

# Breast Cancer

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```
#Using the brca dataset from the dslabs package contains information about breast cancer diagnosis biopsy samples
for tumors determined to be malignant or benign
#Load data and libraries
options(digits = 3)
library(matrixStats)
library(tidyverse)
```

```
## — Attaching packages — tidyverse 1.3.0 —
```

```
## / ggplot2 3.3.2      / purrr  0.3.4
## / tibble  3.0.3      / dplyr  1.0.2
## / tidyr   1.1.0      / stringr 1.4.0
## / readr   1.3.1      / forcats 0.5.0
```

```
## — Conflicts — tidyverse_conflicts() —
## x dplyr::count() masks matrixStats::count()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()   masks stats::lag()
```

```
library(caret)
```

```
## Loading required package: lattice
```

```
##
## Attaching package: 'caret'
```

```
## The following object is masked from 'package:purrr':
## lift
```

```
library(dslabs)
data(brca)
```

```
#Number of samples within dataset
dim(brca$x)[1]
```

```
## [1] 569
```

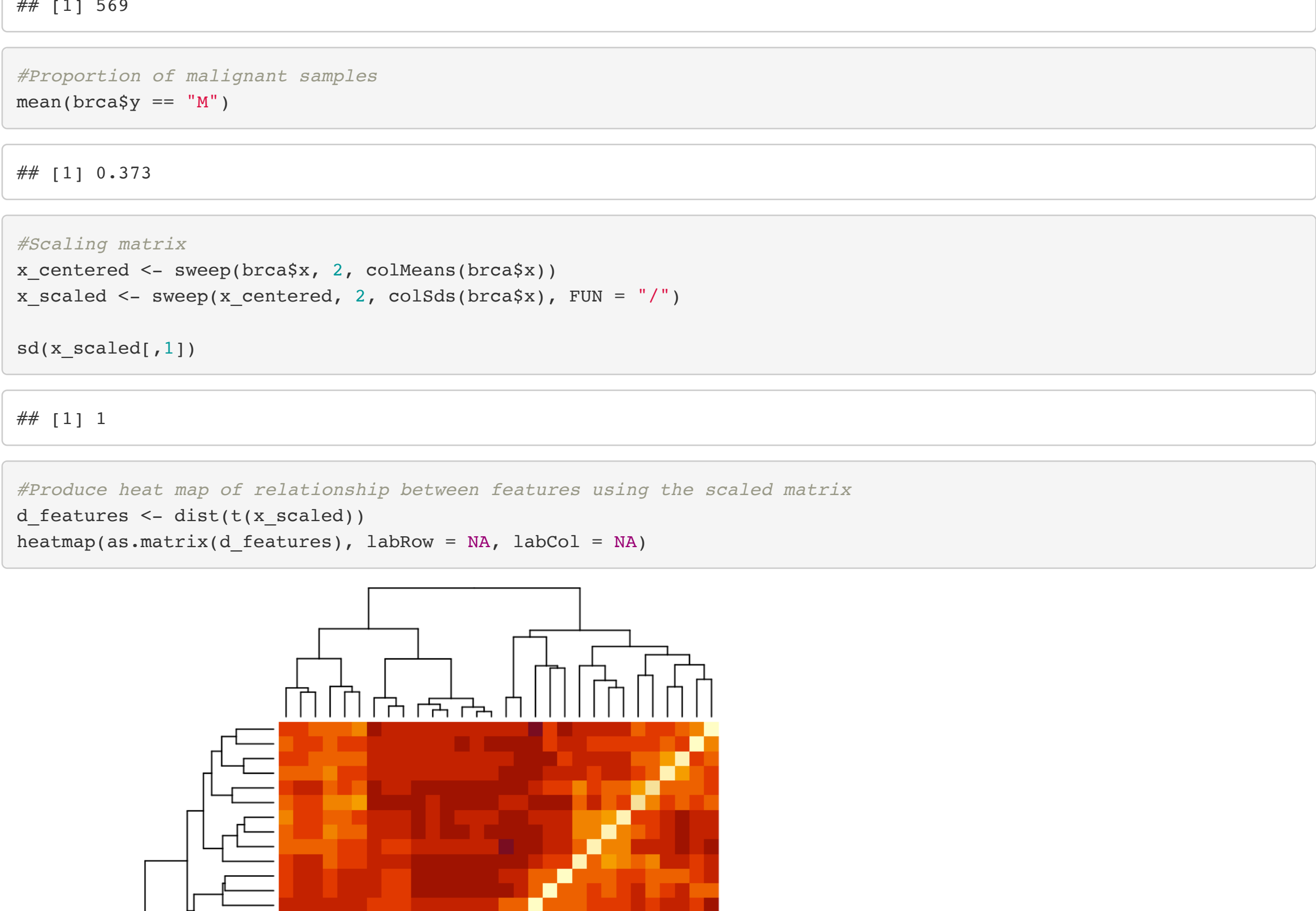
```
#Proportion of malignant samples
mean(brca$y == "M")
```

```
## [1] 0.373
```

```
#Scaling matrix
x_centered <- sweep(brca$x, 2, colMeans(brca$x))
x_scaled <- sweep(x_centered, 2, colSds(brca$x), FUN = "/")
sd(x_scaled[,1])
```

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

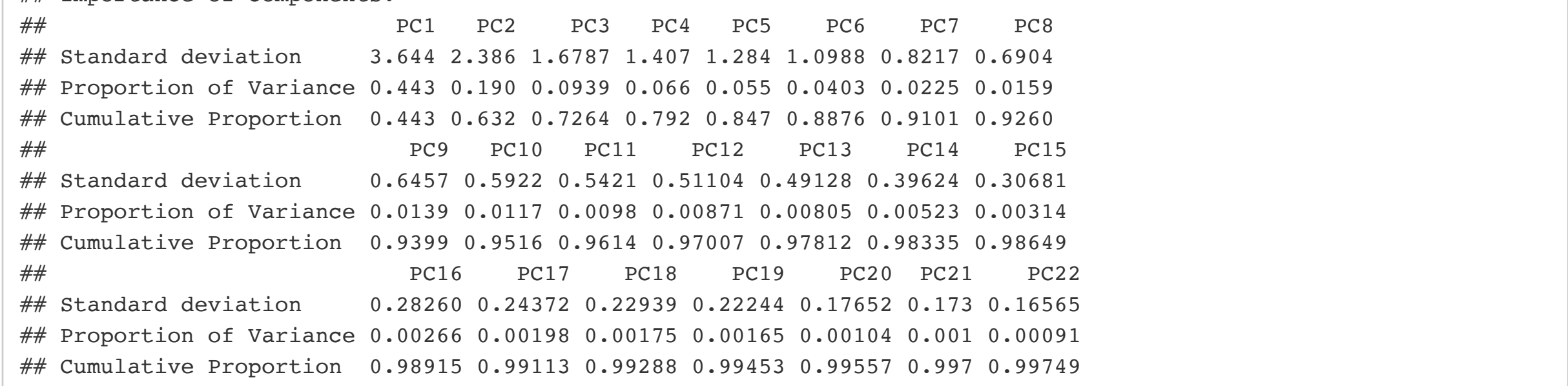
```
#Produce heat map of relationship between features using the scaled matrix
d_features <- dist(t(x_scaled))
heatmap(as.matrix(d_features), labRow = NA, labCol = NA)
```



```
#Principal component analysis of scaled matrix
pca <- prcomp(x_scaled)
summary(pca)
```

```
## Importance of components:
## PC1 PC2 PC3 PC4 PC5 PC6 PC7 PC8
## Standard deviation 3.644 2.386 1.6787 1.407 1.284 1.0988 0.8217 0.6904
## Proportion of Variance 0.443 0.190 0.0939 0.066 0.055 0.0403 0.0225 0.0159
## Cumulative Proportion 0.443 0.632 0.7264 0.792 0.847 0.8876 0.9101 0.9260
## PC9 PC10 PC11 PC12 PC13 PC14 PC15
## Standard deviation 0.6457 0.5922 0.5421 0.51104 0.49128 0.39624 0.30681
## Proportion of Variance 0.0139 0.0117 0.0098 0.00871 0.00805 0.00523 0.00314
## Cumulative Proportion 0.9399 0.9516 0.9614 0.97007 0.97812 0.98335 0.98649
## PC16 PC17 PC18 PC19 PC20 PC21 PC22
## Standard deviation 0.28260 0.24372 0.22939 0.22244 0.17652 0.173 0.16565
## Proportion of Variance 0.00266 0.00198 0.00175 0.00165 0.00104 0.001 0.00091
## Cumulative Proportion 0.98915 0.99113 0.99289 0.99453 0.99557 0.997 0.99749
## PC23 PC24 PC25 PC26 PC27 PC28 PC29
## Standard deviation 0.15602 0.1344 0.12442 0.09043 0.08307 0.03987 0.02736
## Proportion of Variance 0.00081 0.0006 0.00052 0.00027 0.00023 0.00005 0.00002
## Cumulative Proportion 0.99830 0.9989 0.99942 0.99969 0.99992 0.99997 1.00000
## PC30
## Standard deviation 0.0115
## Proportion of Variance 0.0000
## Cumulative Proportion 1.0000
```

```
#Plot two principal components with color representing tumor type (M,B)
data.frame(pca$x[,1:2], type = brca$y) %>%
ggplot(aes(PC1, PC2, color = type)) +
geom_point()
```



```
#Training and test sets
set.seed(1)
test_index <- createDataPartition(brca$y, times = 1, p = 0.2, list = FALSE)
test_x <- x_scaled[test_index,]
test_y <- brca$y[test_index]
train_x <- x_scaled[-test_index,]
train_y <- brca$y[-test_index]
```

```
#Proportion of training set benign
mean(train_y == "B")
```

```
## [1] 0.628
```

```
0.628
```

```
## [1] 0.628
```

```
#Test set
mean(test_y == "B")
```

```
## [1] 0.626
```

```
0.626
```

```
## [1] 0.626
```

```
#Using predict_kmeans() to make predictions on test set
predict_kmeans <- function(x, k) {
  centers <- k$centers
  distances <- sapply(1:nrow(x), function(i){
    apply(centers, 1, function(y) dist(rbind(x[i,], y)))
  })
  max.col(-t(distances)) # select cluster with min distance to center
}
#Overall accuracy
set.seed(3)
k <- kmeans(train_x, centers = 2)
kmeans_preds <- ifelse(predict_kmeans(test_x, k) == 1, "B", "M")
mean(kmeans_preds == test_y)
```

```
## [1] 0.896
```

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0.896
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```
## [1] 0.896
```

```
#Proportion of benign tumors correctly identified
sensitivity(factor(kmeans_preds), test_y, positive = "B")
```

```
## [1] 0.958
```

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0.958
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## [1] 0.958
```

```
#Proportion of malignant tumors correctly identified
sensitivity(factor(kmeans_preds), test_y, positive = "M")
```

```
## [1] 0.791
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0.791
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## [1] 0.791
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```
#Testing accuracy of logistic regression model
train_glm <- train(train_x, train_y, method = "glm")
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