

Elastic Net Test

LIBRARIES

```
# libraries
library(MASS) # Package needed to generate correlated predictors
library(glmnet) # Package to fit ridge/lasso/elastic net models
library(ggplot2)
source("elastic.net.R")
```

GENERATE DATA

```
# seed
set.seed(19875) # Set seed for reproducibility

# globals
n <- 1000 # Number of observations
p <- 5000 # Number of predictors included in model
real_p <- 15 # Number of true predictors
x <- matrix(rnorm(n*p), nrow=n, ncol=p) # this are fake cytokines
y <- apply(x[,1:real_p], 1, sum) + rnorm(n) # fake gene expression
```

SPLIT DATA INTO TEST AND TRAIN

```
# split data
train_rows <- sample(1:n, .66*n) # random data set
x.train <- x[train_rows, ] # train (2/3)
x.test <- x[-train_rows, ] # test (1/3)

y.train <- y[train_rows]
y.test <- y[-train_rows]
```

FIT MODELS

```
# Fit models
fit.lasso <- glmnet(x.train, y.train, family="gaussian", alpha=1)
fit.ridge <- glmnet(x.train, y.train, family="gaussian", alpha=0)
fit.elnet <- glmnet(x.train, y.train, family="gaussian", alpha=.5)

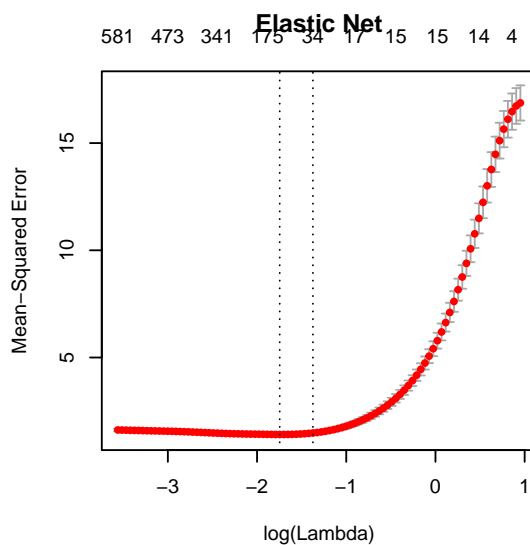
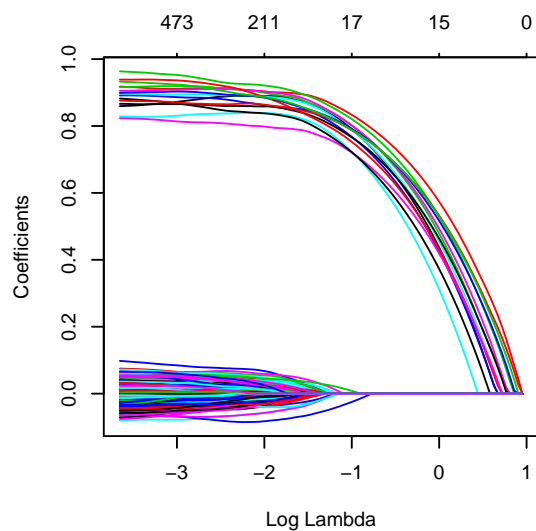
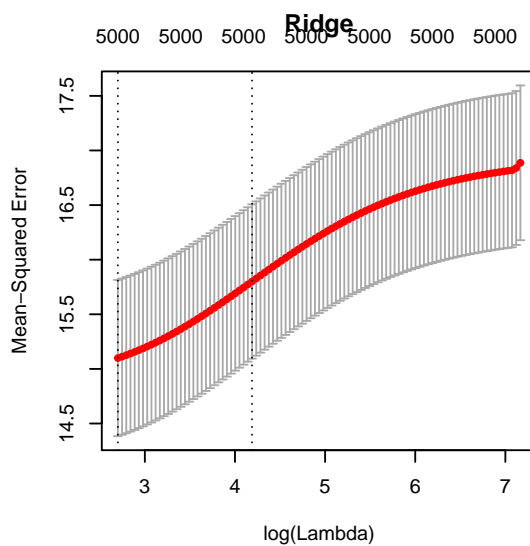
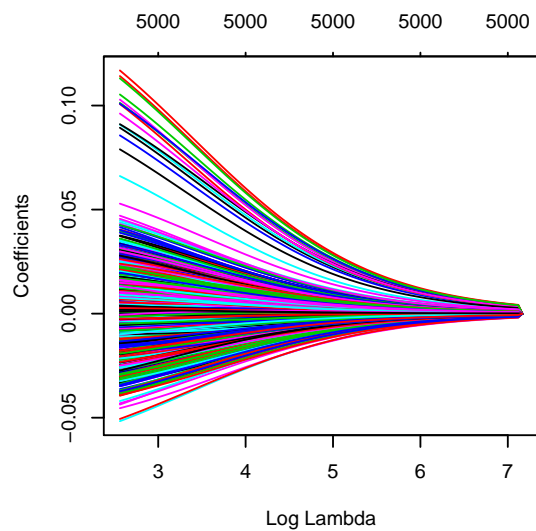
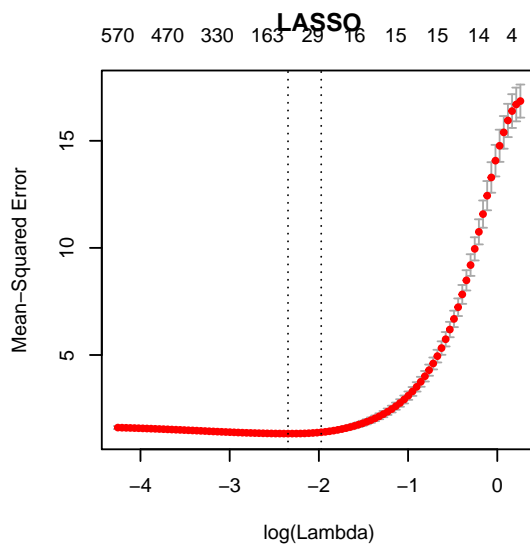
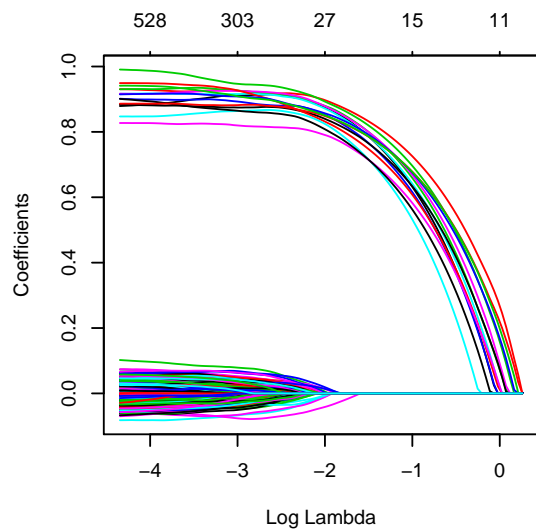
# 10-fold Cross validation for each alpha = 0, 0.1, ... , 0.9, 1.0
# (For plots on Right)
for (i in 0:10) {
  assign(paste("fit", i, sep=""), cv.glmnet(x.train, y.train, type.measure="mse",
                                             alpha=i/10,family="gaussian"))
}
```

PLOT SOLUTION PATH AND CROSS-VALIDATED MSE AS FUNCTION OF λ

```
# Plot solution paths:
par(mfrow=c(3,2))
# For plotting options, type '?plot.glmnet' in R console
plot(fit.lasso, xvar="lambda")
plot(fit10, main="LASSO")

plot(fit.ridge, xvar="lambda")
plot(fit0, main="Ridge")

plot(fit.elnet, xvar="lambda")
plot(fit5, main="Elastic Net")
```

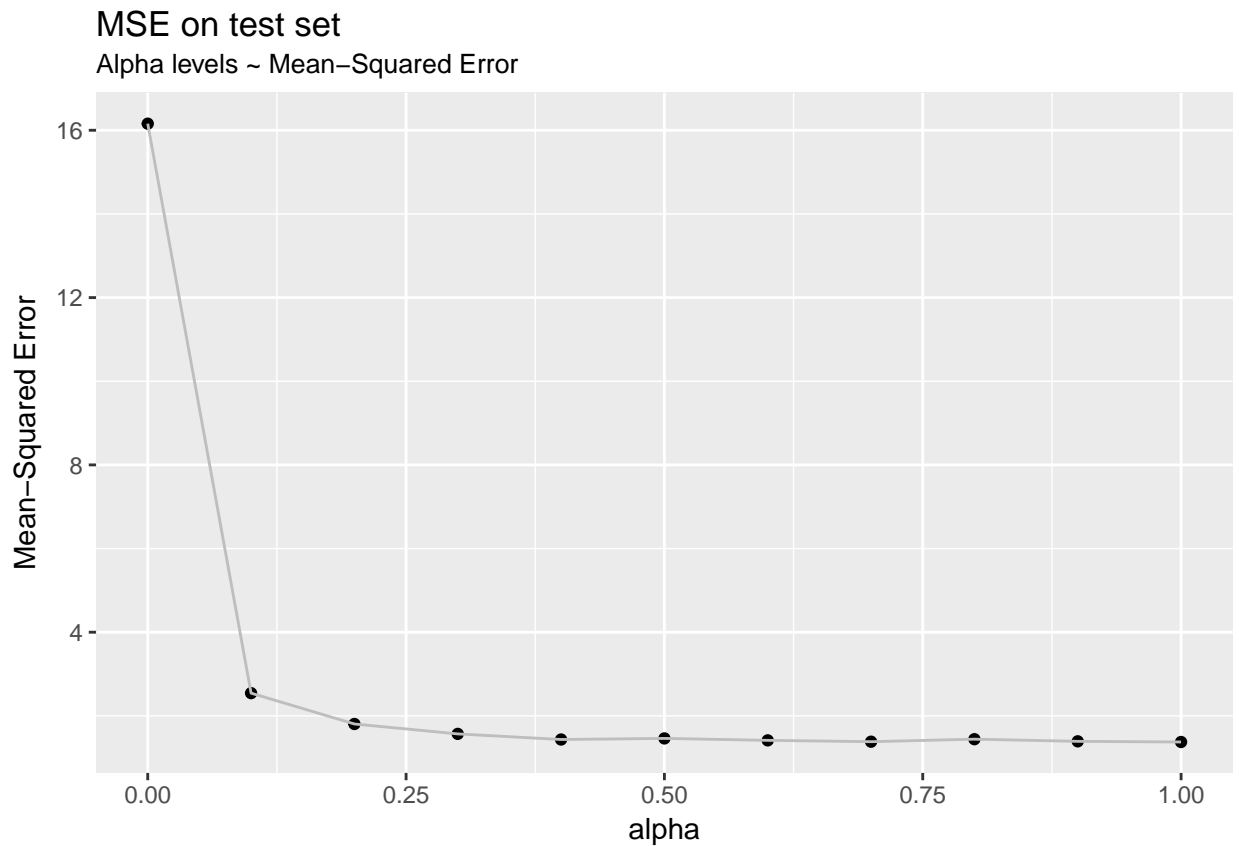


MSE ON TEST SET

```
# Predict fit on test data
for (i in 0:10) {
  assign(paste("yhat", i, sep=""),
    predict(get(paste0("fit", i)),
      s=get(paste0("fit", i))$lambda.1se,
      newx=x.test))
}

# calculate Mean-Squared error of model
a <- seq(0, 1, .1)
mse <- c()
for (i in 0:10) {
  m <- mean((y.test - get(paste0("yhat", i)))^2)
  mse <- c(mse, m)
}

ggplot(data = NULL, aes(a, mse) ) +
  geom_point() +
  geom_line(col="grey") +
  labs(subtitle="Alpha levels ~ Mean-Squared Error",
    x="alpha",
    y="Mean-Squared Error",
    title="MSE on test set")
```



FOLDS FUNCTION

```
Folds <- function(y, k=10) {
  n <- length(y)
  if (n == 0)
    stop('response length is zero')

  uniqY <- unique(y)
  if (!is.factor(y) && length(y) / length(uniqY) >= k) {
    # Interpret the integer-valued y as class labels. Stratify if the number of class labels is <= 5.
    y <- factor(y)
  } else if (is.numeric(y)) {
    # 5-stratum Stratified sampling
    if (n >= 5 * k) {
      breaks <- unique(quantile(y, probs=seq(0, 1, length.out=5)))
      y <- as.integer(cut(y, breaks, include.lowest=TRUE))
    } else
      y <- rep(1, length(y))
  }

  sampList <- tapply(seq_along(y), y, sFolds, k=k, simplify=FALSE)
  list0 <- list()
  length(list0) <- k
  samp <- Reduce(function(list1, list2) {
    mapply(c, list1, list2, SIMPLIFY=FALSE)
  }, sampList, list0)

  return(samp)
}

sFolds <- function(yy, k=10) {
  if (length(yy) > 1)
    allSamp <- sample(yy)
  else
    allSamp <- yy

  n <- length(yy)
  nEach <- n %/% k
  samp <- list()
  length(samp) <- k
  for (i in seq_along(samp)) {
    if (nEach > 0)
      samp[[i]] <- allSamp[1:nEach + (i - 1) * nEach]
    else
      samp[[i]] <- numeric(0)
  }
  restSamp <- allSamp[seq(nEach * k + 1, length(allSamp), length.out=length(allSamp) - nEach * k)]
  restInd <- sample(k, length(restSamp))
  for (i in seq_along(restInd)) {
    sampInd <- restInd[i]
    samp[[sampInd]] <- c(samp[[sampInd]], restSamp[i])
  }
}
```

```

    return(samp)
}

```

GLMNET.WRAPPER

```

# libraries
library(MASS) # Package needed to generate correlated predictors
library(glmnet) # Package to fit ridge/lasso/elastic net models
library(ggplot2)
source("elastic.net.R")
# Generate data
set.seed(19874)
n <- 10 # Number of observations
p <- 500 # Number of predictors included in model
real_p <- 150 # Number of true predictors
x <- matrix(rnorm(n*p), nrow=n, ncol=p)
y <- apply(x[,1:real_p], 1, sum) + rnorm(n)
nrow(x)

## [1] 10

# add colnames
rownames(x) <- sprintf("sample%s", seq(1:nrow(x)))
# vector names
y <- setNames(y, sprintf("sample%s", seq(1:length(y))))
# -----

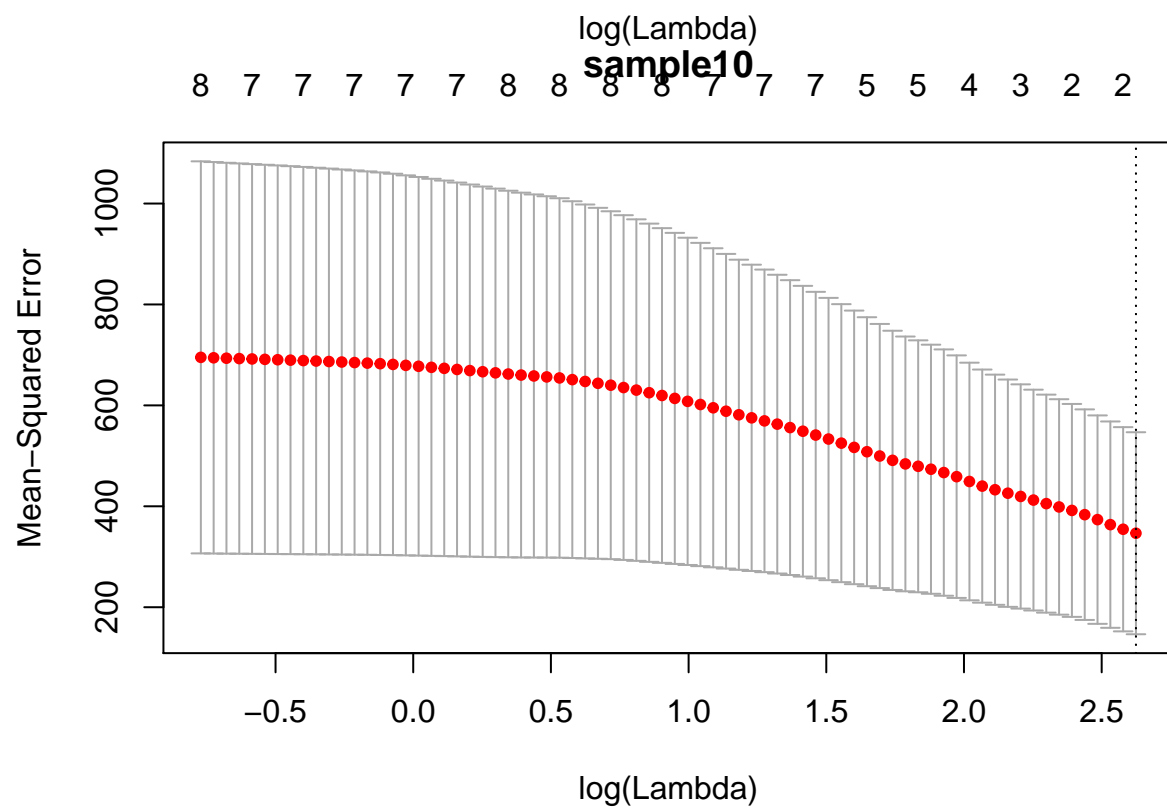
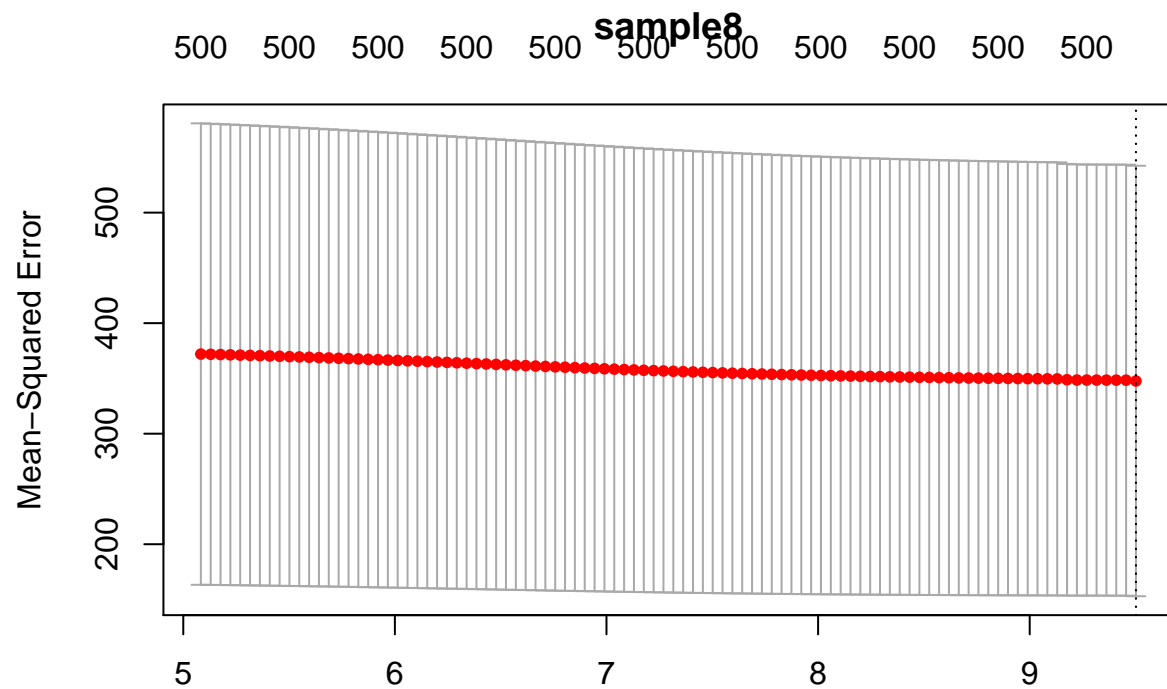
# Remove NA values
y <- y[!is.na(y)]
x <- na.omit(x)
ol <- intersect(rownames(x), names(y))
y <- y[ol]
x <- x[ol, , drop=F]

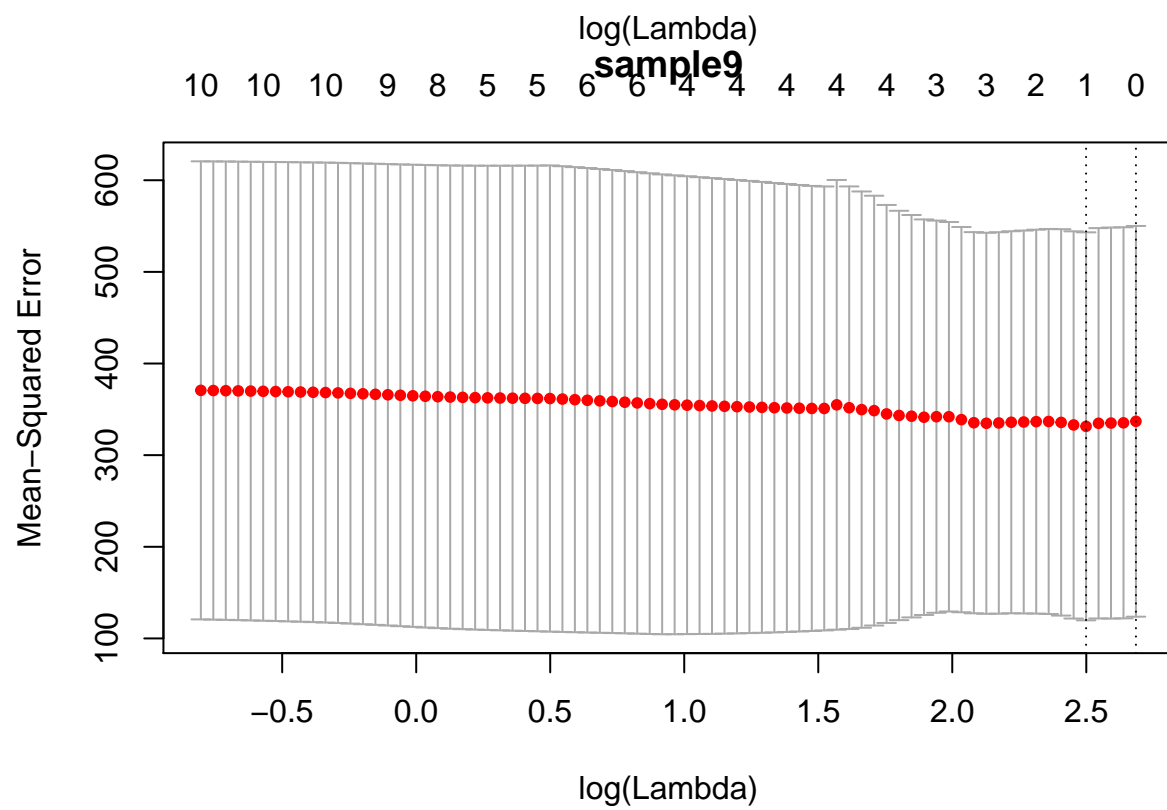
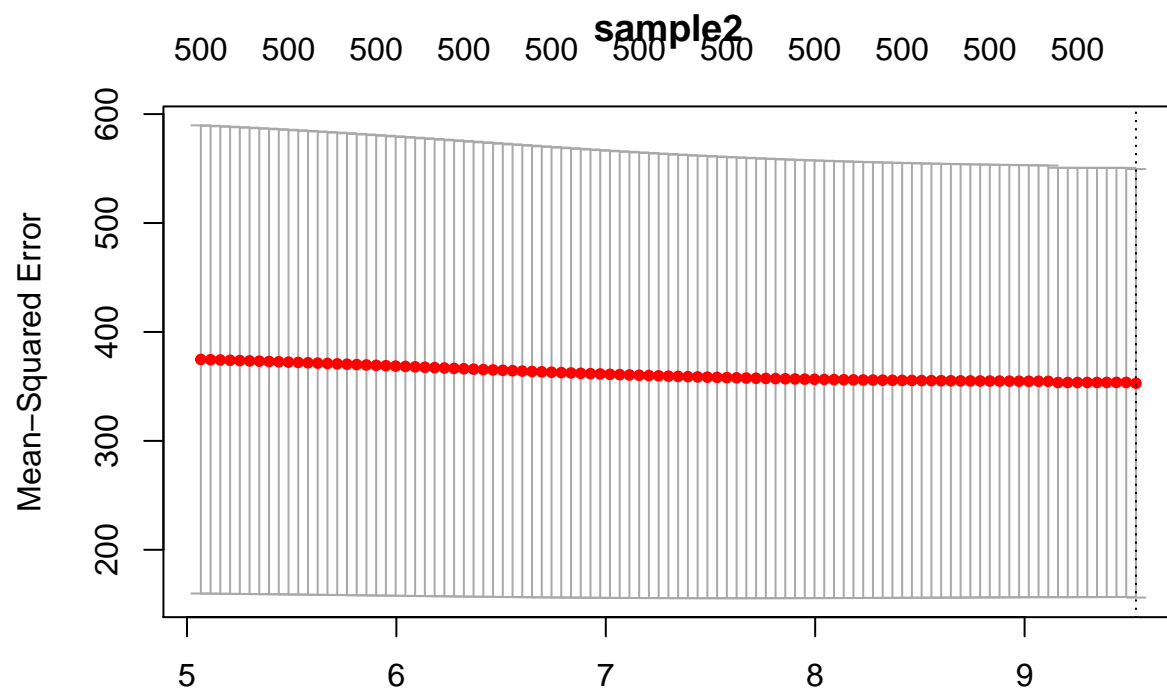
# create a list of length k, containing the test-set indices
folds <- Folds(y, k=10)

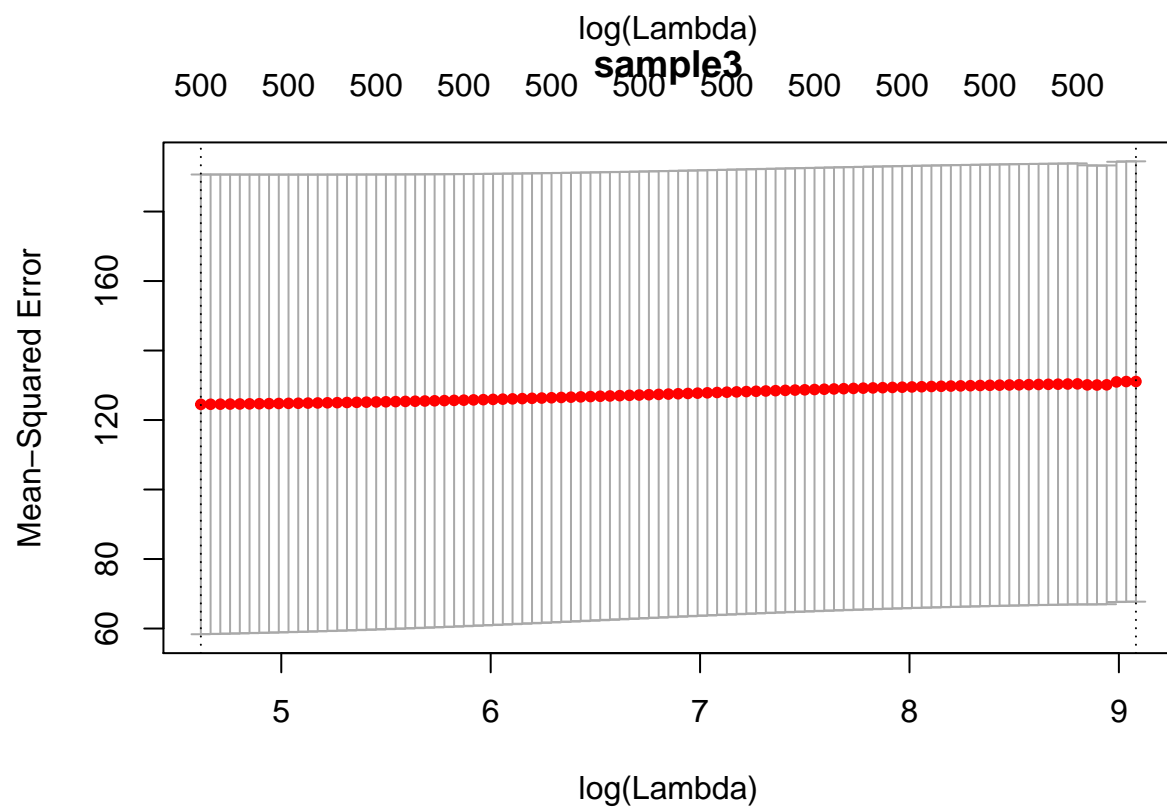
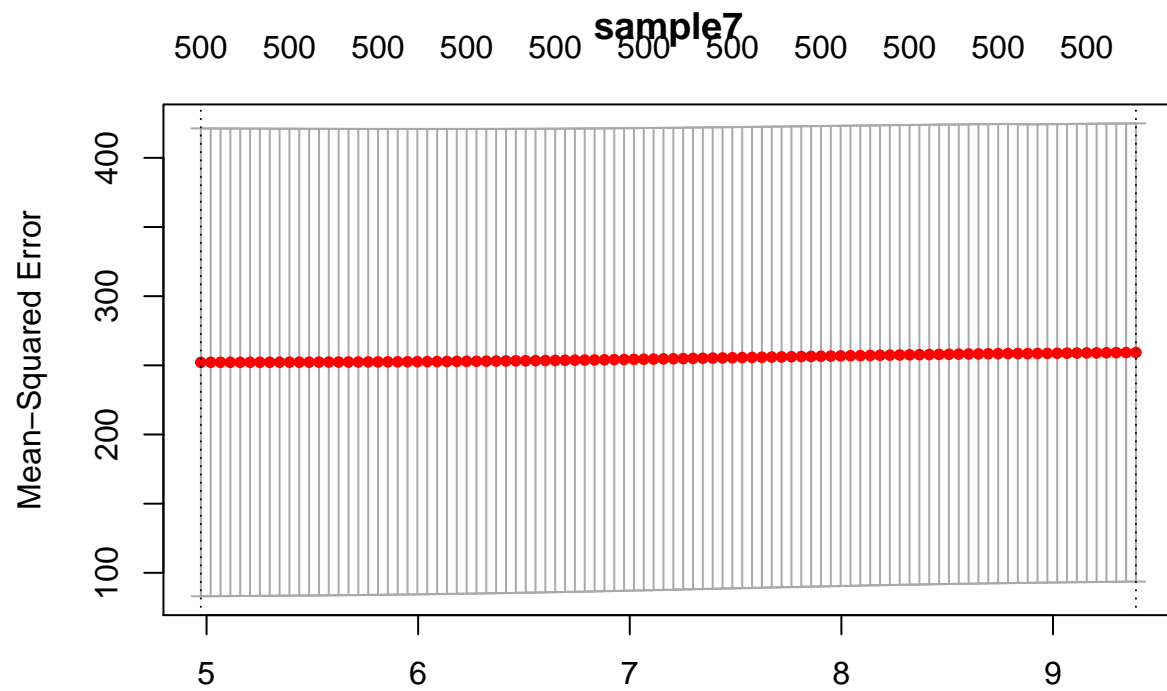
# glmnet
results <- lapply(folds, function(fold, y, x, parallel=F) {
  return(glmnet.wrapper(y=y[-fold],
                        x=x[-fold, , drop=F],
                        newx=x[fold, , drop=F],
                        newy=y[fold]))
}, y=y, x=x)

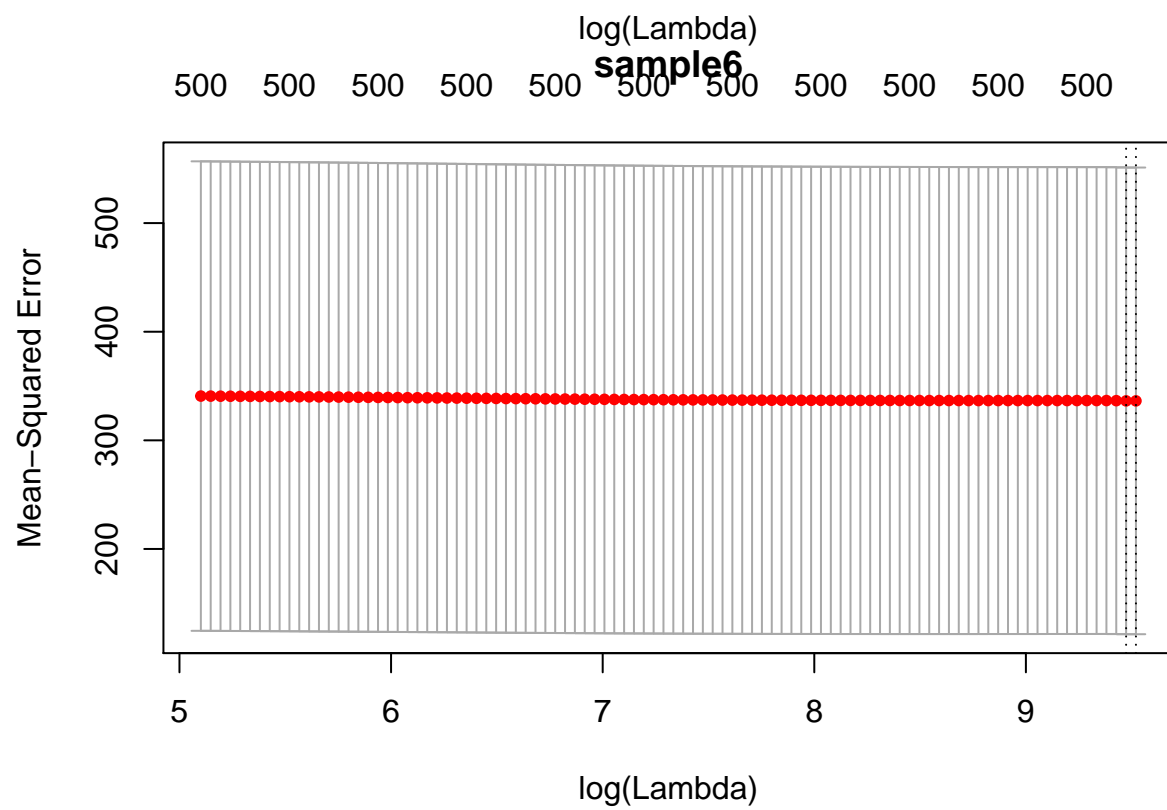
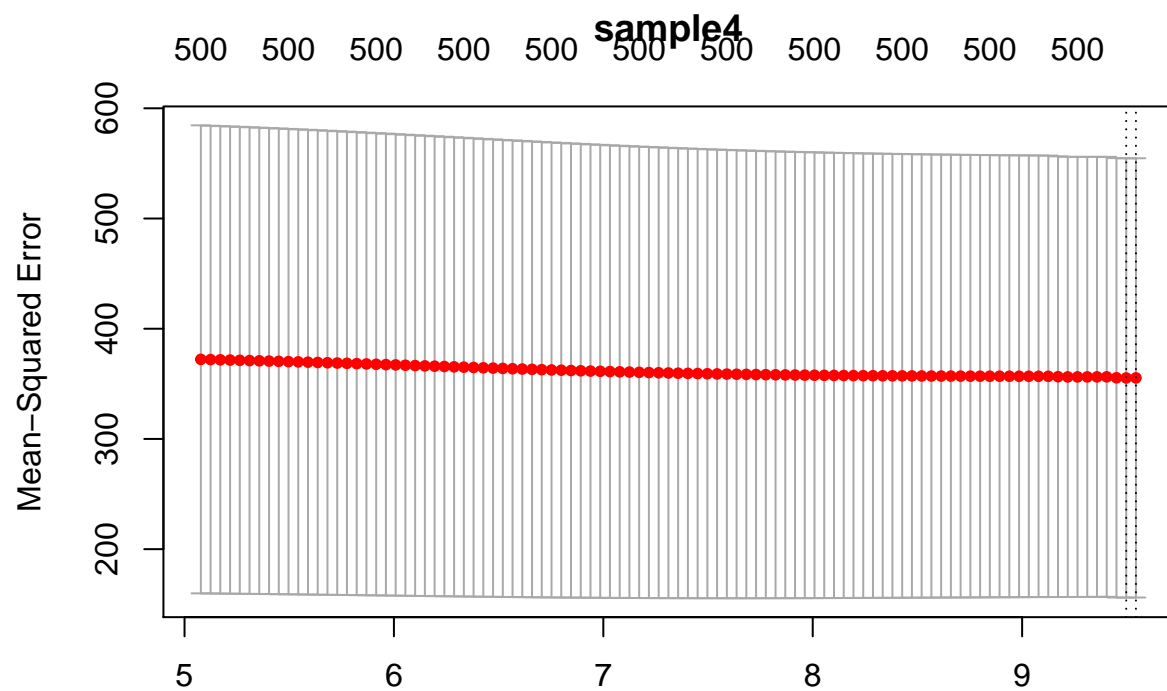
# plot
for (i in 1:length(folds)) {
  plot(results[[i]]$best.model, main=names(results[[i]]$pred))
}

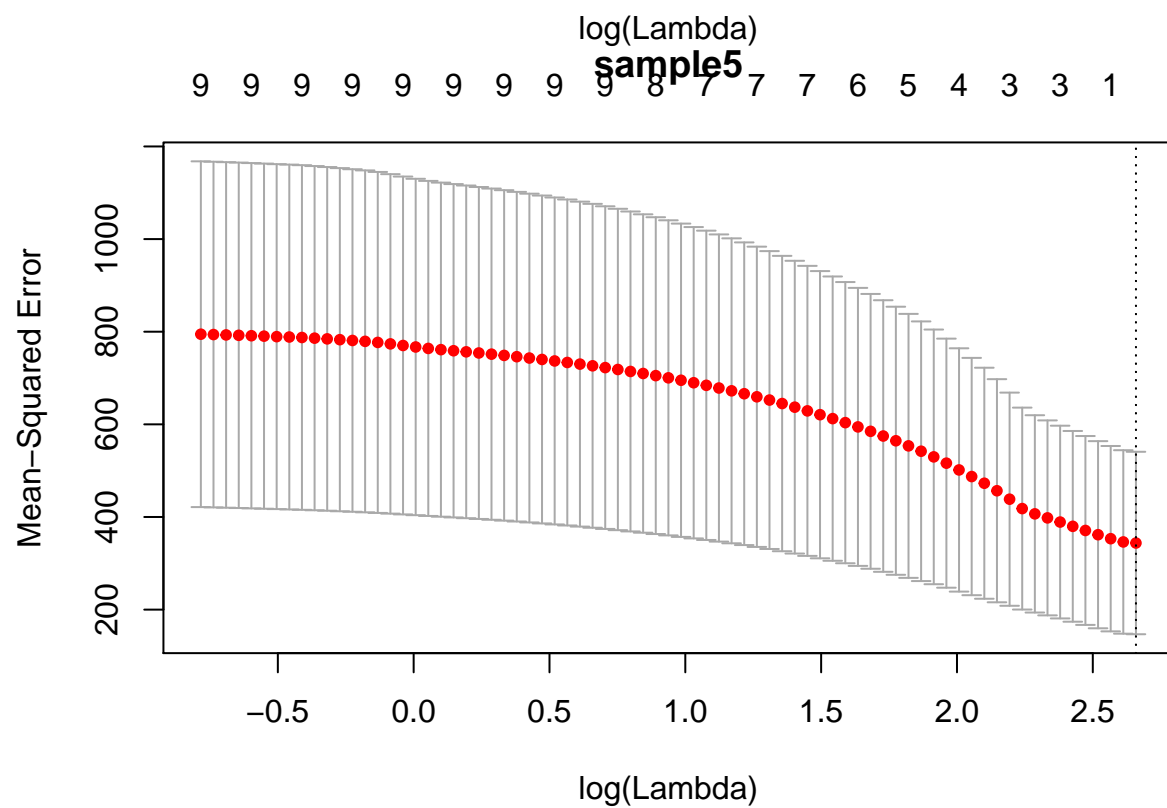
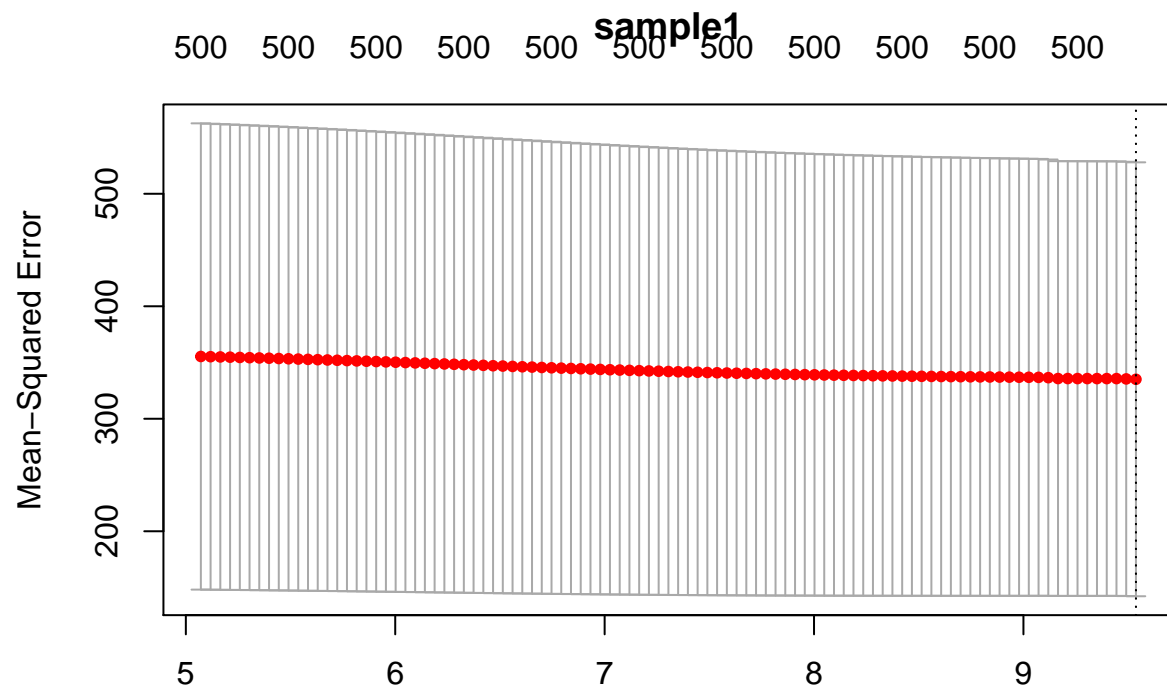
```











```
results[[1]]$mse
```

```
## [1] 71.17961
```

```
# calculate Mean-Squared error of model
```

```
a <- seq(0.1, 1, .1)
```

```
mse <- c()
for (i in 1:10) {
  m <- results[[i]]$mse
  mse <- c(mse, m)
}
length(a)
```

```
## [1] 10
```

```
ggplot(data = NULL, aes(a, mse) ) +
  geom_point() +
  geom_line(col="grey") +
  labs(subtitle="Alpha levels ~ Mean-Squared Error",
       x="alpha",
       y="Mean-Squared Error",
       title="MSE on test set")
```

