Untitled

Linear analysis

```
## Loading required package: Matrix
## Loading required package: foreach
## Loaded glmnet 2.0-2
##
## Loading required package: rpart
## Loading required package: lattice
## Loading required package: ggplot2
```

Additionally, we considered a standard *linear regression* model involving all predictors, as an alternative means to view the significance of each predictor. Note that in this context, performing *k-fold cross-validation* or *bootstrapping* wouldn't allow us to come up with an "averaged" subset, hence we performed an ordinary 80/20 splitting of the data into the testing an training as shown in the code below:

```
set.seed(1000)
test = sample(nrow(Crime), nrow(Crime)*.2)
excluded = c("crmrte", "crmrte_cat", "region_w_nw")
xs = Crime[-which(names(Crime) %in% excluded)]
ys = Crime[which(names(Crime) %in% c("crmrte"))]
xs_test = xs[test,]
xs_train = xs[-test,]
ys_test = ys[test,]
ys_train = ys[-test,]
p = dim(xs)[2]
```

We then run a simple linear fit will all predictors, in order to analyse the significance levels of the parameters, provided that the linear test itself has a significant R^2 value.

```
lm.fit = lm(crmrte ~ ., data = Crime)
summary(lm.fit)
```

```
##
## Call:
## lm(formula = crmrte ~ ., data = Crime)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.027793 -0.005201 -0.000603  0.004163  0.038831
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.115e-01  2.696e-02   4.136 4.03e-05 ***
## county       5.086e-06  6.285e-06   0.809 0.418738
## year        -1.463e-03  3.674e-04  -3.982 7.67e-05 ***
## prbarr      -3.334e-02  3.323e-03 -10.033  < 2e-16 ***
## prbconv     -2.062e-03  2.847e-04  -7.244 1.34e-12 ***
## prbpris      1.952e-03  4.264e-03   0.458 0.647334
```

```
## avgsen      -1.073e-04  1.355e-04  -0.792 0.428543
## polpc        1.725e+00  2.150e-01   8.021 5.51e-15 ***
## density      7.091e-03  5.542e-04  12.795  < 2e-16 ***
## taxpc        1.577e-04  3.932e-05   4.011 6.81e-05 ***
## regionother  4.816e-03  1.010e-03   4.770 2.32e-06 ***
## regionwest  -1.411e-03  1.235e-03  -1.143 0.253584
## smsayes     -3.429e-03  2.448e-03  -1.401 0.161817
## pctmin       1.326e-04  3.421e-05   3.876 0.000118 ***
## wcon        -6.811e-07  3.022e-06  -0.225 0.821741
## wtuc        -1.956e-07  1.330e-06  -0.147 0.883171
## wtrd         4.305e-06  4.261e-06   1.010 0.312703
## wfir        -1.014e-05  1.009e-05  -1.005 0.315466
## wser        -4.180e-06  3.529e-06  -1.184 0.236778
## wmfg        -1.401e-06  5.970e-06  -0.235 0.814550
## wfed         4.413e-05  9.551e-06   4.620 4.70e-06 ***
## wsta        -6.671e-06  9.998e-06  -0.667 0.504907
## wloc         4.167e-05  1.788e-05   2.331 0.020066 *
## mix          4.689e-03  2.218e-03   2.114 0.034926 *
## pctymle      8.609e-02  1.611e-02   5.344 1.29e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.008666 on 601 degrees of freedom
## Multiple R-squared:  0.7544, Adjusted R-squared:  0.7445
## F-statistic:  76.9 on 24 and 601 DF,  p-value: < 2.2e-16
```

as the R^2 value is sufficiently high (0.754353), we decided to perform `best subset selection` on the set of predictors. Although we are aware of the performance penalties of doing this for $p = 23$, the running times were considerably short and hence we decided to stick to this approach:

```
bestsubset=regsubsets(y ~ ., data = data.frame(y = ys_train, x = xs_train), nvmax = p)
```

After getting all best subsets with size $k = 1...p$, we analysed both the *training RSE* and *testing RSE* by performing *k-fold cross validation* with $k = 10$ and then getting the minimum errors on all iterations:

```
set.seed(1000)
x_cols = colnames(xs, do.NULL = FALSE, prefix = "x.")
colnames(xs) <- paste("x", x_cols, sep = ".")
x_cols = colnames(xs)
folds <- createFolds(Crime$crmrte, k=10, list=TRUE, returnTrain=FALSE)
val.test.errors = matrix(, nrow = length(folds), ncol = p)
val.train.errors = matrix(, nrow = length(folds), ncol = p)
pred_train = vector()
pred_test = vector()

for (j in 1:length(folds)) {
  test     = folds[[j]]
  ys_train = ys[-test,]
  ys_test  = ys[test,]
  xs_train = xs[-test,]
  xs_test  = xs[test,]
  for (i in 1:p) {
    coefi = coef(bestsubset, id = i)
```

```
    pred_train = as.matrix(xs_test[, x_cols %in% names(coefi)]) %*% coefi[names(coefi)
                                                                  %in% x_cols]
    pred_test = as.matrix(xs_train[, x_cols %in% names(coefi)]) %*% coefi[names(coefi)
                                                                   %in% x_cols]
    val.train.errors[j,i] = mean((ys_train - pred_test)^2)
    val.test.errors[j,i] = mean((ys_test - pred_train)^2)
  }
}
min_test = which(val.test.errors == min(val.test.errors), arr.ind = TRUE)
min_test
```

```
##      row col
## [1,]   3   8
```

```
min_train = which(val.train.errors == min(val.train.errors), arr.ind = TRUE)
min_train
```

```
##      row col
## [1,]   4   8
```

```
min_test_error.1 = val.test.errors[min_test]
min_test_error.1
```

```
## [1] 0.0001096715
```

```
min_train_error.1 = val.train.errors[min_train]
min_train_error.1
```

```
## [1] 0.0001503665
```

The ratio between *testing RSE* and *training RSE* is very close to 1 (0.7293615) for the subset that minimizes both *RSEs* (which has 8 predictors). Consequently, we can conclude that the predictors yielded by the subset generated by *best subset selection* which minimizes both *RSEs* belong to a consistent model and, hence, can be used as a basis for non linear models. Nevertheless, we decided to run a linear fit with these predictors in order to check our conclusions:

```
lm.2.fit = lm(crmrte ~  prbarr + prbconv + polpc + density
              + as.factor(region) + pctmin + wfed + pctymle, data = Crime)
summary(lm.2.fit)
```

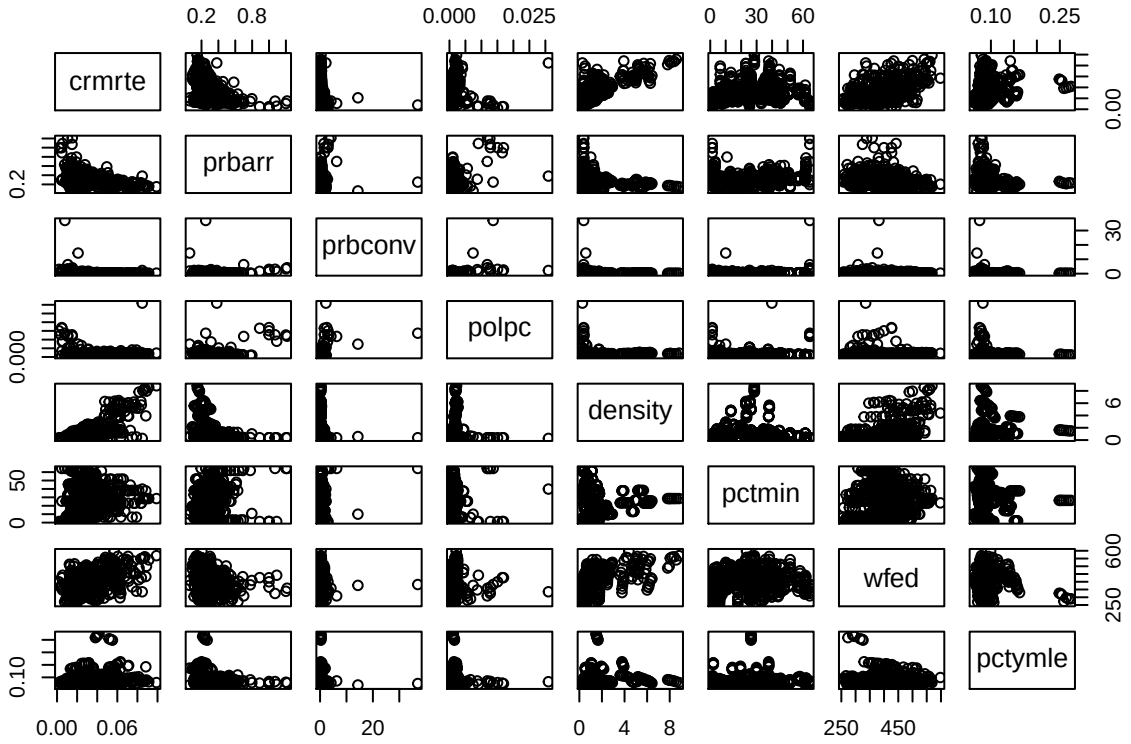
```
##
## Call:
## lm(formula = crmrte ~ prbarr + prbconv + polpc + density + as.factor(region) +
##     pctmin + wfed + pctymle, data = Crime)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.021247 -0.005769 -0.000725  0.004217  0.047783
##
## Coefficients:
```

```
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              7.205e-03  3.586e-03   2.009 0.044942 *
## prbarr                  -3.202e-02  3.098e-03 -10.336  < 2e-16 ***
## prbconv                 -1.807e-03  2.502e-04  -7.222 1.51e-12 ***
## polpc                    1.944e+00  2.112e-01   9.203  < 2e-16 ***
## density                  7.193e-03  3.171e-04  22.684  < 2e-16 ***
## as.factor(region)other   4.681e-03  9.785e-04   4.784 2.15e-06 ***
## as.factor(region)west   -3.471e-03  1.161e-03  -2.990 0.002898 **
## pctmin                   1.243e-04  3.220e-05   3.861 0.000125 ***
## wfed                     2.641e-05  6.936e-06   3.808 0.000154 ***
## pctymle                  7.466e-02  1.546e-02   4.828 1.74e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00887 on 616 degrees of freedom
## Multiple R-squared:  0.7362, Adjusted R-squared:  0.7324
## F-statistic: 191.1 on 9 and 616 DF,  p-value: < 2.2e-16
```

We can note that all coefficients are significant and the R^2, as expected, was reduced but only marginally (0.7362415 versus 0.754353), which confirms that the model with this subset is indeed a good model.

Next, we proceeded to graphically analyse any nonlinearities between these predictors and the response, by looking at all pairwise plots:

```
fitnames = c("prbarr" , "prbconv" , "polpc" , "density" ,
             "as.factor(region)" , "pctmin" , "wfed" ,
             "pctymle", "crmrte")
pairs(Crime[names(Crime) %in% fitnames])
```



It can be seen that `prbrarr`, `prbconvand` `polpc` have a peak structure that would benefit from applying a *log* to them in order to shrink those peaks. Additionally, `wfed` has a nonlinear relationship with `wfed`, which makes it suitable as a polynomial regression predictor. Consequently, we run a new, nonlinear model with these modified predictors:

```
lm.3.fit = lm(crmrte ~  log(prbarr) + log(prbconv) +
                log(polpc) + density + as.factor(region) +
                pctmin + poly(wfed,3) + pctymle, data = Crime)
summary(lm.3.fit)
```

```
##
## Call:
## lm(formula = crmrte ~ log(prbarr) + log(prbconv) + log(polpc) +
##     density + as.factor(region) + pctmin + poly(wfed, 3) + pctymle,
##     data = Crime)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.024202 -0.004384 -0.000246  0.003672  0.045724
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               0.0564773  0.0046897  12.043  < 2e-16 ***
## log(prbarr)              -0.0144423  0.0009070 -15.923  < 2e-16 ***
## log(prbconv)             -0.0113128  0.0006276 -18.024  < 2e-16 ***
## log(polpc)                0.0099603  0.0006892  14.452  < 2e-16 ***
```

```
## density                 0.0052809  0.0003094  17.068  < 2e-16 ***
## as.factor(region)other  0.0039568  0.0008168   4.844 1.61e-06 ***
## as.factor(region)west  -0.0042023  0.0009729  -4.319 1.82e-05 ***
## pctmin                  0.0001813  0.0000271   6.691 5.01e-11 ***
## poly(wfed, 3)1          0.0155450  0.0094692   1.642    0.101
## poly(wfed, 3)2          0.0006990  0.0079938   0.087    0.930
## poly(wfed, 3)3         -0.0101414  0.0076411  -1.327    0.185
## pctymle                 0.0073072  0.0135778   0.538    0.591
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.007408 on 614 degrees of freedom
## Multiple R-squared:  0.8166, Adjusted R-squared:  0.8133
## F-statistic: 248.6 on 11 and 614 DF,  p-value: < 2.2e-16
```

The lack of significance of the polynomials for `wfed` and the increase in R^2 suggests that this model *overfits*. Hence, we decided to remove the polynomials related to `wfed`, but kept the *log* predictors as they have shown to be still very significant.

Next, we analysed all significant interactions between all interaction terms:

```
lm.4.fit = lm(crmrte ~  .*., data = Crime)
summary(lm.4.fit)$r.squared
```

```
## [1] 0.9706801
```

and plugged all interactions to out previous model:

```
lm.5.fit = lm(crmrte ~  log(prbarr) + log(prbconv) +
                log(polpc) + density + as.factor(region) +
                pctmin + poly(wfed,3) + pctymle + .*., data = Crime)
summary(lm.5.fit)$r.squared
```

```
## [1] 0.9725358
```

The number of interactions that we added to the model are:

```
dim(summary(lm.4.fit)$coefficients)
```

```
## [1] 300   4
```

We can see that both models are seriously overfitting (R^2 values are 0.9706801 and 0.9725358 respectively, while the number of predictors has skyrocketed due to all interaction combinations). Even though it is tempting to keep only those interactions with a relevant significance value, since the removal of each of these predictors affects the overall model, we decided instead to choose a final model by using a *Stepwise Algorithm* applying *AIC* to decide. The stepwise procedure is too lengthy and cumbersome to show in text, but the code to generated is displayed below:

```
interaction.fit = stepAIC(lm.5.fit)
```

Once we got the fit, which has the following number of coefficients:

```
length(interaction.fit$coefficients)
```

```
## [1] 190
```

which means a reduction on the number of interactions by 30%, we proceeded to calculate both *training MSE* and *testing MSE*:

```
coefi = coef(interaction.fit)
pred = as.matrix(xs_train[, x_cols %in% names(coefi)]) %*% coefi[names(coefi)
                                                                 %in% x_cols]
val.train.errors = mean((ys_train - pred)^2)
val.train.errors
```

```
## [1] 0.00128208
```

```
pred = as.matrix(xs_test[, x_cols %in% names(coefi)]) %*% coefi[names(coefi)
                                                                %in% x_cols]
val.test.errors = mean((ys_test - pred)^2)
val.test.errors
```

```
## [1] 0.00118466
```

Here, we can see that the error rate remains close to one (0.9240136) which still proves that this model holds. Now that we obtained a complex model consisting of linear variables, *log* variables and *interaction* variables, we're gonna perform *Lasso* in order to remove all interaction terms that are not significant, so that we arrive to a model easy to understand.

Lasso Analysis

With the resulting model from all our previous steps, we performed *k-fold cross validation* using Lasso, in order to obtain the optimum value of λ for our model. The code generating the lasso is the following (note that the first line is a way to manually represent `interaction.fit` as the fit is not recognized by `cv.glmnet`, which requires a formula with a specific formatting):

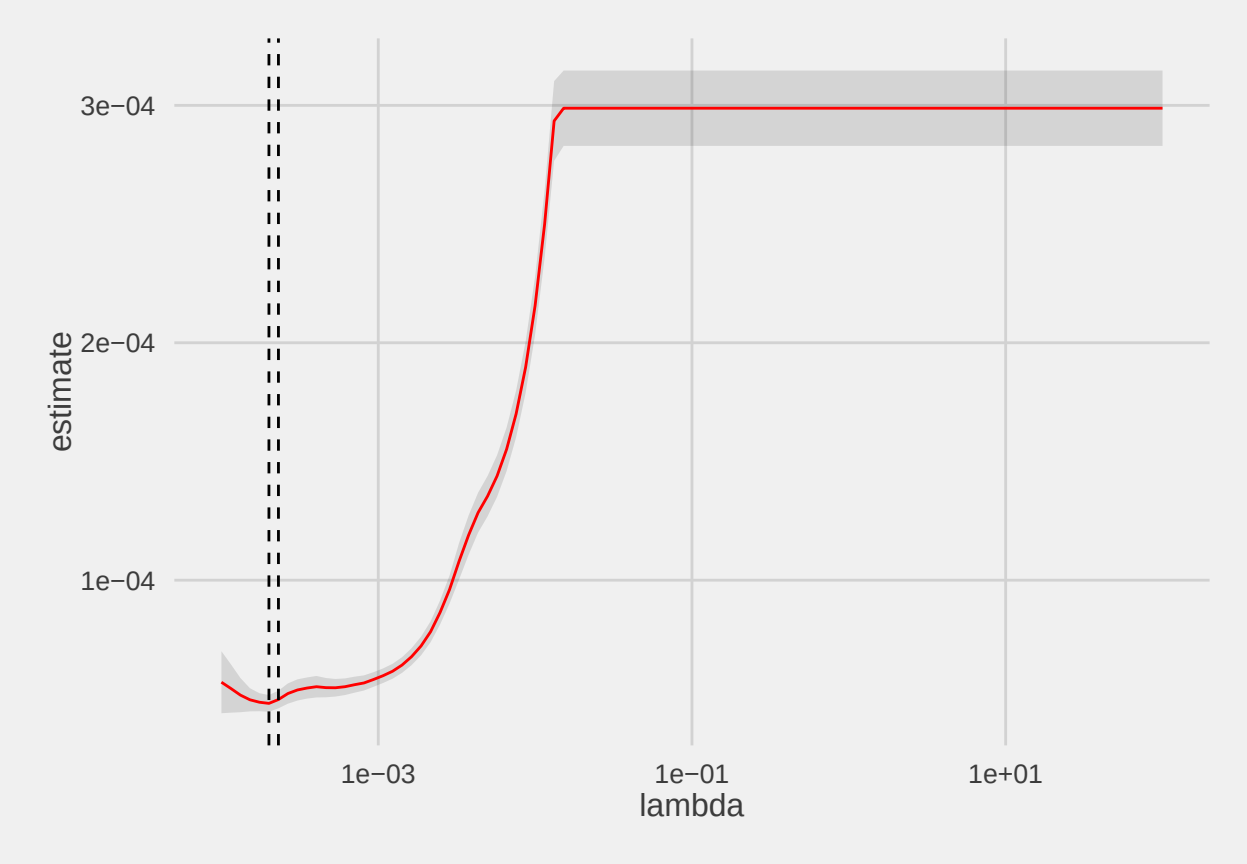
```
formula = "~ log(prbconv) + log(polpc) + density + pctmin +  poly(wfed, 3) +
pctymle + county + year + prbarr + prbconv +   prbpris + avgsen + polpc +
taxpc + region + smsa + wcon +   wtuc + wtrd + wfir + wser + wmfg + wfed +
wsta + wloc + mix +   county:year + county:avgsen + county:polpc +
density:county +  pctmin:county + county:wcon + county:wtuc + county:wtrd +
county:wfir + county:wmfg + county:wsta + county:wloc + pctymle:county +
year:prbconv + year:prbpris + year:polpc + year:region +   year:smsa + pctmin:year +
year:wtrd + year:wfir + year:wmfg +   year:wsta + year:mix + pctymle:year +
prbarr:prbpris + prbarr:polpc +   density:prbarr + prbarr:region + pctmin:prbarr +
prbarr:wcon +   prbarr:wtuc + prbarr:wtrd + prbarr:wfir + prbarr:wfed +
prbconv:prbpris +   prbconv:polpc + prbconv:smsa + pctmin:prbconv + prbconv:wcon +
prbconv:wfir + prbconv:wser + prbconv:wmfg + prbconv:mix +   density:prbpris +
prbpris:taxpc + prbpris:region + pctmin:prbpris +   prbpris:wcon + prbpris:wtrd +
prbpris:wmfg + prbpris:wfed + prbpris:wsta + prbpris:wloc + density:avgsen +
avgsen:taxpc + avgsen:region + avgsen:smsa + pctmin:avgsen + avgsen:wcon +
```

```
avgsen:wtrd + avgsen:wfir + avgsen:wser + avgsen:wfed + avgsen:mix + pctymle:avgsen +
polpc:region + polpc:smsa + pctmin:polpc +   polpc:wtuc + polpc:wtrd + polpc:wser +
polpc:wmfg + polpc:wfed +density:region + density:smsa + density:pctmin +
density:wcon +  density:wtuc + density:wtrd + density:wsta + density:mix +
density:pctymle + taxpc:region + taxpc:smsa + pctmin:taxpc +
taxpc:wmfg + taxpc:wfed + taxpc:wsta + taxpc:wloc + region:smsa +
pctmin:region + region:wcon + region:wtuc + region:wtrd +   region:wfir +
region:wser + region:wmfg + region:wfed + region:wsta +   region:wloc +
region:mix + pctymle:region + pctmin:smsa +   smsa:wtuc + smsa:wtrd +
smsa:wser + smsa:wmfg + smsa:wfed +   smsa:wsta + smsa:mix + pctymle:smsa +
pctmin:wtrd + pctmin:wfir +   pctmin:wser + pctmin:wmfg + pctmin:wfed +
pctmin:wsta + pctmin:wloc +   pctmin:mix + pctmin:pctymle + wcon:wtuc +
wcon:wfir + wcon:wmfg + wcon:wfed + wcon:wsta + wcon:mix + pctymle:wcon +
wtuc:wsta +   wtuc:wloc + wtrd:wfir +wtrd:wmfg + wtrd:wsta + wtrd:mix +
wfir:wmfg + wfir:wfed + wfir:wsta + wfir:wloc + wfir:mix + pctymle:wfir +
wser:wmfg + wser:wfed + wser:wloc + wser:mix + wmfg:wfed + pctymle:wmfg +
wfed:wsta + wfed:wloc + wfed:mix +   wsta:wloc + wsta:mix + pctymle:wsta
+ pctymle:mix"
xs_lasso = model.matrix(as.formula(formula), Crime)
xs_lasso_train = xs_lasso[-test,]
xs_lasso_test = xs_lasso[test,]
grid=10^seq(2,-4,length=100)
lasso.mod=cv.glmnet(xs_lasso[-test ,],ys_train,alpha=1,lambda=grid)
```

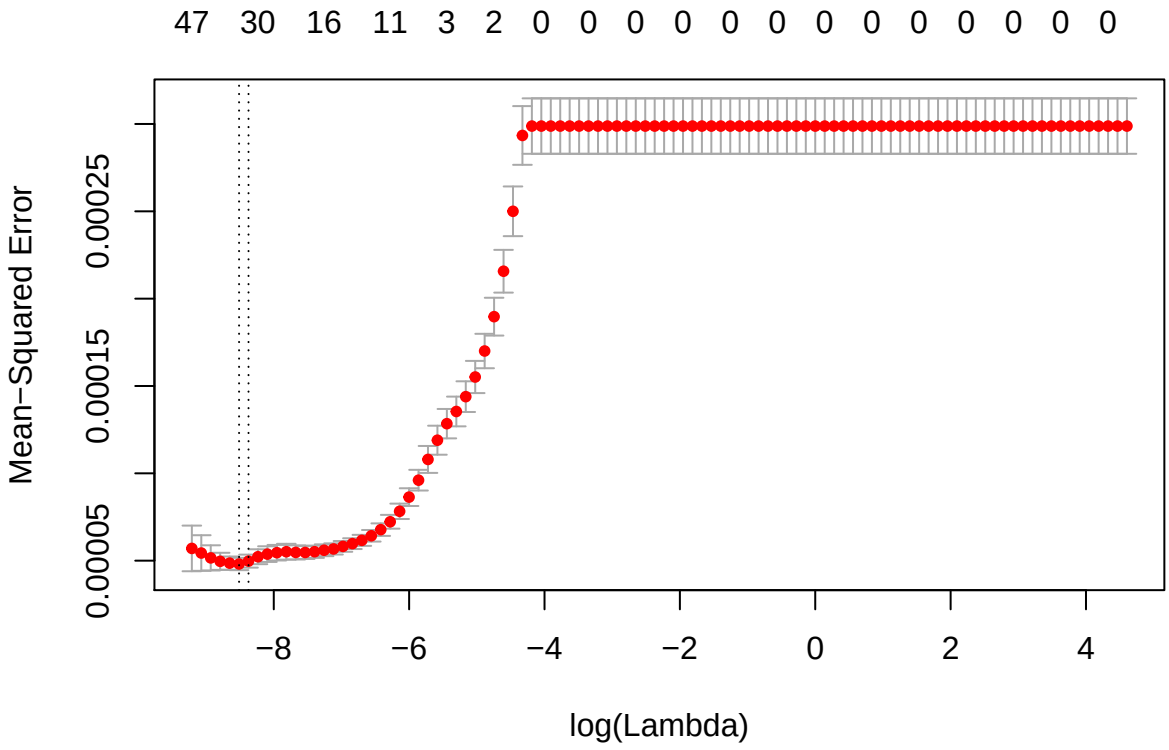
Now that we have computed all possible values for *lambda*, we can create the plot showing the *training RSE* and λ increases:

```
ggplot.glmnet = function(cv.glmnet.obj){
  tidied_cv <- tidy(cv.glmnet.obj)
  glance_cv <- glance(cv.glmnet.obj)

  # plot of MSE as a function of lambda
  g <- ggplot(tidied_cv, aes(lambda, estimate))  + scale_x_log10() +
    geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = .15)+
    geom_line(colour = "red") +
    # geom_line(aes(y=conf.low), linetype = "dashed",size=.4)+
    # geom_line(aes(y=conf.high), linetype = "dashed",size=.4)+
    geom_vline(xintercept = glance_cv$lambda.min, lty = 2) +
    geom_vline(xintercept = glance_cv$lambda.1se, lty = 2) + theme_fivethirtyeight()
g
  return(g)
}
ggplot.glmnet(lasso.mod)
```




```
plot(lasso.mod)
```



We then chose a value of λ within 1 standard deviation from the optimum value, as this is a commonly established good practice. The fit with that value is performed in the code below:

```
lasso.mod.3=glmnet(xs_lasso[-test ,],ys_train,alpha=1,lambda=lasso.mod$lambda.1se)
lasso_vars =  names(coef(lasso.mod.3)[,1][coef(lasso.mod.3)[,1]!=0])[-1]
length(lasso_vars)
```

```
## [1] 32
```

Lasso actually yielded 32 variables with nonzero values, a reduction of 83% with respect to the *stepwise AIC*. The *testing RSE* for this model is obtained using the same *k-folds* generated for the first model:

```
lasso_rse = vector()

for (i in 1:length(folds)) {
  test = folds[[i]]
  xs_lasso_train = xs_lasso[-test,]
  xs_lasso_test = xs_lasso[test,]
  ys_test = ys[test,]
  ys_lasso_pred = predict(lasso.mod.3, xs_lasso_test, s = lasso.mod$lambda.1se)
  lasso_rse[i] = mean((ys_test - ys_lasso_pred)^2)
}

mean(lasso_rse)
```

```
## [1] 4.128223e-05
```

and the error rate w.r.t. to our original model using *best subset selection* is:

```
(mean(lasso_rse) / min_test_error.1) * 100
```

```
## [1] 37.6417
```

Finally, we analyse the relative average $L1$ distance between our estimators and the true model:

```
mean(abs((ys_test - ys_lasso_pred)/ ys_test))
```

```
## [1] 0.2007027
```

which yields a more than reasonable value, since it's below 30%. Consequently, the final set obtained in this section, after performing *linear*, *best subset selection*, *log*, *polynomial* , *stepwise AIC* and *Lasso* yielded a model that will be used in the following sections for more complex fits that will derive in our final model.