Midterm

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Method

Table 1: Data summary

Name Number of rows	hrt_data 920
Number of columns	15
Column type frequency:	
factor	9
numeric	6
Group variables	None

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
diagnosis_heart_disease	0	1.00	FALSE	2	pre: 509, abs: 411
location	0	1.00	FALSE	4	cle: 303, hun: 294, va: 200, swi: 123
sex	0	1.00	FALSE	2	mal: 726, fem: 194
chest_pain_type	0	1.00	FALSE	4	asy: 496, non: 204, aty: 174, typ: 46
fasting_blood_sugar	90	0.90	FALSE	2	fas: 692, fas: 138
resting_ecg	2	1.00	FALSE	3	nor: 551, lef: 188, ST-: 179
exercise_induced_angina	55	0.94	FALSE	2	no: 528, yes: 337
peak_exercise_st_segment	309	0.66	FALSE	3	Fla: 345, Up-: 203, Dow: 63
thalassemia	486	0.47	FALSE	3	nor: 196, rev: 192, fix: 46

Variable type: numeric

skim_variable	n_missing	$complete_rate$	mean	sd	p0	p25	p50	p75	p100
age	0	1.00	53.51	9.42	28.0	47	54.0	60.0	77.0
resting_blood_pressure	59	0.94	132.13	19.07	0.0	120	130.0	140.0	200.0
serum_cholesterol	30	0.97	199.13	110.78	0.0	175	223.0	268.0	603.0
$max_heart_rate_achieved$	55	0.94	137.55	25.93	60.0	120	140.0	157.0	202.0
$st_depression_exercise$	62	0.93	0.88	1.09	-2.6	0	0.5	1.5	6.2
num_major_vessels_flouro	611	0.34	0.68	0.94	0.0	0	0.0	1.0	3.0

Modeling

```
set.seed(123123)
cl = parallel::makePSOCKcluster(5)
doParallel::registerDoParallel(cl)
logistic model =
  train(
    X_tr,
    Y_tr,
    method = "glmnet",
    tuneGrid = expand.grid(alpha = seq(0,1,length=6),
                           lambda = exp(seq(
                             6, to = -6, length = 50
                           ))),
   family = "binomial",
    preProcess = c("knnImpute", "center", "scale"),
    metric = "ROC",
    trControl = TRC
stopCluster(cl)
p_logistics =
  ggplot(logistic_model) +
  scale_x_continuous(trans = "log")+
  labs(title = "Lasso Logistics")
```

```
set.seed(123123)
cl = parallel::makePSOCKcluster(5)
doParallel::registerDoParallel(cl)
```

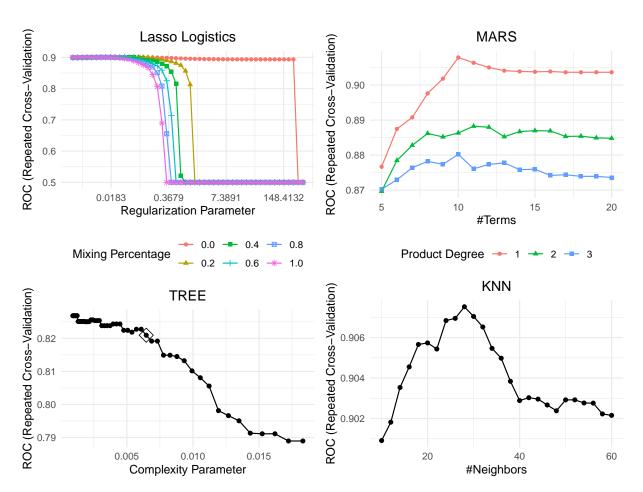
```
mars_model =
 train(X_tr,
       Y tr,
       method = "earth",
        tuneGrid = expand.grid(degree = 1:3,
                               nprune = 5:20),
       preProcess = c("knnImpute", "center", "scale"),
       trControl = TRC,
       metric = "ROC")
stopCluster(cl)
p_mars = ggplot(mars_model) +labs(title ="MARS")
set.seed(123123)
cl = parallel::makePSOCKcluster(5)
doParallel::registerDoParallel(cl)
knn_model =
 train(X_tr,
       Y_tr,
       method = "knn",
       tuneGrid = expand.grid(k = seq(10,60,2)),
       preProcess = c("knnImpute", "center", "scale"),
       trControl = TRC,
       metric = "ROC")
stopCluster(cl)
p_knn = ggplot(knn_model)+labs(title = "KNN")
set.seed(123123)
cl = parallel::makePSOCKcluster(5)
doParallel::registerDoParallel(cl)
lda_model = train(
 X_tr,
 Y tr,
 method = "lda",
 preProcess = c("knnImpute", "center", "scale"),
 trControl = TRC,
 metric = "ROC"
)
stopCluster(cl)
set.seed(123123)
cl = parallel::makePSOCKcluster(5)
doParallel::registerDoParallel(cl)
qda_model = train(
 X_tr,
Y_tr,
```

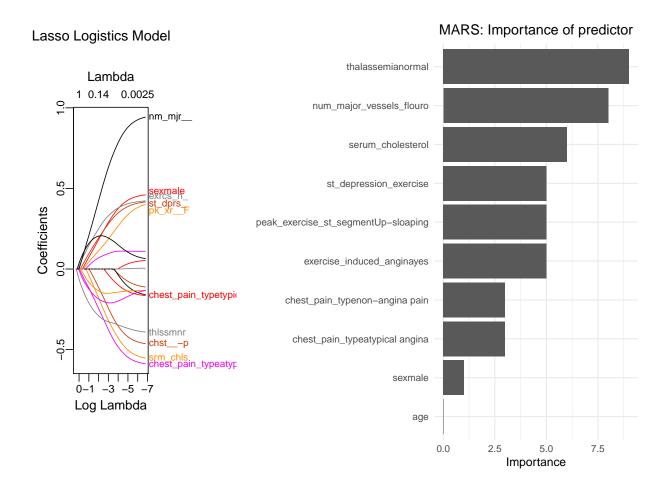
```
method = "qda",
  preProcess = c("knnImpute", "center", "scale"),
  trControl = TRC,
 metric = "ROC"
stopCluster(cl)
set.seed(123123)
cl = parallel::makePSOCKcluster(5)
doParallel::registerDoParallel(cl)
tree_model =
  train(
    X_tr,
    Y_tr,
    method = "rpart",
    tuneGrid = expand.grid(
     cp = exp(seq(-7,-4,length=50))
    preProcess = c("center", "scale"),
    trControl = caret::trainControl(method = "repeatedcv",repeats=5,
                          number = 5,
                          summaryFunction = twoClassSummary,
                          classProbs = T,
                          selectionFunction = "oneSE"),
   metric = "ROC"
  )
stopCluster(cl)
p_tree =
  ggplot(tree_model,highlight = T) + labs(title = "TREE")
coef(logistic_model$finalModel,logistic_model$bestTune$lambda) %>%
  as.vector() %>%
  tibble(term = c("Intercept",colnames(X_tr)),
         coefficient = .) %>%
  knitr::kable(caption = "Coefficient of Lasso Logistic Regression")
```

Table 4: Coefficient of Lasso Logistic Regression

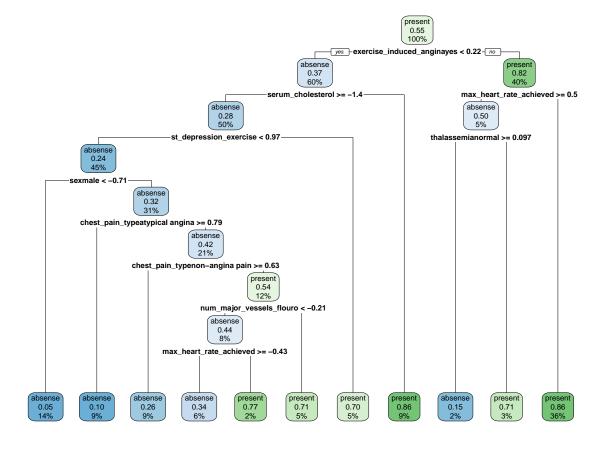
term	coefficient
Intercept	0.333
age	0.097
sexmale	0.296
chest_pain_typeatypical angina	-0.384
chest_pain_typenon-angina pain	-0.251
chest_pain_typetypical angina	-0.040
resting_blood_pressure	0.000
serum_cholesterol	-0.326
fasting_blood_sugarfasting blood sugar $> 120 \text{ mg/dl}$	0.000
resting_ecgnormal	0.000

term	coefficient
resting_ecgST-T wave abnormality	0.000
max_heart_rate_achieved	-0.151
exercise_induced_anginayes	0.334
st_depression_exercise	0.285
peak_exercise_st_segmentFlat	0.191
peak_exercise_st_segmentUp-sloaping	-0.210
num_major_vessels_flouro	0.642
thalassemianormal	-0.329
thalassemiareversible defect	0.190





rpart.plot::rpart.plot(tree_model\$finalModel)



Performance comparison

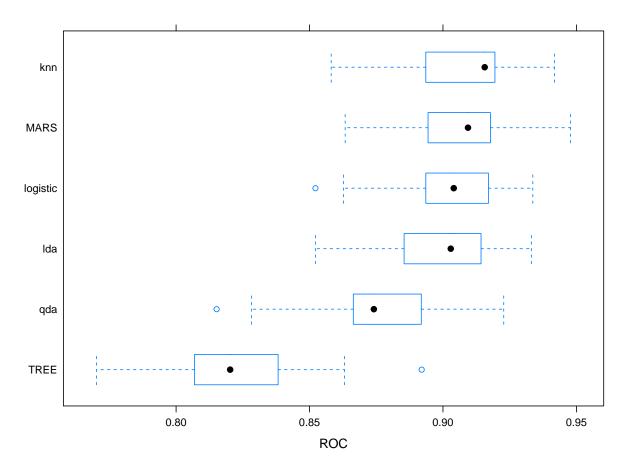
summary.resamples(object = rsmp)

Models: logistic, MARS, knn, lda, qda, TREE

Call:

```
rsmp = resamples(
  list(
    logistic = logistic_model,
    MARS = mars_model,
    knn = knn_model,
    lda = lda_model,
    qda = qda_model,
    TREE = tree_model
),
    metric = c("ROC", "Kappa")
)
summary(rsmp)
```

```
## Number of resamples: 25
##
## ROC
##
           Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
## logistic 0.852
                  0.894 0.904 0.901
                                   0.917 0.934
## MARS
          0.863
                 0.894 0.909 0.908
                                   0.918 0.948
## knn
          0.858
                0.894 0.916 0.908
                                   0.919 0.942
## lda
          0.852
                 0.885 0.903 0.900
                                   0.914 0.933
                                                  0
## qda
         0.815
                 0.866 0.874 0.875
                                   0.892 0.923
                                                  0
## TREE
         0.770 0.807 0.820 0.821
                                   0.838 0.892
                                                  0
##
## Sens
           Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
## logistic 0.682
                  0.758 0.773 0.775 0.803 0.846
## MARS
          0.712
                  0.773 0.800 0.795
                                   0.818 0.879
## knn
          0.697
                  0.758 0.773 0.781
                                     0.818 0.848
                                                  0
## lda
          0.697
                  0.758 0.785 0.783
                                   0.803 0.877
                                                  0
          0.697
                  0.754 0.773 0.779
## qda
                                   0.803 0.877
                  0.667 0.692 0.701 0.727 0.818
## TREE
          0.615
                                                  0
##
## Spec
           Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
                  0.852 0.877 0.868
## logistic 0.815
                                   0.890 0.915
## MARS
          0.778
                  0.840 0.854 0.856
                                    0.878 0.915
## knn
          0.827
                  0.854 0.878 0.880
                                   0.902 0.915
                                                  0
## lda
          0.815
                  0.852 0.864 0.863 0.878 0.915
                                                  0
## qda
          0.778
                  0.817 0.852 0.844
                                   0.866 0.915
                                                  0
## TREE
          bwplot(rsmp,metric = "ROC")
```



```
ROC =
  expand.grid(
   test_X = list(X_ts),
   test_Y = list(Y_ts),
   model = list(logistic_model, mars_model, knn_model, lda_model, qda_model,tree_model)
  ) %>%
  mutate(
    pred = map2(model, test_X, ~ predict(.x, newdata = .y, type = "prob")[, 2]),
   roc = map2(test_Y, pred, ~ pROC::roc(.x, .y))
  ) %>%
 pull(roc)
auc = c()
for (i in 1:6){
  auc = append(auc,ROC[[i]]$auc[1])
  plot(ROC[[i]],col = i, add = T * (i>1), legacy.axes = T * (i==1))
model_name =
  c("lasso logistic", "MARS", "KNN", "LDA", "QDA", "TREE")
legend("bottomright",
```

