

# Package ‘h2o’

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**Type** Package

**Title** R Interface for H2O

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**Author** The H2O.ai team

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**Description** R scripting functionality for H2O, the open source math engine for big data that computes parallel distributed machine learning algorithms such as generalized linear models, gradient boosting machines, random forests, and neural networks (deep learning) within various cluster environments.

**License** Apache License (== 2.0)

**URL** <https://github.com/h2oai/h2o-3>

**BugReports** <http://jira.h2o.ai>

**NeedsCompilation** no

**SystemRequirements** Java (>= 1.7)

**Depends** R (>= 2.13.0), methods, stats

**Imports** graphics, tools, utils, RCurl, jsonlite

**Suggests** ggplot2, mlbench, Matrix, data.table (>= 1.9.8)

**Repository** CRAN

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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: 3.10.5.3  
Branch: rel-vajda  
Date: Fri Jun 30 16:15:10 PDT 2017  
License: Apache License (== 2.0)  
Depends: R (>= 2.13.0), RCurl, jsonlite, statmod, tools, methods, utils

This package allows the user to run basic H2O commands using R commands. In order to use it, you must first have H2O running. 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 H2O is running on a cluster, you must provide the IP and port of the remote machine as arguments to the `h2o.init()` call.

H2O supports a number of standard statistical models, such as GLM, K-means, and Random Forest. For example, to run GLM, call `h2o.glm` with the H2O parsed data and parameters (response variable, error distribution, etc...) as arguments. (The operation will be done on the server associated with the data object where H2O is running, not within the R environment).

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.

If you are using an older version of H2O, use the following porting guide to update your scripts:  
[Porting Scripts](#)

## Author(s)

Anqi Fu, Tom Kraljevic and Petr Maj, with contributions from the H2O.ai team  
Maintainer: Tom Kraljevic <tomk@0xdata.com>

## References

- [H2O.ai Homepage](#)
- [H2O Documentation](#)



- [H2O on GitHub](#)

---

aaa

*Starting H2O For examples*

---

### Description

Starting H2O For examples

### Examples

```
if(Sys.info()['sysname'] == "Darwin" && Sys.info()['release'] == '13.4.0'){
  quit(save="no")
}else{
  h2o.init(nthreads = 2)
}
```

---

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

```
h2o.init()
irisPath <- system.file("extdata", "iris.csv", package="h2o")
iris.hex <- h2o.importFile(path = irisPath, destination_frame = "iris.hex")
summary(apply(iris.hex, 2, sum))
```

---

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.

---

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**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
as.data.frame(prostate.hex)
```

---

`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**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.hex[,2] <- as.factor(prostate.hex[,2])
summary(prostate.hex)
```

---

`as.h2o`*Create H2OFrame*

---

## Description

Import R object to the H2O cloud.

## 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 = "", ...)  
  
## S3 method for class 'Matrix'  
as.h2o(x, destination_frame = "", ...)
```

## Arguments

<code>x</code>	An R object.
<code>destination_frame</code>	A string with the desired name for the H2OFrame.
<code>...</code>	arguments passed to method arguments.

## Details

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

## References

<http://blog.h2o.ai/2016/04/fast-csv-writing-for-r/>

## See Also

[use.package](#)

**Examples**

```

h2o.init()
hi <- as.h2o(iris)
he <- as.h2o(euro)
hl <- as.h2o(letters)
hm <- as.h2o(state.x77)
hh <- as.h2o(hi)
stopifnot(is.h2o(hi), dim(hi)==dim(iris),
          is.h2o(he), dim(he)==c(length(euro),1L),
          is.h2o(hl), dim(hl)==c(length(letters),1L),
          is.h2o(hm), dim(hm)==dim(state.x77),
          is.h2o(hh), dim(hh)==dim(hi))
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)
  hs <- as.h2o(m)
  stopifnot(is.h2o(hs), dim(hs)==dim(m))
}

```

---

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.

---

as.numeric                      *Convert H2O Data to Numeric*

---

### Description

Converts an H2O column into a numeric value column.

### Usage

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

### Arguments

x                                  a column from an H2OFrame data set.  
 ...                                Further arguments to be passed from or to other methods.

### Examples

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.hex[,2] <- as.factor (prostate.hex[,2])
prostate.hex[,2] <- as.numeric(prostate.hex[,2])
```

---

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

---

### 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

---

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

---

**Description**

Temperature, soil moisture, runoff, and other environmental measurements from the Australia coast. The data is available from <http://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.

---

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**

```
h2o.init()
iris.hex <- as.h2o(iris)
dim(iris.hex)
```

---

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

---

**Description**

Column names of an H2OFrame

**Usage**

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

**Arguments**

x                    An H2OFrame

---

h2o.abs	<i>Compute the absolute value of x</i>
---------	--

---

**Description**

Compute the absolute value of x

**Usage**

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

**Arguments**

x                    An H2OFrame object.

**See Also**

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



---

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**

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

---

h2o.aic	<i>Retrieve the AIC. 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".</i>
---------	--

---

**Description**

Retrieve the AIC. 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

---

h2o.all	<i>Given a set of logical vectors, are all of the values true?</i>
---------	--

---

**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 [H2OAutoEncoderModel](#) 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

```
library(h2o)
h2o.init()
prosPath = system.file("extdata", "prostate.csv", package = "h2o")
prostate.hex = h2o.importFile(path = prosPath)
prostate.d1 = h2o.deeplearning(x = 3:9, training_frame = prostate.hex, autoencoder = TRUE,
                             hidden = c(10, 10), epochs = 5)
prostate.anon = h2o.anomaly(prostate.d1, prostate.hex)
head(prostate.anon)
prostate.anon.per.feature = h2o.anomaly(prostate.d1, prostate.hex, per_feature=TRUE)
head(prostate.anon.per.feature)
```

---

h2o.any

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

---

## 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.

---

h2o.anyFactor

*Check H2OFrame columns for factors*

---

## 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**

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris_wheader.csv", package="h2o")
iris.hex <- h2o.importFile(path = irisPath)
h2o.anyFactor(iris.hex)
```

---

h2o.arrange	<i>Sorts H2OFrame by the columns specified. Returns a new H2OFrame, like dplyr::arrange.</i>
-------------	--

---

**Description**

Sorts H2OFrame by the columns specified. 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.

---

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

---

**Description**

Convert H2O Data to Characters

**Usage**

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

**Arguments**

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

**See Also**

[as.character](#) for the base R implementation.

---

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**

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

---

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**

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

---

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

---

**Description**

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

**Usage**

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

**Arguments**

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

---

h2o.as_date	<i>Functions to convert between character representations and objects of class "Date" representing calendar dates.</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 [H2OBinomialMetrics](#). 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> 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

```
library(h2o)
h2o.init()

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

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

---

h2o.betweenss	<i>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".</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

---

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.



---

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

---

h2o.cbind	<i>Combine H2O Datasets by Columns</i>
-----------	--

---

**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

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.cbind <- h2o.cbind(prostate.hex, prostate.hex)
head(prostate.cbind)
```

---

h2o.ceiling	<i>ceiling takes a single numeric argument x and returns a numeric vector containing the smallest integers not less than the corresponding elements of x.</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

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

---

h2o.centers	<i>Retrieve the Model Centers</i>
-------------	-----------------------------------

---

## Description

Retrieve the Model Centers

## Usage

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

## Arguments

object                An [H2OClusteringModel](#) object.

---

h2o.centersSTD	<i>Retrieve the Model Centers STD</i>
----------------	---------------------------------------

---

**Description**

Retrieve the Model Centers STD

**Usage**

h2o.centersSTD(object)

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
--------	---

---

h2o.centroid_stats	<i>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".</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

h2o.clearLog                    *Delete All H2O R Logs*

---

**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**

```
library(h2o)
h2o.init()
h2o.startLogging()
ausPath = system.file("extdata", "australia.csv", package="h2o")
australia.hex = h2o.importFile(path = ausPath)
h2o.stopLogging()
h2o.clearLog()
```

---

h2o.clusterInfo                    *Print H2O cluster info*

---

**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**

```
h2o.init()  
h2o.clusterStatus()
```

---

h2o.cluster_sizes	<i>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".</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

---

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

---

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.

---

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.

---

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

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
h2o.columns_by_type(prostate.hex, coltype="numeric")
```

---

h2o.computeGram     *Compute weighted gram matrix.*

---

### 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    *Access H2O Confusion Matrices*

---

**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 <a href="#">H2OFrame</a> 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**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
hex <- h2o.uploadFile(prosPath)
hex[,2] <- as.factor(hex[,2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = hex, distribution = "bernoulli")
h2o.confusionMatrix(model, hex)
# Generating a ModelMetrics object
perf <- h2o.performance(model, hex)
h2o.confusionMatrix(perf)
```

---

h2o.connect

*Connect to a running H2O instance.*

---

**Description**

Connect to a running H2O instance.

**Usage**

```
h2o.connect(ip = "localhost", port = 54321, strict_version_check = TRUE,
  proxy = NA_character_, https = FALSE, insecure = FALSE,
  username = NA_character_, password = NA_character_,
  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.
insecure	(Optional) Set this to TRUE to disable SSL certificate checking.
username	(Optional) Username to login with.
password	(Optional) Password to login with.
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.

**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)
```

```
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
...	Further arguments to be passed down from other methods.

**Examples**

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

---

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

---

**Description**

Compute the cosine of x

**Usage**

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

**Arguments**

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

**See Also**

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

---

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**

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

---

h2o.createFrame	<i>Data H2OFrame Creation in H2O</i>
-----------------	--------------------------------------

---

**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 has_response = TRUE.
randomize	A logical value indicating whether data values should be randomly generated. This must be TRUE if either categorical_fraction or integer_fraction is non-zero.
value	If randomize = FALSE, 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 has_response = TRUE, 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 TRUE, the total number of columns will be cols+1.
seed	A seed used to generate random values when randomize = TRUE.
seed_for_column_types	A seed used to generate random column types when randomize = TRUE.

### Value

Returns an H2OFrame object.

### Examples

```
library(h2o)
h2o.init()
hex <- h2o.createFrame(rows = 1000, cols = 100, categorical_fraction = 0.1,
                      factors = 5, integer_fraction = 0.5, integer_range = 1,
                      has_response = TRUE)

head(hex)
summary(hex)

hex2 <- h2o.createFrame(rows = 100, cols = 10, randomize = FALSE, value = 5,
                      categorical_fraction = 0, integer_fraction = 0)

summary(hex2)
```

---

`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

---

`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

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

---

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



---

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

---

**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**

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

---

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**

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

---

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**

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

---

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

---

**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.

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**

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris_wheader.csv", package="h2o")
iris.hex <- h2o.uploadFile(path = irisPath, destination_frame = "iris.hex")
summary(iris.hex)

# Cut sepal length column into intervals determined by min/max/quantiles
sepal_len.cut <- cut(iris.hex$sepal_len, c(4.2, 4.8, 5.8, 6, 8))
```

```
head(sepal_len.cut)
summary(sepal_len.cut)
```

---

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 *Convert Milliseconds to Day of Week in H2O Datasets*

---

### 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

*Compute DCT of an H2OFrame*

---

**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**

```

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))

```

---

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.

**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

**See Also**

[ddply](#) for the plyr library implementation.

## Examples

```
library(h2o)
h2o.init()

# Import iris dataset to H2O
irisPath <- system.file("extdata", "iris_wheader.csv", package = "h2o")
iris.hex <- h2o.uploadFile(path = irisPath, destination_frame = "iris.hex")
# Add function taking mean of sepal_len column
fun <- function(df) { sum(df[,1], na.rm = TRUE)/nrow(df) }
# Apply function to groups by class of flower
# uses h2o's ddply, since iris.hex is an H2OFrame object
res <- h2o.ddply(iris.hex, "class", fun)
head(res)
```

---

h2o.deepfeatures

*Feature Generation via H2O Deep Learning or DeepWater Model*

---

## Description

Extract the non-linear feature from an H2O data set using an H2O deep learning model.

## Usage

```
h2o.deepfeatures(object, data, layer)
```

## Arguments

object	An <a href="#">H2OModel</a> object that represents the deep learning model to be used for feature extraction.
data	An H2OFrame object.
layer	Index (for DeepLearning, integer) or Name (for DeepWater, String) of the hidden layer to extract

## Value

Returns an H2OFrame object with as many features as the number of units in the hidden layer of the specified index.

## See Also

`link{h2o.deeplearning}` for making H2O Deep Learning models.

`link{h2o.deepwater}` for making H2O DeepWater models.

**Examples**

```

library(h2o)
h2o.init()
prosPath = system.file("extdata", "prostate.csv", package = "h2o")
prostate.hex = h2o.importFile(path = prosPath)
prostate.dl = h2o.deeplearning(x = 3:9, y = 2, training_frame = prostate.hex,
                             hidden = c(100, 200), epochs = 5)
prostate.deepfeatures_layer1 = h2o.deepfeatures(prostate.dl, prostate.hex, layer = 1)
prostate.deepfeatures_layer2 = h2o.deepfeatures(prostate.dl, prostate.hex, layer = 2)
head(prostate.deepfeatures_layer1)
head(prostate.deepfeatures_layer2)

#if (h2o.deepwater.available()) {
# prostate.dl = h2o.deepwater(x = 3:9, y = 2, backend="mxnet", training_frame = prostate.hex,
#                             hidden = c(100, 200), epochs = 5)
# prostate.deepfeatures_layer1 =
#   h2o.deepfeatures(prostate.dl, prostate.hex, layer = "fc1_w")
# prostate.deepfeatures_layer2 =
#   h2o.deepfeatures(prostate.dl, prostate.hex, layer = "fc2_w")
# head(prostate.deepfeatures_layer1)
# head(prostate.deepfeatures_layer2)
#}

```

---

h2o.deeplearning	<i>Build a Deep Neural Network model using CPUs Builds a feed-forward multilayer artificial neural network on an H2OFrame</i>
------------------	---

---

**Description**

Build a Deep Neural Network model using CPUs 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_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,
                max_hit_ratio_k = 0, 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", "lift_top_group", "misclassification",
"mean_per_class_error"), 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)

```

## 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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
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 N-fold cross-validation (0 to disable or >= 2). Defaults to 0.

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.
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.
max_hit_ratio_k	Max. number (top K) of predictions to use for hit ratio computation (for multi-class only, 0 to disable). Defaults to 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 [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: $rate / (1 + rate\_annealing * samples)$ . Defaults to 1e-06.
rate_decay	Learning rate decay factor between layers (N-th layer: $rate * rate\_decay ^ (n - 1)$ ). 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) Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "mean_per_class_error". 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", "Sort-ByResponse", "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.

**See Also**

[predict.H2OModel](#) for prediction

**Examples**

```
library(h2o)
h2o.init()
iris.hex <- as.h2o(iris)
iris.dl <- h2o.deeplearning(x = 1:4, y = 5, training_frame = iris.hex)

# now make a prediction
predictions <- h2o.predict(iris.dl, iris.hex)
```

---

h2o.deepwater	<i>Build a Deep Learning model using multiple native GPU backends Builds a deep neural network on an H2OFrame containing various data sources</i>
---------------	---

---

**Description**

Build a Deep Learning model using multiple native GPU backends Builds a deep neural network on an H2OFrame containing various data sources

**Usage**

```

h2o.deepwater(x, y, training_frame, model_id = NULL, checkpoint = NULL,
  autoencoder = FALSE, validation_frame = NULL, nfolds = 0,
  balance_classes = FALSE, max_after_balance_size = 5,
  class_sampling_factors = NULL, keep_cross_validation_predictions = FALSE,
  keep_cross_validation_fold_assignment = FALSE, fold_assignment = c("AUTO",
  "Random", "Modulo", "Stratified"), fold_column = NULL,
  offset_column = NULL, weights_column = NULL,
  score_each_iteration = FALSE, categorical_encoding = c("AUTO", "Enum",
  "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder",
  "SortByResponse", "EnumLimited"), overwrite_with_best_model = TRUE,
  epochs = 10, train_samples_per_iteration = -2,
  target_ratio_comm_to_comp = 0.05, seed = -1, standardize = TRUE,
  learning_rate = 0.001, learning_rate_annealing = 1e-06,
  momentum_start = 0.9, momentum_ramp = 10000, momentum_stable = 0.9,
  distribution = c("AUTO", "bernoulli", "multinomial", "gaussian", "poisson",
  "gamma", "tweedie", "laplace", "quantile", "huber"), score_interval = 5,
  score_training_samples = 10000, score_validation_samples = 0,
  score_duty_cycle = 0.1, classification_stop = 0, regression_stop = 0,
  stopping_rounds = 5, stopping_metric = c("AUTO", "deviance", "logloss",
  "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification",
  "mean_per_class_error"), stopping_tolerance = 0, max_runtime_secs = 0,
  ignore_const_cols = TRUE, shuffle_training_data = TRUE,
  mini_batch_size = 32, clip_gradient = 10, network = c("auto", "user",
  "lenet", "alexnet", "vgg", "googlenet", "inception_bn", "resnet"),
  backend = c("mxnet", "caffe", "tensorflow"), image_shape = c(0, 0),
  channels = 3, sparse = FALSE, gpu = TRUE, device_id = c(0),
  cache_data = TRUE, network_definition_file = NULL,
  network_parameters_file = NULL, mean_image_file = NULL,
  export_native_parameters_prefix = NULL, activation = c("Rectifier",
  "Tanh"), hidden = NULL, input_dropout_ratio = 0,
  hidden_dropout_ratios = NULL, problem_type = c("auto", "image",
  "dataset"))

```

**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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
model_id	Destination id for this model; auto-generated if not specified.
checkpoint	Model checkpoint to resume training with.
autoencoder	Logical. Auto-Encoder. Defaults to FALSE.

validation_frame	Id of the validation data frame.
nfolds	Number of folds for N-fold cross-validation (0 to disable or $\geq 2$ ). Defaults to 0.
balance_classes	Logical. Balance training data class counts via over/under-sampling (for imbalanced data). Defaults to FALSE.
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.
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.
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.
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.
score_each_iteration	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
categorical_encoding	Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited". Defaults to AUTO.
overwrite_with_best_model	Logical. If enabled, override the final model with the best model found during training. Defaults to TRUE.
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).
standardize	Logical. If enabled, automatically standardize the data. If disabled, the user must provide properly scaled input data. Defaults to TRUE.
learning_rate	Learning rate (higher => less stable, lower => slower convergence). Defaults to 0.001.
learning_rate_annealing	Learning rate annealing: rate / (1 + rate_annealing * samples). Defaults to 1e-06.
momentum_start	Initial momentum at the beginning of training (try 0.5). Defaults to 0.9.
momentum_ramp	Number of training samples for which momentum increases. Defaults to 10000.
momentum_stable	Final momentum after the ramp is over (try 0.99). Defaults to 0.9.
distribution	Distribution function Must be one of: "AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber". Defaults to AUTO.
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 0.
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) Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "mean_per_class_error". 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.

<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
<code>ignore_const_cols</code>	Logical. Ignore constant columns. Defaults to TRUE.
<code>shuffle_training_data</code>	Logical. Enable global shuffling of training data. Defaults to TRUE.
<code>mini_batch_size</code>	Mini-batch size (smaller leads to better fit, larger can speed up and generalize better). Defaults to 32.
<code>clip_gradient</code>	Clip gradients once their absolute value is larger than this value. Defaults to 10.
<code>network</code>	Network architecture. Must be one of: "auto", "user", "lenet", "alexnet", "vgg", "googlenet", "inception_bn", "resnet". Defaults to auto.
<code>backend</code>	Deep Learning Backend. Must be one of: "mxnet", "caffe", "tensorflow". Defaults to mxnet.
<code>image_shape</code>	Width and height of image. Defaults to [0, 0].
<code>channels</code>	Number of (color) channels. Defaults to 3.
<code>sparse</code>	Logical. Sparse data handling (more efficient for data with lots of 0 values). Defaults to FALSE.
<code>gpu</code>	Logical. Whether to use a GPU (if available). Defaults to TRUE.
<code>device_id</code>	Device IDs (which GPUs to use). Defaults to [0].
<code>cache_data</code>	Logical. Whether to cache the data in memory (automatically disabled if data size is too large). Defaults to TRUE.
<code>network_definition_file</code>	Path of file containing network definition (graph, architecture).
<code>network_parameters_file</code>	Path of file containing network (initial) parameters (weights, biases).
<code>mean_image_file</code>	Path of file containing the mean image data for data normalization.
<code>export_native_parameters_prefix</code>	Path (prefix) where to export the native model parameters after every iteration.
<code>activation</code>	Activation function. Only used if no user-defined network architecture file is provided, and only for <code>problem_type=dataset</code> . Must be one of: "Rectifier", "Tanh".
<code>hidden</code>	Hidden layer sizes (e.g. [200, 200]). Only used if no user-defined network architecture file is provided, and only for <code>problem_type=dataset</code> .
<code>input_dropout_ratio</code>	Input layer dropout ratio (can improve generalization, try 0.1 or 0.2). Defaults to 0.
<code>hidden_dropout_ratios</code>	Hidden layer dropout ratios (can improve generalization), specify one value per hidden layer, defaults to 0.5.

`problem_type` Problem type, auto-detected by default. If set to `image`, the `H2OFrame` must contain a string column containing the path (URI or URL) to the images in the first column. If set to `text`, the `H2OFrame` must contain a string column containing the text in the first column. If set to `dataset`, Deep Water behaves just like any other H2O Model and builds a model on the provided `H2OFrame` (non-String columns). Must be one of: "auto", "image", "dataset". Defaults to `auto`.

---

`h2o.deepwater.available`

*Ask the H2O server whether a Deep Water model can be built (depends on availability of native backends) Returns TRUE if a Deep Water model can be built, or FALSE otherwise.*

---

### Description

Ask the H2O server whether a Deep Water model can be built (depends on availability of native backends) Returns TRUE if a Deep Water model can be built, or FALSE otherwise.

### Usage

```
h2o.deepwater.available(h2oRestApiVersion = .h2o.__REST_API_VERSION)
```

### Arguments

`h2oRestApiVersion`  
(Optional) Specific version of the REST API to use.

---

`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

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.importFile(path = prosPath)
h2o.describe(prostate.hex)
```

---

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.

---

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.

---

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.

---

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 similar-  
ity (0...1)

**Examples**

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

---

h2o.downloadAllLogs     *Download H2O Log Files to Disk*

---

**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**

```
h2o.downloadAllLogs(dirname='./your_directory_name/', filename = 'autoh2o_log.zip')
```

---

h2o.downloadCSV     *Download H2O Data to Disk*

---

**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 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

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris_wheader.csv", package = "h2o")
iris.hex <- h2o.uploadFile(path = irisPath)

myFile <- paste(getwd(), "my_iris_file.csv", sep = .Platform$file.sep)
h2o.downloadCSV(iris.hex, myFile)
file.info(myFile)
file.remove(myFile)
```

---

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

---

## Description

Download the model in MOJO format.

## Usage

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

## 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 folder "path".
genmodel_name	Custom name of genmodel jar.

## Value

Name of the MOJO file written to the path.

## Examples

```
library(h2o)
h <- h2o.init()
fr <- as.h2o(iris)
my_model <- h2o.gbm(x=1:4, y=5, training_frame=fr)
h2o.download_moj(my_model) # save to the current working directory
```

---

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.
getjar	(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

```
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
```



---

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**

```
library(h2o)
h2o.init()
buys <- as.h2o(c("no", "no", "yes", "yes", "yes", "no", "yes", "no", "yes", "yes", "no"))
buys_entropy <- h2o.entropy(buys)
```

---

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**

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

---

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 instance'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, parts = 1)
```

### 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.
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-?????'.

### 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()
irisPath <- system.file("extdata", "iris.csv", package = "h2o")
iris.hex <- h2o.uploadFile(path = irisPath)

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

## End(Not run)
```

---

h2o.exportHDFS	<i>Export a Model to HDFS</i>
----------------	-------------------------------

---

**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.

---

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**

```
library(h2o)
h2o.init()
fr.with.nas = h2o.createFrame(categorical_fraction=0.0,missing_fraction=0.7,rows=6,cols=2,seed=123)
fr <- h2o.fillna(fr.with.nas, "forward", axis=1, maxlen=2L)
```

h2o.filterNACols      *Filter NA Columns*

---

**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

---

h2o.findSynonyms      *Find synonyms using a word2vec model.*

---

**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.

---

`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**

<code>object</code>	H2OBinomialMetrics
<code>threshold</code>	number between 0 and 1

---

`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**

<code>object</code>	H2OBinomialMetrics
<code>metric</code>	"F1," for example

---

h2o.floor	<i>floor takes a single numeric argument x and returns a numeric vector containing the largest integers not greater than the corresponding elements of x.</i>
-----------	---

---

**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**

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

---

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

---

**Description**

Open H2O Flow in your browser

**Usage**

```
h2o.flow()
```

---

h2o.gainsLift	Access H2O Gains/Lift Tables
---------------	------------------------------

---

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

### 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

```
library(h2o)  
h2o.init()  
prosPath <- system.file("extdata", "prostate.csv", package="h2o")  
hex <- h2o.uploadFile(prosPath)  
hex[,2] <- as.factor(hex[,2])
```

```

model <- h2o.gbm(x = 3:9, y = 2, distribution = "bernoulli",
                training_frame = hex, validation_frame = hex, 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=hex) ## score on new data (here: the same)
# Generating a ModelMetrics object
perf <- h2o.performance(model, hex)
h2o.gainsLift(perf)           ## extract from existing metrics object

```

---

h2o.gbm	<i>Builds gradient boosted classification trees and gradient boosted regression trees on a parsed data set.</i>
---------	---

---

## Description

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_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,
        max_hit_ratio_k = 0, 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", "lift_top_group",
        "misclassification", "mean_per_class_error"), 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", "multinomial", "gaussian", "poisson", "gamma", "tweedie",
        "laplace", "quantile", "huber"), 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)

```



**Arguments**

<code>x</code>	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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
<code>training_frame</code>	Id of the training data frame (Not required, to allow initial validation of model parameters).
<code>model_id</code>	Destination id for this model; auto-generated if not specified.
<code>validation_frame</code>	Id of the validation data frame.
<code>nfolds</code>	Number of folds for N-fold cross-validation (0 to disable or $\geq 2$ ). Defaults to 0.
<code>keep_cross_validation_predictions</code>	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
<code>keep_cross_validation_fold_assignment</code>	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
<code>score_each_iteration</code>	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
<code>score_tree_interval</code>	Score the model after every so many trees. Disabled if set to 0. Defaults to 0.
<code>fold_assignment</code>	Cross-validation fold assignment scheme, if <code>fold_column</code> 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.
<code>fold_column</code>	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.
<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> .

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.
max_hit_ratio_k	Max. number (top K) of predictions to use for hit ratio computation (for multi-class only, 0 to disable) Defaults to 0.
ntrees	Number of trees. Defaults to 50.
max_depth	Maximum tree depth. Defaults to 5.
min_rows	Fewest allowed (weighted) observations in a leaf. Defaults to 10.
nbins	For numerical columns (real/int), build a histogram of (at least) this many bins, then split at the best point Defaults to 20.
nbins_top_level	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.
nbins_cats	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.
r2_stopping	r2_stopping is no longer supported and will be ignored if set - please use stopping_rounds, stopping_metric and stopping_tolerance instead. Previous version of H2O would stop making trees when the R <sup>2</sup> metric equals or exceeds this Defaults to 1.797693135e+308.
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) Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "mean_per_class_error". Defaults to AUTO.
stopping_tolerance	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
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.
learn_rate	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", "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.
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 (from 0.0 to 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", "SortByResponse", "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

**See Also**

[predict.H2OModel](#) for prediction

**Examples**

```

library(h2o)
h2o.init()

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

```

---

h2o.getConnection	<i>Retrieve an H2O Connection</i>
-------------------	-----------------------------------

---

**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.

---

`h2o.getFutureModel`     *Get future model*

---

**Description**

Get future model

**Usage**

`h2o.getFutureModel(object)`

**Arguments**

object             H2OModel

---

`h2o.getGLMFullRegularizationPath`  
*Extract full regularization path from glm model (assuming it was run with lambda search option)*

---

**Description**

Extract full regularization path from glm model (assuming it was run with lambda search option)

**Usage**

`h2o.getGLMFullRegularizationPath(model)`

**Arguments**

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

---

h2o.getGrid

*Get a grid object from H2O distributed K/V store.*


---

### 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)
```

### Arguments

<code>grid_id</code>	ID of existing grid object to fetch
<code>sort_by</code>	Sort the models in the grid space by a metric. Choices are "logloss", "residual_deviance", "mse", "auc", "accuracy", "precision", "recall", "f1", etc.
<code>decreasing</code>	Specify whether sort order should be decreasing

### Examples

```
library(h2o)
library(jsonlite)
h2o.init()
iris.hex <- as.h2o(iris)
h2o.grid("gbm", grid_id = "gbm_grid_id", x = c(1:4), y = 5,
        training_frame = iris.hex, 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)})
```

---

h2o.getId

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


---

### 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

---

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**

```
library(h2o)
h2o.init()

iris.hex <- as.h2o(iris, "iris.hex")
model_id <- h2o.gbm(x = 1:4, y = 5, training_frame = iris.hex)@model_id
model.retrieved <- h2o.getModel(model_id)
```

---

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

---

**Description**

Get the Time Zone on the H2O Cloud 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

---

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

---

**Description**

Get h2o version

**Usage**

```
h2o.getVersion()
```



---

h2o.giniCoef	<i>Retrieve the GINI Coefficient</i>
--------------	--------------------------------------

---

### Description

Retrieves the GINI coefficient from an [H2OBinomialMetrics](#). If "train", "valid", and "xval" parameters are FALSE (default), then the training GINI value 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. See [h2o.performance](#) for creating H2OModelMetrics objects. threshold metrics.

### Examples

```
library(h2o)
h2o.init()

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

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

---

h2o.glm	<i>Fits a generalized linear model, specified by a response variable, a set of predictors, and a description of the error distribution.</i>
---------	---

---

### 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, seed = -1, 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("gaussian",
        "binomial", "quasibinomial", "multinomial", "poisson", "gamma", "tweedie"),
        tweedie_variance_power = 0, tweedie_link_power = 1, solver = c("AUTO",
        "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE", "COORDINATE_DESCENT"),
        alpha = NULL, lambda = NULL, lambda_search = FALSE,
        early_stopping = TRUE, nlambda = -1, standardize = TRUE,
        missing_values_handling = c("MeanImputation", "Skip"),
        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"), prior = -1, lambda_min_ratio = -1, beta_constraints = NULL,
        max_active_predictors = -1, interactions = NULL,
        balance_classes = FALSE, class_sampling_factors = NULL,
        max_after_balance_size = 5, max_hit_ratio_k = 0, max_runtime_secs = 0)
```

### 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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
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 N-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_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.
family	Family. Use binomial for classification with logistic regression, others are for regression problems. Must be one of: "gaussian", "binomial", "quasibinomial", "multinomial", "poisson", "gamma", "tweedie". Defaults to gaussian.
tweedie_variance_power	Tweedie variance power Defaults to 0.
tweedie_link_power	Tweedie link power Defaults to 1.
solver	AUTO will set the solver based on given data and the other parameters. IRLSM is fast on on problems with small number of predictors and for lambda-search with L1 penalty, L_BFGS scales better for datasets with many columns. Coordinate descent is experimental (beta). Must be one of: "AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE", "COORDINATE_DESCENT". 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 TRUE.
missing_values_handling	Handling of missing values. Either MeanImputation or Skip. Must be one of: "MeanImputation", "Skip". Defaults to MeanImputation.
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 epsilon, 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	Must be one of: "family_default", "identity", "logit", "log", "inverse", "tweedie". Defaults to family_default.
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.
lambda_min_ratio	Minimum lambda used in lambda search, specified as a ratio of lambda_max. 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 7000 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>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_hit_ratio_k</code>	Maximum number (top K) of predictions to use for hit ratio computation (for multi-class only, 0 to disable) Defaults to 0.
<code>max_runtime_secs</code>	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

### 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

```
h2o.init()
```

```

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

# Run GLM of VOL ~ CAPSULE + AGE + RACE + PSA + GLEASON
myX = setdiff(colnames(prostate.hex), c("ID", "DPROS", "DCAPS", "VOL"))
h2o.glm(y = "VOL", x = myX, training_frame = prostate.hex, 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
data.hex = h2o.importFile(
path = "https://s3.amazonaws.com/h2o-public-test-data/smalldata/demos/bank-additional-full.csv",
destination_frame = "data.hex")
myX = 1:20
myY="y"
my.glm = h2o.glm(x=myX, y=myY, training_frame=data.hex, family="binomial", standardize=TRUE,
lambda_search=TRUE)

```

---

h2o.glm

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


---

## Description

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, 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)

```

**Arguments**

training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
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.
loading_name	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.

**Value**

Returns an object of class [H2ODimReductionModel](#).

**References**

M. Udell, C. Horn, R. Zadeh, S. Boyd (2014). Generalized Low Rank Models[<http://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[<http://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**

```
library(h2o)
h2o.init()
ausPath <- system.file("extdata", "australia.csv", package="h2o")
australia.hex <- h2o.uploadFile(path = ausPath)
h2o.glm(training_frame = australia.hex, k = 5, loss = "Quadratic", regularization_x = "L1",
gamma_x = 0.5, gamma_y = 0, max_iterations = 1000)
```



---

h2o.grep	<i>Searches for matches to argument 'pattern' within each element of a string column.</i>
----------	---

---

## Description

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).

## 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

## Value

H2OFrame holding the matching positions or a logical vector if 'output.logical' is enabled.

## Examples

```
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),]
```

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, ..., hyper_params = list(),
         is_supervised = NULL, do_hyper_params_check = FALSE,
         search_criteria = NULL)
```

**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.
...	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 default strategy 'Cartesian' covers the entire space of hyperparameter combinations. Specify the 'RandomDiscrete' strategy to get random search of all the combinations of your hyperparameters. RandomDiscrete should be usually combined with at least one early stopping criterion, max_models and/or max_runtime_secs, e.g. list(strategy = "RandomDiscrete", max_models = 42, max_runtime_secs = 10) or list(strategy = "RandomDiscrete", stopping_metric = "AUTO", stopping_tolerance = 0.01) or list(strategy = "RandomDiscrete", stopping_metric = "misclassification", stopping_tolerance = 0.01).

**Details**

Launch grid search with given algorithm and parameters.

**Examples**

```

library(h2o)
library(jsonlite)
h2o.init()
iris.hex <- as.h2o(iris)
grid <- h2o.grid("gbm", x = c(1:4), y = 5, training_frame = iris.hex,
               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)})

```

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**

data	an H2OFrame object.
by	a list of column names
gb.control	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 rm.method argument. See Details: for more help.
...	any supported aggregate function. See Details: 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. 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

---

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

```
library(h2o)
h2o.init()
string_to_gsub <- as.h2o("r tutorial")
sub_string <- h2o.gsub("r ", "H2O ", string_to_gsub)
```

---

h2o.head	<i>Return the Head or Tail of an H2O Dataset.</i>
----------	---

---

### Description

Returns the first or last rows of an H2OFrame object.

### Usage

```
h2o.head(x, n = 6L, ...)  
  
## S3 method for class 'H2OFrame'  
head(x, n = 6L, ...)  
  
h2o.tail(x, n = 6L, ...)  
  
## S3 method for class 'H2OFrame'  
tail(x, n = 6L, ...)
```

### 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.
...	Ignored.

### Value

An H2OFrame containing the first or last n rows of an H2OFrame object.

### Examples

```
library(h2o)  
h2o.init(ip <- "localhost", port = 54321, startH2O = TRUE)  
ausPath <- system.file("extdata", "australia.csv", package="h2o")  
australia.hex <- h2o.uploadFile(path = ausPath)  
head(australia.hex, 10)  
tail(australia.hex, 10)
```

---

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).

---

h2o.hit_ratio_table	<i>Retrieve the Hit Ratios 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".</i>
---------------------	---

---

**Description**

Retrieve the Hit Ratios 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

---

h2o.hour	<i>Convert Milliseconds to Hour of Day in H2O Datasets</i>
----------	--

---

**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.ifelse	<i>H2O Apply Conditional Statement</i>
------------	--

---

**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**

```
h2o.init()
ausPath <- system.file("extdata", "australia.csv", package="h2o")
australia.hex <- h2o.importFile(path = ausPath)
australia.hex[,9] <- ifelse(australia.hex[,3] < 279.9, 1, 0)
summary(australia.hex)
```

---

h2o.importFile	<i>Import Files into H2O</i>
----------------	------------------------------

---

**Description**

Imports files into an H2O cloud. 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)

h2o.importFolder(path, pattern = "", destination_frame = "", parse = TRUE,
  header = NA, sep = "", col.names = NULL, col.types = NULL,
  na.strings = NULL)

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)
```



**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.
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**

```

h2o.init(ip = "localhost", port = 54321, startH2O = TRUE)
prosPath = system.file("extdata", "prostate.csv", package = "h2o")
prostate.hex = h2o.importFile(path = prosPath, destination_frame = "prostate.hex")
class(prostate.hex)
summary(prostate.hex)

#Import files with a certain regex pattern by utilizing h2o.importFolder()
#In this example we import all .csv files in the directory prostate_folder
prosPath = system.file("extdata", "prostate_folder", package = "h2o")
prostate_pattern.hex = h2o.importFolder(path = prosPath, pattern = ".*.csv",
                                       destination_frame = "prostate.hex")
class(prostate_pattern.hex)
summary(prostate_pattern.hex)

```

---

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, and MariaDB. Support for Oracle 12g and Microsoft SQL Server

**Usage**

```

h2o.import_sql_select(connection_url, select_query, username, password,
                      optimize = 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
optimize	(Optional) Optimize import of SQL table for faster imports. Experimental. Default is true.

**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 cloud. 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, and MariaDB. Support for Oracle 12g and Microsoft SQL Server

**Usage**

```
h2o.import_sql_table(connection_url, table, username, password,
  columns = NULL, optimize = 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. Experimental. Default is true.

**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**

data	The dataset containing the column to impute.
column	A specific column to impute, default of 0 means impute the whole frame.
method	"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);
combine_method	If method is "median", then choose how to combine quantiles on even sample sizes. This parameter is ignored in all other cases.
by	group by columns
groupByFrame	Impute the column col with this pre-computed grouped frame.
values	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**

```
h2o.init()
fr <- as.h2o(iris, destination_frame="iris")
fr[sample(nrow(fr),40),5] <- NA # randomly replace 50 values with NA
# impute with a group by
fr <- h2o.impute(fr, "Species", "mode", by=c("Sepal.Length", "Sepal.Width"))
```

h2o.init

*Initialize and Connect to H2O***Description**

Attempts to start and/or connect to and H2O instance.

**Usage**

```
h2o.init(ip = "localhost", port = 54321, startH2O = TRUE,
  forceDL = FALSE, enable_assertions = TRUE, license = NULL,
  nthreads = -1, max_mem_size = NULL, min_mem_size = NULL,
  ice_root = tempdir(), strict_version_check = TRUE,
  proxy = NA_character_, https = FALSE, insecure = FALSE,
  username = NA_character_, password = NA_character_,
  cookies = NA_character_, context_path = NA_character_,
  ignore_config = FALSE)
```

**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.
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 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.

<code>min_mem_size</code>	(Optional) A character string specifying the minimum size, in bytes, of the memory allocation pool to H2O. This value must 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.
<code>ice_root</code>	(Optional) A directory to handle object spillage. The default varies by OS.
<code>strict_version_check</code>	(Optional) Setting this to FALSE is unsupported and should only be done when advised by technical support.
<code>proxy</code>	(Optional) A character string specifying the proxy path.
<code>https</code>	(Optional) Set this to TRUE to use https instead of http.
<code>insecure</code>	(Optional) Set this to TRUE to disable SSL certificate checking.
<code>username</code>	(Optional) Username to login with.
<code>password</code>	(Optional) Password to login with.
<code>cookies</code>	(Optional) Vector(or list) of cookies to add to request.
<code>context_path</code>	(Optional) The last part of connection URL: <code>http://&lt;ip&gt;:&lt;port&gt;/&lt;context_path&gt;</code>
<code>ignore_config</code>	(Optional) A logical value indicating whether a search for a <code>.h2oconfig</code> file should be conducted or not. Default value is FALSE.

### 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.jar")`) 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**

```

library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris.csv", package = "h2o")
iris.hex <- h2o.importFile(path = irisPath)
summary(iris.hex)
irismiss.hex <- h2o.insertMissingValues(iris.hex, fraction = 0.25)
head(irismiss.hex)
summary(irismiss.hex)

```

---

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**

```

library(h2o)
h2o.init()

# Create some random data
myframe <- 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
myframe[,5] <- as.factor(myframe[,5])
head(myframe, 20)

# Create pairwise interactions
pairwise <- h2o.interaction(myframe, destination_frame = 'pairwise',
                           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(myframe, destination_frame = 'higherorder', 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(myframe[,5], 20)
trim_integer_levels <- h2o.interaction(myframe, destination_frame = 'trim_integers', factors = "C5",
                                       pairwise = FALSE, max_factors = 3, min_occurrence = 2)

head(trim_integer_levels, 20)

# Put all together
myframe <- h2o.cbind(myframe, pairwise, higherorder, trim_integer_levels)
myframe
head(myframe,20)
summary(myframe)

```

---

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**

[http://www.cs.ucr.edu/~eamonn/iSAX\\_2.0.pdf](http://www.cs.ucr.edu/~eamonn/iSAX_2.0.pdf)

<http://www.cs.ucr.edu/~eamonn/SAX.pdf>

---

h2o.ischaracter	<i>Check if character</i>
-----------------	---------------------------

---

**Description**

Check if character

**Usage**

```
h2o.ischaracter(x)
```

**Arguments**

`x` An H2OFrame object.

**See Also**

[is.character](#) for the base R implementation.

---

h2o.isfactor	<i>Check if factor</i>
--------------	------------------------

---

**Description**

Check if factor

**Usage**

```
h2o.isfactor(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[is.factor](#) for the base R implementation.

---

h2o.isnumeric	<i>Check if numeric</i>
---------------	-------------------------

---

**Description**

Check if numeric

**Usage**

```
h2o.isnumeric(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

[is.numeric](#) for the base R implementation.

---

h2o.is_client	<i>Check Client Mode Connection</i>
---------------	-------------------------------------

---

**Description**

Check Client Mode Connection

**Usage**

h2o.is\_client()

---

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.

---

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	<i>Performs k-means clustering on an H2O dataset.</i>
------------	---

---

### 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_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"))
```

### Arguments

training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
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 N-fold cross-validation (0 to disable or >= 2). Defaults to 0.
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 ( $\leq k$ ) 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", "SortByResponse", "EnumLimited". Defaults to AUTO.

**Value**

Returns 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**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
h2o.kmeans(training_frame = prostate.hex, k = 10, x = c("AGE", "RACE", "VOL", "GLEASON"))
```

---

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**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
h2o.kurtosis(prostate.hex$AGE)
```

---

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**

```
iris.hex <- as.h2o(iris)
h2o.levels(iris.hex, 5) # returns "setosa"    "versicolor" "virginica"
```

---

h2o.listTimezones        *List all of the Time Zones Acceptable by the H2O Cloud.*

---

**Description**

List all of the Time Zones Acceptable by the H2O Cloud.

**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.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. and port of the server running H2O.

**Value**

Returns a [H2OModel](#) object of the class corresponding to the type of model built.

**See Also**

[h2o.saveModel](#), [H2OModel](#)

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prosPath = system.file("extdata", "prostate.csv", package = "h2o")
# prostate.hex = h2o.importFile(path = prosPath, destination_frame = "prostate.hex")
# prostate.glm = h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#   training_frame = prostate.hex, 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.log

*Compute the logarithm of x*

---

**Description**

Compute the logarithm of x

**Usage**

h2o.log(x)

**Arguments**

x                    An H2OFrame object.

**See Also**

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

---

h2o.log10

*Compute the log10 of x*

---

**Description**

Compute the log10 of x

**Usage**

h2o.log10(x)

**Arguments**

`x` An H2OFrame object.

**See Also**

[log10](#) for the base R implementation.

---

`h2o.log1p` *Compute the log1p of x*

---

**Description**

Compute the log1p of x

**Usage**

`h2o.log1p(x)`

**Arguments**

`x` An H2OFrame object.

**See Also**

[log1p](#) for the base R implementation.

---

`h2o.log2` *Compute the log2 of x*

---

**Description**

Compute the log2 of x

**Usage**

`h2o.log2(x)`

**Arguments**

`x` An H2OFrame object.

**See Also**

[log2](#) for the base R implementation.

---

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

---

h2o.ls	<i>List Keys on an H2O Cluster</i>
--------	------------------------------------

---

**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**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
h2o.ls()
```

---

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

```
library(h2o)
h2o.init()
string_to_lstrip <- as.h2o("1234567890")
lstrip_string <- h2o.lstrip(string_to_lstrip,"123") #Remove "123"
```

---

h2o.mae

*Retrieve the Mean Absolute Error Value*

---

## 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

```
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.deeplearning(x=2:5,y=1,training_frame=fr)

h2o.mae(m)
```

---

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 <code>h2o.glm</code> 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)
```

**Arguments**

predicted	An H2OFrame containing predictions
actuals	An H2OFrame containing actual values
domain	Vector with response factors for classification.
distribution	Distribution for regression.

**Value**

Returns an object of the [H2OModelMetrics](#) subclass.

**Examples**

```

library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.hex$CAPSULE <- as.factor(prostate.hex$CAPSULE)
prostate.gbm <- h2o.gbm(3:9, "CAPSULE", prostate.hex)
pred <- h2o.predict(prostate.gbm, prostate.hex)[,3] ## class-1 probability
h2o.make_metrics(pred,prostate.hex$CAPSULE)

```

---

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**

```
h2o.init()
hex <- as.h2o(iris)
h2o.match(hex[,5], c("setosa", "versicolor"))
```

---

h2o.max	<i>Returns the maxima of the input values.</i>
---------	--

---

**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**

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

---

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**

[mean](#) , [rowMeans](#), or [colMeans](#) for the base R implementation

**Examples**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
# Default behavior. Will return list of means per column.
h2o.mean(prostate.hex$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.hex,na.rm=TRUE,axis=1,return_frame=TRUE)
```

---

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**

```
library(h2o)
h2o.init()

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

hex[,2] <- as.factor(hex[,2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = hex, distribution = "bernoulli")
perf <- h2o.performance(model, hex)
h2o.mean_per_class_error(perf)
h2o.mean_per_class_error(model, train=TRUE)
```

---

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**

```
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)
```

---

h2o.median	<i>H2O Median</i>
------------	-------------------

---

**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**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath, destination_frame = "prostate.hex")
h2o.median(prostate.hex)
```

---

h2o.merge	<i>Merge Two H2O Data Frames</i>
-----------	----------------------------------

---

### Description

Merges two H2OFrame objects with the same arguments and meanings as merge() in base R.

### 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 = "hash")
```

### 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, radix, or hash (default)

### Examples

```
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))  
l.hex <- as.h2o(left)  
r.hex <- as.h2o(right)  
left.hex <- h2o.merge(l.hex, r.hex, all.x = TRUE)
```

---

`h2o.metric`*H2O Model Metric Accessor Functions*

---

**Description**

A series of functions that retrieve model metric details.

**Usage**`h2o.metric(object, thresholds, metric)``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.
metric	(Optional) A specified parameter to retrieve.

**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**

```
library(h2o)
h2o.init()

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

hex[,2] <- as.factor(hex[,2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = hex, distribution = "bernoulli")
perf <- h2o.performance(model, hex)
h2o.F1(perf)
```

---

h2o.min

*Returns the minima of the input values.*


---

**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**

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

---

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

---

h2o.month	<i>Convert Milliseconds to Months in H2O Datasets</i>
-----------	---

---

**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	<i>Retrieves Mean Squared Error Value</i>
---------	---

---

**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 [H2OModelMetrics](#) 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

```
library(h2o)
h2o.init()

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

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

---

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

```
h2o.init()
iris.hex <- as.h2o(iris)
h2o.nacnt(iris.hex) # should return all 0s
h2o.insertMissingValues(iris.hex)
h2o.nacnt(iris.hex)
```

h2o.naiveBayes

*Compute naive Bayes probabilities on an H2O dataset.***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_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, max_hit_ratio_k = 0, 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)
```

**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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
model_id	Destination id for this model; auto-generated if not specified.
nfolds	Number of folds for N-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_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.
max_hit_ratio_k	Max. number (top K) of predictions to use for hit ratio computation (for multi-class only, 0 to disable) Defaults to 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.

## Details

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.

## Value

Returns an object of class [H2OBinomialModel](#) if the response has two categorical levels, and [H2OMultinomialModel](#) otherwise.

## Examples

```
h2o.init()
votesPath <- system.file("extdata", "housevotes.csv", package="h2o")
votes.hex <- h2o.uploadFile(path = votesPath, header = TRUE)
h2o.naiveBayes(x = 2:17, y = 1, training_frame = votes.hex, laplace = 3)
```

---

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

---

## Description

Column names of an H2OFrame

## Usage

```
h2o.names(x)
```

## Arguments

x                    An H2OFrame object.

## See Also

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

---

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.

---

h2o.nchar	<i>String length</i>
-----------	----------------------

---

**Description**

String length

**Usage**

```
h2o.nchar(x)
```

**Arguments**

x	The column whose string lengths will be returned.
---	---

**Examples**

```
library(h2o)
h2o.init()
string_to_nchar <- as.h2o("r tutorial")
nchar_string <- h2o.nchar(string_to_nchar)
```

---

h2o.ncol	<i>Return the number of columns present in x.</i>
----------	---

---

**Description**

Return the number of columns present in x.

**Usage**

```
h2o.ncol(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

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

---

h2o.networkTest	<i>View Network Traffic Speed</i>
-----------------	-----------------------------------

---

**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.

---

h2o.no_progress	<i>Disable Progress Bar</i>
-----------------	-----------------------------

---

**Description**

Disable Progress Bar

**Usage**

```
h2o.no_progress()
```

---

h2o.nrow	<i>Return the number of rows present in x.</i>
----------	--

---

**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.

---

h2o.null_deviance	<i>Retrieve the null deviance 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".</i>
-------------------	---

---

**Description**

Retrieve the null deviance 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

---

h2o.null_dof	<i>Retrieve the null degrees of freedom 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".</i>
--------------	--

---

**Description**

Retrieve the null degrees of freedom 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

---

h2o.num\_iterations      *Retrieve the number of iterations.*

---

**Description**

Retrieve the number of iterations.

**Usage**

```
h2o.num_iterations(object)
```

**Arguments**

object	An <a href="#">H2OClusteringModel</a> object.
...	further arguments to be passed on (currently unimplemented)

---

h2o.num\_valid\_substrings  
*Count of substrings  $\geq 2$  chars that are contained in file*

---

**Description**

Find the count of all possible substrings  $\geq 2$  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	<i>View H2O R Logs</i>
-------------	------------------------

---

**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()
ausPath = system.file("extdata", "australia.csv", package="h2o")
australia.hex = h2o.importFile(path = ausPath)
h2o.stopLogging()

# Not run to avoid windows being opened during R CMD check
# h2o.openLog("Command")
# h2o.openLog("Error")

## End(Not run)
```

---

h2o.parseRaw	<i>H2O Data Parsing</i>
--------------	-------------------------

---

**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)
```

**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.
col.types	(Optional) A vector specifying the types to attempt to force over columns.
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

**Details**

Parse the Raw Data produced by the import phase.

**See Also**

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

---

h2o.parseSetup

*Get a parse setup back for the staged data.*

---

**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)
```

**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.
col.types	(Optional) A vector specifying the types to attempt to force over columns.
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

**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)
```

**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 exceed the level count.
plot	A logical specifying whether to plot partial dependence table.
plot_stddev	A logical specifying whether to add std err to partial dependence plot.

**Value**

Plot and list of calculated mean response tables for each feature requested.

**Examples**

```
library(h2o)
h2o.init()
prostate.path <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prostate.path, destination_frame = "prostate.hex")
prostate.hex[, "CAPSULE"] <- as.factor(prostate.hex[, "CAPSULE"] )
prostate.hex[, "RACE"] <- as.factor(prostate.hex[, "RACE"] )
prostate.gbm <- h2o.gbm(x = c("AGE", "RACE"),
  y = "CAPSULE",
  training_frame = prostate.hex,
  ntrees = 10,
  max_depth = 5,
  learn_rate = 0.1)
h2o.partialPlot(object = prostate.gbm, data = prostate.hex, cols = c("AGE", "RACE"))
```

---

h2o.performance

*Model Performance Metrics in H2O*


---

**Description**

Given a trained h2o model, compute its performance on the given dataset

**Usage**

```
h2o.performance(model, newdata = NULL, train = FALSE, valid = FALSE,
  xval = FALSE, data = NULL)
```

**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 balance_classes, 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 <a href="#">H2OFrame</a> . This argument is now called 'newdata'.

**Value**

Returns an object of the [H2OModelMetrics](#) subclass.

**Examples**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.hex$CAPSULE <- as.factor(prostate.hex$CAPSULE)
prostate.gbm <- h2o.gbm(3:9, "CAPSULE", prostate.hex)
h2o.performance(model = prostate.gbm, newdata=prostate.hex)

## If model uses balance_classes
## the results from train = TRUE will not match the results from newdata = prostate.hex
prostate.gbm.balanced <- h2o.gbm(3:9, "CAPSULE", prostate.hex, balance_classes = TRUE)
h2o.performance(model = prostate.gbm.balanced, newdata = prostate.hex)
h2o.performance(model = prostate.gbm.balanced, train = TRUE)
```

---

h2o.pivot

*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*

---

**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

---

h2o.pcomp	<i>Principal components analysis of an H2O data frame using the power method to calculate the singular value decomposition of the Gram matrix.</i>
-----------	--

---

**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.pcomp(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"), k = 1,
  max_iterations = 1000, use_all_factor_levels = FALSE,
  compute_metrics = TRUE, impute_missing = FALSE, seed = -1,
  max_runtime_secs = 0)
```



**Arguments**

training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
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.
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.
pca_method	Method for computing PCA (Caution: GLRM is currently experimental and unstable) Must be one of: "GramSVD", "Power", "Randomized", "GLRM". Defaults to GramSVD.
k	Rank of matrix approximation Defaults to 1.
max_iterations	Maximum training iterations Defaults to 1000.
use_all_factor_levels	Logical. Whether first factor level is included in each categorical expansion Defaults to FALSE.
compute_metrics	Logical. Whether to compute metrics on the training data Defaults to TRUE.
impute_missing	Logical. Whether to impute missing entries with the column mean Defaults to FALSE.
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).
max_runtime_secs	Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

**Value**

Returns 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.g1rm](#)

**Examples**

```
library(h2o)
h2o.init()
ausPath <- system.file("extdata", "australia.csv", package="h2o")
australia.hex <- h2o.uploadFile(path = ausPath)
h2o.prcomp(training_frame = australia.hex, k = 8, transform = "STANDARDIZE")
```

---

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**

<code>model</code>	String with file name of MOJO or POJO Jar
<code>json</code>	JSON String with inputs to model
<code>genmodelpath</code>	(Optional) path name to <code>h2o-genmodel.jar</code> , if not set defaults to same dir as MOJO
<code>labels</code>	(Optional) if TRUE then show output labels in result
<code>classpath</code>	(Optional) Extra items for the class path of where to look for Java classes, e.g., <code>h2o-genmodel.jar</code>
<code>javaoptions</code>	(Optional) Java options string, default if <code>"-Xmx4g"</code>

**Value**

Returns an object with the prediction result

**Examples**

```
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"))
```

---

h2o.print	<i>Print An H2OFrame</i>
-----------	--------------------------

---

**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).
...	Further arguments to be passed from or to other methods.

---

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.

---

h2o.proj\_archetypes     *Convert Archetypes to Features from H2O GLRM Model*

---

### 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

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris_wheader.csv", package="h2o")
iris.hex <- h2o.uploadFile(path = irisPath)
iris.glm <- h2o.glm(training_frame = iris.hex, k = 4, loss = "Quadratic",
                  multi_loss = "Categorical", max_iterations = 1000)
iris.parch <- h2o.proj_archetypes(iris.glm, iris.hex)
head(iris.parch)
```

---

h2o.quantile	<i>Quantiles of H2O Frames.</i>
--------------	---------------------------------

---

**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**

```
# Request quantiles for an H2O parsed data set:
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
# Request quantiles for a subset of columns in an H2O parsed data set
```

```
quantile(prostate.hex[,3])
for(i in 1:ncol(prostate.hex))
  quantile(prostate.hex[,i])
```

---

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

```
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.glm(x=2:5,y=1,training_frame=fr)

h2o.r2(m)
```

---

h2o.randomForest	<i>Builds a Random Forest Model on an H2OFrame</i>
------------------	--

---

## Description

Builds a Random Forest Model on an H2OFrame

## Usage

```
h2o.randomForest(x, y, training_frame, model_id = NULL,
  validation_frame = NULL, nfold = 0,
  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,
  max_hit_ratio_k = 0, 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", "lift_top_group",
  "misclassification", "mean_per_class_error"), stopping_tolerance = 0.001,
  max_runtime_secs = 0, seed = -1, build_tree_one_node = FALSE,
  mtries = -1, sample_rate = 0.632000291, 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)
```

## 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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
model_id	Destination id for this model; auto-generated if not specified.
validation_frame	Id of the validation data frame.

<code>nfolds</code>	Number of folds for N-fold cross-validation (0 to disable or $\geq 2$ ). Defaults to 0.
<code>keep_cross_validation_predictions</code>	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
<code>keep_cross_validation_fold_assignment</code>	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
<code>score_each_iteration</code>	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
<code>score_tree_interval</code>	Score the model after every so many trees. Disabled if set to 0. Defaults to 0.
<code>fold_assignment</code>	Cross-validation fold assignment scheme, if <code>fold_column</code> 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.
<code>fold_column</code>	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.
<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_hit_ratio_k</code>	Max. number (top K) of predictions to use for hit ratio computation (for multi-class only, 0 to disable) Defaults to 0.
<code>ntrees</code>	Number of trees. Defaults to 50.
<code>max_depth</code>	Maximum tree depth. 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.



nbins_top_level	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.
nbins_cats	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.
r2_stopping	r2_stopping is no longer supported and will be ignored if set - please use stopping_rounds, stopping_metric and stopping_tolerance instead. Previous version of H2O would stop making trees when the R <sup>2</sup> metric equals or exceeds this Defaults to 1.797693135e+308.
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) Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "mean_per_class_error". Defaults to AUTO.
stopping_tolerance	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
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 0.6320000291.
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 (from 0.0 to 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

**Value**

Creates a [H2OModel](#) object of the right type.

**See Also**

[predict.H2OModel](#) for prediction

---

h2o.range	<i>Returns a vector containing the minimum and maximum of all the given arguments.</i>
-----------	--

---

**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.

---

h2o.rbind	<i>Combine H2O Datasets by Rows</i>
-----------	-------------------------------------

---

**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**

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

**Examples**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.cbind <- h2o.rbind(prostate.hex, prostate.hex)
head(prostate.cbind)
```

---

h2o.reconstruct	<i>Reconstruct Training Data via H2O GLRM Model</i>
-----------------	---

---

**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**

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris_wheader.csv", package="h2o")
iris.hex <- h2o.uploadFile(path = irisPath)
iris.glm <- h2o.glm(training_frame = iris.hex, k = 4, transform = "STANDARDIZE",
  loss = "Quadratic", multi_loss = "Categorical", max_iterations = 1000)
iris.rec <- h2o.reconstruct(iris.glm, iris.hex, reverse_transform = TRUE)
head(iris.rec)
```

---

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

---

h2o.removeAll	<i>Remove All Objects on the H2O Cluster</i>
---------------	--

---

**Description**

Removes the data from the h2o cluster, but does not remove the local references.

**Usage**

```
h2o.removeAll(timeout_secs = 0)
```

**Arguments**

timeout\_secs    Timeout in seconds. Default is no timeout.

**See Also**

[h2o.rm](#)

**Examples**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package = "h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
h2o.ls()
h2o.removeAll()
h2o.ls()
```

---

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

---

h2o.residual_deviance	<i>Retrieve the residual deviance 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".</i>
-----------------------	---

---

**Description**

Retrieve the residual deviance 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

---

h2o.residual_dof	<i>Retrieve the residual degrees of freedom 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".</i>
------------------	--

---

**Description**

Retrieve the residual degrees of freedom 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

---

h2o.rm	<i>Delete Objects In H2O</i>
--------	------------------------------

---

**Description**

Remove the h2o Big Data object(s) having the key name(s) from ids.

**Usage**

```
h2o.rm(ids)
```

**Arguments**

ids	The object or hex key associated with the object to be removed or a vector/list of those things.
-----	--

**See Also**

[h2o.assign](#), [h2o.ls](#)

---

`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**

<code>object</code>	An <a href="#">H2OModelMetrics</a> object of the correct type.
<code>train</code>	Retrieve the training RMSE
<code>valid</code>	Retrieve the validation RMSE
<code>xval</code>	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**

```
library(h2o)
h2o.init()

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

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



---

h2o.rmsle	<i>Retrieve the Root Mean Squared Log Error</i>
-----------	---

---

**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**

```
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)

m <- h2o.deeplearning(x=2:5,y=1,training_frame=fr)

h2o.rmsle(m)
```

---

h2o.round	<i>Round doubles/floats to the given number of decimal places.</i>
-----------	--

---

**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.

---

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**

```
library(h2o)
h2o.init()
string_to_rstrip <- as.h2o("1234567890")
rstrip_string <- h2o.rstrip(string_to_rstrip,"890") #Remove "890"
```

---

h2o.runif	<i>Produce a Vector of Random Uniform Numbers</i>
-----------	---

---

**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**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.importFile(path = prosPath, destination_frame = "prostate.hex")
s <- h2o.runif(prostate.hex)
summary(s)

prostate.train <- prostate.hex[s <= 0.8,]
prostate.train <- h2o.assign(prostate.train, "prostate.train")
prostate.test <- prostate.hex[s > 0.8,]
prostate.test <- h2o.assign(prostate.test, "prostate.test")
nrow(prostate.train) + nrow(prostate.test)
```

---

h2o.saveModel	<i>Save an H2O Model Object to Disk</i>
---------------	---

---

**Description**

Save an [H2OModel](#) to disk. (Note that ensemble binary models can be saved.)

**Usage**

```
h2o.saveModel(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**

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

**See Also**

[h2o.loadModel](#) for loading a model to H2O from disk

**Examples**

```
## Not run:
# library(h2o)
# h2o.init()
# prostate.hex <- h2o.importFile(path = paste("https://raw.githubusercontent.com",
#     "h2oai/h2o-2/master/smalldata/logreg/prostate.csv", sep = "/"),
#   destination_frame = "prostate.hex")
# prostate.glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#   training_frame = prostate.hex, 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**

object	an <a href="#">H2OModel</a> object.
path	string indicating the directory the model details will be written to.
force	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.hex <- 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.hex, family = "binomial", alpha = 0.5)  
# h2o.saveModelDetails(object = prostate.glm, path = "/Users/UserName/Desktop", force=TRUE)  
  
## End(Not run)
```

---

h2o.saveMojo

*Save an H2O Model Object as Mojo to Disk*

---

## Description

Save an MOJO (Model Object, Optimized) to disk.

## Usage

```
h2o.saveMojo(object, path = "", force = FALSE)
```

## Arguments

<code>object</code>	an <a href="#">H2OModel</a> object.
<code>path</code>	string indicating the directory the model will be written to.
<code>force</code>	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.hex <- 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.hex, family = "binomial", alpha = 0.5)
# h2o.saveMojo(object = prostate.glm, path = "/Users/UserName/Desktop", force=TRUE)

## End(Not run)
```

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)
```

```
## 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**

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris_wheader.csv", package="h2o")
iris.hex <- h2o.uploadFile(path = irisPath, destination_frame = "iris.hex")
summary(iris.hex)

# Scale and center all the numeric columns in iris data set
scale(iris.hex[, 1:4])
```

---

h2o.scoreHistory	<i>Retrieve Model Score History</i>
------------------	-------------------------------------

---

**Description**

Retrieve Model Score History

**Usage**

```
h2o.scoreHistory(object)
```

**Arguments**

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

---

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 <a href="#">H2OFrame</a> object.
na.rm	logical. Should missing values be removed?

**See Also**

[h2o.var](#) for variance, and [sd](#) for the base R implementation.

**Examples**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
sd(prostate.hex$AGE)
```

---

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 [H2ODimReductionModel](#) object.

---

h2o.setLevels	<i>Set Levels of H2O Factor Column</i>
---------------	--

---

**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 (does not make a copy).

**Usage**

h2o.setLevels(x, levels)

**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.

---

h2o.setTimezone	<i>Set the Time Zone on the H2O Cloud</i>
-----------------	---

---

**Description**

Set the Time Zone on the H2O Cloud

**Usage**

h2o.setTimezone(tz)

**Arguments**

tz                    The desired timezone.



---

h2o.show_progress	<i>Enable Progress Bar</i>
-------------------	----------------------------

---

**Description**

Enable Progress Bar

**Usage**

```
h2o.show_progress()
```

---

h2o.shutdown	<i>Shut Down H2O Instance</i>
--------------	-------------------------------

---

**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 cloud
## Not run:
library(h2o)
h2o.init()
h2o.shutdown()

## End(Not run)
```

---

h2o.signif	<i>Round doubles/floats to the given number of significant digits.</i>
------------	--

---

**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**

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

---

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**

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

---

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**

```
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
h2o.skewness(prostate.hex$AGE)
```

---

`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

<code>data</code>	An H2OFrame object representing the dataste to split.
<code>ratios</code>	A numeric value or array indicating the ratio of total rows contained in each split. Must total up to less than 1.
<code>destination_frames</code>	An array of frame IDs equal to the number of ratios specified plus one.
<code>seed</code>	Random seed.

### Value

Returns a list of split H2OFrame's

### Examples

```
library(h2o)
h2o.init()
irisPath <- system.file("extdata", "iris.csv", package = "h2o")
iris.hex <- h2o.importFile(path = irisPath)
iris.split <- h2o.splitFrame(iris.hex, ratios = c(0.2, 0.5))
head(iris.split[[1]])
summary(iris.split[[1]])
```

---

h2o.sqrt	<i>Compute the square root of x</i>
----------	-------------------------------------

---

**Description**

Compute the square root of x

**Usage**

```
h2o.sqrt(x)
```

**Arguments**

x                    An H2OFrame object.

**See Also**

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

---

h2o.stackedEnsemble	<i>Build a stacked ensemble (aka. Super Learner) using the H2O base learning algorithms specified by the user.</i>
---------------------	--

---

**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, base_models = list())
```

**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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).

training\_frame    Id of the training data frame (Not required, to allow initial validation of model parameters).

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

validation\_frame   Id of the validation data frame.

`base_models` List of model ids which we can stack together. Models must have been cross-validated using `nfolds > 1`, and folds must be identical across models. Defaults to `[]`.

### Examples

```
# See example R code here:  
# http://docs.h2o.ai/h2o/latest-stable/h2o-docs/data-science/stacked-ensembles.html
```

---

`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

```
library(h2o)  
h2o.init()  
h2o.startLogging()  
ausPath = system.file("extdata", "australia.csv", package="h2o")  
australia.hex = h2o.importFile(path = ausPath)  
h2o.stopLogging()
```

---

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**

```
library(h2o)
h2o.init()

prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.importFile(prosPath)
prostate.hex[,2] <- as.factor(prostate.hex[,2])
prostate.glm <- h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
                       training_frame = prostate.hex, family = "binomial",
                       nfold = 0, alpha = 0.5, lambda_search = FALSE)
h2o.std_coef_plot(prostate.glm)
```

---

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**

```
library(h2o)
h2o.init()
h2o.startLogging()
ausPath = system.file("extdata", "australia.csv", package="h2o")
australia.hex = h2o.importFile(path = ausPath)
h2o.stopLogging()
```

---

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

---

h2o.stringdist	<i>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.</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"))
```



**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

**Examples**

```
h2o.init()
x <- as.h2o(c("Martha", "Dwayne", "Dixon"))
y <- as.character(as.h2o(c("Marhta", "Duane", "Dicksonx")))
h2o.stringdist(x, y, method = "jw")
```

---

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**

```
library(h2o)
h2o.init()
string_to_split <- as.h2o("Split at every character.")
split_string <- h2o.strsplit(string_to_split,"")
```

---

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

```
library(h2o)
h2o.init()
string_to_sub <- as.h2o("r tutorial")
sub_string <- h2o.sub("r ", "H2O ", string_to_sub)
```

---

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**

```
library(h2o)
h2o.init()
string_to_substring <- as.h2o("1234567890")
substr <- h2o.substring(string_to_substring,2) #Get substring from second index onwards
```

---

h2o.sum	<i>Compute the frame's sum by-column (or by-row).</i>
---------	---

---

**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).
return_frame	A boolean that indicates whether to return an H2O frame or a list. Default is FALSE.

**See Also**

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

---

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

object	An H2OFrame object.
factors	The number of factors to return in the summary. Default is the top 6.
exact_quantiles	Compute exact quantiles or use approximation. Default is to use approximation.
...	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

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.importFile(path = prosPath)
summary(prostate.hex)
summary(prostate.hex$GLEASON)
summary(prostate.hex[,4:6])
summary(prostate.hex, exact_quantiles=TRUE)
```

---

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)
```

### Arguments

training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
x	A vector containing the character names of the predictors in the model.
destination_key	(Optional) The unique hex 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.

### Value

Returns 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.

### Examples

```

library(h2o)
h2o.init()
ausPath <- system.file("extdata", "australia.csv", package="h2o")
australia.hex <- h2o.uploadFile(path = ausPath)
h2o.svd(training_frame = australia.hex, nv = 8)
  
```

---

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**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath, destination_frame = "prostate.hex")
summary(prostate.hex)

# Counts of the ages of all patients
head(h2o.table(prostate.hex[,3]))
h2o.table(prostate.hex[,3])

# Two-way table of ages (rows) and race (cols) of all patients
head(h2o.table(prostate.hex[,c(3,4)]))
h2o.table(prostate.hex[,c(3,4)])
```

---

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 mean Y counts

## Examples

```
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)
```

---

h2o.tan	<i>Compute the tangent of x</i>
---------	---------------------------------

---

## Description

Compute the tangent of x

## Usage

```
h2o.tan(x)
```

## Arguments

x                    An H2OFrame object.

## See Also

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

---

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

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



---

h2o.toFrame	<i>Converts a given word2vec model into H2OFrame. The frame represents learned word embeddings</i>
-------------	--

---

**Description**

Converts a given word2vec model into H2OFrame. The frame represents learned word embeddings

**Usage**

```
h2o.toFrame(word2vec)
```

**Arguments**

word2vec	A word2vec model.
----------	-------------------

**Examples**

```
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
```

---

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**

```
library(h2o)
h2o.init()
string_to_tokenize <- as.h2o("Split at every character and tokenize.")
tokenize_string <- h2o.tokenize(as.character(string_to_tokenize), "")
```

---

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**

```
library(h2o)
h2o.init()
string_to_lower <- as.h2o("ABCDE")
lowered_string <- h2o.tolower(string_to_lower)
```

---

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

---

h2o.totss	<i>Get the total sum of squares. 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".</i>
-----------	--

---

**Description**

Get the total sum of squares. 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

---

h2o.tot_withinss	<i>Get the total within cluster sum of squares. 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".</i>
------------------	---

---

### Description

Get the total within cluster sum of squares. 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

---

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**

```
library(h2o)
h2o.init()
string_to_upper <- as.h2o("abcde")
upper_string <- h2o.toupper(string_to_upper)
```

---

h2o.transform	<i>Transform words (or sequences of words) to vectors using a word2vec model.</i>
---------------	---

---

**Description**

Transform words (or sequences of words) to vectors using a word2vec model.

**Usage**

```
h2o.transform(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**

```
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
```

---

`h2o.trim`*Trim Space*

---

**Description**

Trim Space

**Usage**`h2o.trim(x)`**Arguments**`x`                    The column whose strings should be trimmed.**Examples**

```
library(h2o)
h2o.init()
string_to_trim <- as.h2o("r tutorial")
trim_string <- h2o.trim(string_to_trim)
```

---

`h2o.trunc`*trunc takes a single numeric argument x and returns a numeric vector containing the integers formed by truncating the values in x toward 0.*

---

**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**[trunc](#) for the base R implementation.

---

h2o.unique	<i>H2O Unique</i>
------------	-------------------

---

**Description**

Extract unique values in the column.

**Usage**

```
h2o.unique(x)
```

**Arguments**

x                    An H2OFrame object.

**Value**

Returns an H2OFrame object.

---

h2o.var	<i>Variance of a column or covariance of columns.</i>
---------	---

---

**Description**

Compute the variance or covariance matrix of one or two H2OFrames.

**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**

[var](#) for the base R implementation. [h2o.sd](#) for standard deviation.

**Examples**

```

h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
var(prostate.hex$AGE)

```

---

h2o.varimp	<i>Retrieve the variable importance.</i>
------------	--

---

**Description**

Retrieve the variable importance.

**Usage**

```
h2o.varimp(object)
```

**Arguments**

object            An [H2OModel](#) object.

---

h2o.varimp_plot	<i>Plot Variable Importances</i>
-----------------	----------------------------------

---

**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

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
hex <- h2o.importFile(prosPath)
hex[,2] <- as.factor(hex[,2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = hex, distribution = "bernoulli")
h2o.varimp_plot(model)

# for deep learning set the variable_importance parameter to TRUE
iris.hex <- as.h2o(iris)
iris.dl <- h2o.deeplearning(x = 1:4, y = 5, training_frame = iris.hex,
variable_importances = TRUE)
h2o.varimp_plot(iris.dl)
```

---

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](#)

h2o.weights                      *Retrieve the respective weight matrix*

---

**Description**

Retrieve the respective weight matrix

**Usage**

```
h2o.weights(object, matrix_id = 1)
```

**Arguments**

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

---

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**

```
h2o.init()
iris.hex <- as.h2o(iris)
h2o.which(iris.hex[,1]==4.4)
```

---

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.max](#) for the base R method.

---

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.

---

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"), 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)
```

**Arguments**

training_frame	Id of the training data frame (Not required, to allow initial validation of model parameters).
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	Use the Skip-Gram model Must be one of: "SkipGram". 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

---

h2o.xgboost	<i>Builds a eXtreme Gradient Boosting model using the native XGBoost backend</i>
-------------	--

---

## 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_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", "lift_top_group", "misclassification",
  "mean_per_class_error"), 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, ntrees = 50, max_depth = 5, min_rows = 10,
  min_child_weight = 0, learn_rate = 0.1, eta = 0, sample_rate = 1,
  subsample = 0, col_sample_rate = 1, colsample_bylevel = 0,
  col_sample_rate_per_tree = 1, colsample_bytree = 0,
  max_abs_leafnode_pred = 3.4028235e+38, max_delta_step = 0,
  score_tree_interval = 0, min_split_improvement = 0, max_bin = 255,
  num_leaves = 255, min_sum_hessian_in_leaf = 100, min_data_in_leaf = 0,
  tree_method = c("auto", "exact", "approx", "hist"),
  grow_policy = c("depthwise", "lossguide"), booster = c("gbtree",
  "gblinear", "dart"), gamma = 0, reg_lambda = 1, reg_alpha = 0,
  dmatrix_type = c("auto", "dense", "sparse"), backend = c("auto", "gpu",
  "cpu"), gpu_id = 0)
```

**Arguments**

<code>x</code>	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 of the response variable in the model. If the data does not contain a header, this is the first column index, and increasing from left to right. (The response must be either an integer or a categorical variable).
<code>training_frame</code>	Id of the training data frame (Not required, to allow initial validation of model parameters).
<code>model_id</code>	Destination id for this model; auto-generated if not specified.
<code>validation_frame</code>	Id of the validation data frame.
<code>nfolds</code>	Number of folds for N-fold cross-validation (0 to disable or $\geq 2$ ). Defaults to 0.
<code>keep_cross_validation_predictions</code>	Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
<code>keep_cross_validation_fold_assignment</code>	Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
<code>score_each_iteration</code>	Logical. Whether to score during each iteration of model training. Defaults to FALSE.
<code>fold_assignment</code>	Cross-validation fold assignment scheme, if <code>fold_column</code> 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.
<code>fold_column</code>	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.
<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) Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "mean_per_class_error". Defaults to AUTO.

stopping_tolerance	Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
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).
distribution	Distribution function Must be one of: "AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber". Defaults to AUTO.
tweedie_power	Tweedie power for Tweedie regression, must be between 1 and 2. Defaults to 1.5.
ntrees	(same as n_estimators) Number of trees. Defaults to 50.
max_depth	Maximum tree depth. Defaults to 5.
min_rows	(same as min_child_weight) Fewest allowed (weighted) observations in a leaf. Defaults to 10.
min_child_weight	(same as min_rows) Fewest allowed (weighted) observations in a leaf. Defaults to 0.
learn_rate	(same as eta) Learning rate (from 0.0 to 1.0) Defaults to 0.1.
eta	(same as learn_rate) Learning rate (from 0.0 to 1.0) Defaults to 0.
sample_rate	(same as subsample) Row sample rate per tree (from 0.0 to 1.0) Defaults to 1.
subsample	(same as sample_rate) Row sample rate per tree (from 0.0 to 1.0) Defaults to 0.
col_sample_rate	(same as colsample_bylevel) Column sample rate (from 0.0 to 1.0) Defaults to 1.
colsample_bylevel	(same as col_sample_rate) Column sample rate (from 0.0 to 1.0) Defaults to 0.
col_sample_rate_per_tree	(same as colsample_bytree) Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.
colsample_bytree	(same as col_sample_rate_per_tree) Column sample rate per tree (from 0.0 to 1.0) Defaults to 0.
max_abs_leafnode_pred	(same as max_delta_step) Maximum absolute value of a leaf node prediction Defaults to 3.4028235e+38.
max_delta_step	(same as max_abs_leafnode_pred) Maximum absolute value of a leaf node prediction Defaults to 0.0.
score_tree_interval	Score the model after every so many trees. Disabled if set to 0. Defaults to 0.

min_split_improvement	(same as gamma) Minimum relative improvement in squared error reduction for a split to happen Defaults to 0.0.
max_bin	For tree_method=hist only: maximum number of bins Defaults to 255.
num_leaves	For tree_method=hist only: maximum number of leaves Defaults to 255.
min_sum_hessian_in_leaf	For tree_method=hist only: the minimum sum of hessian in a leaf to keep splitting Defaults to 100.0.
min_data_in_leaf	For tree_method=hist only: the minimum data in a leaf to keep splitting 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.
gamma	(same as min_split_improvement) Minimum relative improvement in squared error reduction for a split to happen Defaults to 0.0.
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 to use. Defaults to 0.

---

`h2o.xgboost.available` *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.*

---

### 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](#)

---

`H2OClusteringModel-class`*The H2OClusteringModel object.*

---

**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 cloud, 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 cloud'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 cloud.

**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 cloud.  
 port A numeric value specifying the port number of the H2O cloud.  
 proxy A character specifying the proxy path of the H2O cloud.  
 https Set this to TRUE to use https instead of http.  
 insecure Set this to TRUE to disable SSL certificate checking.  
 username Username to login with.  
 password Password to login with.  
 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.

---

H2OFrame-class	<i>The H2OFrame class</i>
----------------	---------------------------

---

**Description**

This class represents an H2OFrame object

---

H2OFrame-Extract	<i>Extract or Replace Parts of an H2OFrame Object</i>
------------------	---

---

**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

*H2O Grid*


---

### Description

A class to contain the information about grid results  
 Format grid object in user-friendly way

### 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.

---

H2OModel-class	<i>The H2OModel object.</i>
----------------	-----------------------------

---

**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 cloud, 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 cloud'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.  
 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 'H2OBinomialMetrics'  
show(object)
```

```
## S4 method for signature 'H2OMultinomialMetrics'  
show(object)
```

```
## S4 method for signature 'H2ORegressionMetrics'  
show(object)
```

```
## S4 method for signature 'H2OClusteringMetrics'  
show(object)
```

```
## S4 method for signature 'H2OAutoEncoderMetrics'  
show(object)
```

```
## S4 method for signature 'H2ODimReductionMetrics'  
show(object)
```

**Arguments**

object                    An H2OModelMetrics object

---

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 [<http://www.ics.uci.edu/~mllearn/MLRepository.html>]. Irvine, CA: University of California, Department of Information and Computer Science.

---

iris                                    *Edgar Anderson's Iris Data*

---

**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
---	--------------------

---

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.
---	--------------



---

is.numeric	<i>Check if numeric</i>
------------	-------------------------

---

**Description**

Check if numeric

**Usage**

```
is.numeric(x)
```

**Arguments**

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

---

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

**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.

---

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

---

### Description

Column names of an H2OFrame

### Usage

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

### Arguments

x                    An H2OFrame

---

Ops.H2OFrame	<i>S3 Group Generic Functions for H2O</i>
--------------	---

---

### 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

```
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")
}

```

---

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

[link{h2o.tabulate}](#)

## Examples

```
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)
```

---

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, ...)

h2o.predict(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.

## 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.

---

`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, ...)
```

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

**Arguments**

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

**Details**

For every row in the test set, return a set of factors that identify the leaf placements of the row in all the trees in the model. 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**

```
library(h2o)
h2o.init()
prosPath <- system.file("extdata", "prostate.csv", package="h2o")
prostate.hex <- h2o.uploadFile(path = prosPath)
prostate.hex$CAPSULE <- as.factor(prostate.hex$CAPSULE)
prostate.gbm <- h2o.gbm(3:9, "CAPSULE", prostate.hex)
h2o.predict(prostate.gbm, prostate.hex)
h2o.predict_leaf_node_assignment(prostate.gbm, prostate.hex)
```



---

print.H2OFrame	<i>Print An H2OFrame</i>
----------------	--------------------------

---

**Description**

Print An H2OFrame

**Usage**

```
## S3 method for class 'H2OFrame'
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).
...	Further arguments to be passed from or to other methods.

---

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

---

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

---

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,H2OGrid-method	<i>Format grid object in user-friendly way</i>
------------------------	--

---

**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", FALSE)[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 disabled by default, to enable it set `options("h2o.use.data.table"=TRUE)`. 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/project/xml/downloads.xml?group\\_id=603](https://simtk.org/project/xml/downloads.xml?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)

---

zzz

*Shutdown H2O cloud after examples run*

---

**Description**

Shutdown H2O cloud after examples run

**Examples**

```
library(h2o)
h2o.init()
h2o.shutdown(prompt = FALSE)
Sys.sleep(3)
```

---

**&&***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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