Learning and predicting with statistical models

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Contents

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 distibution.

```
> 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 diferential expression between classes
> trainClass <- factor(c("cyan", "magenta")[1 + 1*(pOut > 0.5)])
> summary(trainClass)
```

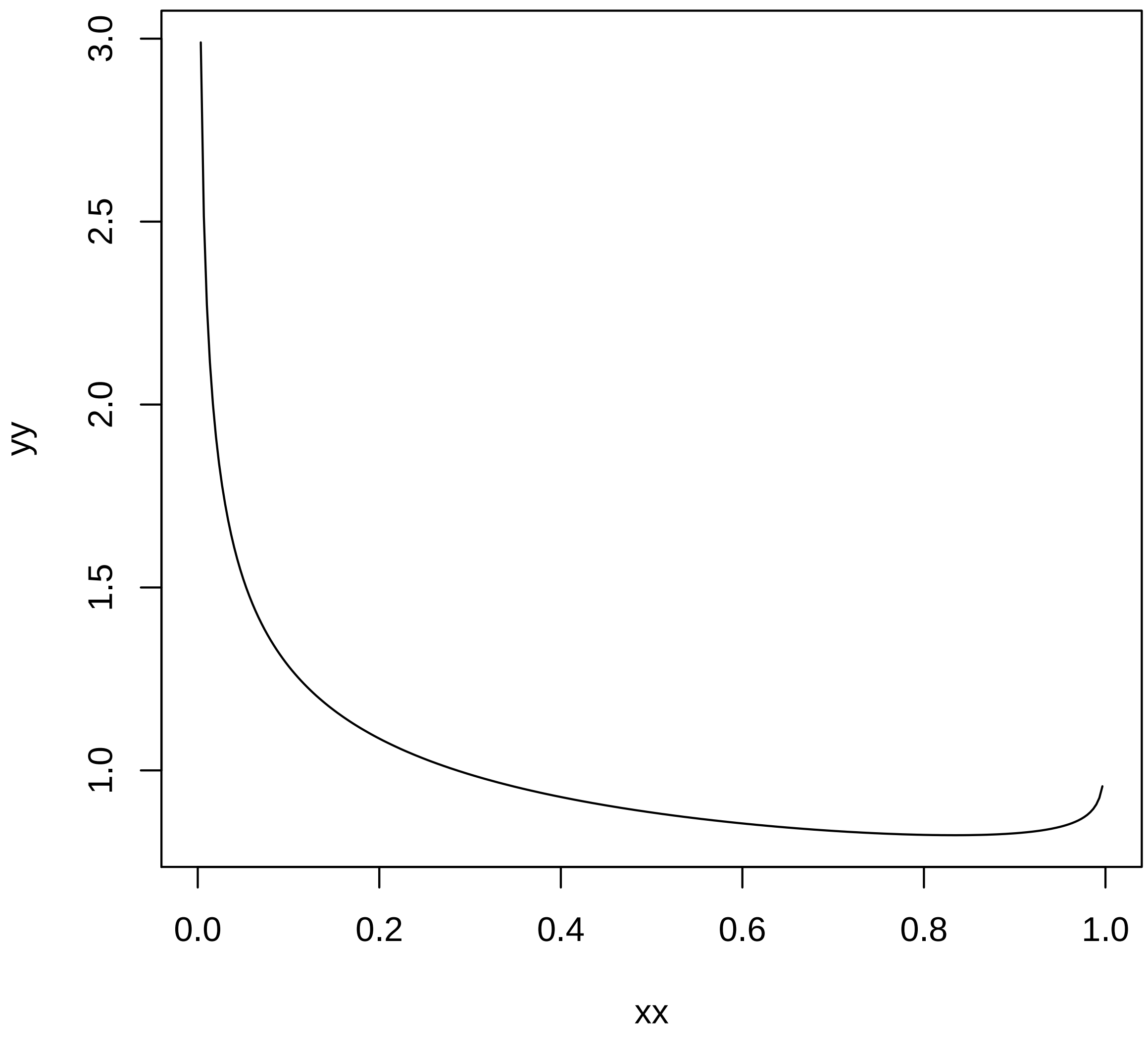
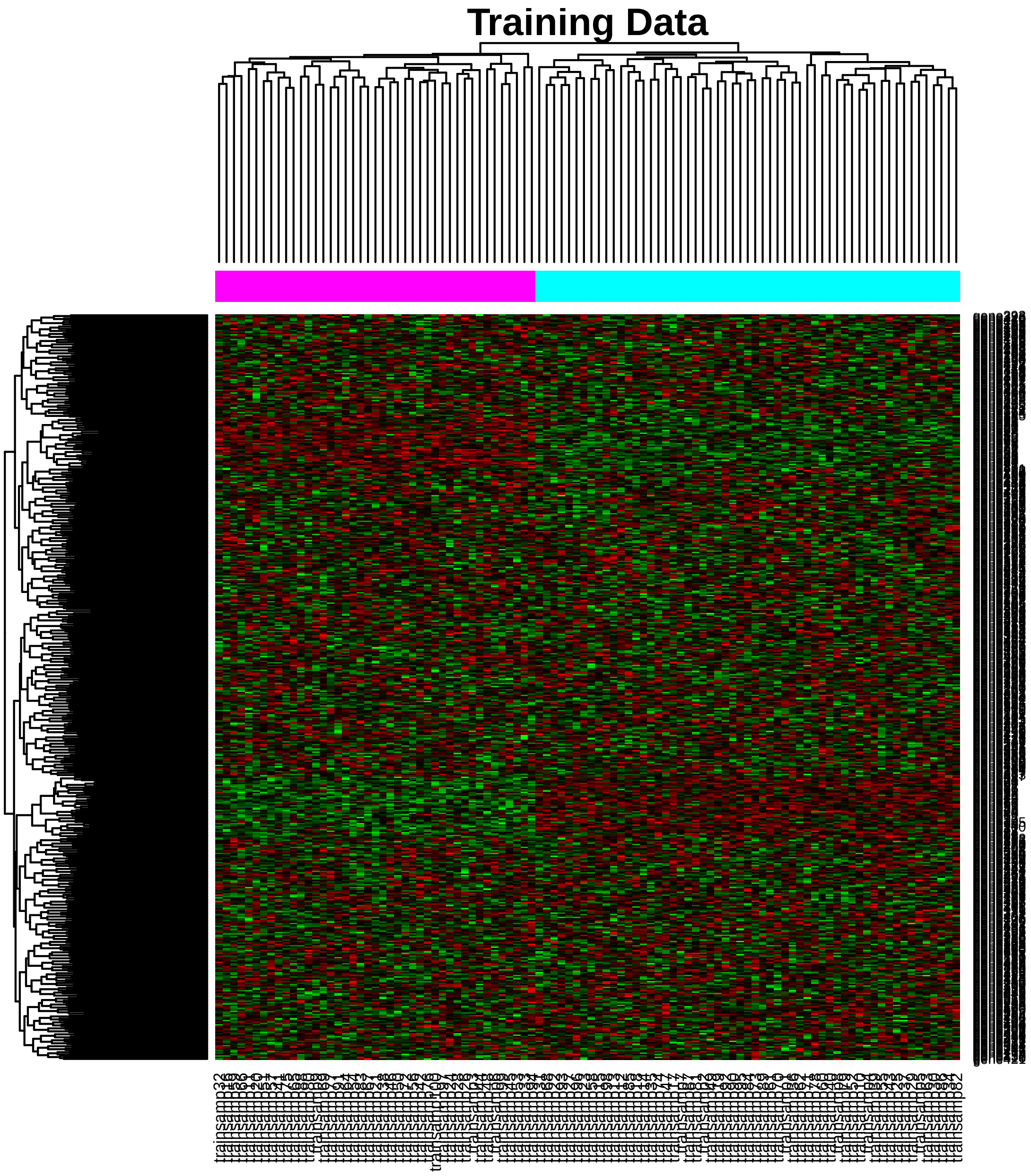


Figure 1: Probability of belonging to class B is simulated from this distribution, Beta(0.75, 0.95).

```
   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.

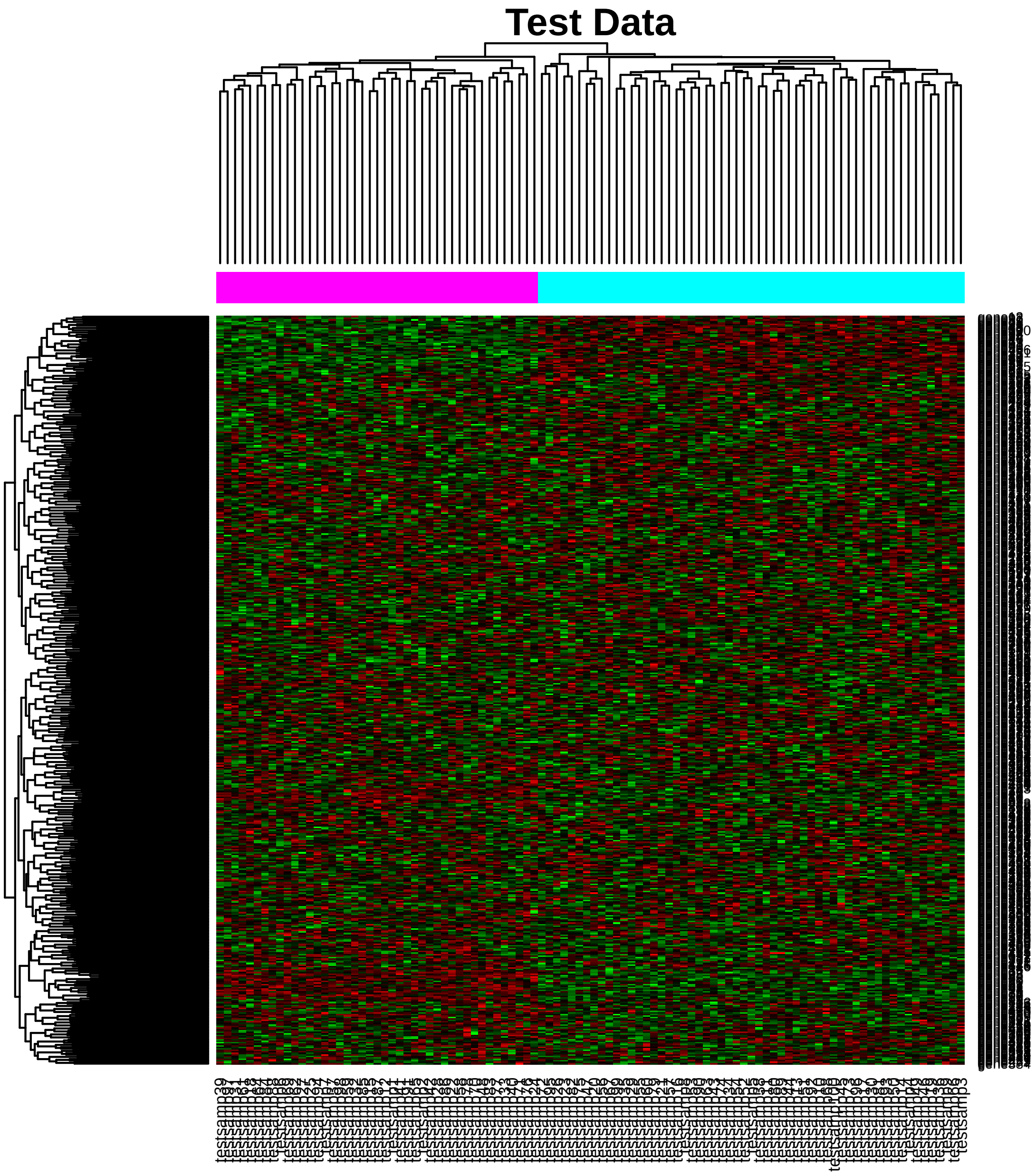
```
> pOut <- rbeta(nTest, alpha, beta)
> testOutcome <- lp(pOut)
```

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=''))
```



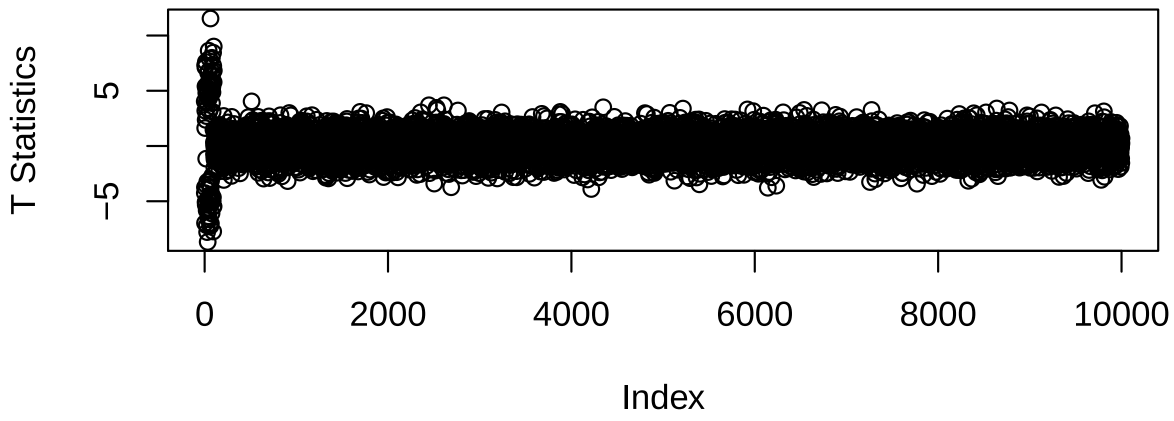
At this point, we can clean up the work space.

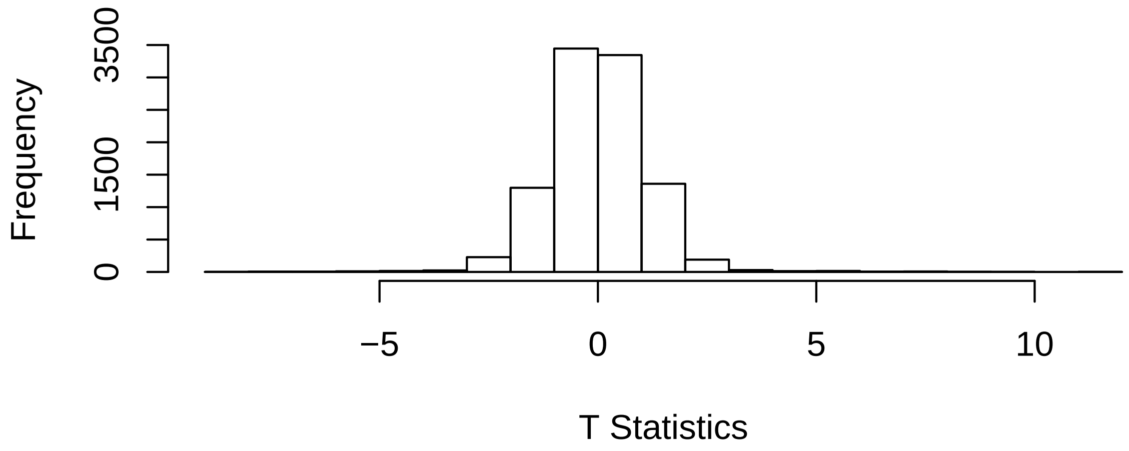
```
> rm(list=paramlist)
> rm(pOut, isB, signed, offsets)
> rm(xx, yy, alpha, beta)
> rm(paramlist)
```

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 exeprssed between the two classes.

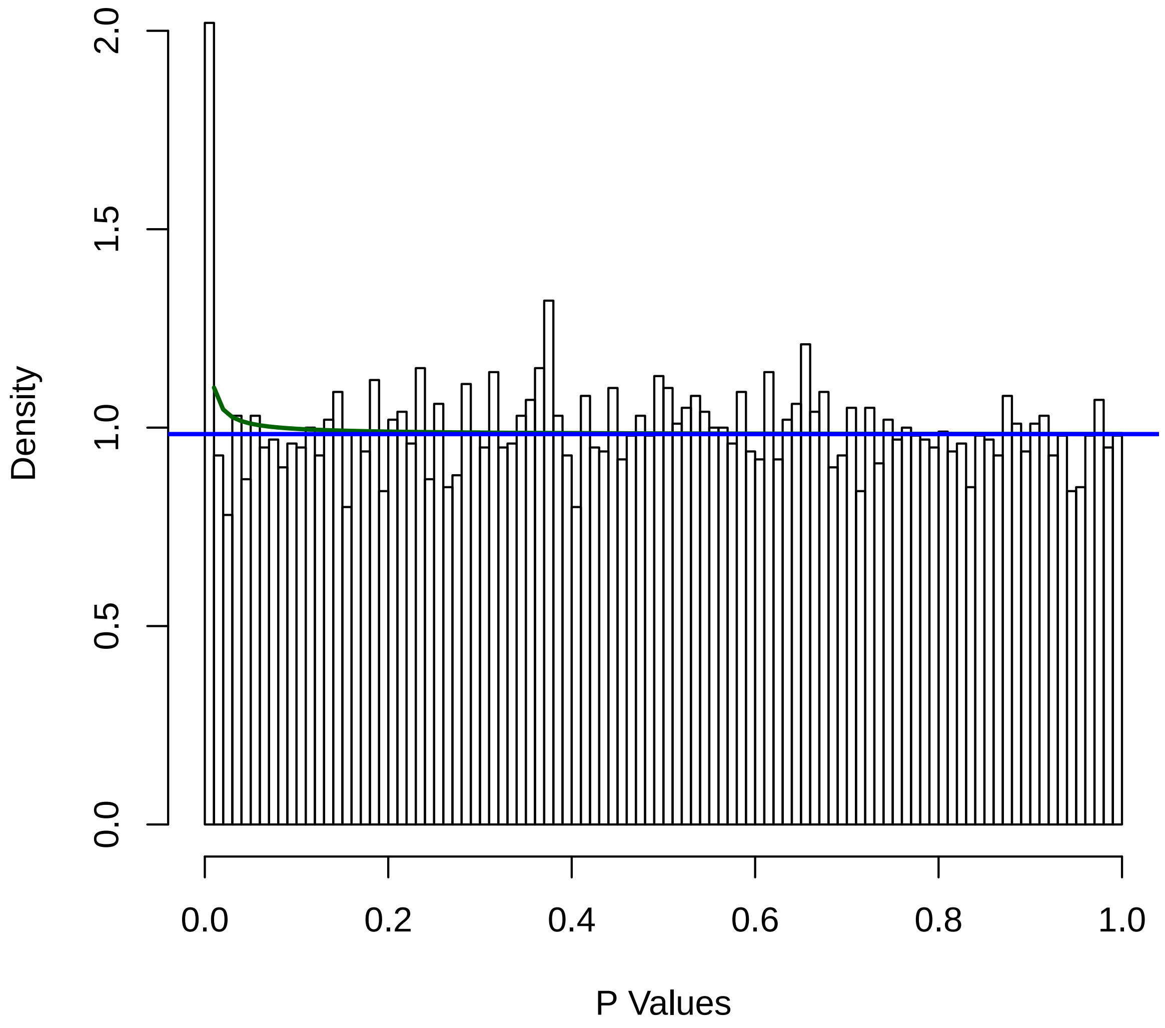
```
> library(ClassComparison)
> mtt <- MultiTtest(trainData, trainClass)
```





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

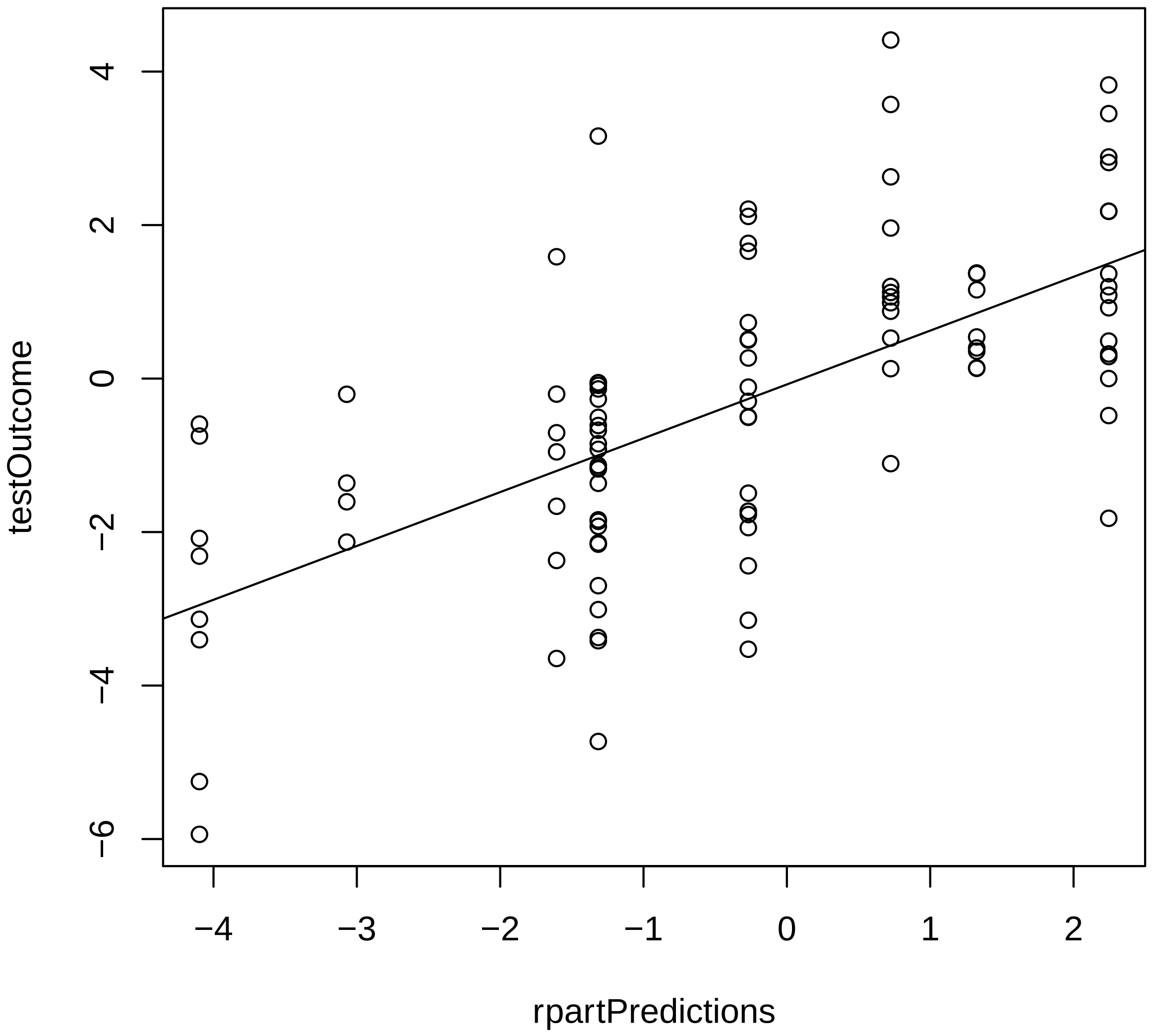
```
> rpartFitted <- learn(modelerRPART, trainSubset, trainOutcome)
> rpartPredictions <- predict(rpartFitted, testSubset)
> table(rpartPredictions > 0, testClass)
```

```
       testClass
        cyan magenta
  FALSE   54      10
  TRUE     3      33
```

```
> cor(rpartPredictions, testOutcome)
```

```
[1] 0.6316475
```

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



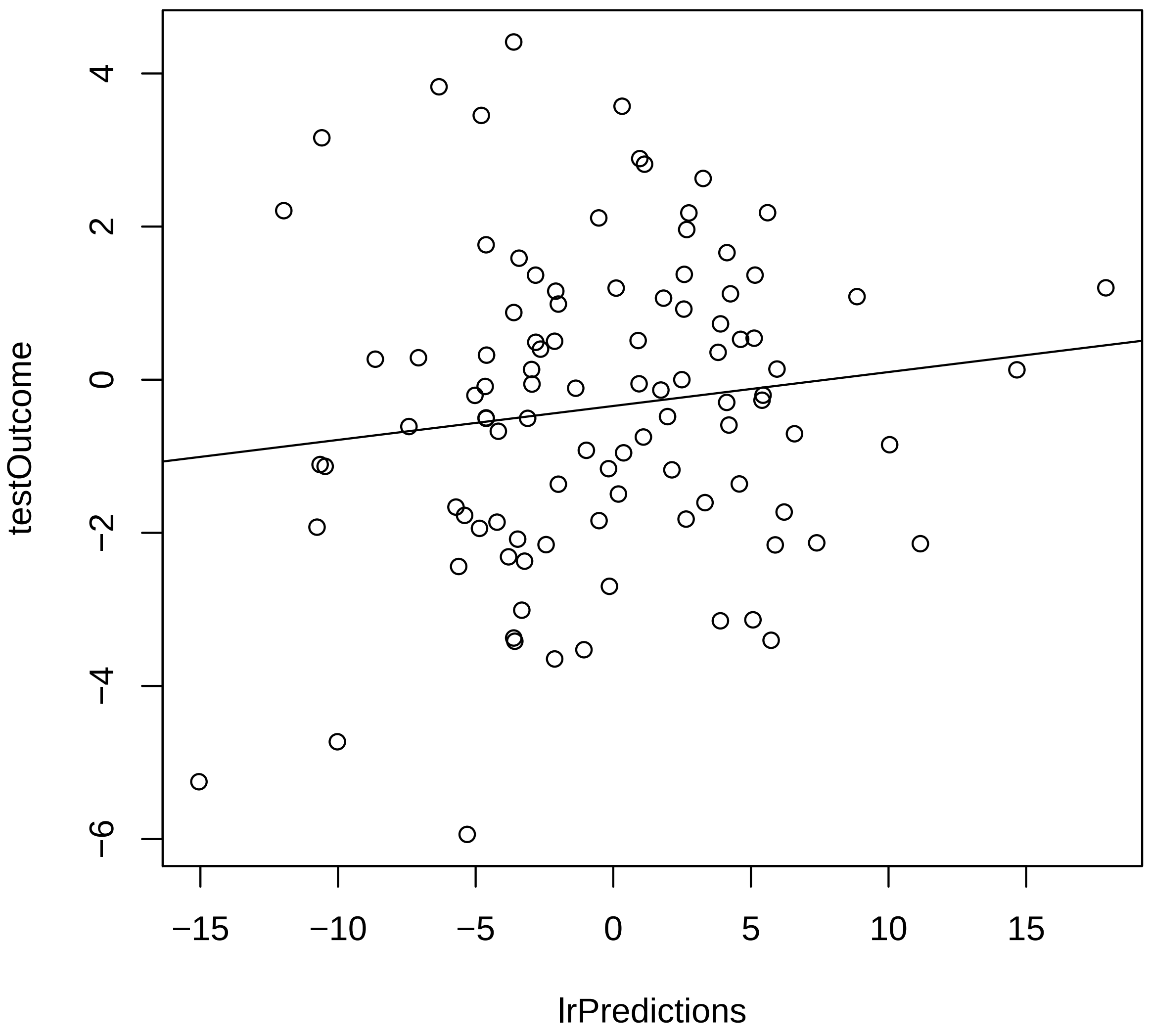
4.3 Linear/Logistic Regression

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

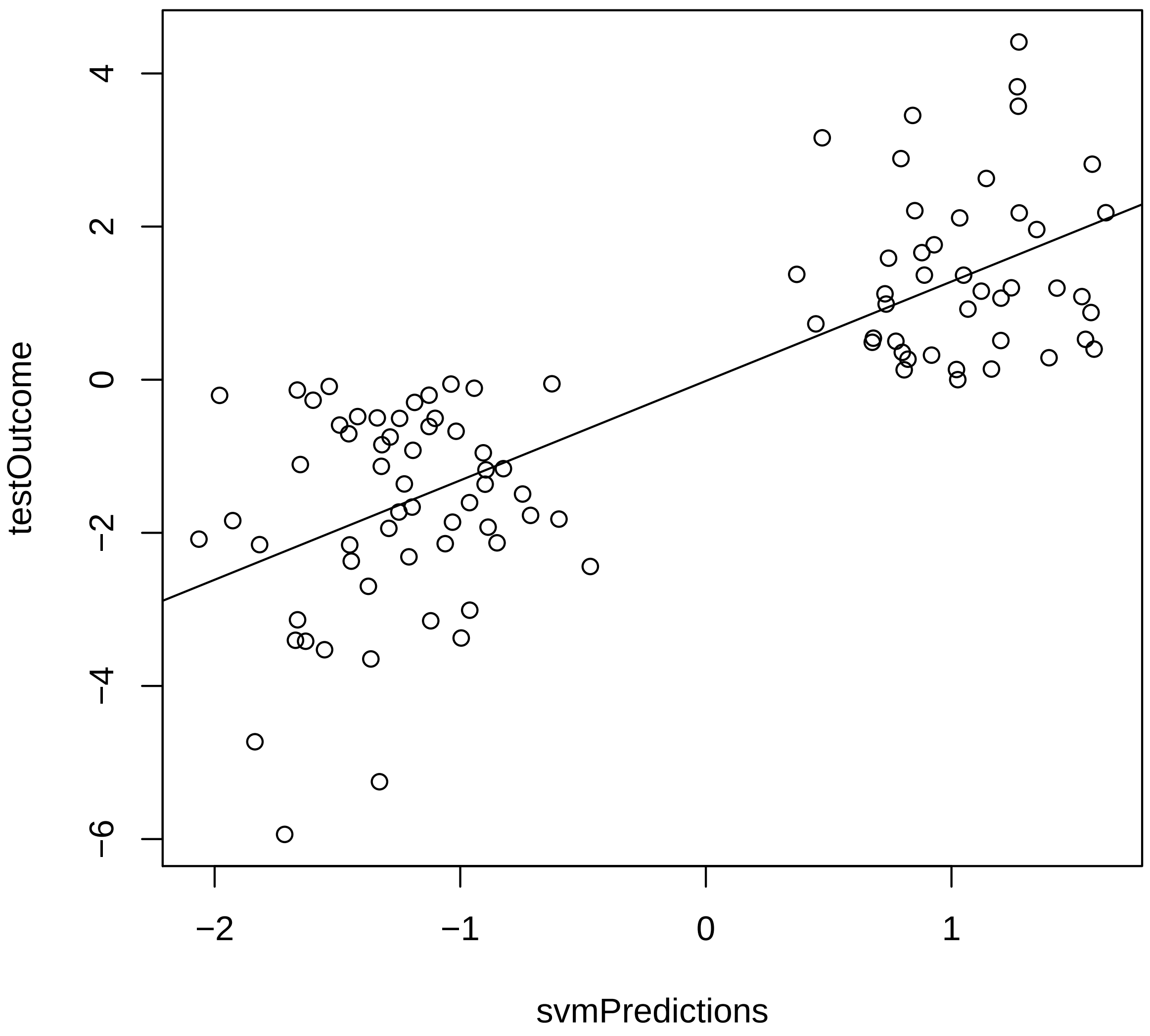
```
> svmFitted <- learn(modelerSVM, trainSubset, trainOutcome)
> svmPredictions <- predict(svmFitted, testSubset)
> table(svmPredictions > 0, testClass)
```

```
       testClass
        cyan magenta
  FALSE   57       0
  TRUE     0      43
```

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

```
[1] 0.7775552
```

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



4.6 Neural Networks

Classification

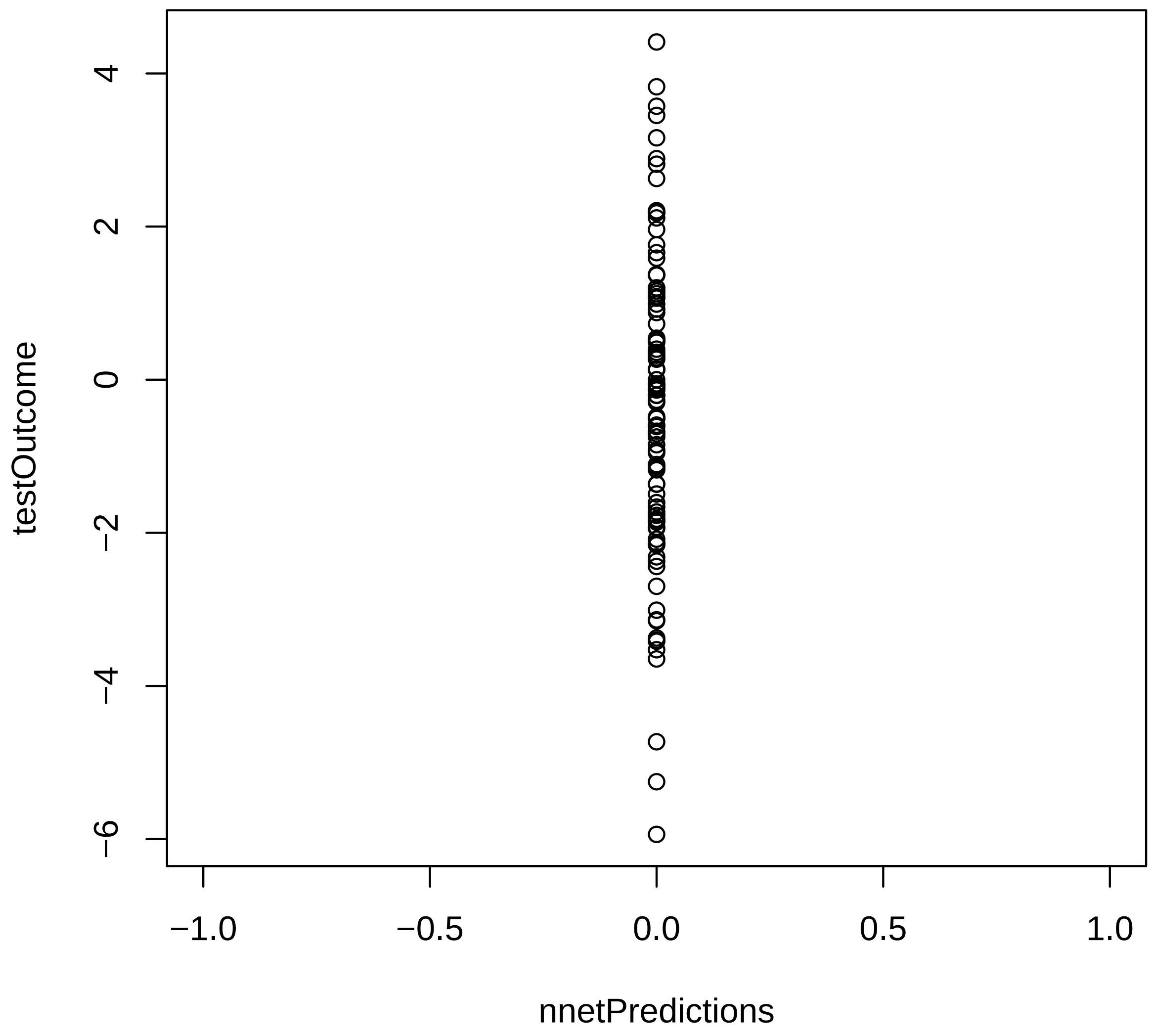
```
> nnetFitted <- learn(modelerNNET, trainSubset, trainClass)
```

```
# 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

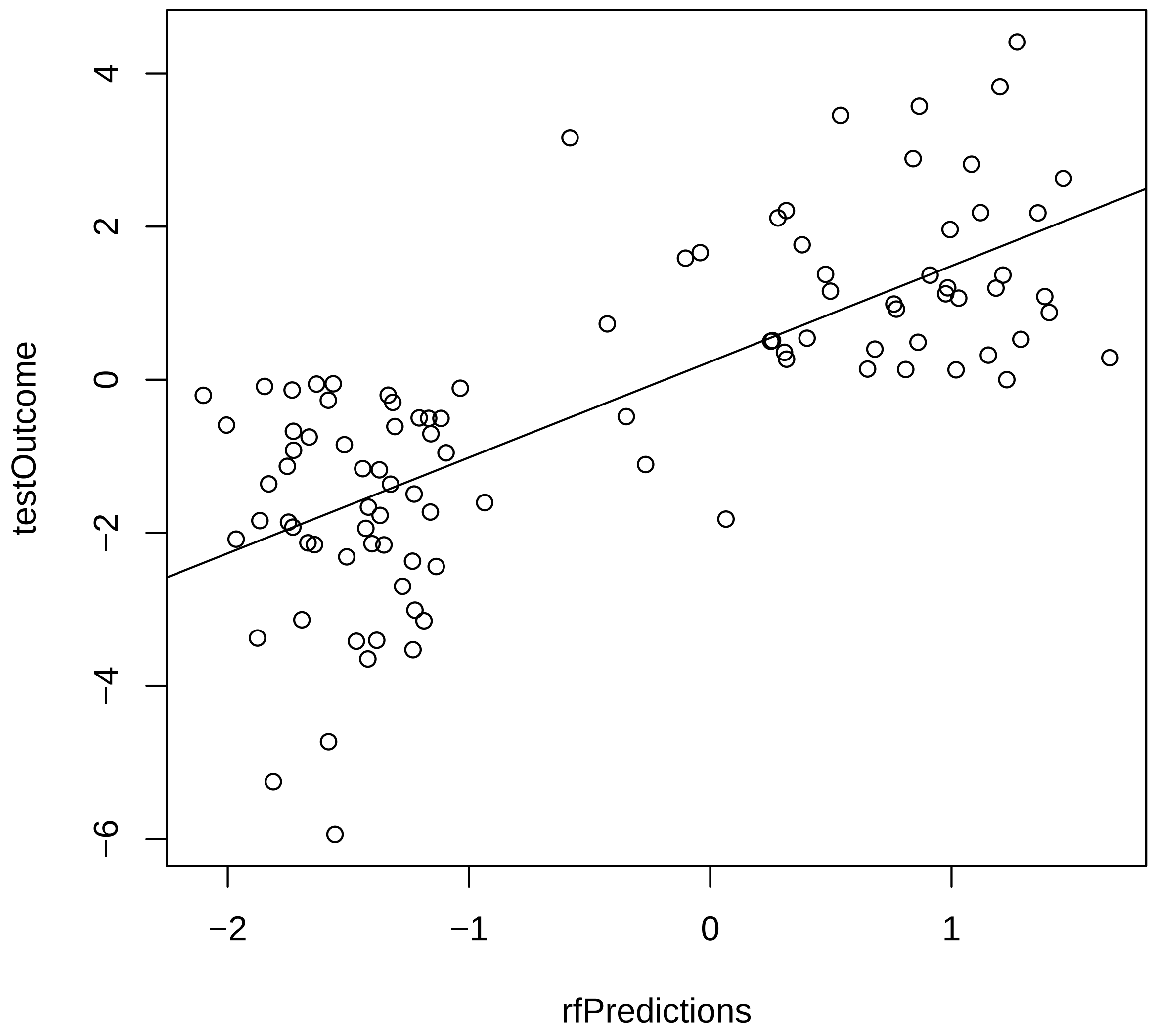
```
> rfFitted <- learn(modelerRF, trainSubset, trainOutcome)
> rfPredictions <- predict(rfFitted, testSubset)
> table(rfPredictions > 0, testClass)
```

```
       testClass
        cyan magenta
  FALSE   56       4
  TRUE     1      39
```

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

```
[1] 0.7343602
```

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



testOutcome
4
2
0
−2
−4
−6
−2
−1
0
1
rfPredictions