Fast Scalable R with H2O

```
> install.packages('h2o')
> library(h2o)
> lh2o = h2o.init(nthreads = -1))
> demo(h2o.deepLearning)
```

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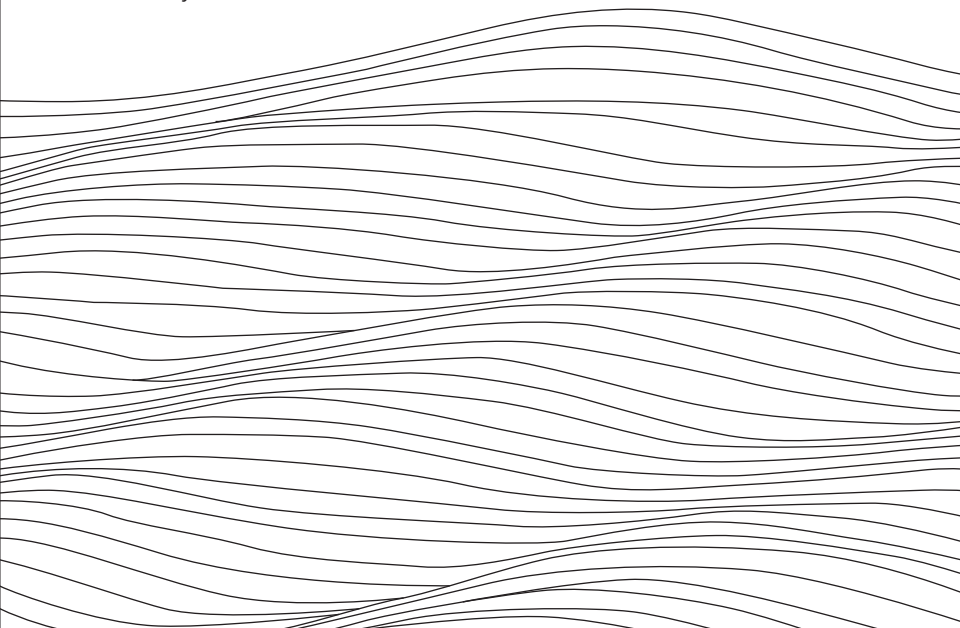

Fast Scalable R in H2O
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1 What is H2O?

H2O is fast scalable open -source machine learning and deep learning for Smarter Applications. With H2O enterprises like PayPal, Nielsen, Cisco and others can use all of their data without sampling and get accurate predictions faster. Advanced algorithms, like Deep Learning, Boosting and Bagging Ensembles are readily available for application designers to build smarter applications through elegant APIs. Some of our earliest customers have built powerful domain-specific predictive engines for Recommendations, Customer Churn, Propensity to Buy, Dynamic Pricing and Fraud Detection for the Insurance, Healthcare, Telecommunications, AdTech, Retail and Payment Systems.

Using in-memory compression techniques, H2O can handle billions of data rows in-memory – even with a fairly small cluster. The platform includes interfaces for R, Python, Scala, Java, JSON and Coffeescript/JavaScript, along with its built-in Flow web interface that make it easier for non-engineers to stitch together complete analytic workflows. The platform was built alongside (and on top of) both Hadoop and Spark Clusters and is typically deployed within minutes.

H2O implements almost all common machine learning algorithms – such as generalized linear modeling (linear regression, logistic regression, etc.), Naive Bayes, principal components analysis, time series, k-means clustering and others. H2O also implements best-in-class algorithms such as Random Forest, Gradient Boosting and Deep Learning at scale. Customers can build thousands of models and compare them to get the best prediction results.

H2O is nurturing a grassroots movement of physicists, mathematicians, computer and data scientists to herald the new wave of discovery with data science. Academic researchers and Industrial data scientists collaborate closely with our team to make this possible. Stanford university giants Stephen Boyd, Trevor Hastie, Rob Tibshirani advise the H2O team to build scalable machine learning algorithms. With 100s of meetups over the past two years, H2O has become a word-of-mouth phenomenon growing amongst the data community by a 100-fold and is now used by 12,000+ users, deployed in 2000+ corporations using R, Python, Hadoop and Spark.

Try it out
H2O offers an R package that can be installed from CRAN. H2O can be downloaded from www.h2o.ai/download.

Join the community
Connect with h2ostream@googlegroups.com and https://github.com/h2oai to learn about our meetups, training sessions, hackathons, and product updates.

Learn more about H2O
Visit www.h2o.ai

2 Introduction

This documentation describes the functionality of R in H2O. Further information on H2O's system and algorithms, as well as R user documentation, can be found at the H2O website at http://docs.h2o.ai This introductory section describes how H2O works with R, followed by a brief overview of generalized linear models (GLM).

R requires a reference object to the H2O instance because it uses a REST API to send functions to H2O. Data sets are not transmitted directly through the REST API. Instead, the user sends a command (containing an HDFS path to the data set, for example) either through the browser or via the REST API to ingest data from disk.

The data set is then assigned a Key in H2O that the user may refer to in future commands to the web server. After preparing your dataset for modeling by defining the significant data and removing the insignificant data, you can create models to represent the results of the data analysis. One of the most popular models for data analysis is GLM.

GLM estimates regression models for outcomes following exponential distributions in general. In addition to the Gaussian (i.e. normal) distribution, these include Poisson, binomial, gamma and Tweedie distributions. Each serves a different purpose, and depending on distribution and link function choice, it can be used either for prediction or classification.

H2O supports Spark, YARN, and all versions of Hadoop. Hadoop is a scalable opensource file system that uses clusters to enable distributed storage and processing of datasets. Depending on your data size, you can get started on your desktop or scale using multiple nodes with Hadoop.

H2O nodes run as JVM invocations on Hadoop nodes. (Note that, for performance reasons, 0xdata recommends you avoid running an H2O node on the same hardware as the Hadoop NameNode if it can be avoided.)

Since H2O nodes run as mapper tasks in Hadoop, administrators can see them in the normal JobTracker and TaskTracker frameworks. This provides process-level (i.e. JVM instance-level) visibility.

H2O helps R users make the leap from laptop-based processing to large-scale environments. Hadoop helps H2O users scale their data processing capabilities based on their current needs. Using H2O, R, and Hadoop, you can create a complete end-to-end data analysis solution. For more information about H2O on Hadoop, refer to http://docs.h2o.ai/bits/hadoop/H2O_on_Hadoop_0xdata.pdf.

This document will walk you through the four steps to data analysis with H2O: installing H2O, preparing your data for modeling (data munging), creating a model using state-of-the-art machine learning algorithms, and scoring your models.

3 Installation

To use H2O with R, you can start H2O outside of R and connect to it, or you can launch H2O from R. However, if you launch H2O from R and close the R session, the H2O instance is closed as well. The client object is used to direct R to datasets and models located in H2O.

3.1 Installing R or R Studio

To download R:

1. Go to http://cran.r-project.org/mirrors.html.
2. Select your closest local mirror.
3. Select your operating system (Linux, OS X, or Windows).
4. Depending on your OS, download the appropriate file, along with any required packages.
5. When the download is complete, unzip the file and install.

To download R Studio:

1. Go to http://www.rstudio.com/products/rstudio/.
2. Select your deployment type (desktop or server).
3. Download the file.
4. When the download is complete, unzip the file and install.

3.2 Installing H2O in R

1. Load the latest CRAN H2O package by running

   ```
   install.packages("h2o")
   ```

2. To get the latest build, download it from http://h2o.ai/download and make sure to run the following (replacing the asterisks [*] with the version number):

   ```
   > if ("package:h2o" %in% search()) { detach("package:h2o", unload=TRUE) }
   > if ("h2o" %in% rownames(installed.packages())) { remove.packages("h2o") }
   > install.packages("h2o", repos=(c("http://s3.amazonaws.com/h2o-release/h2o
   /master/****/R", getOption("repos"))))
   > library(h2o)
   ```

3. Run a demo to see an example classification model using GLM.

   ```
   demo(glm)
   ```

1 Note: Our push to CRAN will be behind the bleeding edge version and due to resource constraints, may be behind the published version. However, there is a best-effort to keep the versions the same.

3.3 Making a build from the Source Code

If you are a developer who wants to make changes to the R package before building and installing it, pull the source code from Git (https://github.com/h2oai/h2o) and follow the instructions in From Source Code (Github) at http://docs.h2o.ai/developuser/quickstart_git.html.

After making the build, navigate to the Rcran folder with the R package in the build's directory, then run (replacing the asterisks [*] with the version number) and install.

```
$ make clean
$ make build
$ cd target/Rcran
$ R CMD INSTALL h2o_****.tar.gz
* installing to library 'C:/Users//Documents/R/win-library/3.0'
* installing *source* package 'h2o' ...
** R
** demo
** inst
...
*** installing help indices
** building package indices
** testing if installed package can be loaded
...
DONE (h2o)
```

4 H2O Initialization

4.1 Launching from R

If you do not specify the argument `max_mem_size` when you run `h2o.init(nthreads = -1)`, the default heap size of the H2O instance running on 32-bit Java is 1g. H2O checks the Java version and suggests an upgrade if you are running 32-bit Java. On 64-bit Java, the heap size is 1/4 of the total memory available on the machine. The nthreads = -1 parameter allows H2O to use all CPUS on the host, which is recommended.

For best performance, the allocated memory should be 4x the size of your data, but never more than the total amount of memory on your computer. For larger data sets, we recommend running on a server or service with more memory available for computing.

To launch H2O from R, run the following in R:

```
> library(h2o) ##Loads required files for H2O
localH2O <- h2o.init(ip = 'localhost', port = 54321, nthreads= -1, max_mem_
size =4g') ##Starts H2O on the localhost, port 54321, with 4g of memory
using all CPUs on the host
```

R displays the following output:

```
Successfully connected to http://localhost:54321
    R is connected to H2O cluster:
H2O cluster uptime:                 11 minutes 35 seconds
H2O cluster version:       2.7.0.1497
H2O cluster name:          H2O_started_from_R
H2O cluster total nodes:   1
H2O cluster total memory:  3.56 GB
H2O cluster total cores:   8
H2O cluster allowed cores: 8
H2O cluster healthy:       TRUE
```

If you are operating on a single node, initialize H2O using

```
h2o_server = h2o.init(nthreads = -1)
```

To connect with an existing H2O cluster node other than the default `localhost:54321`, specify the IP address and port number in the parentheses. For example:

```
h2o_cluster = h2o.init(ip = "192.555.1.123", port = 12345, nthreads= -1)
```


4.2 Launching from Command Line

After launching the H2O instance, initialize the connection by running `h2o.init(nthreads = -1)` with the IP address and port number of a node in the cluster. In the following example, change 192.168.1.161 to your local host.

```
> library(h2o)
> localH2O <- h2o.init(ip = '192.168.1.161', port =54321, nthreads= -1)
```

4.3 Launching from Hadoop

To launch H2O nodes and form a cluster on the Hadoop cluster, run:

```
$ hadoop jar h2odriver_hdp2.1.jar water.hadoop.h2odriver -lib-
jars ../h2o.jar -mapperXmx1g -nodes 1 -output hdfsOutputDirName
```

- For each major release of each distribution of Hadoop, there is a driver jar file that the user will need to launch H2O with. Currently available driver jar files in each build of H2O include `h2odriver_cdh5.jar`, `h2odriver_hdp2.1.jar`, and `mapr2.1.3.jar`.
- The above command launches exactly one 1g node of H2O; however, we recommend launching the cluster with 4 times the memory of your data file.
- `mapperXmx` is the mapper size or the amount of memory allocated to each node.
- `nodes` is the number of nodes requested to form the cluster.
- `output` is the name of the directory created each time a H2O cloud is created so it is necessary for the name to be unique each time it is launched.

4.4 Launching on an EC2

Launch the EC2 instances using the H2O AMI by running `h2o-cluster-launch-instances.py`.which is available on our github, https://github.com/h2oai/h2o/tree/master/ec2.

```
$ python h2o-cluster-launch-instances.py
Using boto version 2.27.0
Launching 2 instances.
Waiting for instance 1 of 2 ...
   .
   .
   instance 1 of 2 is up.
Waiting for instance 2 of 2 ...
   instance 2 of 2 is up.
```

4.5 Checking Cluster Status

To check the status and health of the H2O cluster, use `h2o.clusterInfo( ).`

```
> library(h2o)
> localH2O = h2o.init(ip = 'localhost', port = 54321, nthreads = -1)
> h2o.clusterInfo(localH2O)
```

An easy-to-read summary of information about the cluster displays.

```
R is connected to H2O cluster:
   H2O cluster uptime:            43 minutes 43 seconds
   H2O cluster version:           2.7.0.1497
   H2O cluster name:              H2O_started_from_R
   H2O cluster total nodes:       1
   H2O cluster total memory:      3.56 GB
   H2O cluster total cores:       8
   H2O cluster allowed cores:     8
   H2O cluster healthy:           TRUE
```


5 Data Preparation in R

The following section describes some important points to remember about datapreparation (munging) and some of the tools and methods available in H2O, as well as a data training example.

5.1 Notes

- Although it may seem like you are manipulating the data in R due to the look and feel, once the data has been passed to H2O, all data munging occurs in the H2O instance. The information is passed to R through JSON APIs, so some functions may not have another method.
- You are not limited by R's ability to handle data, but by the total amount of memory allocated to the H2O instance. To process large data sets, make sure to allocate enough memory. For more information, refer to "Launching in R."
- You can manipulate datasets with thousands of factor levels using H2O in R, so if you ask H2O to display a table in R with information from high cardinality factors, the results may overwhelm R's capacity.
- To manipulate data in R and not in H2O, use `as.data.frame()`,`as.h2o()`, and `str()`.
    - `as.data.frame( )` converts an H2O data frame into an R data frame. Be aware that if your request exceeds Rs capabilities due to the amount of data, the R session will crash. If possible, we recommend only taking subsets of the entire data set (the necessary data columns or rows), and not the whole data set.
    - `as.h2o( )` transfers data from R to the H2O instance. We recommend ensuring that you allocate enough memory to the H2O instance for successful data transfer.
    - `str( )` returns the elements of the new object to conrm that the data transferred correctly. It's a good way to verify there were no data loss or conversion issues.

5.2 Tools and Methods

The following section describes some of the tools and methods available in H2O for data preparation.

- **Data Profiling:** Quickly summarize the shape of your dataset to avoid bias or missing information before you start building your model. Missing data, zero values, text, and a visual distribution of the data are visualized automatically upon data ingestion.
- **Summary Statistics:** Visualize your data with summary statistics to get the mean, standard deviation, min, max, or quantile (for numeric columns) or cardinality and counts (for enum columns), and a preview of the data set.
- **Aggregate, Filter, Bin, and Derive Columns:** Build unique views with Group functions, Filtering, Binning, and Derived Columns.
- **Slice, Log Transform, and Anonymize:** Normalize and partition to get your data into the right shape for modeling, and anonymize to remove condential information.
- **Variable Creation:** Highly customizable variable value creation to hone in on the key data characteristics to model.
- **PCA:** Principal Component Analysis makes feature selection easy with a simple interface and standard input values to reduce the many dimensions in your dataset into key components.
- **Training and Validation Sampling Plan:** Design a random or stratified sampling plan to generate data sets for model training and scoring.

5.3 Demo: Creating Aggregates from Split Data

The following section depicts an example of data training using `ddply()`. Using this method, you can split your dataset and apply a function to the subsets.

To apply a user-specified function to each subset of an H2O dataset and combine the results, use `ddply()`, with the name of the H2O object, the variable name, and the function in the parentheses. For more information about functions, refer to `h2o.addFunction` in the Appendix.

```
library(h2o)
localH2O = h2o.init(nthreads = -1)

# Import iris dataset to H2O
irisPath = system.file("extdata", "iris_wheader.csv", package = "h2o")

iris.hex = h2o.importFile(localH2O, path = irisPath, key = "iris.hex")

# Add function taking mean of sepal_len column
fun = function(df) { sum(df[,1], na.rm = T)/nrow(df) }
h2o.addFunction(localH2O, fun)

# Apply function to groups by class of flower
# uses h2o's ddply, since iris.hex is an H2OParsedData object
res = ddply(iris.hex, "class", fun)
head(res)
```

6 Models

The following section describes the features and functions of some common models available in H2O. For more information about running these models in R using H2O, refer to section 5, Running Models.

H2O supports the following models: Deep Learning, Generalized Linear Models (GLM), Gradient Boosted Regression (GBM), K-Means, Naive Bayes, Principal Components Analysis (PCA), Principal Components Regression (PCR), Random Forest (RF), and Cox Proportional Hazards (PH).

The list is growing quickly, so check back often at www.h2o.ai to see the latest additions. The following list describes some common model types and features.

Generalized Linear Models (GLM): A flexible generalization of ordinary linear regression for response variables that have error distribution models other than a normal distribution. GLM unifies various other statistical models, including linear, logistic, Poisson, and more.

Decision trees: used in RF; a decision support tool that uses a tree-like graph or model of decisions and their possible consequences.

Gradient Boosting (GBM): A method to produce a prediction model in the form of an ensemble of weak prediction models. It builds the model in a stage-wise fashion and is generalized by allowing an arbitrary differentiable loss function. It is one of the most powerful methods available today.

K-Means: A method to uncover groups or clusters of data points often used for segmentation. It clusters observations into k certain points with the nearest mean.

Anomaly Detection: Identify the outliers in your data by invoking a powerful pattern recognition model, the Deep Learning Auto-Encoder.

Deep Learning: Model high-level abstractions in data by using non-linear transformations in a layer-by-layer method. Deep learning is an example of supervised learning and can make use of unlabeled data that other algorithms cannot.

Naïve Bayes: A probabilistic classifier that assumes the value of a particular feature is unrelated to the presence or absence of any other feature, given the class variable. It is often used in text categorization.

Grid Search: The standard way of performing hyper-parameter optimization to make model configuration easier. It is measured by cross-validation of an independent data set.

After creating a model, use it to make predictions. For more information about predictions, refer to Section 8.6.

6.1 Demo: GLM

The following demo demonstrates how to import a file, define significant data, view data, create testing and training sets using sampling, define the model, and display the results.


```
# Import dataset and display summary
> airlinesURL = "https://s3.amazonaws.com/h2o-airlines-unpacked/allyears2k.csv"
> airlines.hex = h2o.importFile(localH2O, path = airlinesURL,key = "airlines.hex")
> summary(airlines.hex)

# Define columns to ignore, quantiles and histograms
> high_na_columns = h2o.ignoreColumns(data = airlines.hex)
> delay_quantiles = quantile(x = airlines.hex$ArrDelay, na.rm = TRUE)
> hist(airlines.hex$ArrDelay)

# Find number of flights by airport
> originFlights = h2o.ddply(airlines.hex, 'Origin', nrow)
> originFlights.R = as.data.frame(originFlights)

# Find number of cancellations per month
> flightsByMonth = h2o.ddply(airlines.hex,"Month", nrow)
> flightsByMonth.R = as.data.frame(originFlights)

# Find months with the highest cancellation ratio
> fun = function(df) {sum(df$Cancelled)}
> h2o.addFunction(h, fun)
> cancellationsByMonth = h2o.ddply(airlines.hex,"Month", fun)
> cancellation_rate = cancellationsByMonth$C1/flightsByMonth$C1)
> rates_table = cbind(flightsByMonth$Month, cancellation_rate)
> rates_table.R = as.data.frame(rates.table)

# Construct test and train sets using sampling
> airline.split = h2o.splitFrame(data = airlines.hex,ratios = 0.85)
> airline.train = airline.split[[1]]
> airline.test = airline.split[[2]]

# Display a summary using table-like functions
> summary(as.factor(airline.train$Cancelled))
> summary(as.factor(airline.test$Cancelled))

# Set predictor and response variables
> Y = "IsDepDelayed"
> X = c("Origin", "Dest", "DayofMonth", "Year", "UniqueCarrier", "DayOfWeek",
"Month",
"DepTime", "ArrTime", "Distance")
# Define the data for the model and display the results
> airlines.glm <- h2o.glm(data=airlines.train, x=X, y=Y, family = "binomial",
alpha = 0.5)

# Predict using GLM model
> pred = h2o.predict(object = airlines.glm, newdata = airlines.test)
```

7 Data Manipulation in R

The following section describes some common R commands. For a complete command list, including parameters, refer to http://docs.h2o.ai/bits/h2o_package.pdf. For additional help within R's Help tab, precede the command with a question mark (for example, ?h2o) for suggested commands containing the search terms. For more information on a command, precede the command with two question marks (??h2o).

7.1 Importing Files

The H2O package consolidates all of the various supported import functions using `h2o.importFile( )`. Although `h2o.importFolder` and `h2o.importHDFS` will still work, these functions are deprecated and should be updated to `h2o.importFile( )`.

```
## To import small iris data file from H2O's package
> irisPath = system.file("extdata", "iris.csv", package="h2o")
> iris.hex = h2o.importFile(localH2O, path = irisPath, key ="iris.hex")
       |=================================================| 100%

## To import an entire folder of files as one data object
> pathToFolder = "/Users/data/airlines/"
> airlines.hex = h2o.importFile(localH2O, path = pathToFolder, key =
"airlines.hex")
       |=================================================| 100%

## To import from HDFS, connect to your Hadoop cluster and start an H2O
instance in R using the IP that was specified by Hadoop:
> remoteH2O = h2o.init(ip= <IPAddress>, port =54321, nthreads = -1)
> pathToData = "hdfs://mr-0xd6.h2oai.loc/datasets/airlines_all.csv"
> airlines.hex = h2o.importFile(remoteH2O, path = pathToData, key =
"airlines.hex")
       |=================================================| 100%
```

7.2 Uploading Files

To upload a file from your local disk, we recommend `h2o.importFile`. The alternative is to use `h2o.uploadFile()` which can also upload data local to your H2O instance in addition to uploading data local to your R session. In the parentheses, specify the H2O reference object in R and the complete URL or normalized file path for the file.


```
> irisPath = system.file("extdata", "iris.csv", package="h2o")
> iris.hex = h2o.uploadFile(localH2O, path = irisPath, key =
"iris.hex")
        |=================================================| 100%
```

7.3 Finding Factors

To determine if any column in a data set is a factor, use `h2o.anyFactor()` with the name of the R reference object in the parentheses.

```
> irisPath = system.file("extdata", "iris_wheader.csv", package="h2o")
> iris.hex = h2o.importFile(localH2O, path = irisPath)
|=================================================| 100%
> h2o.anyFactor(iris.hex)
[1] TRUE
```

7.4 Converting to Factors

To convert an integer into a non-ordered factor (also called an enum or categorical), use `as.factor( )` with the name of the R reference object in parentheses followed by the number of the column to convert in brackets.

```
# Import prostate data
> prosPath <- system.file("extdata", "prostate.csv", package="h2o")
> prostate.hex <- h2o.importFile(localH2O, path = prosPath)
|=================================================| 100%
# Converts column 4 (RACE) to an enum
> is.factor(prostate.hex[,4])
[1] FALSE
> prostate.hex[,4]<-as.factor(prostate.hex[,4])
> is.factor(prostate.hex[,4])
[1] TRUE
# Summary will return a count of the factors
> summary(prostate.hex[,4])
RACE
1 :341
2 : 36
0 :  3
```

7.5 Converting Data Frames

To convert an H2O parsed data object into an R data frame that can be manipulated using R commands, use `as.data.frame( )` with the name of the R reference object in the parentheses.

Caution: While this can be very useful, be careful using this command when converting H2O parsed data objects. H2O can easily handle data sets that are often too large to be handled equivalently well in R.

```
# Creates object that defines path
> prosPath <- system.file("extdata", "prostate.csv", package="h2o")
# Imports data set
> prostate.hex = h2o.importFile(localH2O, path = prosPath)
|=================================================| 100%
# Converts current data frame (prostate data set) to an R data frame
> prostate.R <- as.data.frame(prostate.hex)
# Displays a summary of data frame where the summary was executed in R
> summary(prostate.data.frame)
    ID               CAPSULE           AGE             RACE
Min.   : 1.00    Min.   :0.0000   Min.   :43.00   Min.   :0.000
1st Qu.: 95.75   1st Qu.:0.0000   1st Qu.:62.00   1st Qu.:1.000
```

7.6 Transferring Data Frames

To transfer a data frame from the R environment to the H2O instance, use `as.h2o( )`. In the parentheses, specify the name of the `h2o.init` object that communicates with R and H2O and the object in the R environment to be converted to an H2O object. Optionally, you can include the reference to the H2O instance (the key). Precede the key with key= and enclose the key in quotes as in the following example.

```
# Import the iris data into H2O
> data(iris)
> iris
      Sepal.Length   Sepal.Width   Petal.Length   Petal.Width   Species
1              5.1           3.5            1.4           0.2    setosa
2              4.9           3.0            1.4           0.2    setosa
3              4.7           3.2            1.3           0.2    setosa
4              4.6           3.1            1.5           0.2    setosa
5              5.0           3.6            1.4           0.2    setosa
6              5.4           3.9            1.7           0.4    setosa
# Converts R object "iris" into H2O object iris.hex"
> iris.hex = as.h2o(localH2O, iris, key= "iris.hex")
|=================================================| 100%
IP Address: localhost
Port : 54321
Parsed Data Key: iris.hex

      Sepal.Length   Sepal.Width   Petal.Length   Petal.Width   Species
1              5.1           3.5            1.4           0.2    setosa
2              4.9           3.0            1.4           0.2    setosa
3              4.7           3.2            1.3           0.2    setosa
4              4.6           3.1            1.5           0.2    setosa
5              5.0           3.6            1.4           0.2    setosa
6              5.4           3.9            1.7           0.4    setosa
```

7.7 Renaming Data Frames

To rename a dataframe on the server running H2O for a data set manipulated in R, use `h2o.assign( )`. For instance, in the following example, the prostate data set was uploaded to the H2O instance and the data was manipulated to remove outliers. `h2o.assign( )` saves the new data set on the H2O server so that it can be analyzed using H2O without overwriting the original data set.

```
> prosPath <- system.file("extdata", "prostate.csv", package=h2o")
> prostate.hex<-h2o.importFile(localH2O, path = prosPath)
|=================================================| 100%
## Assign a new name to prostate dataset in the KV store
> prostate.hex@key
[1] "prostate.hex"
> prostate.hex <- h2o.assign(data = prostate.hex, key = "newName.hex")
> prostate.hex@key
[1] "newName.hex"
```

7.8 Getting Column Names

To obtain a list of the column names in the data set, use `colnames( )` or `names( )` with the name of the R reference object in the parentheses.

```
##Displays the titles of the columns
> colnames(iris.hex)
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
> names(iris.hex)
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
```

7.9 Getting Minimum and Maximum Values

To obtain the maximum values for the real-valued columns in a data set, use `max( )` with the name of the R reference object in the parentheses. To obtain the minimum values for the real-valued columns in a data set, use `min( )` with the name of the R reference object in the parentheses.

```
> min(prostate.hex$AGE)
[1] 43
> max(prostate.hex$AGE)
[1] 79
```

7.10 Getting Quantiles

To request quantiles for an H2O parsed data set, use `quantile( )` with the name of the R reference object in the parentheses. To request a quantile for a single numerical column, use `quantile(ReferenceObject$ColumnName)`, where `ReferenceObject` represents the R reference object name and `ColumnName` represents the name of the specified column. When you request for a full parsed data set consisting of a single column, `quantile( )` displays a matrix with quantile information for the data set.

```
> prosPath <- system.file("extdata", "prostate.csv", package=h2o")
> prostate.hex <- h2o.importFile(localH2O, path = prosPath)
# Returns the percentiles at 0, 10, 20, ..., 100%
> prostate.qs <- quantile(prostate.hex$PSA, probs = (1:10)/10)
> prostate.qs
    10%    20%    30%    40%    50%    60%    70%    80%    90%    100%
    2.60   4.48   5.77   7.40   8.75   11.00  13.70  20.16  33.21  139.70
# Take the outliers or the bottom and top 10% of data
> PSA.outliers <- prostate.hex[prostate.hex$PSA <= prostate.qs["10%"] |
prostate.hex$PSA
>= prostate.qs["90%"],]
# Check that the number of rows return is about 20% of the original data
> nrow(prostate.hex)
[1] 380
> nrow(PSA.outliers)
[1] 78

> nrow(PSA.outliers)/nrow(prostate.hex)

[1] 0.2052632
```


7.11 Summarizing Data

To generate a summary (similar to the one in R) for each of the columns in the data set, use `summary( )` with the name of the R reference object in the parentheses. For continuous real functions, this produces a summary that includes information on quartiles, min, max, and mean.

For factors, this produces information about counts of elements within each factor level.

```
summary(australia.hex)
premax          salmax         minairtemp      maxairtemp      maxsst
Min.   : 18.0   Min.   :3441   Min.   :272.6   Min.   :285.0   Min.   :285697
1st Qu.: 75.0   1st Qu.:3490   1st Qu.:277.0   1st Qu.:292.0   1st Qu.:290491
Median :150.0   Median :3533   Median :278.8   Median :299.9   Median :293643
Mean   :161.5   Mean   :3529   Mean   :279.9   Mean   :297.5   Mean   :295676
3rd Qu.:250.0   3rd Qu.:3558   3rd Qu.:282.0   3rd Qu.:302.4   3rd Qu.:301942
Max.   :450.0   Max.   :3650   Max.   :290.0   Max.   :310.0   Max.   :303697

maxsoilmoist     Max_czcs         runoffnew
Min.   : 0.000   Min.   : 0.160   Min.   :   0.0
1st Qu.: 0.000   1st Qu.: 0.629   1st Qu.:   0.0
Median : 4.000   Median : 1.020   Median :  19.0
Mean   : 5.117   Mean   : 1.369   Mean   : 232.2
3rd Qu.: 9.000   3rd Qu.: 1.705   3rd Qu.: 300.0
Max.   :16.000   Max.   :11.370   Max.   :2400.0
```

7.12 Summarizing Data in a Table

To summarize the data, use `h2o.table( )`. Because H2O can handle larger data sets, it is possible to generate tables that are larger than R`s capacity.

To summarize multiple columns, use `head(h2o.table (ObjectName[, c(Column Number,ColumnNumber)]))` where `ObjectName` is the name of the object in R and `ColumnNumber` is the number of the column.

```
# Counts of the ages of all patients
> h2o.table(prostate.hex[,"AGE"])
IP Address: localhost
Port : 54321
Parsed Data Key: Last.value.128
```

```
  row.names Count
1        43     1
2        47     1
3        50     2
4        51     3
5        52     2
6        53     4
> h2o.table(prostate.hex[,"AGE"], return.in.R = TRUE)
row.names
43 47 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73
74 75 76 77 78 79
 1  1  2  3  2  4 10  5  7 10 10 13  9 13 20 11 17 24 23 16 28 23 29 24 13 15
13 14 9 4 5 2

# Two-way table of ages (rows) and race (cols) of all patients
# Example: For the first row there is one count of a 43 year old that's la-
beled as RACE = 0
> h2o.table(prostate.hex[,c("AGE","RACE")])
IP Address: localhost
Port : 54321
Parsed Data Key: Last.value.139

  row.names  X0  X1  X2
1        43   1   0   0
2        47   0   1   0
3        50   0   2   0
4        51   0   3   0
5        52   0   2   0
6        53   0   3   1
```

7.13 Generating Random Uniformly Distributed Numbers

To append a column of random numbers to an H2O data frame for facilitating creation of testing/training data splits for analysis and validation in H2O, use `h2o.runif( )` with the name of the R reference object in the parentheses. This method is best for customized frame splitting; otherwise, use `h2o.splitFrame( )`. However, `h2o.runif( )` is not as fast or stable as `h2o.splitFrame( )`.

```
> s <- h2o.runif(phbirths.hex) ##Creates object “s" for h2o.runif on
phbirths data set
> summary (s) ##Summarize the results of h2o.runif
 rnd
 Min. :0.000105
 1st Qu.:0.249472
 Median :0.489969
 Mean :0.492103
 3rd Qu.:0.739377
 Max. :0.998859
```

```
> phbirths.train <- phbirths.hex[s <= 0.8,] ##Create training set with
threshold of 0.8
> phbirths.train <- h2o.assign(phbirths.train, “phbirths.train")
##Assign name to training set
> phbirths.test <- phbirths.hex[s > 0.8,] ##Create test set with
threshold to filter values greater than 0.8
> phbirths.test <- h2o.assign(phbirths.test, “phbirths.test")
##Assign name to test set
> nrow(phbirths.train) + nrow(phbirths.test) ##Combine results of test &
training sets, then display result
[1] 1115
```

7.14 Splitting Frames

To generate two subsets (according to specified ratios) from an existing H2O data set for testing/training, use `h2o.splitFrame( )`. This method is preferred over `h2o.runif` because it is faster and more stable.

```
# Splits data in prostate data frame with a ratio of 0.75
> prostate.split <- h2o.splitFrame(data = prostate.hex , ratios = 0.75)
# Creates training set from 1st data set in split
> prostate.train <- prostate.split[[1]]
# Creates testing set from 2st data set in split
> prostate.test <- prostate.split[[2]]
```

7.15 Getting Frames

To create a reference object to the data frame in H2O, use `h2o.getFrame()`. This is helpful for users that alternate between the web UI and the R API or multiple users accessing the same H2O instance. The following example assumes prostate.hex is in the key-value (KV) store.

```
> prostate.hex <- h2o.getFrame(h2o = localH2O, key = "prostate.hex")
```

7.16 Getting Models

To create a reference object for the model in H2O, use `h2o.getModel( )`. This is helpful for users that alternate between the web UI and the R API or multiple users accessing the same H2O instance. The following example assumes gbm. model is in the key-value (KV) store.

```
gbm.model <- h2o.getModel(h2o = localH2O,
key = "GBM_8e4591a9b413407b983d73fbd9eb44cf")
```

7.17 Listing H2O Objects

To generate a list of all H2O objects generated during a session, along with each object's size in bytes, use `h2o.ls()` with the address of the instance in the parentheses. If the instance is local, use localH2O.

```
> h2o.ls(localH2O)
                                    Key       Bytesize
1       GBM_8e4591a9b413407b983d73fbd9eb44cf       40617
2       GBM_a3ae2edf5dfadbd9ba5dc2e9560c405d        1516
```

7.18 Removing H2O Objects

To remove an H2O object on the server associated with an object in the R environment, use `h2o.rm( )`. For optimal performance, we recommend removing the object from the R environment as well using `remove()`, with the name of the object in the parentheses. If you do not specify an R environment, then the current environment is used.

```
> h2o.rm(object= localH2O, keys= "prostate.train")
```

7.19 Adding Functions

To add a user-defined function in R to the H2O instance, use `h2o.addFunction( )`, with the IP address of the H2O instance and the function in the parentheses.

```
# Send the functional expression to H2O
> simpleFun <- h2o.addFunction(localH2O, function(x) { 2*x + 5 }, "simpleFun")
# Evaluate the expression across prostate's AGE column
> calculated = h2o.exec(expr_to_execute = simpleFun(prostate.hex[,"AGE"]), h2o
= localH2O)
> cbind(prostate.hex[,"AGE"], calculated)
IP Address: localhost
Port : 54321
Parsed Data Key: Last.value.152

  AGE fun
1  65 135
2  72 149
3  70 145
4  76 157
5  69 143
6  71 147
```

8 Running Models

To run the models, use the following commands.

8.1 Gradient Boosted Models (GBM)

To generate gradient boosted models for developing forward-learning ensembles, use `h2o.gbm()`. In the parentheses, define x (the predictor variable vector), y (the integer or categorical response variable), the distribution type (multinomial is the default, gaussian is used for regression), and the name of the H2OParsedData object.

For more information, use `help(h2o.gbm)`

```
> library(h2o)
> localH2O <- h2o.init(nthreads = -1)
> iris.hex <- as.h2o(localH2O, object = iris, headers = T, key = "iris.hex")
> iris.gbm <- h2o.gbm(y = 1, x = 2:5, data = iris.hex, n.trees = 10,
interaction.depth = 3, n.minobsinnode = 2, shrinkage = 0.2, distribution=
"gaussian")
|=================================================| 100%
# To obtain the Mean-squared Error by tree from the model object:
> iris.gbm@model[,"err"]
[1] 0.68112220 0.47215388 0.33393673 0.24465574 0.18596269 0.14500129
[7] 0.11792983 0.10003321 0.08793070 0.07862922 0.07232574
```

To generate a classification model that uses labels, use `distribution= "multinomial"`:

```
> iris.gbm2 <- h2o.gbm(y = 5, x = 1:4, data = iris.hex, n.trees = 15,
interaction.depth = 5, n.minobsinnode = 2, shrinkage = 0.01, distribu-
tion= "multinomial")

IP Address: localhost
Port : 54321
Parsed Data Key: iris.hex

GBM Model Key: GBM_baa2f910e4dcbd61fa60da4f2d034687
```

```
Confusion matrix:
Reported on 0-fold cross-validated data
                                Predicted
Actual        Iris-setosa   Iris-versicolor   Iris-virginica   Error
Iris-setosa            50                 0                0       0
Iris-versicolor         0                50                0       0
Iris-virginica          0                 0               50       0
Totals                 50                50               50       0
Overall Mean-squared Error: 0.3251718
```

8.2 Generalized Linear Models (GLM)

Generalized linear models (GLM) are some of the most commonly-used models for many types of data analysis use cases. While some data analysis can be done using general linear models, if the variables are more complex, general linear models may not be as accurate. For example, if the dependent variable has a non-continuous distribution or if the effect of the predictors is not linear, generalized linear models will produce more accurate results than general linear models.

Generalized Linear Models (GLM) estimate regression models for outcomes following exponential distributions in general. In addition to the Gaussian (i.e. normal) distribution, these include Poisson, binomial, gamma and Tweedie distributions. Each serves a dierent purpose, and depending on distribution and link function choice, it can be used either for prediction or classification.

H2O's GLM algorithm ts the generalized linear model with elastic net penalties. The model fitting computation is distributed, extremely fast,and scales extremely well for models with a limited number (~ low thousands) of predictors with non-zero coefficients. The algorithm can compute models for a single value of a penalty argument or the full regularization path, similar to glmnet. It can compute gaussian (linear), logistic, poisson, and gamma regression models.

To generate a generalized linear model for developing linear models for exponential distributions, use `h2o.glm()`. You can apply regularization to the model by adjusting the lambda and alpha parameters. For more information, use `help(h2o.glm)`.

```
> prostate.hex <- h2o.importFile(localH2O, path =
"https://raw.github.com/h2Oai/h2o/master/smalldata/logreg/prostate.csv",
key = "prostate.hex")
|=================================================| 100%
> h2o.glm(y = "CAPSULE", x = c("AGE","RACE","PSA","DCAPS"), data =
prostate.hex, family = "binomial", nfolds = 10, alpha = 0.5)
|=========================================================| 100%
     Coefficients:
     AGE        RACE        DCAPS        PSA        Intercept
     -0.01104   -0.63136    1.31888      0.04713    -1.10896

     Normalized Coefficients:
     AGE        RACE        DCAPS        PSA        Intercept
     -0.07208   -0.19495    0.40972      0.94253    -0.33707

     Degrees of Freedom: 379 Total (i.e. Null); 375 Residual
     Null Deviance:     514.9
     Residual Deviance: 461.3 AIC: 471.3
     Deviance Explained: 0.10404
     AUC: 0.68875  Best Threshold: 0.328

     Confusion Matrix:
           Predicted
     Actual  false  true   Error
     false     127   100   0.441
     true       51   102   0.333
     Totals    178   202   0.397

     Cross-Validation Models:
                 Nonzeros              Deviance Explained
     Model 1            4       0.6532738    0.048419803
     Model 2            4       0.6316527   -0.006414532
     Model 3            4       0.7100840    0.087779178
     Model 4            4       0.8268698    0.243020554
     Model 5            4       0.6354167    0.153190735
     Model 6            4       0.6888889    0.041892118
     Model 7            4       0.7366071    0.164717509
     Model 8            4       0.6711310    0.004897310
     Model 9            4       0.7803571    0.200384622
     Model 10           4       0.7435897    0.114548543
```

8.3 K-Means

To generate a K-Means model for data characterization, use `h2o.kmeans()`. This algorithm does not rely on a dependent variable. For more information, use `help(h2o.kmeans)`.

```
> iris.km = h2o.kmeans(data = iris.hex, centers = 3, cols = 1:4)
|=================================================| 100%
> print(iris.km)
IP Address: localhost
Port : 54321
Parsed Data Key: iris.hex
K-Means Model Key: KMeans2_937845cadf924db4612c3a7d8f9744a0
K-means clustering with 3 clusters of sizes 50, 38, 62

Cluster means:
        C1       C2       C3       C4
1 5.006000 3.418000 1.464000 0.244000
2 6.850000 3.073684 5.742105 2.071053
3 5.901613 2.748387 4.393548 1.433871
....
```

8.4 Principal Components Analysis (PCA)

To map a set of variables onto a subspace using linear transformations, use `h2o.prcomp()`. This is the first step in Principal Components Regression. For more information, use `help(h2o.prcomp)`.

```
> ausPath = system.file("extdata", "australia.csv", package="h2o")
> australia.hex = h2o.importFile(localH2O, path = ausPath)
|=========================================================| 100%
> australia.pca = h2o.prcomp(data = australia.hex, standardize = TRUE)
|=========================================================| 100%
....

PCA Model Key: PCA_8fbc38e360de5b3c1ae6b7cc754b499c
Standard deviations:
1.750703 1.512142 1.031181 0.8283127 0.6083786 0.5481364 0.4181621
0.2314953
....
```



```
> summary(australia.pca)
Importance of components:  PC1      PC2       PC3        PC4        PC5        PC6
Standard deviation     1.7507032 1.5121421 1.0311814 0.82831266 0.60837860 0.54813639
Proportion of Variance 0.3831202 0.2858217 0.1329169 0.08576273 0.04626556 0.03755669
Cumulative Proportion  0.3831202 0.6689419 0.8018588 0.88762155 0.93388711 0.97144380
```

8.5 Principal Components Regression (PCR)

To map a set of variables to a set of linearly independent variables, use `h2o.pcr( )`. The variables in the new set are linearly independent linear combinations of the original variables and exist in a lower-dimension subspace. This transformation is prepended to the regression model to improve results. For more information, use `help(h2o.pcr)`.

```
> prostate.pcr <- h2o.pcr(x = c("AGE","RACE","PSA","DCAPS"), y = "CAPSULE",
data = prostate.hex, family = "binomial", nfolds = 0, alpha = 0.5, ncomp = 2)

Coefficients:
    PC0        PC1  Intercept
3.55117   1.08603   -0.12964

....
```

8.6 Predictions

The following section describes some of the prediction methods available in H2O.

Predict: Generate outcomes of a data set with any model. Predict with GLM, GBM, Decision Trees or Deep Learning models.

Confusion Matrix: Visualize the performance of an algorithm in a table to understand how a model performs.

Area Under Curve (AUC): A graphical plot to visualize the performance of a model by its sensitivity, true positives, and false positives to select the best model.

Hit Ratio: A classification matrix to visualize the ratio of the number of correctly classified and incorrectly classified cases.

PCA Score: Determine how well your feature selection fits a particular model.

Multi-Model Scoring: Compare and contrast multiple models on a data set to find the best performer to deploy into production.

To apply an H2O model to a holdout set for predictions based on model results, use `h2o.predict( )`. In the following example, H2O generates a model and then displays the predictions for that model.

```
> prostate.fit = h2o.predict(object = prostate.glm, newdata = prostate.hex)
> (prostate.fit)
```

```
predict      X0            X1
      1      0 0.7452267   0.2547732
      2      1 0.3969807   0.6030193
      3      1 0.4120950   0.5879050
      4      1 0.3726134   0.6273866
      5      1 0.6465137   0.3534863
      6      1 0.4331880   0.5668120
```

9 Support

There are multiple ways to request support for H2O:

Email: support@h2o.ai

Google Groups: https://groups.google.com/forum/#!forum/ h2ostream

JIRA: http://jira.0xdata.com/

Meetup information: http://h2o.ai/events

10 References

R Package http://docs.h2o.ai/bits/h2o_package.pdf

R Ensemble documentation http://www.stat.berkeley.edu/~ledell/R/h2oEnsemble.pdf

Slide deck http://0xdata.com/blog/2013/08/big-data-science-in-h2o-with-r/

R project website http://www.r-project.org

11 Appendix: Commands

The following section lists some common commands by function that are available in R and a brief description of each command.

11.1 Data Set Operations

Data Import / Export

`h2o.downloadCSV`: Download a H2O dataset to a CSV file on the local disk.
`h2o.exportFile`: Export H2O Data Frame to a File.
`h2o.importFile`: Import a file from the local path and parse it.

`h2o.parseRaw`: Parse a raw data file.
`h2o.uploadFile`: Upload a file from the local drive and parse it.

Native R -> H2O Coercion

`as.h2o`: Convert an R object to an H2O object

H2O -> Native R Coercion

`as.data.frame`: Check if an object is a data frame, or coerce it if possible.
`as.matrix`: Convert the specified argument to a matrix.
`as.table`: Build a contingency table of the counts at each combination of factor levels.

Data Generation

`h2o.createFrame`: Create an H2O data frame, with optional randomization.
`h2o.runif`: Produce a vector of random uniform numbers.
`h2o.interaction`: Create interaction terms between categorical features of an H2O Frame

Data Sampling / Splitting

`h2o.sample`: Sample an existing H2O Frame by number of observations.
`h2o.splitFrame`: Split an existing H2O data set according to user-specified ratios.
`h2o.nFoldExtractor`: Split an existing H2O data set into N folds and return a specified holdout split, and the rest.

Missing Data Handling

`h2o.impute`: Impute a column of data using the mean, median, or mode.
`h2o.insertMissingValue`: Replaces a user-specified fraction of entries in a H2O dataset with missing values.
`h2o.ignoreColumns`: Returns columns' names of a parsed H2O data object that are recommended to be ignored in an analysis.

11.2 General Data Operations

Subscripting example to pull pieces from data object.

```
x[i]
x[i, j, ... , drop = TRUE]
x[[i]]
x$name
```

```
x[i] <- value
x[i, j, ...] <- value
x[[i]] <- value
x$i <- value
```

Subsetting
`head, tail`: Return the First or Last Part of an Object

Concatenation
`c`: Combine Values into a Vector or List
`cbind`: Take a sequence of H2O datasets and combine them by column.

Data Attributes
`colnames`: Return column names for a parsed H2O data object.
`colnames<-`: Retrieve or set the row or column names of a matrix-like object.
`names`: Get the name of an object.
`names<-`: Set the name of an object.
`dim`: Retrieve the dimension of an object.
`length`: Get the length of vectors (including lists) and factors.
`nrow`: Return a count of the number of rows in an H2OParsedData object.
`ncol`: Return a count of the number of columns in an H2OParsedData object.
`h2o.anyFactor`: Check if an H2O parsed data object has any categorical data columns.
`is.factor`: Check if a given column contains categorical data.

Data Type Coercion
`as.factor`: Convert a column from numeric to factor.
`as.Date`: Converts a column from factor to date.

11.3 Methods from Group Generics

Math (H2O)
`abs`: Compute the absolute value of x.
`sign`: Return a vector with the signs of the corresponding elements of x (the sign of a real number is 1, 0, or -1 if the number is positive, zero, or negative, respectively).
`sqrt`: Computes the (principal) square root of x, √{x}.
`ceiling`: Take a single numeric argument x and return a numeric vector containing the smallest integers not less than the corresponding elements of x.
`floor`: Take a single numeric argument x and return a numeric vector containing the largest integers not greater than the corresponding elements of x.
`trunc`: Take a single numeric argument x and return a numeric vector containing the integers formed by truncating the values in x toward 0.
`log`: Compute logarithms (by default, natural logarithms).
`exp`: Compute the exponential function.

Math (generic)
`cummax`: Display a vector whose elements are the cumulative maxima of the elements of the argument.
`cummin`: Display a vector whose elements are the cumulative minima of the elements of the argument.
`cumprod`: Display a vector whose elements are the cumulative products of the elements of the argument.
`cumsum`: Display a vector whose elements are the cumulative sums of the elements of the argument.
`log10`: Compute common (i.e., base 10) logarithms
`log2`: Compute binary (i.e., base 2) logarithms.
`log1p`: Compute log(1+x) accurately also for |x| << 1.
`acos`: Compute the trigonometric arc-cosine.
`acosh`: Compute the hyperbolic arc-cosine.
`asin`: Compute the trigonometric arc-sine.
`asinh`: Compute the hyperbolic arc-sine.
`atan`: Compute the trigonometric arc-tangent.
`atanh`: Compute the hyperbolic arc-tangent.
`expm1`: Compute exp(x) - 1 accurately also for |x| << 1.
`cos`: Compute the trigonometric cosine.
`cosh`: Compute the hyperbolic cosine.
`cospi`: Compute the trigonometric two-argument arc-cosine.
`sin`: Compute the trigonometric sine.
`sinh`: Compute the hyperbolic sine.
`sinpi`: Compute the trigonometric two-argument arc-sine.
`tan`: Compute the trigonometric tangent.
`tanh`: Compute the hyperbolic tangent.
`tanpi`: Compute the trigonometric two-argument arc-tangent.
`gamma`: Display the gamma function Γ(x)
`lgamma`: Display the natural logarithm of the absolute value of the gamma function.
digamma: Display the first derivative of the logarithm of the gamma function.
`trigamma`: Display the second derivative of the logarithm of the gamma function.

Math2 (H2O)
`round`: Round the values in its first argument to the specified number of decimal places (default 0).
`signif`: Round the values in its first argument to the specified number of significant digits.

Summary (H2O)
`max`: Display the maximum of all the input arguments.
`min`: Display the minimum of all the input arguments.
`range`: Display a vector containing the minimum and maximum of all the given arguments.
`sum`: Calculate the sum of all the values present in its arguments.

Summary (generic)
`prod`: Display the product of all values present in its arguments.
`any`: Given a set of logical vectors, determine if at least one of the values is true.
`all`: Given a set of logical vectors, determine if all of the values are true.

11.4 Other Aggregations

Non-Group Generic Summaries
`mean`: Generic function for the (trimmed) arithmetic mean.
`sd`: Calculate the standard deviation of a column of continuous real valued data.
`var`: Compute the variance of x.
`summary`: Produce result summaries of the results of various model fitting functions.
`quantile`: Obtain and display quantiles for H2O parsed data.

Row / Column Aggregation
`apply`: Apply a function over an H2O parsed data object (an array).

Group By Aggregation
`h2o.ddply`: Split H2O dataset, apply a function (defined in h2o.addFunction), and display results.
`h2o.addFunction`: Add a function defined in R to the H2O server for future use.

Tabulation
`h2o.table`: Use the cross-classifying factors to build a table of counts at each-combination of factor levels.

11.5 Data Munging

Transformation Framework
`h2o.exec`: Directly transmit and execute an R expression in the H2O console.

General Column Manipulations
`is.na`: Display missing elements.
`unique`: Display a vector, data frame, or array with duplicate elements/rows removed.

Element Index Selection
`findInterval`: Find Interval Numbers or Indices.
`which`: Display the row numbers for which the condition is true.

Conditional Element Value Selection
`ifelse`: Apply conditional statements to numeric vectors in H2O parsed data objects.

Numeric Column Manipulations
`h2o.cut`: Convert H2O Numeric Data to Factor.
`diff`: Display suitably lagged and iterated differences.

Character Column Manipulations
`strsplit`: Splits the given factor column on the input split.
`tolower`: Change the elements of a character vector to lower case.
`toupper`: Change the elements of a character vector to lower case.
`trim`: Remove leading and trailing white space.
`h2o.gsub`: Match a pattern and replaces all instances of the matched pattern with the replacement string globally.
`h2o.sub`: Match a pattern and replace the first instance of the matched pattern with the replacement string.

Factor Level Manipulations
`levels`: Display a list of the unique values found in a column of categorical data.
`revalue`: Replace specified values with new values in a factor or character vector.

Date Manipulations
`h2o.month`: Convert the entries of a H2OParsedData object from milliseconds to months (on a 0 to 11 scale).
`h2o.year`: Convert the entries of a H2OParsedData object from milliseconds to years, indexed starting from 1900.

Matrix Operations
`%*%`: Multiply two matrices, if they are conformable.
`t`: Given a matrix or data.frame x, t returns the transpose of x.

11.6 Data Modeling

Model Training
`h2o.coxph`: Fit a Cox Proportional Hazards Model.
`h2o.gbm`: Build gradient boosted classification trees and gradient boosted regression trees on a parsed data set.
`h2o.glm`: Fit a generalized linear model, specified by a response variable, a set of predictors, and a description of the error distribution.
`h2o.kmeans`: Perform k-means clustering on a data set.
`h2o.naiveBayes`: Build gradient boosted classification trees and gradient boosted regression trees on a parsed data set.
`h2o.pcr`: Run GLM regression on PCA results, and allow for transformation of test data to match PCA transformations of training data.
`h2o.prcomp`: Perform principal components analysis on the given data set.
`h2o.randomForest`: Perform random forest classification on a data set.

Deep Learning
`h2o.deeplearning`: Deep Learning neural networks on an H2OParsedData object.
`h2o.anomaly`: Detect anomalies in a H2O dataset using a H2O deep learning model with auto-encoding.
`h2o.deepfeatures`: Extract the non-linear features from a H2O dataset using a H2O deep learning model.

Model Scoring
`h2o.predict`: Obtain predictions from various fitted H2O model objects.

Classification Model Helpers
`h2o.confusionMatrix`: Display prediction errors for classification data from a column of predicted responses and a column of actual (reference) responses in H2O.
`h2o.gains`: Construct the gains table and lift charts for binary outcome algorithms.
`h2o.hitRatio`: Compute the percentage of instances where the actual class of an observation is in the top user-specified number of classes predicted by the model.
`h2o.performance`: Evaluate the predictive performance of a model via various measures.

Clustering Helper
`h2o.gapStatistic`: Measure the suitability of the fit of a clustering algorithm.

Regression Model Helper
`h2o.mse`: Display the mean squared error calculated from a column of predicted responses and a column of actual (reference) responses in H2O.

GLM Helper
`h2o.getGLMLambdaModel`: Retrieve the H2O GLM model built using a specific value of lambda from a lambda search.

11.7 H2O Cluster Operations

H2O Key Value Store Access
`h2o.assign`: Assign H2O hex.keys to objects in their R environment.
`h2o.getFrame`: Get a reference to an existing H2O data set.
`h2o.getModel`: Get a reference to an existing H2O model.
`h2o.ls`: Display a list of object keys in the running instance of H2O.
`h2o.rm`: Remove H2O objects from the server where the instance of H2O is running, but does not remove it from the R environment.

H2O Object Serialization
`h2o.loadAll`: Load all H2OModel object in a directory from disk that was saved using h2o.saveModel or h2o.saveAll.
`h2o.loadModel`: Load an H2OModel object from disk.
`h2o.saveAll`: Save all H2OModel objects to disk to be loaded back into H2O using h2o.loadModel or h2o.loadAll.
`h2o.saveModel`: Save an H2OModel object to disk to be loaded back into H2O using h2o.loadModel.

H2O Cluster Connection
`h2o.init`: Connect to a running H2O instance and check the local H2O R package is the correct version.
`h2o.shutdown`: Shut down the specified H2O instance. All data on the server will be lost!

H2O Load Balancing
`h2o.rebalance`: Rebalance (repartition) an existing H2O data set into given number of chunks (per Vec), for load-balancing across multiple threads or nodes.

H2O Cluster Information
`h2o.clusterInfo`: Display the name, version, uptime, total nodes, total memory, total cores and health of a cluster running H2O.
`h2o.clusterStatus`: Retrieve information on the status of the cluster running H2O.

H2O Logging

`h2o.clearLogs`: Clear all H2O R command and error response logs from local disk.
`h2o.downloadAllLogs`: Download all H2O log files to local disk.
`h2o.logAndEcho`: Write a message to the H2O Java log file and echo it back.
`h2o.openLog`: Open existing logs of H2O R POST commands and error responses on local disk.
`h2o.getLogPath`: Get the file path for the H2O R command and error response logs.
`h2o.setLogPath`: Set the file path for the H2O R command and error response logs.
`h2o.startLogging`: Begin logging H2O R POST commands and error responses.
`h2o.stopLogging`: Stop logging H2O R POST commands and error responses.

Biographies

Patrick Aboyoun
Patrick is a math and data hacker at H2O.ai who has made a career out of creating and delivering software and training for data scientists, particularly those who love R, by having worked on Oracle R Enterprise at Oracle, RevoScaleR at Revo-lution Analytics, Bioconductor at Fred Hutchinson Cancer Research Center, and S-PLUS at Insightful Corporation (now part of the Spotfire division of TIBCO). His most recent employer was Oracle, where he spent 3.5 years using his R expertise to expand the R syntax-driven SQL query generator in ORE and spearheading the effort to leverage the parallel query engine of the Oracle database to create parallel distributed advanced analytics algorithms. Patrick received an M.S. in Statistics from the University of Washington and a B.S. in Statistics from Carnegie Mellon University.

Spencer Aiello
Spencer comes from an unconventional background. After studying Physics and Math as an undergraduate at UCSC, he came to San Francisco to continue his education, earning his MS in Analytics from USF. Since then, Spencer has worked on a number of projects related to analytics in R, python, Java, and SQL. As an engineer at H2O, he works primarily on the R front-end and the backend java R-interpreter. In his free time, Spencer likes to bike, run, swim, and go to shows. He also likes to play the guitar and build furniture.

Anqi Fu
Anqi is a data hacker at H2O.ai. After completing her undergraduate at University of Maryland: College Park, she attended Stanford University. While there she earned her master's degree in Economics, and a second master's degree in Statistics. Her interests include machine learning and optimization.

Jessica Lanford
Jessica is a word hacker and seasoned technical communicator at H2O.ai. She brings our product to life by documenting the many features and functionality of H2O. Having worked for some of the top companies in technology including Dell, AT&T, and Lam Research, she is an expert at translating complex ideas to digestible articles.

"John Chambers (creator of the S language, R-core member) names @hexadata H2O R API in top three promising R projects"

– Erin LeDell