Module 4: Semi and Weakly Supervised Learning

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```
# If a package is installed, it will be loaded. If any
## are not, the missing package(s) will be installed
## from CRAN and then loaded.

## First specify the packages of interest
packages <- c(
  "dplyr", "PheCAP", "glmnet", "randomForestSRC", "PheNorm",
  "MAP", "pROC", "mltools", "data.table", "ggplot2", "parallel"
)

## Now load or install&load all
package.check <- lapply(
  packages,
  FUN = function(x) {
    if (!require(x, character.only = TRUE)) {
      install.packages(x, dependencies = TRUE)
      library(x, character.only = TRUE)
    }
  }
)

# load environment from example 1
load("../module4/environment.RData")
source("../Rscripts/helper_function.R")
```

Semi-supervised Learning

(i) Regress the surrogate on the features with penalized least square to get the direction of beta.

```
x <- all_x %>% select(starts_with("COD") | starts_with("NLP")) # COD + NLP
S <- ehr_data$main_ICDNLP

# Step 1
beta.step1 <- adaptive_lasso_fit(
  y = S, # surrogate
  x = x, # all X
  family = "gaussian",
  tuning = "cv"
)

# Features selected
names(beta.step1[abs(beta.step1) > 0])[-1]
```

```
##   [1] "COD6"   "COD8"   "COD10"  "NLP5"   "NLP7"   "NLP14"  "NLP18"  "NLP21"
##   [9] "NLP24"  "NLP28"  "NLP31"  "NLP33"  "NLP44"  "NLP50"  "NLP56"  "NLP59"
##  [17] "NLP61"  "NLP62"  "NLP66"  "NLP68"  "NLP70"  "NLP73"  "NLP74"  "NLP76"
##  [25] "NLP81"  "NLP89"  "NLP92"  "NLP93"  "NLP95"  "NLP98"  "NLP102" "NLP104"
##  [33] "NLP108" "NLP110" "NLP116" "NLP120" "NLP127" "NLP130" "NLP146" "NLP160"
##  [41] "NLP161" "NLP172" "NLP176" "NLP178" "NLP179" "NLP183" "NLP189" "NLP190"
##  [49] "NLP192" "NLP199" "NLP202" "NLP206" "NLP215" "NLP225" "NLP231" "NLP232"
##  [57] "NLP243" "NLP246" "NLP250" "NLP253" "NLP256" "NLP288" "NLP294" "NLP295"
##  [65] "NLP299" "NLP302" "NLP304" "NLP306" "NLP309" "NLP321" "NLP326" "NLP336"
##  [73] "NLP338" "NLP342" "NLP343" "NLP347" "NLP349" "NLP350" "NLP351" "NLP357"
##  [81] "NLP359" "NLP361" "NLP363" "NLP365" "NLP369" "NLP380" "NLP387" "NLP393"
##  [89] "NLP395" "NLP403" "NLP405" "NLP407" "NLP417" "NLP431" "NLP434" "NLP437"
##  [97] "NLP440" "NLP446" "NLP451" "NLP452" "NLP456" "NLP463" "NLP465" "NLP468"
## [105] "NLP473" "NLP482" "NLP483" "NLP487" "NLP490" "NLP495" "NLP500" "NLP507"
## [113] "NLP522" "NLP529" "NLP534" "NLP536" "NLP539" "NLP541" "NLP544" "NLP554"
## [121] "NLP560" "NLP564" "NLP568" "NLP572"
```

(ii) Regress the outcome on the linear predictor to get the intercept and multiplier for the beta.

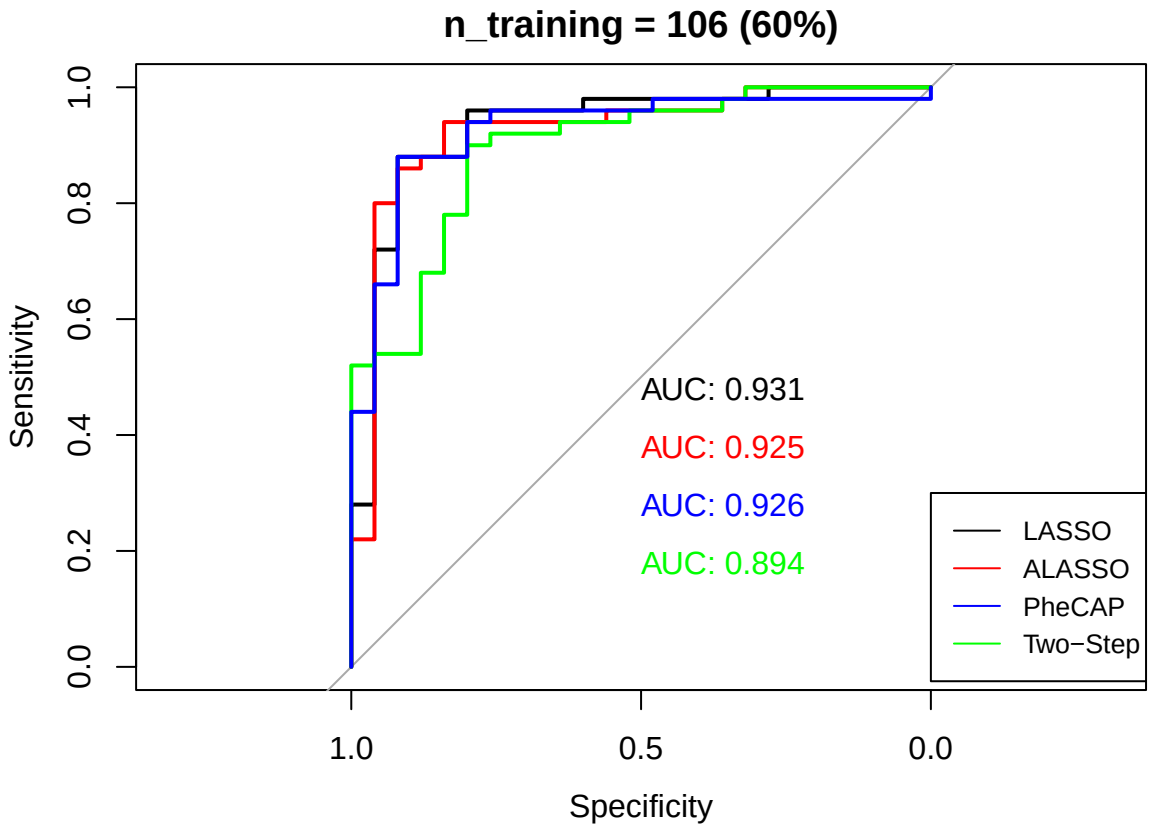
```
# linear predictor without intercept
bhatx <- linear_model_predict(beta = beta.step1, x = as.matrix(x))

# Step 2
step2 <- glm(train_y ~ bhatx[train_data$patient_id] + S[train_data$patient_id] +
  health_count[train_data$patient_id])
beta_step2 <- coef(step2)
beta_step2
```

```
##                          (Intercept)        bhatx[train_data$patient_id]
##                           0.80767522                          0.09193406
##            S[train_data$patient_id] health_count[train_data$patient_id]
##                           0.14335393                         -0.12664878
```

```
# recover beta
beta <- beta_step2[2] * beta.step1
# mu
mu <- beta_step2[1] +
  as.numeric(as.matrix(x[test_data$patient_id, ]) %*% beta[-1]) +
  as.numeric(beta_step2[3] %*% S[test_data$patient_id]) +
  as.numeric(beta_step2[4] %*% health_count[test_data$patient_id])
# expit
y_hat.ss <- plogis(mu)
```

```
plot(roc(test_y, y_hat.lasso),
  print.auc = TRUE, main = "n_training = 106 (60%)"
)
plot(roc(test_y, y_hat.alasso),
  print.auc = TRUE, col = "red", add = TRUE, print.auc.y = 0.4
)
plot(roc(test_y, y_hat.ss),
  print.auc = TRUE, col = "green", add = TRUE, print.auc.y = 0.2
)
plot(roc(test_y, y_hat.phecap),
  print.auc = TRUE, col = "blue", add = TRUE, print.auc.y = 0.3
)
legend(0, 0.3,
```

```
  legend = c("LASSO", "ALASSO", "PheCAP", "Two-Step"),
  col = c("black", "red", "blue", "green"),
  lty = 1, cex = 0.8
)
```



- roc paramter at FPR = 5% and 10% cut-off

```
ss.roc.full <- get_roc(test_y, y_hat.ss) %>% data.frame()
get_roc_parameter(0.05, ss.roc.full)
```

```
##      cutoff  pos.rate  FPR   TPR       PPV       NPV        F1
## 1 0.6992587 0.3600000 0.04 0.525 0.9633028 0.5026178 0.6796117
## 2 0.6945250 0.3666667 0.04 0.530 0.9636364 0.5052632 0.6838710
## 3 0.6944934 0.3733333 0.04 0.535 0.9639640 0.5079365 0.6881029
```

```
get_roc_parameter(0.1, ss.roc.full)
```

```
##     cutoff  pos.rate FPR  TPR       PPV       NPV        F1
## 1 0.693725 0.3933333 0.1 0.54 0.9152542 0.4945055 0.6792453
```

Model Evaluation

```
start <- Sys.time()
auc_twostep <- validate_ss(
  dat = labeled_data, nsim = 600,
  n.train = c(50, 70, 90),
  beta = beta.step1,
  S = S,
```

```
  x = x
)
end <- Sys.time()
end - start
```

```
## Time difference of 27.63318 secs
```

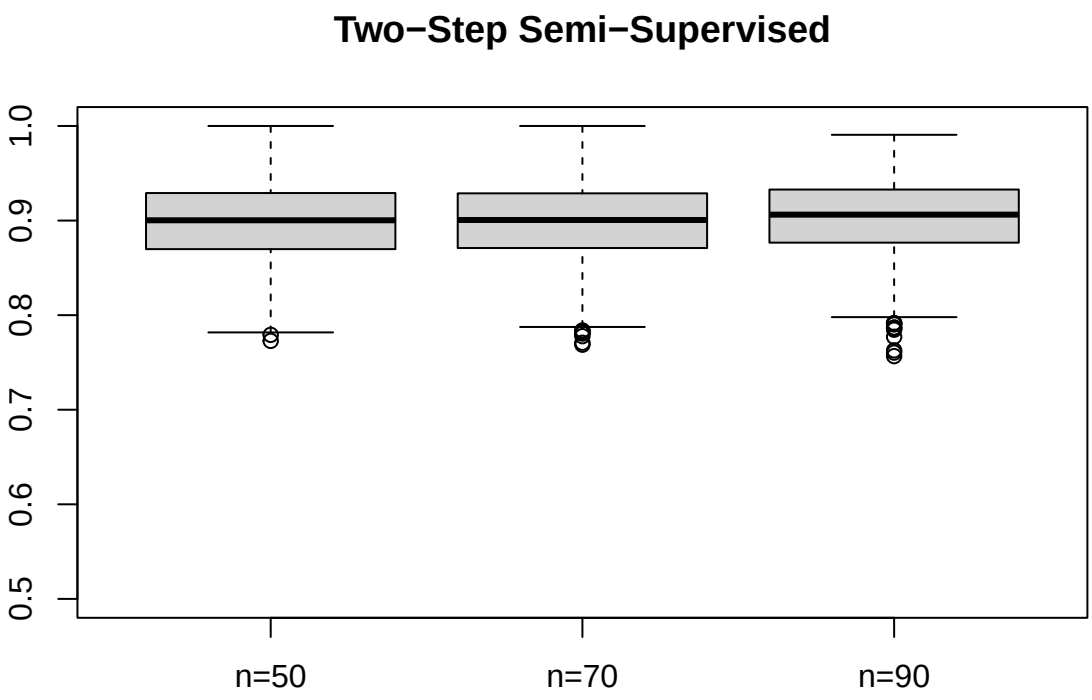
```
# median AUC
apply(auc_twostep, 2, median)
```

```
## n=50,Two-Step n=70,Two-Step n=90,Two-Step
##     0.9002924     0.9005848     0.9062500
```

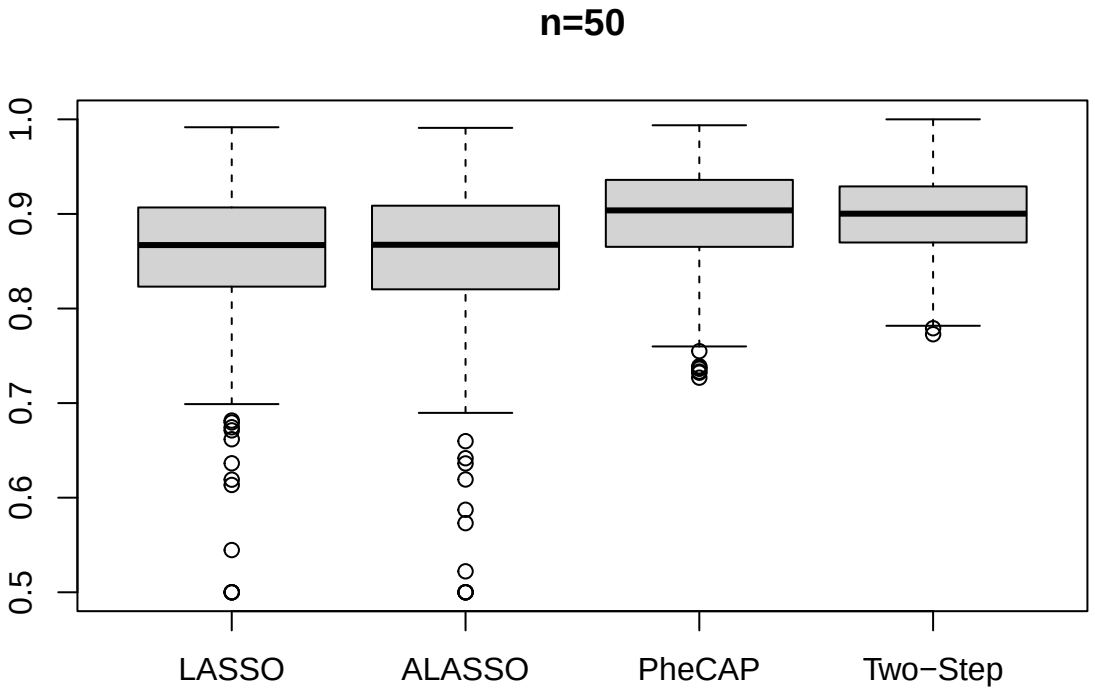
```
# se
apply(auc_twostep, 2, sd)
```

```
## n=50,Two-Step n=70,Two-Step n=90,Two-Step
##    0.04440317    0.04352198    0.04283354
```

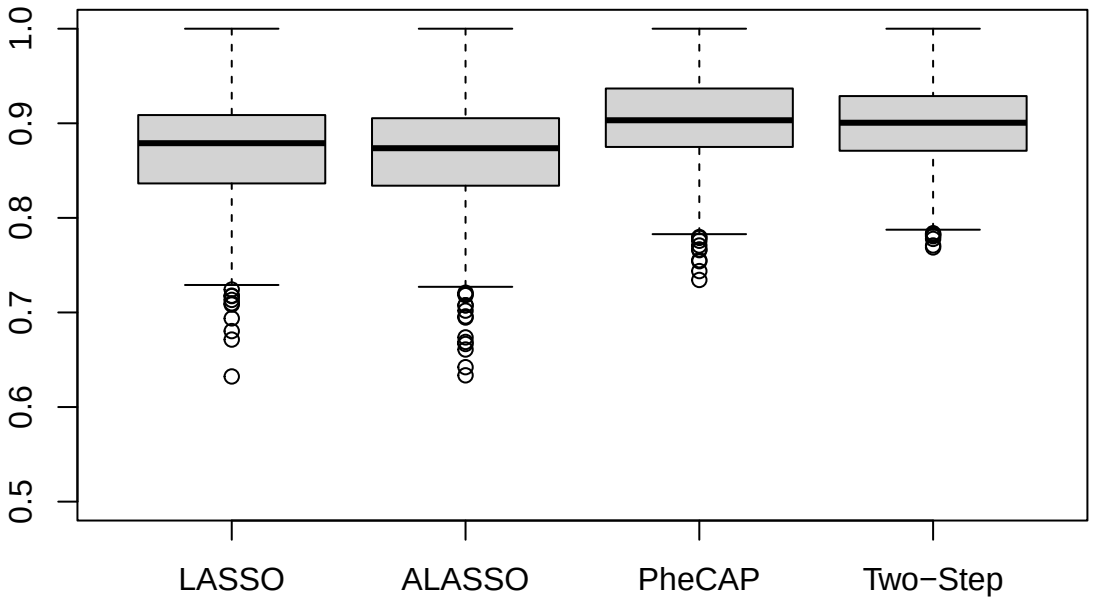
```
boxplot(auc_twostep,
  ylim = c(0.5, 1), names = c("n=50", "n=70", "n=90"),
  main = "Two-Step Semi-Supervised"
)
```




```
# Compare with Previous method
boxplot(cbind(auc_supervised, auc_phecap, auc_twostep)
%>% select(starts_with("n=50")),
ylim = c(0.5, 1), names = c("LASSO", "ALASSO","PheCAP", "Two-Step")
, main = "n=50"
)
```

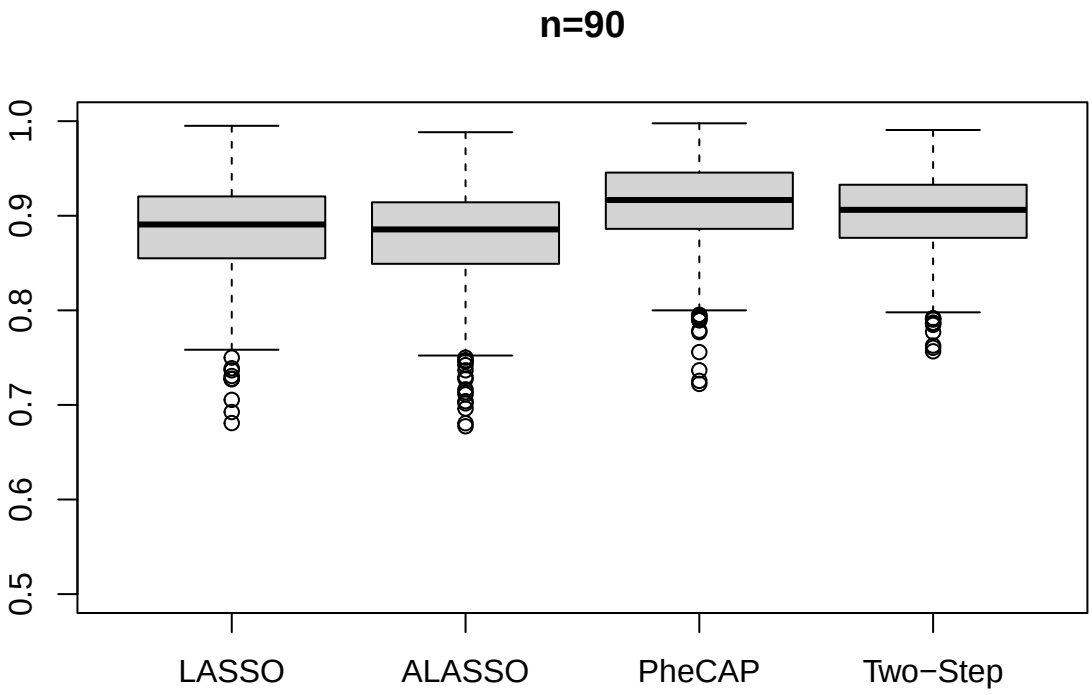



```
boxplot(cbind(auc_supervised, auc_phecap, auc_twostep)
%>% select(starts_with("n=70")),
ylim = c(0.5, 1), names = c("LASSO", "ALASSO","PheCAP", "Two-Step"),
main = "n=70"
)
```




```
boxplot(cbind(auc_supervised, auc_phecap, auc_twostep)
%>% select(starts_with("n=90")),
ylim = c(0.5, 1), names = c("LASSO", "ALASSO","PheCAP","Two-Step"),
main = "n=90"
```

```
)
```

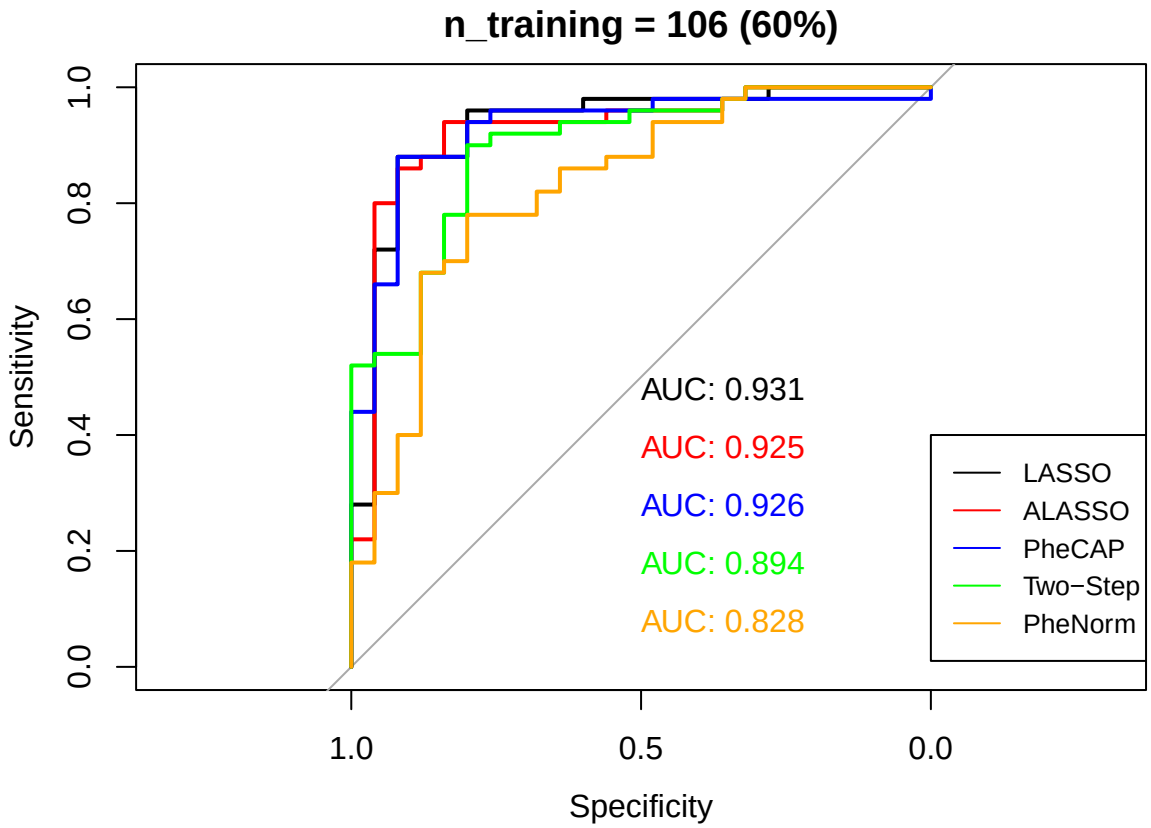


Weakly supervised learning

```
model_phenorm <- PheNorm.Prob(
  nm.logS.ori = "main_ICDNLP", # name of surrogates
  nm.utl = "healthcare_utilization", # name of HU
  nm.X = colnames(ehr_data)[-1:-6], # Other predictors X
  dat = ehr_data %>% select(-patient_id, -main_ICD, -main_NLP),
  train.size = nrow(ehr_data)
)
```

```
y_hat.phenorm <- model_phenorm$probs[data$validation_set]
plot(roc(test_y, y_hat.lasso),
  print.auc = TRUE, main = "n_training = 106 (60%)"
)
plot(roc(test_y, y_hat.alasso),
  print.auc = TRUE, col = "red", add = TRUE, print.auc.y = 0.4
)
plot(roc(test_y, y_hat.phecap),
  print.auc = TRUE, col = "blue", add = TRUE, print.auc.y = 0.3
)
plot(roc(test_y, y_hat.ss),
  print.auc = TRUE, col = "green", add = TRUE, print.auc.y = 0.2
)
plot(roc(test_y, y_hat.phenorm),
  print.auc = TRUE, col = "orange", add = TRUE, print.auc.y = 0.1
)

legend(0, 0.4,
```

```
  legend = c("LASSO", "ALASSO", "PheCAP","Two-Step", "PheNorm"),
  col = c("black", "red", "blue", "green", "orange"),
  lty = 1, cex = 0.8
)
```




```
# Use untransformed data; MAP requires sparse matrix
# Create sparse matrix for surroagtes
data_fit <- sparsify(PheCAP::ehr_data %>%
  select(main_ICD, main_NLP) %>%
  rename(ICD = main_ICD) %>% data.table())

# Create sparse matrix for HU
note <- Matrix(PheCAP::ehr_data$healthcare_utilization, ncol = 1, sparse = TRUE)
model_map <- MAP(mat = data_fit, note = note, full.output = TRUE)
```

```
## ######################
## MAP only considers pateints who have note count data and
##         at least one nonmissing variable!
## ####
## Here is a summary of the input data:
## Total number of patients: 10000
##   ICD main_NLP note  Freq
## 1 YES      YES  YES 10000
## ####
```

```
y_hat.map <- model_map$scores[data$validation_set]
```

```
plot(roc(test_y, y_hat.lasso),
```

```
  print.auc = TRUE, main = "n_training = 106 (60%)"
)
plot(roc(test_y, y_hat.alasso),
  print.auc = TRUE, col = "red", add = TRUE, print.auc.y = 0.4
)
plot(roc(test_y, y_hat.phecap),
  print.auc = TRUE, col = "blue", add = TRUE, print.auc.y = 0.3
)
plot(roc(test_y, y_hat.ss),
  print.auc = TRUE, col = "green", add = TRUE, print.auc.y = 0.2
)
plot(roc(test_y, y_hat.phenorm),
  print.auc = TRUE, col = "orange", add = TRUE, print.auc.y = 0.1
)
plot(roc(test_y, y_hat.map),
  print.auc = TRUE, col = "orchid", add = TRUE, print.auc.y = 0
)

legend(0, 0.4,
  legend = c("LASSO", "ALASSO", "PheCAP","Two-Step",  "PheNorm", "MAP"),
  col = c("black", "red", "blue", "green", "orange", "orchid"),
  lty = 1, cex = 0.8
)
```