. If more than one parameter is set to TRUE, then a named vector of totss' are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.totss(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
train	Retrieve the training total sum of squares
valid	Retrieve the validation total sum of squares
xval	Retrieve the cross-validation total sum of squares

**Examples**

```
## Not run:
library(h2o)
h2o.init()

fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
km <- h2o.kmeans(x = predictors, training_frame = fr, k = 3, nfolds = 3)
h2o.totss(km, train = TRUE)

## End(Not run)
```

---

h2o.tot_withinss	<i>Get the total within cluster sum of squares.</i>
------------------	---

---

**Description**

If "train", "valid", and "xval" parameters are FALSE (default), then the training tot\_withinss value is returned. If more than one parameter is set to TRUE, then a named vector of tot\_withinss' are returned, where the names are "train", "valid" or "xval".

**Usage**

```
h2o.tot_withinss(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
train	Retrieve the training total within cluster sum of squares
valid	Retrieve the validation total within cluster sum of squares
xval	Retrieve the cross-validation total within cluster sum of squares

**Examples**

```
## Not run:
library(h2o)
h2o.init()

fr <- h2o.importFile("https://h2o-public-test-data.s3.amazonaws.com/smalldata/iris/iris_train.csv")
predictors <- c("sepal_len", "sepal_wid", "petal_len", "petal_wid")
km <- h2o.kmeans(x = predictors, training_frame = fr, k = 3, nfolds = 3)
h2o.tot_withinss(km, train = TRUE)

## End(Not run)
```



---

h2o.toupper	<i>Convert strings to uppercase</i>
-------------	-------------------------------------

---

**Description**

Convert strings to uppercase

**Usage**

```
h2o.toupper(x)
```

**Arguments**

x                    An H2OFrame object whose strings should be upper cased

**Value**

An H2OFrame with all entries in uppercase format

**Examples**

```
## Not run:  
library(h2o)  
h2o.init()  
string_to_upper <- as.h2o("abcde")  
upper_string <- h2o.toupper(string_to_upper)  
  
## End(Not run)
```

---

h2o.train_segments	<i>H2O Segmented-Data Bulk Model Training</i>
--------------------	---

---

**Description**

Provides a set of functions to train a group of models on different segments (subpopulations) of the training set.

**Usage**

```
h2o.train_segments(  
  algorithm,  
  segment_columns,  
  segment_models_id,  
  parallelism = 1,  
  ...  
)
```

**Arguments**

algorithm	Name of algorithm to use in training segment models (gbm, randomForest, kmeans, glm, deeplearning, naivebayes, psvm, xgboost, pca, svd, targetencoder, aggregator, word2vec, coxph, isolationforest, kmeans, stackedensemble, glrm, gam).
segment_columns	A list of columns to segment-by. H2O will group the training (and validation) dataset by the segment-by columns and train a separate model for each segment (group of rows).
segment_models_id	Identifier for the returned collection of Segment Models. If not specified it will be automatically generated.
parallelism	Level of parallelism of bulk model building, it is the maximum number of models each H2O node will be building in parallel, defaults to 1.
...	Use to pass along training_frame parameter, x, y, and all non-default parameter values to the algorithm Look at the specific algorithm - h2o.gbm, h2o.glm, h2o.kmeans, h2o.deepLearning - for available parameters.

**Details**

Start Segmented-Data bulk Model Training for a given algorithm and parameters.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
models <- h2o.train_segments(algorithm = "gbm",
                             segment_columns = "Species",
                             x = c(1:3), y = 4,
                             training_frame = iris_hf,
                             ntrees = 5,
                             max_depth = 4)

as.data.frame(models)

## End(Not run)
```

---

h2o.transform	<i>Use H2O Transformation model and apply the underlying transformation</i>
---------------	---

---

**Description**

Use H2O Transformation model and apply the underlying transformation

**Usage**

```
h2o.transform(model, ...)
```

**Arguments**

model	A trained model representing the transformation strategy
...	Transformation model-specific parameters

**Value**

Returns an H2OFrame object with data transformed.

---

h2o.transform,H2OTargetEncoderModel-method

*Applies target encoding to a given dataset*

---

**Description**

Applies target encoding to a given dataset

**Usage**

```
## S4 method for signature 'H2OTargetEncoderModel'
h2o.transform(
  model,
  data,
  blending = NULL,
  inflection_point = -1,
  smoothing = -1,
  noise = NULL,
  as_training = FALSE,
  ...
)
```

**Arguments**

model	A trained model representing the transformation strategy
data	An H2OFrame with data to be transformed
blending	Use blending during the transformation. Respects model settings when not set.
inflection_point	Blending parameter. Only effective when blending is enabled. By default, model settings are respected, if not overridden by this setting.
smoothing	Blending parameter. Only effective when blending is enabled. By default, model settings are respected, if not overridden by this setting.
noise	An amount of random noise added to the encoding, this helps prevent overfitting. By default, model settings are respected, if not overridden by this setting.
as_training	Must be set to True when encoding the training frame. Defaults to False.
...	Mainly used for backwards compatibility, to allow deprecated parameters.

**Value**

Returns an H2OFrame object with data transformed.

---

```
h2o.transform, H2OWordEmbeddingModel-method
```

*Transform words (or sequences of words) to vectors using a word2vec model.*

---

### Description

Transform words (or sequences of words) to vectors using a word2vec model.

### Usage

```
## S4 method for signature 'H2OWordEmbeddingModel'
h2o.transform(model, words, aggregate_method = c("NONE", "AVERAGE"))
```

### Arguments

model	A word2vec model.
words	An H2OFrame made of a single column containing source words.
aggregate_method	Specifies how to aggregate sequences of words. If method is 'NONE' then no aggregation is performed and each input word is mapped to a single word-vector. If method is 'AVERAGE' then input is treated as sequences of words delimited by NA. Each word of a sequences is internally mapped to a vector and vectors belonging to the same sentence are averaged and returned in the result.

### Examples

```
## Not run:
h2o.init()

# Build a simple word2vec model
data <- as.character(as.h2o(c("a", "b", "a")))
w2v_model <- h2o.word2vec(data, sent_sample_rate = 0, min_word_freq = 0, epochs = 1, vec_size = 2)

# Transform words to vectors without aggregation
sentences <- as.character(as.h2o(c("b", "c", "a", NA, "b")))
h2o.transform(w2v_model, sentences) # -> 5 rows total, 2 rows NA ("c" is not in the vocabulary)

# Transform words to vectors and return average vector for each sentence
h2o.transform(w2v_model, sentences, aggregate_method = "AVERAGE") # -> 2 rows

## End(Not run)
```

---

```
h2o.transform_word2vec
```

*Transform words (or sequences of words) to vectors using a word2vec model.*

---

### Description

Transform words (or sequences of words) to vectors using a word2vec model.

**Usage**

```
h2o.transform_word2vec(
  word2vec,
  words,
  aggregate_method = c("NONE", "AVERAGE")
)
```

**Arguments**

word2vec	A word2vec model.
words	An H2OFrame made of a single column containing source words.
aggregate_method	Specifies how to aggregate sequences of words. If method is 'NONE' then no aggregation is performed and each input word is mapped to a single word-vector. If method is 'AVERAGE' then input is treated as sequences of words delimited by NA. Each word of a sequences is internally mapped to a vector and vectors belonging to the same sentence are averaged and returned in the result.

**Examples**

```
## Not run:
h2o.init()

# Build a dummy word2vec model
data <- as.character(as.h2o(c("a", "b", "a")))
w2v_model <- h2o.word2vec(data, sent_sample_rate = 0, min_word_freq = 0, epochs = 1, vec_size = 2)

# Transform words to vectors without aggregation
sentences <- as.character(as.h2o(c("b", "c", "a", NA, "b")))
h2o.transform(w2v_model, sentences) # -> 5 rows total, 2 rows NA ("c" is not in the vocabulary)

# Transform words to vectors and return average vector for each sentence
h2o.transform(w2v_model, sentences, aggregate_method = "AVERAGE") # -> 2 rows

## End(Not run)
```

---

h2o.trim

*Trim Space*


---

**Description**

Trim Space

**Usage**

```
h2o.trim(x)
```

**Arguments**

x	The column whose strings should be trimmed.
---	---

**Examples**

```
## Not run:
library(h2o)
h2o.init()
string_to_trim <- as.h2o("r tutorial")
trim_string <- h2o.trim(string_to_trim)

## End(Not run)
```

---

h2o.trunc	<i>Truncate values in x toward 0</i>
-----------	--------------------------------------

---

**Description**

trunc takes a single numeric argument x and returns a numeric vector containing the integers formed by truncating the values in x toward 0.

**Usage**

```
h2o.trunc(x)
```

**Arguments**

x	An H2OFrame object.
---	---------------------

**See Also**

[Round](#) for the base R implementation, trunc().

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                        categorical_fraction = 0.0,
                        missing_fraction = 0.7,
                        seed = 123)

h2o.trunc(frame["C1"])

## End(Not run)
```

---

h2o.unique	<i>H2O Unique</i>
------------	-------------------

---

**Description**

Extract unique values in the column.

**Usage**

```
h2o.unique(x, include_nas = FALSE)
```

**Arguments**

x	An H2OFrame object.
include_nas	If set to TRUE, NAs are included. FALSE (turned off) by default.

**Value**

Returns an H2OFrame object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://h2o-public-test-data.s3.amazonaws.com/smldata/iris/iris_wheader.csv"
iris <- h2o.importFile(f)
h2o.unique(iris["class"])

## End(Not run)
```

---

h2o.upload_model	<i>Upload a binary model from the provided local path to the H2O cluster. (H2O model can be saved in a binary form either by saveModel() or by download_model() function.)</i>
------------------	--

---

**Description**

Upload a binary model from the provided local path to the H2O cluster. (H2O model can be saved in a binary form either by saveModel() or by download\_model() function.)

**Usage**

```
h2o.upload_model(path)
```

**Arguments**

path	A path on the machine this python session is currently connected to, specifying the location of the model to upload.
------	--

**Value**

Returns a new [H2OModel](#) object.

**See Also**

[h2o.saveModel](#), [h2o.download\\_model](#)

---

h2o.upload_mojo	<i>Imports a MOJO from a local filesystem, creating a Generic model with it.</i>
-----------------	--

---

**Description**

Usage example: `mojo_model <- h2o.upload_mojo(model_file_path = "/path/to/local/mojo.zip")`  
`predictions <- h2o.predict(mojo_model, dataset)`

**Usage**

```
h2o.upload_mojo(mojo_local_file_path)
```

**Arguments**

`mojo_local_file_path`  
 Filesystem path to the model imported

**Value**

Returns H2O Generic Model embedding given MOJO model

**Examples**

```
## Not run:

# Import default Iris dataset as H2O frame
data <- as.h2o(iris)

# Train a very simple GBM model
features <- c("Sepal.Length", "Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
original_model <- h2o.gbm(x = features, y = "Species", training_frame = data)

# Download the trained GBM model as MOJO (temporary directory used in this example)
mojo_original_name <- h2o.download_mojo(model = original_model, path = tempdir())
mojo_original_path <- paste0(tempdir(), "/", mojo_original_name)

# Upload the MOJO from local filesystem and obtain a Generic model
mojo_model <- h2o.upload_mojo(mojo_original_path)

# Perform scoring with the generic model
predictions <- h2o.predict(mojo_model, data)

## End(Not run)
```



---

h2o.var	<i>Variance of a column or covariance of columns.</i>
---------	---

---

**Description**

Compute the variance or covariance matrix of one or two H2OFrame.

**Usage**

```
h2o.var(x, y = NULL, na.rm = FALSE, use)
```

```
var(x, y = NULL, na.rm = FALSE, use)
```

**Arguments**

x	An H2OFrame object.
y	NULL (default) or an H2OFrame. The default is equivalent to y = x.
na.rm	logical. Should missing values be removed?
use	An optional character string indicating how to handle missing values. This must be one of the following: "everything" - outputs NaNs whenever one of its contributing observations is missing "all.obs" - presence of missing observations will throw an error "complete.obs" - discards missing values along with all observations in their rows so that only complete observations are used

**See Also**

[cor](#) for the base R implementation, `var()`. [h2o.sd](#) for standard deviation.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
var(prostate$AGE)

## End(Not run)
```

---

h2o.varimp	<i>Retrieve the variable importance.</i>
------------	--

---

**Description**

Retrieve the variable importance.

**Usage**

```
h2o.varimp(object)
```

**Arguments**

object            An [H2OModel](#) object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/prostate/prostate_complete.csv.zip"
pros <- h2o.importFile(f)
response <- "GLEASON"
predictors <- c("ID", "AGE", "CAPSULE", "DCAPS", "PSA", "VOL", "DPROS")
model <- h2o.glm(x = predictors, y = response, training_frame = pros)
h2o.varimp(model)

## End(Not run)
```

---

h2o.varimp\_heatmap      *Variable Importance Heatmap across multiple models*

---

**Description**

Variable importance heatmap shows variable importance across multiple models. Some models in H2O return variable importance for one-hot (binary indicator) encoded versions of categorical columns (e.g. Deep Learning, XGBoost). In order for the variable importance of categorical columns to be compared across all model types we compute a summarization of the the variable importance across all one-hot encoded features and return a single variable importance for the original categorical feature. By default, the models and variables are ordered by their similarity.

**Usage**

```
h2o.varimp_heatmap(object, top_n = 20)
```

**Arguments**

object            An [H2OAutoML](#) object or list of H2O models.

top\_n            Integer specifying the number models shown in the heatmap (based on leader-board ranking). Defaults to 20.

**Value**

A [ggplot2](#) object.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

# Import the wine dataset into H2O:
f <- "https://h2o-public-test-data.s3.amazonaws.com/smalldata/wine/winequality-redwhite-no-BOM.csv"
```

```

df <- h2o.importFile(f)

# Set the response
response <- "quality"

# Split the dataset into a train and test set:
splits <- h2o.splitFrame(df, ratios = 0.8, seed = 1)
train <- splits[[1]]
test <- splits[[2]]

# Build and train the model:
aml <- h2o.automl(y = response,
                 training_frame = train,
                 max_models = 10,
                 seed = 1)

# Create the variable importance heatmap
varimp_heatmap <- h2o.varimp_heatmap(aml)
print(varimp_heatmap)

## End(Not run)

```

---

h2o.varimp\_plot      *Plot Variable Importances*

---

## Description

Plot Variable Importances

## Usage

```
h2o.varimp_plot(model, num_of_features = NULL)
```

## Arguments

**model**                    A trained model (accepts a trained random forest, GBM, or deep learning model, will use [h2o.std\\_coef\\_plot](#) for a trained GLM)

**num\_of\_features**            The number of features shown in the plot (default is 10 or all if less than 10).

## See Also

[h2o.std\\_coef\\_plot](#) for GLM.

## Examples

```

## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[, 2] <- as.factor(prostate[, 2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
h2o.varimp_plot(model)

```

```
# for deep learning set the variable_importance parameter to TRUE
iris_hf <- as.h2o(iris)
iris_dl <- h2o.deeplearning(x = 1:4, y = 5, training_frame = iris_hf,
variable_importances = TRUE)
h2o.varimp_plot(iris_dl)

## End(Not run)
```

---

h2o.varsplits	<i>Retrieve per-variable split information for a given Isolation Forest model. Output will include: - count - The number of times a variable was used to make a split. - aggregated_split_ratios - The split ratio is defined as "abs(#left_observations - #right_observations) / #before_split". Even splits (#left_observations approx the same as #right_observations) contribute less to the total aggregated split ratio value for the given feature; highly imbalanced splits (eg. #left_observations » #right_observations) contribute more. - aggregated_split_depths - The sum of all depths of a variable used to make a split. (If a variable is used on level N of a tree, then it contributes with N to the total aggregate.)</i>
---------------	--

---

### Description

Retrieve per-variable split information for a given Isolation Forest model. Output will include:

- count - The number of times a variable was used to make a split.
- aggregated\_split\_ratios - The split ratio is defined as "abs(#left\_observations - #right\_observations) / #before\_split". Even splits (#left\_observations approx the same as #right\_observations) contribute less to the total aggregated split ratio value for the given feature; highly imbalanced splits (eg. #left\_observations » #right\_observations) contribute more.
- aggregated\_split\_depths - The sum of all depths of a variable used to make a split. (If a variable is used on level N of a tree, then it contributes with N to the total aggregate.)

### Usage

```
h2o.varsplits(object)
```

### Arguments

object	An Isolation Forest model represented by <a href="#">H2OModel</a> object.
--------	---

---

h2o.week

*Convert Milliseconds to Week of Week Year in H2O Datasets*


---

### Description

Converts the entries of an H2OFrame object from milliseconds to weeks of the week year (starting from 1).

**Usage**

```

h2o.week(x)

week(x)

## S3 method for class 'H2OFrame'
week(x)

```

**Arguments**

x                    An H2OFrame object.

**Value**

An H2OFrame object containing the entries of x converted to weeks of the week year.

**See Also**

[h2o.month](#)

**Examples**

```

## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/jira/v-11-eurodate.csv"
hdf <- h2o.importFile(f)
h2o.week(hdf["ds9"])

## End(Not run)

```

---

h2o.weights	<i>Retrieve the respective weight matrix</i>
-------------	--

---

**Description**

Retrieve the respective weight matrix

**Usage**

```
h2o.weights(object, matrix_id = 1)
```

**Arguments**

object                An [H2OModel](#) or [H2OModelMetrics](#)

matrix\_id            An integer, ranging from 1 to number of layers + 1, that specifies the weight matrix to return.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/chicago/chicagoCensus.csv"
census <- h2o.importFile(f)
census[, 1] <- as.factor(census[, 1])
dl_model <- h2o.deeplearning(x = c(1:3), y = 4, training_frame = census,
                             hidden = c(17, 191),
                             epochs = 1,
                             balance_classes = FALSE,
                             export_weights_and_biases = TRUE)
h2o.weights(dl_model, matrix_id = 1)

## End(Not run)
```

---

h2o.which

*Which indices are TRUE?*


---

**Description**

Give the TRUE indices of a logical object, allowing for array indices.

**Usage**

```
h2o.which(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

Returns an H2OFrame object.

**See Also**

[which](#) for the base R method.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

iris_hf <- as.h2o(iris)
h2o.which(iris_hf[, 1] == 4.4)

## End(Not run)
```

---

h2o.which_max	<i>Which indice contains the max value?</i>
---------------	---

---

### Description

Get the index of the max value in a column or row

### Usage

```
h2o.which_max(x, na.rm = TRUE, axis = 0)
which.max.H2OFrame(x, na.rm = TRUE, axis = 0)
which.min.H2OFrame(x, na.rm = TRUE, axis = 0)
```

### Arguments

x	An H2OFrame object.
na.rm	logical. Indicate whether missing values should be removed.
axis	integer. Indicate whether to calculate the mean down a column (0) or across a row (1).

### Value

Returns an H2OFrame object.

### See Also

[which.min](#) for the base R method, [which.max\(\)](#).

### Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/chicago/chicagoCensus.csv"
census <- h2o.importFile(f)
census[, 1] <- as.factor(census[, 1])
dl_model <- h2o.deeplearning(x = c(1:3), y = 4, hidden = c(17, 191),
                             epochs = 1, training_frame = census,
                             balance_classes = FALSE,
                             export_weights_and_biases = TRUE)
h2o.which_max(census["PER CAPITA INCOME "], na.rm = FALSE, axis = 0)

## End(Not run)
```

---

h2o.which_min	<i>Which index contains the min value?</i>
---------------	--

---

### Description

Get the index of the min value in a column or row

### Usage

```
h2o.which_min(x, na.rm = TRUE, axis = 0)
```

### Arguments

x	An H2OFrame object.
na.rm	logical. Indicate whether missing values should be removed.
axis	integer. Indicate whether to calculate the mean down a column (0) or across a row (1).

### Value

Returns an H2OFrame object.

### See Also

[which.min](#) for the base R method.

### Examples

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/chicago/chicagoCensus.csv"
census <- h2o.importFile(f)
dl_model <- h2o.deeplearning(x = c(1:3), y = 4, hidden = c(17, 191),
                             epochs = 1, training_frame = census,
                             balance_classes = FALSE,
                             export_weights_and_biases = TRUE)
h2o.which_min(census["PER CAPITA INCOME "], na.rm = FALSE, axis = 0)

## End(Not run)
```



---

h2o.withinss	<i>Get the Within SS</i>
--------------	--------------------------

---

**Description**

Get the Within SS

**Usage**

```
h2o.withinss(object)
```

**Arguments**

object      An [H2OClusteringModel](#) object.

---

h2o.word2vec	<i>Trains a word2vec model on a String column of an H2O data frame</i>
--------------	--

---

**Description**

Trains a word2vec model on a String column of an H2O data frame

**Usage**

```
h2o.word2vec(
  training_frame = NULL,
  model_id = NULL,
  min_word_freq = 5,
  word_model = c("SkipGram", "CBOW"),
  norm_model = c("HSM"),
  vec_size = 100,
  window_size = 5,
  sent_sample_rate = 0.001,
  init_learning_rate = 0.025,
  epochs = 5,
  pre_trained = NULL,
  max_runtime_secs = 0,
  export_checkpoints_dir = NULL
)
```

**Arguments**

training\_frame    Id of the training data frame.

model\_id          Destination id for this model; auto-generated if not specified.

min\_word\_freq    This will discard words that appear less than <int> times Defaults to 5.

word\_model        The word model to use (SkipGram or CBOW) Must be one of: "SkipGram", "CBOW". Defaults to SkipGram.

norm\_model        Use Hierarchical Softmax Must be one of: "HSM". Defaults to HSM.

**vec\_size**            Set size of word vectors Defaults to 100.  
**window\_size**        Set max skip length between words Defaults to 5.  
**sent\_sample\_rate**    Set threshold for occurrence of words. Those that appear with higher frequency in the training data will be randomly down-sampled; useful range is (0, 1e-5) Defaults to 0.001.  
**init\_learning\_rate**    Set the starting learning rate Defaults to 0.025.  
**epochs**             Number of training iterations to run Defaults to 5.  
**pre\_trained**        Id of a data frame that contains a pre-trained (external) word2vec model  
**max\_runtime\_secs**    Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.  
**export\_checkpoints\_dir**    Automatically export generated models to this directory.

### Examples

```

## Not run:
library(h2o)
h2o.init()

# Import the CraigslistJobTitles dataset
job_titles <- h2o.importFile(
  "https://s3.amazonaws.com/h2o-public-test-data/smalldata/craigslistJobTitles.csv",
  col.names = c("category", "jobtitle"), col.types = c("String", "String"), header = TRUE
)

# Build and train the Word2Vec model
words <- h2o.tokenize(job_titles, " ")
vec <- h2o.word2vec(training_frame = words)
h2o.findSynonyms(vec, "teacher", count = 20)

## End(Not run)

```

---

h2o.xgboost

*Build an eXtreme Gradient Boosting model*

---

### Description

Builds a eXtreme Gradient Boosting model using the native XGBoost backend.

### Usage

```

h2o.xgboost(
  x,
  y,
  training_frame,
  model_id = NULL,
  validation_frame = NULL,
  nfolds = 0,

```

```
keep_cross_validation_models = TRUE,
keep_cross_validation_predictions = FALSE,
keep_cross_validation_fold_assignment = FALSE,
score_each_iteration = FALSE,
fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
fold_column = NULL,
ignore_const_cols = TRUE,
offset_column = NULL,
weights_column = NULL,
stopping_rounds = 0,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE",
  "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error",
  "custom", "custom_increasing"),
stopping_tolerance = 0.001,
max_runtime_secs = 0,
seed = -1,
distribution = c("AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma",
  "tweedie", "laplace", "quantile", "huber"),
tweedie_power = 1.5,
categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit",
  "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"),
quiet_mode = TRUE,
checkpoint = NULL,
export_checkpoints_dir = NULL,
ntrees = 50,
max_depth = 6,
min_rows = 1,
min_child_weight = 1,
learn_rate = 0.3,
eta = 0.3,
sample_rate = 1,
subsample = 1,
col_sample_rate = 1,
colsample_bylevel = 1,
col_sample_rate_per_tree = 1,
colsample_bytree = 1,
colsample_bynode = 1,
max_abs_leafnode_pred = 0,
max_delta_step = 0,
monotone_constraints = NULL,
interaction_constraints = NULL,
score_tree_interval = 0,
min_split_improvement = 0,
gamma = 0,
auc_type = c("AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO",
  "WEIGHTED_OVO"),
nthread = -1,
save_matrix_directory = NULL,
build_tree_one_node = FALSE,
calibrate_model = FALSE,
calibration_frame = NULL,
max_bins = 256,
```

```

max_leaves = 0,
sample_type = c("uniform", "weighted"),
normalize_type = c("tree", "forest"),
rate_drop = 0,
one_drop = FALSE,
skip_drop = 0,
tree_method = c("auto", "exact", "approx", "hist"),
grow_policy = c("depthwise", "lossguide"),
booster = c("gbtree", "gblinear", "dart"),
reg_lambda = 1,
reg_alpha = 0,
dmatrix_type = c("auto", "dense", "sparse"),
backend = c("auto", "gpu", "cpu"),
gpu_id = NULL,
gainslift_bins = -1,
scale_pos_weight = 1,
verbose = FALSE
)

```

### Arguments

x	(Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y	The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
training_frame	Id of the training data frame.
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.
nfolds	Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
keep_cross_validation_models	Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
fold_assignment	Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column	Column with cross-validation fold index assignment per observation.

<code>ignore_const_cols</code>	Logical. Ignore constant columns. Defaults to TRUE.
<code>offset_column</code>	Offset column. This will be added to the combination of columns before applying the link function.
<code>weights_column</code>	Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor. If you set <code>weight = 0</code> for a row, the returned prediction frame at that row is zero and this is incorrect. To get an accurate prediction, remove all rows with <code>weight == 0</code> .
<code>stopping_rounds</code>	Early stopping based on convergence of <code>stopping_metric</code> . Stop if simple moving average of length <code>k</code> of the <code>stopping_metric</code> does not improve for <code>k:=stopping_rounds</code> scoring events (0 to disable) Defaults to 0.
<code>stopping_metric</code>	Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "AUCPR", "lift_top_group", "misclassification", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
<code>stopping_tolerance</code>	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>seed</code>	Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
<code>distribution</code>	Distribution function Must be one of: "AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber". Defaults to AUTO.
<code>tweedie_power</code>	Tweedie power for Tweedie regression, must be between 1 and 2. Defaults to 1.5.
<code>categorical_encoding</code>	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.
<code>quiet_mode</code>	Logical. Enable quiet mode Defaults to TRUE.
<code>checkpoint</code>	Model checkpoint to resume training with.
<code>export_checkpoints_dir</code>	Automatically export generated models to this directory.
<code>ntrees</code>	(same as <code>n_estimators</code> ) Number of trees. Defaults to 50.
<code>max_depth</code>	Maximum tree depth (0 for unlimited). Defaults to 6.

<code>min_rows</code>	(same as <code>min_child_weight</code> ) Fewest allowed (weighted) observations in a leaf. Defaults to 1.
<code>min_child_weight</code>	(same as <code>min_rows</code> ) Fewest allowed (weighted) observations in a leaf. Defaults to 1.
<code>learn_rate</code>	(same as <code>eta</code> ) Learning rate (from 0.0 to 1.0) Defaults to 0.3.
<code>eta</code>	(same as <code>learn_rate</code> ) Learning rate (from 0.0 to 1.0) Defaults to 0.3.
<code>sample_rate</code>	(same as <code>subsample</code> ) Row sample rate per tree (from 0.0 to 1.0) Defaults to 1.
<code>subsample</code>	(same as <code>sample_rate</code> ) Row sample rate per tree (from 0.0 to 1.0) Defaults to 1.
<code>col_sample_rate</code>	(same as <code>colsample_bylevel</code> ) Column sample rate (from 0.0 to 1.0) Defaults to 1.
<code>colsample_bylevel</code>	(same as <code>col_sample_rate</code> ) Column sample rate (from 0.0 to 1.0) Defaults to 1.
<code>col_sample_rate_per_tree</code>	(same as <code>colsample_bytree</code> ) Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.
<code>colsample_bytree</code>	(same as <code>col_sample_rate_per_tree</code> ) Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.
<code>colsample_bynode</code>	Column sample rate per tree node (from 0.0 to 1.0) Defaults to 1.
<code>max_abs_leafnode_pred</code>	(same as <code>max_delta_step</code> ) Maximum absolute value of a leaf node prediction Defaults to 0.0.
<code>max_delta_step</code>	(same as <code>max_abs_leafnode_pred</code> ) Maximum absolute value of a leaf node prediction Defaults to 0.0.
<code>monotone_constraints</code>	A mapping representing monotonic constraints. Use +1 to enforce an increasing constraint and -1 to specify a decreasing constraint.
<code>interaction_constraints</code>	A set of allowed column interactions.
<code>score_tree_interval</code>	Score the model after every so many trees. Disabled if set to 0. Defaults to 0.
<code>min_split_improvement</code>	(same as <code>gamma</code> ) Minimum relative improvement in squared error reduction for a split to happen Defaults to 0.0.
<code>gamma</code>	(same as <code>min_split_improvement</code> ) Minimum relative improvement in squared error reduction for a split to happen Defaults to 0.0.
<code>auc_type</code>	Set default multinomial AUC type. Must be one of: "AUTO", "NONE", "MACRO_OVR", "WEIGHTED_OVR", "MACRO_OVO", "WEIGHTED_OVO". Defaults to AUTO.
<code>nthread</code>	Number of parallel threads that can be used to run XGBoost. Cannot exceed H2O cluster limits (-nthreads parameter). Defaults to maximum available Defaults to -1.
<code>save_matrix_directory</code>	Directory where to save matrices passed to XGBoost library. Useful for debugging.

build_tree_one_node	Logical. Run on one node only; no network overhead but fewer cpus used. Suitable for small datasets. Defaults to FALSE.
calibrate_model	Logical. Use Platt Scaling to calculate calibrated class probabilities. Calibration can provide more accurate estimates of class probabilities. Defaults to FALSE.
calibration_frame	Calibration frame for Platt Scaling
max_bins	For tree_method=hist only: maximum number of bins Defaults to 256.
max_leaves	For tree_method=hist only: maximum number of leaves Defaults to 0.
sample_type	For booster=dart only: sample_type Must be one of: "uniform", "weighted". Defaults to uniform.
normalize_type	For booster=dart only: normalize_type Must be one of: "tree", "forest". Defaults to tree.
rate_drop	For booster=dart only: rate_drop (0..1) Defaults to 0.0.
one_drop	Logical. For booster=dart only: one_drop Defaults to FALSE.
skip_drop	For booster=dart only: skip_drop (0..1) Defaults to 0.0.
tree_method	Tree method Must be one of: "auto", "exact", "approx", "hist". Defaults to auto.
grow_policy	Grow policy - depthwise is standard GBM, lossguide is LightGBM Must be one of: "depthwise", "lossguide". Defaults to depthwise.
booster	Booster type Must be one of: "gbtree", "gblinear", "dart". Defaults to gbtree.
reg_lambda	L2 regularization Defaults to 1.0.
reg_alpha	L1 regularization Defaults to 0.0.
dmatrix_type	Type of DMatrix. For sparse, NAs and 0 are treated equally. Must be one of: "auto", "dense", "sparse". Defaults to auto.
backend	Backend. By default (auto), a GPU is used if available. Must be one of: "auto", "gpu", "cpu". Defaults to auto.
gpu_id	Which GPU(s) to use.
gainlift_bins	Gains/Lift table number of bins. 0 means disabled.. Default value -1 means automatic binning. Defaults to -1.
scale_pos_weight	Controls the effect of observations with positive labels in relation to the observations with negative labels on gradient calculation. Useful for imbalanced problems. Defaults to 1.0.
verbose	Logical. Print scoring history to the console (Metrics per tree). Defaults to FALSE.

## Examples

```
## Not run:
library(h2o)
h2o.init()

# Import the titanic dataset
f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/gbm_test/titanic.csv"
titanic <- h2o.importFile(f)
```

```

# Set predictors and response; set response as a factor
titanic['survived'] <- as.factor(titanic['survived'])
predictors <- setdiff(colnames(titanic), colnames(titanic)[2:3])
response <- "survived"

# Split the dataset into train and valid
splits <- h2o.splitFrame(data = titanic, ratios = .8, seed = 1234)
train <- splits[[1]]
valid <- splits[[2]]

# Train the XGB model
titanic_xgb <- h2o.xgboost(x = predictors, y = response,
                          training_frame = train, validation_frame = valid,
                          booster = "dart", normalize_type = "tree",
                          seed = 1234)

## End(Not run)

```

---

`h2o.xgboost.available` *Determines whether an XGBoost model can be built*

---

### Description

Ask the H2O server whether a XGBoost model can be built. (Depends on availability of native backend.) Returns True if a XGBoost model can be built, or False otherwise.

### Usage

```
h2o.xgboost.available()
```

---

`h2o.year` *Convert Milliseconds to Years in H2O Datasets*

---

### Description

Convert the entries of an H2OFrame object from milliseconds to years, indexed starting from 1900.

### Usage

```

h2o.year(x)

year(x)

## S3 method for class 'H2OFrame'
year(x)

```

### Arguments

`x` An H2OFrame object.



**Details**

This method calls the function of the `MutableDateTime` class in Java.

**Value**

An `H2OFrame` object containing the entries of `x` converted to years

**See Also**

[h2o.month](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/jira/v-11-eurodate.csv"
hdf <- h2o.importFile(f)
h2o.year(hdf["ds9"])

## End(Not run)
```

---

H2OAutoML-class	<i>The H2OAutoML class</i>
-----------------	----------------------------

---

**Description**

This class represents an `H2OAutoML` object

---

H2OClusteringModel-class	<i>The H2OClusteringModel object.</i>
--------------------------	---------------------------------------

---

**Description**

This virtual class represents a clustering model built by H2O.

**Details**

This object has slots for the `key`, which is a character string that points to the model key existing in the H2O cluster, the data used to build the model (an object of class `H2OFrame`).

**Slots**

- model\_id** A character string specifying the key for the model fit in the H2O cluster's key-value store.
- algorithm** A character string specifying the algorithm that was used to fit the model.
- parameters** A list containing the parameter settings that were used to fit the model that differ from the defaults.
- allparameters** A list containing all parameters used to fit the model.
- model** A list containing the characteristics of the model returned by the algorithm.
- size** The number of points in each cluster.
  - totss** Total sum of squared error to grand mean.
  - withinss** A vector of within-cluster sum of squared error.
  - tot\_withinss** Total within-cluster sum of squared error.
  - betweenss** Between-cluster sum of squared error.

---

H2OConnection-class     *The H2OConnection class.*

---

**Description**

This class represents a connection to an H2O cluster.

**Usage**

```
## S4 method for signature 'H2OConnection'
show(object)
```

**Arguments**

**object**             an H2OConnection object.

**Details**

Because H2O is not a master-slave architecture, there is no restriction on which H2O node is used to establish the connection between R (the client) and H2O (the server).

A new H2O connection is established via the `h2o.init()` function, which takes as parameters the 'ip' and 'port' of the machine running an instance to connect with. The default behavior is to connect with a local instance of H2O at port 54321, or to boot a new local instance if one is not found at port 54321.

**Slots**

- ip** A character string specifying the IP address of the H2O cluster.
- port** A numeric value specifying the port number of the H2O cluster.
- name** A character value specifying the name of the H2O cluster.
- proxy** A character specifying the proxy path of the H2O cluster.
- https** Set this to TRUE to use https instead of http.
- cacert** Path to a CA bundle file with root and intermediate certificates of trusted CAs.

insecure Set this to TRUE to disable SSL certificate checking.  
 username Username to login with.  
 password Password to login with.  
 use\_spnego Set this to TRUE to use SPNEGO authentication.  
 cookies Cookies to add to request  
 context\_path Context path which is appended to H2O server location.  
 mutable An H2OConnectionMutableState object to hold the mutable state for the H2O connection.

---

H2OConnectionMutableState

*The H2OConnectionMutableState class*

---

### Description

This class represents the mutable aspects of a connection to an H2O cluster.

### Slots

session\_id A character string specifying the H2O session identifier.  
 key\_count A integer value specifying count for the number of keys generated for the session\_id.

---

H2OCoxPHModel-class *The H2OCoxPHModel object.*

---

### Description

Virtual object representing H2O's CoxPH Model.

### Usage

```

## S4 method for signature 'H2OCoxPHModel'
show(object)

## S3 method for class 'H2OCoxPHModel'
coef(object, ...)

## S3 method for class 'H2OCoxPHModel'
extractAIC(fit, scale, k = 2, ...)

## S3 method for class 'H2OCoxPHModel'
logLik(object, ...)

survfit.H2OCoxPHModel(formula, newdata, ...)

## S3 method for class 'H2OCoxPHModel'
vcov(object, ...)

```

**Arguments**

object	an H2OCoxPHModel object.
...	additional arguments to pass on.
fit	an H2OCoxPHModel object.
scale	optional numeric specifying the scale parameter of the model.
k	numeric specifying the weight of the equivalent degrees of freedom.
formula	an H2OCoxPHModel object.
newdata	an optional H2OFrame or data.frame with the same variable names as those that appear in the H2OCoxPHModel object.

---

H2OCoxPHModelSummary-class

*The H2OCoxPHModelSummary object.*


---

**Description**

Wrapper object for summary information compatible with survival package.

**Usage**

```
## S4 method for signature 'H2OCoxPHModelSummary'
show(object)

## S3 method for class 'H2OCoxPHModelSummary'
coef(object, ...)
```

**Arguments**

object	An H2OCoxPHModelSummary object.
...	additional arguments to pass on.

**Slots**

summary A list containing the a summary compatible with CoxPH summary used in the survival package.

---

H2OFrame-class

*The H2OFrame class*


---

**Description**

This class represents an H2OFrame object

---

H2OFrame-Extract      *Extract or Replace Parts of an H2OFrame Object*

---

## Description

Operators to extract or replace parts of H2OFrame objects.

## Usage

```
## S3 method for class 'H2OFrame'
data[row, col, drop = TRUE]

## S3 method for class 'H2OFrame'
x$name

## S3 method for class 'H2OFrame'
x[[i, exact = TRUE]]

## S3 method for class 'H2OFrame'
x$name

## S3 method for class 'H2OFrame'
x[[i, exact = TRUE]]

## S3 replacement method for class 'H2OFrame'
data[row, col, ...] <- value

## S3 replacement method for class 'H2OFrame'
data$name <- value

## S3 replacement method for class 'H2OFrame'
data[[name]] <- value
```

## Arguments

data	object from which to extract element(s) or in which to replace element(s).
row	index specifying row element(s) to extract or replace. Indices are numeric or character vectors or empty (missing) or will be matched to the names.
col	index specifying column element(s) to extract or replace.
drop	Unused
x	An H2OFrame
name	a literal character string or a name (possibly backtick quoted).
i	index
exact	controls possible partial matching of [[ when extracting a character
...	Further arguments passed to or from other methods.
value	To be assigned

---

H2OGrid-class	<i>H2O Grid</i>
---------------	-----------------

---

**Description**

A class to contain the information about grid results

**Usage**

```
## S4 method for signature 'H2OGrid'
show(object)
```

**Arguments**

object            an H2OGrid object.

**Slots**

grid\_id the final identifier of grid  
model\_ids list of model IDs which are included in the grid object  
hyper\_names list of parameter names used for grid search  
failed\_params list of model parameters which caused a failure during model building, it can contain a null value  
failure\_details list of detailed messages which correspond to failed parameters field  
failure\_stack\_traces list of stack traces corresponding to model failures reported by failed\_params and failure\_details fields  
failed\_raw\_params list of failed raw parameters  
summary\_table table of models built with parameters and metric information.

**See Also**

[H2OModel](#) for the final model types.

---

H2OLeafNode-class	<i>The H2OLeafNode class.</i>
-------------------	-------------------------------

---

**Description**

This class represents a single leaf node in an H2OTree.

**Details**

```
#' @aliases H2OLeafNode
```

---

H2OModel-class      *The H2OModel object.*

---

### Description

This virtual class represents a model built by H2O.

### Usage

```
## S4 method for signature 'H2OModel'
show(object)
```

### Arguments

object              an H2OModel object.

### Details

This object has slots for the key, which is a character string that points to the model key existing in the H2O cluster, the data used to build the model (an object of class H2OFrame).

### Slots

model\_id A character string specifying the key for the model fit in the H2O cluster's key-value store.

algorithm A character string specifying the algorithm that were used to fit the model.

parameters A list containing the parameter settings that were used to fit the model that differ from the defaults.

allparameters A list containing all parameters used to fit the model.

have\_pojo A logical indicating whether export to POJO is supported

have\_mojo A logical indicating whether export to MOJO is supported

model A list containing the characteristics of the model returned by the algorithm.

---

H2OModelFuture-class      *H2O Future Model*

---

### Description

A class to contain the information for background model jobs.

### Slots

job\_key a character key representing the identification of the job process.

model\_id the final identifier for the model

### See Also

[H2OModel](#) for the final model types.

---

H2OModelMetrics-class *The H2OModelMetrics Object.*

---

**Description**

A class for constructing performance measures of H2O models.

**Usage**

```
## S4 method for signature 'H2OModelMetrics'  
show(object)  
  
## S4 method for signature 'H20BinomialMetrics'  
show(object)  
  
## S4 method for signature 'H20MultinomialMetrics'  
show(object)  
  
## S4 method for signature 'H20OrdinalMetrics'  
show(object)  
  
## S4 method for signature 'H20RegressionMetrics'  
show(object)  
  
## S4 method for signature 'H20ClusteringMetrics'  
show(object)  
  
## S4 method for signature 'H20AutoEncoderMetrics'  
show(object)  
  
## S4 method for signature 'H20DimReductionMetrics'  
show(object)
```

**Arguments**

object            An H2OModelMetrics object

---

H2ONode-class            *The H2ONode class.*

---

**Description**

The H2ONode class.

**Usage**

```
## S4 method for signature 'H2ONode'  
show(object)
```



**Arguments**

object            an H2ONode object.

**Slots**

id    An integer representing node's unique identifier. Generated by H2O.  
 levels    A character representing categorical levels on split from parent's node belonging into this node. NULL for root node or non-categorical splits.  
 #' @aliases H2ONode

---

H2OSegmentModels-class

*H2O Segment Models*

---

**Description**

A class to contain the information for segment models.

**Usage**

```
## S4 method for signature 'H2OSegmentModels'
show(object)
```

**Arguments**

object            an H2OModel object.

**Slots**

segment\_models\_id    the identifier for the segment models collections

---

H2OSegmentModelsFuture-class

*H2O Future Segment Models*

---

**Description**

A class to contain the information for background segment models jobs.

**Slots**

job\_key    a character key representing the identification of the job process.  
 segment\_models\_id    the final identifier for the segment models collections

**See Also**

[H2OSegmentModels](#) for the final segment models types.

---

H2OSplitNode-class      *The H2OSplitNode class.*

---

### Description

This class represents a single non-terminal node in an H2OTree.

### Slots

`threshold` A numeric split threshold, typically when the split column is numerical.

`left_child` A H2ONodeOrNULL representing the left child node, if a node has one.

`right_child` A H2ONodeOrNULL representing the right child node, if a node has one.

`split_feature` A character representing the name of the column this node splits on.

`left_levels` A character representing the levels of a categorical feature heading to the left child of this node. NA for non-categorical split.

`right_levels` A character representing the levels of a categorical feature heading to the right child of this node. NA for non-categorical split.

`na_direction` A character representing the direction of NA values. LEFT means NA values go to the left child node, RIGH means NA values go to the right child node.

---

H2OTree-class      *The H2OTree class.*

---

### Description

This class represents a model of a Tree built by one of H2O's algorithms (GBM, Random Forest).

### Usage

```
## S4 method for signature 'H2OTree'
show(object)
```

### Arguments

`object`      an H2OTree object.

### Slots

`root_node` A H2ONode representing the beginning of the tree behind the model. Allows further tree traversal.

`left_children` An integer vector with left child nodes of tree's nodes

`right_children` An integer vector with right child nodes of tree's nodes

`node_ids` An integer representing identification number of a node. Node IDs are generated by H2O.

`descriptions` A character vector with descriptions for each node to be found in the tree. Contains split threshold if the split is based on numerical column. For cactegorical splits, it contains list of categorical levels for transition from the parent node.

**model\_id** A character with the name of the model this tree is related to.  
**tree\_number** An integer representing the order in which the tree has been built in the model.  
**tree\_class** A character representing name of tree's class. Number of tree classes equals to the number of levels in categorical response column. As there is exactly one class per categorical level, name of tree's class equals to the corresponding categorical level of response column. In case of regression and binomial, the name of the categorical level is ignored can be omitted, as there is exactly one tree built in both cases.  
**thresholds** A numeric split thresholds. Split thresholds are not only related to numerical splits, but might be present in case of categorical split as well.  
**features** A character with names of the feature/column used for the split.  
**levels** A character representing categorical levels on split from parent's node belonging into this node. NULL for root node or non-categorical splits.  
**nas** A character representing if NA values go to the left node or right node. May be NA if node is a leaf.  
**predictions** A numeric representing predictions for each node in the graph.  
**tree\_decision\_path** A character, plain language rules representation of a trained decision tree  
**decision\_paths** A character representing plain language rules that were used in a particular prediction.  
**left\_cat\_split** A character list of categorical levels leading to the left child node. Only present when split is categorical, otherwise none.  
**right\_cat\_split** A character list of categorical levels leading to the right child node. Only present when split is categorical, otherwise none.

---

 housevotes

*United States Congressional Voting Records 1984*


---

### Description

This data set includes votes for each of the U.S. House of Representatives Congressmen on the 16 key votes identified by the CQA. The CQA lists nine different types of votes: voted for, paired for, and announced for (these three simplified to yea), voted against, paired against, and announced against (these three simplified to nay), voted present, voted present to avoid conflict of interest, and did not vote or otherwise make a position known (these three simplified to an unknown disposition).

### Format

A data frame with 435 rows and 17 columns

### Source

Congressional Quarterly Almanac, 98th Congress, 2nd session 1984, Volume XL: Congressional Quarterly Inc., Washington, D.C., 1985

### References

Newman, D.J. & Hettich, S. & Blake, C.L. & Merz, C.J. (1998). UCI Repository of machine learning databases [<https://www.ics.uci.edu/~mlearn/MLRepository.html>]. Irvine, CA: University of California, Department of Information and Computer Science.

---

iris	<i>Edgar Anderson's Iris Data</i>
------	-----------------------------------

---

**Description**

Measurements in centimeters of the sepal length and width and petal length and width, respectively, for three species of iris flowers.

**Format**

A data frame with 150 rows and 5 columns

**Source**

Fisher, R. A. (1936) The use of multiple measurements in taxonomic problems. *Annals of Eugenics*, 7, Part II, 179-188.

The data were collected by Anderson, Edgar (1935). The irises of the Gaspé Peninsula, *Bulletin of the American Iris Society*, 59, 2-5.

---

is.character	<i>Check if character</i>
--------------	---------------------------

---

**Description**

Check if character

**Usage**

```
is.character(x)
```

**Arguments**

x                    An H2OFrame object

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/coxph_test/heart.csv"
heart <- h2o.importFile(f)

heart["transplant"] <- as.character(heart["transplant"])
is.character(heart["transplant"])

## End(Not run)
```

---

is.factor	<i>Check if factor</i>
-----------	------------------------

---

**Description**

Check if factor

**Usage**

```
is.factor(x)
```

**Arguments**

x	An H2OFrame object
---	--------------------

---

is.h2o	<i>Is H2O Frame object</i>
--------	----------------------------

---

**Description**

Test if object is H2O Frame.

**Usage**

```
is.h2o(x)
```

**Arguments**

x	An R object.
---	--------------

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)

is.h2o(frame)

## End(Not run)
```

---

<code>is.numeric</code>	<i>Check if numeric</i>
-------------------------	-------------------------

---

**Description**

Check if numeric

**Usage**

```
is.numeric(x)
```

**Arguments**

<code>x</code>	An H2OFrame object
----------------	--------------------

---

Keyed-class	<i>Virtual Keyed class</i>
-------------	----------------------------

---

**Description**

Base class for all objects having a persistent representation on backend.

---

<code>length,H2OTree-method</code>	<i>Overrides the behavior of length() function on H2OTree class. Returns number of nodes in an H2OTree</i>
------------------------------------	--

---

**Description**

Overrides the behavior of length() function on H2OTree class. Returns number of nodes in an H2OTree

**Usage**

```
## S4 method for signature 'H2OTree'
length(x)
```

**Arguments**

<code>x</code>	An H2OTree to count nodes for.
----------------	--------------------------------

---

Logical-or	<i>Logical or for H2OFrames</i>
------------	---------------------------------

---

**Description**

Logical or for H2OFrames

**Usage**

```
`||`(x, y)
```

**Arguments**

x	An H2OFrame object
y	An H2OFrame object

---

ModelAccessors	<i>Accessor Methods for H2OModel Object</i>
----------------	---

---

**Description**

Function accessor methods for various H2O output fields.

**Usage**

```
getParms(object)

## S4 method for signature 'H2OModel'
getParms(object)

getCenters(object)

getCentersStd(object)

getWithinSS(object)

getTotWithinSS(object)

getBetweenSS(object)

getTotSS(object)

getIterations(object)

getClusterSizes(object)

## S4 method for signature 'H2OClusteringModel'
getCenters(object)
```

```

## S4 method for signature 'H2OClusteringModel'
getCentersStd(object)

## S4 method for signature 'H2OClusteringModel'
getWithinSS(object)

## S4 method for signature 'H2OClusteringModel'
getTotWithinSS(object)

## S4 method for signature 'H2OClusteringModel'
getBetweenSS(object)

## S4 method for signature 'H2OClusteringModel'
getTotSS(object)

## S4 method for signature 'H2OClusteringModel'
getIterations(object)

## S4 method for signature 'H2OClusteringModel'
getClusterSizes(object)

```

### Arguments

object            an [H2OModel](#) class object.

---

model\_cache=class      *Needed to be able to memoise the models*

---

### Description

Needed to be able to memoise the models

---

names.H2OFrame            *Column names of an H2OFrame*

---

### Description

Column names of an H2OFrame

### Usage

```
## S3 method for class 'H2OFrame'
names(x)
```

### Arguments

x                    An H2OFrame



**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                        categorical_fraction = 0.0,
                        missing_fraction = 0.7,
                        seed = 123)

names(frame)

## End(Not run)
```

---

Ops.H2OFrame

*S3 Group Generic Functions for H2O*

---

**Description**

Methods for group generic functions and H2O objects.

**Usage**

```
## S3 method for class 'H2OFrame'
Ops(e1, e2)

## S3 method for class 'H2OFrame'
Math(x, ...)

## S3 method for class 'H2OFrame'
Math(x, ...)

## S3 method for class 'H2OFrame'
Math(x, ...)

## S3 method for class 'H2OFrame'
Summary(x, ..., na.rm)

## S3 method for class 'H2OFrame'
!x

## S3 method for class 'H2OFrame'
is.na(x)

## S3 method for class 'H2OFrame'
t(x)

log(x, ...)

log10(x)

log2(x)
```

```

log1p(x)

trunc(x, ...)

x %**% y

nrow.H2OFrame(x)

ncol.H2OFrame(x)

## S3 method for class 'H2OFrame'
length(x)

h2o.length(x)

## S3 replacement method for class 'H2OFrame'
names(x) <- value

colnames(x) <- value

```

### Arguments

e1	object
e2	object
x	object
...	Further arguments passed to or from other methods.
na.rm	logical. whether or not missing values should be removed
y	object
value	To be assigned

---

plot.H2OModel	<i>Plot an H2O Model</i>
---------------	--------------------------

---

### Description

Plots training set (and validation set if available) scoring history for an H2O Model

### Usage

```

## S3 method for class 'H2OModel'
plot(x, timestep = "AUTO", metric = "AUTO", ...)

```

### Arguments

x	A fitted <a href="#">H2OModel</a> object for which the scoring history plot is desired.
timestep	A unit of measurement for the x-axis.
metric	A unit of measurement for the y-axis.
...	additional arguments to pass on.

**Details**

This method dispatches on the type of H2O model to select the correct scoring history. The timestep and metric arguments are restricted to what is available in the scoring history for a particular type of model.

**Value**

Returns a scoring history plot.

**See Also**

[h2o.deeplearning](#), [h2o.gbm](#), [h2o.glm](#), [h2o.randomForest](#) for model generation in h2o.

**Examples**

```
## Not run:
if (requireNamespace("mlbench", quietly=TRUE)) {
  library(h2o)
  h2o.init()

  df <- as.h2o(mlbench::mlbench.friedman1(10000, 1))
  rng <- h2o.runif(df, seed = 1234)
  train <- df[rng < 0.8,]
  valid <- df[rng >= 0.8,]

  gbm <- h2o.gbm(x = 1:10, y = "y", training_frame = train, validation_frame = valid,
                ntrees = 500, learn_rate = 0.01, score_each_iteration = TRUE)

  plot(gbm)
  plot(gbm, timestep = "duration", metric = "deviance")
  plot(gbm, timestep = "number_of_trees", metric = "deviance")
  plot(gbm, timestep = "number_of_trees", metric = "rmse")
  plot(gbm, timestep = "number_of_trees", metric = "mae")
}

## End(Not run)
```

---

plot.H2OTabulate

*Plot an H2O Tabulate Heatmap*


---

**Description**

Plots the simple co-occurrence based tabulation of X vs Y as a heatmap, where X and Y are two Vecs in a given dataset. This function requires suggested ggplot2 package.

**Usage**

```
## S3 method for class 'H2OTabulate'
plot(x, xlab = x$cols[1], ylab = x$cols[2], base_size = 12, ...)
```

**Arguments**

x	An H2OTabulate object for which the heatmap plot is desired.
xlab	A title for the x-axis. Defaults to what is specified in the given H2OTabulate object.
ylab	A title for the y-axis. Defaults to what is specified in the given H2OTabulate object.
base_size	Base font size for plot.
...	additional arguments to pass on.

**Value**

Returns a ggplot2-based heatmap of co-occurrence.

**See Also**

[h2o.tabulate](#)

**Examples**

```
## Not run:
library(h2o)
h2o.init()
df <- as.h2o(iris)
tab <- h2o.tabulate(data = df, x = "Sepal.Length", y = "Petal.Width",
  weights_column = NULL, nbins_x = 10, nbins_y = 10)
plot(tab)

## End(Not run)
```

---

predict.H2OAutoML      *Predict on an AutoML object*

---

**Description**

Obtains predictions from an AutoML object.

**Usage**

```
## S3 method for class 'H2OAutoML'
predict(object, newdata, ...)

## S3 method for class 'H2OAutoML'
h2o.predict(object, newdata, ...)
```

**Arguments**

object	a fitted <a href="#">H2OAutoML</a> object for which prediction is desired
newdata	An H2OFrame object in which to look for variables with which to predict.
...	additional arguments to pass on.

## Details

This method generated predictions on the leader model from an AutoML run. The order of the rows in the results is the same as the order in which the data was loaded, even if some rows fail (for example, due to missing values or unseen factor levels).

## Value

Returns an H2OFrame object with probabilities and default predictions.

---

predict.H2OModel	<i>Predict on an H2O Model</i>
------------------	--------------------------------

---

## Description

Obtains predictions from various fitted H2O model objects.

## Usage

```
## S3 method for class 'H2OModel'  
predict(object, newdata, ...)  
  
## S3 method for class 'H2OModel'  
h2o.predict(object, newdata, ...)
```

## Arguments

object	a fitted <a href="#">H2OModel</a> object for which prediction is desired
newdata	An H2OFrame object in which to look for variables with which to predict.
...	additional arguments to pass on.

## Details

This method dispatches on the type of H2O model to select the correct prediction/scoring algorithm. The order of the rows in the results is the same as the order in which the data was loaded, even if some rows fail (for example, due to missing values or unseen factor levels).

## Value

Returns an H2OFrame object with probabilities and default predictions.

## See Also

[h2o.deeplearning](#), [h2o.gbm](#), [h2o.glm](#), [h2o.randomForest](#) for model generation in h2o.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smalldata/glm_test/insurance.csv"
insurance <- h2o.importFile(f)
predictors <- colnames(insurance)[1:4]
response <- "Claims"
insurance['Group'] <- as.factor(insurance['Group'])
insurance['Age'] <- as.factor(insurance['Age'])
splits <- h2o.splitFrame(data = insurance, ratios = 0.8, seed = 1234)
train <- splits[[1]]
valid <- splits[[2]]
insurance_gbm <- h2o.gbm(x = predictors, y = response,
                        training_frame = train,
                        validation_frame = valid,
                        distribution = "huber",
                        huber_alpha = 0.9, seed = 1234)
h2o.predict(insurance_gbm, newdata = insurance)

## End(Not run)
```

---

predict\_contributions.H2OModel

*Predict feature contributions - SHAP values on an H2O Model (only DRF, GBM and XGBoost models).*

---

**Description**

Returned H2OFrame has shape (#rows, #features + 1) - there is a feature contribution column for each input feature, the last column is the model bias (same value for each row). The sum of the feature contributions and the bias term is equal to the raw prediction of the model. Raw prediction of tree-based model is the sum of the predictions of the individual trees before the inverse link function is applied to get the actual prediction. For Gaussian distribution the sum of the contributions is equal to the model prediction.

**Usage**

```
predict_contributions.H2OModel(
  object,
  newdata,
  output_format = c("original", "compact"),
  ...
)

h2o.predict_contributions(
  object,
  newdata,
  output_format = c("original", "compact"),
  ...
)
```

**Arguments**

object	a fitted <a href="#">H2OModel</a> object for which prediction is desired
newdata	An H2OFrame object in which to look for variables with which to predict.
output_format	Specify how to output feature contributions in XGBoost - XGBoost by default outputs contributions for 1-hot encoded features, specifying a compact output format will produce a per-feature contribution. Defaults to original.
...	additional arguments to pass on.

**Details**

Note: Multinomial classification models are currently not supported.

**Value**

Returns an H2OFrame contain feature contributions for each input row.

**See Also**

[h2o.gbm](#) and [h2o.randomForest](#) for model generation in h2o.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate_gbm <- h2o.gbm(3:9, "AGE", prostate)
h2o.predict(prostate_gbm, prostate)
h2o.predict_contributions(prostate_gbm, prostate)

## End(Not run)
```

---

predict\_leaf\_node\_assignment.H2OModel

*Predict the Leaf Node Assignment on an H2O Model*

---

**Description**

Obtains leaf node assignment from fitted H2O model objects.

**Usage**

```
predict_leaf_node_assignment.H2OModel(
  object,
  newdata,
  type = c("Path", "Node_ID"),
  ...
)

h2o.predict_leaf_node_assignment(
```

```

    object,
    newdata,
    type = c("Path", "Node_ID"),
    ...
  )

```

### Arguments

object	a fitted <a href="#">H2OModel</a> object for which prediction is desired
newdata	An H2OFrame object in which to look for variables with which to predict.
type	choice of either "Path" when tree paths are to be returned (default); or "Node_ID" when the output
...	additional arguments to pass on.

### Details

For every row in the test set, return the leaf placements of the row in all the trees in the model. Placements can be represented either by paths to the leaf nodes from the tree root or by H2O's internal identifiers. The order of the rows in the results is the same as the order in which the data was loaded

### Value

Returns an H2OFrame object with categorical leaf assignment identifiers for each tree in the model.

### See Also

[h2o.gbm](#) and [h2o.randomForest](#) for model generation in h2o.

### Examples

```

## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
h2o.predict(prostate_gbm, prostate)
h2o.predict_leaf_node_assignment(prostate_gbm, prostate)

## End(Not run)

```

---

print.H2OFrame

*Print An H2OFrame*

---

### Description

Print An H2OFrame



**Usage**

```
## S3 method for class 'H2OFrame'
print(x, n = 6L, m = 200L, ...)
```

**Arguments**

x	An H2OFrame object
n	An (Optional) A single integer. If positive, number of rows in x to return. If negative, all but the n first/last number of rows in x. Anything bigger than 20 rows will require asking the server (first 20 rows are cached on the client).
m	An (Optional) A single integer. If positive, number of columns in x to return. If negative, all but the m first/last number of columns in x.
...	Further arguments to be passed from or to other methods.

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
print(cars, n = 8)

## End(Not run)
```

---

print.H2OTable	<i>Print method for H2OTable objects</i>
----------------	--

---

**Description**

This will print a truncated view of the table if there are more than 20 rows.

**Usage**

```
## S3 method for class 'H2OTable'
print(x, header = TRUE, ...)
```

**Arguments**

x	An H2OTable object
header	A logical value dictating whether or not the table name should be printed.
...	Further arguments passed to or from other methods.

**Value**

The original x object

**Examples**

```
## Not run:
library(h2o)
h2o.init()

f <- "https://s3.amazonaws.com/h2o-public-test-data/smallldata/junit/cars_20mpg.csv"
cars <- h2o.importFile(f)
print(cars, header = TRUE)

## End(Not run)
```

---

prostate	<i>Prostate Cancer Study</i>
----------	------------------------------

---

**Description**

Baseline exam results on prostate cancer patients from Dr. Donn Young at The Ohio State University Comprehensive Cancer Center.

**Format**

A data frame with 380 rows and 9 columns

**Source**

Hosmer and Lemeshow (2000) Applied Logistic Regression: Second Edition.

---

range.H2OFrame	<i>Range of an H2O Column</i>
----------------	-------------------------------

---

**Description**

Range of an H2O Column

**Usage**

```
## S3 method for class 'H2OFrame'
range(..., na.rm = TRUE)
```

**Arguments**

...	An H2OFrame object.
na.rm	ignore missing values

**Examples**

```
## Not run:
library(h2o)
h2o.init()

frame <- h2o.createFrame(rows = 6, cols = 2,
                          categorical_fraction = 0.0,
                          missing_fraction = 0.7,
                          seed = 123)
range(frame, na.rm = TRUE)

## End(Not run)
```

---

scale

*Scaling and Centering of an H2OFrame*

---

**Description**

Centers and/or scales the columns of an H2O dataset.

**Usage**

```
## S3 method for class 'H2OFrame'
scale(x, center = TRUE, scale = TRUE)
```

**Arguments**

x	An H2OFrame object.
center	either a logical value or numeric vector of length equal to the number of columns of x.
scale	either a logical value or numeric vector of length equal to the number of columns of x.

**Examples**

```
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
summary(iris_hf)

# Scale and center all the numeric columns in iris data set
iris_scaled <- scale(iris_hf[, 1:4])

## End(Not run)
```

---

show, H2OAutoML-method *Format AutoML object in user-friendly way*

---

### Description

Format AutoML object in user-friendly way

### Usage

```
## S4 method for signature 'H2OAutoML'
show(object)
```

### Arguments

object            an H2OAutoML object.

---

staged\_predict\_proba.H2OModel

*Predict class probabilities at each stage of an H2O Model*

---

### Description

The output structure is analogous to the output of [h2o.predict\\_leaf\\_node\\_assignment](#). For each tree *t* and class *c* there will be a column *Tt.Cc* (eg. *T3.C1* for tree 3 and class 1). The value will be the corresponding predicted probability of this class by combining the raw contributions of trees *T1.Cc*, ..., *Tt.Cc*. Binomial models build the trees just for the first class and values in columns *Tx.C1* thus correspond to the the probability *p0*.

### Usage

```
staged_predict_proba.H2OModel(object, newdata, ...)
```

```
h2o.staged_predict_proba(object, newdata, ...)
```

### Arguments

object            a fitted [H2OModel](#) object for which prediction is desired  
 newdata           An [H2OFrame](#) object in which to look for variables with which to predict.  
 ...                additional arguments to pass on.

### Value

Returns an [H2OFrame](#) object with predicted probability for each tree in the model.

### See Also

[h2o.gbm](#) and [h2o.randomForest](#) for model generation in [h2o](#).

**Examples**

```
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
h2o.predict(prostate_gbm, prostate)
h2o.staged_predict_proba(prostate_gbm, prostate)

## End(Not run)
```

---

str.H2OFrame	<i>Display the structure of an H2OFrame object</i>
--------------	--

---

**Description**

Display the structure of an H2OFrame object

**Usage**

```
## S3 method for class 'H2OFrame'
str(object, ..., cols = FALSE)
```

**Arguments**

object	An H2OFrame.
...	Further arguments to be passed from or to other methods.
cols	Print the per-column str for the H2OFrame

---

summary, H2OAutoML-method	<i>Format AutoML object in user-friendly way</i>
---------------------------	--

---

**Description**

Format AutoML object in user-friendly way

**Usage**

```
## S4 method for signature 'H2OAutoML'
summary(object)
```

**Arguments**

object	an H2OAutoML object.
--------	----------------------

---

summary,H2OCoxPHModel-method

*Summary method for H2OCoxPHModel objects*

---

### Description

Summary method for H2OCoxPHModel objects

### Usage

```
## S4 method for signature 'H2OCoxPHModel'
summary(object, conf.int = 0.95, scale = 1)
```

### Arguments

object	an H2OCoxPHModel object.
conf.int	a specification of the confidence interval.
scale	a scale.

---

summary,H2OGrid-method

*Format grid object in user-friendly way*

---

### Description

Format grid object in user-friendly way

### Usage

```
## S4 method for signature 'H2OGrid'
summary(object, show_stack_traces = FALSE)
```

### Arguments

object	an H2OGrid object.
show_stack_traces	a flag to show stack traces for model failures

---

 summary,H2OModel-method

*Print the Model Summary*


---

### Description

Print the Model Summary

### Usage

```
## S4 method for signature 'H2OModel'
summary(object, ...)
```

### Arguments

object	An <a href="#">H2OModel</a> object.
...	further arguments to be passed on (currently unimplemented)

---

 use.package

*Use optional package*


---

### Description

Testing availability of optional package, its version, and extra global default. This function is used internally. It is exported and documented because user can control behavior of the function by global option.

### Usage

```
use.package(
  package,
  version = "1.9.8"[package == "data.table"],
  use = getOption("h2o.use.data.table", TRUE)[package == "data.table"]
)
```

### Arguments

package	character scalar name of a package that we Suggests or Enhances on.
version	character scalar required version of a package.
use	logical scalar, extra escape option, to be used as global option.

### Details

We use this function to control csv read/write with optional [data.table](#) package. Currently data.table is enabled by default for some operations, to disable it set options("h2o.use.data.table"=FALSE). It is possible to control just [fread](#) or [fwrite](#) with options("h2o.fread"=FALSE, "h2o.fwrite"=FALSE). h2o.fread and h2o.fwrite options are not handled in this function but next to *fread* and *fwrite* calls.

**See Also**

[as.h2o.data.frame](#), [as.data.frame.H2OFrame](#)

**Examples**

```
op <- options("h2o.use.data.table" = TRUE)
if (use.package("data.table")) {
  cat("optional package data.table 1.9.8+ is available\n")
} else {
  cat("optional package data.table 1.9.8+ is not available\n")
}
options(op)
```

---

walking

*Muscular Actuations for Walking Subject*

---

**Description**

The musculoskeletal model, experimental data, settings files, and results for three-dimensional, muscle-actuated simulations at walking speed as described in Hamner and Delp (2013). Simulations were generated using OpenSim 2.4. The data is available from [https://simtk.org/frs/index.php?group\\_id=603](https://simtk.org/frs/index.php?group_id=603).

**Format**

A data frame with 151 rows and 124 columns

**References**

Hamner, S.R., Delp, S.L. Muscle contributions to fore-aft and vertical body mass center accelerations over a range of running speeds. *Journal of Biomechanics*, vol 46, pp 780-787. (2013)

---

with\_no\_h2o\_progress    *Suppresses h2o progress output from expr*

---

**Description**

Suppresses h2o progress output from expr

**Usage**

```
with_no_h2o_progress(expr)
```

**Arguments**

expr                    expression

**Value**

result of expr



---

zzz

*Shutdown H2O cluster after examples run*

---

### **Description**

Shutdown H2O cluster after examples run

### **Examples**

```
## Not run:
library(h2o)
h2o.init()
h2o.shutdown(prompt = FALSE)
Sys.sleep(3)

## End(Not run)
```

---

&&

*Logical and for H2OFrames*

---

### **Description**

Logical and for H2OFrames

### **Usage**

```
`&&`(x, y)
```

### **Arguments**

x	An H2OFrame object
y	An H2OFrame object

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