Analysis_Chen_Liang_cl4469

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Data preparation

```r
# Load data
recov_df <- get(load("./data/recovery.RData")) |>
  janitor::clean_names() |>
  na.omit()

summary(recov_df)
```

```
##        id              age            gender        race     smoking
##  Min.   :   1.0   Min.   :42.0   Min.   :0.0000   1:1967   0:1822
##  1st Qu.: 750.8   1st Qu.:57.0   1st Qu.:0.0000   2: 158   1: 859
##  Median :1500.5   Median :60.0   Median :0.0000   3: 604   2: 319
##  Mean   :1500.5   Mean   :60.2   Mean   :0.4853   4: 271
##  3rd Qu.:2250.2   3rd Qu.:63.0   3rd Qu.:1.0000
##  Max.   :3000.0   Max.   :79.0   Max.   :1.0000
##      height          weight            bmi         hypertension
##  Min.   :147.8   Min.   : 55.90   Min.   :18.80   Min.   :0.0000
##  1st Qu.:166.0   1st Qu.: 75.20   1st Qu.:25.80   1st Qu.:0.0000
##  Median :169.9   Median : 79.80   Median :27.65   Median :0.0000
##  Mean   :169.9   Mean   : 79.96   Mean   :27.76   Mean   :0.4973
##  3rd Qu.:173.9   3rd Qu.: 84.80   3rd Qu.:29.50   3rd Qu.:1.0000
##  Max.   :188.6   Max.   :103.70   Max.   :38.90   Max.   :1.0000
##     diabetes           sbp             ldl            vaccine
##  Min.   :0.0000   Min.   :105.0   Min.   : 28.0   Min.   :0.000
##  1st Qu.:0.0000   1st Qu.:125.0   1st Qu.: 97.0   1st Qu.:0.000
##  Median :0.0000   Median :130.0   Median :110.0   Median :1.000
##  Mean   :0.1543   Mean   :130.5   Mean   :110.5   Mean   :0.596
##  3rd Qu.:0.0000   3rd Qu.:136.0   3rd Qu.:124.0   3rd Qu.:1.000
##  Max.   :1.0000   Max.   :156.0   Max.   :178.0   Max.   :1.000
##     severity         study           recovery_time
##  Min.   :0.000   Length:3000        Min.   :  2.00
##  1st Qu.:0.000   Class :character   1st Qu.: 31.00
##  Median :0.000   Mode  :character   Median : 39.00
##  Mean   :0.107                      Mean   : 42.17
##  3rd Qu.:0.000                      3rd Qu.: 49.00
##  Max.   :1.000                      Max.   :365.00
```

```
# Create a partition index.(training:test=80:20)
set.seed(2024)
train_index = initial_split(recov_df, prop = .80)

# Extract the training and test data
training_df = training(train_index) |>select(-id)
testing_df = testing(train_index) |>select(-id)
# Training data
x = model.matrix(recovery_time~.,training_df)[, -1]
y = training_df$recovery_time

# Testing data
x2 <- model.matrix(recovery_time~.,testing_df)[, -1]
y2 <- testing_df$recovery_time
```

Linear Model

```
set.seed(2024)

# 10-fold cv
ctrl1 <- trainControl(method = "cv", number = 10)

# Fit Model
lm_fit <- train(x, y, method = "lm", trControl = ctrl1)
summary(lm_fit)
```

```
##
## Call:
## lm(formula = .outcome ~ ., data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -53.037 -10.712  -0.508   8.268 263.578
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.893e+03  1.155e+02 -16.381  < 2e-16 ***
## age           3.024e-01  1.023e-01   2.955 0.003153 **
## gender       -2.988e+00  8.089e-01  -3.694 0.000226 ***
## race2         3.388e+00  1.822e+00   1.859 0.063138 .
## race3        -6.868e-01  1.027e+00  -0.669 0.503720
## race4        -1.427e+00  1.472e+00  -0.969 0.332428
## smoking1      1.749e+00  9.148e-01   1.912 0.055966 .
## smoking2      3.533e+00  1.344e+00   2.628 0.008635 **
## height        1.102e+01  6.773e-01  16.276  < 2e-16 ***
## weight       -1.193e+01  7.152e-01 -16.680  < 2e-16 ***
## bmi           3.608e+01  2.054e+00  17.568  < 2e-16 ***
## hypertension  2.690e+00  1.325e+00   2.030 0.042449 *
## diabetes     -1.670e+00  1.133e+00  -1.474 0.140535
## sbp          -6.707e-04  8.631e-02  -0.008 0.993800
## ldl          -2.969e-02  2.132e-02  -1.393 0.163882
## vaccine      -6.301e+00  8.250e-01  -7.638 3.18e-14 ***
## severity      5.917e+00  1.301e+00   4.549 5.67e-06 ***
## studyB        5.057e+00  8.613e-01   5.871 4.94e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 19.77 on 2382 degrees of freedom
## Multiple R-squared:  0.2256, Adjusted R-squared:   0.22
## F-statistic: 40.81 on 17 and 2382 DF,  p-value: < 2.2e-16
```

```
# Calculate test error
lm_test_pred <- predict(lm_fit, newdata = x2)
lm_test_rmse <- sqrt(mean((lm_test_pred - y2)^2))
lm_test_rmse
```

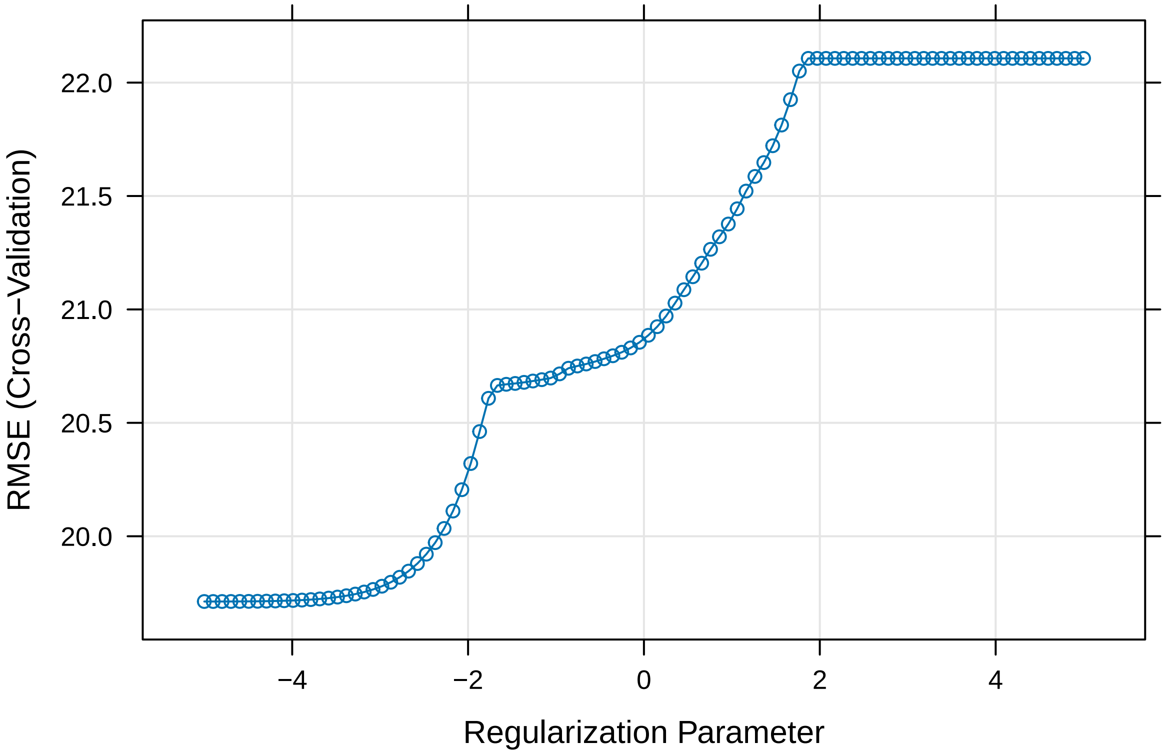
```
## [1] 21.70729
```

Lasso Model

```
set.seed(2024)

# Fit Model
lasso_fit <- train(x, y,
                   data= training_df,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 1,
                                          lambda = exp(seq(5, -5, length = 100))),
                   trControl = ctrl1)
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo,
## : There were missing values in resampled performance measures.
```

```
# Plot RMSE and lambda
plot(lasso_fit, xTrans = log)
```



```
# Check best tune
lasso_fit$bestTune
```

```
##   alpha      lambda
## 2     1 0.007454109
```

```
# Obtain coefficients in the final model
coef(lasso_fit$finalModel, s = lasso_fit$bestTune$lambda)
```

```
## 18 x 1 sparse Matrix of class "dgCMatrix"
##                         s1
## (Intercept)  -1.786727e+03
## age           3.031362e-01
## gender       -2.972141e+00
## race2         3.382522e+00
## race3        -6.654586e-01
## race4        -1.424497e+00
## smoking1      1.719034e+00
## smoking2      3.466992e+00
## height        1.039828e+01
## weight       -1.126692e+01
## bmi           3.417931e+01
## hypertension  2.675531e+00
## diabetes     -1.670466e+00
## sbp           .
## ldl          -2.914713e-02
## vaccine      -6.297203e+00
## severity      5.876002e+00
## studyB        5.042943e+00
```

```
# Calculate test error
lasso_test_pred <- predict(lasso_fit, newdata = x2)
lasso_test_rmse <- mean((lasso_test_pred - y2)^2)
lasso_test_rmse
```

```
## [1] 475.4402
```

Elastic Net Model

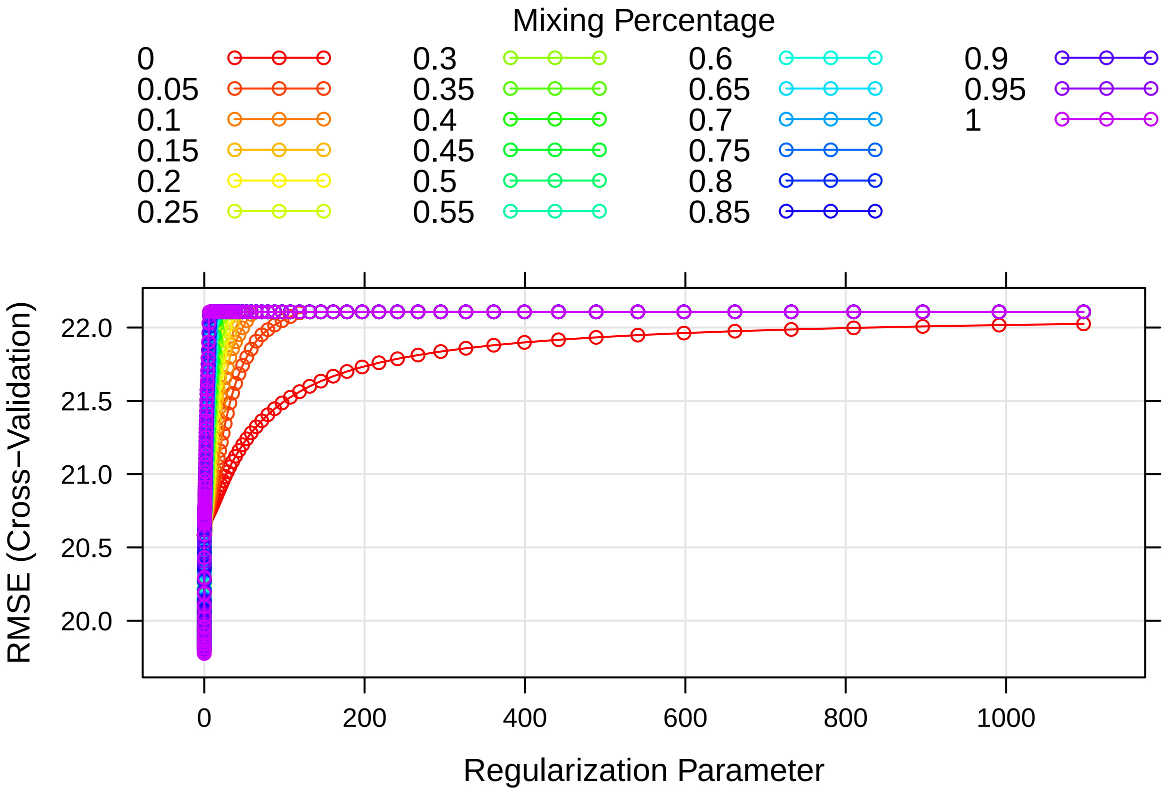
```
set.seed(2024)

# Fit Model
enet_fit <- train(x, y,
                  data = training_df,
                  method = "glmnet",
                  tuneGrid = expand.grid(alpha = seq(0, 1, length = 21),
                                         lambda = exp(seq(7, -3, length = 100))),
                  trControl = ctrl1)
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo,
## : There were missing values in resampled performance measures.
```

```
# Check best tune
enet_fit$bestTune
```

```
##      alpha     lambda
## 2001     1 0.04978707
```

```
# plot RMSE vs lambda and alpha
myCol <- rainbow(25)
myPar <- list(superpose.symbol = list(col = myCol),
              superpose.line = list(col = myCol))

plot(enet_fit, par.settings = myPar)
```



```r
# Obtain coefficients in the final model
coef(enet_fit$finalModel, enet_fit$bestTune$lambda)
```

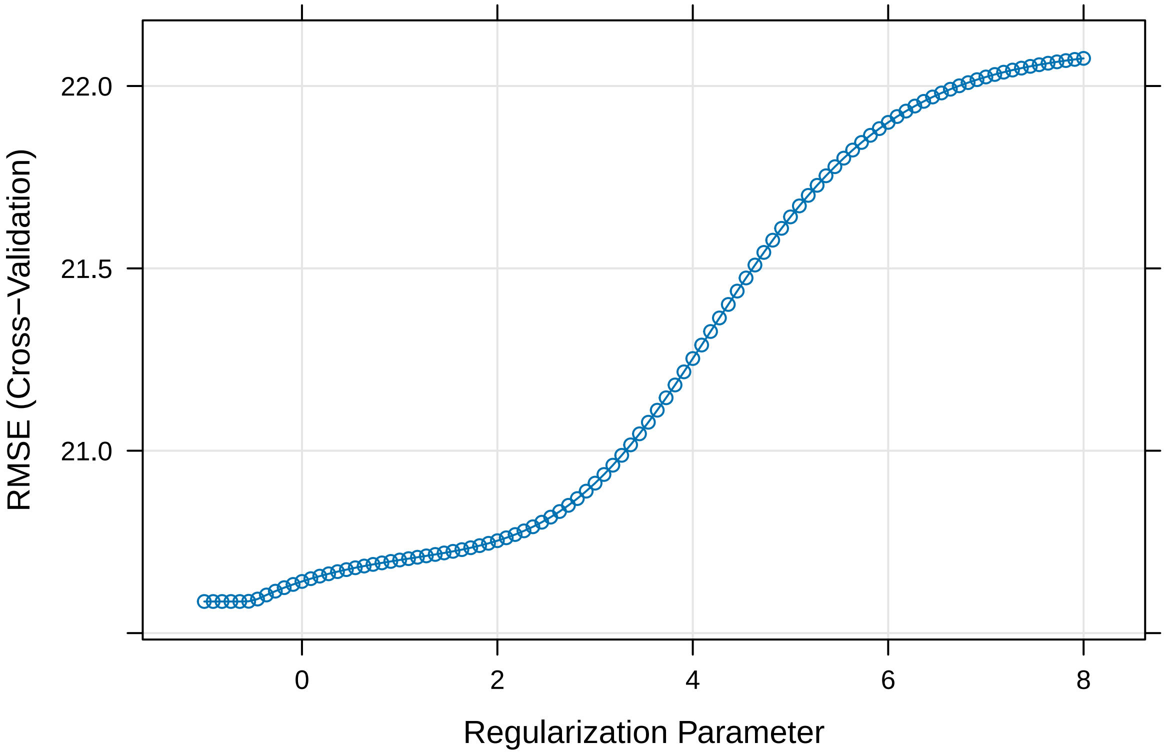
```
## 18 x 1 sparse Matrix of class "dgCMatrix"
##                         s1
## (Intercept)  -1.345823e+03
## age           3.044083e-01
## gender       -2.884762e+00
## race2         3.324496e+00
## race3        -5.441131e-01
## race4        -1.360138e+00
## smoking1      1.561219e+00
## smoking2      3.142061e+00
## height        7.797840e+00
## weight       -8.517852e+00
## bmi           2.628087e+01
## hypertension  2.624536e+00
## diabetes     -1.641080e+00
## sbp           .
## ldl          -2.593299e-02
## vaccine      -6.257870e+00
## severity      5.671095e+00
## studyB        4.960433e+00
```

```
# Calculate test error
enet_test_pred <- predict(enet_fit, newdata = x2)
enet_test_rmse <- mean((enet_test_pred - y2)^2)
enet_test_rmse
```

```
## [1] 496.3542
```

Ridge

```
set.seed(2024)

# Fit Model
ridge_fit <- train(x, y,
                   method = "glmnet",
                   tuneGrid = expand.grid(alpha = 0,
                                          lambda = exp(seq(8, -1, length=100))),
                   trControl = ctrl1)

# plot RMSE
plot(ridge_fit, xTrans = log)
```



```r
# Check best tune
ridge_fit$bestTune
```

```
##   alpha    lambda
## 5     0 0.5292133
```

```r
# Obtain coefficients in the final model
coef(ridge_fit$finalModel, s = ridge_fit$bestTune$lambda)
```

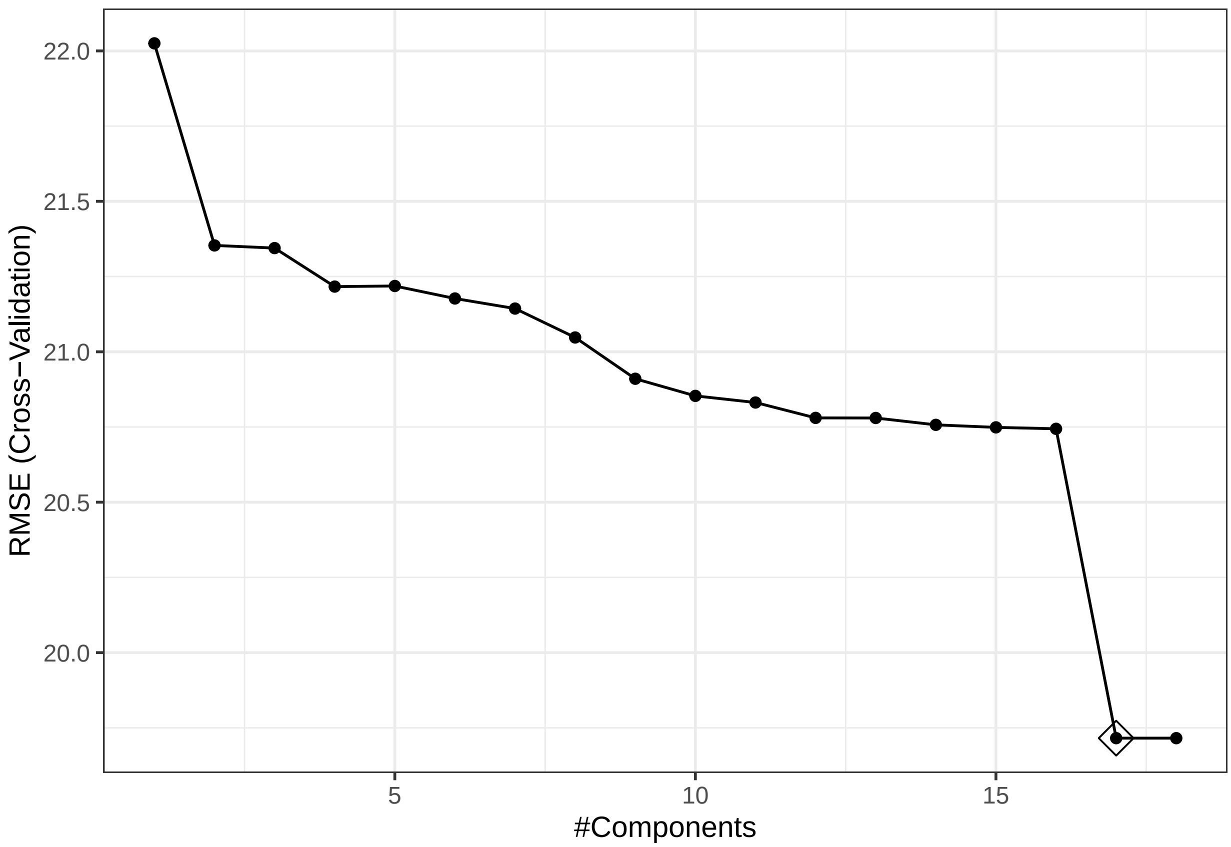
```
## 18 x 1 sparse Matrix of class "dgCMatrix"
##                         s1
## (Intercept)  -88.793877369
## age            0.337716864
## gender        -2.887487626
## race2          3.653136318
## race3         -0.670122648
## race4         -1.893301307
## smoking1       1.533851174
## smoking2       2.852821090
## height         0.388447289
## weight        -0.672787548
## bmi            3.714325264
## hypertension   2.787728002
## diabetes      -1.968811271
## sbp           -0.004322627
## ldl           -0.028329531
## vaccine       -6.350093251
## severity       5.448595072
## studyB         4.965623471
```

```r
# Calculate test error
ridge_test_pred <- predict(ridge_fit, newdata = x2)
ridge_test_mse <- mean((ridge_test_pred - y2)^2)
ridge_test_mse
```

```
## [1] 584.6444
```

Principal Component Regression (PCR)

```r
set.seed(2024)

# Fit Model
pcr_fit <-  train(x, y,
                  method = "pcr",
                  tuneGrid = data.frame(ncomp = 1:18),
                  trControl = ctrl1,
                  preProcess = c("center", "scale"))

# plot RMSE
ggplot(pcr_fit, highlight = TRUE) + theme_bw()
```



```
# Check best tune
pcr_fit$bestTune
```

```
##    ncomp
## 17    17
```

```
# Obtain coefficients in the final model
coef(pcr_fit$finalModel, s = pcr_fit$bestTune)
```

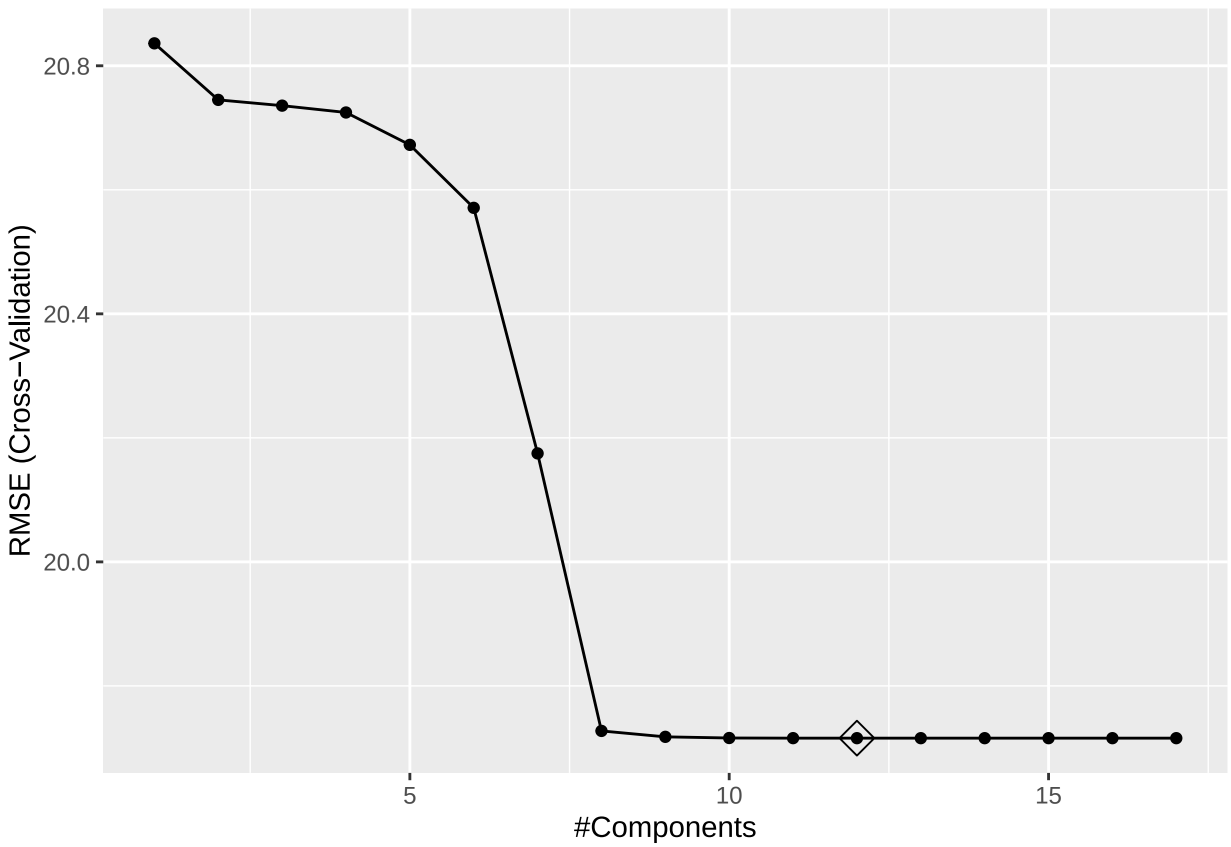
```
## , , 17 comps
## 
##                    .outcome
## age             1.345229648
## gender         -1.493769451
## race2           0.761325281
## race3          -0.276690264
## race4          -0.399028343
## smoking1        0.795261992
## smoking2        1.090904515
## height         65.818417321
## weight        -85.066995624
## bmi           100.591853512
## hypertension    1.345339735
## diabetes       -0.596426494
## sbp            -0.005358771
## ldl           -0.586903327
## vaccine       -3.095789007
## severity       1.842629752
## studyB         2.374295409
```

```
# Calculate test error
pcr_test_pred <- predict(pcr_fit, newdata = x2)
pcr_test_mse <- mean((pcr_test_pred - y2)^2)
pcr_test_mse
```

```
## [1] 471.2063
```

Partial Least Squares model (PLS)

```
set.seed(2024)

# Fit Model
pls_fit <- train(x, y,
                 method = "pls",
                 tuneGrid = data.frame(ncomp = 1:17),
                 trControl = ctrl1,
                 preProcess = c("center", "scale"))

# Plot RMSE
ggplot(pls_fit, highlight = TRUE)
```



```
# Check best tune
pls_fit$bestTune
```

```
##    ncomp
## 12    12
```

```
# Obtain coefficients in the final model
coef(pls_fit$finalModel, s = pls_fit$bestTune)
```

```
## , , 12 comps
##
##                    .outcome
## age             1.345158171
## gender         -1.493772824
## race2           0.761188904
## race3          -0.276878330
## race4          -0.399096705
## smoking1        0.795166426
## smoking2        1.090788616
## height         65.818448742
## weight        -85.066976536
## bmi           100.591848304
## hypertension    1.345385989
## diabetes       -0.596479918
## sbp            -0.005320082
## ldl           -0.586950522
## vaccine       -3.095844913
## severity       1.842596287
## studyB         2.374347318
```

```
# Calculate test error
pls_test_pred <- predict(pls_fit, newdata = x2)
pls_test_mse <- mean((pls_test_pred - y2)^2)
pls_test_mse
```

```
## [1] 471.2062
```

GAM

```
set.seed(2024)

# Fit Model
gam_fit = train(x, y,
                method = "gam",
                tuneGrid = data.frame(method = "GCV.Cp",
                                      select = c(TRUE, FALSE)),
                trControl = ctrl1)

# Parameters that fit the best model
gam_fit$bestTune
```

```
##   select method
## 1  FALSE GCV.Cp
```

```
gam_fit$finalModel
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension + diabetes + vaccine + severity + studyB + s(age) +
##     s(sbp) + s(ldl) + s(bmi) + s(height) + s(weight)
##
## Estimated degrees of freedom:
## 1.00 1.20 1.00 8.61 1.00 2.75  total = 27.55
##
## GCV score: 355.0009
```

```
# View the model summary
summary(gam_fit$finalModel)
```

```
##
```

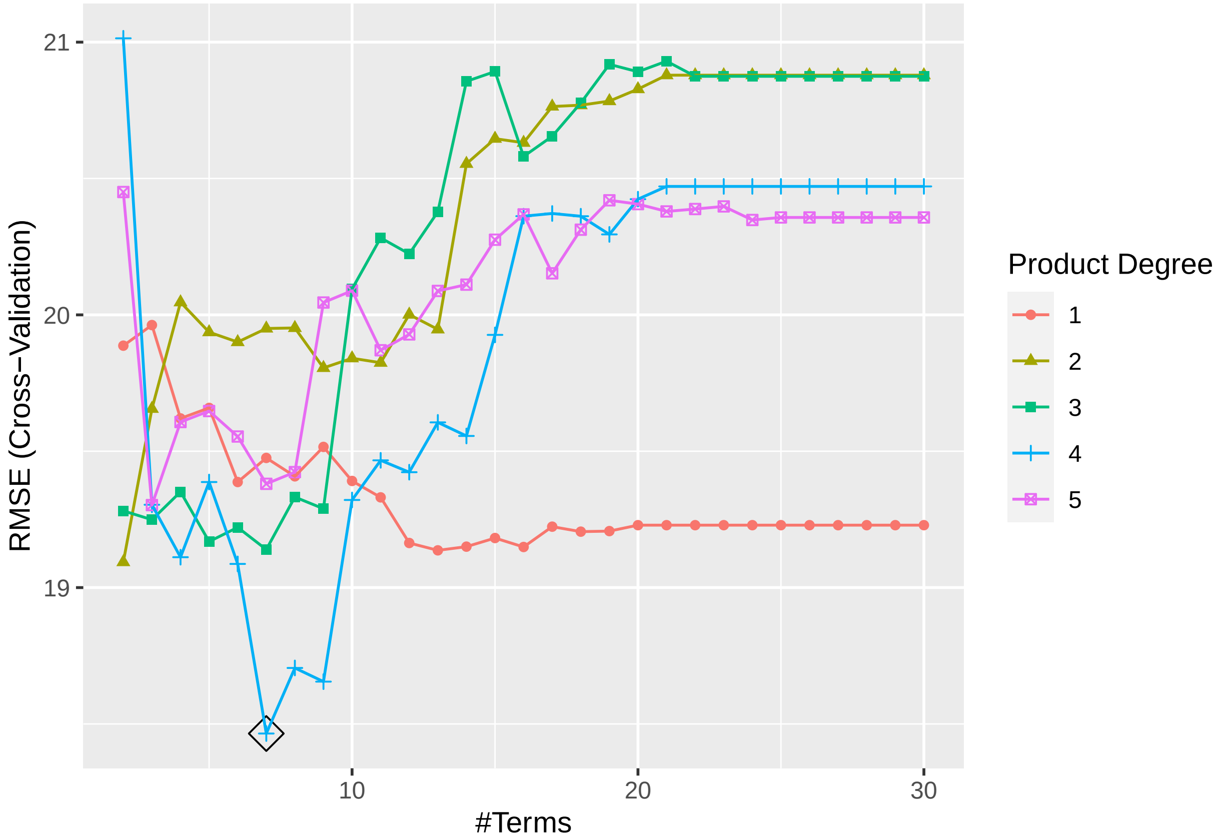
```
## Family: gaussian
## Link function: identity
##
## Formula:
## .outcome ~ gender + race2 + race3 + race4 + smoking1 + smoking2 +
##     hypertension + diabetes + vaccine + severity + studyB + s(age) +
##     s(sbp) + s(ldl) + s(bmi) + s(height) + s(weight)
##
## Parametric coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   43.1568     1.0646  40.540  < 2e-16 ***
## gender        -3.3920     0.7687  -4.413 1.07e-05 ***
## race2          2.5889     1.7284   1.498  0.13431
## race3         -0.5280     0.9743  -0.542  0.58789
## race4         -1.2561     1.3982  -0.898  0.36906
## smoking1       1.9909     0.8684   2.293  0.02195 *
## smoking2       4.1584     1.2778   3.254  0.00115 **
## hypertension   2.7655     1.2687   2.180  0.02937 *
## diabetes      -1.4274     1.0750  -1.328  0.18433
## vaccine       -6.3431     0.7834  -8.097 8.88e-16 ***
## severity       5.9477     1.2351   4.816 1.56e-06 ***
## studyB         4.6537     0.8190   5.682 1.50e-08 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Approximate significance of smooth terms:
##             edf Ref.df      F p-value
## s(age)    1.000  1.000  6.114 0.01348 *
## s(sbp)    1.196  1.367  0.093 0.91631
## s(ldl)    1.000  1.000  1.617 0.20368
## s(bmi)    8.607  8.945 63.287 < 2e-16 ***
## s(height) 1.000  1.000  5.495 0.01915 *
## s(weight) 2.750  3.732  4.360 0.00163 **
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## R-sq.(adj) =    0.3   Deviance explained = 30.8%
## GCV =    355  Scale est. = 350.93    n = 2400
```

```r
# Calculate test error
gam_test_pred <- predict(gam_fit, newdata = x2)
gam_test_mse <- mean((gam_test_pred - y2)^2)
gam_test_mse
```

```
## [1] 427.107
```

Multivariate Adaptive Regression Splines (MARS)

```r
set.seed(2024)

mars_grid <- expand.grid(degree = 1:5,
                         nprune = 2:30)


mars_fit <- train(x, y,
                  method = "earth",
                  tuneGrid = mars_grid,
                  metric = "RMSE",
                  trControl = ctrl1)

# Plot RMSE
ggplot(mars_fit, highlight = T)
```



```
# Parameters that fit the best model
mars_fit$bestTune
```

```
##    nprune degree
## 93      7      4
```

```
coef(mars_fit$finalModel)
```

```
##                        (Intercept)                       h(30.3-bmi)
##                          22.435204                          3.574363
##                  h(bmi-30.3) * studyB                          vaccine
##                           9.782606                         -6.264022
##  h(164-height) * h(bmi-30.3) * studyB                           h(bmi-25.7)
##                              2.990501                              4.898496
## h(87.6-weight) * h(bmi-30.3) * studyB
##                             -2.640353
```

```r
summary(mars_fit$finalModel)
```

```
## Call: earth(x=matrix[2400,17], y=c(33,44,33,27,6...), keepxy=TRUE, degree=4,
##             nprune=7)
##
##                                        coefficients
## (Intercept)                               22.435204
## vaccine                                   -6.264022
## h(bmi-25.7)                                4.898496
## h(30.3-bmi)                                3.574364
## h(bmi-30.3) * studyB                       9.782606
## h(164-height) * h(bmi-30.3) * studyB       2.990502
## h(87.6-weight) * h(bmi-30.3) * studyB     -2.640353
##
## Selected 7 of 22 terms, and 5 of 17 predictors (nprune=7)
## Termination condition: Reached nk 35
## Importance: bmi, studyB, height, weight, vaccine, age-unused, ...
## Number of terms at each degree of interaction: 1 3 1 2
## GCV 305.1695    RSS 722673.9    GRSq 0.3915679    RSq 0.3991527
```

```r
mars_test_pred <- predict(gam_fit, newdata = x2)
mars_test_mse <- mean((mars_test_pred - y2)^2)
mars_test_mse
```

```
## [1] 427.107
```

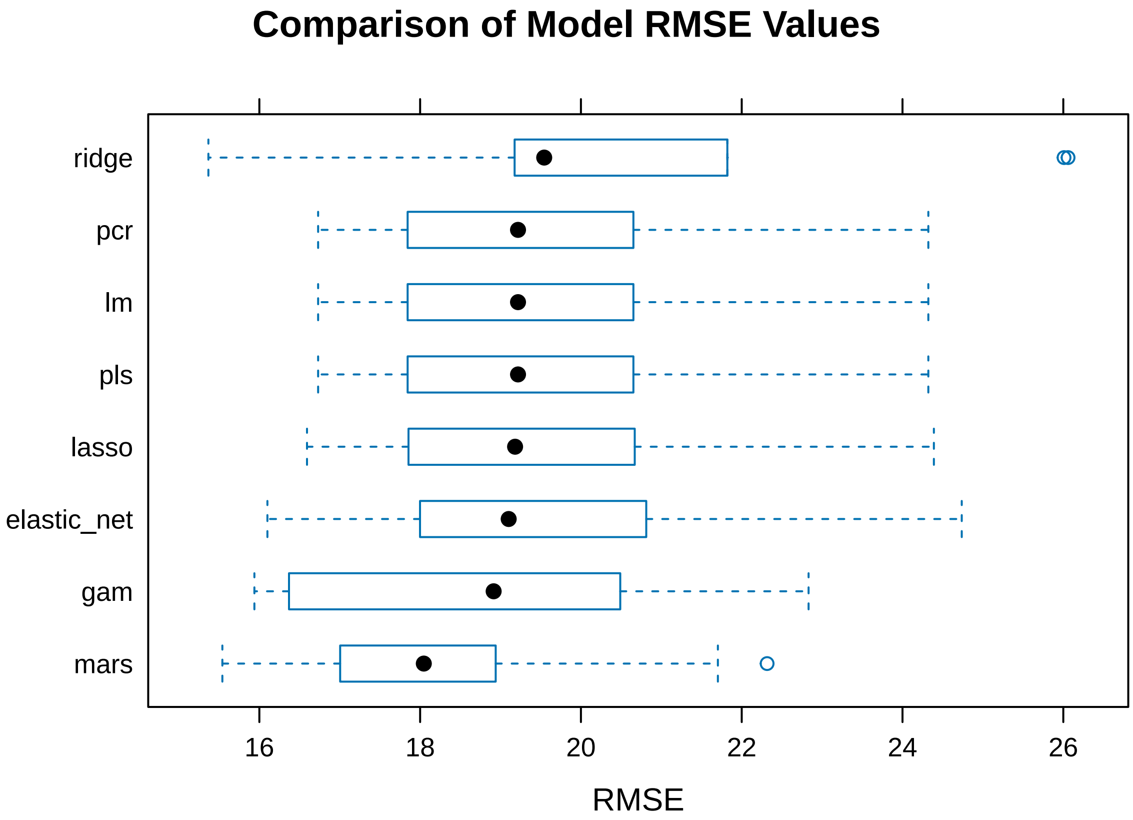
Model Comparing

```r
# resample
resamp <- resamples(list(
  lm = lm_fit,
  lasso = lasso_fit,
  ridge = ridge_fit,
  elastic_net = enet_fit,
  pcr = pcr_fit,
  pls = pls_fit,
  gam = gam_fit,
  mars = mars_fit
))

summary(resamp)
```

```
##
## Call:
## summary.resamples(object = resamp)
```

```
##
## Models: lm, lasso, ridge, elastic_net, pcr, pls, gam, mars
## Number of resamples: 10
##
## MAE
##                 Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lm          11.74160 12.57542 13.05304 12.96649 13.35735 14.01804    0
## lasso       11.68936 12.47988 12.99726 12.91362 13.29877 13.96370    0
## ridge       11.61061 12.89322 13.00231 13.07056 13.44631 14.29571    0
## elastic_net 11.54759 12.25975 12.84822 12.76980 13.15859 13.83584    0
## pcr         11.74160 12.57542 13.05304 12.96649 13.35735 14.01804    0
## pls         11.74160 12.57540 13.05304 12.96648 13.35735 14.01805    0
## gam         11.18041 12.14532 12.58068 12.46836 12.96641 13.51204    0
## mars        11.29074 11.69608 11.96643 12.04453 12.56542 12.82283    0
##
## RMSE
##                 Min.  1st Qu.   Median     Mean  3rd Qu.     Max. NA's
## lm          16.73131 17.89516 19.21757 19.71575 20.50813 24.32138    0
## lasso       16.59288 17.90516 19.18095 19.71227 20.52341 24.39038    0
## ridge       15.36616 19.20411 19.54329 20.58662 21.68757 26.05950    0
## elastic_net 16.10032 18.04364 19.10151 19.77650 20.66412 24.73699    0
## pcr         16.73131 17.89516 19.21757 19.71575 20.50813 24.32138    0
## pls         16.73129 17.89516 19.21756 19.71574 20.50813 24.32139    0
## gam         15.93861 16.89042 18.91441 18.98713 20.21679 22.83180    0
## mars        15.54017 17.25203 18.04581 18.46486 18.75092 22.31588    0
##
## Rsquared
##                   Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
## lm          0.06611697 0.2019001 0.2268777 0.2122074 0.2473751 0.2819362    0
## lasso       0.07046686 0.2000951 0.2272111 0.2117903 0.2465348 0.2796740    0
## ridge       0.09486261 0.1145127 0.1348116 0.1368990 0.1477628 0.2011960    0
## elastic_net 0.08959695 0.1870300 0.2235610 0.2059847 0.2411988 0.2652584    0
## pcr         0.06611697 0.2019001 0.2268777 0.2122074 0.2473751 0.2819362    0
## pls         0.06611802 0.2019003 0.2268774 0.2122076 0.2473758 0.2819355    0
## gam         0.09606751 0.2020966 0.2670992 0.2781279 0.3666627 0.4376890    0
## mars        0.04864786 0.2039051 0.3015203 0.3135288 0.3970823 0.6892535    0
```

```
# visualization
modelcomp <- bwplot(resamp, metric = "RMSE",main = "Comparison of Model RMSE Values")

modelcomp
```



```r
png(filename = "./plots/modelcomp.png", width = 3, height = 1, units = "in", res = 80)
```