H2O.ai

H2O WORLD TRAINING 2015

H2O WORLD 2015

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H2O Tutorials

This document contains tutorials and training materials for H2O-3. For questions or feature requests, visit the H2O community forum at https://community.h2o.ai, or join the "H2O Stream" Google Group:

- Web: https://groups.google.com/forum/#!forum/h2ostream
- E-mail: h2ostream@googlegroups.com

Finding tutorial material in Github

Most current material

Tutorials in the master branch are intended to work with the lastest stable version of H2O.

	URL
Training material	https://github.com/h2oai/h2o-tutorials/blob/master/SUMMARY.md
Latest stable H2O release	http://h2o.ai/download

Historical events

Tutorial versions in named branches are snapshotted for specific events. Scripts should work unchanged for the version of H2O used at that time.

H2O World 2015 Training

	URL
Training material	https://github.com/h2oai/h2o-tutorials/blob/h2o-world-2015-training/SUMMARY.md
Tibshirani-3 H2O release	http://h2o-release.s3.amazonaws.com/h2o/rel-tibshirani/3/index.html

R Tutorials

- Intro to H2O in R
- H2O Grid Search & Model Selection
- H2O Deep Learning in R
- H2O Stacked Ensembles
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Python Tutorials

- Intro to H2O in Python
- H2O Grid Search & Model Selection
- H2O Stacked Ensembles

What is H2O?

H2O is fast, scalable, open-source machine learning and deep learning for Smarter Applications. With H2O, enterprises like PayPal, Nielsen Catalina, 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 a built-in web interface, Flow, 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.), Naïve 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, and a python package that can be installed from PyPI.

H2O can also be downloaded directly from http://h2o.ai/download.

Join the community

Visit the open source community forum at https://groups.google.com/d/forum/h2ostream.

To learn about our meetups, training sessions, hackathons, and product updates, visit http://h2o.ai.

Intro to Data Science

Slides

- PDF
- Keynote

Building a Smarter Application

Slides

- PDF
- PowerPoint

Code

The source code for this example is here: https://github.com/h2oai/app-consumer-loan

Classification and Regression with H2O Deep Learning

Introduction

This tutorial shows how a H2O Deep Learning model can be used to do supervised classification and regression. A great tutorial about Deep Learning is given by Quoc Le here and here. This tutorial covers usage of H2O from R. A python version of this tutorial will be available as well in a separate document. This file is available in plain R, R markdown and regular markdown formats, and the plots are available as PDF files. All documents are available on Github.

If run from plain R, execute R in the directory of this script. If run from RStudio, be sure to setwd() to the location of this script. h2o.init() starts H2O in R's current working directory. h2o.importFile() looks for files from the perspective of where H2O was started.

More examples and explanations can be found in our H2O Deep Learning booklet and on our H2O Github Repository. The PDF slide deck can be found on Github.

H2O R Package

Load the H2O R package:

```
## R installation instructions are at http://h2o.ai/download
library(h2o)
```

Start H2O

Start up a 1-node H2O server on your local machine, and allow it to use all CPU cores and up to 2GB of memory:

```
h2o.init(nthreads=-1, max_mem_size="2G")
h2o.removeAll() ## clean slate - just in case the cluster was already running
```

The `h2o.deeplearning` function fits H2O's Deep Learning models from within R. We can run the example from the man page using the `example` function, or run a longer demonstration from the `h2o` package using the `demo` function:

```
args(h2o.deeplearning)
help(h2o.deeplearning)
example(h2o.deeplearning)
#demo(h2o.deeplearning)  #requires user interaction
```

While H2O Deep Learning has many parameters, it was designed to be just as easy to use as the other supervised training methods in H2O. Early stopping, automatic data standardization and handling of categorical variables and missing values and adaptive learning rates (per weight) reduce the amount of parameters the user has to specify. Often, it's just the number and sizes of hidden layers, the number of

epochs and the activation function and maybe some regularization techniques.

Let's have some fun first: Decision Boundaries

We start with a small dataset representing red and black dots on a plane, arranged in the shape of two nested spirals. Then we task H2O's machine learning methods to separate the red and black dots, i.e., recognize each spiral as such by assigning each point in the plane to one of the two spirals.

We visualize the nature of H2O Deep Learning (DL), H2O's tree methods (GBM/DRF) and H2O's generalized linear modeling (GLM) by plotting the decision boundary between the red and black spirals:

```
setwd("~/h2o-tutorials/tutorials/deeplearning") ##For RStudio
spiral <- h2o.importFile(path = normalizePath("../data/spiral.csv"))
grid   <- h2o.importFile(path = normalizePath("../data/grid.csv"))
# Define helper to plot contours
plotC <- function(name, model, data=spiral, g=grid) {
  data <- as.data.frame(data) #get data from into R
  pred <- as.data.frame(h2o.predict(model, g))
  n=0.5*(sqrt(nrow(g))-1); d <- 1.5; h <- d*(-n:n)/n
  plot(data[,-3],pch=19,col=data[,3],cex=0.5,
       xlim=c(-d,d),ylim=c(-d,d),main=name)
  contour(h,h,z=array(ifelse(pred[,1]=="Red",0,1),
          dim=c(2*n+1,2*n+1)),col="blue",lwd=2,add=T)
}
```

We build a few different models:

```
#dev.new(noRStudioGD=FALSE) #direct plotting output to a new window
par(mfrow=c(2,2)) #set up the canvas for 2x2 plots
plotC( "DL", h2o.deeplearning(1:2,3,spiral,epochs=1e3))
plotC("GBM", h2o.gbm         (1:2,3,spiral))
plotC("DRF", h2o.randomForest(1:2,3,spiral))
plotC("GLM", h2o.glm         (1:2,3,spiral,family="binomial"))
```

Let's investigate some more Deep Learning models. First, we explore the evolution over training time (number of passes over the data), and we use checkpointing to continue training the same model:

```
#dev.new(noRStudioGD=FALSE) #direct plotting output to a new window
par(mfrow=c(2,2)) #set up the canvas for 2x2 plots
ep <- c(1,250,500,750)
plotC(paste0("DL ",ep[1]," epochs"),
      h2o.deeplearning(1:2,3,spiral,epochs=ep[1],
                               model_id="dl_1"))
plotC(paste0("DL ",ep[2]," epochs"),
      h2o.deeplearning(1:2,3,spiral,epochs=ep[2],
            checkpoint="dl_1",model_id="dl_2"))
plotC(paste0("DL ",ep[3]," epochs"),
      h2o.deeplearning(1:2,3,spiral,epochs=ep[3],
            checkpoint="dl_2",model_id="dl_3"))
plotC(paste0("DL ",ep[4]," epochs"),
      h2o.deeplearning(1:2,3,spiral,epochs=ep[4],
            checkpoint="dl_3",model_id="dl_4"))
```

You can see how the network learns the structure of the spirals with enough training time. We explore different network architectures next:

```
#dev.new(noRStudioGD=FALSE) #direct plotting output to a new window
par(mfrow=c(2,2)) #set up the canvas for 2x2 plots
for (hidden in list(c(11,13,17,19),c(42,42,42),c(200,200),c(1000))) {
  plotC(paste0("DL hidden=",paste0(hidden, collapse="x")),
        h2o.deeplearning(1:2,3,spiral,hidden=hidden,epochs=500))
}
```

It is clear that different configurations can achieve similar performance, and that tuning will be required for optimal performance. Next, we

compare between different activation functions, including one with 50% dropout regularization in the hidden layers:

```
#dev.new(noRStudioGD=FALSE) #direct plotting output to a new window
par(mfrow=c(2,2)) #set up the canvas for 2x2 plots
for (act in c("Tanh","Maxout","Rectifier","RectifierWithDropout")) {
  plotC(paste0("DL ",act," activation"),
        h2o.deeplearning(1:2,3,spiral,
              activation=act,hidden=c(100,100),epochs=1000))
}
```

Clearly, the dropout rate was too high or the number of epochs was too low for the last configuration, which often ends up performing the best on larger datasets where generalization is important.

More information about the parameters can be found in the H2O Deep Learning booklet.

Cover Type Dataset

We important the full cover type dataset (581k rows, 13 columns, 10 numerical, 3 categorical). We also split the data 3 ways: 60% for training, 20% for validation (hyper parameter tuning) and 20% for final testing.

```
df <- h2o.importFile(path = normalizePath("../data/covtype.full.csv"))
dim(df)
df
splits <- h2o.splitFrame(df, c(0.6,0.2), seed=1234)
train  <- h2o.assign(splits[[1]], "train.hex") # 60%
valid  <- h2o.assign(splits[[2]], "valid.hex") # 20%
test   <- h2o.assign(splits[[3]], "test.hex")  # 20%
```

Here's a scalable way to do scatter plots via binning (works for categorical and numeric columns) to get more familiar with the dataset.

```
#dev.new(noRStudioGD=FALSE) #direct plotting output to a new window
par(mfrow=c(1,1)) # reset canvas
plot(h2o.tabulate(df, "Elevation",                      "Cover_Type"))
plot(h2o.tabulate(df, "Horizontal_Distance_To_Roadways", "Cover_Type"))
plot(h2o.tabulate(df, "Soil_Type",                      "Cover_Type"))
plot(h2o.tabulate(df, "Horizontal_Distance_To_Roadways", "Elevation" ))
```

First Run of H2O Deep Learning

Let's run our first Deep Learning model on the covtype dataset. We want to predict the `Cover_Type` column, a categorical feature with 7 levels, and the Deep Learning model will be tasked to perform (multi-class) classification. It uses the other 12 predictors of the dataset, of which 10 are numerical, and 2 are categorical with a total of 44 levels. We can expect the Deep Learning model to have 56 input neurons (after automatic one-hot encoding).

```
response <- "Cover_Type"
predictors <- setdiff(names(df), response)
predictors
```

To keep it fast, we only run for one epoch (one pass over the training data).

```
m1 <- h2o.deeplearning(
  model_id="dl_model_first",
  training_frame=train,
  validation_frame=valid,   ## validation dataset: used for scoring and early stopping
  x=predictors,
  y=response,
  #activation="Rectifier",  ## default
  #hidden=c(200,200),       ## default: 2 hidden layers with 200 neurons each
  epochs=1,
  variable_importances=T    ## not enabled by default
)
summary(m1)
```

Inspect the model in Flow for more information about model building etc. by issuing a cell with the content `getModel "dl_model_first"`, and pressing Ctrl-Enter.

Variable Importances

Variable importances for Neural Network models are notoriously difficult to compute, and there are many pitfalls. H2O Deep Learning has implemented the method of Gedeon, and returns relative variable importances in descending order of importance.

```
head(as.data.frame(h2o.varimp(m1)))
```

Early Stopping

Now we run another, smaller network, and we let it stop automatically once the misclassification rate converges (specifically, if the moving average of length 2 does not improve by at least 1% for 2 consecutive scoring events). We also sample the validation set to 10,000 rows for faster scoring.

```
m2 <- h2o.deeplearning(
  model_id="dl_model_faster",
  training_frame=train,
  validation_frame=valid,
  x=predictors,
  y=response,
  hidden=c(32,32,32),                  ## small network, runs faster
  epochs=1000000,                      ## hopefully converges earlier...
  score_validation_samples=10000,      ## sample the validation dataset (faster)
  stopping_rounds=2,
  stopping_metric="misclassification", ## could be "MSE","logloss","r2"
  stopping_tolerance=0.01
)
summary(m2)
plot(m2)
```

Adaptive Learning Rate

By default, H2O Deep Learning uses an adaptive learning rate (ADADELTA) for its stochastic gradient descent optimization. There are only two tuning parameters for this method: `rho` and `epsilon`, which balance the global and local search efficiencies. `rho` is the similarity to prior weight updates (similar to momentum), and `epsilon` is a parameter that prevents the optimization to get stuck in local optima. Defaults are `rho=0.99` and `epsilon=1e-8`. For cases where convergence speed is very important, it might make sense to perform a few runs to optimize these two parameters (e.g., with `rho in c(0.9,0.95,0.99,0.999)` and `epsilon in c(1e-10,1e-8,1e-6,1e-4)`). Of course, as always with grid searches, caution has to be applied when extrapolating grid search results to a different parameter regime (e.g., for more epochs or different layer topologies or activation functions, etc.).

If `adaptive_rate` is disabled, several manual learning rate parameters become important: `rate`, `rate_annealing`, `rate_decay`, `momentum_start`, `momentum_ramp`, `momentum_stable` and `nesterov_accelerated_gradient`, the discussion of which we leave to H2O Deep Learning booklet.

Tuning

With some tuning, it is possible to obtain less than 10% test set error rate in about one minute. Error rates of below 5% are possible with larger models. Note that deep tree methods can be more effective for this dataset than Deep Learning, as they directly partition the space into sectors, which seems to be needed here.

```
m3 <- h2o.deeplearning(
  model_id="dl_model_tuned",
  training_frame=train,
  validation_frame=valid,
  x=predictors,
  y=response,
  overwrite_with_best_model=F,    ## Return the final model after 10 epochs, even if not the best
  hidden=c(128,128,128),          ## more hidden layers -> more complex interactions
  epochs=10,                      ## to keep it short enough
  score_validation_samples=10000, ## downsample validation set for faster scoring
  score_duty_cycle=0.025,         ## don't score more than 2.5% of the wall time
  adaptive_rate=F,                ## manually tuned learning rate
  rate=0.01,
  rate_annealing=2e-6,
  momentum_start=0.2,             ## manually tuned momentum
  momentum_stable=0.4,
  momentum_ramp=1e7,
  l1=1e-5,                        ## add some L1/L2 regularization
  l2=1e-5,
  max_w2=10                       ## helps stability for Rectifier
)
summary(m3)
```

Let's compare the training error with the validation and test set errors

```
h2o.performance(m3, train=T)          ## sampled training data (from model building)
h2o.performance(m3, valid=T)          ## sampled validation data (from model building)
h2o.performance(m3, newdata=train)    ## full training data
h2o.performance(m3, newdata=valid)    ## full validation data
h2o.performance(m3, newdata=test)     ## full test data
```

To confirm that the reported confusion matrix on the validation set (here, the test set) was correct, we make a prediction on the test set and compare the confusion matrices explicitly:

```
pred <- h2o.predict(m3, test)
pred
test$Accuracy <- pred$predict == test$Cover_Type
1-mean(test$Accuracy)
```

Hyper-parameter Tuning with Grid Search

Since there are a lot of parameters that can impact model accuracy, hyper-parameter tuning is especially important for Deep Learning:

For speed, we will only train on the first 10,000 rows of the training dataset:

```
sampled_train=train[1:10000,]
```

The simplest hyperparameter search method is a brute-force scan of the full Cartesian product of all combinations specified by a grid search:

```
hyper_params <- list(
  hidden=list(c(32,32,32),c(64,64)),
  input_dropout_ratio=c(0,0.05),
  rate=c(0.01,0.02),
  rate_annealing=c(1e-8,1e-7,1e-6)
)
hyper_params
grid <- h2o.grid(
  algorithm="deeplearning",
  grid_id="dl_grid",
  training_frame=sampled_train,
  validation_frame=valid,
  x=predictors,
  y=response,
  epochs=10,
  stopping_metric="misclassification",
  stopping_tolerance=1e-2,        ## stop when misclassification does not improve by >=1% for 2 scoring events
  stopping_rounds=2,
  score_validation_samples=10000, ## downsample validation set for faster scoring
  score_duty_cycle=0.025,         ## don't score more than 2.5% of the wall time
  adaptive_rate=F,                ## manually tuned learning rate
  momentum_start=0.5,             ## manually tuned momentum
  momentum_stable=0.9,
  momentum_ramp=1e7,
  l1=1e-5,
  l2=1e-5,
  activation=c("Rectifier"),
  max_w2=10,                      ## can help improve stability for Rectifier
  hyper_params=hyper_params
)
grid
```

Let's see which model had the lowest validation error:

```
grid <- h2o.getGrid("dl_grid",sort_by="err",decreasing=FALSE)
grid

## To see what other "sort_by" criteria are allowed
#grid <- h2o.getGrid("dl_grid",sort_by="wrong_thing",decreasing=FALSE)

## Sort by logloss
h2o.getGrid("dl_grid",sort_by="logloss",decreasing=FALSE)

## Find the best model and its full set of parameters
grid@summary_table[1,]
best_model <- h2o.getModel(grid@model_ids[[1]])
best_model

print(best_model@allparameters)
print(h2o.performance(best_model, valid=T))
print(h2o.logloss(best_model, valid=T))
```

Random Hyper-Parameter Search

Often, hyper-parameter search for more than 4 parameters can be done more efficiently with random parameter search than with grid search. Basically, chances are good to find one of many good models in less time than performing an exhaustive grid search. We simply build up to `max_models` models with parameters drawn randomly from user-specified distributions (here, uniform). For this example, we use the adaptive learning rate and focus on tuning the network architecture and the regularization parameters. We also let the grid search stop automatically once the performance at the top of the leaderboard doesn't change much anymore, i.e., once the search has converged.

```
hyper_params <- list(
  activation=c("Rectifier","Tanh","Maxout","RectifierWithDropout","TanhWithDropout","MaxoutWithDropout"),
  hidden=list(c(20,20),c(50,50),c(30,30,30),c(25,25,25,25)),
  input_dropout_ratio=c(0,0.05),
  l1=seq(0,1e-4,1e-6),
  l2=seq(0,1e-4,1e-6)
)
hyper_params

## Stop once the top 5 models are within 1% of each other (i.e., the windowed average varies less than 1%)
search_criteria = list(strategy = "RandomDiscrete", max_runtime_secs = 360, max_models = 100, seed=1234567, stopping_rounds=5, st
dl_random_grid <- h2o.grid(
  algorithm="deeplearning",
  grid_id = "dl_grid_random",
  training_frame=sampled_train,
  validation_frame=valid,
  x=predictors,
  y=response,
  epochs=1,
  stopping_metric="logloss",
  stopping_tolerance=1e-2,        ## stop when logloss does not improve by >=1% for 2 scoring events
  stopping_rounds=2,
  score_validation_samples=10000, ## downsample validation set for faster scoring
  score_duty_cycle=0.025,         ## don't score more than 2.5% of the wall time
  max_w2=10,                      ## can help improve stability for Rectifier
  hyper_params = hyper_params,
  search_criteria = search_criteria
)
grid <- h2o.getGrid("dl_grid_random",sort_by="logloss",decreasing=FALSE)
grid

grid@summary_table[1,]
best_model <- h2o.getModel(grid@model_ids[[1]]) ## model with lowest logloss
best_model
```

Let's look at the model with the lowest validation misclassification rate:

```
grid <- h2o.getGrid("dl_grid",sort_by="err",decreasing=FALSE)
best_model <- h2o.getModel(grid@model_ids[[1]]) ## model with lowest classification error (on validation, since it was available
h2o.confusionMatrix(best_model,valid=T)
best_params <- best_model@allparameters
best_params$activation
best_params$hidden
best_params$input_dropout_ratio
best_params$l1
best_params$l2
```

Checkpointing

Let's continue training the manually tuned model from before, for 2 more epochs. Note that since many important parameters such as `epochs, l1, l2, max_w2, score_interval, train_samples_per_iteration, input_dropout_ratio, hidden_dropout_ratios, score_duty_cycle, classification_stop, regression_stop, variable_importances, force_load_balance` can be modified between checkpoint restarts, it is best to specify as many parameters as possible explicitly.

```
max_epochs <- 12 ## Add two more epochs
m_cont <- h2o.deeplearning(
  model_id="dl_model_tuned_continued",
  checkpoint="dl_model_tuned",
  training_frame=train,
  validation_frame=valid,
  x=predictors,
  y=response,
  hidden=c(128,128,128),          ## more hidden layers -> more complex interactions
  epochs=max_epochs,              ## hopefully long enough to converge (otherwise restart again)
  stopping_metric="logloss",      ## logloss is directly optimized by Deep Learning
  stopping_tolerance=1e-2,        ## stop when validation logloss does not improve by >=1% for 2 scoring events
  stopping_rounds=2,
  score_validation_samples=10000, ## downsample validation set for faster scoring
  score_duty_cycle=0.025,         ## don't score more than 2.5% of the wall time
  adaptive_rate=F,                ## manually tuned learning rate
  rate=0.01,
  rate_annealing=2e-6,
  momentum_start=0.2,             ## manually tuned momentum
  momentum_stable=0.4,
  momentum_ramp=1e7,
  l1=1e-5,                        ## add some L1/L2 regularization
  l2=1e-5,
  max_w2=10                       ## helps stability for Rectifier
)
summary(m_cont)
plot(m_cont)
```

Once we are satisfied with the results, we can save the model to disk (on the cluster). In this example, we store the model in a directory called `mybest_deeplearning_covtype_model`, which will be created for us since `force=TRUE`.

```
path <- h2o.saveModel(m_cont,
          path="./mybest_deeplearning_covtype_model", force=TRUE)
```

It can be loaded later with the following command:

```
print(path)
m_loaded <- h2o.loadModel(path)
summary(m_loaded)
```

This model is fully functional and can be inspected, restarted, or used to score a dataset, etc. Note that binary compatibility between H2O versions is currently not guaranteed.

Cross-Validation

For N-fold cross-validation, specify `nfolds>1` instead of (or in addition to) a validation frame, and `N+1` models will be built: 1 model on the full training data, and N models with each 1/N-th of the data held out (there are different holdout strategies). Those N models then score on the held out data, and their combined predictions on the full training data are scored to get the cross-validation metrics.

```
dlmodel <- h2o.deeplearning(
  x=predictors,
  y=response,
  training_frame=train,
  hidden=c(10,10),
  epochs=1,
  nfolds=5,
  fold_assignment="Modulo" # can be "AUTO", "Modulo", "Random" or "Stratified"
  )
dlmodel
```

N-fold cross-validation is especially useful with early stopping, as the main model will pick the ideal number of epochs from the convergence behavior of the cross-validation models.

Regression and Binary Classification

Assume we want to turn the multi-class problem above into a binary classification problem. We create a binary response as follows:

```
train$bin_response <- ifelse(train[,response]=="class_1", 0, 1)
```

Let's build a quick model and inspect the model:

```
dlmodel <- h2o.deeplearning(
  x=predictors,
  y="bin_response",
  training_frame=train,
  hidden=c(10,10),
  epochs=0.1
)
summary(dlmodel)
```

Instead of a binary classification model, we find a regression model (`H2ORegressionModel`) that contains only 1 output neuron (instead of 2). The reason is that the response was a numerical feature (ordinal numbers 0 and 1), and H2O Deep Learning was run with `distribution=AUTO` , which defaulted to a Gaussian regression problem for a real-valued response. H2O Deep Learning supports regression for distributions other than `Gaussian` such as `Poisson` , `Gamma` , `Tweedie` , `Laplace` . It also supports `Huber` loss and per-row offsets specified via an `offset_column` . We refer to our H2O Deep Learning regression code examples for more information.

To perform classification, the response must first be turned into a categorical (factor) feature:

```
train$bin_response <- as.factor(train$bin_response) ##make categorical
dlmodel <- h2o.deeplearning(
  x=predictors,
  y="bin_response",
  training_frame=train,
  hidden=c(10,10),
  epochs=0.1
  #balance_classes=T    ## enable this for high class imbalance
)
summary(dlmodel) ## Now the model metrics contain AUC for binary classification
plot(h2o.performance(dlmodel)) ## display ROC curve
```

Now the model performs (binary) classification, and has multiple (2) output neurons.

Unsupervised Anomaly detection

For instructions on how to build unsupervised models with H2O Deep Learning, we refer to our previous Tutorial on Anomaly Detection with H2O Deep Learning and our MNIST Anomaly detection code example, as well as our Stacked AutoEncoder R code example and another one for Unsupervised Pretraining with an AutoEncoder R code example.

H2O Deep Learning Tips & Tricks

Performance Tuning

The Definitive H2O Deep Learning Performance Tuning blog post covers many of the following points that affect the computational efficiency, so it's highly recommended.

Activation Functions

While sigmoids have been used historically for neural networks, H2O Deep Learning implements `Tanh` , a scaled and shifted variant of the sigmoid which is symmetric around 0. Since its output values are bounded by -1..1, the stability of the neural network is rarely endangered. However, the derivative of the tanh function is always non-zero and back-propagation (training) of the weights is more

computationally expensive than for rectified linear units, or `Rectifier`, which is `max(0,x)` and has vanishing gradient for `x<=0`, leading to much faster training speed for large networks and is often the fastest path to accuracy on larger problems. In case you encounter instabilities with the `Rectifier` (in which case model building is automatically aborted), try a limited value to re-scale the weights: `max_w2=10`. The `Maxout` activation function is computationally more expensive, but can lead to higher accuracy. It is a generalized version of the Rectifier with two non-zero channels. In practice, the `Rectifier` (and `RectifierWithDropout`, see below) is the most versatile and performant option for most problems.

Generalization Techniques

L1 and L2 penalties can be applied by specifying the `l1` and `l2` parameters. Intuition: L1 lets only strong weights survive (constant pulling force towards zero), while L2 prevents any single weight from getting too big. Dropout has recently been introduced as a powerful generalization technique, and is available as a parameter per layer, including the input layer. `input_dropout_ratio` controls the amount of input layer neurons that are randomly dropped (set to zero), while `hidden_dropout_ratios` are specified for each hidden layer. The former controls overfitting with respect to the input data (useful for high-dimensional noisy data), while the latter controls overfitting of the learned features. Note that `hidden_dropout_ratios` require the activation function to end with `...WithDropout`.

Early stopping and optimizing for lowest validation error

By default, Deep Learning training stops when the `stopping_metric` does not improve by at least `stopping_tolerance` (0.01 means 1% improvement) for `stopping_rounds` consecutive scoring events on the training (or validation) data. By default, `overwrite_with_best_model` is enabled and the model returned after training for the specified number of epochs (or after stopping early due to convergence) is the model that has the best training set error (according to the metric specified by `stopping_metric`), or, if a validation set is provided, the lowest validation set error. Note that the training or validation set errors can be based on a subset of the training or validation data, depending on the values for `score_validation_samples` or `score_training_samples`, see below. For early stopping on a predefined error rate on the *training data* (accuracy for classification or MSE for regression), specify `classification_stop` or `regression_stop`.

Training Samples per MapReduce Iteration

The parameter `train_samples_per_iteration` matters especially in multi-node operation. It controls the number of rows trained on for each MapReduce iteration. Depending on the value selected, one MapReduce pass can sample observations, and multiple such passes are needed to train for one epoch. All H2O compute nodes then communicate to agree on the best model coefficients (weights/biases) so far, and the model may then be scored (controlled by other parameters below). The default value of `-2` indicates auto-tuning, which attemps to keep the communication overhead at 5% of the total runtime. The parameter `target_ratio_comm_to_comp` controls this ratio. This parameter is explained in more detail in the H2O Deep Learning booklet,

Categorical Data

For categorical data, a feature with K factor levels is automatically one-hot encoded (horizontalized) into K-1 input neurons. Hence, the input neuron layer can grow substantially for datasets with high factor counts. In these cases, it might make sense to reduce the number of hidden neurons in the first hidden layer, such that large numbers of factor levels can be handled. In the limit of 1 neuron in the first hidden layer, the resulting model is similar to logistic regression with stochastic gradient descent, except that for classification problems, there's still a softmax output layer, and that the activation function is not necessarily a sigmoid (`Tanh`). If variable importances are computed, it is recommended to turn on `use_all_factor_levels` (K input neurons for K levels). The experimental option `max_categorical_features` uses feature hashing to reduce the number of input neurons via the hash trick at the expense of hash collisions and reduced accuracy. Another way to reduce the dimensionality of the (categorical) features is to use `h2o.glrm()`, we refer to the GLRM tutorial for more details.

Sparse Data

If the input data is sparse (many zeros), then it might make sense to enable the `sparse` option. This will result in the input not being standardized (0 mean, 1 variance), but only de-scaled (1 variance) and 0 values remain 0, leading to more efficient back-propagation. Sparsity is also a reason why CPU implementations can be faster than GPU implementations, because they can take advantage of if/else statements more effectively.

Missing Values

H2O Deep Learning automatically does mean imputation for missing values during training (leaving the input layer activation at 0 after standardizing the values). For testing, missing test set values are also treated the same way by default. See the `h2o.impute` function to do your own mean imputation.

Loss functions, Distributions, Offsets, Observation Weights

H2O Deep Learning supports advanced statistical features such as multiple loss functions, non-Gaussian distributions, per-row offsets and observation weights. In addition to `Gaussian` distributions and `Squared` loss, H2O Deep Learning supports `Poisson`, `Gamma`, `Tweedie` and `Laplace` distributions. It also supports `Absolute` and `Huber` loss and per-row offsets specified via an `offset_column`. Observation weights are supported via a user-specified `weights_column`.

We refer to our H2O Deep Learning R test code examples for more information.

Exporting Weights and Biases

The model parameters (weights connecting two adjacent layers and per-neuron bias terms) can be stored as H2O Frames (like a dataset) by enabling `export_weights_and_biases`, and they can be accessed as follows:

```
iris_dl <- h2o.deeplearning(1:4,5,as.h2o(iris),
            export_weights_and_biases=T)
h2o.weights(iris_dl, matrix_id=1)
h2o.weights(iris_dl, matrix_id=2)
h2o.weights(iris_dl, matrix_id=3)
h2o.biases(iris_dl,  vector_id=1)
h2o.biases(iris_dl,  vector_id=2)
h2o.biases(iris_dl,  vector_id=3)
#plot weights connecting `Sepal.Length` to first hidden neurons
plot(as.data.frame(h2o.weights(iris_dl,  matrix_id=1))[,1])
```

Reproducibility

Every run of DeepLearning results in different results since multithreading is done via Hogwild! that benefits from intentional lock-free race conditions between threads. To get reproducible results for small datasets and testing purposes, set `reproducible=T` and set `seed=1337` (pick any integer). This will not work for big data for technical reasons, and is probably also not desired because of the significant slowdown (runs on 1 core only).

Scoring on Training/Validation Sets During Training

The training and/or validation set errors *can* be based on a subset of the training or validation data, depending on the values for `score_validation_samples` (defaults to 0: all) or `score_training_samples` (defaults to 10,000 rows, since the training error is only used for early stopping and monitoring). For large datasets, Deep Learning can automatically sample the validation set to avoid spending too much time in scoring during training, especially since scoring results are not currently displayed in the model returned to R.

Note that the default value of `score_duty_cycle=0.1` limits the amount of time spent in scoring to 10%, so a large number of scoring samples won't slow down overall training progress too much, but it will always score once after the first MapReduce iteration, and once at the end of training.

Stratified sampling of the validation dataset can help with scoring on datasets with class imbalance. Note that this option also requires `balance_classes` to be enabled (used to over/under-sample the training dataset, based on the max. relative size of the resulting training dataset, `max_after_balance_size`):

More information can be found in the H2O Deep Learning booklet, in our H2O SlideShare Presentations, our H2O YouTube channel, as well as on our H2O Github Repository, especially in our H2O Deep Learning R tests, and H2O Deep Learning Python tests.

All done, shutdown H2O

```
h2o.shutdown(prompt=FALSE)
```

GBM and Random Forest in H2O

Slides

- PDF

Code

- The source code for this example is here: R script

Introduction

This tutorial shows how a H2O GLM model can be used to do binary and multi-class classification. This tutorial covers usage of H2O from R. A python version of this tutorial will be available as well in a separate document. This file is available in plain R, R markdown and regular markdown formats, and the plots are available as PDF files. All documents are available on Github.

If run from plain R, execute R in the directory of this script. If run from RStudio, be sure to `setwd()` to the location of this script. `h2o.init()` starts H2O in R's current working directory. h2o.importFile() looks for files from the perspective of where H2O was started.

More examples and explanations can be found in our H2O GLM booklet and on our H2O Github Repository.

H2O R Package

Load the H2O R package:

```
## R installation instructions are at http://h2o.ai/download
library(h2o)
```

Start H2O

Start up a 1-node H2O server on your local machine, and allow it to use all CPU cores and up to 2GB of memory:

```
h2o.init(nthreads=-1, max_mem_size="2G")
h2o.removeAll() ## clean slate - just in case the cluster was already running
```

Cover Type Data

Predicting forest cover type from cartographic variables only (no remotely sensed data). Let's import the dataset:

```
D = h2o.importFile(path = normalizePath("../data/covtype.full.csv"))
h2o.summary(D)
```

We have 11 numeric and two categorical features. Response is "Cover_Type" and has 7 classes. Let's split the data into Train/Test/Validation with train having 70% and Test and Validation 15% each:

```
data = h2o.splitFrame(D,ratios=c(.7,.15),destination_frames = c("train","test","valid"))
names(data)
```

Multinomial Model

We imported our data, so let's run GLM. As we mentioned previously, Cover_Type is the response and we use all other columns as predictors. We have multi-class problem so we pick family=multinomial. L-BFGS solver tends to be faster on multinomial problems, so we pick L-BFGS for our first try. The rest can use the default settings.

```
m1 = h2o.glm(training_frame = data$Train, validation_frame = data$Valid, x = x, y = y,family='multinomial',solver='L_BFGS')
h2o.confusionMatrix(m1, valid=TRUE)
```

The model predicts only the majority class so it's not useful at all! Maybe we regularized it too much, let's try again without regularization:

```
m2 = h2o.glm(training_frame = data$Train, validation_frame = data$Valid, x = x, y = y,family='multinomial',solver='L_BFGS', lambd
h2o.confusionMatrix(m2, valid=FALSE) # get confusion matrix in the training data
h2o.confusionMatrix(m2, valid=TRUE)  # get confusion matrix in the validation data
```

No overfitting (as train and test performance are the same), regularization is not needed in this case.

This model is actually useful. It got 28% classification error, down from 51% obtained by predicting majority class only.

Binomial Model

Since multinomial models are difficult and time consuming, let's try a simpler binary classification. We'll take a subset of the data with only `class_1` and `class_2` (the two majority classes) and build a binomial model deciding between them.

```
D_binomial = D[D$Cover_Type %in% c("class_1","class_2"),]
h2o.setLevels(D_binomial$Cover_Type,c("class_1","class_2"))
# split to train/test/validation again
data_binomial = h2o.splitFrame(D_binomial,ratios=c(.7,.15),destination_frames = c("train_b","test_b","valid_b"))
names(data_binomial)
```

We can run a binomial model now:

```
m_binomial = h2o.glm(training_frame = data_binomial$Train, validation_frame = data_binomial$Valid, x = x, y = y, family='binomial
h2o.confusionMatrix(m_binomial, valid = TRUE)
h2o.confusionMatrix(m_binomial, valid = TRUE)
```

The output for a binomial problem is slightly different from multinomial. The confusion matrix now has a threshold attached to it.

The model produces probability of `class_1` and `class_2` similarly to multinomial example earlier. However, this time we only have two classes and we can tune the classification to our needs.

The classification errors in binomial cases have a particular meaning: we call them false-positive and false negative. In reality, each can have a different cost associated with it, so we want to tune our classifier accordingly.

The common way to evaluate a binary classifier performance is to look at its ROC curve. The ROC curve plots the true positive rate versus false positive rate. We can plot it from the H2O model output:

```
fpr = m_binomial@model$training_metrics@metrics$thresholds_and_metric_scores$fpr
tpr = m_binomial@model$training_metrics@metrics$thresholds_and_metric_scores$tpr
fpr_val = m_binomial@model$validation_metrics@metrics$thresholds_and_metric_scores$fpr
tpr_val = m_binomial@model$validation_metrics@metrics$thresholds_and_metric_scores$tpr
plot(fpr,tpr, type='l')
title('AUC')
lines(fpr_val,tpr_val,type='l',col='red')
legend("bottomright",c("Train", "Validation"),col=c("black","red"),lty=c(1,1),lwd=c(3,3))
```

The area under the ROC curve (AUC) is a common "good fit" metric for binary classifiers. For this example, the results were:

```
h2o.auc(m_binomial,valid=FALSE) # on train
h2o.auc(m_binomial,valid=TRUE)  # on test
```

The default confusion matrix is computed at thresholds that optimize the F1 score. We can choose different thresholds - the H2O output shows optimal thresholds for some common metrics.

```
m_binomial@model$training_metrics@metrics$max_criteria_and_metric_scores
```

The model we just built gets 23% classification error at the F1-optimizing threshold, so there is still room for improvement. Let's add some features:

- There are 11 numerical predictors in the dataset, we will cut them into intervals and add a categorical variable for each
- We can add interaction terms capturing interactions between categorical variables

Let's make a convenience function to cut the column into intervals working on all three of our datasets (Train/Validation/Test). We'll use `h2o.hist` to determine interval boundaries (but there are many more ways to do that!) on the Train set.
We'll take only the bins with non-trivial support:

```
cut_column <- function(data,="" col)="" {="" #="" need="" lower="" upper="" bound="" due="" to="" h2o.cut="" behavior="" (points=
  min_val = min(data$Train[,col])-1
  max_val = max(data$Train[,col])+1
  x = h2o.hist(data$Train[, col])
  # use only the breaks with enough support
  breaks = x$breaks[which(x$counts > 1000)]
  # assign level names
  lvls = c("min",paste("i_",breaks[2:length(breaks)-1],sep=""),"max")
  col_cut
```

Now let's make a convenience function generating interaction terms on all three of our datasets. We'll use `h2o.interaction` :

```
interactions
```

Finally, let's wrap addition of the features into a separate function call, as we will use it again later. We'll add intervals for each numeric column and interactions between each pair of binary columns.

```
# add features to our cover type example
# let's cut all the numerical columns into intervals and add interactions between categorical terms
add_features
```

Now we generate new features and add them to the dataset. We'll also need to generate column names again, as we added more columns:

```
# Add Features
data_binomial_ext
```

Let's build the model! We should add some regularization this time because we added correlated variables, so let's try the default:

```
m_binomial_1_ext = try(h2o.glm(training_frame = data_binomial_ext$Train, validation_frame = data_binomial_ext$Valid, x = x, y = y
```

Oops, doesn't run - well, we know have more features than the default method can solve with 2GB of RAM. Let's try L-BFGS instead.

```
m_binomial_1_ext = h2o.glm(training_frame = data_binomial_ext$Train, validation_frame = data_binomial_ext$Valid, x = x, y = y, fa
h2o.confusionMatrix(m_binomial_1_ext)
h2o.auc(m_binomial_1_ext,valid=TRUE)
```

Not much better, maybe too much regularization? Let's pick a smaller lambda and try again.

```
m_binomial_2_ext = h2o.glm(training_frame = data_binomial_ext$Train, validation_frame = data_binomial_ext$Valid, x = x, y = y, fa
h2o.confusionMatrix(m_binomial_2_ext, valid=TRUE)
h2o.auc(m_binomial_2_ext,valid=TRUE)
```

Way better, we got an AUC of .91 and classification error of 0.180838. We picked our regularization strength arbitrarily. Also, we used only the l2 penalty but we added lot of extra features, some of which may be useless. Maybe we can do better with an l1 penalty. So now we want to run a lambda search to find optimal penalty strength and we want to have a non-zero l1 penalty to get sparse solution. We'll use the IRLSM solver this time as it does much better with lambda search and l1 penalty. Recall we were not able to use it before. We can use it now as we are running a lambda search that will filter out a large portion of the inactive (coefficient==0) predictors.

```
m_binomial_3_ext = h2o.glm(training_frame = data_binomial_ext$Train, validation_frame = data_binomial_ext$Valid, x = x, y = y, fa
h2o.confusionMatrix(m_binomial_3_ext, valid=TRUE)
h2o.auc(m_binomial_3_ext,valid=TRUE)
```

Better yet, we have 17% error and we used only 3000 out of 7000 features. Ok, our new features improved the binomial model significantly, so let's revisit our former multinomial model and see if they make a difference there (they should!):

```
# Multinomial Model 2
# let's revisit the multinomial case with our new features
data_ext
```

Improved considerably, 21% instead of 28%.

Generalized Low Rank Models

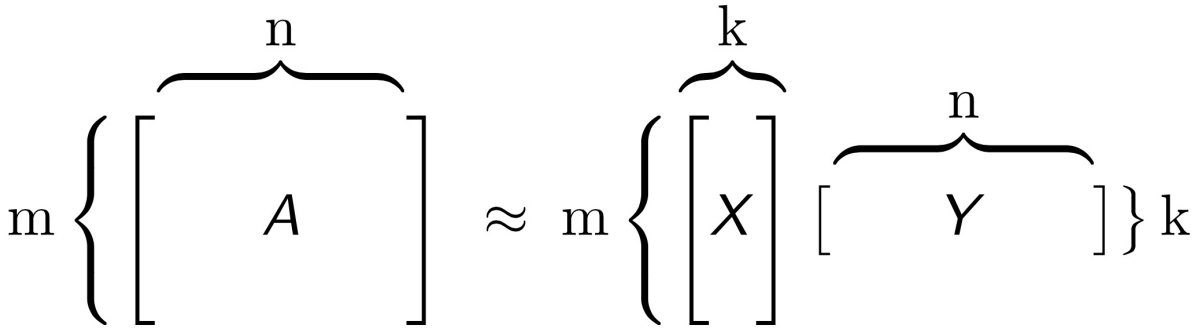
Overview

This tutorial introduces the Generalized Low Rank Model (GLRM) [1], a new machine learning approach for reconstructing missing values and identifying important features in heterogeneous data. It demonstrates how to build a GLRM in H2O and integrate it into a data science pipeline to make better predictions.

What is a Low Rank Model?

Across business and research, analysts seek to understand large collections of data with numeric and categorical values. Many entries in this table may be noisy or even missing altogether. Low rank models facilitate the understanding of tabular data by producing a condensed vector representation for every row and column in the data set.

Specifically, given a data table A with m rows and n columns, a GLRM consists of a decomposition of A into numeric matrices X and Y. The matrix X has the same number of rows as A, but only a small, user-specified number of columns k. The matrix Y has k rows and d columns, where d is equal to the total dimension of the embedded features in A. For example, if A has 4 numeric columns and 1 categorical column with 3 distinct levels (e.g., *red*, *blue* and *green*), then Y will have 7 columns. When A contains only numeric features, the number of columns in A and Y are identical, as shown below.



Both X and Y have practical interpretations. Each row of Y is an archetypal feature formed from the columns of A, and each row of X corresponds to a row of A projected into this reduced dimension feature space. We can approximately reconstruct A from the matrix product XY, which has rank k. The number k is chosen to be much less than both m and n: a typical value for 1 million rows and 2,000

columns of numeric data is k = 15. The smaller k is, the more compression we gain from our low rank representation.

GLRMs are an extension of well-known matrix factorization methods such as Principal Components Analysis (PCA). While PCA is limited to numeric data, GLRMs can handle mixed numeric, categorical, ordinal and Boolean data with an arbitrary number of missing values. It allows the user to apply regularization to X and Y, imposing restrictions like non-negativity appropriate to a particular data science context. Thus, it is an extremely flexible approach for analyzing and interpreting heterogeneous data sets.

Why use Low Rank Models?

- **Memory:** By saving only the X and Y matrices, we can significantly reduce the amount of memory required to store a large data set. A file that is 10 GB can be compressed down to 100 MB. When we need the original data again, we can reconstruct it on the fly from X and Y with minimal loss in accuracy.
- **Speed:** We can use GLRM to compress data with high-dimensional, heterogeneous features into a few numeric columns. This leads to a huge speed-up in model building and prediction, especially by machine learning algorithms that scale poorly with the size of the feature space. Below, we will see an example with 10x speed-up and no accuracy loss in deep learning.
- **Feature Engineering:** The Y matrix represents the most important combination of features from the training data. These condensed features, called archetypes, can be analyzed, visualized and incorporated into various data science applications.
- **Missing Data Imputation:** Reconstructing a data set from X and Y will automatically impute missing values. This imputation is accomplished by intelligently leveraging the information contained in the known values of each feature, as well as user-provided parameters such as the loss function.

Example 1: Visualizing Walking Stances

For our first example, we will use data on Subject 01's walking stances from an experiment carried out by *Hamner and Delp (2013)* [2]. Each of the 151 rows of the data set contains the (x, y, z) coordinates of major body parts recorded at a specific point in time.

Basic Model Building

Initialize the H2O server and import our walking stance data. We use all available cores on our computer and allocate a maximum of 2 GB of memory to H2O.

```
library(h2o)
h2o.init(nthreads = -1, max_mem_size = "2G")
gait.hex <- h2o.importFile(path = normalizePath("../data/subject01_walk1.csv"), destination_frame = "gait.hex")
```

Get a summary of the imported data set.

```
dim(gait.hex)
summary(gait.hex)
```

Build a basic GLRM using quadratic loss and no regularization. Since this data set contains only numeric features and no missing values, this is equivalent to PCA. We skip the first column since it is the time index, set the rank k = 10, and allow the algorithm to run for a maximum of 1,000 iterations.

```
gait.glrm <- h2o.glrm(training_frame = gait.hex, cols = 2:ncol(gait.hex), k = 10, loss = "Quadratic",
                      regularization_x = "None", regularization_y = "None", max_iterations = 1000)
```

To ensure our algorithm converged, we should always plot the objective function value per iteration after model building is complete.

```
plot(gait.glrm)
```

Plotting Archetypal Features

The rows of the Y matrix represent the principal stances that Subject 01 took while walking. We can visualize each of the 10 stances by plotting the (x, y) coordinate weights of each body part.

```
gait.y <- gait.glrm@model$archetypes
gait.y.mat <- as.matrix(gait.y)
x_coords <- seq(1, ncol(gait.y), by = 3)
y_coords <- seq(2, ncol(gait.y), by = 3)
feat_nams <- sapply(colnames(gait.y), function(nam) { substr(nam, 1, nchar(nam)-1) })
feat_nams <- as.character(feat_nams[x_coords])
for(k in 1:10) {
    plot(gait.y.mat[k,x_coords], gait.y.mat[k,y_coords], xlab = "X-Coordinate Weight", ylab = "Y-Coordinate Weight", main = paste
    text(gait.y.mat[k,x_coords], gait.y.mat[k,y_coords], labels = feat_nams, cex = 0.7, pos = 3)
    cat("Press [Enter] to continue")
    line <- readline()
}
```

The rows of the X matrix decompose each bodily position Subject 01 took at a specific time into a combination of the principal stances. Let's plot each principal stance over time to see how they alternate.

```
gait.x <- h2o.getFrame(gait.glrm@model$representation_name)
time.df <- as.data.frame(gait.hex$Time[1:150])[,1]
gait.x.df <- as.data.frame(gait.x[1:150,])
matplot(time.df, gait.x.df, xlab = "Time", ylab = "Archetypal Projection", main = "Archetypes over Time", type = "l", lty = 1, co
legend("topright", legend = colnames(gait.x.df), col = 1:5, pch = 1)
```

We can reconstruct our original training data from X and Y.

```
gait.pred <- predict(gait.glrm, gait.hex)
head(gait.pred)
```

For comparison, let's plot the original and reconstructed data of a specific feature over time: the x-coordinate of the left acromium.

```
lacro.df <- as.data.frame(gait.hex$L.Acromium.X[1:150])
lacro.pred.df <- as.data.frame(gait.pred$reconstr_L.Acromium.X[1:150])
matplot(time.df, cbind(lacro.df, lacro.pred.df), xlab = "Time", ylab = "X-Coordinate of Left Acromium", main = "Position of Left
legend("topright", legend = c("Original", "Reconstructed"), col = c(1,4), pch = 1)
```

Imputing Missing Values

Suppose that due to a sensor malfunction, our walking stance data has missing values randomly interspersed. We can use GLRM to reconstruct these missing values from the existing data.

Import walking stance data containing 15% missing values and get a summary.

```
gait.miss <- h2o.importFile(path = normalizePath("../data/subject01_walk1_miss15.csv"), destination_frame = "gait.miss")
dim(gait.miss)
summary(gait.miss)
```

Count the total number of missing values in the data set.

```
sum(is.na(gait.miss))
```

Build a basic GLRM with quadratic loss and no regularization, validating on our original data set that has no missing values. We change the algorithm initialization method, increase the maximum number of iterations to 2,000, and reduce the minimum step size to 1e-6 to ensure convergence.

```
gait.glrm2 <- h2o.glrm(training_frame = gait.miss, validation_frame = gait.hex, cols = 2:ncol(gait.miss), k = 10, init = "SVD", s
                       loss = "Quadratic", regularization_x = "None", regularization_y = "None", max_iterations = 2000, min_step_s
plot(gait.glrm2)
```

Impute missing values in our training data from X and Y.

```
gait.pred2 <- predict(gait.glrm2, gait.miss)
head(gait.pred2)
sum(is.na(gait.pred2))
```

Plot the original and reconstructed values of the x-coordinate of the left acromium. Red x's mark the points where the training data contains a missing value, so we can see how accurate our imputation is.

```
lacro.pred.df2 <- as.data.frame(gait.pred2$reconstr_L.Acromium.X[1:150])
matplot(time.df, cbind(lacro.df, lacro.pred.df2), xlab = "Time", ylab = "X-Coordinate of Left Acromium", main = "Position of Left
legend("topright", legend = c("Original", "Imputed"), col = c(1,4), pch = 1)
lacro.miss.df <- as.data.frame(gait.miss$L.Acromium.X[1:150])
idx_miss <- which(is.na(lacro.miss.df))
points(time.df[idx_miss], lacro.df[idx_miss,1], col = 2, pch = 4, lty = 2)
```

Example 2: Compressing Zip Codes

For our second example, we will be using two data sets. The first is compliance actions carried out by the U.S. Labor Department's Wage and Hour Division (WHD) from 2014-2015. This includes information on each investigation, including the zip code tabulation area (ZCTA) where the firm is located, number of violations found and civil penalties assessed. We want to predict whether a firm is a repeat and/or willful violator. In order to do this, we need to encode the categorical ZCTA column in a meaningful way. One common approach is to replace ZCTA with indicator variables for every unique level, but due to its high cardinality (there are over 32,000 ZCTAs!), this is slow and leads to overfitting.

Instead, we will build a GLRM to condense ZCTAs into a few numeric columns representing the demographics of that area. Our second data set is the 2009-2013 American Community Survey (ACS) 5-year estimates of household characteristics. Each row contains information for a unique ZCTA, such as average household size, number of children and education. By transforming the WHD data with our GLRM, we not only address the speed and overfitting issues, but also transfer knowledge between similar ZCTAs in our model.

Condensing Categorical Data

Initialize the H2O server and import the ACS data set. We use all available cores on our computer and allocate a maximum of 2 GB of memory to H2O.

```
library(h2o)
h2o.init(nthreads = -1, max_mem_size = "2G")
acs_orig <- h2o.importFile(path = "../data/ACS_13_5YR_DP02_cleaned.zip", col.types = c("enum", rep("numeric", 149)))
```

Separate out the zip code tabulation area column.

```
acs_zcta_col <- acs_orig$ZCTA5
acs_full <- acs_orig[,-which(colnames(acs_orig) == "ZCTA5")]
```

Get a summary of the ACS data set.

```
dim(acs_full)
summary(acs_full)
```

Build a GLRM to reduce ZCTA demographics to k = 10 archetypes. We standardize the data before model building to ensure a

good fit. For the loss function, we select quadratic again, but this time, apply regularization to X and Y in order to sparsify the condensed features.

```
acs_model <- h2o.glrm(training_frame = acs_full, k = 10, transform = "STANDARDIZE",
                      loss = "Quadratic", regularization_x = "Quadratic",
                      regularization_y = "L1", max_iterations = 100, gamma_x = 0.25, gamma_y = 0.5)
plot(acs_model)
```

The rows of the X matrix map each ZCTA into a combination of demographic archetypes.

```
zcta_arch_x <- h2o.getFrame(acs_model@model$representation_name)
head(zcta_arch_x)
```

Plot a few interesting ZCTAs on the first two archetypes. We should see cities with similar demographics, such as Sunnyvale and Cupertino, grouped close together, while very different cities, such as the rural town McCune and the upper east side of Manhattan, fall far apart on the graph.

```
idx <- ((acs_zcta_col == "10065") |   # Manhattan, NY (Upper East Side)
        (acs_zcta_col == "11219") |   # Manhattan, NY (East Harlem)
        (acs_zcta_col == "66753") |   # McCune, KS
        (acs_zcta_col == "84104") |   # Salt Lake City, UT
        (acs_zcta_col == "94086") |   # Sunnyvale, CA
        (acs_zcta_col == "95014"))    # Cupertino, CA

city_arch <- as.data.frame(zcta_arch_x[idx,1:2])
xeps <- (max(city_arch[,1]) - min(city_arch[,1])) / 10
yeps <- (max(city_arch[,2]) - min(city_arch[,2])) / 10
xlims <- c(min(city_arch[,1]) - xeps, max(city_arch[,1]) + xeps)
ylims <- c(min(city_arch[,2]) - yeps, max(city_arch[,2]) + yeps)
plot(city_arch[,1], city_arch[,2], xlim = xlims, ylim = ylims, xlab = "First Archetype", ylab = "Second Archetype", main = "Arche
text(city_arch[,1], city_arch[,2], labels = c("Upper East Side", "East Harlem", "McCune", "Salt Lake City", "Sunnyvale", "Cuperti
```

Runtime and Accuracy Comparison

We now build a deep learning model on the WHD data set to predict repeat and/or willful violators. For comparison purposes, we train our model using the original data, the data with the ZCTA column replaced by the compressed GLRM representation (the X matrix), and the data with the ZCTA column replaced by all the demographic features in the ACS data set.

Import the WHD data set and get a summary.

```
whd_zcta <- h2o.importFile(path = "../data/whd_zcta_cleaned.zip", col.types = c(rep("enum", 7), rep("numeric", 97)))
dim(whd_zcta)
summary(whd_zcta)
```

Split the WHD data into test and train with a 20/80 ratio.

```
split <- h2o.runif(whd_zcta)
train <- whd_zcta[split <= 0.8,]
test <- whd_zcta[split > 0.8,]
```

Build a deep learning model on the WHD data set to predict repeat/willful violators. Our response is a categorical column with four levels: N/A = neither repeat nor willful, R = repeat, W = willful, and RW = repeat and willful violator. Thus, we specify a multinomial distribution. We skip the first four columns, which consist of the case ID and location information that is already captured by the ZCTA.

```
myY <- "flsa_repeat_violator"
myX <- setdiff(5:ncol(train), which(colnames(train) == myY))
orig_time <- system.time(dl_orig <- h2o.deeplearning(x = myX, y = myY, training_frame = train,
                                                    validation_frame = test, distribution = "multinomial",
                                                    epochs = 0.1, hidden = c(50,50,50)))
```

Replace each ZCTA in the WHD data with the row of the X matrix corresponding to its condensed demographic representation. In the end, our single categorical column will be replaced by k = 10 numeric columns.

```
zcta_arch_x$zcta5_cd <- acs_zcta_col
whd_arch <- h2o.merge(whd_zcta, zcta_arch_x, all.x = TRUE, all.y = FALSE)
whd_arch$zcta5_cd <- NULL
summary(whd_arch)
```

Split the reduced WHD data into test/train and build a deep learning model to predict repeat/willful violators.

```
train_mod <- whd_arch[split <= 0.8,]
test_mod  <- whd_arch[split > 0.8,]
myX <- setdiff(5:ncol(train_mod), which(colnames(train_mod) == myY))
mod_time <- system.time(dl_mod <- h2o.deeplearning(x = myX, y = myY, training_frame = train_mod,
                                                   validation_frame = test_mod, distribution = "multinomial",
                                                   epochs = 0.1, hidden = c(50,50,50)))
```

Replace each ZCTA in the WHD data with the row of ACS data containing its full demographic information.

```
colnames(acs_orig)[1] <- "zcta5_cd"
whd_acs <- h2o.merge(whd_zcta, acs_orig, all.x = TRUE, all.y = FALSE)
whd_acs$zcta5_cd <- NULL
summary(whd_acs)
```

Split the combined WHD-ACS data into test/train and build a deep learning model to predict repeat/willful violators.

```
train_comb <- whd_acs[split <= 0.8,]
test_comb <- whd_acs[split > 0.8,]
myX <- setdiff(5:ncol(train_comb), which(colnames(train_comb) == myY))
comb_time <- system.time(dl_comb <- h2o.deeplearning(x = myX, y = myY, training_frame = train_comb,
                                                    validation_frame = test_comb, distribution = "multinomial",
                                                    epochs = 0.1, hidden = c(50,50,50)))
```

Compare the performance between the three models. We see that the model built on the reduced WHD data set finishes almost 10 times faster than the model using the original data set, and it yields a lower log-loss error. The model with the combined WHD-ACS data set does not improve significantly on this error. We can conclude that our GLRM compressed the ZCTA demographics with little informational loss.

```
data.frame(original = c(orig_time[3], h2o.logloss(dl_orig, train = TRUE), h2o.logloss(dl_orig, valid = TRUE)),
              reduced  = c(mod_time[3], h2o.logloss(dl_mod, train = TRUE), h2o.logloss(dl_mod, valid = TRUE)),
           combined = c(comb_time[3], h2o.logloss(dl_comb, train = TRUE), h2o.logloss(dl_comb, valid = TRUE)),
           row.names = c("runtime", "train_logloss", "test_logloss"))
```

References

[1] M. Udell, C. Horn, R. Zadeh, S. Boyd (2014). Generalized Low Rank Models. Unpublished manuscript, Stanford Electrical Engineering Department.

[2] Hamner, S.R., Delp, S.L. Muscle contributions to fore-aft and vertical body mass center accelerations over a range of running speeds. Journal of Biomechanics, vol 46, pp 780-787. (2013)

Ensembles: Stacking, Super Learner

- Overview
- What is Ensemble Learning?
  - Bagging
  - Boosting
  - Stacking / Super Learning
- H2O Ensemble: Super Learning in H2O

Overview

In this tutorial, we will discuss ensemble learning with a focus on a type of ensemble learning called stacking or Super Learning. In this tutorial, we present an H2O implementation of the Super Learner algorithm (aka. Stacking, Stacked Ensembles).

Following the introduction to ensemble learning, we will dive into a hands-on code demo of the h2oEnsemble R package. Note that as of H2O 3.10.3.1, Stacked Ensembles are now available as part of base H2O. The documentation for H2O Stacked Ensembles, including R and Python code examples, can be found here. The **h2oEnsemble** R package is the predecessor to the base H2O implementation and although this package will contibue to be supported, new development efforts will be focused on the native H2O version of stacked ensembles, and for new projects we'd recommend using native H2O.

H2O World slides accompanying this tutorial are here.

The GitHub page for the ensembles is here.

What is Ensemble Learning?

Ensemble machine learning methods use multiple learning algorithms to obtain better predictive performance than could be obtained from any of the constituent learning algorithms.

Many of the popular modern machine learning algorithms are actually ensembles. For example, Random Forest and Gradient Boosting Machine are both ensemble learners.

Common types of ensembles:

- Bagging
- Boosting
- Stacking

Bagging

Bootstrap aggregating, or bagging, is an ensemble method designed to improve the stability and accuracy of machine learning algorithms. It reduces variance and helps to avoid overfitting. Bagging is a special case of the model averaging approach and is relatively robust against noisy data and outliers.

One of the most well known bagging ensembles is the Random Forest algorithm, which applies bagging to decision trees.

Boosting

Boosting is an ensemble method designed to reduce bias and variance. A boosting algorithm iteratively learns weak classifiers and adds them to a final strong classifier.

After a weak learner is added, the data is reweighted: examples that are misclassified gain weight and examples that are classified correctly

lose weight. Thus, future weak learners focus more on the examples that previous weak learners misclassified. This causes boosting methods to be not very robust to noisy data and outliers.

Both bagging and boosting are ensembles that take a collection of weak learners and forms a single, strong learner.

Stacking / Super Learning

Stacking is a broad class of algorithms that involves training a second-level "metalearner" to ensemble a group of base learners. The type of ensemble learning implemented in H2O is called "super learning", "stacked regression" or "stacking." Unlike bagging and boosting, the goal in stacking is to ensemble strong, diverse sets of learners together.

Some Background

Leo Breiman, known for his work on classification and regression trees and the creator of the Random Forest algorithm, formalized stacking in his 1996 paper, "Stacked Regressions". Although the idea originated with David Wolpert in 1992 under the name "Stacked Generalization", the modern form of stacking that uses internal k-fold cross-validation was Dr. Breiman's contribution.

However, it wasn't until 2007 that the theoretical background for stacking was developed, which is when the algorithm took on the name, "Super Learner". Until this time, the mathematical reasons for why stacking worked were unknown and stacking was considered a "black art." The Super Learner algorithm learns the optimal combination of the base learner fits. In an article titled, "Super Learner", by Mark van der Laan et al., proved that the Super Learner ensemble represents an asymptotically optimal system for learning.

Super Learner Algorithm

Here is an outline of the tasks involved in training and testing a Super Learner ensemble.

Set up the ensemble

- Specify a list of L base algorithms (with a specific set of model parameters).
- Specify a metalearning algorithm.

Train the ensemble

- Train each of the L base algorithms on the training set.
- Perform k-fold cross-validation on each of these learners and collect the cross-validated predicted values from each of the L algorithms.
- The N cross-validated predicted values from each of the L algorithms can be combined to form a new N x L matrix. This matrix, along wtih the original response vector, is called the "level-one" data. (N = number of rows in the training set)
- Train the metalearning algorithm on the level-one data.
- The "ensemble model" consists of the L base learning models and the metalearning model, which can then be used to generate predictions on a test set.

Predict on new data

- To generate ensemble predictions, first generate predictions from the base learners.
- Feed those predictions into the metalearner to generate the ensemble prediction.

H2O Ensemble: Super Learning in H2O

H2O Ensemble has been implemented as a stand-alone R package called h2oEnsemble. The package is an extension to the h2o R package that allows the user to train an ensemble in the H2O cluster using any of the supervised machine learning algorithms H2O. As in the **h2o** R package, all of the actual computation in **h2oEnsemble** is performed inside the H2O cluster, rather than in R memory.

The main computational tasks in the Super Learner ensemble algorithm are the training and cross-validation of the base learners and

metalearner. Therefore, implementing the "plumbing" of the ensemble in R (rather than in Java) does not incur a loss of performance. All training and data processing are performed in the high-performance H2O cluster.

H2O Ensemble currently supports regression and binary classification. Multi-class support will be added in a future release.

Install H2O Ensemble

To install the **h2oEnsemble** package, you just need to follow the installation instructions on the README file, also documented here for convenience.

H2O R Package

First you need to install the H2O R package if you don't already have it installed. The R installation instructions are at: http://h2o.ai/download

H2O Ensemble R Package

The recommended way of installing the **h2oEnsemble** R package is directly from GitHub using the devtools package (however, H2O World tutorial attendees should install the package from the provided USB stick).

Install from GitHub

```
library(devtools)
install_github("h2oai/h2o-3/h2o-r/ensemble/h2oEnsemble-package")
```

Higgs Demo

This is an example of binary classification using the `h2o.ensemble` function, which is available in **h2oEnsemble**. This demo uses a subset of the HIGGS dataset, which has 28 numeric features and a binary response. The machine learning task in this example is to distinguish between a signal process which produces Higgs bosons (Y = 1) and a background process which does not (Y = 0). The dataset contains approximately the same number of positive vs negative examples. In other words, this is a balanced, rather than imbalanced, dataset.

If run from plain R, execute R in the directory of this script. If run from RStudio, be sure to setwd() to the location of this script. h2o.init() starts H2O in R's current working directory. h2o.importFile() looks for files from the perspective of where H2O was started.

Start H2O Cluster

```
library(h2oEnsemble)  # This will load the `h2o` R package as well
h2o.init(nthreads = -1)  # Start an H2O cluster with nthreads = num cores on your machine
h2o.removeAll() # (Optional) Remove all objects in H2O cluster
```

Load Data into H2O Cluster

First, import a sample binary outcome train and test set into the H2O cluster.

```
train <- h2o.importFile("https://s3.amazonaws.com/erin-data/higgs/higgs_train_5k.csv")
test <- h2o.importFile("https://s3.amazonaws.com/erin-data/higgs/higgs_test_5k.csv")
y <- "response"
x <- setdiff(names(train), y)
family <- "binomial"
```

For binary classification, the response should be encoded as a factor type (also known as the enum type in Java or categorial in Python Pandas). The user can specify column types in the `h2o.importFile` command, or you can convert the response column as follows:

```
train[,y] <- as.factor(train[,y])
test[,y] <- as.factor(test[,y])
```

Specify Base Learners & Metalearner

For this example, we will use the default base learner library for `h2o.ensemble`, which includes the default H2O GLM, Random Forest, GBM and Deep Neural Net (all using default model parameter values). We will also use the default metalearner, the H2O GLM.

```
learner <- c("h2o.glm.wrapper", "h2o.randomForest.wrapper",
             "h2o.gbm.wrapper", "h2o.deeplearning.wrapper")
metalearner <- "h2o.glm.wrapper"
```

Train an Ensemble

Train the ensemble (using 5-fold internal CV) to generate the level-one data. Note that more CV folds will take longer to train, but should increase performance.

```
fit <- h2o.ensemble(x = x, y = y,
                    training_frame = train,
                    family = family,
                    learner = learner,
                    metalearner = metalearner,
                    cvControl = list(V = 5))
```

Evaluate Model Performance

Since the response is binomial, we can use Area Under the ROC Curve (AUC) to evaluate the model performance. Compute test set performance, and sort by AUC (the default metric that is printed for a binomial classification):

```
perf <- h2o.ensemble_performance(fit, newdata = test)
```

Print the base learner and ensemble performance:

```
> perf

Base learner performance, sorted by specified metric:
                   learner       AUC
1          h2o.glm.wrapper 0.6824304
4 h2o.deeplearning.wrapper 0.7006335
2 h2o.randomForest.wrapper 0.7570211
3          h2o.gbm.wrapper 0.7780807


H2O Ensemble Performance on <newdata>:
----------------
Family: binomial

Ensemble performance (AUC): 0.781580655670451
```

We can compare the performance of the ensemble to the performance of the individual learners in the ensemble.

So we see the best individual algorithm in this group is the GBM with a test set AUC of 0.778, as compared to 0.782 for the ensemble. At first thought, this might not seem like much, but in many industries like medicine or finance, this small advantage can be highly valuable.

To increase the performance of the ensemble, we have several options. One of them is to increase the number of internal cross-validation folds using the `cvControl` argument. The other options are to change the base learner library or the metalearning algorithm.

Note that the ensemble results above are not reproducible since `h2o.deeplearning` is not reproducible when using multiple cores, and we did not set a seed for `h2o.randomForest.wrapper`.

If we want to evaluate the model by a different metric, say "MSE", then we can pass that metric to the `print` method for and ensemble performance object as follows:

```
> print(perf, metric = "MSE")

Base learner performance, sorted by specified metric:
                  learner       MSE
4 h2o.deeplearning.wrapper 0.2305775
1          h2o.glm.wrapper 0.2225176
2 h2o.randomForest.wrapper 0.2014339
3          h2o.gbm.wrapper 0.1916273


H2O Ensemble Performance on <newdata>:
----------------
Family: binomial

Ensemble performance (MSE): 0.1898735479034431
```

Predict

If you actually need to generate the predictions (instead of looking only at model performance), you can use the `predict()` function with a test set. Generate predictions on the test set and store as an H2O Frame:

```
pred <- predict(fit, newdata = test)
```

If you need to bring the predictions back into R memory for futher processing, you can convert `pred` to a local R data.frame as follows:

```
predictions <- as.data.frame(pred$pred)[,3]  #third column is P(Y==1)
labels <- as.data.frame(test[,y])[,1]
```

The `predict` method for an `h2o.ensemble` fit will return a list of two objects. The `pred$pred` object contains the ensemble predictions, and `pred$basepred` is a matrix of predictions from each of the base learners. In this particular example where we used four base learners, the `pred$basepred` matrix has four columns. Keeping the base learner predictions around is useful for model inspection and will allow us to calculate performance of each of the base learners on the test set (for comparison to the ensemble).

Specifying new learners

Now let's try again with a more extensive set of base learners. The **h2oEnsemble** packages comes with four functions by default that can be customized to use non-default parameters.

Here is an example of how to generate a custom learner wrappers:

```
h2o.glm.1 <- function(..., alpha = 0.0) h2o.glm.wrapper(..., alpha = alpha)
h2o.glm.2 <- function(..., alpha = 0.5) h2o.glm.wrapper(..., alpha = alpha)
h2o.glm.3 <- function(..., alpha = 1.0) h2o.glm.wrapper(..., alpha = alpha)
h2o.randomForest.1 <- function(..., ntrees = 200, nbins = 50, seed = 1) h2o.randomForest.wrapper(..., ntrees = ntrees, nbins = nb
h2o.randomForest.2 <- function(..., ntrees = 200, sample_rate = 0.75, seed = 1) h2o.randomForest.wrapper(..., ntrees = ntrees, sa
h2o.randomForest.3 <- function(..., ntrees = 200, sample_rate = 0.85, seed = 1) h2o.randomForest.wrapper(..., ntrees = ntrees, sa
h2o.randomForest.4 <- function(..., ntrees = 200, nbins = 50, balance_classes = TRUE, seed = 1) h2o.randomForest.wrapper(..., ntr
h2o.gbm.1 <- function(..., ntrees = 100, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, seed = seed)
h2o.gbm.2 <- function(..., ntrees = 100, nbins = 50, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, nbins = nbins, seed = seed)
h2o.gbm.3 <- function(..., ntrees = 100, max_depth = 10, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, max_depth = max_depth, s
h2o.gbm.4 <- function(..., ntrees = 100, col_sample_rate = 0.8, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, col_sample_rate =
h2o.gbm.5 <- function(..., ntrees = 100, col_sample_rate = 0.7, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, col_sample_rate =
h2o.gbm.6 <- function(..., ntrees = 100, col_sample_rate = 0.6, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, col_sample_rate =
h2o.gbm.7 <- function(..., ntrees = 100, balance_classes = TRUE, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, balance_classes
h2o.gbm.8 <- function(..., ntrees = 100, max_depth = 3, seed = 1) h2o.gbm.wrapper(..., ntrees = ntrees, max_depth = max_depth, se
h2o.deeplearning.1 <- function(..., hidden = c(500,500), activation = "Rectifier", epochs = 50, seed = 1)  h2o.deeplearning.wrapp
h2o.deeplearning.2 <- function(..., hidden = c(200,200,200), activation = "Tanh", epochs = 50, seed = 1)  h2o.deeplearning.wrappe
h2o.deeplearning.3 <- function(..., hidden = c(500,500), activation = "RectifierWithDropout", epochs = 50, seed = 1)  h2o.deeplea
h2o.deeplearning.4 <- function(..., hidden = c(500,500), activation = "Rectifier", epochs = 50, balance_classes = TRUE, seed = 1)
h2o.deeplearning.5 <- function(..., hidden = c(100,100,100), activation = "Rectifier", epochs = 50, seed = 1)  h2o.deeplearning.w
h2o.deeplearning.6 <- function(..., hidden = c(50,50), activation = "Rectifier", epochs = 50, seed = 1)  h2o.deeplearning.wrapper
h2o.deeplearning.7 <- function(..., hidden = c(100,100), activation = "Rectifier", epochs = 50, seed = 1)  h2o.deeplearning.wrapp
```

Let's grab a subset of these learners for our base learner library and re-train the ensemble.

Customized base learner library

```
learner <- c("h2o.glm.wrapper",
             "h2o.randomForest.1", "h2o.randomForest.2",
             "h2o.gbm.1", "h2o.gbm.6", "h2o.gbm.8",
             "h2o.deeplearning.1", "h2o.deeplearning.6", "h2o.deeplearning.7")
```

Train with new library:

```
fit <- h2o.ensemble(x = x, y = y,
                    training_frame = train,
                    family = family,
                    learner = learner,
                    metalearner = metalearner,
                    cvControl = list(V = 5))
```

Evaluate the test set performance:

```
perf <- h2o.ensemble_performance(fit, newdata = test)
```

We see an increase in performance by including a more diverse library.

Base learner test AUC (for comparison)

```
> perf

Base learner performance, sorted by specified metric:
             learner       AUC
1    h2o.glm.wrapper 0.6824304
7 h2o.deeplearning.1 0.6897187
8 h2o.deeplearning.6 0.6998472
9 h2o.deeplearning.7 0.7048874
2 h2o.randomForest.1 0.7668024
3 h2o.randomForest.2 0.7697849
4          h2o.gbm.1 0.7751240
6          h2o.gbm.8 0.7752852
5          h2o.gbm.6 0.7771115


H2O Ensemble Performance on <newdata>:
----------------
Family: binomial

Ensemble performance (AUC): 0.780924502576107
```

So what happens to the ensemble if we remove some of the weaker learners? Let's remove the GLM and DL from the learner library and see what happens...

Here is a more stripped down version of the base learner library used above:

```
learner <- c("h2o.randomForest.1", "h2o.randomForest.2",
             "h2o.gbm.1", "h2o.gbm.6", "h2o.gbm.8")
```

Again re-train the ensemble and evaluate the performance:

```
fit <- h2o.ensemble(x = x, y = y,
                    training_frame = train,
                    family = family,
                    learner = learner,
                    metalearner = metalearner,
                    cvControl = list(V = 5))

perf <- h2o.ensemble_performance(fit, newdata = test)
```

We actually lose ensemble performance by removing the weak learners! This demonstrates the power of stacking with a large and diverse set of base learners.

```
> perf

Base learner performance, sorted by specified metric:
             learner       AUC
1 h2o.randomForest.1 0.7668024
2 h2o.randomForest.2 0.7697849
3          h2o.gbm.1 0.7751240
5          h2o.gbm.8 0.7752852
4          h2o.gbm.6 0.7771115


H2O Ensemble Performance on <newdata>:
----------------
Family: binomial

Ensemble performance (AUC): 0.778853964308554
```

At first thought, you may assume that removing less performant models would increase the perforamnce of the ensemble. However, each learner has it's own unique contribution to the ensemble and the added diversity among learners usually improves performance. The Super Learner algorithm learns the optimal way of combining all these learners together in a way that is superior to other combination/blending methods.

Stacking Existing Model Sets

You can also use an existing (cross-validated) list of H2O models as the starting point and use the `h2o.stack()` function to ensemble them together via a specified metalearner. The base models must have been trained on the same dataset with same response and for cross-validation, must have all used the same folds.

An example follows. As above, start up the H2O cluster and load the training and test data.

```
library(h2oEnsemble)
h2o.init(nthreads = -1) # Start H2O cluster using all available CPU threads


# Import a sample binary outcome train/test set into R
train <- h2o.importFile("https://s3.amazonaws.com/erin-data/higgs/higgs_train_5k.csv")
test <- h2o.importFile("https://s3.amazonaws.com/erin-data/higgs/higgs_test_5k.csv")
y <- "response"
x <- setdiff(names(train), y)
family <- "binomial"

#For binary classification, response should be a factor
train[,y] <- as.factor(train[,y])
test[,y] <- as.factor(test[,y])
```

Cross-validate and train a handful of base learners and then use the `h2o.stack()` function to create the ensemble:

```
# The h2o.stack function is an alternative to the h2o.ensemble function, which
# allows the user to specify H2O models individually and then stack them together
# at a later time.  Saved models, re-loaded from disk, can also be stacked.

# The base models must use identical cv folds; this can be achieved in two ways:
# 1. they be specified explicitly by using the fold_column argument, or
# 2. use same value for `nfolds` and set `fold_assignment = "Modulo"`

nfolds <- 5

glm1 <- h2o.glm(x = x, y = y, family = family,
                training_frame = train,
                nfolds = nfolds,
                fold_assignment = "Modulo",
                keep_cross_validation_predictions = TRUE)

gbm1 <- h2o.gbm(x = x, y = y, distribution = "bernoulli",
                training_frame = train,
                seed = 1,
                nfolds = nfolds,
                fold_assignment = "Modulo",
                keep_cross_validation_predictions = TRUE)

rf1 <- h2o.randomForest(x = x, y = y, # distribution not used for RF
                        training_frame = train,
                        seed = 1,
                        nfolds = nfolds,
                        fold_assignment = "Modulo",
                        keep_cross_validation_predictions = TRUE)

dl1 <- h2o.deeplearning(x = x, y = y, distribution = "bernoulli",
                        training_frame = train,
                        nfolds = nfolds,
                        fold_assignment = "Modulo",
                        keep_cross_validation_predictions = TRUE)

models <- list(glm1, gbm1, rf1, dl1)
metalearner <- "h2o.glm.wrapper"

stack <- h2o.stack(models = models,
                   response_frame = train[,y],
                   metalearner = metalearner,
                   seed = 1,
                   keep_levelone_data = TRUE)


# Compute test set performance:
perf <- h2o.ensemble_performance(stack, newdata = test)
```

Print base learner and ensemble test set performance:

```
> print(perf)

Base learner performance, sorted by specified metric:
                                learner       AUC
1          GLM_model_R_1480128759162_16643 0.6822933
4 DeepLearning_model_R_1480128759162_18909 0.7016809
3          DRF_model_R_1480128759162_17790 0.7546005
2          GBM_model_R_1480128759162_16661 0.7780807


H2O Ensemble Performance on <newdata>:
----------------
Family: binomial

Ensemble performance (AUC): 0.781241759877087
```

All done, shutdown H2O

```
h2o.shutdown()
```

Roadmap for h2oEnsemble

h2oEnsemble is only available as an R package. A list of open tickets (bugs, feature requests) for the package can be found here (JIRA tickets with the "h2oEnsemble" tag).

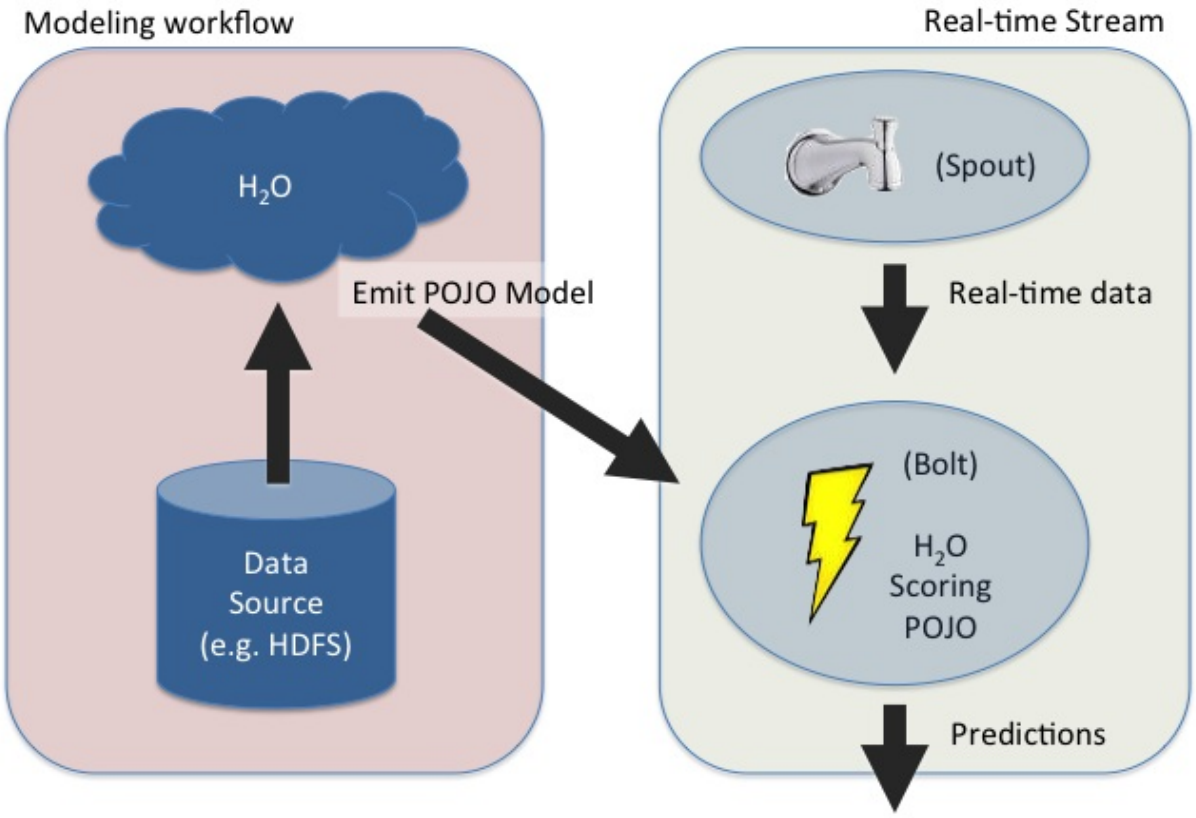
Open tickets for the native H2O version of Stacked Ensembles can be found here (JIRA tickets with the "StackedEnsemble" tag).

Real-time Predictions With H2O on Storm

This tutorial shows how to create a Storm topology can be used to make real-time predictions with H2O.

1. What this tutorial covers

In this tutorial, we explore a combined modeling and streaming workflow as seen in the picture below:



We produce a GBM model by running H2O and emitting a Java POJO used for scoring. The POJO is very lightweight and does not depend on any other libraries, not even H2O. As such, the POJO is perfect for embedding into third-party environments, like a Storm bolt.

This tutorial walks you through the following sequence:

- Installing the required software
- A brief discussion of the data
- Using R to build a gbm model in H2O
- Exporting the gbm model as a Java POJO
- Copying the generated POJO files into a Storm bolt build environment
- Building Storm and the bolt for the model
- Running a Storm topology with your model deployed
- Watching predictions in real-time

(Note that R is not strictly required, but is used for convenience by this tutorial.)

2. Installing the required software

2.1. Clone the required repositories from Github

```
git clone https://github.com/apache/storm.git
git clone https://github.com/h2oai/h2o-world-2015-training.git
```

- *NOTE*: Building storm (c.f. Section 5) requires Maven. You can install Maven (version 3.x) by following the Maven installation instructions.

Navigate to the directory for this tutorial inside the h2o-world-2015-training repository:

```
cd h2o-world-2015-training/tutorials/streaming/storm
```

You should see the following files in this directory:

- ***README.md*** (This document)
- ***example.R*** (The R script that builds the GBM model and exports it as a Java POJO)
- ***training_data.csv*** (The data used to build the GBM model)
- ***live_data.csv*** (The data that predictions are made on; used to feed the spout in the Storm topology)
- ***H2OStormStarter.java*** (The Storm topology with two bolts: a prediction bolt and a classifying bolt)
- ***TestH2ODataSpout.java*** (The Storm spout which reads data from the live_data.csv file and passes each observation to the prediction bolt one observation at a time; this simulates the arrival of data in real-time)

And the following directories:

- ***premade_generated_model*** (For those people who have trouble building the model but want to try running with Storm anyway; you can ignore this directory if you successfully build your own generated_model later in the tutorial)
- ***images*** (Images for the tutorial documentation, you can ignore these)
- ***web*** (Contains the html and image files for watching the real-time prediction output (c.f. Section 8))

2.2. Install R

Get the latest version of R from CRAN and install it on your computer.

2.3. Install the H2O package for R

> Note: The H2O package for R includes both the R code as well as the main H2O jar file. This is all you need to run H2O locally on your laptop.

Step 1: Start R (at the command line or via RStudio)

Step 2: Install H2O from CRAN

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

Note: For convenience, this tutorial was created with the Slater stable release of H2O (3.2.0.3) from CRAN, as shown above. Later versions of H2O will also work.

2.4. Development environment

This tutorial was developed with the following software environment. (Other environments will work, but this is what we used to develop and test this tutorial.)

- H2O 3.3.0.99999 (Slater)
- MacOS X (Mavericks)
- java version "1.7.0_79"
- R 3.2.2
- Storm git hash: 99285bb719357760f572d6f4f0fb4cd02a8fd389

- curl 7.30.0 (x86_64-apple-darwin13.0) libcurl/7.30.0 SecureTransport zlib/1.2.5
- Maven (Apache Maven 3.3.3)

For viewing predictions in real-time (Section 8) you will need the following:

- npm (1.3.11) (`brew install npm`)
- http-server (`npm install http-server -g`)
- A modern web browser (animations depend on D3)

3. A brief discussion of the data

Let's take a look at a small piece of the training_data.csv file for a moment. This is a synthetic data set created for this tutorial.

```
head -n 20 training_data.csv
```

Label	Has4Legs	CoatColor	HairLength	TailLength	EnjoysPlay	StaresOutWindow	HoursSp
dog	1	Brown	0	2	1	1	2
dog	1	Brown	1	1	1	1	5
dog	1	Grey	1	10	1	1	2
dog	1	Grey	1	1	1	1	2
dog	1	Brown	1	5	1	0	10
cat	1	Grey	1	6	1	1	3
dog	1	Spotted	1	1	1	1	2
cat	1	Spotted	1	7	0	1	5
dog	1	Grey	1	1	1	1	2
cat	1	Black	0	7	0	1	5
dog	1	Grey	1	1	1	0	2
dog	1	Spotted	0	1	1	1	2
dog	1	Spotted	1	4	1	1	2
cat	1	Spotted	1	8	1	1	3
cat	1	White	1	8	0	1	5
cat	1	Black	1	5	1	1	2
cat	1	Grey	1	7	1	1	3
cat	1	Spotted	1	8	0	0	10

Note that the first row in the training data set is a header row specifying the column names.

The response column (i.e. the "y" column) we want to make predictions for is Label. It's a binary column, so we want to build a classification model. The response column is categorical, and contains two levels, 'cat' and 'dog'. Note that the ratio of dogs to cats is 3:1.

The remaining columns are all input features (i.e. the "x" columns) we use to predict whether each new observation is a 'cat' or a 'dog'. The input features are a mix of integer, real, and categorical columns.

4. Using R to build a gbm model in H2O and export it as a Java POJO

4.1. Build and export the model

The `example.R` script builds the model and exports the Java POJO to the generated_model temporary directory. Run `example.R` at the command line as follows:

```
R -f example.R
```

You will see the following output:

```
R version 3.2.2 (2015-08-14) -- "Fire Safety"
Copyright (C) 2015 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> #
> # Example R code for generating an H2O Scoring POJO.
> #
>
> # "Safe" system.  Error checks process exit status code.  stop() if it failed.
> safeSystem <- function(x)"" {="" +="" print(sprintf("+="" CMD:="" %s",="" x))="" res="" <-="" system(x)="" print(res)="" if="""
> library(h2o)
Loading required package: statmod

----------------------------------------------------------------------

Your next step is to start H2O:
    > h2o.init()

For H2O package documentation, ask for help:
    > ??h2o

After starting H2O, you can use the Web UI at http://localhost:54321
For more information visit http://docs.h2o.ai

----------------------------------------------------------------------


Attaching package: ‘h2o’

The following objects are masked from ‘package:stats’:

    sd, var

The following objects are masked from ‘package:base’:

    %*%, %in%, apply, as.factor, as.numeric, colnames, colnames<-, ifelse,="" is.factor,="" is.numeric,="" log,="" range,="" trur
> cat("Starting H2O\n")
Starting H2O
> myIP <- "localhost"="">> myPort <- 54321="">> h <- 1="" 2="" 8="" 738="" h2o.init(ip="myIP," port="myPort," startH2O="TRUE)" H2O=
           > h2o.init(nthreads = -1)

>
> cat("Building GBM model\n")
Building GBM model
> df <- h2o.importFile(path="normalizePath("./training_data.csv"));" |="==========
```

```
> cat("Downloading Java prediction model code from H2O\n")
Downloading Java prediction model code from H2O
> model_id <- gbm.h2o.fit@model_id="">
> tmpdir_name <- "generated_model"="> cmd <- sprintf("rm="" -fr="" %s",="" tmpdir_name)="> safeSystem(cmd)
[1] "+ CMD: rm -fr generated_model"
[1] 0
> cmd <- sprintf("mkdir="" %s",="" tmpdir_name)="> safeSystem(cmd)
[1] "+ CMD: mkdir generated_model"
[1] 0
>
> h2o.download_pojo(gbm.h2o.fit, "./generated_model/")
[1] "POJO written to: ./generated_model//GBMPojo.java"
>
> cat("Note: H2O will shut down automatically if it was started by this R script and the script exits\n")
Note: H2O will shut down automatically if it was started by this R script and the script exits
>
```

4.2. Look at the output

The generated_model directory is created and now contains two files:

```
ls -l generated_model
```

```
ls -l generated_model/
total 72
-rw-r--r--  1 ludirehak  staff  19764 Sep 25 12:36 GBMPojo.java
-rw-r--r--  1 ludirehak  staff  23655 Sep 25 12:36 h2o-genmodel.jar
```

The h2o-genmodel.jar file contains the interface definition, and the GBMPojo.java file contains the Java code for the POJO model.

The following three sections from the generated model are of special importance.

4.2.1. Class name

```
public class GBMPojo extends GenModel {
```

This is the class to instantiate in the Storm bolt to make predictions.

4.2.2. Predict method

```
public final double[] score0( double[] data, double[] preds )
```

score0() is the method to call to make a single prediction for a new observation. ***data*** is the input, and ***preds*** is the output. The return value is just ***preds***, and can be ignored.

Inputs and Outputs must be numerical. Categorical columns must be translated into numerical values using the DOMAINS mapping on the way in. Even if the response is categorical, the result will be numerical. It can be mapped back to a level string using DOMAINS, if desired. When the response is categorical, the preds response is structured as follows:

```
preds[0] contains the predicted level number
preds[1] contains the probability that the observation is level0
preds[2] contains the probability that the observation is level1
...
preds[N] contains the probability that the observation is levelN-1

sum(preds[1] ... preds[N]) == 1.0
```

In this specific case, that means:

```
preds[0] contains 0 or 1
preds[1] contains the probability that the observation is ColInfo_15.VALUES[0]
preds[2] contains the probability that the observation is ColInfo_15.VALUES[1]
```

4.2.3. DOMAINS array

```
  // Column domains. The last array contains domain of response column.
  public static final String[][] DOMAINS = new String[][] {
    /* Has4Legs */ null,
    /* CoatColor */ GBMPojo_ColInfo_1.VALUES,
    /* HairLength */ null,
    /* TailLength */ null,
    /* EnjoysPlay */ null,
    /* StaresOutWindow */ null,
    /* HoursSpentNapping */ null,
    /* RespondsToCommands */ null,
    /* EasilyFrightened */ null,
    /* Age */ null,
    /* Noise1 */ null,
    /* Noise2 */ null,
    /* Noise3 */ null,
    /* Noise4 */ null,
    /* Noise5 */ null,
    /* Label */ GBMPojo_ColInfo_15.VALUES
  };
```

The DOMAINS array contains information about the level names of categorical columns. Note that Label (the column we are predicting) is the last entry in the DOMAINS array.

5. Building Storm and the bolt for the model

5.1 Build storm and import into IntelliJ

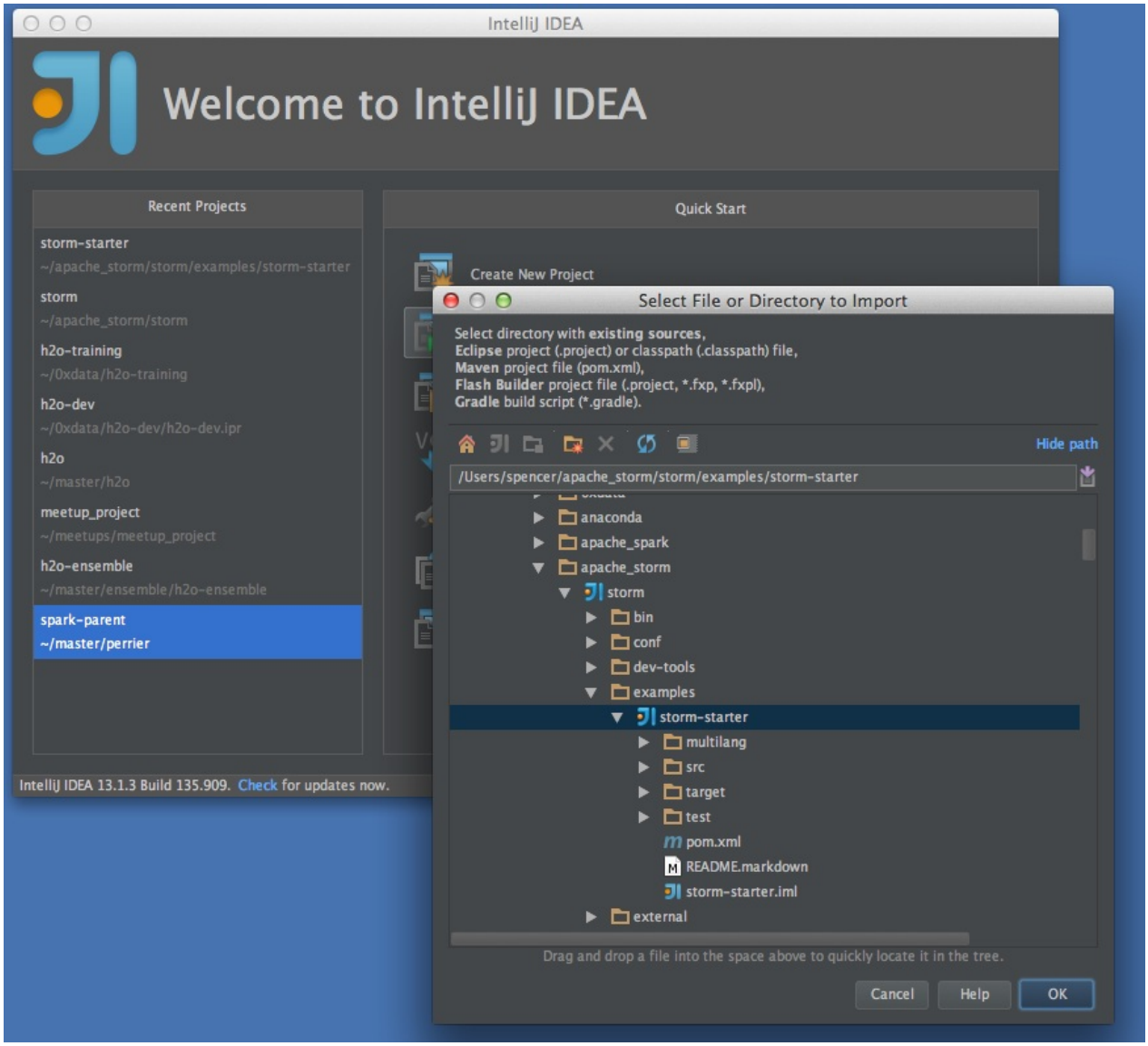
To build storm navigate to the cloned repo and install via Maven:

```
cd storm && mvn clean install -DskipTests=true
```

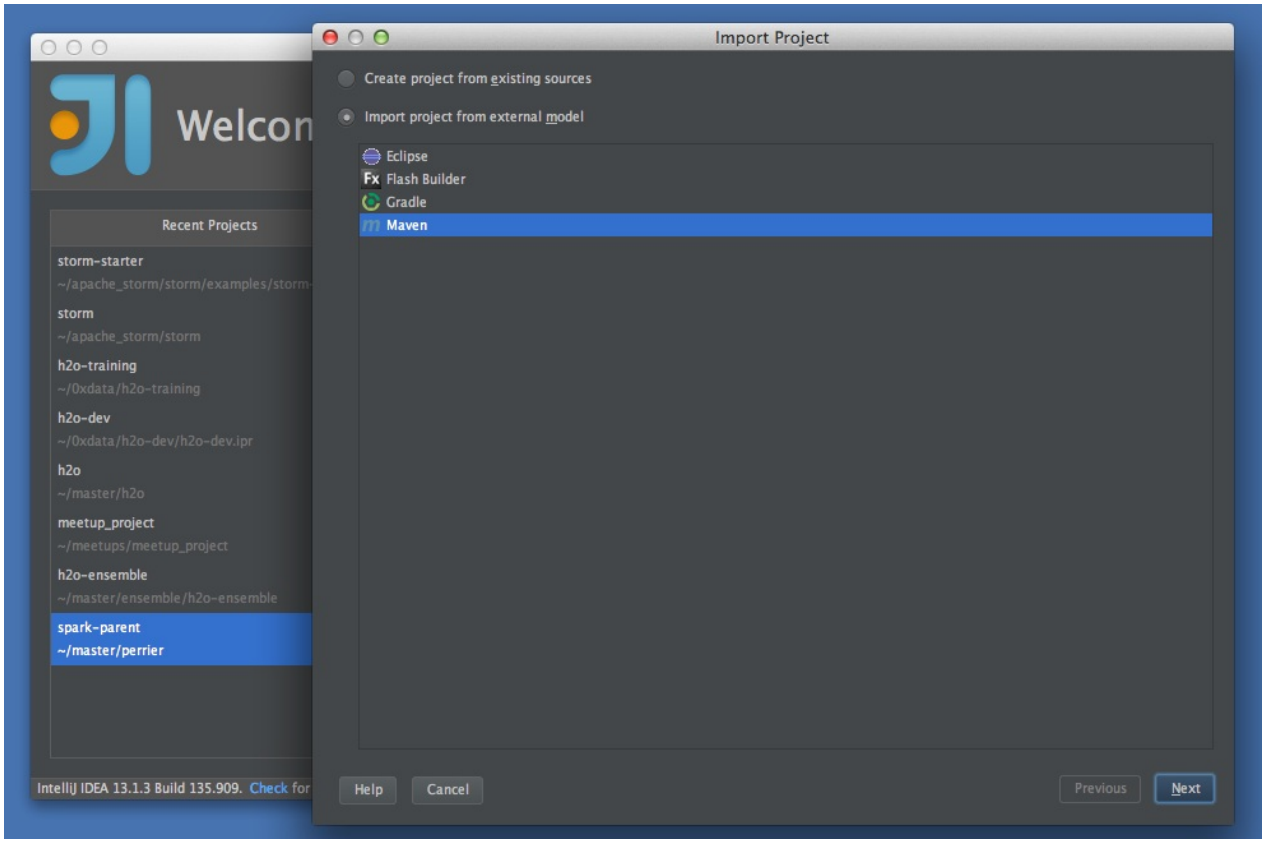
Once storm is built, open up your favorite IDE to start building the h2o streaming topology. In this tutorial, we will be using IntelliJ.

To import the storm-starter project into your IntelliJ please follow these screenshots:

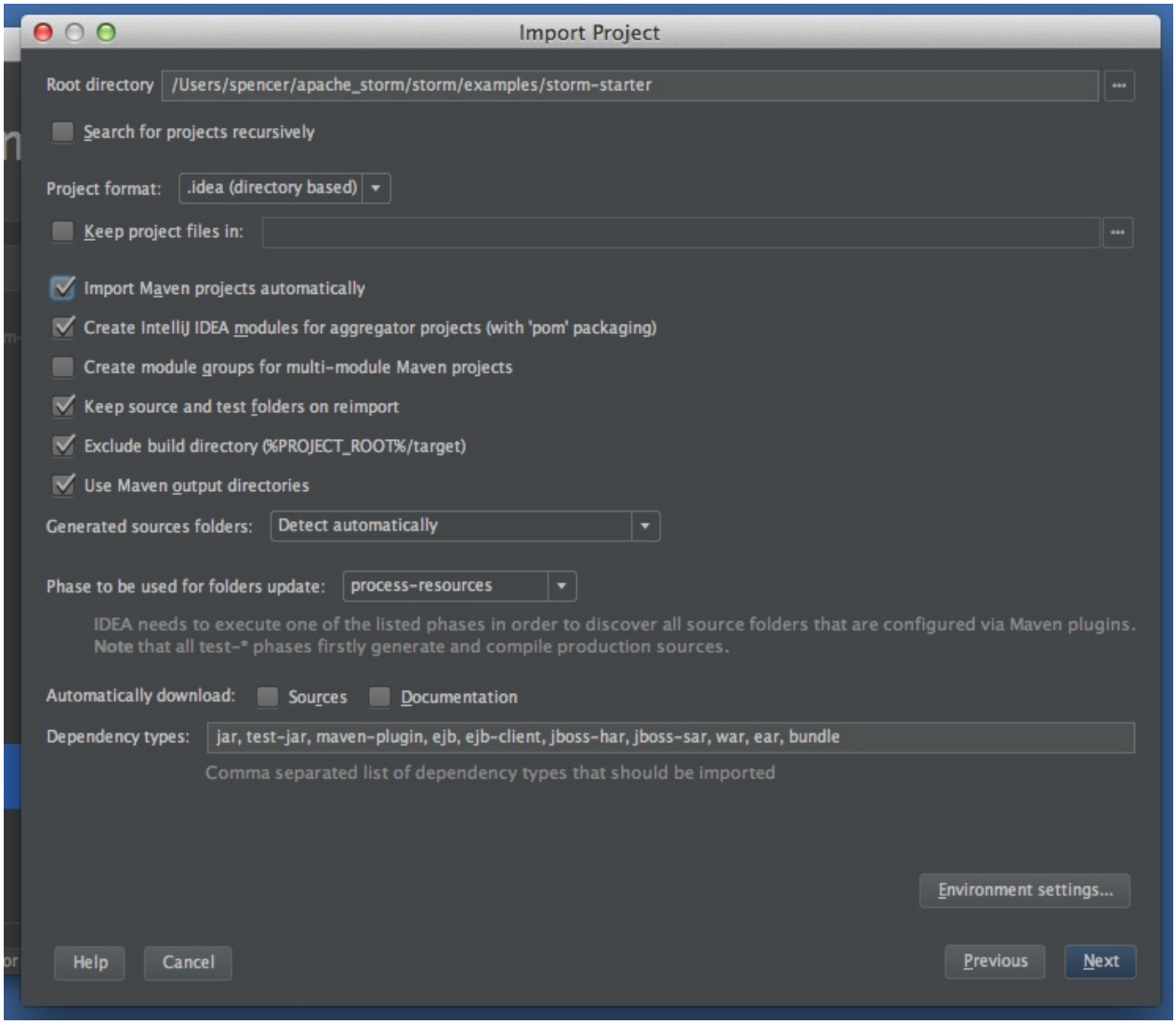
Click on "Import Project" and find the storm repo. Select storm-starter and click "OK"



Import the project from extrenal model using Maven, click "Next"



Ensure that "Import Maven projects automatically" check box is clicked (it's off by default), click "Next"



That's it! Now click through the remaining prompts (Next -> Next -> Next -> Finish).

Once inside the project, open up *storm-starter/test/jvm/storm.starter*. Yes, we'll be working out of the test directory.

5.2 Build the topology

The topology we've prepared has one spout TestH2ODataSpout and two bolts (a "Predict Bolt" and a "Classifier Bolt"). Please copy the pre-built bolts and spout into the *test* directory in IntelliJ.

Edit L100 of H2OStormStarter.java so that the file path is: `PATH_TO_H2O_WORLD_2015_TRAINING/h2o-world-2015-training/tutorials/streaming/storm/web/out`

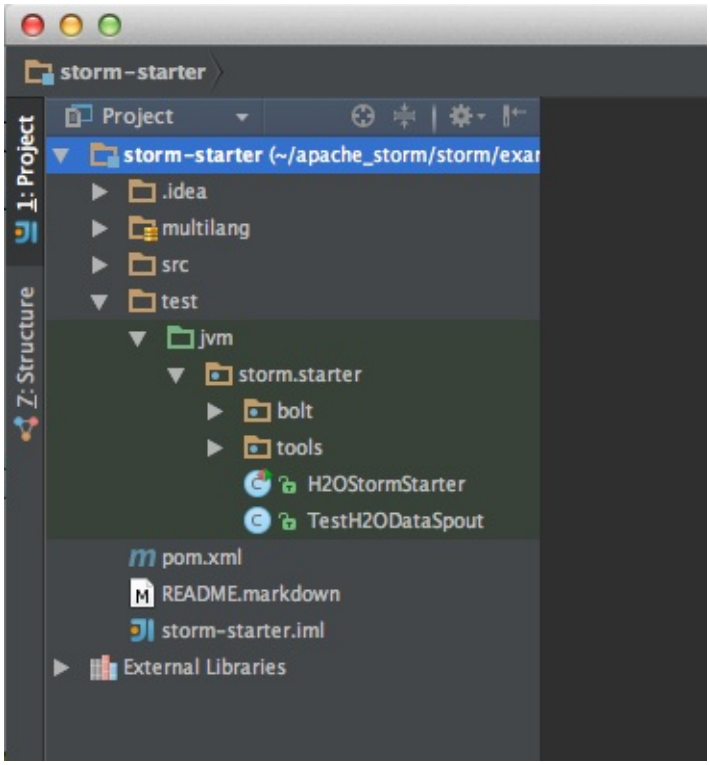
Likewise, edit L46 of TestH2ODataSpout.java so that the file path is: `PATH_TO_H2O_WORLD_2015_TRAINING/h2o-world-2015-training/tutorials/streaming/storm/live_data.csv`

Now copy.

```
cp H2OStormStarter.java /PATH_TO_STORM/storm/examples/storm-starter/test/jvm/storm/starter/
```

```
cp TestH2ODataSpout.java /PATH_TO_STORM/storm/examples/storm-starter/test/jvm/storm/starter/
```

Your project should now look like this:

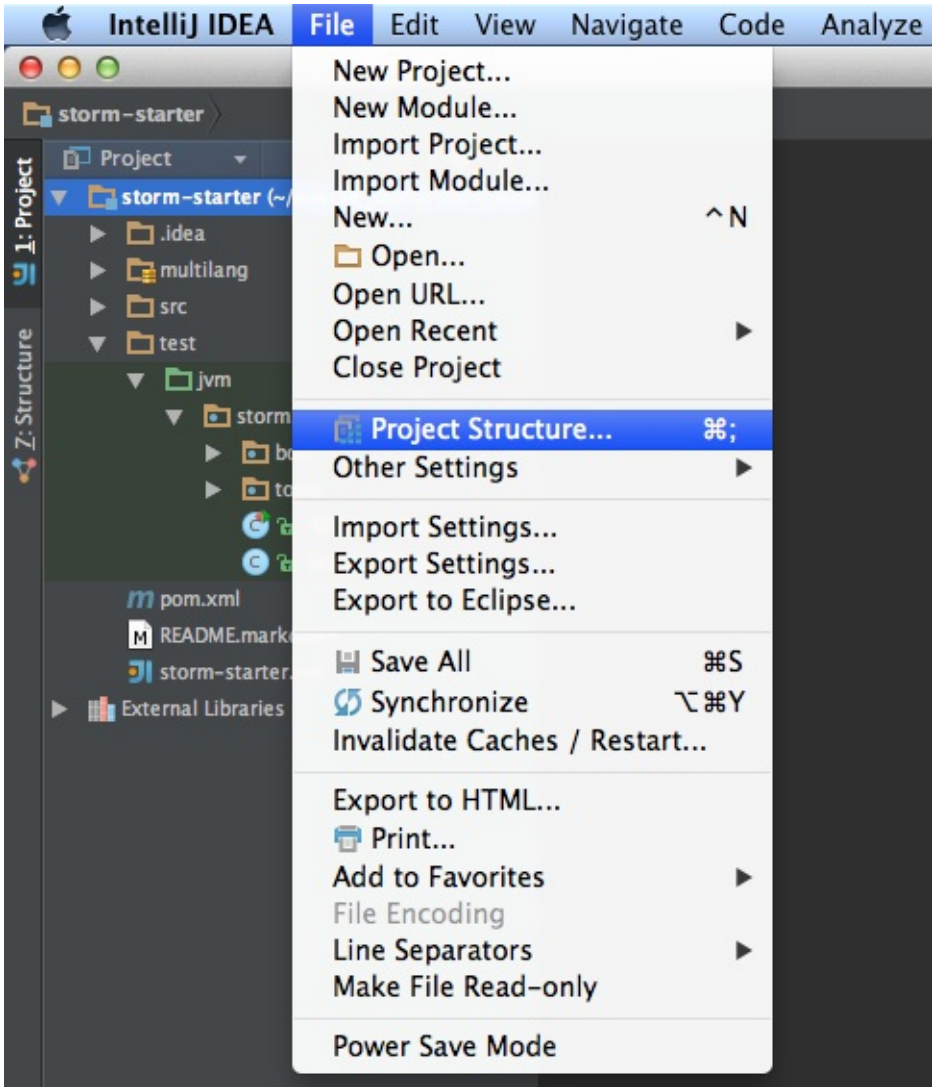


6. Copying the generated POJO files into a Storm bolt build environment

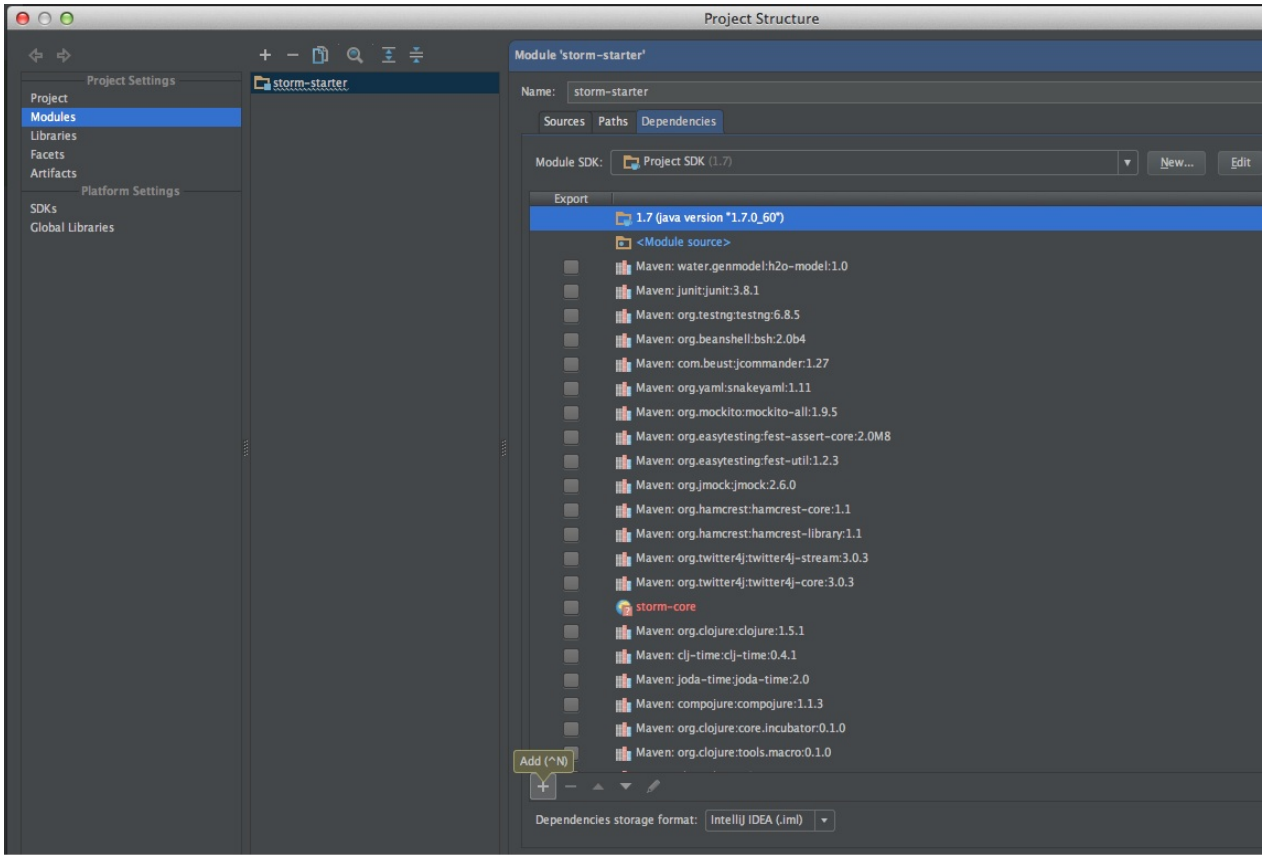
We are now ready to import the H2O pieces into the IntelliJ project. We'll need to add the *h2o-genmodel.jar* and the scoring POJO.

To import the *h2o-genmodel.jar* into your IntelliJ project, please follow these screenshots:

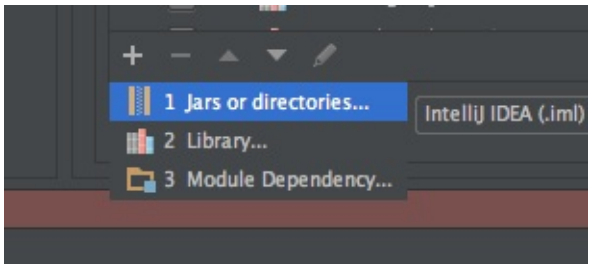
File > Project Structure…



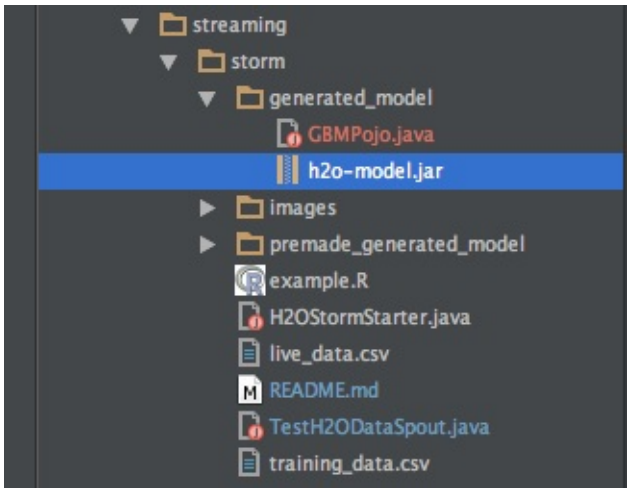
Click the "+" to add a new dependency



Click on Jars or directories…



Find the h2o-genmodel.jar that we previously downloaded with the R script in section 4



Click "OK", then "Apply", then "OK".

You now have the h2o-genmodel.jar as a dependency in your project.

Modify GBMPojo.java to add `package storm.starter;` as the first line.

```
sed -i -e '1i\'$'\n''package storm.starter;'$'\n' ./generated_model/GBMPojo.java
```

We now copy over the POJO from section 4 into our storm project.

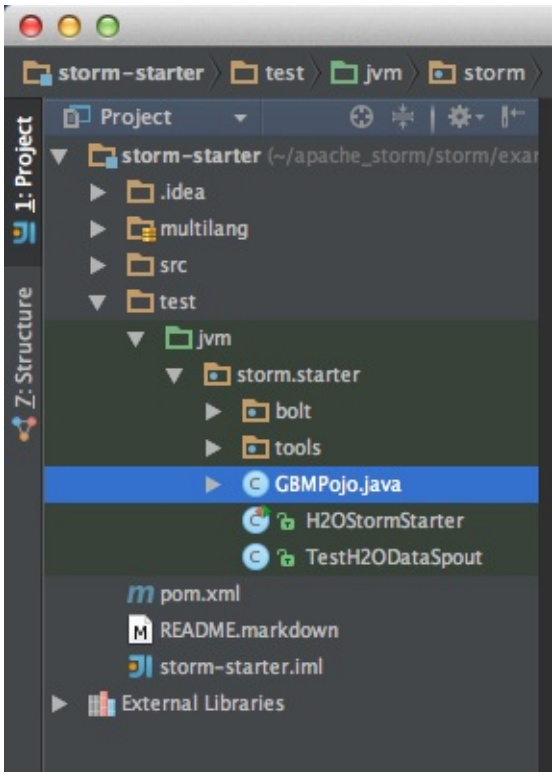
```
cp ./generated_model/GBMPojo.java /PATH_TO_STORM/storm/examples/storm-starter/test/jvm/storm/starter/
```

OR if you were not able to build the GBMPojo, copy over the pre-made version:

```
cp ./premade_generated_model/GBMPojo.java /PATH_TO_STORM/storm/examples/storm-starter/test/jvm/storm/starter/
```

If copying over the pre-made version of GBMPojo, also repeat the above steps in this section to import the pre-made *h2o-genmodel.jar* from the *premade_generated_model* directory.

Your storm-starter project directory should now look like this:



In order to use the GBMPojo class, our ***PredictionBolt*** in H2OStormStarter has the following "execute" block:

```
@Override public void execute(Tuple tuple) {

  GBMPojo p = new GBMPojo();

  // get the input tuple as a String[]
  ArrayList<String> vals_string = new ArrayList<String>();
  for (Object v : tuple.getValues()) vals_string.add((String)v);
  String[] raw_data = vals_string.toArray(new String[vals_string.size()]);

  // the score pojo requires a single double[] of input.
  // We handle all of the categorical mapping ourselves
  double data[] = new double[raw_data.length-1]; //drop the Label

  String[] colnames = tuple.getFields().toList().toArray(new String[tuple.size()]);

  // if the column is a factor column, then look up the value, otherwise put the double
  for (int i = 1; i < raw_data.length; ++i) {
    data[i-1] = p.getDomainValues(colnames[i]) == null
            ? Double.valueOf(raw_data[i])
            : p.mapEnum(p.getColIdx(colnames[i]), raw_data[i]);
  }

  // get the predictions
  double[] preds = new double [GBMPojo.NCLASSES+1];
  //p.predict(data, preds);
  p.score0(data, preds);

  // emit the results
  _collector.emit(tuple, new Values(raw_data[0], preds[1]));
  _collector.ack(tuple);
}
```

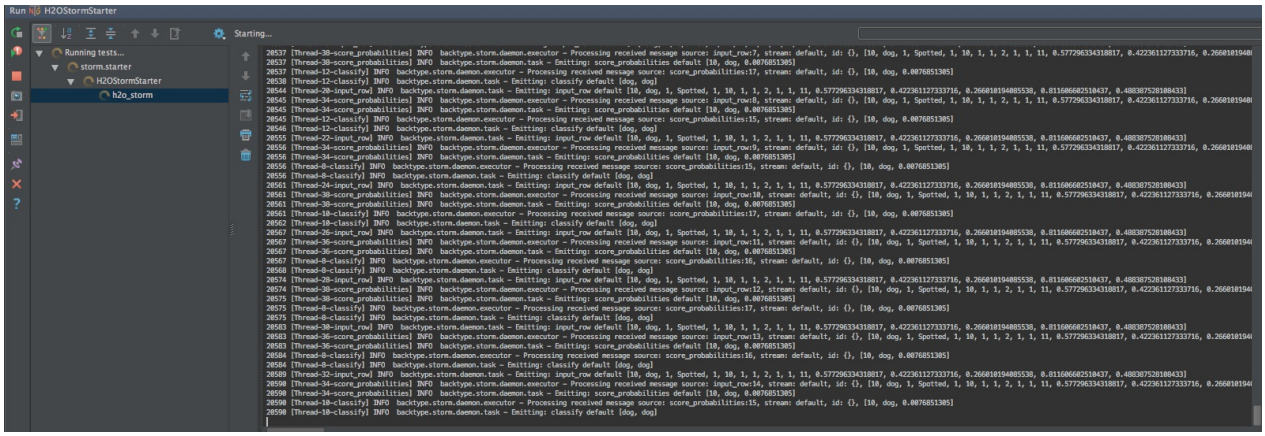
The probability emitted is the probability of being a 'dog'. We use this probability to decide whether the observation is of type 'cat' or 'dog' depending on some threshold. This threshold was chosen such that the F1 score was maximized for the testing data (please see AUC and/or h2o.performance() from R).

The ***ClassifierBolt*** then looks like:

```
public static class ClassifierBolt extends BaseRichBolt {
  OutputCollector _collector;
  final double _thresh = 0.54;

  @Override
  public void prepare(Map conf, TopologyContext context, OutputCollector collector) {
    _collector = collector;
  }

  @Override
  public void execute(Tuple tuple) {
    String expected=tuple.getString(0);
    double dogProb = tuple.getDouble(1);
    String content = expected + "," + (dogProb <= _thresh ? "dog" : "cat");
    try {
      File file = new File("/Users/ludirehak/other_h2o/h2o-world-2015-training/tutorials/streaming/storm/web/out");
      if (!file.exists())  file.createNewFile();
      FileWriter fw = new FileWriter(file.getAbsoluteFile());
      BufferedWriter bw = new BufferedWriter(fw);
      bw.write(content);
      bw.close();
    } catch (IOException e) {
      e.printStackTrace();
    }
    _collector.emit(tuple, new Values(expected, dogProb <= _thresh ? "dog" : "cat"));
    _collector.ack(tuple);
  }

  @Override
  public void declareOutputFields(OutputFieldsDeclarer declarer) {
    declarer.declare(new Fields("expected_class", "class"));
  }
}
```

7. Running a Storm topology with your model deployed

Finally, we can run the topology by right-clicking on H2OStormStarter and running. Here's a screen shot of what that looks like:



8. Watching predictions in real-time

To watch the predictions in real time, we start up an http-server on port 4040 and navigate to http://localhost:4040.

In order to get http-server, install *npm* (you may need sudo):

```
brew install npm
npm install http-server -g
```

Once these are installed, you may navigate to the *web* directory and start the server:

```
cd web
http-server -p 4040 -c-1
```

Now open up your browser and navigate to http://localhost:4040. Requires a modern browser (depends on D3 for animation).

Here's a short video showing what it looks like all together.

Enjoy!

References

- CRAN
- GBM

  The Elements of Statistical Learning. Vol.1. N.p., page 339
  Hastie, Trevor, Robert Tibshirani, and J Jerome H Friedman.
  Springer New York, 2001.

  Data Science with H2O (GBM)

  Gradient Boosting (Wikipedia)

- H2O
- H2O Markov stable release
- Java POJO
- R
- Storm

H2OWorld - Building Machine Learning Applications with Sparkling Water

Requirements

- Oracle Java 7+ (USB)
- Spark 1.5.1 (USB)
- Sparkling Water 1.5.6 (USB)
- SMS dataset (USB)

Provided on USB

- Binaries
- SMS dataset
- Slides
- Scala Script

Machine Learning Workflow

Goal: For a given text message, identify if it is spam or not.

1. Extract data
2. Transform & tokenize messages
3. Build Spark's Tf-IDF model and expand messages to feature vectors
4. Create and evaluate H2O's Deep Learning model
5. Use the models to detect spam messages

Prepare environment

1. Run Sparkling shell with an embedded Spark cluster:

```
cd "path/to/sparkling/water"
export SPARK_HOME="/path/to/spark/installation"
export MASTER="local-cluster[3,2,4096]"
bin/sparkling-shell --conf spark.executor.memory=2G
```

> Note: To avoid flooding output with Spark INFO messages, I recommend editing your `$SPARK_HOME/conf/log4j.properties` and configuring the log level to `WARN`.

2. Open Spark UI: Go to http://localhost:4040/ to see the Spark status.

3. Prepare the environment:

```
// Input data
val DATAFILE="../data/smsData.txt"
// Common imports from H2O and Sparks
import _root_.hex.deeplearning.{DeepLearningModel, DeepLearning}
import _root_.hex.deeplearning.DeepLearningParameters
import org.apache.spark.examples.h2o.DemoUtils._
import org.apache.spark.h2o._
import org.apache.spark.mllib
import org.apache.spark.mllib.feature.{IDFModel, IDF, HashingTF}
import org.apache.spark.rdd.RDD
import water.Key
```

4. Define the representation of the training message:

```
// Representation of a training message
case class SMS(target: String, fv: mllib.linalg.Vector)
```

5. Define the data loader and parser:

```
def load(dataFile: String): RDD[Array[String]] = {
 // Load file into memory, split on TABs and filter all empty lines
 sc.textFile(dataFile).map(l => l.split("\t")).filter(r => !r(0).isEmpty)
}
```

6. Define the input messages tokenizer:

```
// Tokenizer
// For each sentence in input RDD it provides array of string representing individual interesting words in the sentence
def tokenize(dataRDD: RDD[String]): RDD[Seq[String]] = {
 // Ignore all useless words
 val ignoredWords = Seq("the", "a", "", "in", "on", "at", "as", "not", "for")
 // Ignore all useless characters
 val ignoredChars = Seq(',', ':', ';', '/', '<', '>', '"', '.', '(', ')', '?', '-', '\'','!','0', '1')

 // Invoke RDD API and transform input data
 val textsRDD = dataRDD.map( r => {
   // Get rid of all useless characters
   var smsText = r.toLowerCase
   for( c <- ignoredChars) {
     smsText = smsText.replace(c, ' ')
   }
   // Remove empty and uninteresting words
   val words = smsText.split(" ").filter(w => !ignoredWords.contains(w) && w.length>2).distinct

   words.toSeq
 })
 textsRDD
}
```

7. Configure Spark's Tf-IDF model builder:

```
def buildIDFModel(tokensRDD: RDD[Seq[String]],
                  minDocFreq:Int = 4,
                  hashSpaceSize:Int = 1 << 10): (HashingTF, IDFModel, RDD[mllib.linalg.Vector]) = {
 // Hash strings into the given space
 val hashingTF = new HashingTF(hashSpaceSize)
 val tf = hashingTF.transform(tokensRDD)

 // Build term frequency-inverse document frequency model
 val idfModel = new IDF(minDocFreq = minDocFreq).fit(tf)
 val expandedTextRDD = idfModel.transform(tf)
 (hashingTF, idfModel, expandedTextRDD)
}
```

> **Wikipedia** defines TF-IDF as: "tf–idf, short for term frequency–inverse document frequency, is a numerical statistic that is intended to reflect how important a word is to a document in a collection or corpus. It is often used as a weighting factor in information retrieval and text mining. The tf-idf value increases proportionally to the number of times a word appears in the document, but is offset by the frequency of the word in the corpus, which helps to adjust for the fact that some words appear more frequently in general."

8. Configure H2O's DeepLearning model builder:

```
def buildDLModel(trainHF: Frame, validHF: Frame,
              epochs: Int = 10, l1: Double = 0.001, l2: Double = 0.0,
              hidden: Array[Int] = Array[Int](200, 200))
             (implicit h2oContext: H2OContext): DeepLearningModel = {
 import h2oContext._
 import _root_.hex.deeplearning.DeepLearning
 import _root_.hex.deeplearning.DeepLearningParameters
 // Create algorithm parameres
 val dlParams = new DeepLearningParameters()
 // Name for target model
 dlParams._model_id = Key.make("dlModel.hex")
 // Training dataset
 dlParams._train = trainHF
 // Validation dataset
 dlParams._valid = validHF
 // Column used as target for training
 dlParams._response_column = 'target
 // Number of passes over data
 dlParams._epochs = epochs
 // L1 penalty
 dlParams._l1 = l1
 // Number internal hidden layers
 dlParams._hidden = hidden

 // Create a DeepLearning job
 val dl = new DeepLearning(dlParams)
 // And launch it
 val dlModel = dl.trainModel.get

 // Force computation of model metrics on both datasets
 dlModel.score(trainHF).delete()
 dlModel.score(validHF).delete()

 // And return resulting model
 dlModel
}
```

9. Initialize `H2OContext` and start H2O services on top of Spark:

```
// Create SQL support
import org.apache.spark.sql._
implicit val sqlContext = SQLContext.getOrCreate(sc)
import sqlContext.implicits._

// Start H2O services
import org.apache.spark.h2o._
val h2oContext = new H2OContext(sc).start()
```

10. Open H2O UI and verify that H2O is running:

```
h2oContext.openFlow
```

> At this point, you can use the H2O UI and see the status of the H2O cloud by typing `getCloud`.

11. Build the final workflow using all building pieces:

```
// Data load
val dataRDD = load(DATAFILE)
// Extract response column from dataset
val hamSpamRDD = dataRDD.map( r => r(0))
// Extract message from dataset
val messageRDD = dataRDD.map( r => r(1))
// Tokenize message content
val tokensRDD = tokenize(messageRDD)

// Build IDF model on tokenized messages
// It returns
//   - hashingTF: hashing function to hash a word to a vector space
//   - idfModel: a model to transform hashed sentence to a feature vector
//   - tfidf: transformed input messages
var (hashingTF, idfModel, tfidfRDD) = buildIDFModel(tokensRDD)

// Merge response with extracted vectors
val resultDF = hamSpamRDD.zip(tfidfRDD).map(v => SMS(v._1, v._2)).toDF

// Publish Spark DataFrame as H2OFrame
val tableHF = h2oContext.asH2OFrame(resultDF, "messages_table")

// Transform target column into categorical!
tableHF.replace(tableHF.find("target"), tableHF.vec("target").toCategoricalVec()).remove()
tableHF.update(null)

// Split table into training and validation parts
val keys = Array[String]("train.hex", "valid.hex")
val ratios = Array[Double](0.8)
val frs = split(tableHF, keys, ratios)
val (trainHF, validHF) = (frs(0), frs(1))
tableHF.delete()

// Build final DeepLearning model
val dlModel = buildDLModel(trainHF, validHF)(h2oContext)
```

12. Evaluate the model's quality:

```
// Collect model metrics and evaluate model quality
import water.app.ModelMetricsSupport
val trainMetrics = ModelMetricsSupport.binomialMM(dlModel, trainHF)
val validMetrics = ModelMetricsSupport.binomialMM(dlModel, validHF)
println(trainMetrics.auc._auc)
println(validMetrics.auc._auc)
```

> You can also open the H2O UI and type `getPredictions` to visualize the model's performance or type `getModels` to see model output.

13. Create a spam detector:

```
// Spam detector
def isSpam(msg: String,
       dlModel: DeepLearningModel,
       hashingTF: HashingTF,
       idfModel: IDFModel,
       h2oContext: H2OContext,
       hamThreshold: Double = 0.5):String = {
  val msgRdd = sc.parallelize(Seq(msg))
  val msgVector: DataFrame = idfModel.transform(
                              hashingTF.transform (
                                tokenize (msgRdd))).map(v => SMS("?", v)).toDF
  val msgTable: H2OFrame = h2oContext.asH2OFrame(msgVector)
  msgTable.remove(0) // remove first column
  val prediction = dlModel.score(msgTable)

  if (prediction.vecs()(1).at(0) < hamThreshold) "SPAM DETECTED!" else "HAM"
}
```

14. Try to detect spam:

```
isSpam("Michal, h2oworld party tonight in MV?", dlModel, hashingTF, idfModel, h2oContext)
//
isSpam("We tried to contact you re your reply to our offer of a Video Handset? 750 anytime any networks mins? UNLIMITED TEXT
```

15. At this point, you have finished your 1st Sparkling Water Machine Learning application. Hack and enjoy! Thank you!

1. Define Spark Context

```
sc
```

```
<pyspark.context.SparkContext at 0x102cea1d0>
```

2. Start H2O Context

```
from pysparkling import *
sc
hc= H2OContext(sc).start()

Warning: Version mismatch. H2O is version 3.6.0.2, but the python package is version 3.7.0.99999.
```

H2O cluster uptime:	2 seconds 217 milliseconds
H2O cluster version:	3.6.0.2
H2O cluster name:	sparkling-water-nidhimehta
H2O cluster total nodes:	2
H2O cluster total memory:	3.83 GB
H2O cluster total cores:	16
H2O cluster allowed cores:	16
H2O cluster healthy:	True
H2O Connection ip:	172.16.2.98
H2O Connection port:	54329

3. Define H2O Context

```
hc

H2OContext: ip=172.16.2.98, port=54329
```

4. Import H2O Python library

```
import h2o
```

5. View all available H2O Python functions

```
#dir(h2o)
```

6. Parse Chicago Crime dataset into H2O

```
column_type = ['Numeric','String','String','Enum','Enum','Enum','Enum','Enum','Enum','Enum','Numeric','Numeric','Numeric','Numeri
f_crimes = h2o.import_file(path ="../data/chicagoCrimes10k.csv",col_types =column_type)

print(f_crimes.shape)
f_crimes.summary()


Parse Progress: [##################################################] 100%
(9999, 22)
```

	ID	Case Number	Date	Block	IUCR	Primary Type	Description
type	int	string	string	enum	enum	enum	enum
mins	21735.0	NaN	NaN	0.0	0.0	0.0	0.0
mean	9931318.73737	NaN	NaN	NaN	NaN	NaN	NaN
maxs	9962898.0	NaN	NaN	6517.0	212.0	26.0	198.0
sigma	396787.564221	NaN	NaN	NaN	NaN	NaN	NaN
zeros	0	0	0	3	16	11	933
missing	0	0	0	0	0	0	0
0	9955810.0	HY144797	02/08/2015 11:43:40 PM	081XX S COLES AVE	1811	NARCOTICS	POSS: CANNABIS 30GMS OR LESS
1	9955861.0	HY144838	02/08/2015 11:41:42 PM	118XX S STATE ST	0486	BATTERY	DOMESTIC BATTERY SIMPLE
2	9955801.0	HY144779	02/08/2015 11:30:22 PM	002XX S LARAMIE AVE	2026	NARCOTICS	POSS: PCP
3	9956197.0	HY144787	02/08/2015 11:30:23 PM	006XX E 67TH ST	1811	NARCOTICS	POSS: CANNABIS 30GMS OR LESS
4	9955846.0	HY144829	02/08/2015 11:30:58 PM	0000X S MAYFIELD AVE	0610	BURGLARY	FORCIBLE ENTRY
5	9955835.0	HY144778	02/08/2015 11:30:21 PM	010XX W 48TH ST	0486	BATTERY	DOMESTIC BATTERY SIMPLE
6	9955872.0	HY144822	02/08/2015 11:27:24 PM	015XX W ARTHUR AVE	1320	CRIMINAL DAMAGE	TO VEHICLE
7	21752.0	HY144738	02/08/2015 11:26:12 PM	060XX W GRAND AVE	0110	HOMICIDE	FIRST DEGREE MURDER
8	9955808.0	HY144775	02/08/2015 11:20:33 PM	001XX W WACKER DR	0460	BATTERY	SIMPLE
9	9958275.0	HY146732	02/08/2015 11:15:36 PM	001XX W WACKER DR	0460	BATTERY	SIMPLE

7. Look at the distribution of the IUCR column

```
f_crimes["IUCR"].table()
```

IUCR	Count
0110	16
0261	2
0263	2
0265	5
0266	2
0281	41
0291	3
0312	18
0313	20
031A	136

8. Look at the distribution of the Arrest column

```
f_crimes["Arrest"].table()
```

Arrest	Count
false	7071
true	2928

9. Modify column names to replace blank spaces with underscores

```
col_names = map(lambda s: s.replace(' ', '_'), f_crimes.col_names)
f_crimes.set_names(col_names)
```

ID	Case_Number	Date	Block	IUCR	Primary_Type	Description	Locat
9.95581e+06	HY144797	02/08/2015 11:43:40 PM	081XX S COLES AVE	1811	NARCOTICS	POSS: CANNABIS 30GMS OR LESS	STRE
9.95586e+06	HY144838	02/08/2015 11:41:42 PM	118XX S STATE ST	0486	BATTERY	DOMESTIC BATTERY SIMPLE	APAF
9.9558e+06	HY144779	02/08/2015 11:30:22 PM	002XX S LARAMIE AVE	2026	NARCOTICS	POSS: PCP	SIDE
9.9562e+06	HY144787	02/08/2015 11:30:23 PM	006XX E 67TH ST	1811	NARCOTICS	POSS: CANNABIS 30GMS OR LESS	STRE
9.95585e+06	HY144829	02/08/2015 11:30:58 PM	0000X S MAYFIELD AVE	0610	BURGLARY	FORCIBLE ENTRY	APAF
9.95584e+06	HY144778	02/08/2015 11:30:21 PM	010XX W 48TH ST	0486	BATTERY	DOMESTIC BATTERY SIMPLE	APAF
9.95587e+06	HY144822	02/08/2015 11:27:24 PM	015XX W ARTHUR AVE	1320	CRIMINAL DAMAGE	TO VEHICLE	STRE
21752	HY144738	02/08/2015 11:26:12 PM	060XX W GRAND AVE	0110	HOMICIDE	FIRST DEGREE MURDER	STRE
9.95581e+06	HY144775	02/08/2015 11:20:33 PM	001XX W WACKER DR	0460	BATTERY	SIMPLE	OTHE
9.95828e+06	HY146732	02/08/2015 11:15:36 PM	001XX W WACKER DR	0460	BATTERY	SIMPLE	HOTE

10. Set time zone to UTC for date manipulation

```
h2o.set_timezone("Etc/UTC")
```

11. Refine the date column

```
def refine_date_col(data, col, pattern):
    data[col]         = data[col].as_date(pattern)
    data["Day"]       = data[col].day()
    data["Month"]     = data[col].month()    # Since H2O indexes from 0
    data["Year"]      = data[col].year()
    data["WeekNum"]   = data[col].week()
    data["WeekDay"]   = data[col].dayOfWeek()
    data["HourOfDay"] = data[col].hour()

    # Create weekend and season cols
    data["Weekend"] = (data["WeekDay"] == "Sun" or data["WeekDay"] == "Sat").ifelse(1, 0)[0]
    data["Season"] = data["Month"].cut([0, 2, 5, 7, 10, 12], ["Winter", "Spring", "Summer", "Autumn", "Winter"])

refine_date_col(f_crimes, "Date", "%m/%d/%Y %I:%M:%S %p")
f_crimes = f_crimes.drop("Date")
```

12. Parse Census data into H2O

```
f_census = h2o.import_file("../data/chicagoCensus.csv",header=1)

## Update column names in the table
col_names = map(lambda s: s.strip().replace(' ', '_'), f_census.col_names)
f_census.set_names(col_names)
f_census = f_census[1:78,:]
print(f_census.dim)
#f_census.summary()


Parse Progress: [##################################################] 100%
[77, 9]
```

13. Parse Weather data into H2O

```
f_weather = h2o.import_file("../data/chicagoAllWeather.csv")
f_weather = f_weather[1:]
print(f_weather.dim)
#f_weather.summary()


Parse Progress: [##################################################] 100%
[5162, 6]
```

14. Look at all the null entires in the Weather table

```
f_weather[f_weather["meanTemp"].isna()]
```

month	day	year	maxTemp	meanTemp	minTemp
6	19	2008	nan	nan	nan
9	23	2008	nan	nan	nan
9	24	2008	nan	nan	nan
9	25	2008	nan	nan	nan
9	26	2008	nan	nan	nan
9	27	2008	nan	nan	nan
9	28	2008	nan	nan	nan
9	29	2008	nan	nan	nan
9	30	2008	nan	nan	nan
3	4	2009	nan	nan	nan

15. Look at the help on `as_h2o_frame`

```
hc.as_spark_frame?
f_weather

H2OContext: ip=172.16.2.98, port=54329
```

month	day	year	maxTemp	meanTemp	minTemp
1	1	2001	23	14	6
1	2	2001	18	12	6
1	3	2001	28	18	8
1	4	2001	30	24	19
1	5	2001	36	30	21
1	6	2001	33	26	19
1	7	2001	34	28	21
1	8	2001	26	20	14
1	9	2001	23	16	10
1	10	2001	34	26	19

16. Copy data frames to Spark from H2O

```
df_weather = hc.as_spark_frame(f_weather,)
df_census = hc.as_spark_frame(f_census)
df_crimes = hc.as_spark_frame(f_crimes)
```

17. Look at the weather data as parsed in Spark

(only showing top 2 rows)

```
df_weather.show(2)

+-----+---+----+-------+--------+-------+
|month|day|year|maxTemp|meanTemp|minTemp|
+-----+---+----+-------+--------+-------+
|    1|  1|2001|     23|      14|      6|
|    1|  2|2001|     18|      12|      6|
+-----+---+----+-------+--------+-------+
```

18. Join columns from Crime, Census and Weather DataFrames in Spark

```
## Register DataFrames as tables in SQL context
sqlContext.registerDataFrameAsTable(df_weather, "chicagoWeather")
sqlContext.registerDataFrameAsTable(df_census, "chicagoCensus")
sqlContext.registerDataFrameAsTable(df_crimes, "chicagoCrime")


crimeWithWeather = sqlContext.sql("""SELECT
a.Year, a.Month, a.Day, a.WeekNum, a.HourOfDay, a.Weekend, a.Season, a.WeekDay,
a.IUCR, a.Primary_Type, a.Location_Description, a.Community_Area, a.District,
a.Arrest, a.Domestic, a.Beat, a.Ward, a.FBI_Code,
b.minTemp, b.maxTemp, b.meanTemp,
c.PERCENT_AGED_UNDER_18_OR_OVER_64, c.PER_CAPITA_INCOME, c.HARDSHIP_INDEX,
c.PERCENT_OF_HOUSING_CROWDED, c.PERCENT_HOUSEHOLDS_BELOW_POVERTY,
c.PERCENT_AGED_16__UNEMPLOYED, c.PERCENT_AGED_25__WITHOUT_HIGH_SCHOOL_DIPLOMA
FROM chicagoCrime a
JOIN chicagoWeather b
ON a.Year = b.year AND a.Month = b.month AND a.Day = b.day
JOIN chicagoCensus c
ON a.Community_Area = c.Community_Area_Number""")
```

19. Print the `crimeWithWeather` data table from Spark

```
crimeWithWeather.show(2)

+----+-----+---+-------+---------+-------+------+-------+----+-----------------+--------------------+--------------+--------+----
|Year|Month|Day|WeekNum|HourOfDay|Weekend|Season|WeekDay|IUCR|     Primary_Type|Location_Description|Community_Area|District|Arre
+----+-----+---+-------+---------+-------+------+-------+----+-----------------+--------------------+--------------+--------+----
|2015|    1| 23|      4|       22|      0|Winter|    Fri|143A|WEAPONS VIOLATION|              ALLEY|            31|      12|  tr
|2015|    1| 23|      4|       19|      0|Winter|    Fri|4625|    OTHER OFFENSE|           SIDEWALK|            31|      10|  tr
+----+-----+---+-------+---------+-------+------+-------+----+-----------------+--------------------+--------------+--------+----
only showing top 2 rows
```

20. Copy table from Spark to H2O

```
hc.as_h2o_frame?
crimeWithWeatherHF = hc.as_h2o_frame(crimeWithWeather,framename="crimeWithWeather")

H2OContext: ip=172.16.2.98, port=54329



crimeWithWeatherHF.summary()
```

	Year	Month	Day	WeekNum	HourOfDay	Weekend
type	int	int	int	int	int	int
mins	2015.0	1.0	1.0	4.0	0.0	0.0
mean	2015.0	1.41944194419	17.6839683968	5.18081808181	13.6319631963	0.159115911591
maxs	2015.0	2.0	31.0	6.0	23.0	1.0
sigma	0.0	0.493492406787	11.1801043358	0.738929830409	6.47321735807	0.365802434041
zeros	0	0	0	0	374	8408
missing	0	0	0	0	0	0
0	2015.0	1.0	24.0	4.0	22.0	0.0
1	2015.0	1.0	24.0	4.0	21.0	0.0
2	2015.0	1.0	24.0	4.0	18.0	0.0
3	2015.0	1.0	24.0	4.0	18.0	0.0
4	2015.0	1.0	24.0	4.0	13.0	0.0
5	2015.0	1.0	24.0	4.0	9.0	0.0
6	2015.0	1.0	24.0	4.0	8.0	0.0
7	2015.0	1.0	24.0	4.0	1.0	0.0
8	2015.0	1.0	24.0	4.0	0.0	0.0
9	2015.0	1.0	31.0	5.0	23.0	0.0

21. Assign column types to the `CrimeWeatherHF` data table in H2O

```
crimeWithWeatherHF["Season"]= crimeWithWeatherHF["Season"].asfactor()
crimeWithWeatherHF["WeekDay"]= crimeWithWeatherHF["WeekDay"].asfactor()
crimeWithWeatherHF["IUCR"]= crimeWithWeatherHF["IUCR"].asfactor()
crimeWithWeatherHF["Primary_Type"]= crimeWithWeatherHF["Primary_Type"].asfactor()
crimeWithWeatherHF["Location_Description"]= crimeWithWeatherHF["Location_Description"].asfactor()
crimeWithWeatherHF["Arrest"]= crimeWithWeatherHF["Arrest"].asfactor()
crimeWithWeatherHF["Domestic"]= crimeWithWeatherHF["Domestic"].asfactor()
crimeWithWeatherHF["FBI_Code"]= crimeWithWeatherHF["FBI_Code"].asfactor()
crimeWithWeatherHF["Season"]= crimeWithWeatherHF["Season"].asfactor()



crimeWithWeatherHF.summary()
```

	Year	Month	Day	WeekNum	HourOfDay	Weekend
type	int	int	int	int	int	int
mins	2015.0	1.0	1.0	4.0	0.0	0.0
mean	2015.0	1.41944194419	17.6839683968	5.18081808181	13.6319631963	0.159115911591
maxs	2015.0	2.0	31.0	6.0	23.0	1.0
sigma	0.0	0.493492406787	11.1801043358	0.738929830409	6.47321735807	0.365802434041
zeros	0	0	0	0	374	8408
missing	0	0	0	0	0	0
0	2015.0	1.0	24.0	4.0	22.0	0.0
1	2015.0	1.0	24.0	4.0	21.0	0.0
2	2015.0	1.0	24.0	4.0	18.0	0.0
3	2015.0	1.0	24.0	4.0	18.0	0.0
4	2015.0	1.0	24.0	4.0	13.0	0.0
5	2015.0	1.0	24.0	4.0	9.0	0.0
6	2015.0	1.0	24.0	4.0	8.0	0.0
7	2015.0	1.0	24.0	4.0	1.0	0.0
8	2015.0	1.0	24.0	4.0	0.0	0.0
9	2015.0	1.0	31.0	5.0	23.0	0.0

22. Split final H2O data table into train test and validation sets

```
ratios = [0.6,0.2]
frs = crimeWithWeatherHF.split_frame(ratios,seed=12345)
train = frs[0]
train.frame_id = "Train"
valid = frs[2]
valid.frame_id = "Validation"
test = frs[1]
test.frame_id = "Test"
```

23. Import Model Builders from H2O Python

```
from h2o.estimators.gbm import H2OGradientBoostingEstimator
from h2o.estimators.deeplearning import H2ODeepLearningEstimator
```

24. Inspect the availble GBM parameters

```
H2OGradientBoostingEstimator?
```

25. Define Predictors

```
predictors = crimeWithWeatherHF.names[:]
response = "Arrest"
predictors.remove(response)
```

26. Create a Simple GBM model to Predict Arrests

```
model_gbm = H2OGradientBoostingEstimator(ntrees         =50,
                                         max_depth      =6,
                                         learn_rate     =0.1,
                                         #nfolds         =2,
                                         distribution   ="bernoulli")

model_gbm.train(x              =predictors,
                y              ="Arrest",
                training_frame  =train,
                validation_frame=valid
                )
```

27. Create a Simple Deep Learning model to Predict Arrests

```
model_dl = H2ODeepLearningEstimator(variable_importances=True,
                                    loss               ="Automatic")

model_dl.train(x               =predictors,
               y               ="Arrest",
               training_frame  =train,
               validation_frame=valid)


gbm Model Build Progress: [##################################################] 100%

deeplearning Model Build Progress: [##################################################] 100%
```

28. Print confusion matrices for the training and validation datasets

```
print(model_gbm.confusion_matrix(train = True))
print(model_gbm.confusion_matrix(valid = True))
```

Confusion Matrix (Act/Pred) for max f1 @ threshold = 0.335827722991:

	false	true	Error	Rate
false	4125.0	142.0	0.0333	(142.0/4267.0)
true	251.0	1504.0	0.143	(251.0/1755.0)
Total	4376.0	1646.0	0.0653	(393.0/6022.0)

Confusion Matrix (Act/Pred) for max f1 @ threshold = 0.432844055866:

	false	true	Error	Rate
false	1362.0	61.0	0.0429	(61.0/1423.0)
true	150.0	443.0	0.253	(150.0/593.0)
Total	1512.0	504.0	0.1047	(211.0/2016.0)

```
print(model_gbm.auc(train=True))
print(model_gbm.auc(valid=True))
model_gbm.plot(metric="AUC")

0.974667176776
0.92596751276
```

29. Print variable importances

```
model_gbm.varimp(True)
```

	variable	relative_importance	scaled_importance	percentage
0	IUCR	4280.939453	1.000000e+00	8.234218e-01
1	Location_Description	487.323059	1.138355e-01	9.373466e-02
2	WeekDay	55.790558	1.303232e-02	1.073109e-02
3	HourOfDay	55.419220	1.294557e-02	1.065967e-02
4	PERCENT_AGED_16__UNEMPLOYED	34.422894	8.040967e-03	6.621107e-03
5	Beat	31.468222	7.350775e-03	6.052788e-03
6	PERCENT_HOUSEHOLDS_BELOW_POVERTY	29.103352	6.798356e-03	5.597915e-03
7	PER_CAPITA_INCOME	26.233143	6.127894e-03	5.045841e-03
8	PERCENT_AGED_UNDER_18_OR_OVER_64	24.077402	5.624327e-03	4.631193e-03
9	Day	23.472567	5.483041e-03	4.514855e-03
...	...	...	...	...
15	maxTemp	11.300793	2.639793e-03	2.173663e-03
16	Community_Area	10.252146	2.394835e-03	1.971960e-03
17	HARDSHIP_INDEX	10.116072	2.363049e-03	1.945786e-03
18	Domestic	9.294327	2.171095e-03	1.787727e-03
19	District	8.304654	1.939914e-03	1.597367e-03
20	minTemp	6.243027	1.458331e-03	1.200822e-03
21	WeekNum	4.230102	9.881246e-04	8.136433e-04
22	FBI_Code	2.363182	5.520241e-04	4.545486e-04
23	Month	0.000018	4.187325e-09	3.447935e-09
24	Weekend	0.000000	0.000000e+00	0.000000e+00

25 rows × 4 columns

30. Inspect Deep Learning model output

```
model_dl

Model Details
=============
H2ODeepLearningEstimator :  Deep Learning
Model Key:  DeepLearning_model_python_1446861372065_4

Status of Neuron Layers: predicting Arrest, 2-class classification, bernoulli distribution, CrossEntropy loss, 118,802 weights/bi
```

	layer	units	type	dropout	l1	l2	mean_rate	rate_RMS	momentum	mean_w
	1	390	Input	0.0						
	2	200	Rectifier	0.0	0.0	0.0	0.1	0.3	0.0	-0.0
	3	200	Rectifier	0.0	0.0	0.0	0.1	0.2	0.0	-0.0
	4	2	Softmax		0.0	0.0	0.0	0.0	0.0	0.0

ModelMetricsBinomial: deeplearning

Reported on train data.

```
MSE: 0.0737426129728
R^2: 0.642891439669
LogLoss: 0.242051500943
AUC: 0.950131166302
Gini: 0.900262332604
```

Confusion Matrix (Act/Pred) for max f1 @ threshold = 0.343997370612:

	false	true	Error	Rate
false	4003.0	264.0	0.0619	(264.0/4267.0)
true	358.0	1397.0	0.204	(358.0/1755.0)
Total	4361.0	1661.0	0.1033	(622.0/6022.0)

Maximum Metrics: Maximum metrics at their respective thresholds

metric	threshold	value	idx
max f1	0.3	0.8	195.0
max f2	0.2	0.9	278.0
max f0point5	0.7	0.9	86.0
max accuracy	0.5	0.9	149.0
max precision	1.0	1.0	0.0
max absolute_MCC	0.3	0.7	195.0
max min_per_class_accuracy	0.2	0.9	247.0

```
ModelMetricsBinomial: deeplearning
** Reported on validation data. **

MSE: 0.0843305429737
R^2: 0.593831388139
LogLoss: 0.280203809486
AUC: 0.930515181213
Gini: 0.861030362427
```

Confusion Matrix (Act/Pred) for max f1 @ threshold = 0.493462351545:

	false	true	Error	Rate
false	1361.0	62.0	0.0436	(62.0/1423.0)
true	158.0	435.0	0.2664	(158.0/593.0)
Total	1519.0	497.0	0.1091	(220.0/2016.0)

Maximum Metrics: Maximum metrics at their respective thresholds

metric	threshold	value	idx
max f1	0.5	0.8	137.0
max f2	0.1	0.8	303.0
max f0point5	0.7	0.9	82.0
max accuracy	0.7	0.9	91.0
max precision	1.0	1.0	0.0
max absolute_MCC	0.7	0.7	91.0
max min_per_class_accuracy	0.2	0.8	236.0

Scoring History:

	timestamp	duration	training_speed	epochs	samples	training_MSE	training_r2	training_
	2015-11-06 17:57:05	0.000 sec	None	0.0	0.0	nan	nan	nan
	2015-11-06 17:57:09	2.899 sec	2594 rows/sec	1.0	6068.0	0.1	0.3	0.6
	2015-11-06 17:57:15	9.096 sec	5465 rows/sec	7.3	43742.0	0.1	0.6	0.3
	2015-11-06 17:57:19	12.425 sec	6571 rows/sec	12.0	72478.0	0.1	0.6	0.2

Variable Importances:

variable	relative_importance	scaled_importance	percentage
Domestic.false	1.0	1.0	0.0
Primary_Type.NARCOTICS	0.9	0.9	0.0
IUCR.0860	0.8	0.8	0.0
FBI_Code.18	0.8	0.8	0.0
IUCR.4625	0.7	0.7	0.0
---	---	---	---
Location_Description.missing(NA)	0.0	0.0	0.0
Primary_Type.missing(NA)	0.0	0.0	0.0
FBI_Code.missing(NA)	0.0	0.0	0.0
WeekDay.missing(NA)	0.0	0.0	0.0
Domestic.missing(NA)	0.0	0.0	0.0

31. Predict on the test set using the GBM model

```
predictions = model_gbm.predict(test)
predictions.show()
```

predict	false	true
false	0.946415	0.0535847
false	0.862165	0.137835
false	0.938661	0.0613392
false	0.870186	0.129814
false	0.980488	0.0195118
false	0.972006	0.0279937
false	0.990995	0.00900489
true	0.0210692	0.978931
false	0.693061	0.306939
false	0.992097	0.00790253

32. Look at test set performance (if it includes true labels)

```
test_performance = model_gbm.model_performance(test)
test_performance


ModelMetricsBinomial: gbm
** Reported on test data. **

MSE: 0.0893676876445
R^2: 0.57094394422
LogLoss: 0.294019576922
AUC: 0.922152238508
Gini: 0.844304477016
```

Confusion Matrix (Act/Pred) for max f1 @ threshold = 0.365461652105:

	false	true	Error	Rate
false	1297.0	84.0	0.0608	(84.0/1381.0)
true	153.0	427.0	0.2638	(153.0/580.0)
Total	1450.0	511.0	0.1209	(237.0/1961.0)

Maximum Metrics: Maximum metrics at their respective thresholds

metric	threshold	value	idx
max f1	0.4	0.8	158.0
max f2	0.1	0.8	295.0
max f0point5	0.7	0.9	97.0
max accuracy	0.6	0.9	112.0
max precision	1.0	1.0	0.0
max absolute_MCC	0.6	0.7	112.0
max min_per_class_accuracy	0.2	0.8	235.0

33. Create Plots of Crime type vs Arrest Rate and Proportion of reported Crime

```
# Create table to report Crimetype, Arrest count per crime, total reported count per Crime
sqlContext.registerDataFrameAsTable(df_crimes, "df_crimes")
allCrimes = sqlContext.sql("""SELECT Primary_Type, count(*) as all_count FROM df_crimes GROUP BY Primary_Type""")
crimesWithArrest = sqlContext.sql("SELECT Primary_Type, count(*) as crime_count FROM chicagoCrime WHERE Arrest = 'true' GROUP BY

sqlContext.registerDataFrameAsTable(crimesWithArrest, "crimesWithArrest")
sqlContext.registerDataFrameAsTable(allCrimes, "allCrimes")

crime_type = sqlContext.sql("Select a.Primary_Type as Crime_Type, a.crime_count, b.all_count \
FROM crimesWithArrest a \
JOIN allCrimes b \
ON a.Primary_Type = b.Primary_Type ")

crime_type.show(12)

+--------------------+-----------+---------+
|          Crime_Type|crime_count|all_count|
+--------------------+-----------+---------+
|       OTHER OFFENSE|        183|      720|
|   WEAPONS VIOLATION|         96|      118|
|  DECEPTIVE PRACTICE|         25|      445|
|            BURGLARY|         14|      458|
|             BATTERY|        432|     1851|
|             ROBBERY|         17|      357|
| MOTOR VEHICLE THEFT|         17|      414|
|        PROSTITUTION|        106|      106|
|     CRIMINAL DAMAGE|         76|     1003|
|          KIDNAPPING|          1|        7|
|            GAMBLING|          3|        3|
|LIQUOR LAW VIOLATION|         12|       12|
+--------------------+-----------+---------+
only showing top 12 rows
```

34. Copy Crime_type table from Spark to H2O

```
crime_typeHF = hc.as_h2o_frame(crime_type,framename="crime_type")
```

35. Create Additional columns Arrest_rate and Crime_propotion

```
crime_typeHF["Arrest_rate"] = crime_typeHF["crime_count"]/crime_typeHF["all_count"]
crime_typeHF["Crime_proportion"] = crime_typeHF["all_count"]/crime_typeHF["all_count"].sum()
crime_typeHF["Crime_Type"] = crime_typeHF["Crime_Type"].asfactor()
# h2o.assign(crime_typeHF,crime_type)
crime_typeHF.frame_id = "Crime_type"


crime_typeHF
```

Crime_Type	crime_count	all_count	Arrest_rate	Crime_proportion
OTHER OFFENSE	183	720	0.254167	0.0721226
WEAPONS VIOLATION	96	118	0.813559	0.0118201
DECEPTIVE PRACTICE	25	445	0.0561798	0.0445758
BURGLARY	14	458	0.0305677	0.045878
BATTERY	432	1851	0.233387	0.185415
ROBBERY	17	357	0.047619	0.0357608
MOTOR VEHICLE THEFT	17	414	0.0410628	0.0414705
PROSTITUTION	106	106	1	0.0106181
CRIMINAL DAMAGE	76	1003	0.0757727	0.100471
KIDNAPPING	1	7	0.142857	0.000701192

```
hc
```

```
H2OContext: ip=172.16.2.98, port=54329
```

36. Plot in Flow

```
plot (g) -> g(
  g.rect(
    g.position "Crime_Type", "Arrest_rate"
    g.fillColor g.value 'blue'
    g.fillOpacity g.value 0.75
  )
  g.rect(
    g.position "Crime_Type", "Crime_proportion"
    g.fillColor g.value 'red'
    g.fillOpacity g.value 0.65
  )
  g.from inspect "data", getFrame "Crime_type"
)
```

```
#hc.stop()
```

Resources

More information about machine learning with H2O

H2O

- **Documentation for H2O and Sparkling Water**: http://docs.h2o.ai/
- **Glossary of terms**: https://github.com/h2oai/h2o-3/blob/master/h2o-docs/src/product/tutorials/glossary.md
- **Open forum for questions about H2O (Google account required)**: https://groups.google.com/forum/#!forum/h2ostream
- **Track or file bug reports for H2O** : https://jira.h2o.ai
- **GitHub repository for H2O**: https://github.com/h2oai

Python

- **About Python**: https://www.python.org/
- **Latest Python H2O documentation**: http://h2o-release.s3.amazonaws.com/h2o/latest_stable_Pydoc.html

R

- **About R**: https://www.r-project.org/about.html
- **Download R**: https://cran.r-project.org/mirrors.html
- **Latest R API H2O documentation**: http://h2o-release.s3.amazonaws.com/h2o/latest_stable_Rdoc.html

Sparkling Water

- **About Spark**: http://spark.apache.org/
- **Download Spark**: http://spark.apache.org/downloads.html
- **Sparkling Water Developer documentation**: https://github.com/h2oai/sparkling-water/blob/master/DEVEL.md