1 Solution – Assignment 1

This document is produced with Sweave. For that reason all uses of ggplot2 functions for plotting need to be done inside a print – otherwise there will be no figures.

```
> require(MASS)
> require(ggplot2)
> setwd("~/courses/statlearn/statlearn_2009/R/")
> load("Assignment1.RData")
```

1.1 Question 1

```
> X <- as.matrix(Assignment1Train[, -16])
> y <- Assignment1Train[, 16]</pre>
```

It seems that 230 has some outlier values and it is exclude.

> X <- X[-230,] > y <- y[-230]

Computing group means and the estimate of the covariance matrix.

```
> groupMeans <- apply(X, 2, function(x) tapply(x, y, mean))
> SigmaHat <- t(X - groupMeans[y, ]) %*% (X - groupMeans[y, ])/(dim(X)[1] -
+ 3)</pre>
```

FGA	45.82	43.93	45.30																		
D5S818	23.24	23.02	22.61			FGA	-0.01	-0.15	0.18	0.39	-0.37	-0.04	-0.07	-0.06	0.15	-0.25	0.32	-0.03	0.14	0.01	9.01
D18S51	32.40	30.23	30.61			D5S818	0.13	-0.12	-0.04	0.22	-0.03	0.04	0.12	0.17	-0.11	-0.09	-0.17	-0.07	0.18	3.07	0.01
TPOX	17.76	18.37	18.81			D18S51	-0.34	0.07	0.48	0.17	0.35	0.05	0.04	-0.00	0.27	0.17	-0.30	0.19	11.09	0.18	0.14
vWA	32.87	33.40	33.04			TPOX	0.30	-0.04	0.13	0.05	-0.02	0.24	-0.06	-0.04	-1.00	-0.09	-0.08	5.15	0.19	-0.07	-0.03
D19S433	26.91	27.84	27.56			vWA	-0.17	0.07	0.02	0.04	-0.19	-0.10	-0.17	0.22	0.14	-0.28	3.96	-0.08	-0.30	-0.17	0.32
D2S1338 D	41.74	41.43	40.16			D19S433	0.17	-0.16	0.15	-0.15	0.01	-0.15	-0.07	0.22	0.14	2.85	-0.28	-0.09	0.17	-0.09	-0.25
D16S539 I	21.68	22.80	22.41			D2S1338	-0.75	0.10	-0.15	-0.35	0.29	-0.51	-0.14	0.08	16.48	0.14	0.14	-1.00	0.27	-0.11	0.15
D13S317 L	23.28	22.17	21.68	Means		D16S539	0.02	-0.20	0.01	0.06	-0.18	0.15	0.29	4.09	0.08	0.22	0.22	-0.04	-0.00	0.17	-0.06
TH01 D	15.12	15.95	15.58	Table 1: Group Means		D13S317	0.26	-0.29	0.17	0.13	-0.11	-0.10	4.88	0.29	-0.14	-0.07	-0.17	-0.06	0.04	0.12	-0.07
D3S1358	31.70	32.18	32.01	Table 1		TH01	0.29	-0.05	-0.15	0.05	-0.03	3.39	-0.10	0.15	-0.51	-0.15	-0.10	0.24	0.05	0.04	-0.04
CSF1PO L	21.28	22.70	22.30			D3S1358	-0.06	-0.22	-0.39	-0.37	2.55	-0.03	-0.11	-0.18	0.29	0.01	-0.19	-0.02	0.35	-0.03	-0.37
D7S820 C	19.70	20.02	20.59			CSF1PO	-0.10	-0.16	0.31	3.22	-0.37	0.05	0.13	0.06	-0.35	-0.15	0.04	0.05	0.17	0.22	0.39
D21S11 I	59.57	59.79	60.20			D7S820	0.06	0.30	3.63	0.31	-0.39	-0.15	0.17	0.01	-0.15	0.15	0.02	0.13	0.48	-0.04	0.18
D8S1179 I	27.17	25.57	25.99			D21S11	0.01	6.07	0.30	-0.16	-0.22	-0.05	-0.29	-0.20	0.10	-0.16	0.07	-0.04	0.07	-0.12	-0.15
Ц	nerican	Caucasian	Hispanic			D8S1179	5.11	0.01	0.06	-0.10	-0.06	0.29	0.26	0.02	-0.75	0.17	-0.17	0.30	-0.34	0.13	-0.01
	African American	Cat	H				D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA

Table 2: Sigmahat

2

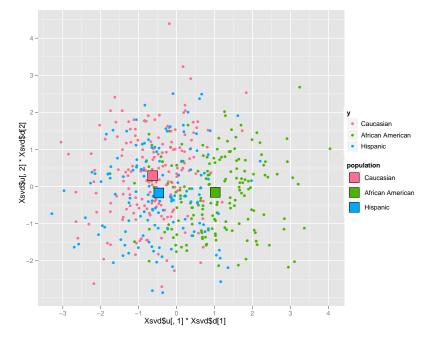
For later use in subsequent plots we compute the group means after a centering and scaling.

> groupMeans <- apply(scale(X), 2, function(x) tapply(x, y, mean))</pre>

1.2 Question 2

We make this plot after centering (compulsory) and scaling (optional, but generally recommended).

```
> Xsvd <- svd(scale(X))
> population <- levels(Assignment1Train[, 16])[c(2, 1, 3)]
> print(qplot(Xsvd$u[, 1] * Xsvd$d[1], Xsvd$u[, 2] * Xsvd$d[2],
+ colour = y) + geom_point(aes(groupMeans[c(2, 1, 3), ] %*%
+ Xsvd$v[, 1], groupMeans[c(2, 1, 3), ] %*% Xsvd$v[, 2], fill = population),
+ colour = I("black"), shape = 22, size = 8))
```

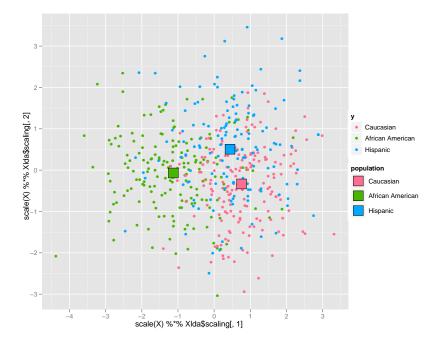


1.3 Question 3

We do this using centered and scaled X's. The actual lda classifier is not affected by this (just remember that new observations should be centered and scaled using the same estimated means and variances) but the resulting plots are then in a standardized form, which is common.

```
> Xlda <- lda(scale(X), y)
> print(qplot(scale(X) %*% Xlda$scaling[, 1], scale(X) %*% Xlda$scaling[,
+ 2], colour = y) + geom_point(aes(groupMeans[c(2, 1, 3), ] %*%
```

- + Xlda\$scaling[, 1], groupMeans[c(2, 1, 3),] %*% Xlda\$scaling[,
- + 2], fill = population), colour = I("black"), shape = 22,
- + size = 8))



1.4 Question 4

> X <- X[y != "Hispanic",]
> y <- y[y != "Hispanic", drop = TRUE]
> Xlda <- lda(X, y)</pre>

Computing misclassification tables.

```
> pred <- table(predict(Xlda)$class, y)
> print(pred)
```

2	7		
	African	American	Caucasian
African American		143	22
Caucasian		30	154

> print(pred/sum(pred), digits = 3)

2	7		
	${\tt African}$	American	Caucasian
African American		0.410	0.063
Caucasian		0.086	0.441

Then computing the number of misclassifications and the relative number of misclassifications.

```
> print(pred[1, 2] + pred[2, 1])
[1] 52
> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)
[1] 0.149
```

1.5 Question 5

```
> Xglm <- glm(population ~ ., data = cbind(X, data.frame(population = y)),
+ family = binomial)
```

Computing misclassification tables.

```
> pred <- table(levels(y)[round(predict(Xglm, type = "response")) +
+ 1], y)
> print(pred)
```

y African American Caucasian African American 144 24 Caucasian 29 152

> print(pred/sum(pred), digits = 3)

2	7		
	African	American	Caucasian
African American		0.4126	0.0688
Caucasian		0.0831	0.4355

Then computing the number of misclassifications and the relative number of misclassifications.

> print(pred[1, 2] + pred[2, 1])

[1] 53

> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)

[1] 0.152

1.6 Question 6

```
> mu1Hat <- Xlda$means[2, ]
> mu0Hat <- Xlda$means[1, ]
> residuals <- X - Xlda$means[y, ]
> SigmaHat <- t(residuals) %*% residuals/(dim(X)[1] - 2)
> tauHatBeta0 <- log(Xlda$prior[2]/Xlda$prior[1]) + (t(mu0Hat) %*%
+ solve(SigmaHat, mu0Hat) - t(mu1Hat) %*% solve(SigmaHat, mu1Hat))/2
> tauHatBeta <- solve(SigmaHat, mu1Hat - mu0Hat)
> hat <- data.frame(tauHat = c(tauHatBeta0, tauHatBeta), Hat = Xglm$coef)
> print(hat)
```

	tauHat	Hat
	-18.3628	-20.9147
D8S1179	-0.3760	-0.3948
D21S11	0.0473	0.0897
D7S820	0.1326	0.1534
CSF1PO	0.5268	0.5846
D3S1358	0.3123	0.2789
TH01	0.2931	0.2979
D13S317	-0.2494	-0.2969
D16S539	0.2356	0.2106
D2S1338	-0.0151	-0.0171
D19S433	0.4000	0.4427
vWA	0.1815	0.2094
TPOX	0.0762	0.0921
D18S51	-0.2497	-0.2392
D5S818	-0.1165	-0.1152
FGA	-0.2238	-0.2539

When we do two class classification the scalings from lda and the $\hat{\beta}$ coefficient from logistic regression are not directly comparable, but tauHatBeta above, which is comparable with $\hat{\beta}$, is in fact proportional to the scaling. The constant of proportionality comes from two facts. First, there is a different "centering" used for the scaling in the affine space spanned by $\hat{\mu}_1$ and $\hat{\mu}_2$, and second, the scaling vector is by definition of unit length when we use the inner product given by $\hat{\Sigma}$.

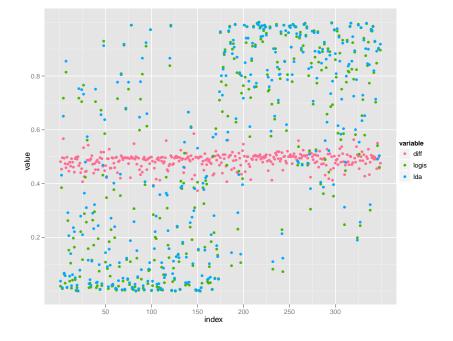
```
> tildeBeta <- solve(SigmaHat, mu1Hat - (Nk[2] * mu1Hat + Nk[1] *
+ mu0Hat)/sum(Nk))
> tildeBeta <- tildeBeta/sqrt(tildeBeta %*% SigmaHat %*% tildeBeta)
> lda(X, y)$scaling/tildeBeta
LD1
D8S1179 1
D21S11 1
```

D7S820 1 CSF1P0 1 D3S1358 1 TH01 1

D13S317	1
D16S539	1
D2S1338	1
D19S433	1
vWA	1
TPOX	1
D18S51	1
D5S818	1
FGA	1

If you turn to classification problems with the number of groups $K \geq 3$ the $\hat{\beta}_1, \ldots, \hat{\beta}_{K-1}$ vectors from multinomial regression are in general not comparable in any direct way to the scalings computed from lda. In this situation the only way to get something out of lda that is comparable to the estimates from the multinomial regression is to compute the plug-in estimates of the parameter function τ .

```
> trainPosterior <- data.frame(logis = predict(Xglm, type = "response"),
+ lda = predict(Xlda)$posterior[, 2])[order(y), ]
> print(ggplot(data = melt(cbind(data.frame(index = 1:(dim(X)[1]),
+ diff = trainPosterior[, 1] - trainPosterior[, 2] + 0.5),
+ trainPosterior), id = "index"), aes(x = index, y = value,
+ col = variable)) + geom_point())
```

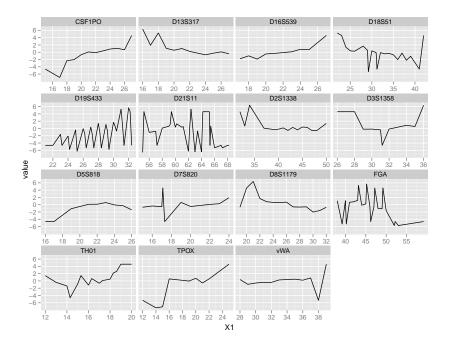


1.7 Question 7

```
> allLevels <- levels(factor(c(unlist(Assignment1Train[, -16]),
+ unlist(Assignment1Test[, -16]))))
```

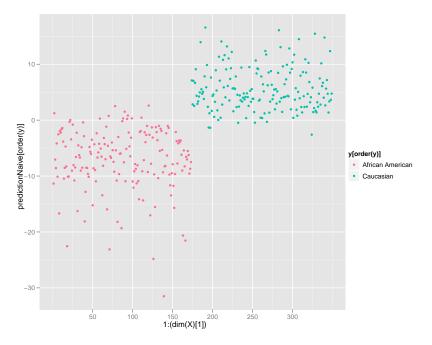
We compute the estimates of the marginal distributions.

```
> counts <- lapply(Assignment1TrainMod, function(x) tapply(x, y,
+ table))
> epsilon <- 0.01
> h <- lapply(counts, function(x) lapply(x, function(x) (x + epsilon)/sum(x +
+ epsilon)))
> logit <- sapply(h, function(x) log((x[[2]])/(x[[1]])))
> logitMelt <- melt(logit)
> print(qplot(x = X1, y = value, data = logitMelt[abs(logitMelt$value) >
+ 0.02, ], geom = "line") + facet_wrap(~X2, scale = "free_x"))
```



Computing the training error.

```
> Nk <- table(y)
> intercept <- log(Nk[2]/Nk[1])
> predictionNaive <- apply(X, 1, function(x) intercept + sum(diag(logit[as.character(x),
+ ])))
> print(qplot(1:(dim(X)[1]), predictionNaive[order(y)], shape = I(20),
+ colour = y[order(y)]))
```



Computing the misclassification tables.

```
> pred <- table(levels(y)[(predictionNaive > 0) + 1], y)
> print(pred)
```

У		
African	American	Caucasian
African American	161	6
Caucasian	12	170

> print(pred/sum(pred), digits = 3)

3	7		
	${\tt African}$	American	Caucasian
African American		0.4613	0.0172
Caucasian		0.0344	0.4871

Then computing the number of misclassifications and the relative number of misclassifications.

> print(pred[1, 2] + pred[2, 1])
[1] 18
> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)
[1] 0.0516

1.8 Question 8

```
> yTest <- as.factor(as.vector(Assignment1Test[, 16]))
> XTest <- Assignment1Test[, -16]
> predictionNaive <- apply(XTest, 1, function(x) intercept + sum(diag(logit[as.character(x),
+ ])))</pre>
```

Naive test error:

```
> pred <- table(levels(yTest)[(predictionNaive > 0) + 1], yTest)
> print(pred)
```

	yTest		
	African	American	Caucasian
African American		65	12
Caucasian		17	75

> print(pred/sum(pred), digits = 3)

yTest		
African	American	Caucasian
African American	0.385	0.071
Caucasian	0.101	0.444

Then computing the number of misclassifications and the relative number of misclassifications.

> print(pred[1, 2] + pred[2, 1])

[1] 29

> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)

[1] 0.172

LDA test error:

> pred <- table(predict(Xlda, XTest)\$class, yTest)
> print(pred)

2	yTest		
	African	American	Caucasian
African American		61	19
Caucasian		21	68

> print(pred/sum(pred), digits = 3)

yTest		
Afri	can American	Caucasian
African American	0.361	0.112
Caucasian	0.124	0.402

Then computing the number of misclassifications and the relative number of misclassifications.

> print(pred[1, 2] + pred[2, 1])

[1] 40

```
> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)
```

[1] 0.237

Glm test error:

yTest				
Af	rican	American	Caucasian	
African American		65	21	
Caucasian		17	66	

> print(pred/sum(pred), digits = 3)

7	Jest		
	African	American	Caucasian
African American		0.385	0.124
Caucasian		0.101	0.391

Then computing the number of misclassifications and the relative number of misclassifications.

> print(pred[1, 2] + pred[2, 1])

[1] 38

> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)

[1] 0.225

The Naive Bayes method seems to be able to make the best predictions - also on the test data. The method does adapt a lot to the concrete dataset and we see a considerable increase in the estimated expected prediction error on the test data compared to misclassification rate on the training data for the Naive Bayes procedure. However, it also seems that the Naive Bayes procedure captures some important, non-linear effects that improves on the prediction.

Some have noted that there is an implementation of "naive Bayes" in the e1071 library. In effect this is a diagonal QDA – a quadratic discriminant analysis but where the covariance matrices are assumed diagonal. It turns out that is method performs surprisingly well and seems to have the smallest generalization error. It does not suffer from the many free parameters that are in my hand-crafted naive Bayes procedure above, but it incorporates quadratic terms, which seem to be very important.

1.9 Generalizations

If we think of include quadratic terms in a more direct way, we can do so, either explicitly using a logistic regression model or though more general non-linear effects in a generalized additive model. Using logistic regression with quadratic terms included:

```
> form <- as.formula(paste("population~", paste(colnames(X), collapse = "+"),</pre>
      "+", paste("I(", colnames(X), "^2)", sep = "", collapse = "+")))
+
> XQglm <- glm(form, data = cbind(X, data.frame(population = y)),</pre>
      family = binomial)
> pred <- table(levels(y)[round(predict(XQglm, XTest, type = "response")) +</pre>
      1], yTest)
> print(pred)
                  vTest
                    African American Caucasian
 African American
                                  66
                                             18
 Caucasian
                                   16
                                             69
> print(pred/sum(pred), digits = 3)
                   vTest
                    African American Caucasian
                                         0.1065
 African American
                              0.3905
 Caucasian
                              0.0947
                                         0.4083
> print(pred[1, 2] + pred[2, 1])
[1] 34
> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)
[1] 0.201
```

Using a generalized additive model

```
> require(gam)
> form <- as.formula(paste("population~", paste("s(", colnames(X),</pre>
      ",df=3)", sep = "", collapse = "+")))
+
> Xgam <- gam(form, data = cbind(X, data.frame(population = y)),</pre>
     family = binomial)
+
> pred <- table(levels(y)[round(predict(Xgam, XTest, type = "response")) +</pre>
     1], yTest)
+
> print(pred)
                  yTest
                   African American Caucasian
  African American
                                  66
                                            15
                                            72
 Caucasian
                                  16
> print(pred/sum(pred), digits = 3)
                  yTest
                   African American Caucasian
                             0.3905 0.0888
  African American
 Caucasian
                              0.0947
                                        0.4260
> print(pred[1, 2] + pred[2, 1])
[1] 31
> print((pred[1, 2] + pred[2, 1])/sum(pred), digits = 3)
[1] 0.183
```