

Learning and predicting with statistical models

Kevin R. Coombes

July 6, 2017

Contents

1	Introduction	1
2	Simulated DataSet	1
2.1	Training Data	2
2.2	Test Data	5
3	Feature Selection	8
4	Fitting Models and Making Predictions	10
4.1	K Nearest Neighbors	10
4.2	Classification and regression trees	10
4.3	Linear/Logistic Regression	12
4.4	Compound Covariate Prediction	13
4.5	Support Vector Machines	14
4.6	Neural Networks	15
4.7	Random Forests	17

1 Introduction

We start, as usual, by loading the appropriate package:

```
> library(Modeler)
```

2 Simulated DataSet

In order to have something to test our models against, we simulate a dataset that has enough underlying structure to make it interesting. First, we set the random seed so that the results will be reproducible.

```
> set.seed(234843)
```

Next, we define the simulation parameters. We will simulate a dataset with `nFeatures` rows representing genes, only `nSignif` of which are significantly associated with the outcome of interest. We assume that both the training set and test set come from the same population, which is actually a mixture of two types, A and B , where the probability of belonging to type B is given by `pB`. The significant genes are assumed to be differentially expressed between the two types, with the difference in means following a normal distribution ($\Delta \sim \text{Norm}(\delta, \sigma)$).

```

> nFeatures <- 10000
> nSignif <- 100
> pB <- 0.4
> delta <- 1
> sigma <- 0.3
> nTrain <- 100
> nTest <- 100

```

For cleanup purposes, we specify the names of things we can safely remove later.

```

> paramlist <- c("nFeatures", "nSignif", "pB",
+               "delta", "sigma", "nTrain", "nTest")

```

In addition to simulating the class assignment (A or B), we will also simulate a continuous outcome that represents a probability of belonging to class B . The continuous outcome (Figure 1) will follow a beta distribution with parameters α and β .

```

> alpha <- 0.75
> beta <- 0.95
> round(100*pbeta(seq(0.1, 0.9, 0.1), alpha, beta), 1)

```

```

[1] 17.1 28.8 39.1 48.7 57.7 66.4 74.9 83.2 91.4

```

```

> xx <- seq(0, 1, length=300)
> yy <- dbeta(xx, alpha, beta)

```

Now we can actually start the simulation. For the differentially expressed genes, we make it equally likely that they are higher in A or higher in B .

```

> signed <- -1 + 2*rbinom(nSignif, 1, 0.5)

```

As noted above, the magnitude of the difference follows a normal distribution.

```

> offsets <- c(signed*rnorm(nSignif, delta, sigma), # can change in either direction
+             rep(0, nFeatures - nSignif))        # but most don't change at all

```

2.1 Training Data

To simulate the training dataset, we first simulate the continuous outcomes (interpreted as the probability of belonging to class B). These are transformed using a logit function so they lie on the entire real line.

```

> lp <- function(p) log(p/(1-p))
> ea <- function(a) 1/(1+exp(-a))
> pOut <- rbeta(nTrain, alpha, beta)
> trainOutcome <- lp(pOut)

```

The binary classes for the simulated samples are obtained by dichotomizing the probabilities.

```

> # TODO: Fix this so it looks at correlation with the continuous outcome
> # instead of just differential expression between classes
> trainClass <- factor(c("cyan", "magenta")[1 + 1*(pOut > 0.5)])
> summary(trainClass)

```

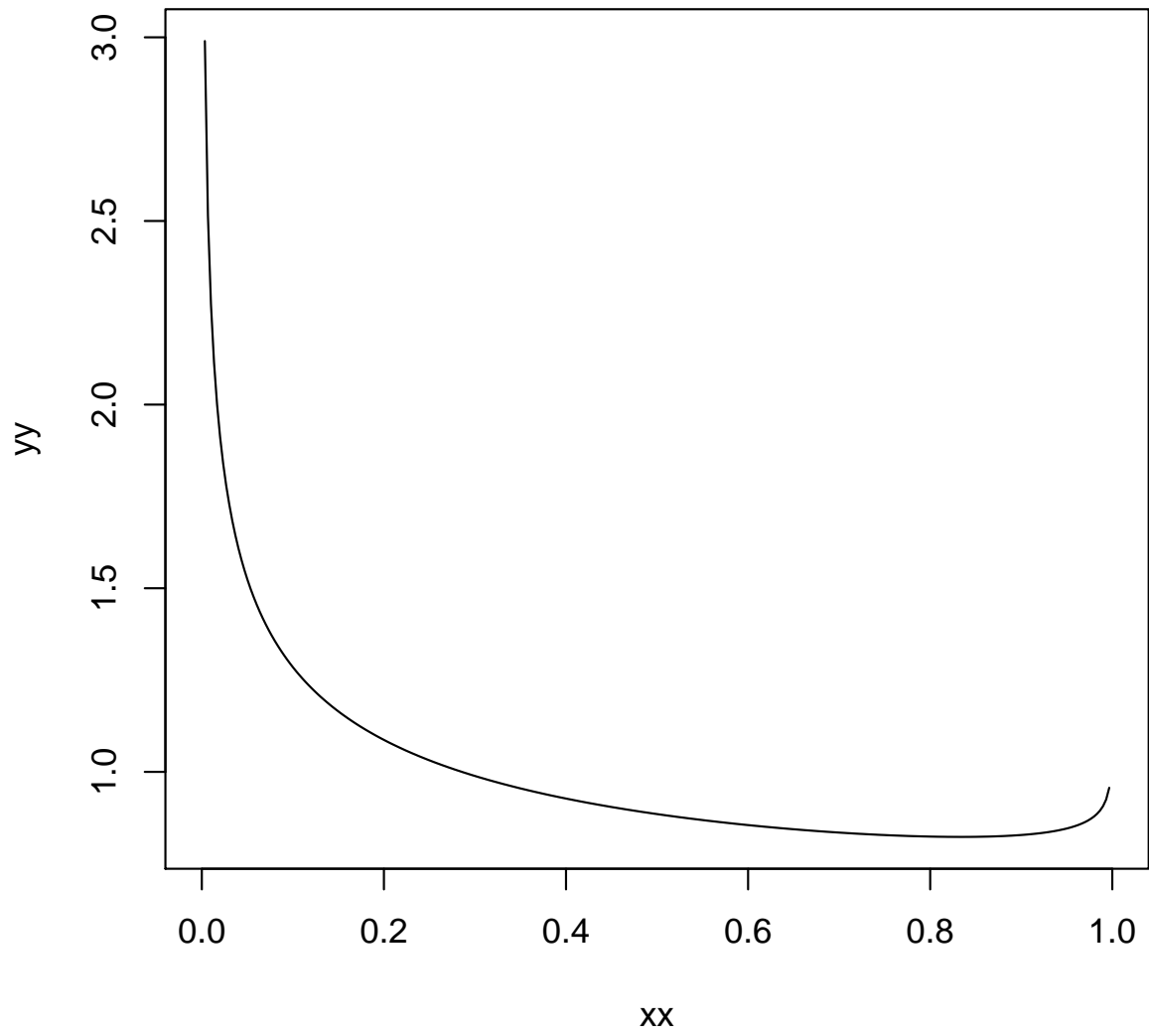


Figure 1: Probability of belonging to class B is simulated from this distribution, $\text{Beta}(0.75, 0.95)$.

```

      cyan magenta
      57      43

> isB <- trainClass=="magenta"
> summary(isB)

      Mode    FALSE     TRUE
logical      57      43

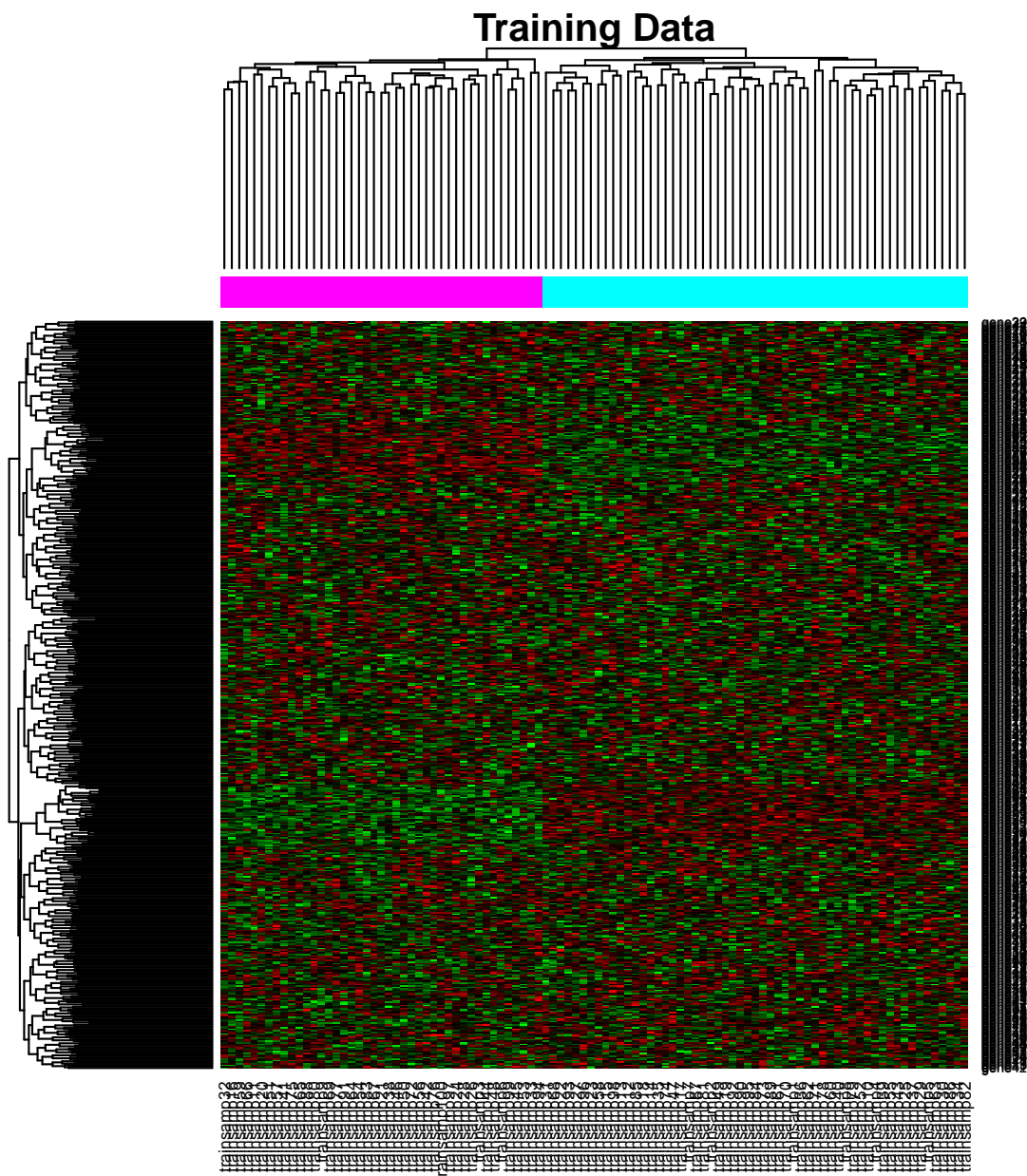
```

Now we put together the training dataset.

```

> trainData <- matrix(rnorm(nFeatures*nTrain), ncol=nTrain) # pure noise
> trainData[,isB] <- sweep(trainData[,isB], 1, offsets, "+")
> trainData <- t(scale(t(trainData)))
> dimnames(trainData) <- list(paste("gene", 1:nFeatures, sep=''),
+                             paste("trainsamp", 1:nTrain, sep=''))
>

```



2.2 Test Data

We use the same procedure to simulate the test dataset, starting with continuous outcomes.

```
> pOut <- rbeta(nTest, alpha, beta)
> testOutcome <- lp(pOut)
```

We convert the continuous outcomes to binary class assignments.

```
> testClass <- factor(c("cyan", "magenta")[1 + 1*(pOut > 0.5)])
> summary(testClass)
```

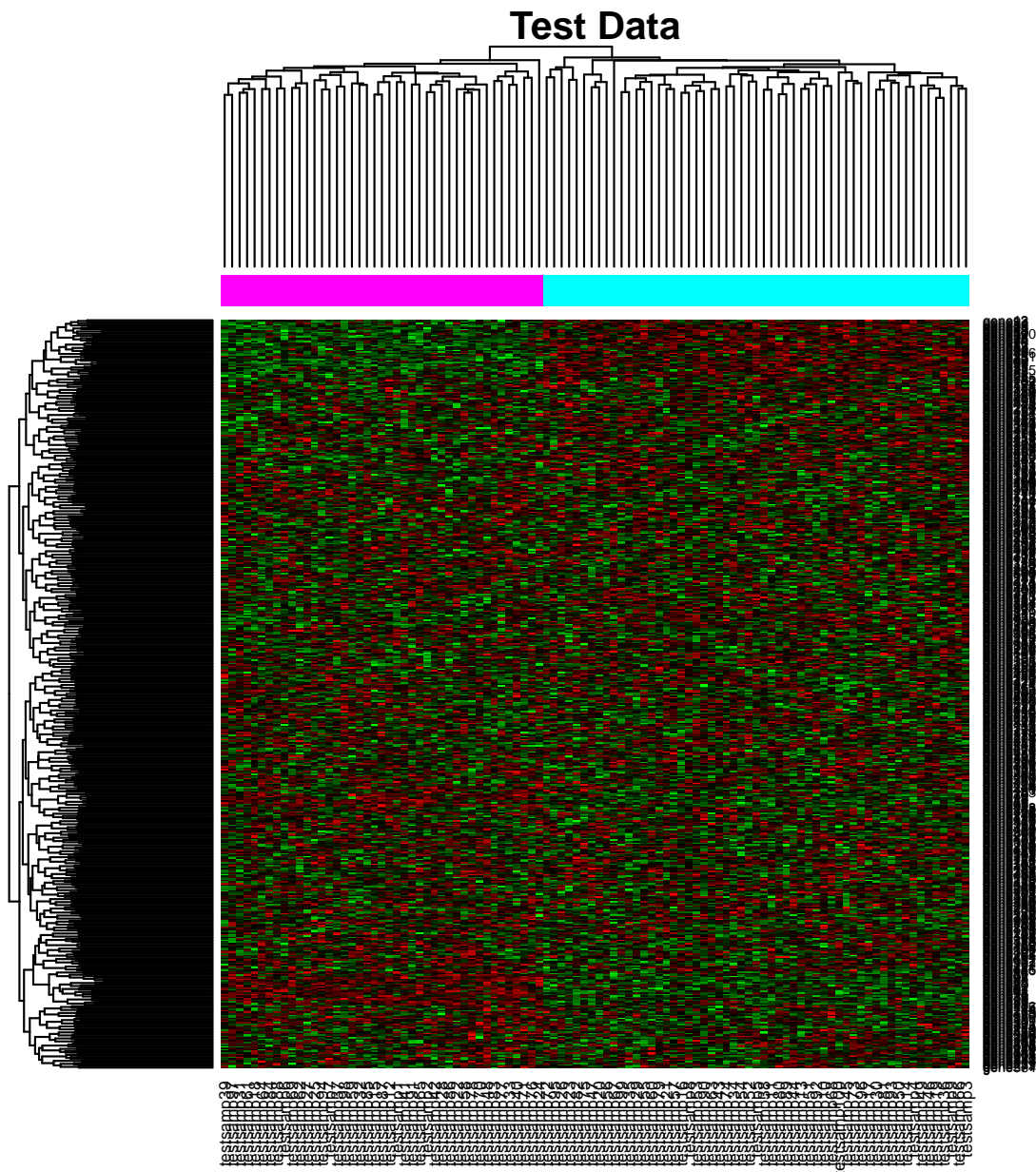
```
   cyan magenta
     57      43
```

```
> isB <- testClass=="magenta"
> summary(isB)
```

```
   Mode   FALSE   TRUE
logical    57    43
```

And we then generate the simulated microarray data.

```
> testData <- matrix(rnorm(nFeatures*nTest), ncol=nTest) # pure noise
> testData[,isB] <- sweep(testData[,isB], 1, offsets, "+")
> testData <- t(scale(t(testData)))
> dimnames(testData) <- list(paste("gene", 1:nFeatures, sep=''),
+                             paste("testsamp", 1:nTest, sep=''))
```



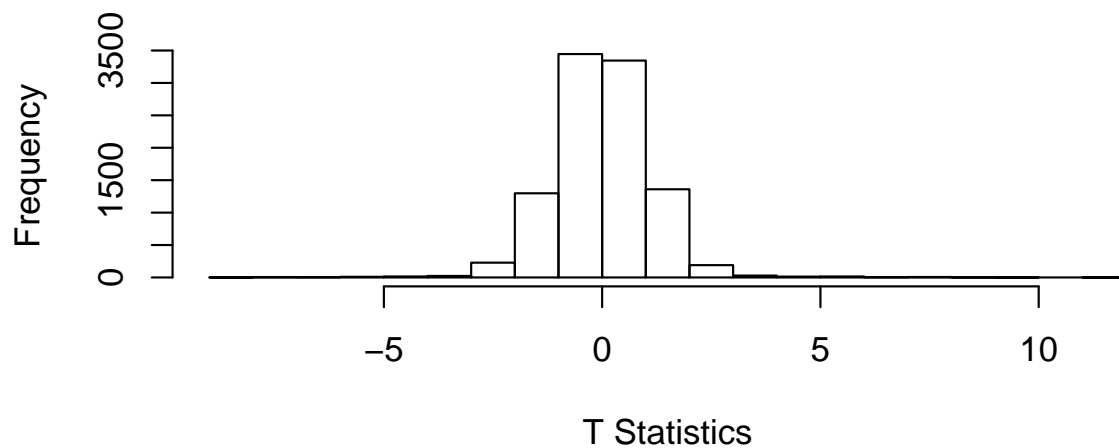
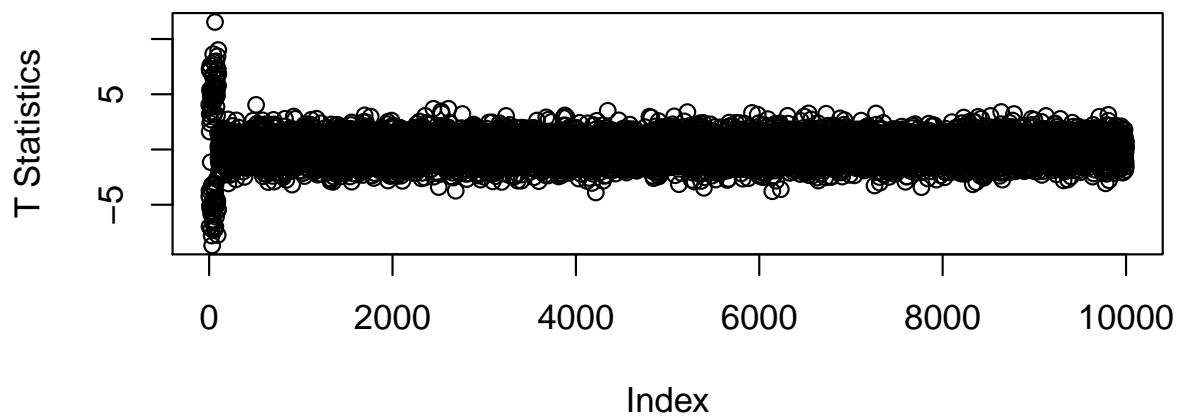
At this point, we can clean up the work space.

```
> rm(list=paramlist)
> rm(pOut, isB, signed, offsets)
> rm(xx, yy, alpha, beta)
> rm(paramlist)
```

3 Feature Selection

Here we implement a simple feature selection scheme. We first perform gene-by-gene t-tests on the training data to identify genes that are differentially expressed between the two classes.

```
> library(ClassComparison)
> mtt <- MultiTtest(trainData, trainClass)
```



We then use a beta-uniform-mixture (BUM) model to estimate the false discover rate (FDR).


```

> bum <- Bum(mtt@p.values)
> countSignificant(bum, alpha=0.01, by="FDR")

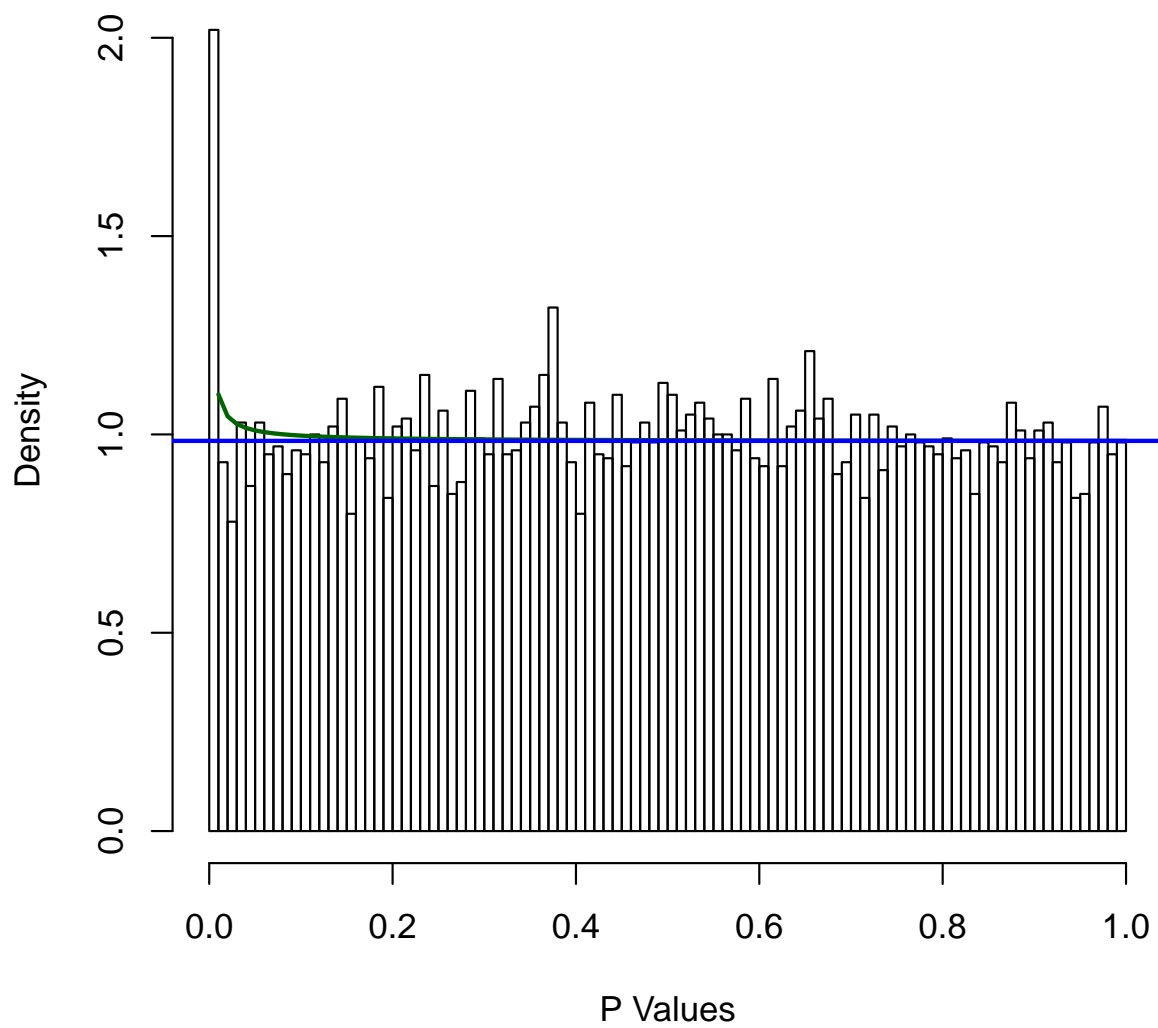
[1] 78

> countSignificant(bum, alpha=0.05, by="FDR")

[1] 91

>

```



```

> geneset <- rownames(trainData)[selectSignificant(bum, alpha=0.05, by="FDR")]
> length(geneset)

[1] 91

> trainSubset <- trainData[geneset,]
> testSubset <- testData[geneset,]

```

4 Fitting Models and Making Predictions

4.1 K Nearest Neighbors

Note that the KNN method works for binary class prediction, but does not work for regression.

```

> knnFitted <- learn(modeler3NN, trainSubset, trainClass)
> knnPredictions <- predict(knnFitted, testSubset)
> table(knnPredictions, testClass)

```

	testClass	
knnPredictions	cyan	magenta
cyan	57	0
magenta	0	43

```

>

```

```

> knnFitted <- learn(modeler5NN, trainSubset, trainClass)
> knnPredictions <- predict(knnFitted, testSubset)
> table(knnPredictions, testClass)

```

	testClass	
knnPredictions	cyan	magenta
cyan	57	0
magenta	0	43

4.2 Classification and regression trees

Classification

```

> rpartFitted <- learn(modelerRPART, trainSubset, trainClass)
> rpartPredictions <- predict(rpartFitted, testSubset, type='class')
> table(rpartPredictions, testClass)

```

	testClass	
rpartPredictions	cyan	magenta
cyan	49	4
magenta	8	39

Regression

```

> rpartFitted <- learn(modelerRPART, trainSubset, trainOutcome)
> rpartPredictions <- predict(rpartFitted, testSubset)
> table(rpartPredictions > 0, testClass)

```

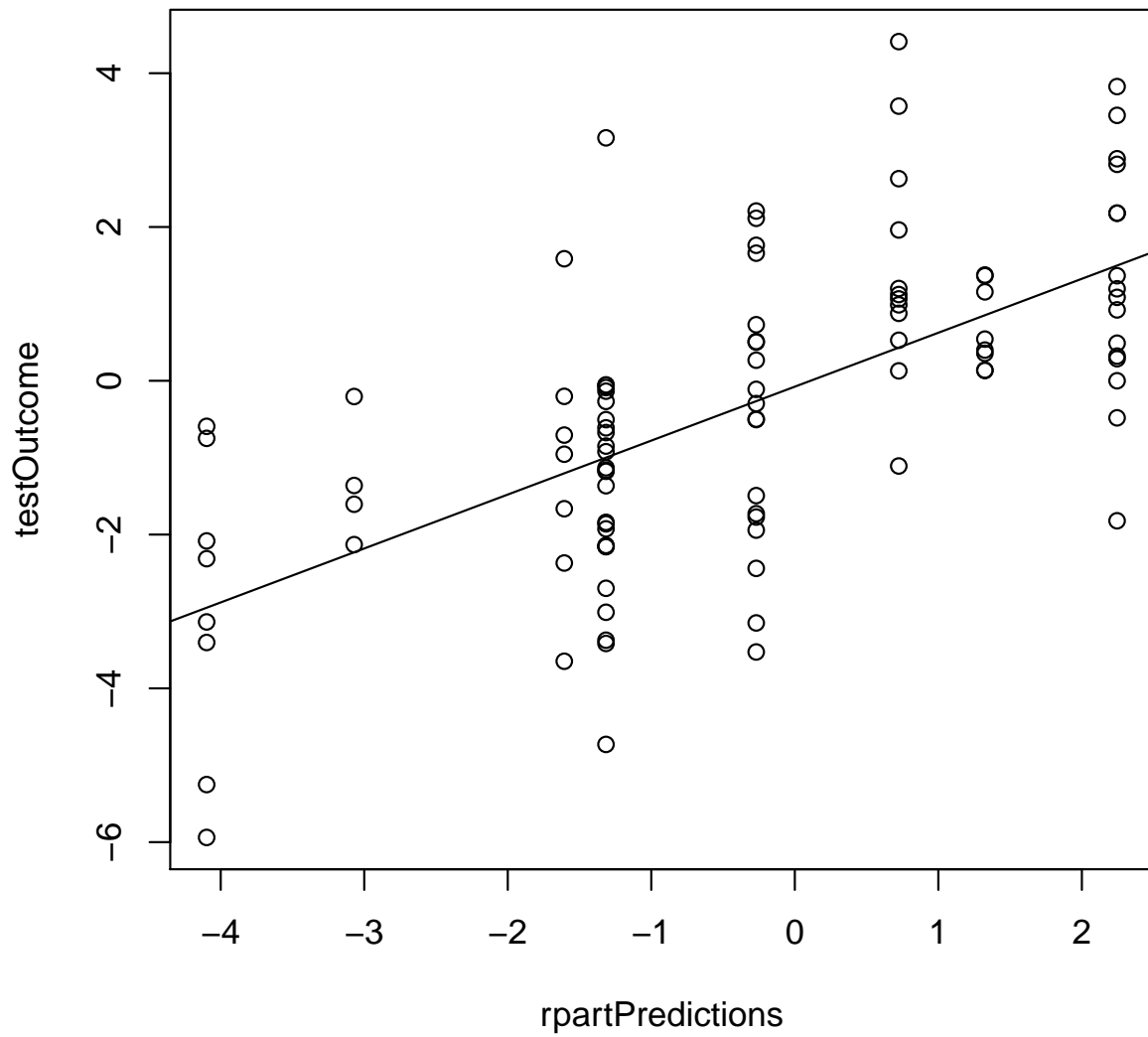
```

      testClass
      cyan magenta
FALSE    54     10
 TRUE     3     33

> cor(rpartPredictions, testOutcome)
[1] 0.6316475

> temp <- lm(testOutcome ~ rpartPredictions)

```



4.3 Linear/Logistic Regression

Classification

```
> # takes too long for the vignette, because of the "step"
> # across glm fits.
> lrFitted <- learn(modelerLR, trainSubset, trainClass)
> lrPredictions <- predict(lrFitted, testSubset)
> table(lrPredictions, testClass)
```

Regression

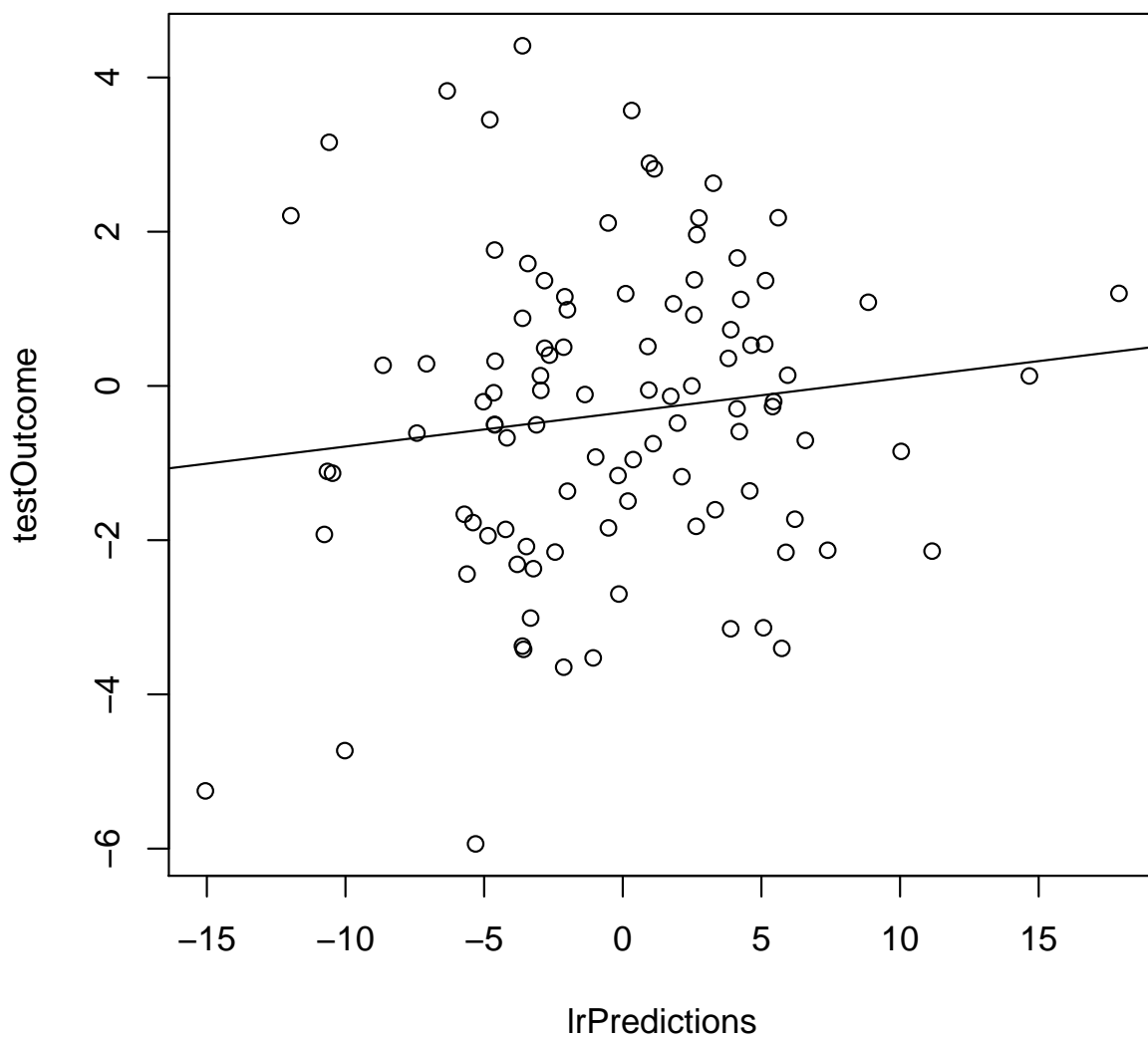
```
> lrFitted <- learn(modelerLR, trainSubset, trainOutcome)
> lrPredictions <- predict(lrFitted, testSubset)
> table(lrPredictions > 0, testClass)
```

	testClass	
	cyan	magenta
FALSE	34	19
TRUE	23	24

```
> cor(lrPredictions, testOutcome)
```

```
[1] 0.12484
```

```
> temp <- lm(testOutcome ~ lrPredictions)
```



4.4 Compound Covariate Prediction

Classification only

```
> ccpFitted <- learn(modelerCCP, trainSubset, trainClass)
> ccpPredictions <- predict(ccpFitted, testSubset)
> table(ccpPredictions, testClass)
```

	testClass	
ccpPredictions	cyan	magenta
cyan	57	0
magenta	0	43

4.5 Support Vector Machines

Classification

```
> # takes too long for the vignette, because of the "step"
> # across glm fits.
> svmFitted <- learn(modelerSVM, trainSubset, trainClass)
> svmPredictions <- predict(svmFitted, testSubset)
> table(svmPredictions, testClass)
```

	testClass	
svmPredictions	cyan	magenta
cyan	57	0
magenta	0	43

Regression

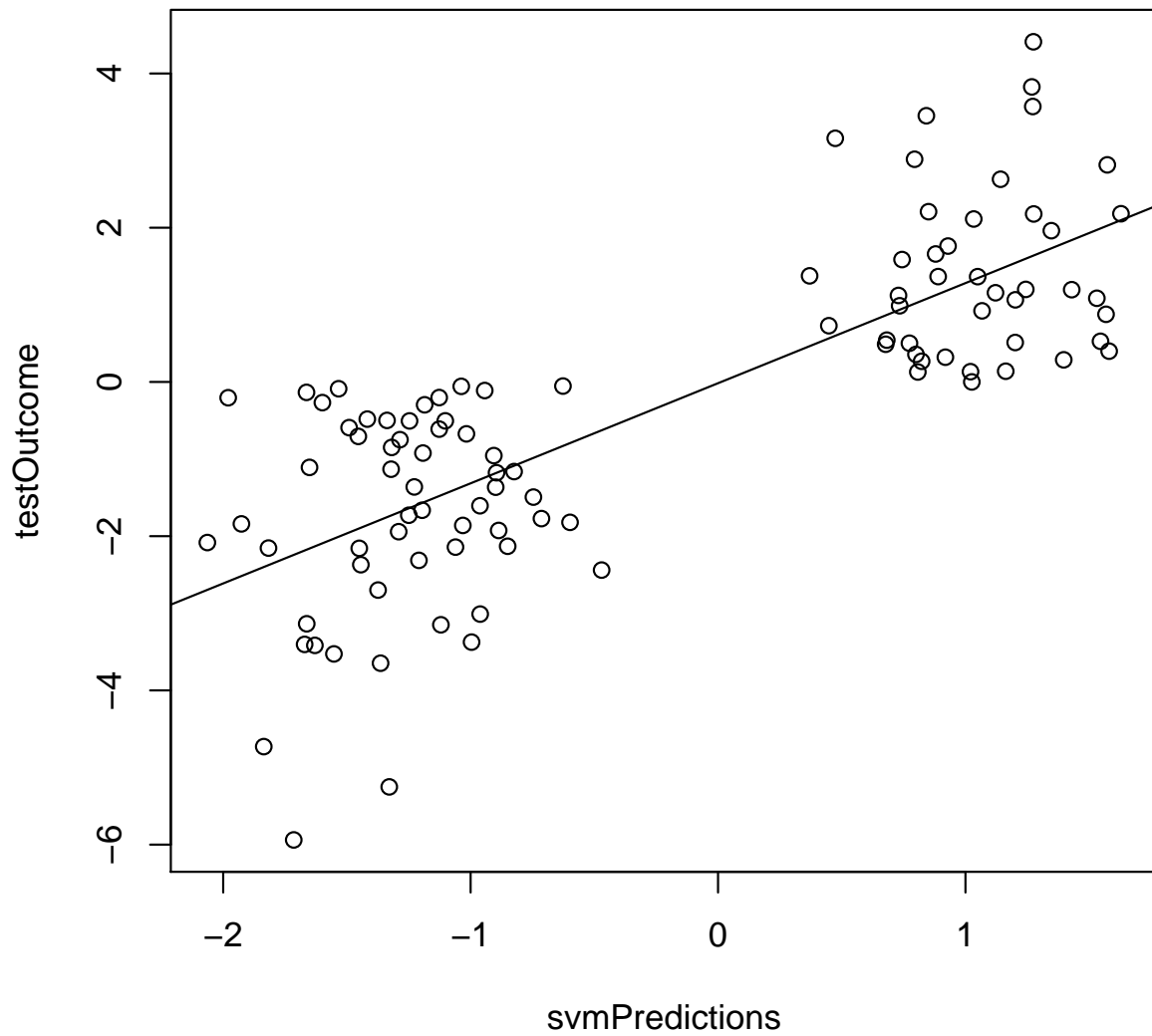
```
> svmFitted <- learn(modelerSVM, trainSubset, trainOutcome)
> svmPredictions <- predict(svmFitted, testSubset)
> table(svmPredictions > 0, testClass)
```

	testClass	
	cyan	magenta
FALSE	57	0
TRUE	0	43

```
> cor(svmPredictions, testOutcome)
```

```
[1] 0.7775552
```

```
> temp <- lm(testOutcome ~ svmPredictions)
```



4.6 Neural Networks

Classification

```
> nnetFitted <- learn(modelerNNET, trainSubset, trainClass)
```

```
# weights: 466
```

```
initial value 78.889878
```

```

final value 0.000037
converged

> nnetPredictions <- predict(nnetFitted, testSubset)
> table(nnetPredictions, testClass)

      testClass
nnetPredictions  cyan magenta
      0           57         0
0.999999128699143  0         1
0.999999128723069  0        42

Regression

> nnetFitted <- learn(modelerNNET, trainSubset, trainOutcome)

# weights: 466
initial value 570.848014
final value 484.616805
converged

> nnetPredictions <- predict(nnetFitted, testSubset)
> table(nnetPredictions > 0, testClass)

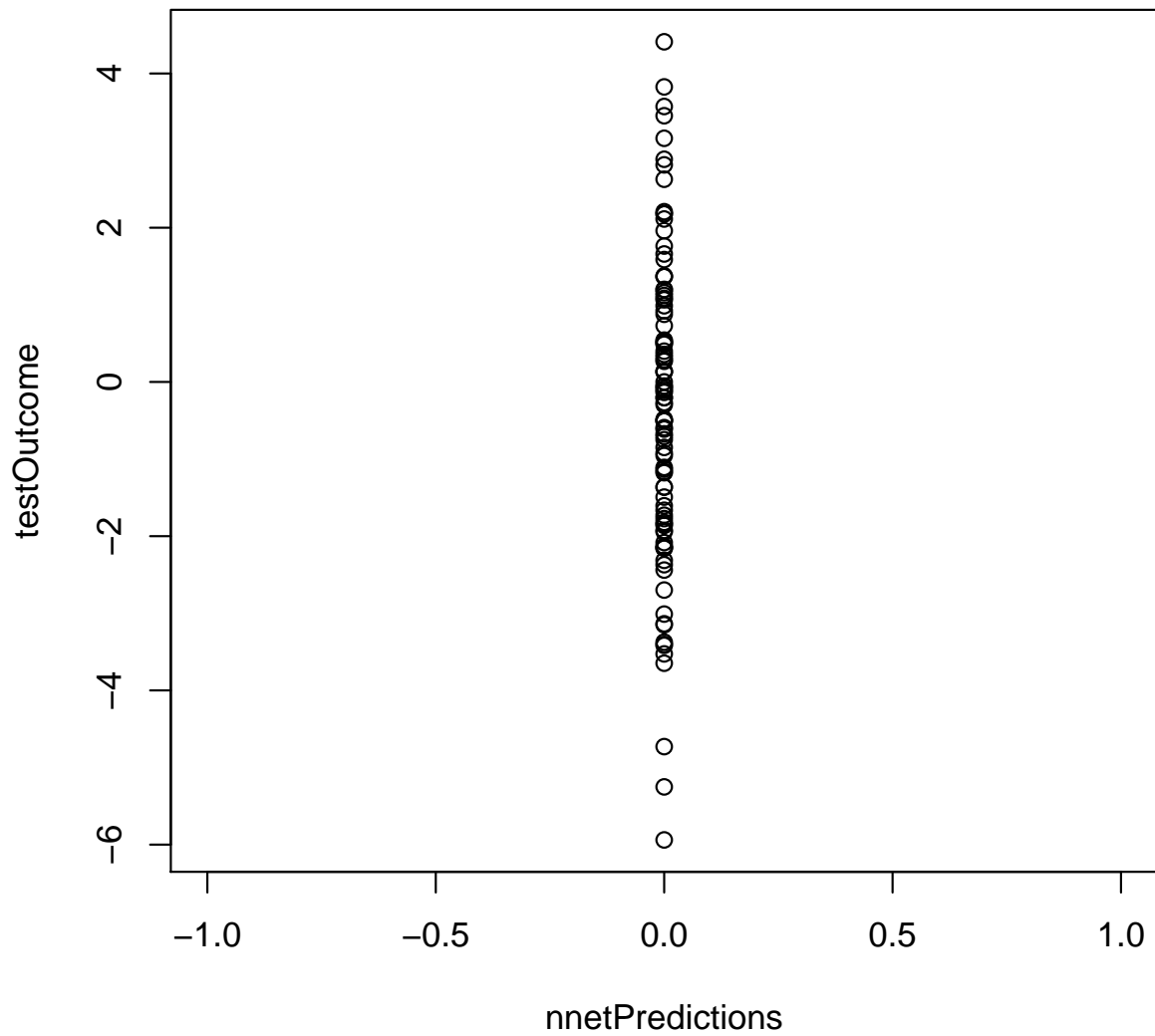
      testClass
      cyan magenta
FALSE    57      43

> cor(nnetPredictions, testOutcome)

      [,1]
[1,]    NA

> temp <- lm(testOutcome ~ nnetPredictions)

```

4.7 Random Forests

Classification

```
> rfFitted <- learn(modelerRF, trainSubset, trainClass)
> rfPredictions <- predict(rfFitted, testSubset)
> table(rfPredictions, testClass)
```

	testClass	
rfPredictions	cyan	magenta
cyan	57	0
magenta	0	43

Regression

```
> rfFitted <- learn(modelerRF, trainSubset, trainOutcome)
> rfPredictions <- predict(rfFitted, testSubset)
> table(rfPredictions > 0, testClass)
```

	testClass	
	cyan	magenta
FALSE	56	4
TRUE	1	39

```
> cor(rfPredictions, testOutcome)
```

```
[1] 0.7343602
```

```
> temp <- lm(testOutcome ~ rfPredictions)
```

