

Myocardial Infarction Complications

Lennox Garay

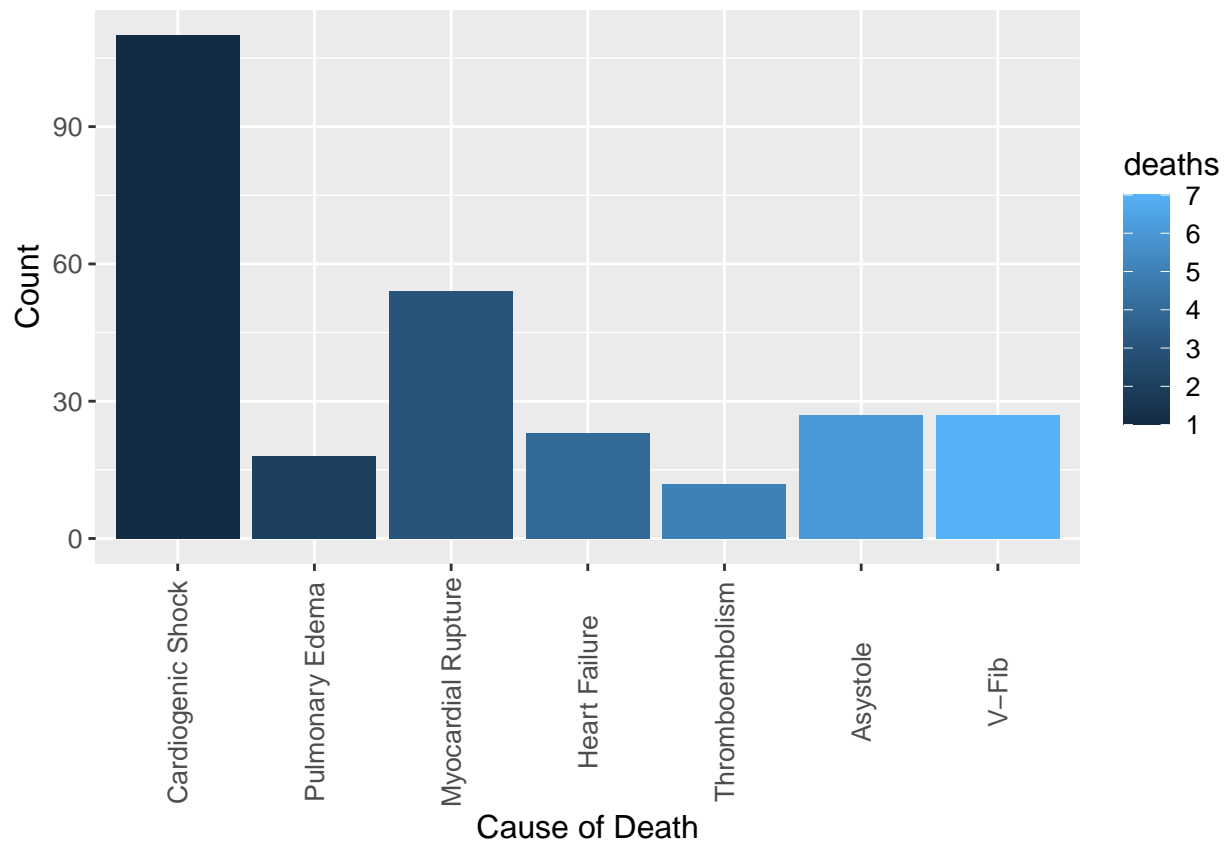
2023-11-04

```
data = read.csv("Myocardial.csv")
attach(data)

data = data %>% mutate_if(is.numeric, na.aggregate, FUN = median) %>%
  mutate_if(is.integer, na.aggregate, FUN = median) %>%
  mutate_if(is.double, na.aggregate, FUN = median)

cause_death = data.frame(deaths = data$LET_IS[which(data$LET_IS > 0)]) ## 16% of the patients with MI h

ggplot(data = cause_death, aes(x=factor(deaths), fill = deaths)) + geom_bar(stat = 'count') + xlab('Cause of Death')
scale_x_discrete(name='Cause of Death', labels=c("0" = "Alive", "1" = "Cardiogenic Shock", "2" = "Pulmonary Edema", "3" = "Myocardial Rupture", "4" = "Heart Failure", "5" = "Thromboembolism", "6" = "Asystole", "7" = "V-Fib"))
```



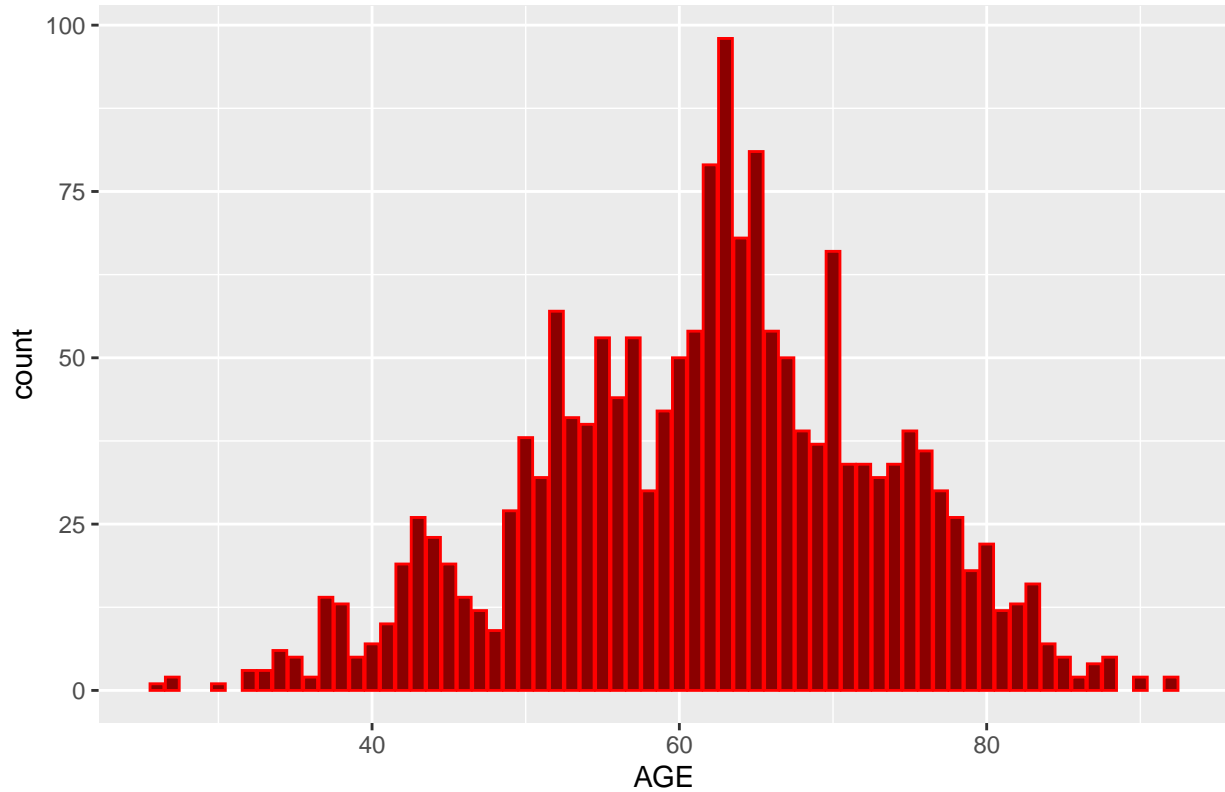
```
response = data[,113:124]
```

```
ggplot(data = data, aes(x = AGE)) + geom_histogram(stat = 'count', color = 'red', fill = 'darkred') + g
```

```
## Warning in geom_histogram(stat = "count", color = "red", fill = "darkred"):
```

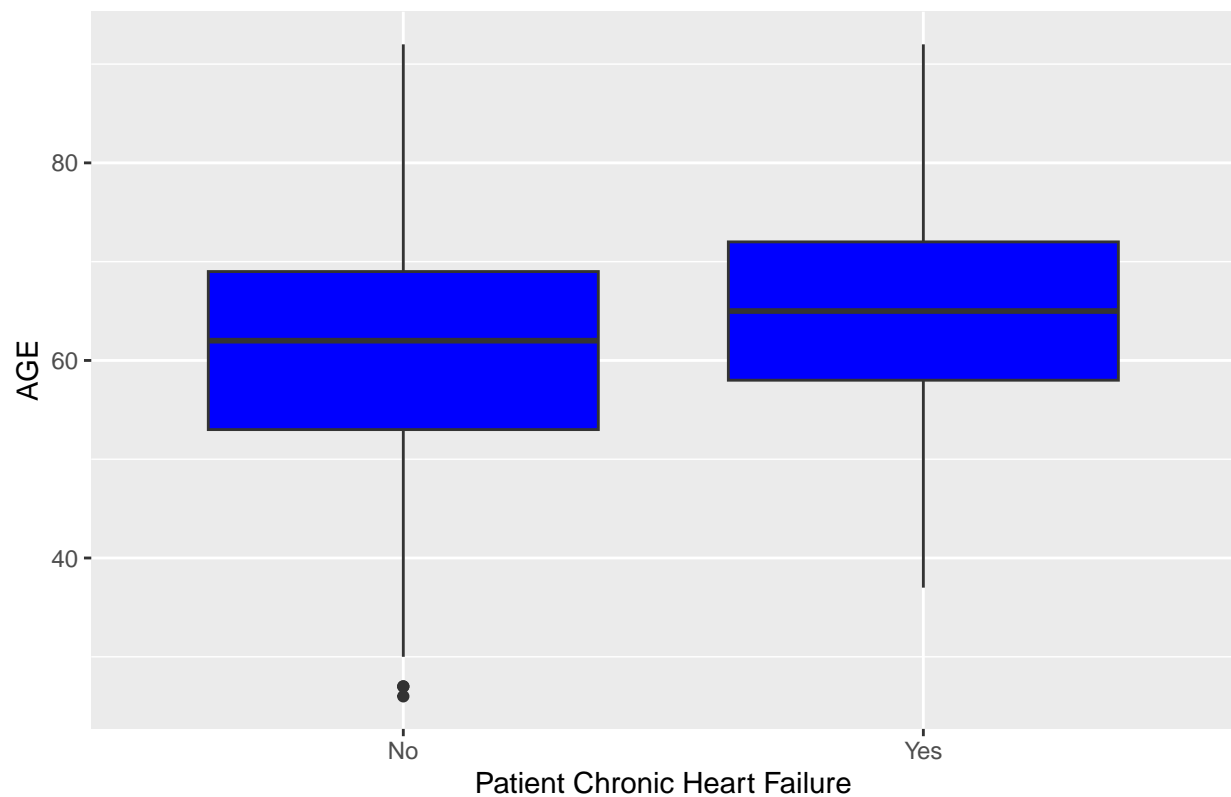
```
## Ignoring unknown parameters: `binwidth`, `bins`, and `pad`
```

Distribution of Age in MI Patients (Fig 1.)



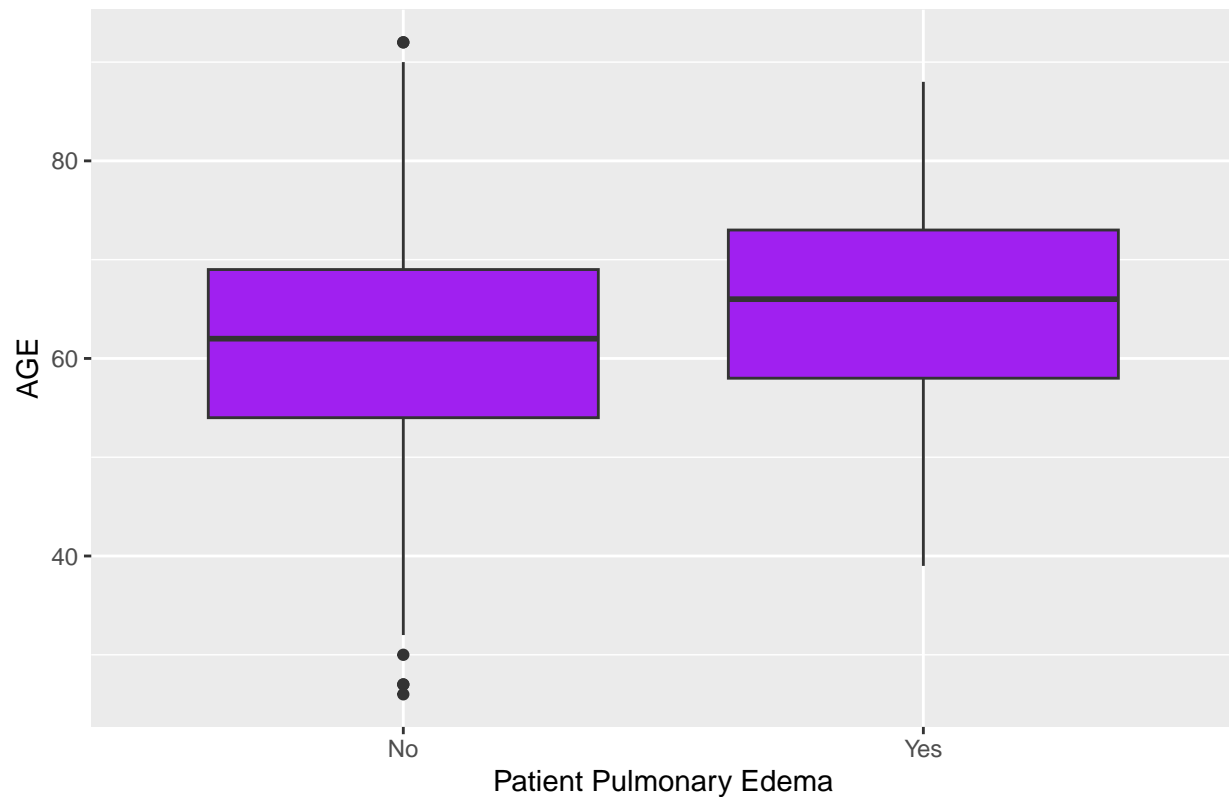
```
ggplot(data = data, aes(x = factor(ZSN), y = AGE)) +  
  geom_boxplot(fill='blue') +  
  ggtitle(label = 'Boxplot of Chronic Heart Failure vs Patient age (Fig 2.)') +  
  scale_x_discrete(name='Patient Chronic Heart Failure', labels=c("0" = "No", "1" = "Yes"))
```

Boxplot of Chronic Heart Failure vs Patient age (Fig 2.)



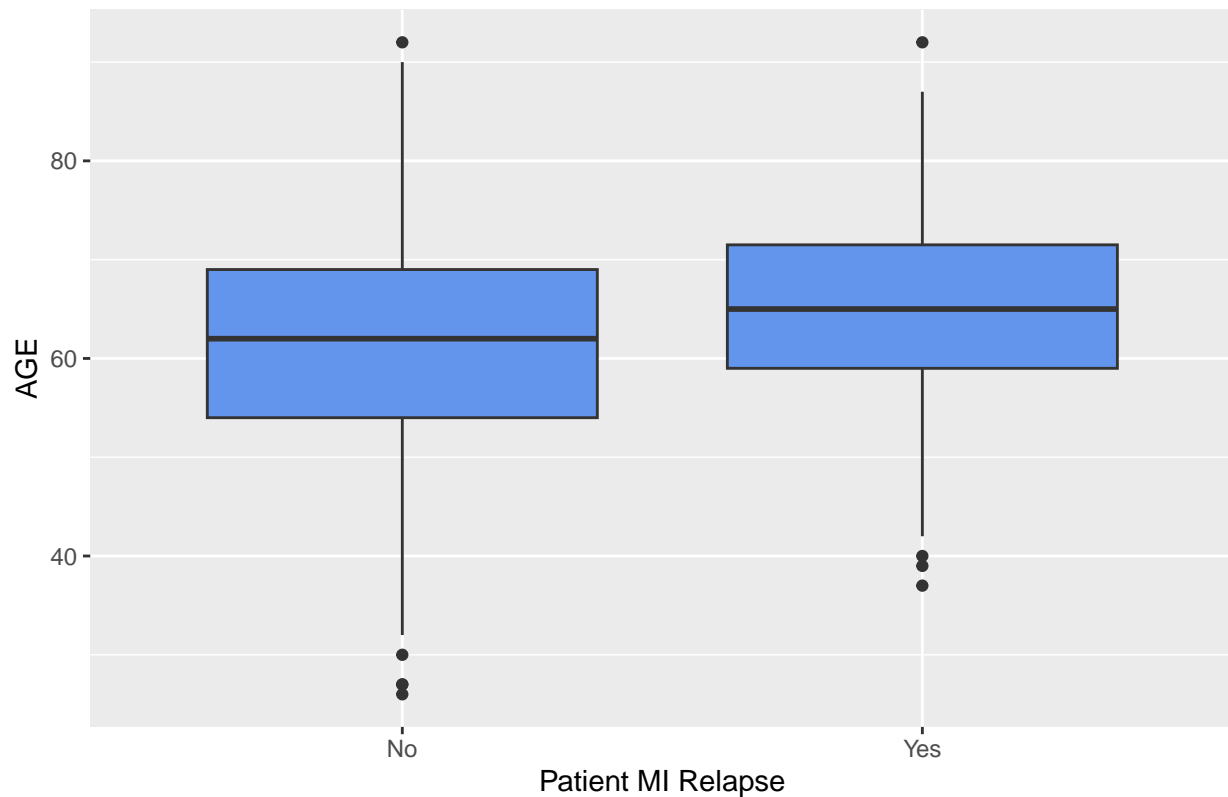
```
ggplot(data = data, aes(x = factor(OTЕК_LANC), y = AGE)) +  
  geom_boxplot(fill='purple') +  
  ggtitle(label = 'Boxplot of Pulmonary Edema vs Patient age (Fig 2.1)') +  
  scale_x_discrete(name='Patient Pulmonary Edema', labels=c("0" = "No", "1" = "Yes"))
```

Boxplot of Pulmonary Edema vs Patient age (Fig 2.1)



```
ggplot(data = data, aes(x = factor(REC_IM), y = AGE)) +  
  geom_boxplot(fill='cornflowerblue') +  
  ggtitle(label = 'Boxplot of Patient Relapse of MI vs Patient age (Fig 2.2)') +  
  scale_x_discrete(name='Patient MI Relapse', labels=c("0" = "No", "1" = "Yes"))
```

Boxplot of Patient Relapse of MI vs Patient age (Fig 2.2)



```
EDEMA_VS_MI_RELAPSE = matrix(c(OTЕК_LANC, REC_IM), ncol = 2)
tetrachoric(EDEMA_VS_MI_RELAPSE)
```

```
## Call: tetrachoric(x = EDEMA_VS_MI_RELAPSE)
## tetrachoric correlation
##      C1   C2
## R1 1.00
## R2 0.39 1.00
##
## with tau of
## [1] 1.3 1.3
```

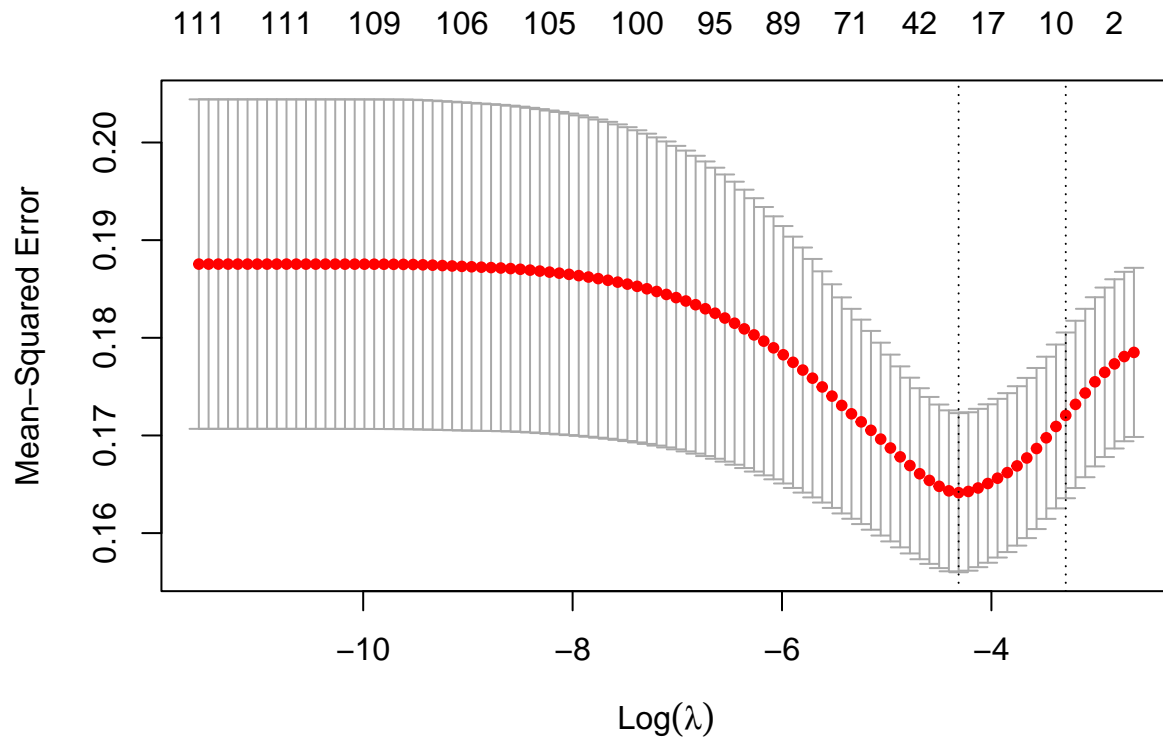
```
FAILURE_VS_RELAPSE = matrix(c(ZSN, REC_IM), ncol = 2)
tetrachoric(FAILURE_VS_RELAPSE)
```

```
## Call: tetrachoric(x = FAILURE_VS_RELAPSE)
## tetrachoric correlation
##      C1   C2
## R1 1.00
## R2 0.19 1.00
##
## with tau of
## [1] 0.73 1.32
```

```
x = data[,2:112]
y = data[, 'ZSN']
```

```
cv_model = cv.glmnet(as.matrix(x),y, alpha=1) ## 10-fold cross validation

best_lambda = cv_model$lambda.min ## 0.01339178
plot(cv_model)
```



```
## LASSO
```

```
lasso_model = glmnet(x,y, alpha=1, lambda = best_lambda) ##alpha=1 is LASSO
```

```
coef(lasso_model)
```

```
## 112 x 1 sparse Matrix of class "dgCMatrix"
```

```
##              s0
## (Intercept) -0.0601954774
## AGE         0.0032515506
## SEX        -0.0006022468
## INF_ANAM    .
## STENOK_AN   .
## FK_STENOK  -0.0064042039
## IBS_POST   .
## IBS_NASL   -0.0343223303
## GB         .
## SIM_GIPERT .
## DLIT_AG    .
## ZSN_A      0.0757012149
## nr_11     .
```

```

## nr_01      .
## nr_02      .
## nr_03      .
## nr_04      .
## nr_07      0.2647561330
## nr_08      .
## np_01      .
## np_04      .
## np_05      .
## np_07      .
## np_08      -0.0042956653
## np_09      0.4184150360
## np_10      .
## endocr_01   0.0879128520
## endocr_02   .
## endocr_03   .
## zab_leg_01  0.1241515734
## zab_leg_02  .
## zab_leg_03  .
## zab_leg_04  .
## zab_leg_06  .
## S_AD_KBRIG  .
## D_AD_KBRIG  .
## S_AD_ORIT   .
## D_AD_ORIT   .
## O_L_POST    .
## K_SH_POST   -0.1513260593
## MP_TP_POST  .
## SVT_POST    .
## GT_POST     .
## FIB_G_POST  .
## ant_im      .
## lat_im      0.0253219456
## inf_im      .
## post_im     .
## IM_PG_P     .
## ritm_ecg_p_01 .
## ritm_ecg_p_02 0.0672579473
## ritm_ecg_p_04 .
## ritm_ecg_p_06 0.1305754934
## ritm_ecg_p_07 .
## ritm_ecg_p_08 .
## n_r_ecg_p_01 .
## n_r_ecg_p_02 -0.0192638936
## n_r_ecg_p_03 .
## n_r_ecg_p_04 .
## n_r_ecg_p_05 .
## n_r_ecg_p_06 0.0696467377
## n_r_ecg_p_08 .
## n_r_ecg_p_09 .
## n_r_ecg_p_10 .
## n_p_ecg_p_01 .
## n_p_ecg_p_03 .
## n_p_ecg_p_04 .

```

```

## n_p_ecg_p_05 .
## n_p_ecg_p_06 .
## n_p_ecg_p_07 .
## n_p_ecg_p_08 .
## n_p_ecg_p_09 .
## n_p_ecg_p_10 .
## n_p_ecg_p_11 .
## n_p_ecg_p_12 .
## fibr_ter_01 .
## fibr_ter_02 .
## fibr_ter_03 .
## fibr_ter_05 .
## fibr_ter_06 .
## fibr_ter_07 .
## fibr_ter_08 .
## GIPO_K .
## K_BLOOD .
## GIPER_NA .
## NA_BLOOD .
## ALT_BLOOD 0.0253636194
## AST_BLOOD .
## KFK_BLOOD .
## L_BLOOD .
## ROE .
## TIME_B_S .
## R_AB_1_n .
## R_AB_2_n .
## R_AB_3_n 0.0061743908
## NA_KB .
## NOT_NA_KB 0.0209955362
## LID_KB 0.0085734823
## NITR_S .
## NA_R_1_n .
## NA_R_2_n 0.0624263680
## NA_R_3_n 0.0985947304
## NOT_NA_1_n 0.0157578267
## NOT_NA_2_n .
## NOT_NA_3_n .
## LID_S_n .
## B_BLOK_S_n .
## ANT_CA_S_n .
## GEPAR_S_n -0.0099349438
## ASP_S_n .
## TIKL_S_n .
## TRENT_S_n .

```

```

x = data[,2:112]
y = data[, 'REC_IM']

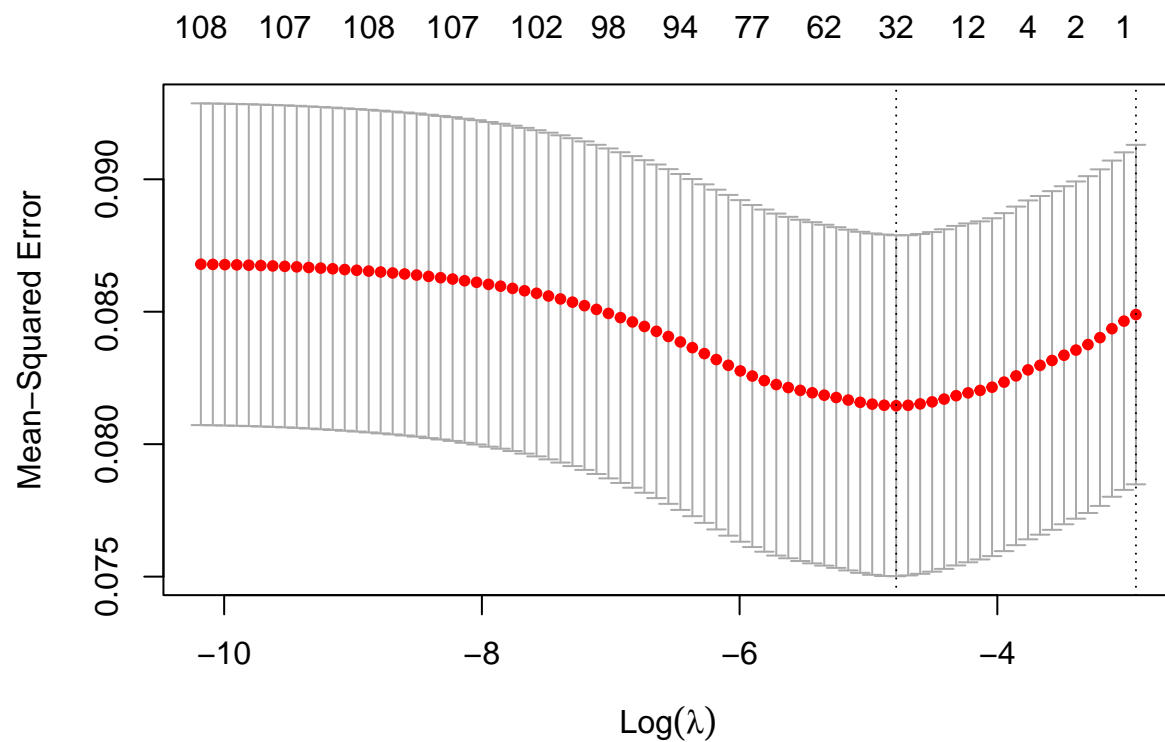
```

```

cv_model = cv.glmnet(as.matrix(x),y, alpha=1) ## 10-fold cross validation

best_lambda = cv_model$lambda.min ## 0.01339178
plot(cv_model)

```

```
## LASSO
```

```
lasso_model = glmnet(x,y, alpha=1, lambda = best_lambda) ##alpha=1 is LASSO
```

```
coef(lasso_model)
```

```
## 112 x 1 sparse Matrix of class "dgCMatrix"
```

```
##              s0
## (Intercept) -0.0376688120
## AGE         0.0010370397
## SEX         -0.0044599629
## INF_ANAM    .
## STENOK_AN   0.0075441960
## FK_STENOK   .
## IBS_POST    0.0059883330
## IBS_NASL    .
## GB          .
## SIM_GIPERT  .
## DLIT_AG     .
## ZSN_A       .
## nr_11       .
## nr_01       .
## nr_02       .
## nr_03       0.0402408641
## nr_04       .
## nr_07       .
```

```

## nr_08 .
## np_01 0.6323311551
## np_04 .
## np_05 .
## np_07 .
## np_08 .
## np_09 .
## np_10 0.0594247505
## endocr_01 0.0059498843
## endocr_02 .
## endocr_03 .
## zab_leg_01 -0.0207001131
## zab_leg_02 0.0334371408
## zab_leg_03 .
## zab_leg_04 .
## zab_leg_06 .
## S_AD_KBRIG .
## D_AD_KBRIG .
## S_AD_ORIT .
## D_AD_ORIT .
## O_L_POST .
## K_SH_POST -0.0547746265
## MP_TP_POST .
## SVT_POST .
## GT_POST 0.1650972264
## FIB_G_POST 0.0036998215
## ant_im 0.0015787898
## lat_im 0.0003735782
## inf_im .
## post_im .
## IM_PG_P .
## ritm_ecg_p_01 .
## ritm_ecg_p_02 -0.0107063723
## ritm_ecg_p_04 .
## ritm_ecg_p_06 .
## ritm_ecg_p_07 0.0067364141
## ritm_ecg_p_08 .
## n_r_ecg_p_01 .
## n_r_ecg_p_02 .
## n_r_ecg_p_03 .
## n_r_ecg_p_04 .
## n_r_ecg_p_05 .
## n_r_ecg_p_06 -0.0376731704
## n_r_ecg_p_08 .
## n_r_ecg_p_09 0.0917148846
## n_r_ecg_p_10 .
## n_p_ecg_p_01 .
## n_p_ecg_p_03 .
## n_p_ecg_p_04 .
## n_p_ecg_p_05 .
## n_p_ecg_p_06 .
## n_p_ecg_p_07 .
## n_p_ecg_p_08 .
## n_p_ecg_p_09 .

```

```
## n_p_ecg_p_10      .
## n_p_ecg_p_11      0.0374898418
## n_p_ecg_p_12      .
## fibr_ter_01       .
## fibr_ter_02       .
## fibr_ter_03       .
## fibr_ter_05       .
## fibr_ter_06       .
## fibr_ter_07       .
## fibr_ter_08       .
## GIPO_K            .
## K_BLOOD           .
## GIPER_NA          0.0288109190
## NA_BLOOD          .
## ALT_BLOOD         .
## AST_BLOOD         .
## KFK_BLOOD         .
## L_BLOOD           0.0027686056
## ROE               .
## TIME_B_S         .
## R_AB_1_n         .
## R_AB_2_n         .
## R_AB_3_n         0.1251436955
## NA_KB             .
## NOT_NA_KB        .
## LID_KB           -0.0030615932
## NITR_S           0.0019354032
## NA_R_1_n         0.0035326449
## NA_R_2_n         0.0336397371
## NA_R_3_n         0.0067432103
## NOT_NA_1_n       .
## NOT_NA_2_n       0.0021473474
## NOT_NA_3_n       .
## LID_S_n          .
## B_BLOK_S_n       .
## ANT_CA_S_n       -0.0092336644
## GEPAR_S_n        0.0130147926
## ASP_S_n          .
## TIKL_S_n         .
## TRENT_S_n        -0.0082192527
```

```
#x, response
```

```
newd = cor(x[sapply(x,is.numeric)])
```

```
melted = melt(newd)
```

```
ggplot(melted, aes(x = Var1, y = Var2, fill = value)) + geom_tile() + scale_fill_gradient(high = "red",
  labs(title = "Correlation Heatmap of Covariates") +
  theme(text = element_text(size=4), axis.text.x = element_text(angle=90, hjust = .5, vjust = .5))
```

Correlation Heatmap of Covariates

