"h2o"
October 18, 2019

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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:** 3.26.0.8
- **Branch:** rel-yau
- **Date:** Fri Oct 18 01:34:17 UTC 2019
- **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)

Maintainer: Erin LeDell <erin@h2o.ai>

### References

- H2O.ai Homepage
- H2O Documentation
- H2O on GitHub

---

### Description

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

### Usage

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

### Arguments

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

### Details

Contained here are a set of helper methods that perform type checking on the value passed in.
**.collapse**  
*Helper Collapse Function*

**Description**

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

**Usage**

```
collapse(v)
```

**Arguments**

- `v`  
  Character vector.

---

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

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A list object as described above
.h2o.doPOST

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

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A list object as described above

---

.h2o.doRawGET

Perform a low-level HTTP GET operation on an H2O instance

**Description**

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

**Usage**

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

**Arguments**

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

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

Value

A list object as described above

.h2o.doRawPOST
Perform a low-level HTTP POST operation on an H2O instance

Description

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

Usage

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

Arguments

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

Details

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

Value

A list object as described above
**.h2o.doSafeGET**

*Perform a safe (i.e. error-checked) HTTP GET request to an H2O cluster.*

**Description**

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

**Usage**

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

**Arguments**

- **h2oRestApiVersion**
  - (Optional) A version number to prefix to the urlSuffix. If no version is provided, a default version is chosen for you.

- **urlSuffix**
  - The partial URL suffix to add to the calculated base URL for the instance

- **parms**
  - (Optional) Parameters to include in the request

- **...**
  - (Optional) Additional parameters.

**Value**

The raw response payload as a character vector

---

**.h2o.doSafePOST**

*Perform a safe (i.e. error-checked) HTTP POST request to an H2O cluster.*

**Description**

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

**Usage**

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

**Arguments**

- **h2oRestApiVersion**
  (Optional) A version number to prefix to the urlSuffix. If no version is provided, a default version is chosen for you.

- **urlSuffix**
  The partial URL suffix to add to the calculated base URL for the instance

- **parms**
  (Optional) Parameters to include in the request

- **fileUploadInfo**
  (Optional) Information to POST (NOTE: changes Content-type from XXX-www-url-encoded to multi-part). Use fileUpload(normalizePath("/path/to/file")).

- **...**
  (Optional) Additional parameters.

**Value**

The raw response payload as a character vector

---

.h2o.is_progress

**Check if Progress Bar is Enabled**

**Description**

Check if Progress Bar is Enabled

**Usage**

.h2o.is_progress()

---

.h2o.locate

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

**Description**

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

**Usage**

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

**Arguments**

- **pathStub**
  relative path

- **root.parent**
  search root directory
Description
Map of operations known to H2O

Usage
.h2o.primitives

Format
An object of class character of length 39.

Capabilities endpoints

Description
Capabilities endpoints

Usage
.h2o.__ALL_CAPABILITIES

Format
An object of class character of length 1.

Check H2O Server Health

Description
Warn if there are sick nodes.

Usage
.h2o.__checkConnectionHealth()
.h2o.__CREATE_FRAME  

**H2OFrame Manipulation**

### Description

H2OFrame Manipulation

### Usage

```r
.h2o.__CREATE_FRAME
```

### Format

An object of class character of length 1.

---

.h2o.__DECRYPTION_SETUP  

**Decryption Endpoints**

### Description

Decryption Endpoints

### Usage

```r
.h2o.__DECRYPTION_SETUP
```

### Format

An object of class character of length 1.

---

.h2o.__DKV  

**Removal Endpoints**

### Description

Removal Endpoints

### Usage

```r
.h2o.__DKV
```

### Format

An object of class character of length 1.
.h2o.__EXPORT_FILES

Export Files Endpoint Generator

Description
Export Files Endpoint Generator

Usage
.h2o.__EXPORT_FILES(frame)

Arguments
frame H2OFrame

.h2o.__FRAMES

Inspect/Summary Endpoints

Description
Inspect/Summary Endpoints

Usage
.h2o.__FRAMES

Format
An object of class character of length 1.

.h2o.__IMPORT

Import/Export Endpoints

Description
Import/Export Endpoints

Usage
.h2o.__IMPORT

Format
An object of class character of length 1.
.h2o.__JOBS

**Administrative Endpoints**

**Description**

Administrative Endpoints

**Usage**

.h2o.__JOBS

**Format**

An object of class character of length 1.

---

.h2o.__LOGANDECHO

**Log and Echo Endpoint**

**Description**

Log and Echo Endpoint

**Usage**

.h2o.__LOGANDECHO

**Format**

An object of class character of length 1.

---

.h2o.__MODELS

**Model Endpoint**

**Description**

Model Endpoint

**Usage**

.h2o.__MODELS

**Format**

An object of class character of length 1.
.h2o.__MODEL_BUILDERS  Model Builder Endpoint Generator

**Description**

Model Builder Endpoint Generator

**Usage**

.h2o.__MODEL_BUILDERS(algo)

**Arguments**

algo Cannonical identifier of H2O algorithm.

---

.h2o.__MODEL_METRICS  Model Metrics Endpoint

**Description**

Model Metrics Endpoint

**Usage**

.h2o.__MODEL_METRICS(model, data)

**Arguments**

model H2OModel.

data H2OFrame.

---

.h2o.__PARSE_SETUP  Parse Endpoints

**Description**

Parse Endpoints

**Usage**

.h2o.__PARSE_SETUP

**Format**

An object of class character of length 1.
Rapids Endpoint

Description
Rapids Endpoint

Usage
.h2o.__RAPIDS

Format
An object of class character of length 1.

H2O Package Constants

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

Usage
.h2o.__REST_API_VERSION

Format
An object of class integer of length 1.

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

Word2Vec Endpoints

Description
Word2Vec Endpoints

Usage
.h2o.__W2V_SYNONYMS

Format
An object of class character of length 1.
The H2O Package Environment

Description

The H2O Package Environment

Usage

.pkg.env

Format

An object of class `environment` of length 4.

H2O <-> R Communication and Utility Methods

Description

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

Usage

.skip_if_not_developer()

.verify_dataxy

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

Description

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

Usage

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

Arguments

data H2OFrame
x features
y response
autoencoder autoencoder flag
Description

Starting H2O For examples

Examples

```r
## Not run:
if (Sys.info()
['sysname'] == "Darwin" 
&

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

apply

Apply on H2O Datasets

Description

Method for apply on H2OFrame objects.

Usage

```r
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

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

## End(Not run)
```

### as.character.H2OFrame

Convert an H2OFrame to a String

**Description**

Convert an H2OFrame to a String

**Usage**

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

**Arguments**

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

**Examples**

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

## End(Not run)
```

### as.data.frame.H2OFrame

Converts parsed H2O data into an R data frame

**Description**

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

**Usage**

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

Arguments

x
   An H2OFrame object.

Details

Method as.data.frame.H2OFrame will use fread if data.table package is installed in required version.

See Also

table, as.data.frame

Examples

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

## End(Not run)

---

as.factor  
Convert H2O Data to Factors

Description

Convert a column into a factor column.

Usage

as.factor(x)

Arguments

x
   a column from an H2OFrame data set.

See Also

as.factor.

Examples

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

## End(Not run)
as.h2o

Create H2OFrame

Description
Import R object to the H2O cluster.

Usage
as.h2o(x, destination_frame = "", ...)

## Default S3 method:
as.h2o(x, destination_frame = "", ...)

## S3 method for class 'H2OFrame'
as.h2o(x, destination_frame = "", ...)

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

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

Arguments
x An R object.
destination_frame A string with the desired name for the H2OFrame.
... arguments passed to method arguments.

Details
Method as.h2o.data.frame will use fwrite if data.table package is installed in required version.
To speedup execution time for large sparse matrices, use h2o datatable. Make sure you have in-
stalled and imported data.table and slam packages. Turn on h2o datatable by options("h2o.use.data.table"=TRUE)

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

See Also
use.package

Examples
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
euro_hf <- as.h2o(euro)
letters_hf <- as.h2o(letters)
state_hf <- as.h2o(state.x77)
as.matrix.H2OFrame

Convert an H2OFrame to a matrix

Description

Convert an H2OFrame to a matrix

Usage

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

Arguments

x
An H2OFrame object

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

Examples

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

## End(Not run)
as.numeric

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

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

as.vector.H2OFrame

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
Examples

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

### Australia

#### Australia Coastal Data

**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](http://cs.colby.edu/courses/S11/cs251/labs/lab07/AustraliaSubset.csv).

**Format**

A data frame with 251 rows and 8 columns

---

### colnames

**Description**

Returns the column names of an H2OFrame

**Usage**

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

**Arguments**

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

**Examples**

```r
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
colnames(iris_hf) # Returns "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
## End(Not run)
```
dim.H2OFrame

Returns the Dimensions of an H2OFrame

Description

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

Usage

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

Arguments

- `x`: An H2OFrame object.

See Also

- `dim` for the base R method.

Examples

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

dimnames.H2OFrame

Column names of an H2OFrame

Description

Set column names of an H2O Frame

Usage

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

Arguments

- `x`: An H2OFrame
Examples

```r
## Not run:
h2o.init()
n <- 2000
# Generate variables V1, ... V10
X <- matrix(rnorm(10 * n), n, 10)
# y = +1 if sum_i x_{ij}^2 > chisq median on 10 df
y <- rep(-1, n)
y[apply(X*X, 1, sum) > qchisq(.5, 10)] <- 1
# Assign names to the columns of X:
dimnames(X)[[2]] <- c("V1", "V2", "V3", "V4", "V5", "V6", "V7", "V8", "V9", "V10")
## End(Not run)
```

---

**feature_frequencies.H2OModel**

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

Description

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

Usage

```r
feature_frequencies.H2OModel(object, newdata, ...)
h2o.feature_frequencies(object, newdata, ...)
```

Arguments

- **object**: a fitted **H2OModel** object for which prediction is desired
- **newdata**: An H2OFrame object in which to look for variables with which to predict.
- **...**: additional arguments to pass on.

Value

Returns an H2OFrame contain per-feature frequencies on the predict path for each input row.

See Also

- `h2o.gbm` and `h2o.randomForest` for model generation in h2o.
**generate_col_ind**

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

**Description**

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

**Usage**

`generate_col_ind(data, by)`

**Arguments**

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

---

**get_seed.H2OModel**

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

**Description**

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

**Usage**

`get_seed.H2OModel(object)`

`h2o.get_seed(object)`

**Arguments**

- `object`: a fitted H2OModel object.

**Value**

_Returns seed to be used during training a model. Could be numeric or string._
Examples

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

## End(Not run)

h2o.abs

Compute the absolute value of x

Description

Compute the absolute value of x

Usage

h2o.abs(x)

Arguments

x

An H2OFrame object.

See Also

abs for the base R implementation.

Examples

## Not run:
h2o.init()
smtrees_hf <- h2o.importFile(url)
model <- h2o.gbm(x = c("girth", "height"), y = "vol", ntrees = 3, max_depth = 1,
  distribution = "gaussian", min_rows = 2, learn_rate = .1,
  training_frame = smtrees_hf)
pred <- as.data.frame(predict(model, newdata = smtrees_hf))
diff <- pred - smtrees_df[, 4]
diff_abs <- abs(diff)
print(diff_abs)

## End(Not run)
h2o.acos

Compute the arc cosine of x

Description

Compute the arc cosine of x

Usage

h2o.acos(x)

Arguments

x An H2OFrame object.

See Also

acos for the base R implementation.

Examples

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

---

h2o.aggregated_frame

Retrieve an aggregated frame from an Aggregator model

Description

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

Usage

h2o.aggregated_frame(model)

Arguments

model an H2OClusteringModel corresponding from a h2o.aggregator call.
## Examples

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

df <- h2o.createFrame(rows=100, cols=5, categorical_fraction=0.6, integer_fraction=0,
  binary_fraction=0, real_range=100, integer_range=100, missing_fraction=0)
target_num_exemplars=1000
rel_tol_num_exemplars=0.5
encoding="Eigen"

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

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

## End(Not run)
```

---

### h2o.aggregator

#### Build an Aggregated Frame

**Description**

Builds an Aggregated Frame of an H2OFrame.

**Usage**

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

**Arguments**

- **training_frame**  
  Id of the training data frame.
- **x**  
  A vector containing the character names of the predictors in the model.
- **model_id**  
  Destination id for this model; auto-generated if not specified.
- **ignore_const_cols**  
  Logical. Ignore constant columns. Defaults to TRUE.
- **target_num_exemplars**  
  Targeted number of exemplars Defaults to 5000.
- **rel_tol_num_exemplars**  
  Relative tolerance for number of exemplars (e.g, 0.5 is +/- 50 percents) Defaults to 0.5.
- **transform**  
  Transformation of training data Must be one of: "NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE". Defaults to NORMALIZE.
categorical_encoding
- Encoding scheme for categorical features. Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited". Defaults to AUTO.

save_mapping_frame
- Logical. Whether to export the mapping of the aggregated frame. Defaults to FALSE.

num_iteration_without_new_exemplar
- The number of iterations to run before the aggregator exits if the number of exemplars collected didn't change. Defaults to 500.

export_checkpoints_dir
- Automatically export generated models to this directory.

Examples
```r
## Not run:
library(h2o)
h2o.init()
df <- h2o.createFrame(rows=100, cols=5, categorical_fraction=0.6, integer_fraction=0,
                   binary_fraction=0, real_range=100, integer_range=100, missing_fraction=0)
target_num_exemplars=1000
rel_tol_num_exemplars=0.5
encoding="Eigen"
agg <- h2o.aggregator(training_frame=df,
                   target_num_exemplars=target_num_exemplars,
                   rel_tol_num_exemplars=rel_tol_num_exemplars,
                   categorical_encoding=encoding)
## End(Not run)
```

---

h2o.aic

Retrieve the Akaike information criterion (AIC) value

Description

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

Usage

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

Arguments

- object: An H2OModel or H2OModelMetrics.
- train: Retrieve the training AIC
- valid: Retrieve the validation AIC
- xval: Retrieve the cross-validation AIC
Examples

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

---

**h2o.all**

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

**Description**

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

**Usage**

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

**Arguments**

- `x`: An H2OFrame object.

**See Also**

`all` for the base R implementation.

---

**h2o.anomaly**

*Anomaly Detection via H2O Deep Learning Model*

**Description**

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

**Usage**

```r
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

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

---

### h2o.any

*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

```r
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**

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

**Arguments**

- `x`: An H2OFrame object.

**Value**

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

**Examples**

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

### h2o.arrange

**Sorts an H2O frame by columns**

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

**Usage**

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

**Arguments**

- `x`: The H2OFrame input to be sorted.
- `...`: The column names to sort by.
**h2o.ascharacter**  
*Convert H2O Data to Characters*

**Description**
Convert H2O Data to Characters

**Usage**
```r
h2o.ascharacter(x)
```

**Arguments**
- `x`  
  An H2OFrame object.

**See Also**
- `as.character` for the base R implementation.

---

**h2o.asfactor**  
*Convert H2O Data to Factors*

**Description**
Convert H2O Data to Factors

**Usage**
```r
h2o.asfactor(x)
```

**Arguments**
- `x`  
  An H2OFrame object.

**See Also**
- `as.factor` for the base R implementation.
**h2o.asnumeric**

Convert H2O Data to Numerics

**Description**

Convert H2O Data to Numerics

**Usage**

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

**Arguments**

- `x` An H2OFrame object.

**See Also**

`as.numeric` for the base R implementation.

---

**h2o.assign**

Rename an H2O object.

**Description**

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

**Usage**

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

**Arguments**

- `data` An H2OFrame object
- `key` The key to be associated with the H2O parsed data object
h2o.as_date

Convert between character representations and objects of Date class

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

Retrieve the AUC

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 H2OBinomialMetrics 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

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

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

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

## End(Not run)
```

h2o.automl

Automatic Machine Learning

Description

The Automatic Machine Learning (AutoML) function automates the supervised machine learning model training process. The current version of AutoML trains and cross-validates a Random Forest, an Extremely-Randomized Forest, a random grid of Gradient Boosting Machines (GBMs), a random grid of Deep Neural Nets, and then trains a Stacked Ensemble using all of the models.

Usage

```r
h2o.automl(x, y, training_frame, validation_frame = NULL,
leaderboard_frame = NULL, blending_frame = NULL, nfolds = 5,
fold_column = NULL, weights_column = NULL, balance_classes = FALSE,
class_sampling_factors = NULL, max_after_balance_size = 5,
max_runtime_secs = 3600, max_runtime_secs_per_model = NULL,
max_models = NULL, stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "mean_per_class_error"),
stopping_tolerance = NULL, stopping_rounds = 3, seed = NULL,
project_name = NULL, exclude_algos = NULL, include_algos = NULL,
keep_cross_validation_predictions = FALSE,
keep_cross_validation_models = FALSE,
keep_cross_validation_fold_assignment = FALSE,
sort_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "mean_per_class_error"), export_checkpoints_dir = NULL,
verbosity = 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 or index of the response variable in the model. For classification, the y column must be a factor, otherwise regression will be performed. Indexes are 1-based in R.
h2o.automl

training_frame  Training frame (H2OFrame or ID).
validation_frame  Validation frame (H2OFrame or ID); Optional. This argument is ignored unless the user sets nfolds = 0. If cross-validation is turned off, then a validation frame can be specified and used for early stopping of individual models and early stopping of the grid searches. By default and when nfolds > 1, cross-validation metrics will be used for early stopping and thus validation_frame will be ignored.
leaderboard_frame  Leaderboard frame (H2OFrame or ID); Optional. If provided, the Leaderboard will be scored using this data frame instead of using cross-validation metrics, which is the default.
blending_frame  Blending frame (H2OFrame or ID) used to train the metalearning algorithm in Stacked Ensembles (instead of relying on cross-validated predicted values); Optional.
nfolds  Number of folds for k-fold cross-validation. Defaults to 5. Use 0 to disable cross-validation; this will also disable Stacked Ensemble (thus decreasing the overall model performance).
fold_column  Column with cross-validation fold index assignment per observation; used to override the default, randomized, 5-fold cross-validation scheme for individual models in the AutoML run.
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.
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_runtime_secs  Maximum allowed runtime in seconds for the entire model training process. Use 0 to disable. Defaults to 3600 secs (1 hour).
max_runtime_secs_per_model  Maximum runtime in seconds dedicated to each individual model training process. Use 0 to disable. Defaults to 0.
max_models  Maximum number of models to build in the AutoML process (does not include Stacked Ensembles). Defaults to NULL.
stopping_metric  Metric to use for early stopping ("AUTO" is logloss for classification, deviance for regression). Must be one of "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "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). This value defaults to 0.001 if the dataset is at least 1 million rows; otherwise it defaults to a bigger value determined by the size of the dataset and the non-NA-rate. In that case, the value is computed as 1/sqrt(nrows * non-NA-rate).

stopping_rounds

Integer. 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. Defaults to 3 and must be an non-zero integer. Use 0 to disable early stopping.

seed

Integer. Set a seed for reproducibility. AutoML can only guarantee reproducibility if max_models or early stopping is used because max_runtime_secs is resource limited, meaning that if the resources are not the same between runs, AutoML may be able to train more models on one run vs another.

project_name

Character string to identify an AutoML project. Defaults to NULL, which means a project name will be auto-generated based on the training frame ID.

exclude_algos

Vector of character strings naming the algorithms to skip during the model-building phase. An example use is exclude_algos = c("GLM", "DeepLearning", "DRF"), and the full list of options is: "DRF" (Random Forest and Extremely-Randomized Trees), "GLM", "XGBoost", "GBM", "DeepLearning" and "StackedEnsemble".

include_algos

Vector of character strings naming the algorithms to restrict to during the model-building phase. This can’t be used in combination with exclude_algos param.

keep_cross_validation_predictions

Logical. Whether to keep the predictions of the cross-validation predictions. This needs to be set to TRUE if running the same AutoML object for repeated runs because CV predictions are required to build additional Stacked Ensemble models in AutoML. This option defaults to FALSE.

keep_cross_validation_models

Logical. Whether to keep the cross-validated models. Keeping cross-validation models may consume significantly more memory in the H2O cluster. This option defaults to FALSE.

keep_cross_validation_fold_assignment

Logical. Whether to keep fold assignments in the models. Deleting them will save memory in the H2O cluster. Defaults to FALSE.

sort_metric

Metric to sort the leaderboard by. For binomial classification choose between "AUC", "logloss", "mean_per_class_error", "RMSE", "MSE". For regression choose between "mean_residual_deviance", "RMSE", "MSE", "MAE", and "RM-SLE". For multinomial classification choose between "mean_per_class_error", "logloss", "RMSE", "MSE". Default is "AUTO". If set to "AUTO", then "AUC" will be used for binomial classification, "mean_per_class_error" for multinomial classification, and "mean_residual_deviance" for regression.

export_checkpoints_dir

(Optional) Path to a directory where every model will be stored in binary form.

verbosity

Verbosity of the backend messages printed during training; Optional. Must be one of "debug", "info", "warn". Defaults to NULL (disable live log).
**Details**

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

**Value**

An H2OAutoML object.

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
votes_path <- system.file("extdata", "housevotes.csv", package = "h2o")
votes_hf <- h2o.uploadFile(path = votes_path, header = TRUE)
aml <- h2o.automl(y = "Class", training_frame = votes_hf, max_runtime_secs = 30)
## End(Not run)
```

---

**h2o.betweenss**

*Get the between cluster sum of squares*

**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**

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

**Arguments**

- **object**: An H2OClusteringModel 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  

**Return the respective bias vector**

**Description**

Return the respective bias vector

**Usage**

h2o.biases(object, vector_id = 1)

**Arguments**

- **object**
  An H2OModel or H2OModelMetrics

- **vector_id**
  An integer, ranging from 1 to number of layers + 1, that specifies the bias vector to return.

h2o.bottomN  

**H2O bottomN**

**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  

Combine H2O Datasets by Columns

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

Usage
h2o.cbind(...)

Arguments

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

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

See Also
cbind for the base R method.

Examples

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

h2o.ceiling  

Take a single numeric argument and return a numeric vector with the smallest integers

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

\texttt{ceiling} for the base R implementation.

\begin{verbatim}
\textbf{h2o.centers} \hspace{1cm} \textit{Retrieve the Model Centers}
\end{verbatim}

\textbf{Description}

Retrieve the Model Centers

\textbf{Usage}

\texttt{h2o.centers(object)}

\textbf{Arguments}

\begin{itemize}
\item \texttt{object} \hspace{0.5cm} An \texttt{H2OClusteringModel} object.
\end{itemize}

\begin{verbatim}
\textbf{h2o.centersSTD} \hspace{1cm} \textit{Retrieve the Model Centers STD}
\end{verbatim}

\textbf{Description}

Retrieve the Model Centers STD

\textbf{Usage}

\texttt{h2o.centersSTD(object)}

\textbf{Arguments}

\begin{itemize}
\item \texttt{object} \hspace{0.5cm} An \texttt{H2OClusteringModel} object.
\end{itemize}

\begin{verbatim}
\textbf{h2o.centroid_stats} \hspace{1cm} \textit{Retrieve centroid statistics}
\end{verbatim}

\textbf{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".

\textbf{Usage}

\texttt{h2o.centroid_stats(object, train = FALSE, valid = FALSE, xval = FALSE)}
**h2o.clearLog**

**Arguments**

- **object**
  - An `H2OClusteringModel` object.

- **train**
  - Retrieve the training centroid statistics

- **valid**
  - Retrieve the validation centroid statistics

- **xval**
  - Retrieve the cross-validation centroid statistics

**Description**

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

**Usage**

```r
h2o.clearLog()
```

**See Also**

- `h2o.startLogging`
- `h2o.stopLogging`
- `h2o.openLog`

**Examples**

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

## End(Not run)
```

---

**h2o.clusterInfo**

**Print H2O clustering info**

**Description**

Print H2O cluster info

**Usage**

```r
h2o.clusterInfo()
```
h2o.clusterIsUp  

_Determine if an H2O cluster is up or not_

**Description**

Determine if an H2O cluster is up or not.

**Usage**

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

**Arguments**

- `conn`  
  - H2OConnection object

**Value**

TRUE if the cluster is up; FALSE otherwise.

---

h2o.clusterStatus  

_Return the status of the cluster_

**Description**

Retrieve information on the status of the cluster running H2O.

**Usage**

```r
h2o.clusterStatus()
```

**See Also**

H2OConnection, h2o.init

**Examples**

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

Retrieve the cluster sizes

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 H2OClusteringModel object.
- train: Retrieve the training cluster sizes
- valid: Retrieve the validation cluster sizes
- xval: Retrieve the cross-validation cluster sizes

h2o.coef

Return the coefficients that can be applied to the non-standardized data.

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

Usage
h2o.coef(object)

Arguments
- object: an H2OModel object.
h2o.coef_norm

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

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

Return column names of an H2OFrame

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)

Arguments

... Ignored

Value

A list of column indices that correspond to "type"

Examples

## Not run:

h2o.init()

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

prostate <- h2o.uploadFile(path = prostate_path)

h2o.columns_by_type(prostate, coltype="numeric")

## End(Not run)

h2o.computeGram

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
weights
use_all_factor_levels
standardize
skip_missing

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
... 
newdata
valid
thresholds
metrics

Details

The H2OModelMetrics version of this function will only take H2OBinomialMetrics or H2OMultinomialMetrics objects. If no threshold is specified, all possible thresholds are selected.
Value
Calling this function on H2OModel objects returns a confusion matrix corresponding to the predict function. If used on an H2OBinomialMetrics object, returns a list of matrices corresponding to the number of thresholds specified.

See Also
predict for generating prediction frames, h2o.performance for creating H2OModelMetrics.

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

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

## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
cor(prostate$AGE)
## End(Not run)

h2o.cos Compute the cosine of x

Description

Compute the cosine of x

Usage

h2o.cos(x)

Arguments

x An H2OFrame object.

See Also

cos for the base R implementation.

h2o.cosh Compute the hyperbolic cosine of x

Description

Compute the hyperbolic cosine of x

Usage

h2o.cosh(x)

Arguments

x An H2OFrame object.
**h2o.coxph**

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

### Description

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

### Usage

```r
h2o.coxph(x, event_column, training_frame, model_id = NULL, 
start_column = NULL, stop_column = NULL, weights_column = NULL, 
offset_column = NULL, stratify_by = NULL, ties = c("efron", 
"breslow"), init = 0, lre_min = 9, max_iterations = 20, 
interactions = NULL, interaction_pairs = NULL, 
interactions_only = NULL, use_all_factor_levels = FALSE, 
export_checkpoints_dir = NULL)
```

### Arguments

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

interaction_pairs
A list of pairwise (first order) column interactions.

interactions_only
A list of columns that should only be used to create interactions but should not itself participate in model training.

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

export_checkpoints_dir
Automatically export generated models to this directory.

---

**h2o.createFrame**

**Data H2OFrame Creation in H2O**

**Description**

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

**Usage**

```r
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.
**h2o.cross_validation_fold_assignment**

Retrieve the cross-validation fold assignment

**Description**

Retrieve the cross-validation fold assignment

**Usage**

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

---

**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**

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

hf <- h2o.createFrame(rows = 100, cols = 10, randomize = FALSE, value = 5,
                     categorical_fraction = 0, integer_fraction = 0)
summary(hf)
## End(Not run)
```
**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

Return the cumulative max over a column or across a row

Description

Return the cumulative max over a column or across a row

Usage

h2o.cummax(x, axis = 0)

Arguments

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

See Also

cummax for the base R implementation.
h2o.cummin

Return the cumulative min over a column or across a row

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

Return the cumulative product over a column or across a row

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

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

**Description**

Return the cumulative sum over a column or across a row

**Usage**

```r
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**

```r
h2o.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 sing "(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

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

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

## End(Not run)
```

---

**h2o.day**

*Convert Milliseconds to Day of Month in H2O Datasets*

**Description**

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

**Usage**

```r
h2o.day(x)
day(x)
```

```r
## 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**

```r
h2o.dayOfWeek(x)
```

```r
dayOfWeek(x)
```

```r
## 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**

```r
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

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

h2o.ddply

Split H2O Dataset, Apply Function, and Return Results

Description

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

Usage

```r
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.
## h2o.decryptionSetup

### Setup a Decryption Tool

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

#### Usage

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

#### Arguments

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

#### See Also

- `h2o.importFile`, `h2o.parseSetup`
### Examples

```r
## Not run:
library(h2o)
h2o.init()
ks_path <- system.file("extdata", "keystore.jks", package = "h2o")
keystore <- h2o.importFile(path = ks_path, parse = FALSE) # don't parse, keep as a binary file
cipher <- "AES/ECB/PKCS5Padding"
pwd <- "Password123"
alias <- "secretKeyAlias"
dt <- h2o.decryptionSetup(keystore, key_alias = alias, password = pwd, cipher_spec = cipher)
data_path <- system.file("extdata", "prostate.csv.aes", package = "h2o")
data <- h2o.importFile(data_path, decrypt_tool = dt)
summary(data)
## End(Not run)
```

## 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

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

#### Arguments

- **object**: An H2OModel 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

- `h2o.deeplearning` for making H2O Deep Learning models.
- `h2o.deepwater` for making H2O DeepWater models.
Examples

```r
## Not run:
library(h2o)
h2o.init()
prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
prostate_dl = h2o.deeplearning(x = 3:9, y = 2, training_frame = prostate,
    hidden = c(100L, 200L), epochs = 5)
prostate_deepfeatures_layer1 = h2o.deepfeatures(prostate_dl, prostate, layer = 1)
prostate_deepfeatures_layer2 = h2o.deepfeatures(prostate_dl, prostate, layer = 2)
head(prostate_deepfeatures_layer1)
head(prostate_deepfeatures_layer2)

# if (h2o.deepwater.available()) {
  prostate_dl = h2o.deepwater(x = 3:9, y = 2, backend="mxnet", training_frame = prostate,
    hidden = c(100L, 200L), epochs = 5)
  prostate_deepfeatures_layer1 =
    h2o.deepfeatures(prostate_dl, prostate, layer = "fc1_w")
  prostate_deepfeatures_layer2 =
    h2o.deepfeatures(prostate_dl, prostate, layer = "fc2_w")
  head(prostate_deepfeatures_layer1)
  head(prostate_deepfeatures_layer2)
#}

## End(Not run)
```

h2o.deeplearning

Build a Deep Neural Network model using CPUs

Description

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

Usage

```r
h2o.deeplearning(x, y, training_frame, model_id = NULL,
    validation_frame = NULL, nfolds = 0,
    keep_cross_validation_models = TRUE,
    keep_cross_validation_predictions = FALSE,
    keep_cross_validation_fold_assignment = FALSE,
    fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
    fold_column = NULL, ignore_const_cols = TRUE,
    score_each_iteration = FALSE, weights_column = NULL,
    offset_column = NULL, balance_classes = FALSE,
    class_sampling_factors = NULL, max_after_balance_size = 5,
    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(200L, 200L), 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_annnealing = 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", "RMSELE", "AUC", "lift_top_group", "misclassification", "AUCPR",
"mean_per_class_error", "custom", "custom_increasing"),
stopping_tolerance = 0, max_runtime_secs = 0,
score_validation_sampling = c("Uniform", "Stratified"),
diagnostics = TRUE, fast_mode = TRUE, force_load_balance = TRUE,
variable_importances = TRUE, replicate_training_data = TRUE,
single_node_mode = FALSE, shuffle_training_data = FALSE,
missing_values_handling = c("MeanImputation", "Skip"),
quiet_mode = FALSE, autoencoder = FALSE, sparse = FALSE,
col_major = FALSE, average_activation = 0, sparsity_beta = 0,
max_categorical_features = 2147483647, reproducible = FALSE,
export_weights_and_biases = FALSE, mini_batch_size = 1,
categorical_encoding = c("AUTO", "Enum", "OneHotInternal",
"OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse",
"EnumLimited"), elastic_averaging = FALSE,
estatic_averaging_moving_rate = 0.9,
estatic_averaging_regularization = 0.001,
export_checkpoints_dir = NULL, verbose = FALSE)

Arguments

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

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

training_frame Id of the training data frame.
model_id Destination id for this model; auto-generated if not specified.
validation_frame Id of the validation data frame.
nfolds Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
keep_cross_validation_models Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions
Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.

keep_cross_validation_fold_assignment
Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.

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

fold_column
Column with cross-validation fold index assignment per observation.

ignore_const_cols
Logical. Ignore constant columns. Defaults to TRUE.

score_each_iteration
Logical. Whether to score during each iteration of model training. Defaults to FALSE.

weights_column
Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor.

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.


hidden Hidden layer sizes (e.g. [100, 100]). Defaults to c(200, 200).

epochs How many times the dataset should be iterated (streamed), can be fractional. Defaults to 10.

train_samples_per_iteration Number of training samples (globally) per MapReduce iteration. Special values are 0: one epoch, -1: all available data (e.g., replicated training data), -2: automatic. Defaults to -2.

target_ratio_comm_to_comp Target ratio of communication overhead to computation. Only for multi-node operation and train_samples_per_iteration = -2 (auto-tuning). Defaults to 0.05.

seed Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Note: only reproducible when running single threaded. Defaults to -1 (time-based random number).

adaptive_rate Logical. Adaptive learning rate. Defaults to TRUE.

rho Adaptive learning rate time decay factor (similarity to prior updates). Defaults to 0.99.

epsilon Adaptive learning rate smoothing factor (to avoid divisions by zero and allow progress). Defaults to 1e-08.

rate Learning rate (higher => less stable, lower => slower convergence). Defaults to 0.005.

rate_annealing Learning rate annealing: 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_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**

**distribution**
- Distribution function. Must be one of: "AUTO", "bernoulli", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber". Defaults to AUTO.

**quantile_alpha**
- Desired quantile for Quantile regression, must be between 0 and 1. Defaults to 0.5.

**tweedie_power**
- Tweedie power for Tweedie regression, must be between 1 and 2. Defaults to 1.5.

**huber_alpha**
- Desired quantile for Huber/M-regression (threshold between quadratic and linear loss, must be between 0 and 1). Defaults to 0.9.

**score_interval**
- Shortest time interval (in seconds) between model scoring. Defaults to 5.

**score_training_samples**
- Number of training set samples for scoring (0 for all). Defaults to 10000.

**score_validation_samples**
- Number of validation set samples for scoring (0 for all). Defaults to 0.

**score_duty_cycle**
- Maximum duty cycle fraction for scoring (lower: more training, higher: more scoring). Defaults to 0.1.

**classification_stop**
- Stopping criterion for classification error fraction on training data (-1 to disable). Defaults to 0.

**regression_stop**
- Stopping criterion for regression error (MSE) on training data (-1 to disable). Defaults to 1e-06.

**stopping_rounds**
- Early stopping based on convergence of stopping_metric. Stop if simple moving average of length k of the stopping_metric does not improve for k:=stopping_rounds scoring events (0 to disable) Defaults to 5.

**stopping_metric**
- Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "AUCPR", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.

**stopping_tolerance**
- Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.

**max_runtime_secs**
- Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
score_validation_sampling
    Method used to sample validation dataset for scoring. Must be one of: "Uniform", "Stratified". Defaults to Uniform.

diagnostics Logical. Enable diagnostics for hidden layers. Defaults to TRUE.

fast_mode Logical. Enable fast mode (minor approximation in back-propagation). Defaults to TRUE.

force_load_balance Logical. Force extra load balancing to increase training speed for small datasets (to keep all cores busy). Defaults to TRUE.

variable_importances Logical. Compute variable importances for input features (Gedeon method) - can be slow for large networks. Defaults to TRUE.

replicate_training_data Logical. Replicate the entire training dataset onto every node for faster training on small datasets. Defaults to TRUE.

single_node_mode Logical. Run on a single node for fine-tuning of model parameters. Defaults to FALSE.

shuffle_training_data Logical. Enable shuffling of training data (recommended if training data is replicated and train_samples_per_iteration is close to #nodes x #rows, of 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.
Build a Deep Learning model using multiple native GPU backends

Builds a deep neural network on an H2OFrame containing various data sources.

Usage

```r
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_models = TRUE,
               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,
```

See Also

`predict.H2OModel` for prediction

Examples

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

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

## End(Not run)
```
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", "AUCPR",
"mean_per_class_error", "custom", "custom_increasing"),
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", "googlelenet", "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"),
export_checkpoints_dir = NULL)

Arguments

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

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

fication model.

training_frame  Id of the training data frame.
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 K-fold cross-validation (0 to disable or >= 2). Defaults to
0.
balance_classes  Logical. Balance training data class counts via over/under-sampling (for im-
balanced 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 bal-
ance during training. Requires balance_classes.
**keep_cross_validation_models**
Logical. Whether to keep the cross-validation models. Defaults to TRUE.

**keep_cross_validation_predictions**
Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.

**keep_cross_validation_fold_assignment**
Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.

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

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

**offset_column**
Offset column. This will be added to the combination of columns before applying the link function.

**weights_column**
Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor.

**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 and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "AUCPR", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.

stopping_tolerance
   Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.

max_runtime_secs
   Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

ignore_const_cols
   Logical. Ignore constant columns. Defaults to TRUE.

shuffle_training_data
   Logical. Enable global shuffling of training data. Defaults to TRUE.

mini_batch_size
   Mini-batch size (smaller leads to better fit, larger can speed up and generalize better). Defaults to 32.

clip_gradient
   Clip gradients once their absolute value is larger than this value. Defaults to 10.
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Default</th>
</tr>
</thead>
<tbody>
<tr>
<td>backend</td>
<td>Deep Learning Backend. Must be one of: &quot;mxnet&quot;, &quot;caffe&quot;, &quot;tensorflow&quot;. Defaults to mxnet.</td>
<td></td>
</tr>
<tr>
<td>image_shape</td>
<td>Width and height of image. Defaults to c(0, 0).</td>
<td></td>
</tr>
<tr>
<td>channels</td>
<td>Number of (color) channels. Defaults to 3.</td>
<td></td>
</tr>
<tr>
<td>sparse</td>
<td>Logical. Sparse data handling (more efficient for data with lots of 0 values). Defaults to FALSE.</td>
<td></td>
</tr>
<tr>
<td>gpu</td>
<td>Logical. Whether to use a GPU (if available). Defaults to TRUE.</td>
<td></td>
</tr>
<tr>
<td>device_id</td>
<td>Device IDs (which GPUs to use). Defaults to c(0).</td>
<td></td>
</tr>
<tr>
<td>cache_data</td>
<td>Logical. Whether to cache the data in memory (automatically disabled if data size is too large). Defaults to TRUE.</td>
<td></td>
</tr>
<tr>
<td>network_definition_file</td>
<td>Path of file containing network definition (graph, architecture).</td>
<td></td>
</tr>
<tr>
<td>network_parameters_file</td>
<td>Path of file containing network (initial) parameters (weights, biases).</td>
<td></td>
</tr>
<tr>
<td>mean_image_file</td>
<td>Path of file containing the mean image data for data normalization.</td>
<td></td>
</tr>
<tr>
<td>export_native_parameters_prefix</td>
<td>Path (prefix) where to export the native model parameters after every iteration.</td>
<td></td>
</tr>
<tr>
<td>activation</td>
<td>Activation function. Only used if no user-defined network architecture file is provided, and only for problem_type=dataset. Must be one of: &quot;Rectifier&quot;, &quot;Tanh&quot;.</td>
<td></td>
</tr>
<tr>
<td>hidden</td>
<td>Hidden layer sizes (e.g. [200, 200]). Only used if no user-defined network architecture file is provided, and only for problem_type=dataset.</td>
<td></td>
</tr>
<tr>
<td>input_dropout_ratio</td>
<td>Input layer dropout ratio (can improve generalization, try 0.1 or 0.2). Defaults to 0.</td>
<td></td>
</tr>
<tr>
<td>hidden_dropout_ratios</td>
<td>Hidden layer dropout ratios (can improve generalization), specify one value per hidden layer, defaults to 0.5.</td>
<td></td>
</tr>
<tr>
<td>problem_type</td>
<td>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: &quot;auto&quot;, &quot;image&quot;, &quot;dataset&quot;. Defaults to auto.</td>
<td></td>
</tr>
<tr>
<td>export_checkpoints_dir</td>
<td>Automatically export generated models to this directory.</td>
<td></td>
</tr>
</tbody>
</table>
h2o.deepwater.available

Determines whether Deep Water is available

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/maxes/missing/zero counts/standards/number of levels

Usage

h2o.describe(frame)

Arguments

frame

An H2OFrame object.

Value

A table with the Frame stats.

Examples

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

## End(Not run)
**h2o.difflag1**

*Conduct a lag 1 transform on a numeric H2OFrame column*

**Description**

Conduct a lag 1 transform on a numeric H2OFrame column

**Usage**

```r
h2o.difflag1(object)
```

**Arguments**

- `object` H2OFrame object

**Value**

Returns an H2OFrame object.

---

**h2o.dim**

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

**Description**

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

**Usage**

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

**Arguments**

- `x` An H2OFrame object.

**See Also**

`dim` for the base R implementation.
h2o.dimnames  

Column names of an H2OFrame

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  

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

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, \( \geq 0 \)) "l2" - Euclidean distance (L2-norm, \( \geq 0 \)) "cosine" - Cosine similarity (-1...1) "cosine_sq" - Squared Cosine similarity (0...1)

Examples
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.distance(prostate[11:30,], prostate[1:10,], "cosine")
## End(Not run)
h2o.downloadAllLogs  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
## Not run:
```
h2o.downloadAllLogs(dirname="/your_directory_name/", filename = "autoh2o_log.zip")
```
## End(Not run)

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 accommodate the entire file.
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)

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

## End(Not run)

### Description

Download the model in MOJO format.

### Usage

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

### Arguments

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

### Value

Name of the MOJO file written to the path.

### Examples

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

## End(Not run)
```
**h2o.download_pojo**

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

**Description**

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

**Usage**

```r
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 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**

```r
## Not run:
library(h2o)
h <- h2o.init()
fr <- as.h2o(iris)
my_model <- h2o.gbm(x = 1:4, y = 5, training_frame = fr)
h2o.download_pojo(my_model) # print the model to screen
# h2o.download_pojo(my_model, getwd()) # save the POJO and jar file to the current working directory, NOT RUN
# h2o.download_pojo(my_model, getwd(), get_jar = FALSE ) # save only the POJO to the current working directory, NOT RUN
h2o.download_pojo(my_model, getwd()) # save to the current working directory

## End(Not run)
```
**h2o.entropy**  
*Shannon entropy*

**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**

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

---

**h2o.exp**  
*Compute the exponential function of x*

**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**  
*Export an H2O Data Frame (H2OFrame) to a File or to a collection of Files.*

**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**
```r
h2o.exportFile(data, path, force = FALSE, sep = ",", compression = NULL, 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.
- **sep**: The field separator character. Values on each line of the file will be separated by this character (default ",").
- **compression**: How to compress the exported dataset
- **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**
```r
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)

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

## End(Not run)
```
**h2o.exportHDFS**  
*Export a Model to HDFS*

**Description**
Exports an H2OModel to HDFS.

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

**Arguments**
- `object`: an H2OModel 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**  
*fillna*

**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**
```r
## Not run:
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)
## End(Not run)
```
**h2o.filterNACols**  
*Filter NA Columns*

**Description**
Filter NA Columns

**Usage**
```r
h2o.filterNACols(data, frac = 0.2)
```

**Arguments**
- **data**: A dataset to filter on.
- **frac**: The threshold of NAs to allow per column (columns >= 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**
```r
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

**Usage**

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

**Arguments**

- **object**: H2OBinomialMetrics
- **threshold**: 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**

- **object**: H2OBinomialMetrics
- **metric**: "F1," for example
**h2o.floor**

Take a single numeric argument and return a numeric vector with the largest integers

**Description**

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

**Usage**

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

**Arguments**

- \( x \): An H2OFrame object.

**See Also**

- `floor` for the base R implementation.

---

**h2o.flow**

Open H2O Flow

**Description**

Open H2O Flow in your browser

**Usage**

```r
h2o.flow()
```

---

**h2o.gainsLift**

Access H2O Gains/Lift Tables

**Description**

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

**Usage**

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

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

## S4 method for signature 'H2OModelMetrics'  
h2o.gainsLift(object)
```
h2o.gbm

Build gradient boosted classification or regression trees

Description

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

Arguments

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

Details

The H2OModelMetrics version of this function will only take H2OBinomialMetrics objects.

Value

Calling this function on H2OModel objects returns a Gains/Lift table corresponding to the predict function.

See Also

predict for generating prediction frames, h2o.performance for creating H2OModelMetrics.

Examples

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

## End(Not run)
Usage

h2o.gbm(x, y, training_frame, model_id = NULL, validation_frame = NULL, nfolds = 0, keep_cross_validation_models = TRUE, keep_cross_validation_predictions = FALSE, keep_cross_validation_fold_assignment = FALSE, score_each_iteration = FALSE, score_tree_interval = 0, fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"), fold_column = NULL, ignore_const_cols = TRUE, offset_column = NULL, weights_column = NULL, balance_classes = FALSE, class_sampling_factors = NULL, max_after_balance_size = 5, 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", "AUCPR", "mean_per_class_error", "custom", "custom_increasing"), stopping_tolerance = 0.001, max_runtime_secs = 0, seed = -1, build_tree_one_node = FALSE, learn_rate = 0.1, learn_rate_annealing = 1, distribution = c("AUTO", "bernoulli", "quasibinomial", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber", "custom"), quantile_alpha = 0.5, tweedie_power = 1.5, huber_alpha = 0.9, checkpoint = NULL, sample_rate = 1, sample_rate_per_class = NULL, col_sample_rate = 1, col_sample_rate_change_per_level = 1, col_sample_rate_per_tree = 1, min_split_improvement = 1e-05, histogram_type = c("AUTO", "UniformAdaptive", "Random", "QuantilesGlobal", "RoundRobin"), max_abs_leafnode_pred = Inf, pred_noise_bandwidth = 0, categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"), calibrate_model = FALSE, calibration_frame = NULL, custom_metric_func = NULL, custom_distribution_func = NULL, export_checkpoints_dir = NULL, monotone_constraints = NULL, check_constant_response = TRUE, verbose = FALSE)

Arguments

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

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

training_frame
Id of the training data frame.

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

validation_frame
Id of the validation data frame.

nfolds
Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.

keep_cross_validation_models
Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions
Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.

keep_cross_validation_fold_assignment
Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.

score_each_iteration
Logical. Whether to score during each iteration of model training. Defaults to FALSE.

score_tree_interval
Score the model after every so many trees. Disabled if set to 0. Defaults to 0.

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

fold_column
Column with cross-validation fold index assignment per observation.

ignore_const_cols
Logical. Ignore constant columns. Defaults to TRUE.

offset_column
Offset column. This will be added to the combination of columns before applying the link function.

weights_column
Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor.

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.

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^2 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 and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "AUCPR", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.
stopping_tolerance: Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.
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", "quasibinomial", "multinomial", "gaussian", "poisson", "gamma", "tweedie", "laplace", "quantile", "huber", "custom". Defaults to AUTO.
quantile_alpha: Desired quantile for Quantile regression, must be between 0 and 1. Defaults to 0.5.
tweedie_power: Tweedie power for Tweedie regression, must be between 1 and 2. Defaults to 1.5.
huber_alpha: Desired quantile for Huber/M-regression (threshold between quadratic and linear loss, must be between 0 and 1). Defaults to 0.9.
checkpoint: Model checkpoint to resume training with.
sample_rate: Row sample rate per tree (from 0.0 to 1.0) Defaults to 1.
sample_rate_per_class: A list of row sample rates per class (relative fraction for each class, from 0.0 to 1.0), for each tree.
col_sample_rate: Column sample rate (from 0.0 to 1.0) Defaults to 1.
col_sample_rate_change_per_level
Relative change of the column sampling rate for every level (must be > 0.0 and <= 2.0) Defaults to 1.

col_sample_rate_per_tree
Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.

min_split_improvement
Minimum relative improvement in squared error reduction for a split to happen Defaults to 1e-05.

histogram_type
What type of histogram to use for finding optimal split points Must be one of: "AUTO", "UniformAdaptive", "Random", "QuantilesGlobal", "RoundRobin". Defaults to AUTO.

max_abs_leafnode_pred
Maximum absolute value of a leaf node prediction Defaults to 1.797693135e+308.

pred_noise_bandwidth
Bandwidth (sigma) of Gaussian multiplicative noise \~N(1,sigma) for tree node predictions Defaults to 0.

categorical_encoding
Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.

calibrate_model
Logical. Use Platt Scaling to calculate calibrated class probabilities. Calibration can provide more accurate estimates of class probabilities. Defaults to FALSE.

calibration_frame
Calibration frame for Platt Scaling

custom_metric_func
Reference to custom evaluation function, format: 'language:keyName=funcName'

custom_distribution_func
Reference to custom distribution, format: 'language:keyName=funcName'

export_checkpoints_dir
Automatically export generated models to this directory.

monotone_constraints
A mapping representing monotonic constraints. Use +1 to enforce an increasing constraint and -1 to specify a decreasing constraint.

check_constant_response
Logical. Check if response column is constant. If enabled, then an exception is thrown if the response column is a constant value. If disabled, then model will train regardless of the response column being a constant value or not. Defaults to TRUE.

verbose
Logical. Print scoring history to the console (Metrics per tree). Defaults to FALSE.

See Also

predict.H2OModel for prediction
Examples

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

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

## End(Not run)
```

---

h2o.generic

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

Description

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

Usage

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

Arguments

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

Examples

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

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

## End(Not run)
```
h2o.genericModel

Imports a model under given path, creating a Generic model with it.

Description

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

Usage

h2o.genericModel(mojo_file_path)

Arguments

mojo_file_path  Filesystem path to the model imported

Value

Returns H2O Generic Model based on given embedded model

Examples

## Not run:

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

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

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

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

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

## End(Not run)

h2o.getAutoML

Get an R object that is a subclass of H2OAutoML

Description

Get an R object that is a subclass of H2OAutoML
Usage

h2o.getAutoML(project_name)

Arguments

project_name  A string indicating the project_name of the automl instance to retrieve.

Value

Returns an object that is a subclass of H2OAutoML.

Examples

## Not run:
library(h2o)
h2o.init()
votes_path <- system.file("extdata", "housevotes.csv", package = "h2o")
votes_hf <- h2o.uploadFile(path = votes_path, header = TRUE)
aml <- h2o.automl(y = "Class", project_name="aml_housevotes",
                 training_frame = votes_hf, max_runtime_secs = 30)
automl_retrieved <- h2o.getAutoML("aml_housevotes")
## End(Not run)

h2o.getConnection

Retrieve an H2O Connection

Description

Attempt to recover an h2o connection.

Usage

h2o.getConnection()

Value

Returns an H2OConnection object.

h2o.getFrame

Get an R Reference to an H2O Dataset, that will NOT be GC’d by default

Description

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

Usage

h2o.getFrame(id)
**h2o.getFutureModel**

**Arguments**

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

**Description**

Get future model

**Usage**

```r
h2o.getFutureModel(object, verbose = FALSE)
```

**Arguments**

- `object`: H2OModel
- `verbose`: Print model progress to console. Default is FALSE

---

**h2o.getGLMFullRegularizationPath**

*Extract full regularization path from a GLM model*

**Description**

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

**Usage**

```r
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

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

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

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

Examples

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

h2o.getId

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)
**h2o.getModel**

**Get an R reference to an H2O model**

**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**

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

iris_hf <- as.h2o(iris)
model_id <- h2o.gbm(x = 1:4, y = 5, training_frame = iris_hf)@model_id
model_retrieved <- h2o.getModel(model_id)
## End(Not run)
```

**h2o.getModelTree**

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

**Description**

Usage example:

```r
airlines.data <- h2o.importFile(path = '/path/to/airlines_train.csv')
gbm.model = h2o.gbm(x=c("Origin", "Dest", "Distance"),y="IsDepDelayed",training_frame=airlines.data,model_id="gbm_trees_model")
tree <- h2o.getModelTree(gbm.model, 1, 1);
```
Usage

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

Arguments

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

Value

Returns an H2OTree object with detailed information about a tree.

h2o.getTimezone

Get the Time Zone on the H2O cluster Returns a string

Description

Get the Time Zone on the H2O cluster Returns a string

Usage

h2o.getTimezone()

h2o.getTypes

Get the types-per-column

Description

Get the types-per-column

Usage

h2o.getTypes(x)

Arguments

x An H2OFrame

Value

A list of types per column
h2o.getVector

Get h2o version

Description
Get h2o version

Usage
h2o.getVector()

h2o.giniCoef
Retrieve the GINI Coefficient

Description
Retrieves the GINI coefficient from an H2OBinomialMetrics. If "train", "valid", and "xval" parameters are FALSE (default), then the training 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 H2OBinomialMetrics object.
train Retrieve the training GINI Coefficient
valid Retrieve the validation GINI Coefficient
xval Retrieve the cross-validation GINI Coefficient

See Also
h2o.auc for AUC, h2o.giniCoef for the GINI coefficient, and h2o.metric for the various threshold metrics. See h2o.performance for creating H2OModelMetrics objects.

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

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

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

## End(Not run)
h2o.glm

Fit a generalized linear model

Description

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

Usage

h2o.glm(x, y, training_frame, model_id = NULL, validation_frame = NULL, nfolds = 0, seed = -1, keep_cross_validation_models = TRUE, keep_cross_validation_predictions = 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", "ordinal", "multinomial", "poisson", "gamma", "tweedie", "negativebinomial"), tweedie_variance_power = 0, tweedie_link_power = 1, theta = 1e-10, solver = c("AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE", "COORDINATE_DESCENT", "GRADIENT_DESCENT_LH", "GRADIENT_DESCENT_SQERR"), alpha = NULL, lambda = NULL, lambda_search = FALSE, early_stopping = TRUE, nlambdas = -1, standardize = TRUE, missing_values_handling = c("MeanImputation", "Skip", "PlugValues"), plug_values = NULL, compute_p_values = FALSE, remove_collinear_columns = FALSE, intercept = TRUE, non_negative = FALSE, max_iterations = -1, objective_epsilon = -1, beta_epsilon = 1e-04, gradient_epsilon = -1, link = c("family_default", "identity", "logit", "log", "inverse", "tweedie", "ologit"), prior = -1, lambda_min_ratio = -1, beta_constraints = NULL, max_active_predictors = -1, interactions = NULL, interaction_pairs = NULL, obj_reg = -1, export_checkpoints_dir = NULL, balance_classes = FALSE, class_sampling_factors = NULL, max_after_balance_size = 5, max_hit_ratio_k = 0, max_runtime_secs = 0, custom_metric_func = NULL)

Arguments

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

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

training_frame Id of the training data frame.

model_id Destination id for this model; auto-generated if not specified.
validation_frame
Id of the validation data frame.
nfolds
Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
seed
Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
keep_cross_validation_models
Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions
Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment
Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
fold_assignment
Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column
Column with cross-validation fold index assignment per observation.
ignore_const_cols
Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration
Logical. Whether to score during each iteration of model training. Defaults to FALSE.
offset_column
Offset column. This will be added to the combination of columns before applying the link function.
weights_column
Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor.
family
tweedie_variance_power
Tweedie variance power Defaults to 0.
tweedie_link_power
Tweedie link power Defaults to 1.
theta
Theta Defaults to 1e-10.
solver
AUTO will set the solver based on given data and the other parameters. IRLSM is fast on problems with small number of predictors and for lambda-search with L1 penalty. L_BFGS scales better for datasets with many columns. Must be one of: "AUTO", "IRLSM", "L_BFGS", "COORDINATE_DESCENT_NAIVE", "COORDINATE_DESCENT", "GRADIENT_DESCENT_LH", "GRADIENT_DESCENT_SQERR". Defaults to AUTO.
**h2o.glm**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>alpha</strong></td>
<td>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.</td>
</tr>
<tr>
<td><strong>lambda</strong></td>
<td>Regularization strength</td>
</tr>
<tr>
<td><strong>lambda_search</strong></td>
<td>Logical. Use lambda search starting at lambda max, given lambda is then interpreted as lambda min Defaults to FALSE.</td>
</tr>
<tr>
<td><strong>early_stopping</strong></td>
<td>Logical. Stop early when there is no more relative improvement on train or validation (if provided) Defaults to TRUE.</td>
</tr>
<tr>
<td><strong>nlambdas</strong></td>
<td>Number of lambdas to be used in a search. Default indicates: If alpha is zero, with lambda search set to True, the value of nlambdas is set to 30 (fewer lambdas are needed for ridge regression) otherwise it is set to 100. Defaults to -1.</td>
</tr>
<tr>
<td><strong>standardize</strong></td>
<td>Logical. Standardize numeric columns to have zero mean and unit variance Defaults to TRUE.</td>
</tr>
<tr>
<td><strong>missing_values_handling</strong></td>
<td>Handling of missing values. Either MeanImputation, Skip or PlugValues. Must be one of: &quot;MeanImputation&quot;, &quot;Skip&quot;, &quot;PlugValues&quot;. Defaults to MeanImputation.</td>
</tr>
<tr>
<td><strong>plug_values</strong></td>
<td>Plug Values (a single row frame containing values that will be used to impute missing values of the training/validation frame, use with conjunction missing_values_handling = PlugValues)</td>
</tr>
<tr>
<td><strong>compute_p_values</strong></td>
<td>Logical. Request p-values computation, p-values work only with IRLSM solver and no regularization Defaults to FALSE.</td>
</tr>
<tr>
<td><strong>remove_collinear_columns</strong></td>
<td>Logical. In case of linearly dependent columns, remove some of the dependent columns Defaults to FALSE.</td>
</tr>
<tr>
<td><strong>intercept</strong></td>
<td>Logical. Include constant term in the model Defaults to TRUE.</td>
</tr>
<tr>
<td><strong>non_negative</strong></td>
<td>Logical. Restrict coefficients (not intercept) to be non-negative Defaults to FALSE.</td>
</tr>
<tr>
<td><strong>max_iterations</strong></td>
<td>Maximum number of iterations Defaults to -1.</td>
</tr>
<tr>
<td><strong>objective_epsilon</strong></td>
<td>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.</td>
</tr>
<tr>
<td><strong>beta_epsilon</strong></td>
<td>Converge if beta changes less (using L-infinity norm) than beta epsilon, ONLY applies to IRLSM solver Defaults to 0.0001.</td>
</tr>
<tr>
<td><strong>gradient_epsilon</strong></td>
<td>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.</td>
</tr>
<tr>
<td><strong>link</strong></td>
<td>Link function. Must be one of: &quot;family_default&quot;, &quot;identity&quot;, &quot;logit&quot;, &quot;log&quot;, &quot;inverse&quot;, &quot;tweedie&quot;, &quot;ologit&quot;. Defaults to family_default.</td>
</tr>
</tbody>
</table>
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 (the smallest lambda that drives all coefficients to zero). Default indicates: if the number of observations is greater than the number of variables, then lambda_min_ratio is set to 0.0001; if the number of observations is less than the number of variables, then lambda_min_ratio is set to 0.01. Defaults to -1.

beta_constraints  Beta constraints

max_active_predictors  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 max_active_predictors is set to 5000 otherwise it is set to 100000000. Defaults to -1.

interactions  A list of predictor column indices to interact. All pairwise combinations will be computed for the list.

interaction_pairs  A list of pairwise (first order) column interactions.

obj_reg  Likelihood divider in objective value computation, default is 1/nobs Defaults to -1.

export_checkpoints_dir  Automatically export generated models to this directory.

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  Maximum number (top K) of predictions to use for hit ratio computation (for multi-class only, 0 to disable) Defaults to 0.

max_runtime_secs  Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

custom_metric_func  Reference to custom evaluation function, format: 'language:keyName=funcName'

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

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

# Run GLM of CAPSULE ~ AGE + RACE + PSA + DCAPS
prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)

h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"), training_frame = prostate,
       family = "binomial", nfolds = 0, alpha = 0.5, lambda_search = FALSE)

# Run GLM of VOL ~ CAPSULE + AGE + RACE + PSA + GLEASON
predictors = setdiff(colnames(prostate), c("ID", "DPROS", "DCAPS", "VOL"))

h2o.glm(y = "VOL", x = predictors, training_frame = prostate, family = "gaussian",
        nfolds = 0, alpha = 0.1, lambda_search = FALSE)

# GLM variable importance
# Also see:
# https://github.com/h2oai/h2o/blob/master/R/tests/testdir_demos/runit_demo_VI_all_algos.R
bank = h2o.importFile(path="https://s3.amazonaws.com/h2o-public-test-data/smalldata/demos/bank-additional-full.csv")
predictors = 1:20
target="y"

glm = h2o.glm(x=predictors, y=target, training_frame=bank, family="binomial", standardize=TRUE, lambda_search=TRUE)

h2o.std_coef_plot(glm, num_of_features = 20)
## End(Not run)
```

---

**h2o.glrm**

Generalized low rank decomposition of an H2O data frame

Description

Builds a generalized low rank decomposition of an H2O data frame

Usage

```r
h2o.glrm(training_frame, cols = NULL, model_id = NULL, validation_frame = NULL, ignore_const_cols = TRUE,
          score_each_iteration = FALSE, transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"),
          k = 1, loss = c("Quadratic", "Absolute", "Huber", "Poisson", "Hinge",
```

Arguments

training_frame  
Id of the training data frame.

cols  
(Optional) A vector containing the data columns on which k-means operates.

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

validation_frame  
Id of the validation data frame.

ignore_const_cols  
Logical. Ignore constant columns. Defaults to TRUE.

score_each_iteration  
Logical. Whether to score during each iteration of model training. Defaults to FALSE.

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  

loss_by_col  
Loss function by column (override) Must be one of: "Quadratic", "Absolute", "Huber", "Poisson", "Hinge", "Logistic", "Periodic", "Categorical", "Ordinal".

loss_by_col_idx  
Loss function by column index (override)

multi_loss  
Categorical loss function Must be one of: "Categorical", "Ordinal". Defaults to Categorical.

period  
Length of period (only used with periodic loss function) Defaults to 1.

regularization_x  
Regularization function for X matrix Must be one of: "None", "Quadratic", "L2", "L1", "NonNegative", "OneSparse", "UnitOneSparse", "Simplex". Defaults to None.

regularization_y  
Regularization function for Y matrix Must be one of: "None", "Quadratic", "L2", "L1", "NonNegative", "OneSparse", "UnitOneSparse", "Simplex". Defaults to None.

gamma_x  
Regularization weight on X matrix Defaults to 0.

gamma_y  
Regularization weight on Y matrix Defaults to 0.
max_iterations  Maximum number of iterations Defaults to 1000.
max_updates    Maximum number of updates, defaults to 2*max_iterations Defaults to 2000.
init_step_size Initial step size Defaults to 1.
min_step_size  Minimum step size Defaults to 0.0001.
seed          Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
init           Initialization mode Must be one of: "Random", "SVD", "PlusPlus", "User". Defaults to PlusPlus.
svd_method     Method for computing SVD during initialization (Caution: Randomized is currently experimental and unstable) Must be one of: "GramSVD", "Power", "Randomized". Defaults to Randomized.
user_y         User-specified initial Y
user_x         User-specified initial X
expand_user_y Logical. Expand categorical columns in user-specified initial Y Defaults to TRUE.
impute_original Logical. Reconstruct original training data by reversing transform Defaults to FALSE.
recover_svd    Logical. Recover singular values and eigenvectors of XY Defaults to FALSE.
max_runtime_secs Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.
export_checkpoints_dir Automatically export generated models to this directory.

Value
an object of class H2ODimReductionModel.

References

See Also
h2o.kmeans, h2o.svd, h2o.prcomp

Examples
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
h2o.glrm(training_frame = australia, k = 5, loss = "Quadratic", regularization_x = "L1",
          gamma_x = 0.5, gamma_y = 0, max_iterations = 1000)
## Search for matches to an argument pattern

**Description**

Searches for matches to argument ‘pattern’ within each element of a string column.

**Usage**

```r
h2o.grep(pattern, x, ignore.case = FALSE, invert = FALSE,
output.logical = FALSE)
```

**Arguments**

- `pattern`: A character string containing a regular expression.
- `x`: An H2O frame that wraps a single string column.
- `ignore.case`: If TRUE case is ignored during matching.
- `invert`: Identify elements that do not match the pattern.
- `output.logical`: If TRUE returns logical vector of indicators instead of list of matching positions

**Details**

This function has similar semantics as R’s native grep function and it supports a subset of its parameters. Default behavior is to return indices of the elements matching the pattern. Parameter ‘output.logical’ can be used to return a logical vector indicating if the element matches the pattern (1) or not (0).

**Value**

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

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
addresses <- as.h2o(c("2307", "Leghorn St", "Mountain View", "CA", "94043"))
zip.codes <- addresses[h2o.grep("[0-9]{5}\", addresses, output.logical = TRUE),]
## End(Not run)
```
**h2o.grid**

**H2O Grid Support**

**Description**
Provides a set of functions to launch a grid search and get its results.

**Usage**

```r
h2o.grid(algorithm, grid_id, x, y, training_frame, ..., 
  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 autogen-
  erated.

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

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

- **training_frame**
  Id of the training data frame.

- **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 al-
  gorithm.

- **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 combi-
  nations. 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.
  or list(strategy = "RandomDiscrete", stopping_metric = "AUTO", stopping_tolerance = 
  or list(strategy = "RandomDiscrete", stopping_metric = "misclassification", stopping

**Details**
Launch grid search with given algorithm and parameters.
Examples

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

---

**h2o.group_by**  
*Group and Apply by Column*

**Description**

Performs a group by and apply similar to ddply.

**Usage**

```r
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
- `...`  
  any supported aggregate function. See Details: for more help.
- `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.

**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 \texttt{sum(col="X1", na="all").mean(col="X5", na="all").max()})

Value

Returns a new H2OFrame object with columns equivalent to the number of groups created

<table>
<thead>
<tr>
<th>h2o.gsub</th>
<th>String Global Substitute</th>
</tr>
</thead>
</table>

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

\texttt{h2o.gsub(pattern, replacement, x, ignore.case = FALSE)}

Arguments

- \texttt{pattern} The pattern to replace.
- \texttt{replacement} The replacement pattern.
- \texttt{x} The column on which to operate.
- \texttt{ignore.case} Case sensitive or not

Examples

```r
## Not run:
library(h2o)
h2o.init()
string_to_gsub <- as.h2o("r tutorial")
sub_string <- h2o.gsub("r ", "H2O ", string_to_gsub)
## End(Not run)
```
Return the Head or Tail of an H2O Dataset.

Description

Returns the first or last rows of an H2OFrame object.

Usage

h2o.head(x, n = 6L, ...)

## 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

## Not run:
library(h2o)
h2o.init(ip = "localhost", port = 54321, startH2O = TRUE)
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
head(australia, 10)
tail(australia, 10)

## End(Not run)
h2o.hist  

**Compute A Histogram**

**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**

```r
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  

**Retrieve the Hit Ratios**

**Description**

If "train", "valid", and "xval" parameters are FALSE (default), then the training Hit Ratios value is returned. If more than one parameter is set to TRUE, then a named list of Hit Ratio tables are returned, where the names are "train", "valid" or "xval".

**Usage**

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

**Arguments**

- **object**  
  An H2OModel object.

- **train**  
  Retrieve the training Hit Ratio

- **valid**  
  Retrieve the validation Hit Ratio

- **xval**  
  Retrieve the cross-validation Hit Ratio
h2o.hour  

*Convert Milliseconds to Hour of Day in H2O Datasets*

**Description**  
Converts the entries of an H2OFrame object from milliseconds to hours of the day (on a 0 to 23 scale).

**Usage**  

```r
h2o.hour(x)
```

```r
hour(x)
```

```r
## 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  

*H2O Apply Conditional Statement*

**Description**  
Applies conditional statements to numeric vectors in H2O parsed data objects when the data are numeric.

**Usage**  

```r
h2o.ifelse(test, yes, no)
```

```r
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

```r
## Not run:
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.importFile(path = australia_path)
australia[,9] <- ifelse(australia[,3] < 279.9, 1, 0)
summary(australia)
## End(Not run)
```

h2o.importFile

Import Files into H2O

Description

Imports files into an H2O cluster. The default behavior is to pass-through to the parse phase automatically.

Usage

```r
h2o.importFile(path, destination_frame = "", parse = TRUE,
    header = NA, sep = "", col.names = NULL, col.types = NULL,
    na.strings = NULL, decrypt_tool = NULL, skipped_columns = NULL,
    custom_non_data_line_markers = NULL)
```

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

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

```r
h2o.uploadFile(path, destination_frame = "", parse = TRUE,
    header = NA, sep = "", col.names = NULL, col.types = NULL,
    na.strings = NULL, progressBar = FALSE, parse_type = NULL,
    decrypt_tool = NULL, skipped_columns = NULL)
```
**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 `h2o.parseRaw`.

**header**
(Optional) A logical value indicating whether the first line of the file contains column headers. If left empty, the parser will try to automatically detect this.

**sep**
(Optional) The field separator character. Values on each line of the file are separated by this character. If sep = "", the parser will automatically detect the separator.

**col.names**
(Optional) An H2OFrame object containing a single delimited line with the column names for the file.

**col.types**
(Optional) A vector to specify whether columns should be forced to a certain type upon import parsing.

**na.strings**
(Optional) H2O will interpret these strings as missing.

**decrypt_tool**
(Optional) Specify a Decryption Tool (key-reference acquired by calling `h2o.decryptionSetup`.

**skipped_columns**
a list of column indices to be skipped during parsing.

**custom_non_data_line_markers**
(Optional) If a line in imported file starts with any character in given string it will NOT be imported. Empty string means all lines are imported, NULL means that default behaviour for given format will be used

**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

```r
## Not run:
#h2o.init(ip = "localhost", port = 54321, startH2O = TRUE)
prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
prostate = h2o.importFile(path = prostate_path)
class(prostate)
summary(prostate)

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

## End(Not run)
```

h2o.import_hive_table

Import Hive Table into H2O

Description

Import Hive table to H2OFrame in memory. Make sure to start H2O with Hive on classpath. Uses hive-site.xml on classpath to connect to Hive.

Usage

```r
h2o.import_hive_table(database, table, partitions = NULL,
allow_multi_format = FALSE)
```

Arguments

- **database**: Name of Hive database (default database will be used by default)
- **table**: Name of Hive table to import
- **partitions**: a list of lists of strings - partition key column values of partitions you want to import.
- **allow_multi_format**: enable import of partitioned tables with different storage formats used. WARNING: this may fail on out-of-memory for tables with a large number of small partitions.

Details

For example, `my_citibike_data = h2o.import_hive_table("default", "citibike20k", partitions = list(c("2017", "01"), c("2017", "02")))`
**h2o.import_mojo**

*Imports a MOJO under given path, creating a Generic model with it.*

**Description**

Usage example:

```r
mojo_model <- h2o.import_mojo(model_file_path = "/path/to/mojo.zip")
predictions <- h2o.predict(mojo_model, dataset)
```

**Usage**

```r
h2o.import_mojo(mojo_file_path)
```

**Arguments**

- **mojo_file_path**: Filesystem path to the model imported

**Value**

Returns H2O Generic Model embedding given MOJO model

**Examples**

```r
## Not run:
# Import default Iris dataset as H2O frame
data <- as.h2o(iris)

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

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

# Import the MOJO and obtain a Generic model
mojo_model <- h2o.import_mojo(mojo_original_path)

# Perform scoring with the generic model
predictions <- h2o.predict(mojo_model, data)
## End(Not run)
```

---

**h2o.import_sql_select**

*Import SQL table that is result of SELECT SQL query into H2O*

**Description**

Creates a temporary SQL table from the specified sql_query. Runs multiple SELECT SQL queries on the temporary table concurrently for parallel ingestion, then drops the table. Be sure to start the h2o.jar in the terminal with your downloaded JDBC driver in the classpath: 'java -cp <path_to_h2o_jar>:<path_to_jdbc_driver_jar> water.H2OApp' Also see h2o.import_sql_table. Currently supported SQL databases are MySQL, PostgreSQL, MariaDB, Hive, Oracle and Microsoft SQL Server.

---
**Usage**

```r
h2o.import_sql_select(connection_url, select_query, username, password,
                       use_temp_table = NULL, temp_table_name = NULL, optimize = NULL,
                       fetch_mode = NULL)
```

**Arguments**

- **connection_url**: URL of the SQL database connection as specified by the Java Database Connectivity (JDBC) Driver. For example, "jdbc:mysql://localhost:3306/menagerie?&useSSL=false"
- **select_query**: SQL query starting with 'SELECT' that returns rows from one or more database tables.
- **username**: Username for SQL server
- **password**: Password for SQL server
- **use_temp_table**: Whether a temporary table should be created from select_query
- **temp_table_name**: Name of temporary table to be created from select_query
- **optimize**: (Optional) Optimize import of SQL table for faster imports. Experimental. Default is true.
- **fetch_mode**: (Optional) Set to DISTRIBUTED to enable distributed import. Set to SINGLE to force a sequential read from the database. Can be used for databases that do not support OFFSET-like clauses in SQL statements.

**Details**

For example, my_sql_conn_url <- "jdbc:mysql://172.16.2.178:3306/ingestSQL?&useSSL=false"
select_query <- "SELECT bikeid from citibike20k" username <- "root" password <- "abc123"
my_citibike_data <- h2o.import_sql_select(my_sql_conn_url, select_query, username, password)

---

**h2o.import_sql_table**  
Import SQL Table into H2O

**Description**

Imports SQL table into an H2O cluster. Assumes that the SQL table is not being updated and is stable. Runs multiple SELECT SQL queries concurrently for parallel ingestion. Be sure to start the h2o.jar in the terminal with your downloaded JDBC driver in the classpath: 'java -cp <path_to_h2o_jar>:<path_to_jdbc_driver_jar> water.H2OApp' Also see h2o.import_sql_select. Currently supported SQL databases are MySQL, PostgreSQL, MariaDB, Hive, Oracle and Microsoft SQL Server.

**Usage**

```r
h2o.import_sql_table(connection_url, table, username, password,
                      columns = NULL, optimize = NULL, fetch_mode = NULL)
```
Arguments

collection_url     URL of the SQL database connection as specified by the Java Database Connectivity (JDBC) Driver. For example, "jdbc:mysql://localhost:3306/menagerie?&useSSL=false"
table              Name of SQL table
username           Username for SQL server
password           Password for SQL server
columns            (Optional) Character vector of column names to import from SQL table. Default is to import all columns.
optimize           (Optional) Optimize import of SQL table for faster imports. Default is true. Ignored - use fetch_mode instead.
fetch_mode         (Optional) Set to DISTRIBUTED to enable distributed import. Set to SINGLE to force a sequential read from the database Can be used for databases that do not support OFFSET-like clauses in SQL statements.

Details

For example, my_sql_conn_url <- "jdbc:mysql://172.16.2.178:3306/ingestSQL?&useSSL=false" table <- "citibike20k" username <- "root" password <- "abc123" my_citibike_data <- h2o.import_sql_table(my_sql_conn_url, table, username, password)

---

h2o.impute       Basic Imputation of H2O Vectors

Description

Perform inplace imputation by filling missing values with aggregates computed on the "na.rm'd" vector. Additionally, it's possible to perform imputation based on groupings of columns from within data; these columns can be passed by index or name to the by parameter. If a factor column is supplied, then the method must be "mode".

Usage

h2o.impute(data, column = 0, method = c("mean", "median", "mode"),
            combine_method = c("interpolate", "average", "lo", "hi"), by = NULL,
            groupByFrame = NULL, values = NULL)

Arguments

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

```r
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
iris_hf[sample(nrow(iris_hf), 40), 5] <- NA  # randomly replace 50 values with NA
# impute with a group by
iris_hf <- h2o.impute(iris_hf, "Species", "mode", by = c("Sepal.Length", "Sepal.Width"))
## End(Not run)
```

h2o.init

Initialize and Connect to H2O

Description

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

Usage

```r
h2o.init(ip = "localhost", port = 54321, name = NA_character_,
         startH2O = TRUE, forceDL = FALSE, enable Assertions = TRUE,
         license = NULL, nthreads = -1, max_mem_size = NULL,
         min_mem_size = NULL, ice_root = tempdir(), log_dir = NA_character_,
         log_level = NA_character_, strict_version_check = TRUE,
         proxy = NA_character_, https = FALSE, cacert = NA_character_,
         insecure = FALSE, username = NA_character_,
         password = NA_character_, use_spnego = FALSE,
         cookies = NA_character_, context_path = NA_character_,
         ignore_config = FALSE, extra_classpath = NULL,
         jvm_custom_args = NULL, bind_to_localhost = TRUE)
```

Arguments

- **ip**: Object of class character representing the IP address of the server where H2O is running.
- **port**: Object of class numeric representing the port number of the H2O server.
- **name** (Optional): A character string representing the H2O cluster name.
- **startH2O** (Optional): A logical value indicating whether to try to start H2O from R if no connection with H2O is detected. This is only possible if `ip` = "localhost" or `ip` = "127.0.0.1". If an existing connection is detected, R does not start H2O.
**forceDL** *(Optional) A logical value indicating whether to force download of the H2O executable. Defaults to FALSE, so the executable will only be downloaded if it does not already exist in the h2o R library resources directory h2o/java/h2o.jar. This value is only used when R starts H2O.*

**enable_assertions** *(Optional) A logical value indicating whether H2O should be launched with assertions enabled. Used mainly for error checking and debugging purposes. This value is only used when R starts H2O.*

**license** *(Optional) A character string value specifying the full path of the license file. This value is only used when R starts H2O.*

**nthreads** *(Optional) Number of threads in the thread pool. This relates very closely to the number of CPUs used. -1 means use all CPUs on the host (Default). A positive integer specifies the number of CPUs directly. This value is only used when R starts H2O.*

**max_mem_size** *(Optional) A character string specifying the maximum size, in bytes, of the memory allocation pool to H2O. This value must 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.*

**min_mem_size** *(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.*

**ice_root** *(Optional) A directory to handle object spillage. The default varies by OS.*

**log_dir** *(Optional) A directory where H2O server logs are stored. The default varies by OS.*

**log_level** *(Optional) The level of logging of H2O server. The default is INFO.*

**strict_version_check** *(Optional) Setting this to FALSE is unsupported and should only be done when advised by technical support.*

**proxy** *(Optional) A character string specifying the proxy path.*

**https** *(Optional) Set this to TRUE to use https instead of http.*

**cacert** *(Optional) Path to a CA bundle file with root and intermediate certificates of trusted CAs.*

**insecure** *(Optional) Set this to TRUE to disable SSL certificate checking.*

**username** *(Optional) Username to login with.*

**password** *(Optional) Password to login with.*

**use_spnego** *(Optional) Set this to TRUE to enable SPNEGO authentication.*

**cookies** *(Optional) Vector(or list) of cookies to add to request.*

**context_path** *(Optional) The last part of connection URL: http://<ip>:<port>/<context_path>*

**ignore_config** *(Optional) A logical value indicating whether a search for a .h2oconfig file should be conducted or not. Default value is FALSE.*

**extra_classpath** *(Optional) A vector of paths to libraries to be added to the Java classpath when H2O is started from R.*

**jvm_custom_args** *(Optional) A character list of custom arguments for the JVM where new H2O instance is going to run, if started. Ignored when connecting to an existing instance.*
bind_to_localhost

(Optional) A logical flag indicating whether access to the H2O instance should be restricted to the local machine (default) or if it can be reached from other computers on the network. Only applicable when H2O is started from R.

Details

By default, this method first checks if an H2O instance is connectible. If it cannot connect and `start = TRUE` with `ip = "localhost"`, it will attempt to start an instance of H2O at localhost:54321. If an open ip and port of your choice are passed in, then this method will attempt to start an H2O instance at that specified ip port.

When initializing H2O locally, this method searches for h2o.jar in the R library resources (`system.file("java", "h2o.jar", package = "h2o")`), and if the file does not exist, it will automatically attempt to download the correct version from Amazon S3. The user must have Internet access for this process to be successful.

Once connected, the method checks to see if the local H2O R package version matches the version of H2O running on the server. If there is a mismatch and the user indicates she wishes to upgrade, it will remove the local H2O R package and download/install the H2O R package from the server.

Value

this method will load it and return a H2OConnection object containing the IP address and port number of the H2O server.

Note

Users may wish to manually upgrade their package (rather than waiting until being prompted), which requires that they fully uninstall and reinstall the H2O package, and the H2O client package. You must unload packages running in the environment before upgrading. It’s recommended that users restart R or R studio after upgrading

See Also

H2O R package documentation for more details. h2o.shutdown for shutting down from R.

Examples

```r
## 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

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

iris_hf <- as.h2o(iris)
summary(iris_hf)

irismiss <- h2o.insertMissingValues(iris_hf, fraction = 0.25)
head(irismiss)
summary(irismiss)

## End(Not run)
```
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

```r
## Not run:
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,
    factors = list(c(1, 2), c("C2", "C3", "C4")),
    pairwise = TRUE)
```

h2o.isax

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, 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)

## End(Not run)

---

**h2o.isax**

**iSAX**

**Description**

Compute the iSAX index for a DataFrame which is assumed to be numeric time series data

**Usage**

```r
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/SAX.pdf
h2o.ischaracter

Check if character

Description
Check if character

Usage
h2o.ischaracter(x)

Arguments
x An H2OFrame object.

See Also
is.character for the base R implementation.

h2o.isfactor

Check if factor

Description
Check if factor

Usage
h2o.isfactor(x)

Arguments
x An H2OFrame object.

See Also
is.factor for the base R implementation.
### h2o.isnumeric

**Check if numeric**

**Description**

Check if numeric

**Usage**

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

**Arguments**

- **x**
  - An H2OFrame object.

**See Also**

- `is.numeric` for the base R implementation.

### h2o.isolationForest

**Trains an Isolation Forest model**

**Description**

Trains an Isolation Forest model

**Usage**

```r
h2o.isolationForest(training_frame, x, model_id = NULL,
                      score_each_iteration = FALSE, score_tree_interval = 0,
                      ignore_const_cols = TRUE, ntrees = 50, max_depth = 8,
                      min_rows = 1, max_runtime_secs = 0, seed = -1,
                      build_tree_one_node = FALSE, mtries = -1, sample_size = 256,
                      sample_rate = -1, col_sample_rate_change_per_level = 1,
                      col_sample_rate_per_tree = 1, categorical_encoding = c("AUTO",
                      "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen",
                      "LabelEncoder", "SortByResponse", "EnumLimited"), stopping_rounds = 0,
                      stopping_metric = c("AUTO", "anomaly_score"),
                      stopping_tolerance = 0.01, export_checkpoints_dir = NULL)
```

**Arguments**

- **training_frame**
  - Id of the training data frame.
- **x**
  - A vector containing the character names of the predictors in the model.
- **model_id**
  - Destination id for this model; auto-generated if not specified.
- **score_each_iteration**
  - Logical. Whether to score during each iteration of model training. Defaults to FALSE.
score_tree_interval
Score the model after every so many trees. Disabled if set to 0. Defaults to 0.

ignore_const_cols
Logical. Ignore constant columns. Defaults to TRUE.

ntrees
Number of trees. Defaults to 50.

max_depth
Maximum tree depth. Defaults to 8.

min_rows
Fewest allowed (weighted) observations in a leaf. Defaults to 1.

max_runtime_secs
Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

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

build_tree_one_node
Logical. Run on one node only; no network overhead but fewer cpus used. Suitable for small datasets. Defaults to FALSE.

mtries
Number of variables randomly sampled as candidates at each split. If set to -1, defaults (number of predictors)/3. Defaults to -1.

sample_size
Number of randomly sampled observations used to train each Isolation Forest tree. Only one of parameters sample_size and sample_rate should be defined. If sample_rate is defined, sample_size will be ignored. Defaults to 256.

sample_rate
Rate of randomly sampled observations used to train each Isolation Forest tree. Needs to be in range from 0.0 to 1.0. If set to -1, sample_rate is disabled and sample_size will be used instead. Defaults to -1.

col_sample_rate_change_per_level
Relative change of the column sampling rate for every level (must be > 0.0 and <= 2.0) Defaults to 1.

col_sample_rate_per_tree
Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.

categorical_encoding
Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.

stopping_rounds
Early stopping based on convergence of stopping_metric. Stop if simple moving average of length k of the stopping_metric does not improve for k:=stopping_rounds scoring events (0 to disable) Defaults to 0.

stopping_metric
Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "anomaly_score". Defaults to AUTO.

stopping_tolerance
Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.01.

export_checkpoints_dir
Automatically export generated models to this directory.
**h2o.is_client**

*Check Client Mode Connection*

**Description**

Check Client Mode Connection

**Usage**

h2o.is_client()

---

**h2o.keyof**

*Method on Keyed objects allowing to obtain their key.*

**Description**

Method on Keyed objects allowing to obtain their key.

**Usage**

h2o.keyof(object)

```
## S4 method for signature 'Keyed'
h2o.keyof(object)

## S4 method for signature 'H2OModel'
h2o.keyof(object)

## S4 method for signature 'H2OFrame'
h2o.keyof(object)

## S4 method for signature 'H2OAutoML'
h2o.keyof(object)
```

**Arguments**

object A Keyed object

**Value**

the string key holding the persistent object.
h2o.kfold_column  
**Produce a k-fold column vector.**

**Description**
Create a k-fold vector useful for H2O algorithms that take a fold_assignments argument.

**Usage**
```r
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  
**Dump the stack into the JVM’s stdout.**

**Description**
A poor man’s profiler, but effective.

**Usage**
```r
h2o.killMinus3()
```

h2o.kmeans  
**Performs k-means clustering on an H2O dataset**

**Description**
Performs k-means clustering on an H2O dataset
h2o.kmeans

Usage

h2o.kmeans(training_frame, x, model_id = NULL, validation_frame = NULL, nfolds = 0, keep_cross_validation_models = TRUE, keep_cross_validation_predictions = FALSE, keep_cross_validation_fold_assignment = FALSE, fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"), fold_column = NULL, ignore_const_cols = TRUE, score_each_iteration = FALSE, k = 1, estimate_k = FALSE, user_points = NULL, max_iterations = 10, standardize = TRUE, seed = -1, init = c("Random", "PlusPlus", "Furthest", "User"), max_runtime_secs = 0, categorical_encoding = c("AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited"), export_checkpoints_dir = NULL)

Arguments

training_frame  Id of the training data frame.
x  A vector containing the character names of the predictors in the model.
model_id  Destination id for this model; auto-generated if not specified.
validation_frame  Id of the validation data frame.
nfolds  Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
keep_cross_validation_models  Logical. Whether to keep the cross-validation models. Defaults to TRUE.
keep_cross_validation_predictions  Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment  Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.
fold_assignment  Cross-validation fold assignment scheme, if fold_column is not specified. The 'Stratified' option will stratify the folds based on the response variable, for classification problems. Must be one of: "AUTO", "Random", "Modulo", "Stratified". Defaults to AUTO.
fold_column  Column with cross-validation fold index assignment per observation.
ignore_const_cols  Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration  Logical. Whether to score during each iteration of model training. Defaults to FALSE.
k  The max. number of clusters. If estimate_k is disabled, the model will find k centroids, otherwise it will find up to k centroids. Defaults to 1.
estimate_k  Logical. Whether to estimate the number of clusters (<=k) iteratively and deterministically.Defaults to FALSE.
user_points  This option allows you to specify a dataframe, where each row represents an initial cluster center. The user- specified points must have the same number of columns as the training observations. The number of rows must equal the number of clusters.
h2o.kurtosis

Kurtosis of a column

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)
### h2o.levels

Return the levels from the column requested column.

Description

Return the levels from the column requested column.

Usage

```
h2o.levels(x, i)
```

Arguments

- **x**: An H2OFrame object.
- **i**: Optional, the index of the column whose domain is to be returned.

See Also

`levels` for the base R method.

Examples

```
## Not run:
iris_hf <- as.h2o(iris)
h2o.levels(iris_hf, 5) # returns "setosa" "versicolor" "virginica"
```

## End(Not run)

```
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.kurtosis(prostate$AGE)
## End(Not run)
```
h2o.listTimezones

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

Description
List all of the Time Zones Acceptable by the H2O cluster.

Usage
h2o.listTimezones()

h2o.list_all_extensions

List all H2O registered extensions

Description
List all H2O registered extensions

Usage
h2o.list_all_extensions()

h2o.list_api_extensions

List registered API extensions

Description
List registered API extensions

Usage
h2o.list_api_extensions()

h2o.list_core_extensions

List registered core extensions

Description
List registered core extensions

Usage
h2o.list_core_extensions()
**h2o.list_jobs**

*Return list of jobs performed by the H2O cluster*

**Description**

Return list of jobs performed by the H2O cluster

**Usage**

```r
h2o.list_jobs()
```

**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**

```r
h2o.loadModel(path)
```

**Arguments**

- `path` The path of the H2O Model to be imported.

**Value**

Returns a `H2OModel` object of the class corresponding to the type of model loaded.

**See Also**

`h2o.saveModel`, `H2OModel`

**Examples**

```r
## Not run:
# library(h2o)
# h2o.init()
# prostate_path = system.file("extdata", "prostate.csv", package = "h2o")
# prostate = h2o.importFile(path = prostate_path)
# prostate_glm = h2o.glm(y = "CAPSULE", x = c("AGE", "RACE", "PSA", "DCAPS"),
#  training_frame = prostate, family = "binomial", alpha = 0.5)
# glmmodel_path = h2o.saveModel(prostate_glm, dir = "/Users/UserName/Desktop")
# glmmodel_load = h2o.loadModel(glmmodel_path)

## End(Not run)
```
h2o.log

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

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  
Log a message on the server-side logs

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  
Retrieve the Log Loss Value

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 H2OModelMetrics object of the correct type.
train  Retrieve the training Log Loss
valid  Retrieve the validation Log Loss
xval  Retrieve the cross-validation Log Loss
**List Keys on an H2O Cluster**

**Description**
Accesses a list of object keys in the running instance of H2O.

**Usage**
```
h2o.ls()
```

**Value**
Returns a list of hex keys in the current H2O instance.

**Examples**
```r
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.ls()
## End(Not run)
```

---

**Strip set from left**

**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**
```r
## Not run:
library(h2o)
h2o.init()
string_to_lstrip <- as.h2o("1234567890")
lstrip_string <- h2o.lstrip(string_to_lstrip, "123") #Remove "123"
## End(Not run)
```
**h2o.mae**  
*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 H2OModel 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**  
```r  
## Not run:  
library(h2o)  
h <- h2o.init()  
fr <- as.h2o(iris)  
m <- h2o.deeplearning(x = 2:5, y = 1, training_frame = fr)  
h2o.mae(m)  
## End(Not run)
```

**h2o.makeGLMModel**  
*Set betas of an existing H2O GLM Model*

**Description**  
This function allows setting betas of an existing glm model.

**Usage**  
$h2o.makeGLMModel(model, beta)$

**Arguments**  
- **model**: an H2OModel corresponding from a h2o.glm call.  
- **beta**: a new set of betas (a named vector)
**h2o.make_metrics**

Create Model Metrics from predicted and actual values in H2O

### Description

Given predicted values (target for regression, class-1 probabilities or binomial or per-class probabilities for multinomial), compute a model metrics object.

### Usage

```r
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

```r
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
pred <- h2o.predict(prostate_gbm, prostate)[,3]  ## class-1 probability
h2o.make_metrics(pred, prostate$CAPSULE)
## End(Not run)
```

---

**h2o.match**

Value Matching in H2O

### Description

`match` and `%in%` return values similar to the base R generic functions.

### Usage

```r
h2o.match(x, table, nomatch = 0, incomparables = NULL)
machine.H2OFrame(x, table, nomatch = 0, incomparables = NULL)
x %in% table
```
h2o.max

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

```r
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
h2o.match(iris_hf[, 5], c("setosa", "versicolor"))
## End(Not run)
```

h2o.max

Returns the maxima of the input values.

Description

Returns the maxima of the input values.

Usage

```r
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**

**Compute the frame's mean by-column (or by-row).**

**Description**

Compute the frame’s mean by-column (or by-row).

**Usage**

```r
h2o.mean(x, na.rm = FALSE, axis = 0, return_frame = FALSE, ...)
```

```r
## 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**

```r
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
# Default behavior. Will return list of means per column.
h2o.mean(prostate$AGE)
# return_frame set to TRUE. This will return an H2O Frame
# with mean per row or column (depends on axis argument)
h2o.mean(prostate, na.rm=TRUE, axis=1, return_frame=TRUE)
## End(Not run)
```
h2o.mean_per_class_error

Retrieve the mean per class error

Description

Retrieves the mean per class error from an H2OBinomialMetrics. If “train”, “valid”, and “xval” parameters are FALSE (default), then the training mean per class error value is returned. If more than one parameter is set to TRUE, then a named vector of mean per class errors are returned, where the names are “train”, “valid” or “xval”.

Usage

h2o.mean_per_class_error(object, train = FALSE, valid = FALSE, xval = FALSE)

Arguments

object An H2OBinomialMetrics object.
train Retrieve the training mean per class error
valid Retrieve the validation mean per class error
xval Retrieve the cross-validation mean per class error

See Also

h2o.mse for MSE, and h2o.metric for the various threshold metrics. See h2o.performance for creating H2OModelMetrics objects.

Examples

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

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

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

## End(Not run)
h2o.mean_residual_deviance

Retrieve the Mean Residual Deviance value

Description

Retrieves the Mean Residual Deviance value from an H2O model. If "train", "valid", and "xval" parameters are FALSE (default), then the training Mean Residual Deviance value is returned. If more than one parameter is set to TRUE, then a named vector of Mean Residual Deviances are returned, where the names are "train", "valid" or "xval".

Usage

h2o.mean_residual_deviance(object, train = FALSE, valid = FALSE, xval = FALSE)

Arguments

object An H2OModel object.
train Retrieve the training Mean Residual Deviance
valid Retrieve the validation Mean Residual Deviance
xval Retrieve the cross-validation Mean Residual Deviance

Examples

## Not run:
library(h2o)

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

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

h2o.mean_residual_deviance(m)
## End(Not run)

h2o.median

H2O Median

Description

Compute the median of an H2OFrame.

Usage

h2o.median(x, na.rm = TRUE)

## S3 method for class 'H2OFrame'
median(x, na.rm = TRUE)
h2o.melt

Converts a frame to key-value representation while optionally skipping NA values. Inverse operation to h2o.pivot.

Description

Pivot the frame designated by the three columns: index, column, and value. Index and column should be of type enum, int, or time. For cases of multiple indexes for a column label, the aggregation method is to pick the first occurrence in the data frame.

Usage

h2o.melt(x, id_vars, value_vars = NA_character_, var_name = "variable", value_name = "value", skipna = FALSE)

Arguments

x an H2OFrame
id_vars the columns used as identifiers
value_vars what columns will be converted to key-value pairs (optional, if not specified complement to id_vars will be used)
var_name name of the key-column (default: "variable")
value_name name of the value-column (default: "value")
skipna if enabled, do not include NAs in the result (default: FALSE)

Value

an unpivoted H2OFrame
h2o.merge

Merge Two H2O Data Frames

Description

Merges two H2OFrame objects with the same arguments and meanings as merge() in base R. However, we do not support all=TRUE, all.x=TRUE and all.y=TRUE. The default method is auto and it will default to the radix method. The radix method will return the correct merge result regardless of duplicated rows in the right frame. In addition, the radix method can perform merge even if you have string columns in your frames. If there are duplicated rows in your right frame, they will not be included if you use the hash method. The hash method cannot perform merge if you have string columns in your left frame. Hence, we consider the radix method superior to the hash method and is the default method to use.

Usage

h2o.merge(x, y, by = intersect(names(x), names(y)), by.x = by,
by.y = by, all = FALSE, all.x = all, all.y = all,
method = "auto")

Arguments

x, y H2OFrame objects
by columns used for merging by default the common names
by.x x columns used for merging by name or number
by.y y columns used for merging by name or number
all TRUE includes all rows in x and all rows in y even if there is no match to the other
all.x If all.x is true, all rows in the x will be included, even if there is no matching row in y, and vice-versa for all.y.
all.y see all.x
method auto(default), radix, hash

Examples

## Not run:
h2o.init()
left <- data.frame(fruit = c('apple', 'orange', 'banana', 'lemon', 'strawberry', 'blueberry'),
color <- c('red', 'orange', 'yellow', 'yellow', 'red', 'blue'))
right <- data.frame(fruit = c('apple', 'orange', 'banana', 'lemon', 'strawberry', 'watermelon'),
citrus <- c(FALSE, TRUE, FALSE, TRUE, FALSE, FALSE))
left_hf <- as.h2o(left)
right_hf <- as.h2o(right)
merged <- h2o.merge(left_hf, right_hf, all.x = TRUE)

## End(Not run)
**h2o.metric**

**H2O Model Metric Accessor Functions**

**Description**

A series of functions that retrieve model metric details.

**Usage**

```r
h2o.metric(object, thresholds, metric, transform = NULL)
h2o.F0point5(object, thresholds)
h2o.F1(object, thresholds)
h2o.F2(object, thresholds)
h2o.accuracy(object, thresholds)
h2o.error(object, thresholds)
h2o.maxPerClassError(object, thresholds)
h2o.mean_per_class_accuracy(object, thresholds)
h2o.mcc(object, thresholds)
h2o.precision(object, thresholds)
h2o.tpr(object, thresholds)
h2o.fpr(object, thresholds)
h2o.fnr(object, thresholds)
h2o.tnr(object, thresholds)
h2o.recall(object, thresholds)
h2o.sensitivity(object, thresholds)
h2o.fallout(object, thresholds)
h2o.missrate(object, thresholds)
h2o.specificity(object, thresholds)
```

**Arguments**

- **object**: An `H2OModelMetrics` object of the correct type.
h2o.min

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, the 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

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

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.F1(perf)

## End(Not run)
```

---

h2o.min

*Returns the minima of the input values.*

Description

Returns the minima of the input values.

Usage

```r
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**

*Compute msec since the Unix Epoch*

Description

Compute msec since the Unix Epoch

Usage

```r
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.mojo_predict_csv**

*H2O Prediction from R without having H2O running*

Description

Provides the method `h2o.mojo_predict_csv` with which you can predict a MOJO model from R.

Usage

```r
h2o.mojo_predict_csv(input_csv_path, mojo_zip_path, 
                       output_csv_path = NULL, genmodel_jar_path = NULL, classpath = NULL, 
                       java_options = NULL, verbose = F, setInvNumNA = F)
```
Arguments

- **input_csv_path**: Path to input CSV file.
- **mojo_zip_path**: Path to MOJO zip downloaded from H2O.
- **output_csv_path**: Optional, path to the output CSV file with computed predictions. If NULL (default), then predictions will be saved as prediction.csv in the same folder as the MOJO zip.
- **genmodel_jar_path**: Optional, path to genmodel jar file. If NULL (default) then the h2o-genmodel.jar in the same folder as the MOJO zip will be used.
- **classpath**: Optional, specifies custom user defined classpath which will be used when scoring. If NULL (default) then the default classpath for this MOJO model will be used.
- **java_options**: Optional, custom user defined options for Java. By default `-Xmx4g -XX:ReservedCodeCacheSize=256m` is used.
- **verbose**: Optional, if TRUE, then additional debug information will be printed. FALSE by default.
- **setInvNumNA**: Optional, if TRUE, then for an string that cannot be parsed into a number an N/A value will be produced, if false the command will fail. FALSE by default.

Value

Returns a data.frame containing computed predictions

---

**h2o.mojo_predict_df**   
*H2O Prediction from R without having H2O running*

Description

Provides the method `h2o.mojo_predict_df` with which you can predict a MOJO model from R.

Usage

```r
h2o.mojo_predict_df(frame, mojo_zip_path, genmodel_jar_path = NULL, 
                      classpath = NULL, java_options = NULL, verbose = F, 
                      setInvNumNA = F)
```

Arguments

- **frame**: data.frame to score.
- **mojo_zip_path**: Path to MOJO zip downloaded from H2O.
- **genmodel_jar_path**: Optional, path to genmodel jar file. If NULL (default) then the h2o-genmodel.jar in the same folder as the MOJO zip will be used.
- **classpath**: Optional, specifies custom user defined classpath which will be used when scoring. If NULL (default) then the default classpath for this MOJO model will be used.
Optional, custom user defined options for Java. By default `-Xmx4g -XX:ReservedCodeCacheSize=256m` is used.

Optional, if TRUE, then additional debug information will be printed. FALSE by default.

Optional, if TRUE, then for an string that cannot be parsed into a number an N/A value will be produced, if false the command will fail. FALSE by default.

Returns a data.frame containing computed predictions

Convert Milliseconds to Months in H2O Datasets

Converts the entries of an H2OFrame object from milliseconds to months (on a 1 to 12 scale).

h2o.month(x)

month(x)

## S3 method for class 'H2OFrame'
month(x)

An H2OFrame object.

An H2OFrame object containing the entries of x converted to months of the year.

h2o.year
h2o.mse

Retrieves Mean Squared Error Value

Description

Retrieves the mean squared error value from an H2OModelMetrics object. If "train", "valid", and "xval" parameters are FALSE (default), then the training MSE value is returned. If more than one parameter is set to TRUE, then a named vector of MSEs are returned, where the names are "train", "valid" or "xval".

Usage

h2o.mse(object, train = FALSE, valid = FALSE, xval = FALSE)

Arguments

object An 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

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

**Count of NAs per column**

**Description**

Gives the count of NAs per column.

**Usage**

```r
h2o.nacnt(x)
```

**Arguments**

- `x`  
  An H2OFrame object.

**Value**

Returns a list containing the count of NAs per column.

**Examples**

```r
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
h2o.nacnt(iris_hf) # should return all 0s
h2o.insertMissingValues(iris_hf)
h2o.nacnt(iris_hf)
## End(Not run)
```

---

### h2o.naiveBayes

**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**

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

score_each_iteration = FALSE, balance_classes = FALSE,
class_sampling_factors = NULL, max_after_balance_size = 5,
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,
export_checkpoints_dir = NULL)

Arguments

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

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

training_frame Id of the training data frame.

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

nfolds Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to
0.

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

fold_assignment Cross-validation fold assignment scheme, if fold_column is not specified. The
'Stratified' option will stratify the folds based on the response variable, for clas-
sification problems. Must be one of: "AUTO", "Random", "Modulo", "Strati-
fied". Defaults to AUTO.

fold_column Column with cross-validation fold index assignment per observation.

keep_cross_validation_models Logical. Whether to keep the cross-validation models. Defaults to TRUE.

keep_cross_validation_predictions Logical. Whether to keep the predictions of the cross-validation models. De-
faults 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 im-
balanced 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 bal-
ance 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.

**export_checkpoints_dir**

Automatically export generated models to this directory.

### Value

An object of class `H2OBinomialModel` if the response has two categorical levels, and `H2OMultinomialModel` otherwise.

### Examples

```r
## Not run:
h2o.init()
votes_path <- system.file("extdata", "housevotes.csv", package = "h2o")
votes <- h2o.uploadFile(path = votes_path, header = TRUE)
h2o.naiveBayes(x = 2:17, y = 1, training_frame = votes, laplace = 3)

## End(Not run)
```

---

**h2o.names**

*Column names of an H2OFrame*

### Description

Column names of an H2OFrame

### Usage

```r
h2o.names(x)
```
Arguments

x  An H2OFrame object.

See Also

names for the base R implementation.

h2o.na_omit  Remove Rows With NAs

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  String length

Description

String length

Usage

h2o.nchar(x)

Arguments

x  The column whose string lengths will be returned.

Examples

```r
## Not run:
library(h2o)
h2o.init()
string_to_nchar <- as.h2o("r tutorial")
nchar_string <- h2o.nchar(string_to_nchar)
## End(Not run)
```
h2o.ncol

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

View Network Traffic Speed

Description
View speed with various file sizes.

Usage
h2o.networkTest()

Value
Returns a table listing the network speed for 1B, 10KB, and 10MB.

h2o.nlevels

Get the number of factor levels for this frame.

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**

*Disable Progress Bar*

**Description**

Disable Progress Bar

**Usage**

```r
h2o.no_progress()
```

**h2o.nrow**

*Return the number of rows present in x.*

**Description**

Return the number of rows present in x.

**Usage**

```r
h2o.nrow(x)
```

**Arguments**

- `x`  
An H2OFrame object.

**See Also**

`nrow` for the base R implementation.

**h2o.null_deviance**

*Retrieve the null deviance*

**Description**

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

**Usage**

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

**Arguments**

- `object`  
An `H2OModel` or `H2OModelMetrics`
- `train`  
Retrieve the training null deviance
- `valid`  
Retrieve the validation null deviance
- `xval`  
Retrieve the cross-validation null deviance
**h2o.null_dof**  
*Retrieve the null degrees of freedom*

**Description**

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

**Usage**

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

**Arguments**

- `object`  
  An H2OModel or H2OModelMetrics
- `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 H2OClusteringModel object.
- `...`  
  further arguments to be passed on (currently unimplemented)
h2o.num_valid_substrings

-message-of-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

View H2O R Logs

Description
Open existing logs of H2O R POST commands and error responses on local disk. Used primarily for debugging purposes.

Usage
h2o.openLog(type)

Arguments

See Also
h2o.startLogging, h2o.stopLogging, h2o.clearLog

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

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

## End(Not run)
**Description**

The second phase in the data ingestion step.

**Usage**

```r
h2o.parseRaw(data, pattern = "", destination_frame = "", header = NA,
          sep = "", col.names = NULL, col.types = NULL, na.strings = NULL,
          blocking = FALSE, parse_type = NULL, chunk_size = NULL,
          decrypt_tool = NULL, skipped_columns = NULL,
          custom_non_data_line_markers = NULL)
```

**Arguments**

- `data`: An H2OFrame object to be parsed.
- `pattern`: (Optional) Character string containing a regular expression to match file(s) in the folder.
- `destination_frame`: (Optional) The hex key assigned to the parsed file.
- `header`: (Optional) A logical value indicating whether the first row is the column header. If missing, H2O will automatically try to detect the presence of a header.
- `sep`: (Optional) The field separator character. Values on each line of the file are separated by this character. If `sep = " "`, the parser will automatically detect the separator.
- `col.names`: (Optional) An H2OFrame object containing a single delimited line with the column names for the file. If skipped_columns are specified, only list column names of columns that are not skipped.
- `col.types`: (Optional) A vector specifying the types to attempt to force over columns. If skipped_columns are specified, only list column types of columns that are not skipped.
- `na.strings`: (Optional) H2O will interpret these strings as missing.
- `blocking`: (Optional) Tell H2O parse call to block synchronously instead of polling. This can be faster for small datasets but loses the progress bar.
- `parse_type`: (Optional) Specify which parser type H2O will use. Valid types are "ARFF", "XLS", "CSV", "SVMLight"
- `chunk_size`: size of chunk of (input) data in bytes
- `decrypt_tool`: (Optional) Specify a Decryption Tool (key-reference acquired by calling `h2o.decryptionSetup`.
- `skipped_columns`: a list of column indices to be excluded from parsing
- `custom_non_data_line_markers`: (Optional) If a line in imported file starts with any character in given string it will NOT be imported. Empty string means all lines are imported, NULL means that default behaviour for given format will be used
h2o.parseSetup

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, decrypt_tool = NULL, skipped_columns = NULL, custom_non_data_line_markers = 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. If skipped_columns are specified, only list column names of columns that are not skipped.
col.types (Optional) A vector specifying the types to attempt to force over columns. If skipped_columns are specified, only list column types of columns that are not skipped.
na.strings (Optional) H2O will interpret these strings as missing.
parse_type (Optional) Specify which parser type H2O will use. Valid types are "ARFF", "XLS", "CSV", "SVMLight"
chunk_size size of chunk of (input) data in bytes
decrypt_tool (Optional) Specify a Decryption Tool (key-reference acquired by calling h2o.decryptionSetup).
skipped_columns a list of column indices to be excluded from parsing
custom_non_data_line_markers (Optional) If a line in imported file starts with any character in given string it will NOT be imported. Empty string means all lines are imported, NULL means that default behaviour for given format will be used
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 randomForest’s partialPlot when plotting partial dependence the mean response (probabilities) is returned rather than the mean of the log class probability.

**Usage**

```r
h2o.partialPlot(object, data, cols, destination_key, nbins = 20, plot = TRUE, plot_stddev = TRUE, weight_column = -1, include_na = FALSE, user_splits = NULL, col_pairs_2dpdp = NULL, save_to = NULL, row_index = -1)
```

**Arguments**

- `object`: An H2OModel object.
- `data`: An H2OFrame object used for scoring and constructing the plot.
- `cols`: Feature(s) for which partial dependence will be calculated.
- `destination_key`: An key reference to the created partial dependence tables in H2O.
- `nbins`: Number of bins used. For categorical columns make sure the number of bins exceeds the level count. If you enable add_missing_NA, the returned length will be nbins+1.
- `plot`: A logical specifying whether to plot partial dependence table.
- `plot_stddev`: A logical specifying whether to add std err to partial dependence plot.
- `weight_column`: A string denoting which column of data should be used as the weight column.
- `include_na`: A logical specifying whether missing value should be included in the Feature values.
- `user_splits`: A two-level nested list containing user defined split points for pdp plots for each column. If there are two columns using user defined split points, there should be two lists in the nested list. Inside each list, the first element is the column name followed by values defined by the user.
- `col_pairs_2dpdp`: A two-level nested list like this: `col_pairs_2dpdp = list(c("col1_name", "col2_name"), c("col1_name", "col3_name"), ...)` where a 2D partial plots will be generated for col1_name, col2_name pair, for col1_name, col3_name pair and whatever other pairs that are specified in the nested list.
- `save_to`: Fully qualified prefix of the image files the resulting plots should be saved to, e.g. `/home/user/pdp`. Plots for each feature are saved separately in PNG format, each file receives a suffix equal to the corresponding feature name, e.g. `/home/user/pdp_AGE.png`. If the files already exists, they will be overridden. Files are only saves if plot = TRUE (default).
**h2o.performance**

Row for which partial dependence will be calculated instead of the whole input frame.

**Value**

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

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate[, "CAPSULE"] <- as.factor(prostate[, "CAPSULE"])
prostate[, "RACE"] <- as.factor(prostate[, "RACE"])
prostate_gbm <- h2o.gbm(x = c("AGE", "RACE"),
                      y = "CAPSULE",
                      training_frame = prostate,
                      ntree = 10,
                      max_depth = 5,
                      learn_rate = 0.1)
h2o.partialPlot(object = prostate_gbm, data = prostate, cols = c("AGE", "RACE"))
## End(Not run)
```

---

**h2o.performance**

*Model Performance Metrics in H2O*

**Description**

Given a trained h2o model, compute its performance on the given dataset. However, if the dataset does not contain the response/target column, no performance will be returned. Instead, a warning message will be printed.

**Usage**

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

**Arguments**

- **model**
  - An `H2OModel` object
- **newdata**
  - An H2OFrame. 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: [https://0xdata.atlassian.net/browse/TN-9](https://0xdata.atlassian.net/browse/TN-9)
h2o.pivot

Pivot a frame

Description

Pivot the frame designated by the three columns: index, column, and value. Index and column should be of type enum, int, or time. For cases of multiple indexes for a column label, the aggregation method is to pick the first occurrence in the data frame.

Usage

h2o.pivot(x, index, column, value)

Arguments

x an H2OFrame
index the column where pivoted rows should be aligned on
column the column to pivot
value values of the pivoted table

Value

An H2OFrame with columns from the columns arg, aligned on the index arg, with values from values arg.

Examples

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

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

## End(Not run)
**h2o.prcomp**

Principal component analysis of an H2O data frame

**Description**

Principal components analysis of an H2O data frame using the power method to calculate the singular value decomposition of the Gram matrix.

**Usage**

```r
h2o.prcomp(training_frame, x, model_id = NULL, validation_frame = NULL, 
ignore_const_cols = TRUE, score_each_iteration = FALSE, 
transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"), 
pca_method = c("GramSVD", "Power", "Randomized", "GLRM"), 
pca_impl = c("MTJ_EVD_DENSEMATRIX", "MTJ_EVD_SYMMATRIX", 
"MTJ_SVD_DENSEMATRIX", "JAMA"), k = 1, max_iterations = 1000, 
use_all_factor_levels = FALSE, compute_metrics = TRUE, 
impute_missing = FALSE, seed = -1, max_runtime_secs = 0, 
export_checkpoints_dir = NULL)
```

**Arguments**

- **training_frame**: Id of the training data frame.
- **x**: A vector containing the character names of the predictors in the model.
- **model_id**: Destination id for this model; auto-generated if not specified.
- **validation_frame**: Id of the validation data frame.
- **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**: Specify the algorithm to use for computing the principal components: GramSVD - uses a distributed computation of the Gram matrix, followed by a local SVD; Power - computes the SVD using the power iteration method (experimental); Randomized - uses randomized subspace iteration method; GLRM - fits a generalized low-rank model with L2 loss function and no regularization and solves for the SVD using local matrix algebra (experimental) Must be one of: "GramSVD", "Power", "Randomized", "GLRM". Defaults to GramSVD.
h2o.predict

**Description**

Predict on an H2O Model

**Value**

an object of class H2ODimReductionModel.

**References**


**See Also**

h2o.svd, h2o.glm

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
h2o.pcomp(training_frame = australia, k = 8, transform = "STANDARDIZE")

## End(Not run)
```

---

**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.

**export_checkpoints_dir**

Automatically export generated models to this directory.
Usage

h2o.predict(object, newdata, ...)

Arguments

object  a fitted model object for which prediction is desired.
newdata An H2OFrame object in which to look for variables with which to predict.
...    additional arguments to pass on.

Value

Returns an H2OFrame object with probabilites and default predictions.

Description

Provides the method h2o.predict with which you can predict a MOJO or POJO Jar model from R.

Usage

h2o.predict_json(model, json, genmodelpath, labels, classpath, javaoptions)

Arguments

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

Value

Returns an object with the prediction result

Examples

```r
## Not run:
library(h2o)
h2o.predict_json(~/GBM_model_python_1473313897851_6.zip, '{"C7":1}')
h2o.predict_json(~/GBM_model_python_1473313897851_6.zip, '{"C7":1}', c('.', "lib"))
## End(Not run)
```
h2o.print

Print An H2OFrame

Description

Print An H2OFrame

Usage

h2o.print(x, n = 6L)

Arguments

x

An H2OFrame object

n

An (Optional) A 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

Return the product of all the values present in its arguments.

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 `H2ODimReductionModel` 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.glrm` for making an `H2ODimReductionModel`.

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_glrm <- h2o.glrm(training_frame = iris_hf, k = 4, loss = "Quadratic",
                      multi_loss = "Categorical", max_iterations = 1000)
iris_parch <- h2o.proj_archetypes(iris_glrm, iris_hf)
head(iris_parch)
## End(Not run)
```
h2o.pr_auc

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

Usage

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

Arguments

object
An H2OBinomialMetrics object.

train
Retrieve the training pr_auc

valid
Retrieve the validation pr_auc

xval
Retrieve the cross-validation pr_auc

See Also

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

Examples

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

h2o.psvm

Trains a Support Vector Machine model on an H2O dataset

Description

Alpha version. Supports only binomial classification problems.
h2o.psvm

Usage

h2o.psvm(x, y, training_frame, model_id = NULL,
validation_frame = NULL, ignore_const_cols = TRUE, hyper_param = 1,
kernel_type = c("gaussian"), gamma = -1, rank_ratio = -1,
positive_weight = 1, negative_weight = 1,
disable_training_metrics = TRUE, sv_threshold = 1e-04,
fact_threshold = 1e-05, feasible_threshold = 0.001,
surrogate_gap_threshold = 0.001, mu_factor = 10,
max_iterations = 200, seed = -1)

Arguments

x (Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
y The name or column index of the response variable in the data. The response must be either a binary categorical/factor variable or a numeric variable with values -1/1 (for compatibility with SVMlight format).
training_frame Id of the training data frame.
model_id Destination id for this model; auto-generated if not specified.
validation_frame Id of the validation data frame.
ignore_const_cols Logical. Ignore constant columns. Defaults to TRUE.
hyper_param Penalty parameter C of the error term Defaults to 1.
kernel_type Type of used kernel Must be one of: "gaussian". Defaults to gaussian.
gamma Coefficient of the kernel (currently RBF gamma for gaussian kernel. -1 means 1/#features) Defaults to -1.
rank_ratio Desired rank of the ICF matrix expressed as an ration of number of input rows (-1 means use sqrt(#rows)). Defaults to -1.
positive_weight Weight of positive (+1) class of observations Defaults to 1.
negative_weight Weight of positive (-1) class of observations Defaults to 1.
disable_training_metrics Logical. Disable calculating training metrics (expensive on large datasets) Defaults to TRUE.
sv_threshold Threshold for accepting a candidate observation into the set of support vectors Defaults to 0.0001.
fact_threshold Convergence threshold of the Incomplete Cholesky Factorization (ICF) Defaults to 1e-05.
feasible_threshold Convergence threshold for primal-dual residuals in the IPM iteration Defaults to 0.001.
surrogate_gap_threshold Feasibility criterion of the surrogate duality gap (eta) Defaults to 0.001.
mu_factor Increasing factor mu Defaults to 10.
max_iterations Maximum number of iteration of the algorithm Defaults to 200.
seed Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
h2o.quantile

Quantiles of H2O Frames.

Description

Obtain and display quantiles for H2O parsed data.

Usage

h2o.quantile(x, probs = c(0.001, 0.01, 0.1, 0.25, 0.333, 0.5, 0.667, 
0.75, 0.9, 0.99, 0.999), combine_method = c("interpolate", "average", 
"avg", "low", "high"), weights_column = NULL, ...)

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 inter-
polation. E.g., If method is "lo", then it will take the lo value of the quantile. 
Abbreviations for average, low, and high are acceptable (avg, lo, hi).
weights_column
(Optional) String name of the observation weights column in x or an H2OFrame 
object with a single numeric column of observation weights.
...
Further arguments passed to or from other methods.

Details

quantile.H2OFrame, a method for the quantile generic. Obtain and return quantiles for an 
H2OFrame object.

Value

A vector describing the percentiles at the given cutoffs for the H2OFrame object.

Examples

## Not run:
# Request quantiles for an H2O parsed data set:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
# Request quantiles for a subset of columns in an H2O parsed data set
quantile(prostate[,3])
for(i in 1:ncol(prostate))
  quantile(prostate[,i])

## End(Not run)
**h2o.r2**  
*Retrieve the R2 value*

**Description**

Retrieves the R2 value from an H2O model. Will return R² 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**

```r
h2o.r2(object, train = FALSE, valid = FALSE, xval = FALSE)
```

**Arguments**

- `object`: An H2OModel 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**

```r
## Not run:
library(h2o)

h <- h2o.init()
fr <- as.h2o(iris)
m <- h2o.glm(x = 2:5, y = 1, training_frame = fr)
h2o.r2(m)
## End(Not run)
```

---

**h2o.randomForest**  
*Build a Random Forest model*

**Description**

Builds a Random Forest model on an H2OFrame.
Usage

```r
h2o.randomForest(x, y, training_frame, model_id = NULL,
    validation_frame = NULL, nfolds = 0,
    keep_cross_validation_models = TRUE,
    keep_cross_validation_predictions = FALSE,
    keep_cross_validation_fold_assignment = FALSE,
    score_each_iteration = FALSE, score_tree_interval = 0,
    fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"),
    fold_column = NULL, ignore_const_cols = TRUE, offset_column = NULL,
    weights_column = NULL, balance_classes = FALSE,
    class_sampling_factors = NULL, max_after_balance_size = 5,
    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", "AUCPR", "mean_per_class_error",
        "custom", "custom_increasing"), stopping_tolerance = 0.001,
    max_runtime_secs = 0, seed = -1, build_tree_one_node = FALSE,
    mtries = 0, sample_rate = 0.6320000291,
    sample_rate_per_class = NULL, binomial_double_trees = FALSE,
    checkpoint = NULL, col_sample_rate_change_per_level = 1,
    col_sample_rate_per_tree = 1, min_split_improvement = 1e-05,
    histogram_type = c("AUTO", "UniformAdaptive", "Random",
        "QuantilesGlobal", "RoundRobin"), categorical_encoding = c("AUTO",
        "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen",
        "LabelEncoder", "SortByResponse", "EnumLimited"),
    calibrate_model = FALSE, calibration_frame = NULL,
    distribution = c("AUTO", "bernoulli", "multinomial", "gaussian",
        "poisson", "gamma", "tweedie", "laplace", "quantile", "huber"),
    custom_metric_func = NULL, export_checkpoints_dir = NULL,
    check_constant_response = TRUE, verbose = FALSE)
```

Arguments

- **x** (Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
- **y** The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
- **training_frame** Id of the training data frame.
- **model_id** Destination id for this model; auto-generated if not specified.
- **validation_frame** Id of the validation data frame.
- **nfolds** Number of folds for K-fold cross-validation (0 to disable or >= 2). Defaults to 0.
- **keep_cross_validation_models** Logical. Whether to keep the cross-validation models. Defaults to TRUE.
- **keep_cross_validation_predictions** Logical. Whether to keep the predictions of the cross-validation models. Defaults to FALSE.
keep_cross_validation_fold_assignment
   Logical. Whether to keep the cross-validation fold assignment. Defaults to FALSE.

score_each_iteration
   Logical. Whether to score during each iteration of model training. Defaults to FALSE.

score_tree_interval
   Score the model after every so many trees. Disabled if set to 0. Defaults to 0.

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

fold_column
   Column with cross-validation fold index assignment per observation.

ignore_const_cols
   Logical. Ignore constant columns. Defaults to TRUE.

offset_column
   Offset column. This argument is deprecated and has no use for Random Forest.

weights_column
   Column with observation weights. Giving some observation a weight of zero is equivalent to excluding it from the dataset; giving an observation a relative weight of 2 is equivalent to repeating that row twice. Negative weights are not allowed. Note: Weights are per-row observation weights and do not increase the size of the data frame. This is typically the number of times a row is repeated, but non-integer values are supported as well. During training, rows with higher weights matter more, due to the larger loss function pre-factor.

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.

ntrees
   Number of trees. Defaults to 50.

max_depth
   Maximum tree depth. Defaults to 20.

min_rows
   Fewest allowed (weighted) observations in a leaf. Defaults to 1.

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^2 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 and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "AUCPR", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.

stopping_tolerance  
Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.

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 (must be > 0.0 and <= 2.0) Defaults to 1.

col_sample_rate_per_tree  
Column sample rate per tree (from 0.0 to 1.0) Defaults to 1.

min_split_improvement  
Minimum relative improvement in squared error reduction for a split to happen Defaults to 1e-05.

histogram_type  
What type of histogram to use for finding optimal split points Must be one of: "AUTO", "UniformAdaptive", "Random", "QuantilesGlobal", "RoundRobin". Defaults to AUTO.
categorical_encoding

Encoding scheme for categorical features. Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "Sort-ByResponse", "EnumLimited". Defaults to AUTO.

calibrate_model

Logical. Use Platt Scaling to calculate calibrated class probabilities. Calibration can provide more accurate estimates of class probabilities. Defaults to FALSE.

calibration_frame

Calibration frame for Platt Scaling

distribution

Distribution. This argument is deprecated and has no use for Random Forest.

custom_metric_func

Reference to custom evaluation function, format: 'language:keyName=funcName'

export_checkpoints_dir

Automatically export generated models to this directory.

check_constant_response

Logical. Check if response column is constant. If enabled, then an exception is thrown if the response column is a constant value. If disabled, then model will train regardless of the response column being a constant value or not. Defaults to TRUE.

verbose

Logical. Print scoring history to the console (Metrics per tree). Defaults to FALSE.

Value

Creates a H2OModel object of the right type.

See Also

predict.H2OModel for prediction

---

h2o.range

Returns a vector containing the minimum and maximum of all the given arguments.

Description

Returns a vector containing the minimum and maximum of all the given arguments.

Usage

h2o.range(x, na.rm = FALSE, finite = FALSE)

Arguments

x

An H2OFrame object.

na.rm

Logical indicating whether missing values should be removed.

finite

Logical indicating if all non-finite elements should be omitted.

See Also

range for the base R implementation.
h2o.rank_within_group_by

This function will add a new column rank where the ranking is produced as follows: 1. sorts the H2OFrame by columns specified in group_by_cols and sort_cols in the directions specified by the ascending for the sort_cols. The sort directions for the group_by_cols are ascending only. 2. A new rank column is added to the frame which will contain a rank assignment performed next. The user can choose to assign a name to this new column. The default name is New_Rank_column. 3. For each groupby groups, a rank is assigned to the row starting from 1, 2, ... to the end of that group. 4. If sort_cols_sorted is TRUE, a final sort on the frame will be performed frame according to the sort_cols and the sort directions in ascending. If sort_cols_sorted is FALSE (by default), the frame from step 3 will be returned as is with no extra sort. This may provide a small speedup if desired.

Usage

h2o.rank_within_group_by(x, group_by_cols, sort_cols, ascending = NULL, new_col_name = "New_Rank_column", sort_cols_sorted = FALSE)

Arguments

x The H2OFrame input to be sorted.
group_by_cols a list of column names or indices to form the groupby groups
sort_cols a list of column names or indices for sorting
ascending a list of Boolean to determine if ascending sort (set to TRUE) is needed for each column in sort_cols (optional). Default is ascending sort for all. To perform descending sort, set value to FALSE
new_col_name new column name for the newly added rank column if specified (optional). Default name is New_Rank_column.
sort_cols_sorted Boolean to determine if the final returned frame is to be sorted according to the sort_cols and sort directions in ascending. Default is FALSE.

The following example is generated by Nidhi Mehta.
h2o.rbind

Combine H2O Datasets by Rows

Description

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

Usage

h2o.rbind(...)
h2o.reconstruct

Reconstruct Training Data via H2O GLRM Model

Description

Reconstruct the training data and impute missing values from the H2O GLRM model by computing the matrix product of X and Y, and transforming back to the original feature space by minimizing each column’s loss function.

Usage

h2o.reconstruct(object, data, reverse_transform = FALSE)

Arguments

- **object**: An H2ODimReductionModel 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.glrm for making an H2ODimReductionModel.

Examples

```r
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_glrm <- h2o.glrm(training_frame = iris_hf, k = 4, transform = "STANDARDIZE",
                      loss = "Quadratic", multi_loss = "Categorical", max_iterations = 1000)
iris_rec <- h2o.reconstruct(iris_glrm, iris_hf, reverse_transform = TRUE)
head(iris_rec)
## End(Not run)
```

h2o.relevel

Reorders levels of an H2O factor, similarly to standard R’s `relevel`.

Description

The levels of a factor are reordered so that the reference level is at level 0, remaining levels are moved down as needed.

Usage

h2o.relevel(x, y)

Arguments

- `x`: factor column in h2o frame
- `y`: reference level (string)

Value

new reordered factor column

Examples

```r
## Not run:
library(h2o)
h2o.init()
# Convert iris dataset to an H2OFrame
iris_hf <- as.h2o(iris)
# Look at current ordering of the Species column levels
h2o.levels(iris_hf["Species"])
# "setosa" "versicolor" "virginica"
# Change the reference level to "virginica"
iris_hf["Species"] <- h2o.relevel(x = iris_hf["Species"], y = "virginica")
# Observe new ordering
h2o.levels(iris_hf["Species"])
# "virginica" "setosa" "versicolor"
```
## h2o.removeAll

**Remove All Objects on the H2O Cluster**

### Description

Removes the data from the h2o cluster, but does not remove the local references. Retains frames and vectors specified in retained_elements argument. Retained keys must be keys of models and frames only. For models retained, training and validation frames are retained as well. Cross validation models of a retained model are NOT retained automatically, those must be specified explicitly.

### Usage

```r
h2o.removeAll(timeout_secs = 0, retained_elements = c())
```

### Arguments

- `timeout_secs` Timeout in seconds. Default is no timeout.
- `retained_elements` Frames and vectors to be retained. Other keys provided are ignored.

### See Also

- `h2o.rm`

### Examples

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

---

## h2o.removeVecs

**Delete Columns from an H2OFrame**

### Description

Delete the specified columns from the H2OFrame. Returns an H2OFrame without the specified columns.

### Usage

```r
h2o.removeVecs(data, cols)
```
h2o.rep_len

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>data</td>
<td>The H2OFrame.</td>
</tr>
<tr>
<td>cols</td>
<td>The columns to remove.</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>an H2O frame</td>
</tr>
<tr>
<td>length.out</td>
<td>non negative integer. The desired length of the output vector.</td>
</tr>
</tbody>
</table>

Value

Creates an H2OFrame of the same type as \( x \)

h2o.residual_deviance

Retrieve the residual deviance

Description

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

Usage

h2o.residual_deviance(object, train = FALSE, valid = FALSE, xval = FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An H2OModel or H2OModelMetrics</td>
</tr>
<tr>
<td>train</td>
<td>Retrieve the training residual deviance</td>
</tr>
<tr>
<td>valid</td>
<td>Retrieve the validation residual deviance</td>
</tr>
<tr>
<td>xval</td>
<td>Retrieve the cross-validation residual deviance</td>
</tr>
</tbody>
</table>
h2o.residual_dof

Retrieve the residual degrees of freedom

Description

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

Usage

h2o.residual_dof(object, train = FALSE, valid = FALSE, xval = FALSE)

Arguments

- object: An H2OModel or H2OModelMetrics
- 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

Delete Objects In H2O

Description

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

Usage

h2o.rm(ids, cascade = TRUE)

Arguments

- ids: The object or hex key associated with the object to be removed or a vector/list of those things.
- cascade: Boolean, if set to TRUE (default), the object dependencies (e.g. submodels) are also removed.

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
- object: An H2OModelMetrics object of the correct type.
- train: Retrieve the training RMSE
- valid: Retrieve the validation RMSE
- xval: Retrieve the cross-validation RMSE

Details
This function only supports H2OBinomialMetrics, H2OMultinomialMetrics, and H2ORegressionMetrics objects.

See Also
h2o.auc for AUC, h2o.mse for RMSE, and h2o.metric for the various threshold metrics. See h2o.performance for creating H2OModelMetrics objects.

Examples
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(prostate_path)
prostate[,2] <- as.factor(prostate[,2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
perf <- h2o.performance(model, prostate)
h2o.rmse(perf)
## End(Not run)
**h2o.rmsle**  
*Retrieve the Root Mean Squared Log Error*

**Description**  
Retrieves the root mean squared log error (RMSLE) value from an H2O model. If "train", "valid", and "xval" parameters are FALSE (default), then the training rmsle value is returned. If more than one parameter is set to TRUE, then a named vector of rmsles are returned, where the names are "train", "valid" or "xval".

**Usage**  
```r  
h2o.rmsle(object, train = FALSE, valid = FALSE, xval = FALSE)  
```

**Arguments**  
- `object`: An H2OModel 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**  
```r  
## Not run:  
library(h2o)  
h <- h2o.init()  
fr <- as.h2o(iris)  
m <- h2o.deeplearning(x = 2:5, y = 1, training_frame = fr)  
h2o.rmsle(m)  
## End(Not run)  
```

**h2o.round**  
*Round doubles/floats to the given number of decimal places.*

**Description**  
Round doubles/floats to the given number of decimal places.

**Usage**  
```r  
h2o.round(x, digits = 0)  
```  
```r  
round(x, digits = 0)  
```
**h2o.rstrip**

**Strip set from right**

**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**

```r
h2o.rstrip(x, set = " ")
```

**Arguments**

- `x`: The column whose strings should be rstrip-ed.
- `set`: string of characters to be removed

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
string_to_rstrip <- as.h2o("1234567890")
rstrip_string <- h2o.rstrip(string_to_rstrip, "890") #Remove "890"

## End(Not run)
```

**h2o.runif**

**Produce a Vector of Random Uniform Numbers**

**Description**

Creates a vector of random uniform numbers equal in length to the length of the specified H2O dataset.

**Usage**

```r
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**

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

prostate_train <- prostate[s <= 0.8,]
prostate_test <- prostate[s > 0.8,]
nrow(prostate_train) + nrow(prostate_test)

## End(Not run)
```

---

**Description**

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

**Usage**

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

**Arguments**

- **object**: an H2OModel 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

```r
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.importFile(path = paste("https://raw.githubusercontent.com/h2oai/h2o-2/master/smalldata/logreg/prostate.csv", sep = "/"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE","RACE","PSA","DCAPS"),
# training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.saveModel(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)
## End(Not run)
```

---

**h2o.saveModelDetails**  
Save an H2O Model Details

**Description**

Save Model Details of an H2O Model in JSON Format

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an <strong>H2OModel</strong> object.</td>
</tr>
<tr>
<td>path</td>
<td>string indicating the directory the model details will be written to.</td>
</tr>
<tr>
<td>force</td>
<td>logical, indicates how to deal with files that already exist.</td>
</tr>
</tbody>
</table>

**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**

```r
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.uploadFile(path = system.file("extdata", "prostate.csv", package = "h2o"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE","RACE","PSA","DCAPS"),
# training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.saveModelDetails(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)
## End(Not run)
```
### h2o.saveMojo

Save an H2O Model Object as Mojo to Disk

**Description**

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

**Usage**

\[
\text{h2o.saveMojo(object, path = "", force = FALSE)}
\]

**Arguments**

- **object**: an H2OModel object.
- **path**: string indicating the directory the model will be written to.
- **force**: logical, indicates how to deal with files that already exist.

**Details**

MOJO will download as a zip file. In the case of existing files `force = TRUE` will overwrite the file. Otherwise, the operation will fail.

**See Also**

- `h2o.saveModel` for saving a model to disk as a binary object.

**Examples**

```r
## Not run:
# library(h2o)
# h2o.init()
# prostate <- h2o.uploadFile(path = system.file("extdata", "prostate.csv", package="h2o"))
# prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE","RACE","PSA","DCAPS"),
# training_frame = prostate, family = "binomial", alpha = 0.5)
# h2o.saveMojo(object = prostate_glm, path = "/Users/UserName/Desktop", force = TRUE)
## End(Not run)
```

### h2o.scale

Scaling and Centering of an H2OFrame

**Description**

Centers and/or scales the columns of an H2O dataset.

**Usage**

\[
\text{h2o.scale(x, center = TRUE, scale = TRUE, inplace = FALSE)}
\]
Arguments

- x: An H2OFrame object.
- center: either a logical value or numeric vector of length equal to the number of columns of x.
- scale: either a logical value or numeric vector of length equal to the number of columns of x.
- inplace: a logical values indicating whether directly overwrite original data (disabled by default). Exposed for backwards compatibility (prior versions of this functions were always doing an inplace update).

Examples

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

# Scale and center all the numeric columns in iris data set
iris_scaled <- h2o.scale(iris_hf[, 1:4])
## End(Not run)
```

h2o.scoreHistory

Retrieve Model Score History

Description

Retrieve Model Score History

Usage

h2o.scoreHistory(object)

Arguments

- object: An H2OModel object.

h2o.sd

Standard Deviation of a column of data.

Description

Obtain the standard deviation of a column of data.

Usage

h2o.sd(x, na.rm = FALSE)

sd(x, na.rm = FALSE)
Arguments

x  An H2OFrame object.
na.rm  logical. Should missing values be removed?

See Also

h2o.var for variance, and sd for the base R implementation.

Examples

## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
sd(prostate$AGE)
## End(Not run)

---

h2o.sdev  

Retrieve the standard deviations of principal components

Description

Retrieve the standard deviations of principal components

Usage

h2o.sdev(object)

Arguments

object  An H2ODimReductionModel object.

---

h2o.setLevels  

Set Levels of H2O Factor Column

Description

Works on a single categorical vector. New domains must be aligned with the old domains. This call has SIDE EFFECTS and mutates the column in place (change of the levels will also affect all the frames that are referencing this column). If you want to make a copy of the column instead, use parameter in.place = FALSE.

Usage

h2o.setLevels(x, levels, in.place = TRUE)
Arguments

x  A single categorical column.
levels  A character vector specifying the new levels. The number of new levels must match the number of old levels.
in.place  Indicates whether new domain will be directly applied to the column (in place change) or if a copy of the column will be created with the given domain levels.

Examples

## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
new.levels <- c("setosa", "versicolor", "caroliniana")
iris_hf$Species <- h2o.setLevels(iris_hf$Species, new.levels, in.place = FALSE)
h2o.levels(iris_hf$Species)
## End(Not run)

h2o.setTimezone  Set the Time Zone on the H2O cluster

Description

Set the Time Zone on the H2O cluster

Usage

h2o.setTimezone(tz)

Arguments

tz  The desired timezone.

h2o.set_s3_credentials  Creates a new Amazon S3 client internally with specified credentials.

Description

There are no validations done to the credentials. Incorrect credentials are thus revealed with first S3 import call.

Usage

h2o.set_s3_credentials(secretKeyId, secretAccessKey)

Arguments

secretKeyId  Amazon S3 Secret Key ID (provided by Amazon)
secretAccessKey  Amazon S3 Secret Access Key (provided by Amazon)
**h2o.show_progress**  
*Enable Progress Bar*

**Description**  
Enable Progress Bar

**Usage**  
```r
h2o.show_progress()
```

**h2o.shutdown**  
*Shut Down H2O Instance*

**Description**  
Shut down the specified instance. All data will be lost.

**Usage**  
```r
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
h2o.signif

Examples

# Don't run automatically to prevent accidentally shutting down a cluster
## Not run:
library(h2o)
h2o.init()
h2o.shutdown()

## End(Not run)

h2o.signif

Round doubles/floats to the given number of significant digits.

Description

Round doubles/floats to the given number of significant digits.

Usage

h2o.signif(x, digits = 6)
signif(x, digits = 6)

Arguments

x An H2OFrame object.
digits Number of significant digits to round doubles/floats.

See Also

signif for the base R implementation.

h2o.sin

Compute the sine of x

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**

**Skewness of a column**

**Description**

Obtain the skewness of a column of a parsed H2O data object.

**Usage**

```r
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**

```r
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
h2o.skewness(prostate$AGE)
## End(Not run)
```

---

**h2o.splitFrame**

**Split an H2O Data Set**

**Description**

Split an existing H2O data set according to user-specified ratios. The number of subsets is always 1 more than the number of given ratios. Note that this does not give an exact split. H2O is designed to be efficient on big data using a probabilistic splitting method rather than an exact split. For example, when specifying a split of 0.75/0.25, H2O will produce a test/train split with an expected value of 0.75/0.25 rather than exactly 0.75/0.25. On small datasets, the sizes of the resulting splits will deviate from the expected value more than on big data, where they will be very close to exact.

**Usage**

```r
h2o.splitFrame(data, ratios = 0.75, destination_frames, seed = -1)
```
h2o.sqrt

Compute the square root of \( x \)

**Description**

Compute the square root of \( x \)

**Usage**

h2o.sqrt(x)

**Arguments**

\( x \) 

An H2OFrame object.

**See Also**

`sqrt` for the base R implementation.

---

**Arguments**

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

**Value**

Returns a list of split H2OFrame’s

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
iris_hf <- as.h2o(iris)
iris_split <- h2o.splitFrame(iris_hf, ratios = c(0.2, 0.5))
head(iris_split[[1]])
summary(iris_split[[1]])
## End(Not run)
```
h2o.stackedEnsemble  Builds a Stacked Ensemble

Description

Build a stacked ensemble (aka. Super Learner) using the H2O base learning algorithms specified by the user.

Usage

h2o.stackedEnsemble(x, y, training_frame, model_id = NULL, validation_frame = NULL, blending_frame = NULL, base_models = list(), metalearner_algorithm = c("AUTO", "glm", "gbm", "drf", "deeplearning"), metalearner_nfolds = 0, metalearner_fold_assignment = c("AUTO", "Random", "Modulo", "Stratified"), metalearner_fold_column = NULL, metalearner_params = NULL, seed = -1, keep_levelone_frame = FALSE, export_checkpoints_dir = NULL)

Arguments

x  (Optional). A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used. Training frame is used only to compute ensemble training metrics.

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

training_frame  Id of the training data frame.

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

validation_frame  Id of the validation data frame.

blending_frame  Frame used to compute the predictions that serve as the training frame for the metalearner (triggers blending mode if provided)

base_models  List of models (or model ids) to ensemble/stack together. If not using blending frame, then models must have been cross-validated using nfolds > 1, and folds must be identical across models.

metalearner_algorithm  Type of algorithm to use as the metalearner. Options include 'AUTO' (GLM with non negative weights; if validation_frame is present, a lambda search is performed), 'glm' (GLM with default parameters), 'gbm' (GBM with default parameters), 'drf' (Random Forest with default parameters), or 'deeplearning' (Deep Learning with default parameters). Must be one of: "AUTO", "glm", "gbm", "drf", "deeplearning". Defaults to AUTO.

metalearner_nfolds  Number of folds for K-fold cross-validation of the metalearner algorithm (0 to disable or >= 2). Defaults to 0.
### Description

Begin logging H2O R POST commands and error responses to local disk. Used primarily for debugging purposes.

### Usage

```r
h2o.startLogging(file)
```

### Arguments

- **file**: a character string name for the file, automatically generated

### See Also

- `h2o.stopLogging`, `h2o.clearLog`, `h2o.openLog`
Examples

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

---

**h2o.std_coef_plot**  
Plot Standardized Coefficient Magnitudes

**Description**
Plot a GLM model’s standardized coefficient magnitudes.

**Usage**

```r
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**

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

prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[,2] <- as.factor(prostate[,2])
prostate_glm <- h2o.glm(y = "CAPSULE", x = c("AGE","RACE","PSA","DCAPS"),
                        training_frame = prostate, family = "binomial",
                        nfolds = 0, alpha = 0.5, lambda_search = FALSE)
h2o.std_coef_plot(prostate_glm)
## End(Not run)
```
## h2o.stopLogging

**Stop Writing H2O R Logs**

**Description**

Halt logging of H2O R POST commands and error responses to local disk. Used primarily for debugging purposes.

**Usage**

```
h2o.stopLogging()
```

**See Also**

`h2o.startLogging`, `h2o.clearLog`, `h2o.openLog`

**Examples**

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

## h2o.str

**Display the structure of an H2OFrame object**

**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

Description
Compute element-wise string distances between two H2OFrames. Both frames need to have the same shape (N x M) and only contain string/factor columns. Return a matrix (H2OFrame) of shape N x M.

Usage
h2o.stringdist(x, y, method = c("lv", "lcs", "qgram", "jaccard", "jw", "soundex"), compare_empty = TRUE)

Arguments
- x: An H2OFrame
- y: A comparison H2OFrame
- method: A string identifier indicating what string distance measure to use. Must be one of: "lv" - Levenshtein distance "lcs" - Longest common substring distance "qgram" - q-gram distance "jaccard" - Jaccard distance between q-gram profiles "jw" - Jaro, or Jaro-Winker distance "soundex" - Distance based on soundex encoding
- compare_empty: if set to FALSE, empty strings will be handled as NaNs

Examples
## Not run:
h2o.init()
x <- as.h2o(c("Martha", "Dwayne", "Dixon"))
y <- as.character(as.h2o(c("Marhta", "Duane", "Dicksonx")))
h2o.stringdist(x, y, method = "jw")
## End(Not run)

h2o.strsplit

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

```r
## Not run:
library(h2o)
h2o.init()
string_to_split <- as.h2o("Split at every character.")
split_string <- h2o.strsplit(string_to_split,"")
## End(Not run)
```

---

### 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

```r
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

```r
## Not run:
library(h2o)
h2o.init()
string_to_sub <- as.h2o("r tutorial")
sub_string <- h2o.sub("r ", "H2O ", string_to_sub)
## End(Not run)
```
h2o.substring  Substring

Description
Returns a copy of the target column that is a substring at the specified start and stop indices, inclusive. If the stop index is not specified, then the substring extends to the end of the original string. If start is longer than the number of characters in the original string, or is greater than stop, an empty string is returned. Negative start is coerced to 0.

Usage
h2o.substring(x, start, stop = "[]")
h2o.substr(x, start, stop = "[]")

Arguments
x The column on which to operate.
start The index of the first element to be included in the substring.
stop Optional, The index of the last element to be included in the substring.

Examples
## Not run:
library(h2o)
h2o.init()
string_to_substring <- as.h2o("1234567890")
substr <- h2o.substring(string_to_substring, 2) #Get substring from second index onwards
## End(Not run)

h2o.sum  Compute the frame’s sum by-column (or by-row).

Description
Compute the frame’s sum by-column (or by-row).

Usage
h2o.sum(x, na.rm = FALSE, axis = 0, return_frame = FALSE)

Arguments
x An H2OFrame object.
na.rm logical, indicating whether missing values should be removed.
axis An int that indicates whether to do down a column (0) or across a row (1). For row or column sums, the return_frame parameter must be TRUE.
return_frame A boolean that indicates whether to return an H2O frame or one single aggregated value. Default is FALSE.
h2o.summary

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

## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path)
summary(prostate)
summary(prostate$GLEASON)
summary(prostate[,4:6])
summary(prostate, exact_quantiles=TRUE)

## End(Not run)
Singular value decomposition of an H2O data frame using the power method

Usage

h2o.svd(training_frame, x, destination_key, model_id = NULL, validation_frame = NULL, ignore_const_cols = TRUE, score_each_iteration = FALSE, transform = c("NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE"), svd_method = c("GramSVD", "Power", "Randomized"), nv = 1, max_iterations = 1000, seed = -1, keep_u = TRUE, u_name = NULL, use_all_factor_levels = TRUE, max_runtime_secs = 0, export_checkpoints_dir = NULL)

Arguments

training_frame  Id of the training data frame.
x  A vector containing the character names of the predictors in the model.
destination_key  (Optional) The unique key assigned to the resulting model. Automatically generated if none is provided.
model_id  Destination id for this model; auto-generated if not specified.
validation_frame  Id of the validation data frame.
ignore_const_cols  Logical. Ignore constant columns. Defaults to TRUE.
score_each_iteration  Logical. Whether to score during each iteration of model training. Defaults to FALSE.
transform  Transformation of training data Must be one of: "NONE", "STANDARDIZE", "NORMALIZE", "DEMEAN", "DESCALE". Defaults to NONE.
svd_method  Method for computing SVD (Caution: Randomized is currently experimental and unstable) Must be one of: "GramSVD", "Power", "Randomized". Defaults to GramSVD.
nv  Number of right singular vectors Defaults to 1.
max_iterations  Maximum iterations Defaults to 1000.
seed  Seed for random numbers (affects certain parts of the algo that are stochastic and those might or might not be enabled by default). Defaults to -1 (time-based random number).
keep_u  Logical. Save left singular vectors? Defaults to TRUE.
u_name  Frame key to save left singular vectors
use_all_factor_levels  Logical. Whether first factor level is included in each categorical expansion. Defaults to TRUE.
max_runtime_secs
Maximum allowed runtime in seconds for model training. Use 0 to disable.
Defaults to 0.

export_checkpoints_dir
Automatically export generated models to this directory.

Value
an object of class H2ODimReductionModel.

References

Examples
## Not run:
library(h2o)
h2o.init()
australia_path <- system.file("extdata", "australia.csv", package = "h2o")
australia <- h2o.uploadFile(path = australia_path)
h2o.svd(training_frame = australia, nv = 8)

## End(Not run)
Examples

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

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

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

## End(Not run)
```

---

**h2o.tabulate**

### Tabulation between Two Columns of an H2OFrame

**Description**

Simple Co-Occurrence based tabulation of X vs Y, where X and Y are two Vecs in a given dataset. Uses histogram of given resolution in X and Y. Handles numerical/categorical data and missing values. Supports observation weights.

**Usage**

```r
h2o.tabulate(data, x, y, weights_column = NULL, nbins_x = 50, nbins_y = 50)
```

**Arguments**

- `data` : An H2OFrame object.
- `x` : predictor column
- `y` : response column
- `weights_column` : (optional) observation weights column
- `nbins_x` : number of bins for predictor column
- `nbins_y` : number of bins for response column

**Value**

Returns two TwoDimTables of 3 columns each: count_table: X Y counts, response_table: X meanY counts.
**Examples**

```r
## Not run:
library(h2o)
h2o.init()
df <- as.h2o(iris)
tab <- h2o.tabulate(data = df, x = "Sepal.Length", y = "Petal.Width",
                   weights_column = NULL, nbins_x = 10, nbins_y = 10)
plot(tab)
## End(Not run)
```

---

**h2o.tan**  
*Compute the tangent of x*

**Description**

Compute the tangent of x

**Usage**

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

**Arguments**

- `x`  
  An H2OFrame object.

**See Also**

- `tan` for the base R implementation.

---

**h2o.tanh**  
*Compute the hyperbolic tangent of x*

**Description**

Compute the hyperbolic tangent of x

**Usage**

```r
h2o.tanh(x)
```

**Arguments**

- `x`  
  An H2OFrame object.

**See Also**

- `tanh` for the base R implementation.
**Description**

Transformation of a categorical variable with a mean value of the target variable

**Usage**

```r
h2o.targetencoder(x, y, training_frame, blending = FALSE, k = 20,
                    f = 10, data_leakage_handling = c("None", "KFold", "LeaveOneOut"),
                    model_id = NULL, fold_column = NULL)
```

**Arguments**

- **x**: (Optional) A vector containing the names or indices of the predictor variables to use in building the model. If x is missing, then all columns except y are used.
- **y**: The name or column index of the response variable in the data. The response must be either a numeric or a categorical/factor variable. If the response is numeric, then a regression model will be trained, otherwise it will train a classification model.
- **training_frame**: Id of the training data frame.
- **blending**: Logical. Blending enabled/disabled. Defaults to FALSE.
- **k**: Inflection point. Used for blending (if enabled). Blending is to be enabled separately using the 'blending' parameter. Defaults to 20.
- **f**: Smoothing. Used for blending (if enabled). Blending is to be enabled separately using the 'blending' parameter. Defaults to 10.
- **data_leakage_handling**: Data leakage handling strategy. Default to None. Must be one of: "None", "KFold", "LeaveOneOut". Defaults to None.
- **model_id**: Destination id for this model; auto-generated if not specified.
- **fold_column**: Column with cross-validation fold index assignment per observation.

**Examples**

```r
## Not run:
# library(h2o)
# h2o.init()
#
# Create a target encoder
# target_encoder <- h2o.targetencoder(training_frame = data, encoded_columns= encoded_columns,
# target_column = "survived", fold_column = "pclass", data_leakage_handling = "KFold")
#
# Apply the Target Encoder transformation
# encoded_data <- h2o.transform(target_encoder, data)

## End(Not run)
```
h2o.target_encode_apply

Apply Target Encoding Map to Frame

Description


Usage

h2o.target_encode_apply(data, x, y, target_encode_map, holdout_type, fold_column = NULL, blended_avg = TRUE, noise_level = NULL, seed = -1)

Arguments

data An H2OFrame object with which to apply the target encoding map.

x A list containing the names or indices of the variables to encode. A target encoding column will be created for each element in the list. Items in the list can be multiple columns. For example, if 'x = list(c("A"), c("B", "C"))', then the resulting frame will have a target encoding column for A and a target encoding column for B & C (in this case, we group by two columns).

y The name or column index of the response variable in the data. The response variable can be either numeric or binary.

target_encode_map A list of H2OFrame objects that is the results of the h2o.target_encode_create function.

holdout_type The holdout type used. Must be one of: "LeaveOneOut", "KFold", "None".

fold_column (Optional) The name or column index of the fold column in the data. Defaults to NULL (no 'fold_column'). Only required if 'holdout_type' = "KFold".

blended_avg Logical. (Optional) Whether to perform blended average.

noise_level (Optional) The amount of random noise added to the target encoding. This helps prevent overfitting. Defaults to 0.01 * range of y.

seed (Optional) A random seed used to generate draws from the uniform distribution for random noise. Defaults to -1.

Value

Returns an H2OFrame object containing the target encoding per record.

See Also

h2o.target_encode_create for creating the target encoding map
h2o.target_encode_create

Create Target Encoding Map

Description

Creates a target encoding map based on group-by columns ('x') and a numeric or binary target column ('y'). Computing target encoding for high cardinality categorical columns can improve performance of supervised learning models. A Target Encoding tutorial is available here: https://github.com/h2oai/h2o-tutorials/blob/master/best-practices/categorical-predictors/target_encoding.md.

Usage

h2o.target_encode_create(data, x, y, fold_column = NULL)

Arguments

data: An H2OFrame object with which to create the target encoding map.
x: A list containing the names or indices of the variables to encode. A target encoding map will be created for each element in the list. Items in the list can be multiple columns. For example, if `x = list(c("A"), c("B", "C"))`, then there will be one mapping frame for A and one mapping frame for B & C (in this case, we group by two columns).
y: The name or column index of the response variable in the data. The response variable can be either numeric or binary.
fold_column: (Optional) The name or column index of the fold column in the data. Defaults to NULL (no 'fold_column').
Value

Returns a list of H2OFrame objects containing the target encoding mapping for each column in 'x'.

See Also

`h2o.target_encode_apply` for applying the target encoding mapping to a frame.

Examples

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

# Get Target Encoding Map on bank-additional-full data with numeric response
data <- h2o.importFile(
  path = "https://s3.amazonaws.com/h2o-public-test-data/smalldata/demos/bank-additional-full.csv")
mapping_age <- h2o.target_encode_create(data = data, x = list(c("job"), c("job", "marital")),
                                         y = "age")
head(mapping_age)

# Get Target Encoding Map on bank-additional-full data with binary response
mapping_y <- h2o.target_encode_create(data = data, x = list(c("job"), c("job", "marital")),
                                       y = "y")
head(mapping_y)

## End(Not run)
```

---

**h2o.target_encode_fit**  
*Deprecated API. Please use h2o.targetencoder model instead.*

Description

Create Target Encoding Map

Usage

```r
h2o.target_encode_fit(frame, x, y, fold_column = NULL)
```

Arguments

- `frame` An H2OFrame object with which to create the target encoding map.
- `x` List of categorical column names or indices that we want apply target encoding to. Case when item in the list is a list of multiple columns itself is not supported for now.
- `y` The name or column index of the response variable in the frame.
- `fold_column` (Optional) The name or column index of the fold column in the frame.
Details

This is an API for a new target encoding implemented in JAVA. Creates a target encoding map based on group-by columns ('x') and binary target column ('y'). Computing target encoding for high cardinality categorical columns can improve performance of supervised learning models.

Value

Returns an object containing the target encoding mapping for each column in 'x'.

See Also

h2o.target_encode_transform for applying the target encoding mapping to a frame.

---

h2o.target_encode_transform

*Deprecated API. Please use h2o.targetencoder model instead.* Trans- form Frame by Target Encoding Map

Description

This is an API for a new target encoding implemented in JAVA. Applies a target encoding map to an H2OFrame object. Computing target encoding for high cardinality categorical columns can improve performance of supervised learning models.

Usage

h2o.target_encode_transform(frame, x, y, target_encode_map, holdout_type, fold_column = NULL, blended_avg = TRUE, inflection_point = 10, smoothing = 20, noise = -1, seed = -1)

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>frame</td>
<td>An H2OFrame object with which to apply the target encoding map.</td>
</tr>
<tr>
<td>x</td>
<td>List of categorical column names or indices that we want apply target encoding to. Case when item in the list is a list of multiple columns itself is not supported for now.</td>
</tr>
<tr>
<td>y</td>
<td>The name or column index of the response variable in the frame.</td>
</tr>
<tr>
<td>target_encode_map</td>
<td>An object that is a result of the calling h2o.target_encode_fit function.</td>
</tr>
<tr>
<td>holdout_type</td>
<td>Supported options:</td>
</tr>
<tr>
<td></td>
<td>1) &quot;kfold&quot; - encodings for a fold are generated based on out-of-fold data.</td>
</tr>
<tr>
<td></td>
<td>2) &quot;loo&quot; - leave one out. Current row’s response value is subtracted from the pre-calculated per-level frequencies.</td>
</tr>
<tr>
<td></td>
<td>3) &quot;none&quot; - we do not holdout anything. Using whole frame for training</td>
</tr>
<tr>
<td>fold_column</td>
<td>(Optional) The name or column index of the fold column in the frame.</td>
</tr>
<tr>
<td>blended_avg</td>
<td>Logical. (Optional) Whether to perform blended average. Defaults to TRUE</td>
</tr>
</tbody>
</table>
inflection_point
(Optional) Parameter for blending. Used to calculate 'lambda'. Determines half of the minimal sample size for which we completely trust the estimate based on the sample in the particular level of categorical variable. Default value is 10.

smoothing
(Optional) Parameter for blending. Used to calculate 'lambda'. Controls the rate of transition between the particular level’s posterior probability and the prior probability. For smoothing values approaching infinity it becomes a hard threshold between the posterior and the prior probability. Default value is 20.

noise
(Optional) The amount of random noise added to the target encoding. This helps prevent overfitting. Defaults to 0.01 * range of y.

seed
(Optional) A random seed used to generate draws from the uniform distribution for random noise. Defaults to -1.

Value

Returns an H2OFrame object containing the target encoding per record.

See Also

h2o.target_encode_fit for creating the target encoding map

Description

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

Usage

h2o.toFrame(word2vec)

Arguments

word2vec
A word2vec model.

Examples

## Not run:
h2o.init()

# Build a dummy word2vec model
data <- as.character(as.h2o(c("a", "b", "a")))
w2v_model <- h2o.word2vec(data, sent_sample_rate = 0, min_word_freq = 0, epochs = 1, vec_size = 2)

# Transform words to vectors and return average vector for each sentence
h2o.toFrame(w2v_model) # -> Frame made of 2 rows and 2 columns

## End(Not run)
h2o.tokenize  

**Tokenize String**

**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**

```r
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**

```r
## Not run:
library(h2o)
h2o.init()
string_to_tokenize <- as.h2o("Split at every character and tokenize.")
tokenize_string <- h2o.tokenize(as.character(string_to_tokenize), "]")
## End(Not run)
```

---

h2o.tolower  

**Convert strings to lowercase**

**Description**

Convert strings to lowercase

**Usage**

```r
h2o.tolower(x)
```

**Arguments**

- `x`  
An H2OFrame object whose strings should be lower cased

**Value**

An H2OFrame with all entries in lowercase format
Examples

```r
## Not run:
library(h2o)
h2o.init()
string_to_lower <- as.h2o("ABCDE")
lowered_string <- h2o.tolower(string_to_lower)
## End(Not run)
```

### Description

Extract the top N percent of values of a column and return it in a H2OFrame.

### Usage

```r
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

---

### Description

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

### Usage

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

### Arguments

- `object`: An H2OClusteringModel 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  
Get the total within cluster sum of squares.

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

Usage
h2o.tot_withinss(object, train = FALSE, valid = FALSE, xval = FALSE)

Arguments
object  
An H2OClusteringModel 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  
Convert strings to uppercase

Description
Convert strings to uppercase

Usage
h2o.toupper(x)

Arguments
x  
An H2OFrame object whose strings should be upper cased

Value
An H2OFrame with all entries in uppercase format

Examples
## Not run:
library(h2o)
h2o.init()
string_to_upper <- as.h2o("abcde")
upper_string <- h2o.toupper(string_to_upper)

## End(Not run)
### h2o.transform

**Description**

Use H2O Transformation model and apply the underlying transformation

**Usage**

```r
h2o.transform(model, ...)
```

**Arguments**

- `model` A trained model representing the transformation strategy
- `...` Transformation model-specific parameters

**Value**

Returns an H2OFrame object with data transformed.

### h2o.transform,H2OTargetEncoderModel-method

**Description**

Applies target encoding to a given dataset

**Usage**

```r
## S4 method for signature 'H2OTargetEncoderModel'

h2o.transform(model, data,
              data_leakage_handling = NULL, use_blending = NULL,
              inflection_point = -1, smoothing = -1)
```

**Arguments**

- `model` A trained model representing the transformation strategy
- `data` An H2OFrame with data to be transformed
- `data_leakage_handling` Handling of data leakage. Available options are: "None", "LeaveOneOut", "KFold". Defaults to "None".
- `use_blending` Use blending during the transformation. Respects model settings when not set.
- `inflection_point` Blending parameter. Only effective when blending is enabled. By default, model settings are respected, if not overridden by this setting.
- `smoothing` Blending parameter. Only effective when blending is enabled. By default, model settings are respected, if not overridden by this setting.
Value

Returns an H2OFrame object with data transformed.

Description

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

Usage

```r
## S4 method for signature 'H2OWordEmbeddingModel'

h2o.transform(model, words,
               aggregate_method = c("NONE", "AVERAGE"))
```

Arguments

- `model`: A word2vec model.
- `words`: An H2OFrame made of a single column containing source words.
- `aggregate_method`: Specifies how to aggregate sequences of words. If method is ‘NONE’ then no aggregation is performed and each input word is mapped to a single word-vector. If method is ‘AVERAGE’ then input is treated as sequences of words delimited by NA. Each word of a sequences is internally mapped to a vector and vectors belonging to the same sentence are averaged and returned in the result.

Examples

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

# Build a simple word2vec model
data <- as.character(as.h2o(c("a", "b", "a")))
w2v_model <- h2o.word2vec(data, sent_sample_rate = 0, min_word_freq = 0, epochs = 1, vec_size = 2)

# Transform words to vectors without aggregation
sentences <- as.character(as.h2o(c("b", "c", "a", NA, "b")))
h2o.transform(w2v_model, sentences) # -> 5 rows total, 2 rows NA ("c" is not in the vocabulary)

# Transform words to vectors and return average vector for each sentence
h2o.transform(w2v_model, sentences, aggregate_method = "AVERAGE") # -> 2 rows

## End(Not run)
```
h2o.transform_word2vec

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

Description

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

Usage

h2o.transform_word2vec(word2vec, words, aggregate_method = c("NONE", "AVERAGE"))

Arguments

word2vec A word2vec model.
words An H2OFrame made of a single column containing source words.
aggregate_method Specifies how to aggregate sequences of words. If method is 'NONE' then no aggregation is performed and each input word is mapped to a single word-vector. If method is 'AVERAGE' then input is treated as sequences of words delimited by NA. Each word of a sequences is internally mapped to a vector and vectors belonging to the same sentence are averaged and returned in the result.

Examples

## Not run:
h2o.init()

# Build a dummy word2vec model
data <- as.character(as.h2o(c("a", "b", "a")))
w2v_model <- h2o.word2vec(data, sent_sample_rate = 0, min_word_freq = 0, epochs = 1, vec_size = 2)

# Transform words to vectors without aggregation
sentences <- as.character(as.h2o(c("b", "c", "a", NA, "b")))
h2o.transform(w2v_model, sentences) # -> 5 rows total, 2 rows NA ("c" is not in the vocabulary)

# Transform words to vectors and return average vector for each sentence
h2o.transform(w2v_model, sentences, aggregate_method = "AVERAGE") # -> 2 rows

## End(Not run)

h2o.trim

Trim Space

Description

Trim Space
Usage

h2o.trim(x)

Arguments

x

The column whose strings should be trimmed.

Examples

## Not run:
library(h2o)
h2o.init()
string_to_trim <- as.h2o("r tutorial")
trim_string <- h2o.trim(string_to_trim)
## End(Not run)

h2o.trunc

Truncate 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

H2O Unique

Description

Extract unique values in the column.

Usage

h2o.unique(x)

Arguments

x

An H2OFrame object.
h2o.upload_mojo

**Value**

Returns an H2OFrame object.

**Description**

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

**Usage**

```
h2o.upload_mojo(mojo_local_file_path)
```

**Arguments**

`mojo_local_file_path`

Filesystem path to the model imported

**Value**

Returns H2O Generic Model embedding given MOJO model

**Examples**

```
## Not run:
# Import default Iris dataset as H2O frame
data <- as.h2o(iris)

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

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

# Upload the MOJO from local filesystem and obtain a Generic model
mojo_model <- h2o.upload_mojo(mojo_original_path)

# Perform scoring with the generic model
predictions <- h2o.predict(mojo_model, data)

## End(Not run)
```
**h2o.var**

Variance of a column or covariance of columns.

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

```r
## Not run:
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
var(prostate$AGE)
## End(Not run)
```

**h2o.varimp**

Retrieve the variable importance.

Description

Retrieve the variable importance.

Usage

h2o.varimp(object)

Arguments

- **object**: An H2OModel object.
h2o.varimp_plot

Plot Variable Importances

Description
Plot Variable Importances

Usage
h2o.varimp_plot(model, num_of_features = NULL)

Arguments
- model: A trained model (accepts a trained random forest, GBM, or deep learning model, will use h2o.std_coef_plot for a trained GLM
- num_of_features: The number of features shown in the plot (default is 10 or all if less than 10).

See Also
h2o.std_coef_plot for GLM.

Examples
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(prostate_path)
prostate[,2] <- as.factor(prostate[,2])
model <- h2o.gbm(x = 3:9, y = 2, training_frame = prostate, distribution = "bernoulli")
h2o.varimp_plot(model)

# for deep learning set the variable_importance parameter to TRUE
iris_hf <- as.h2o(iris)
iris_dl <- h2o.deeplearning(x = 1:4, y = 5, training_frame = iris_hf,
variable_importances = TRUE)
h2o.varimp_plot(iris_dl)
## End(Not run)

h2o.varsplits

Retrieve per-variable split information for a given Isolation Forest model. Output will include:
- count: The number of times a variable was used to make a split.
- aggregated_split_ratios: The split ratio is defined as "abs(#left_observations - #right_observations) / #before_split". Even splits (#left_observations approx the same as #right_observations) contribute less to the total aggregated split ratio value for the given feature; highly imbalanced splits (eg. #left_observations » #right_observations) contribute more.
- aggregated_split_depths: The sum of all depths of a variable used to make a split. (If a variable is used on level N of a tree, then it contributes with N to the total aggregate.)
Description

Retrieve per-variable split information for a given Isolation Forest model. Output will include:
- count - The number of times a variable was used to make a split. - aggregated_split_ratios -
  The split ratio is defined as "abs(#left_observations - #right_observations) / #before_split". Even
  splits (#left_observations approx the same as #right_observations) contribute less to the total ag-
  gregated split ratio value for the given feature; highly imbalanced splits (eg. #left_observations »
  #right_observations) contribute more. - aggregated_split_depths - The sum of all depths of a vari-
  able used to make a split. (If a variable is used on level N of a tree, then it contributes with N to the
  total aggregate.)

Usage

h2o.varsplits(object)

Arguments

object An Isolation Forest model represented by H2OModel object.

h2o.week

Convert Milliseconds to Week of Week Year in H2O Datasets

Description

Converts the entries of an H2OFrame object from milliseconds to weeks of the week year (starting
from 1).

Usage

h2o.week(x)

week(x)

## S3 method for class 'H2OFrame'

week(x)

Arguments

x An H2OFrame object.

Value

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

See Also

h2o.month
h2o.weights

Retrieve the respective weight matrix

Description
Retrieve the respective weight matrix

Usage
h2o.weights(object, matrix_id = 1)

Arguments
object  An H2OModel or H2OModelMetrics
matrix_id  An integer, ranging from 1 to number of layers + 1, that specifies the weight matrix to return.

h2o.which
Which indices are TRUE?

Description
Give the TRUE indices of a logical object, allowing for array indices.

Usage
h2o.which(x)

Arguments
x  An H2OFrame object.

Value
Returns an H2OFrame object.

See Also
which for the base R method.

Examples
## Not run:
h2o.init()
iris_hf <- as.h2o(iris)
h2o.which(iris_hf[, 1] == 4.4)
## End(Not run)
**h2o.which_max**

*Which indice contains the max value?*

**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**

*Which index contains the min value?*

**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).
h2o.withinss

Value
Returns an H2OFrame object.

See Also
which.min for the base R method.

---

h2o.withinss Get the Within SS

Description
Get the Within SS

Usage
h2o.withinss(object)

Arguments
- object: An H2OClusteringModel object.

---

h2o.word2vec Trains a word2vec model on a String column of an H2O data frame

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, max_runtime_secs = 0, export_checkpoints_dir = NULL)

Arguments
- training_frame: Id of the training data frame.
- model_id: Destination id for this model; auto-generated if not specified.
- min_word_freq: This will discard words that appear less than <int> times. Defaults to 5.
- word_model: 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

max_runtime_secs
Maximum allowed runtime in seconds for model training. Use 0 to disable. Defaults to 0.

export_checkpoints_dir
Automatically export generated models to this directory.

---

**h2o.xgboost**

**Build an eXtreme Gradient Boosting model**

**Description**

Builds a eXtreme Gradient Boosting model using the native XGBoost backend.

**Usage**

```r
h2o.xgboost(x, y, training_frame, model_id = NULL,
validation_frame = NULL, nfolds = 0,
keep_cross_validation_models = TRUE,
keep_cross_validation_predictions = FALSE,
keep_cross_validation_fold_assignment = FALSE,
score_each_iteration = FALSE, fold_assignment = c("AUTO", "Random",
"Modulo", "Stratified"), fold_column = NULL,
ignore_const_cols = TRUE, offset_column = NULL,
weights_column = NULL, stopping_rounds = 0,
stopping_metric = c("AUTO", "deviance", "logloss", "MSE", "RMSE",
"MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "AUCPR",
"mean_per_class_error", "custom", "custom_increasing"),
stopping_tolerance = 0.001, max_runtime_secs = 0, seed = -1,
distribution = c("AUTO", "bernoulli", "multinomial", "gaussian",
"poisson", "gamma", "tweedie", "laplace", "quantile", "huber"),
tweedie_power = 1.5, categorical_encoding = c("AUTO", "Enum",
"OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder",
"SortByResponse", "EnumLimited"), quiet_mode = TRUE,
export_checkpoints_dir = NULL, ntrees = 50, max_depth = 6,
min_rows = 1, min_child_weight = 1, learn_rate = 0.3, eta = 0.3,
sample_rate = 1, subsample = 1, col_sample_rate = 1,
colsample_bylevel = 1, col_sample_rate_per_tree = 1,
colsample_bytree = 1, max_abs_leafnode_pred = 0,
min_split_improvement = 0, gammax = 0,
max_delta_step = 0, monotone_constraints = NULL,
min_sum_hessian_in_leaf = 100, min_data_in_leaf = 0,
```
```r
sample_type = c("uniform", "weighted"), normalize_type = c("tree", "forest"), rate_drop = 0, one_drop = FALSE, skip_drop = 0,
tree_method = c("auto", "exact", "approx", "hist"),
grow_policy = c("depthwise", "lossguide"), booster = c("gbtree", "gblinear", "dart"), reg_lambda = 1, reg_alpha = 0,
dmatrix_type = c("auto", "dense", "sparse"), backend = c("auto", "gpu", "cpu"), gpu_id = 0, verbose = FALSE)
```

**Arguments**

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

stopping_metric
Metric to use for early stopping (AUTO: logloss for classification, deviance for regression and anomaly_score for Isolation Forest). Note that custom and custom_increasing can only be used in GBM and DRF with the Python client. Must be one of: "AUTO", "deviance", "logloss", "MSE", "RMSE", "MAE", "RMSLE", "AUC", "lift_top_group", "misclassification", "AUCPR", "mean_per_class_error", "custom", "custom_increasing". Defaults to AUTO.

stopping_tolerance
Relative tolerance for metric-based stopping criterion (stop if relative improvement is not at least this much) Defaults to 0.001.

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.

categorical_encoding
Encoding scheme for categorical features Must be one of: "AUTO", "Enum", "OneHotInternal", "OneHotExplicit", "Binary", "Eigen", "LabelEncoder", "SortByResponse", "EnumLimited". Defaults to AUTO.

quiet_mode
Logical. Enable quiet mode Defaults to TRUE.

export_checkpoints_dir
Automatically export generated models to this directory.

ntrees
(same as n_estimators) Number of trees. Defaults to 50.

max_depth
Maximum tree depth. Defaults to 6.

min_rows
(same as min_child_weight) Fewest allowed (weighted) observations in a leaf. Defaults to 1.

min_child_weight
(same as min_rows) Fewest allowed (weighted) observations in a leaf. Defaults to 1.

learn_rate
(same as eta) Learning rate (from 0.0 to 1.0) Defaults to 0.3.

eta
(same as learn_rate) Learning rate (from 0.0 to 1.0) Defaults to 0.3.

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 1.

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 1.
**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 1.

**max_abs_leafnode_pred**
(same as _max_delta_step_) Maximum absolute value of a leaf node prediction Defaults to 0.0.

**max_delta_step**
(same as _max_abs_leafnode_pred_) Maximum absolute value of a leaf node prediction Defaults to 0.0.

**monotone_constraints**
A mapping representing monotonic constraints. Use +1 to enforce an increasing constraint and -1 to specify a decreasing constraint.

**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.

**gamma**
(same as _min_split_improvement_) Minimum relative improvement in squared error reduction for a split to happen Defaults to 0.0.

**nthread**
Number of parallel threads that can be used to run XGBoost. Cannot exceed H2O cluster limits (-nthreads parameter). Defaults to maximum available Defaults to -1.

**max_bins**
For tree_method=hist only: maximum number of bins Defaults to 256.

**max_leaves**
For tree_method=hist only: maximum number of leaves Defaults to 0.

**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.

**sample_type**
For booster=dart only: sample_type Must be one of: "uniform", "weighted". Defaults to uniform.

**normalize_type**
For booster=dart only: normalize_type Must be one of: "tree", "forest". Defaults to tree.

**rate_drop**
For booster=dart only: rate_drop (0..1) Defaults to 0.0.

**one_drop**
Logical. For booster=dart only: one_drop Defaults to FALSE.

**skip_drop**
For booster=dart only: skip_drop (0..1) Defaults to 0.0.

**tree_method**
Tree method Must be one of: "auto", "exact", "approx", "hist". Defaults to auto.

**grow_policy**
Grow policy - depthwise is standard GBM, lossguide is LightGBM Must be one of: "depthwise", "lossguide". Defaults to depthwise.

**booster**
Booster type Must be one of: "gbtree", "gblinear", "dart". Defaults to gbtree.

**reg_lambda**
L2 regularization Defaults to 1.0.

**reg_alpha**
L1 regularization Defaults to 0.0.

**dmatrix_type**
Type of DMatrix. For sparse, NAs and 0 are treated equally. Must be one of: "auto", "dense", "sparse". Defaults to auto.
### h2o.xgboost.available

Determines whether an XGBoost model can be built

**Description**

Ask the H2O server whether a XGBoost model can be built. (Depends on availability of native backend.) Returns True if a XGBoost model can be built, or False otherwise.

**Usage**

```
h2o.xgboost.available()
```

### h2o.year

Convert Milliseconds to Years in H2O Datasets

**Description**

Convert the entries of an H2OFrame object from milliseconds to years, indexed starting from 1900.

**Usage**

```
h2o.year(x)
year(x)
```

**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`
**H2OAutoML-class**

*The H2OAutoML class*

**Description**

This class represents an H2OAutoML object

**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 cluster, the data used to build the model (an object of class H2OFrame).

**Slots**

- `model_id` A character string specifying the key for the model fit in the H2O cluster’s key-value store.
- `algorithm` A character string specifying the algorithm that was used to fit the model.
- `parameters` A list containing the parameter settings that were used to fit the model that differ from the defaults.
- `allparameters` A list containing all parameters used to fit the model.
- `model` A list containing the characteristics of the model returned by the algorithm.
  - `size` The number of points in each cluster.
  - `totss` Total sum of squared error to grand mean.
  - `withinss` A vector of within-cluster sum of squared error.
  - `tot_withinss` Total within-cluster sum of squared error.
  - `betweenss` Between-cluster sum of squared error.
H2OConnection-class

The H2OConnection class.

Description

This class represents a connection to an H2O cluster.

Usage

## S4 method for signature 'H2OConnection'
show(object)

Arguments

object an H2OConnection object.

Details

Because H2O is not a master-slave architecture, there is no restriction on which H2O node is used to establish the connection between R (the client) and H2O (the server).

A new H2O connection is established via the h2o.init() function, which takes as parameters the 'ip' and 'port' of the machine running an instance to connect with. The default behavior is to connect with a local instance of H2O at port 54321, or to boot a new local instance if one is not found at port 54321.

Slots

ip A character string specifying the IP address of the H2O cluster.
port A numeric value specifying the port number of the H2O cluster.
name A character value specifying the name of the H2O cluster.
proxy A character specifying the proxy path of the H2O cluster.
https Set this to TRUE to use https instead of http.
cacert Path to a CA bundle file with root and intermediate certificates of trusted CAs.
insecure Set this to TRUE to disable SSL certificate checking.
username Username to login with.
password Password to login with.
use_spnego Set this to TRUE to use SPNEGO authentication.
cookies Cookies to add to request
context_path Context path which is appended to H2O server location.
mutable An H2OConnectionMutableState object to hold the mutable state for the H2O connection.
**H2OConnectionMutableState**

*The H2OConnectionMutableState class*

**Description**

This class represents the mutable aspects of a connection to an H2O cluster.

**Slots**

- `session_id` A character string specifying the H2O session identifier.
- `key_count` A integer value specifying count for the number of keys generated for the `session_id`.

**H2OCoxPHModel-class**

*The H2OCoxPHModel object.*

**Description**

Virtual object representing H2O’s CoxPH Model.

**Usage**

```r
## S4 method for signature 'H2OCoxPHModel'
show(object)

## S3 method for class 'H2OCoxPHModel'
coef(object, ...)

## S3 method for class 'H2OCoxPHModel'
evaluateAIC(fit, scale, k = 2, ...)

## S3 method for class 'H2OCoxPHModel'
logLik(object, ...)

survfit.H2OCoxPHModel(formula, newdata, ...)

## S3 method for class 'H2OCoxPHModel'
vcov(object, ...)
```

**Arguments**

- `object` an H2OCoxPHModel object.
- `...` additional arguments to pass on.
- `fit` an H2OCoxPHModel object.
- `scale` optional numeric specifying the scale parameter of the model.
- `k` numeric specifying the weight of the equivalent degrees of freedom.
- `formula` an H2OCoxPHModel object.
- `newdata` an optional H2OFrame or data.frame with the same variable names as those that appear in the H2OCoxPHModel object.
H2OCoxPHModelSummary-class

The H2OCoxPHModelSummary object.

Description

Wrapper object for summary information compatible with survival package.

Usage

## S4 method for signature 'H2OCoxPHModelSummary'
show(object)

## S3 method for class 'H2OCoxPHModelSummary'
coef(object, ...)

Arguments

object An H2OCoxPHModelSummary object.
...
additional arguments to pass on.

Slots

summary A list containing the summary compatible with CoxPH summary used in the survival package.

H2OFrame-class

The H2OFrame class

Description

This class represents an H2OFrame object

H2OFrame-Extract

Extract or Replace Parts of an H2OFrame Object

Description

Operators to extract or replace parts of H2OFrame objects.
Usage

```r
## 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
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**

The H2OModel object.

**Description**

This virtual class represents a model built by H2O.

**Usage**

```r
## S4 method for signature 'H2OModel'
show(object)
```

**Arguments**

- `object`: an H2OModel object.

**Details**

This object has slots for the key, which is a character string that points to the model key existing in the H2O cluster, the data used to build the model (an object of class H2OFrame).

**Slots**

- `model_id`: A character string specifying the key for the model fit in the H2O cluster's key-value store.
- `algorithm`: A character string specifying the algorithm that were used to fit the model.
- `parameters`: A list containing the parameter settings that were used to fit the model that differ from the defaults.
- `allparameters`: A list containing all parameters used to fit the model.
- `have_pojo`: A logical indicating whether export to POJO is supported.
- `have_mojo`: A logical indicating whether export to MOJO is supported.
- `model`: A list containing the characteristics of the model returned by the algorithm.

---

**H2OModelFuture-class**

H2O Future Model

**Description**

A class to contain the information for background model jobs.

**Slots**

- `job_key`: a character key representing the identification of the job process.
- `model_id`: the final identifier for the model

**See Also**

- H2OModel for the final model types.
The H2OModelMetrics Class

Description

A class for constructing performance measures of H2O models.

Usage

```r
## 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 'H2OOrdinalMetrics'
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

The H2ONode Class

Description

The H2ONode class.

Usage

```r
## S4 method for signature 'H2ONode'
show(object)
```
**H2OSplitNode-class**

**Arguments**

- `object` an H2ONode object.

**Slots**

- `id` An integer representing node’s unique identifier. Generated by H2O.
- `levels` A character representing categorical levels on split from parent’s node belonging into this node. NULL for root node or non-categorical splits.

**H2OTree-class**

**Description**

This class represents a model of a Tree built by one of H2O’s algorithms (GBM, Random Forest).

**Usage**

```r
## S4 method for signature 'H2OTree'
show(object)
```

**Arguments**

- `object` an H2OTree object.
Slots

root_node A H2ONode representing the beginning of the tree behind the model. Allows further
tree traversal.

left_children An integer vector with left child nodes of tree’s nodes

right_children An integer vector with right child nodes of tree’s nodes

node_ids An integer representing identification number of a node. Node IDs are generated by
H2O.

descriptions A character vector with descriptions for each node to be found in the tree. Con-
tains split threshold if the split is based on numerical column. For cactegorical splits, it con-
tains list of categorical levels for transition from the parent node.

model_id A character with the name of the model this tree is related to.

tree_number An integer representing the order in which the tree has been built in the model.

tree_class A character representing name of tree’s class. Number of tree classes equals to the
number of levels in categorical response column. As there is exactly one class per categorical
level, name of tree’s class equals to the corresponding categorical level of response column.
In case of regression and binomial, the name of the categorical level is ignored can be omitted,
as there is exactly one tree built in both cases.

thresholds A numeric split thresholds. Split thresholds are not only related to numerical splits,
but might be present in case of categorical split as well.

features A character with names of the feature/column used for the split.

levels A character representing categorical levels on split from parent’s node belonging into
this node. NULL for root node or non-categorical splits.

nas A character representing if NA values go to the left node or right node. May be NA if node
is a leaf.

predictions A numeric representing predictions for each node in the graph.

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

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
The data were collected by Anderson, Edgar (1935). The irises of the Gaspe Peninsula, Bulletin of the American Iris Society, 59, 2-5.

is.character

*Check if character*

Description
Check if character

Usage

`is.character(x)`

Arguments

*x* 
An H2OFrame object
### is.factor

**Description**
Check if factor

**Usage**

```r
is.factor(x)
```

**Arguments**

- `x` An H2OFrame object

### is.h2o

**Description**
Test if object is H2O Frame.

**Usage**

```r
is.h2o(x)
```

**Arguments**

- `x` An R object.

### is.numeric

**Description**
Check if numeric

**Usage**

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

**Arguments**

- `x` An H2OFrame object
Keyed-class

Virtual Keyed class

Description

Base class for all objects having a persistent representation on backend.

length,H2OTree-method

Overrides the behavior of length() function on H2OTree class. Returns number of nodes in an H2OTree

Description

Overrides the behavior of length() function on H2OTree class. Returns number of nodes in an H2OTree

Usage

## S4 method for signature 'H2OTree'
length(x)

Arguments

x An H2OTree to count nodes for.

Logical-or

Logical or for H2OFrames

Description

Logical or for H2OFrames

Usage

"||"(x, y)

Arguments

x An H2OFrame object
y An H2OFrame object
ModelAccessors  Accessor Methods for H2OModel 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

*Column names of an H2OFrame*

**Description**

Column names of an H2OFrame

**Usage**

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

**Arguments**

- x: An H2OFrame

---

### Ops.H2OFrame

*S3 Group Generic Functions for H2O*

**Description**

Methods for group generic functions and H2O objects.

**Usage**

```r
## S3 method for class 'H2OFrame'
Ops(e1, e2)
```

```r
## S3 method for class 'H2OFrame'
Math(x, ...)
```

```r
## S3 method for class 'H2OFrame'
Summary(x, ..., na.rm)
```

```r
## S3 method for class 'H2OFrame'
!x
```
plot.H2OModel

## 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  Plot an H2O Model

### Description

Plots training set (and validation set if available) scoring history for an H2O Model
## plot.H2OModel

### Usage

```r
## S3 method for class 'H2OModel'
plot(x, timestep = "AUTO", metric = "AUTO", ...)
```

### Arguments

- **x**: A fitted **H2OModel** 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

```r
## Not run:
if (requireNamespace("mlbench", quietly=TRUE)) {
  library(h2o)
  h2o.init()
  df <- as.h2o(mlbench::mlbench.friedman1(10000,1))
  rng <- h2o.runif(df, seed=1234)
  train <- df[rng<0.8,]
  valid <- df[rng>=0.8,]
  gbm <- h2o.gbm(x = 1:10, y = "y", training_frame = train, validation_frame = valid,
                 ntree=500, learn_rate=0.01, score_each_iteration = TRUE)
  plot(gbm)
  plot(gbm, timestep = "duration", metric = "deviance")
  plot(gbm, timestep = "number_of_trees", metric = "deviance")
  plot(gbm, timestep = "number_of_trees", metric = "rmse")
  plot(gbm, timestep = "number_of_trees", metric = "mae")
}
## End(Not run)
```
plot.H2OTabulate    *Plot an H2O Tabulate Heatmap*

**Description**

Plots the simple co-occurrence based tabulation of X vs Y as a heatmap, where X and Y are two Vecs in a given dataset. This function requires suggested ggplot2 package.

**Usage**

```r
## S3 method for class 'H2OTabulate'
plot(x, xlab = x$cols[1], ylab = x$cols[2],
     base_size = 12, ...)
```

**Arguments**

- `x`  
  An H2OTabulate object for which the heatmap plot is desired.
- `xlab`  
  A title for the x-axis. Defaults to what is specified in the given H2OTabulate object.
- `ylab`  
  A title for the y-axis. Defaults to what is specified in the given H2OTabulate object.
- `base_size`  
  Base font size for plot.
- `...`  
  Additional arguments to pass on.

**Value**

Returns a ggplot2-based heatmap of co-occurrence.

**See Also**

`h2o.tabulate`

**Examples**

```r
## Not run:
library(h2o)
h2o.init()
df <- as.h2o(iris)
tab <- h2o.tabulate(data = df, x = "Sepal.Length", y = "Petal.Width",
                    weights_column = NULL, nbins_x = 10, nbins_y = 10)
plot(tab)
## End(Not run)
```
predict.H2OAutoML

Predict on an AutoML object

Description

Obtains predictions from an AutoML object.

Usage

## S3 method for class 'H2OAutoML'
predict(object, newdata, ...)

## S3 method for class 'H2OAutoML'
h2o.predict(object, newdata, ...)

Arguments

- **object**: a fitted H2OAutoML object for which prediction is desired
- **newdata**: An H2OFrame object in which to look for variables with which to predict.
- **...**: additional arguments to pass on.

Details

This method generated predictions on the leader model from an AutoML run. The order of the rows in the results is the same as the order in which the data was loaded, even if some rows fail (for example, due to missing values or unseen factor levels).

Value

Returns an H2OFrame object with probabilities and default predictions.

predict.H2OModel

Predict on an H2O Model

Description

Obtains predictions from various fitted H2O model objects.

Usage

## S3 method for class 'H2OModel'
predict(object, newdata, ...)

## S3 method for class 'H2OModel'
h2o.predict(object, newdata, ...)

Arguments

- **object**: a fitted H2OModel object for which prediction is desired
- **newdata**: An H2OFrame object in which to look for variables with which to predict.
- **...**: additional arguments to pass on.
**predict_contributions.H2OModel**

**Arguments**
- **object** a fitted H2OModel object for which prediction is desired
- **newdata** An H2OFrame object in which to look for variables with which to predict.
- **...** additional arguments to pass on.

**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 probabilites and default predictions.

**See Also**
h2o.deeplearning, h2o.gbm, h2o.glm, h2o.randomForest for model generation in h2o.

---

**predict_contributions.H2OModel**

Predict feature contributions - SHAP values on an H2O Model (only GBM and XGBoost models).

**Description**
Returned H2OFrame has shape (#rows, #features + 1) - there is a feature contribution column for each input feature, the last column is the model bias (same value for each row). The sum of the feature contributions and the bias term is equal to the raw prediction of the model. Raw prediction of tree-based model is the sum of the predictions of the individual trees before the inverse link function is applied to get the actual prediction. For Gaussian distribution the sum of the contributions is equal to the model prediction.

**Usage**

predict_contributions.H2OModel(object, newdata, ...)
h2o.predict_contributions(object, newdata, ...)

**Arguments**
- **object** a fitted H2OModel object for which prediction is desired
- **newdata** An H2OFrame object in which to look for variables with which to predict.
- **...** additional arguments to pass on.

**Details**
Note: Multinomial classification models are currently not supported.
Value

Returns an H2OFrame contain feature contributions for each input row.

See Also

h2o.gbm and h2o.randomForest for model generation in h2o.

Examples

```r
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate_gbm <- h2o.gbm(3:9, "AGE", prostate)
h2o.predict(prostate_gbm, prostate)
h2o.predict_contributions(prostate_gbm, prostate)
## End(Not run)
```

**predict_leaf_node_assignment.H2OModel**

*Predict the Leaf Node Assignment on an H2O Model*

Description

Obtains leaf node assignment from fitted H2O model objects.

Usage

```r
predict_leaf_node_assignment.H2OModel(object, newdata, type = c("Path", "Node_ID"), ...)
```

```r
h2o.predict_leaf_node_assignment(object, newdata, type = c("Path", "Node_ID"), ...)
```

Arguments

- **object**: a fitted H2OModel object for which prediction is desired
- **newdata**: An H2OFrame object in which to look for variables with which to predict.
- **type**: choice of either "Path" when tree paths are to be returned (default); or "Node_ID" when the output
- **...**: additional arguments to pass on.

Details

For every row in the test set, return the leaf placements of the row in all the trees in the model. Placements can be represented either by paths to the leaf nodes from the tree root or by H2O’s internal identifiers. The order of the rows in the results is the same as the order in which the data was loaded.
Value

Returns an H2OFrame object with categorical leaf assignment identifiers for each tree in the model.

See Also

h2o.gbm and h2o.randomForest for model generation in h2o.

Examples

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

print.H2OFrame

Print An H2OFrame

Description

Print An H2OFrame

Usage

```r
## 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

---

### Description

This will print a truncated view of the table if there are more than 20 rows.

### Usage

```r
## 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

**Prostate Cancer Study**

---

### 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

## H2OFrame

### Description

Range of an H2O Column

### Usage

```r
## S3 method for class 'H2OFrame'
range(..., na.rm = TRUE)
```

### Arguments

- `...`: An H2OFrame object.
- `na.rm`: Ignore missing values.

---

## scale

### Description

Centers and/or scales the columns of an H2O dataset.

### Usage

```r
## 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

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

# Scale and center all the numeric columns in iris data set
iris_scaled <- scale(iris_hf[, 1:4])

## End(Not run)
```
staged_predict_proba.H2OModel

Predict class probabilities at each stage of an H2O Model

Description

The output structure is analogous to the output of h2o.predict_leaf_node_assignment. For each tree t and class c there will be a column Tt.Cc (e.g. T3.C1 for tree 3 and class 1). The value will be the corresponding predicted probability of this class by combining the raw contributions of trees T1.Cc, Tt.Cc. Binomial models build the trees just for the first class and values in columns Tx.C1 thus correspond to the probability p0.

Usage

staged_predict_proba.H2OModel(object, newdata, ...)

h2o.staged_predict_proba(object, newdata, ...)

Arguments

object a fitted H2OModel object for which prediction is desired
newdata An H2OFrame object in which to look for variables with which to predict.
... additional arguments to pass on.

Value

Returns an H2OFrame object with predicted probability for each tree in the model.

See Also

h2o.gbm and h2o.randomForest for model generation in h2o.

Examples

```r
## Not run:
library(h2o)
h2o.init()
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.uploadFile(path = prostate_path)
prostate$CAPSULE <- as.factor(prostate$CAPSULE)
prostate_gbm <- h2o.gbm(3:9, "CAPSULE", prostate)
h2o.predict(prostate_gbm, prostate)
h2o.staged_predict_proba(prostate_gbm, prostate)
## End(Not run)
```
str.H2OFrame

Display the structure of an H2OFrame object

Description

Display the structure of an H2OFrame object

Usage

```r
## 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.H2OCoxPHModel-method

Summary method for H2OCoxPHModel objects

Description

Summary method for H2OCoxPHModel objects

Usage

```r
## S4 method for signature 'H2OCoxPHModel'
summary(object, conf.int = 0.95, scale = 1)
```

Arguments

- **object**
  - an H2OCoxPHModel object.

- **conf.int**
  - a specification of the confidence interval.

- **scale**
  - a scale.
**summary,H2OGrid-method**

Format grid object in user-friendly way

**Description**

Format grid object in user-friendly way

**Usage**

```r
## 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**

```r
## S4 method for signature 'H2OModel'
summary(object, ...)
```

**Arguments**

- `object`: An H2OModel 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

```r
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.

Format

A data frame with 151 rows and 124 columns

References


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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