

```
setwd("F:\\NIS_SEPSIS\\test\\")
```

```
#####
```

```
# Install and import Dependencies
```

```
#####
```

```
# install packages required for the models
```

```
libraries <- c("glmnet", "rpart", "party", "partykit", "gbm", "SuperLearner", "fastDummies", "tensorflow",  
              "ranger", "rms", "pROC", "keras", "data.table", "xgboost", "reportROC", "SHAPforxgboost",  
              "parallel")
```

```
lapply(libraries, require, character.only = TRUE)
```

```
#New package
```

```
library(microbenchmark)
```

```
library(h2o)
```

```
h2o.init(nthreads=detectCores()-1, max_mem_size="40G")
```

```
h2o.removeAll() ## clean slate - just in case the cluster was already running
```

```
#####
```

```
# Import a binary outcome train/test set into H2O#
```

```
#####
```

```
# Import a sample binary outcome train/test set into H2O
```

```
train <- h2o.importFile("sepsis_train.txt")
```

```
test <- h2o.importFile("sepsis_validation.txt")
```

```
y <- "DIED"
```

```
x <- setdiff(names(train), y)
```

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

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

```
nfolds <- 10
```

```
#####
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```
# glm model #
```

```
#####
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```
# Train & cross-validate a Lasso Logistic Model:
```

```
s1 <- Sys.time()
```

```
lasso2 <- h2o.glm(x = x,
```

```
  y = y,
```

```
  training_frame = train,
```

```
  family = "binomial",
```

```
  alpha = 1,
```

```
  nfolds = 10,
```

```
  stopping_metric = "MSE",
```

```
  keep_cross_validation_models=TRUE,
```

```
  seed = 1 )
```

```
t1 <- Sys.time()-s1
```

```
# Save this module for the future
```

```
saveRDS(lasso2, 'Lasso2.rds')
```

```
h2o.saveModel(object = lasso2, path = getwd(), force = TRUE)
```

```
fwrite(as.list(t1), "t1.txt")
```

```
#####
```

```
# rf model #
```

```
#####
```

```
s2 <- Sys.time()
```

```
rf <- h2o.randomForest(x = x,  
  y = y,  
  training_frame = train,  
  ntrees = 400,  
  mtries=500,  
  keep_cross_validation_predictions = TRUE,  
  seed = 555)
```

```
t2 <- Sys.time()-s2
```

```
# Save this module for the future
```

```
saveRDS(rf, 'rf.rds')
```

```
h2o.saveModel(object = rf, path = getwd(), force = TRUE)
```

```
fwrite(as.list(t2), "t2.txt")
```

```
#####
```

```
# XGB model not available on windows OS#
```

```
#####
```

```
s3 <- Sys.time()
```

```
XGB <- h2o.xgboost(x = x,  
  y = y,  
  training_frame = train,  
  eta = 0.15,  
  max_depth = 10,  
  nthread = 10,  
  stopping_metric = "AUC",  
  stopping_rounds = 50,  
  ntrees = 400,  
  nfolds=10,
```

```

        distribution = 'bernoulli',
        seed=1)
t3 <- Sys.time()-s3
# Save this module for the future
saveRDS(XGB, 'XGB.rds')
h2o.saveModel(object = XGB, path = getwd(), force = TRUE)
fwrite(as.list(t3), "t3.txt")

#####
# ensemble model not available on windows OS#
#####

s4 <- Sys.time()
ensemble <- h2o.stackedEnsemble(x = x,
                               y = y,
                               training_frame = train,
                               base_models = list(rf,XGB))
t4 <- Sys.time()-s4
# Save this module for the future
saveRDS(ensemble, 'ensemble.rds')
h2o.saveModel(object = ensemble, path = getwd(), force = TRUE)
fwrite(as.list(t4), "t4.txt")

#####
# Performance#
#####

perf <- h2o.performance(ensemble, newdata = test)
ensemble_auc_test <- h2o.auc(perf)

```

```
#perf_gbm_test <- h2o.performance(my_gbm, newdata = test)
perf_lasso_test <- h2o.performance(lasso2, newdata = test)
perf_rf_test <- h2o.performance(rf, newdata = test)
perf_XGB_test <- h2o.performance(XGB, newdata = test)

baselearner_best_auc_test <- max(h2o.auc(perf_lasso_test),
                                h2o.auc(perf_rf_test))

# DNN_best_auc_test <- max(h2o.auc(perf_DNN))

# print(sprintf("DNN Test AUC: %s", h2o.auc(perf_DNN)))
print(sprintf("Best Base-learner Test AUC: %s", baselearner_best_auc_test))
print(sprintf("Ensemble Test AUC: %s", ensemble_auc_test))

# [1] "Best Base-learner Test AUC: 0.76979821502548"
# [1] "Ensemble Test AUC: 0.773501212640419"
```