

# KaitlinRMD

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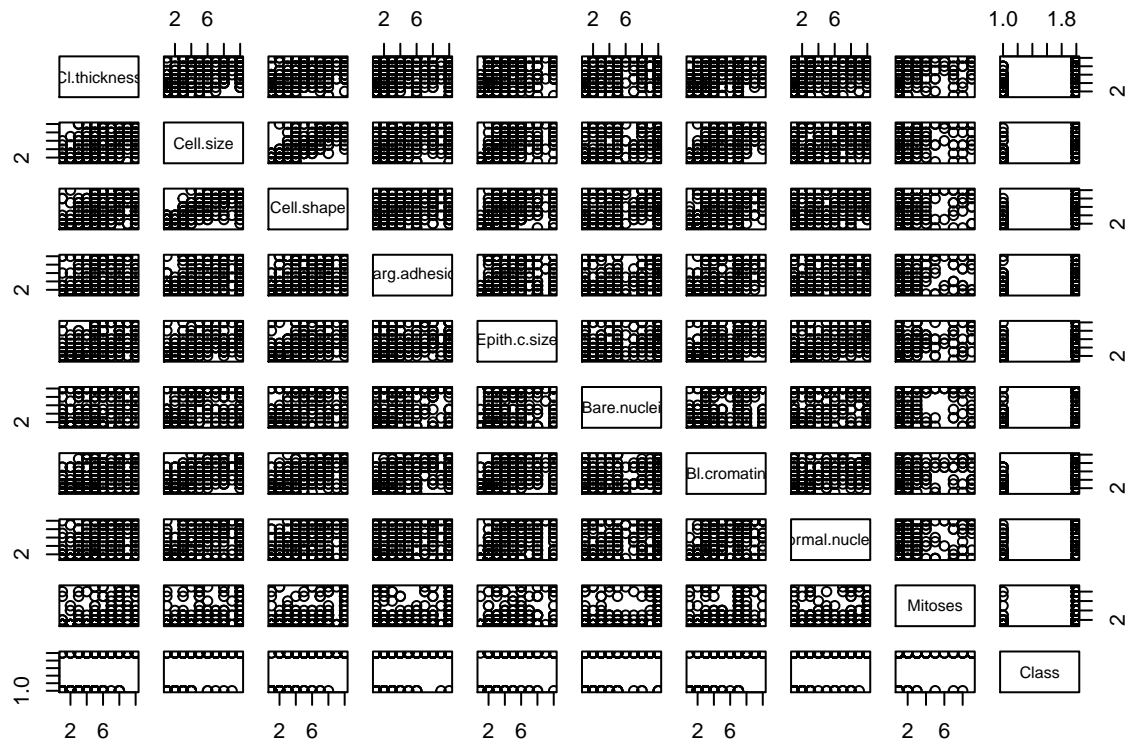
*April 26, 2018*

```
### Summary stuff for DS2 final project
```

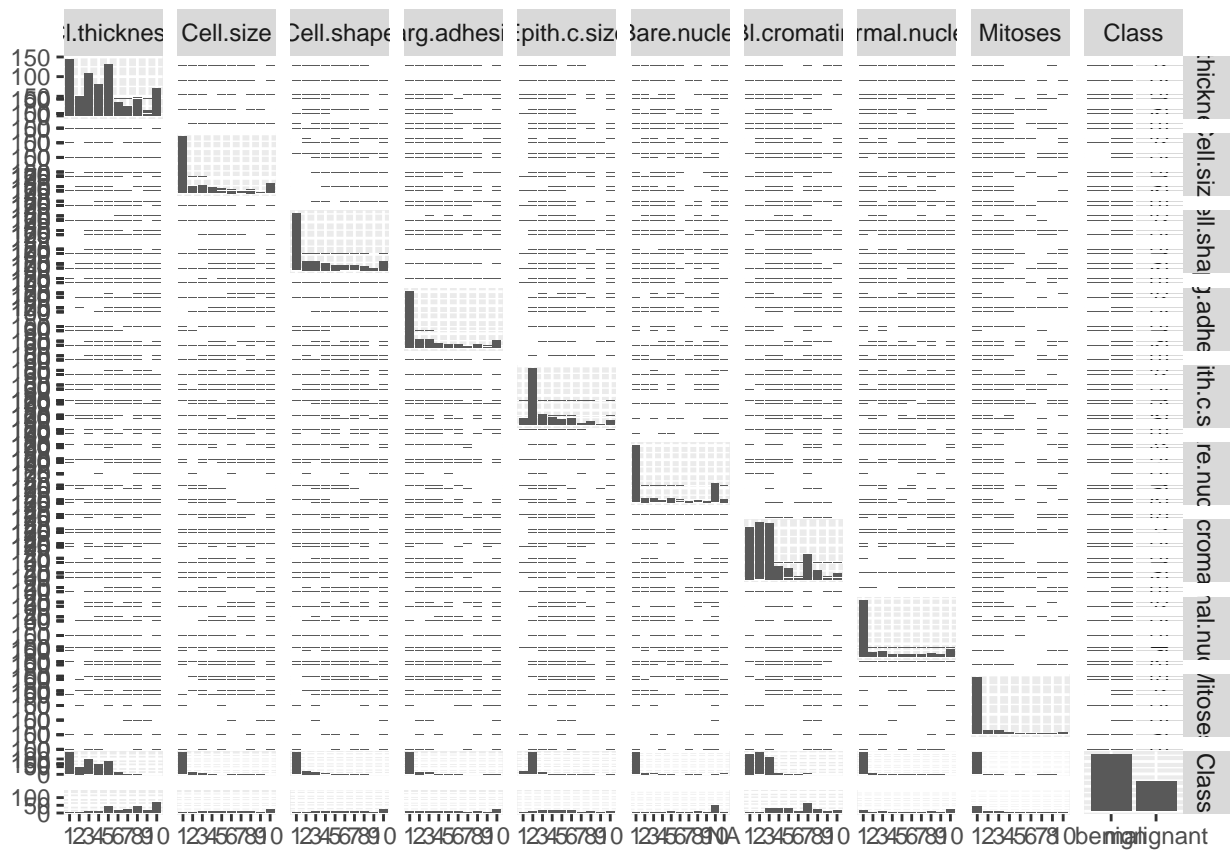
```
library(mlbench)
data(BreastCancer)
attach(BreastCancer)
library(dplyr)
BreastCancer <- BreastCancer[,-1] # remove ID column
summary(BreastCancer) # note that everything is factor
```

```
##   Cl.thickness   Cell.size   Cell.shape   Marg.adhesion   Epith.c.size
## 1      :145     1      :384     1      :353     1      :407     2      :386
## 5      :130    10      : 67     2      : 59     2      : 58     3      : 72
## 3      :108     3      : 52    10      : 58     3      : 58     4      : 48
## 4      : 80     2      : 45     3      : 56    10      : 55     1      : 47
## 10     : 69     4      : 40     4      : 44     4      : 33     6      : 41
## 2      : 50     5      : 30     5      : 34     8      : 25     5      : 39
## (Other):117   (Other): 81   (Other): 95   (Other): 63   (Other): 66
##   Bare.nuclei   Bl.cromatin   Normal.nucleoli   Mitoses   Class
## 1      :402     2      :166     1      :443     1      :579   benign :458
## 10     :132     3      :165    10      : 61     2      : 35   malignant:241
## 2      : 30     1      :152     3      : 44     3      : 33
## 5      : 30     7      : 73     2      : 36    10      : 14
## 3      : 28     4      : 40     8      : 24     4      : 12
## (Other): 61     5      : 34     6      : 22     7      : 9
## NA's      : 16   (Other): 69   (Other): 69   (Other): 17
```

```
plot(BreastCancer)
```



```
library(GGally)
ggpairs(BreastCancer) # note all are factors
```



```

BreastCancer = BreastCancer %>%
  mutate(Cl.thickness=as.numeric(Cl.thickness)) %>%
  mutate(Cell.size=as.numeric(Cell.size)) %>%
  mutate(Cell.shape=as.numeric(Cell.shape)) %>%
  mutate(Marg.adhesion=as.numeric(Marg.adhesion)) %>%
  mutate(Epith.c.size=as.numeric(Epith.c.size)) %>%
  mutate(Bare.nuclei=as.numeric(Bare.nuclei)) %>%
  mutate(Bl.cromatin=as.numeric(Bl.cromatin)) %>%
  mutate(Normal.nucleoli=as.numeric(Normal.nucleoli)) %>%
  mutate(Mitoses=as.numeric(Mitoses))

ggpairs(BreastCancer) # all but response are numeric

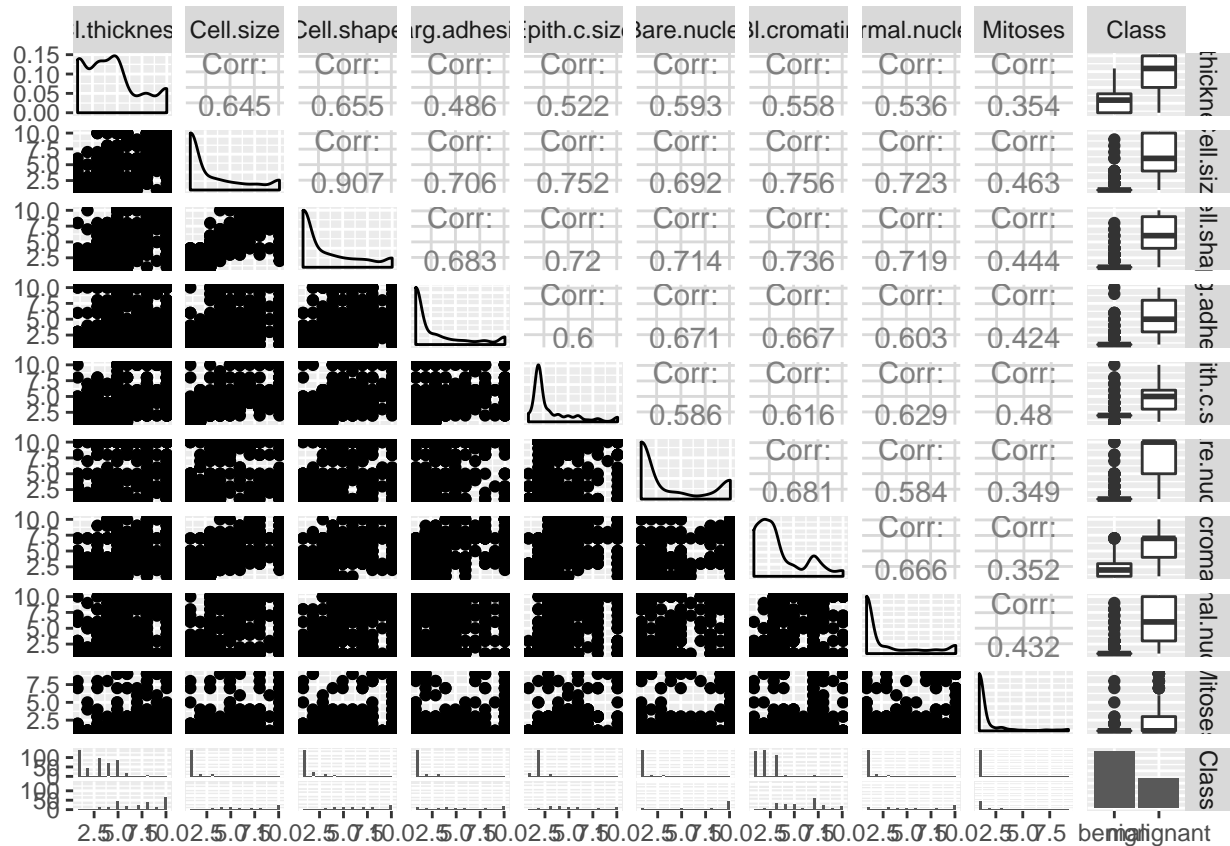
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 16 rows containing missing values
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## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 16 rows containing missing values
## Warning: Removed 16 rows containing missing values (geom_point).
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## Warning: Removed 16 rows containing missing values (geom_point).
## Warning: Removed 16 rows containing missing values (geom_point).
## Warning: Removed 16 rows containing non-finite values (stat_density).
## Warning in (function (data, mapping, alignPercent = 0.6, method =
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## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 16 rows containing missing values
## Warning: Removed 16 rows containing non-finite values (stat_boxplot).
## Warning: Removed 16 rows containing missing values (geom_point).
## Warning: Removed 16 rows containing missing values (geom_point).
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## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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```

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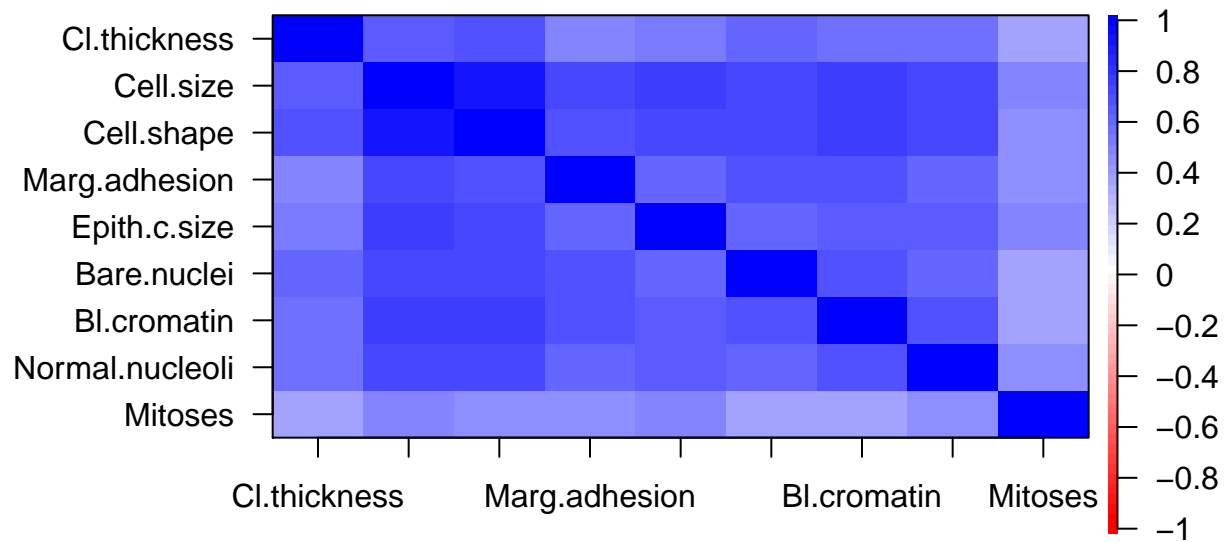
## Warning: Removed 16 rows containing non-finite values (stat_bin).

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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```



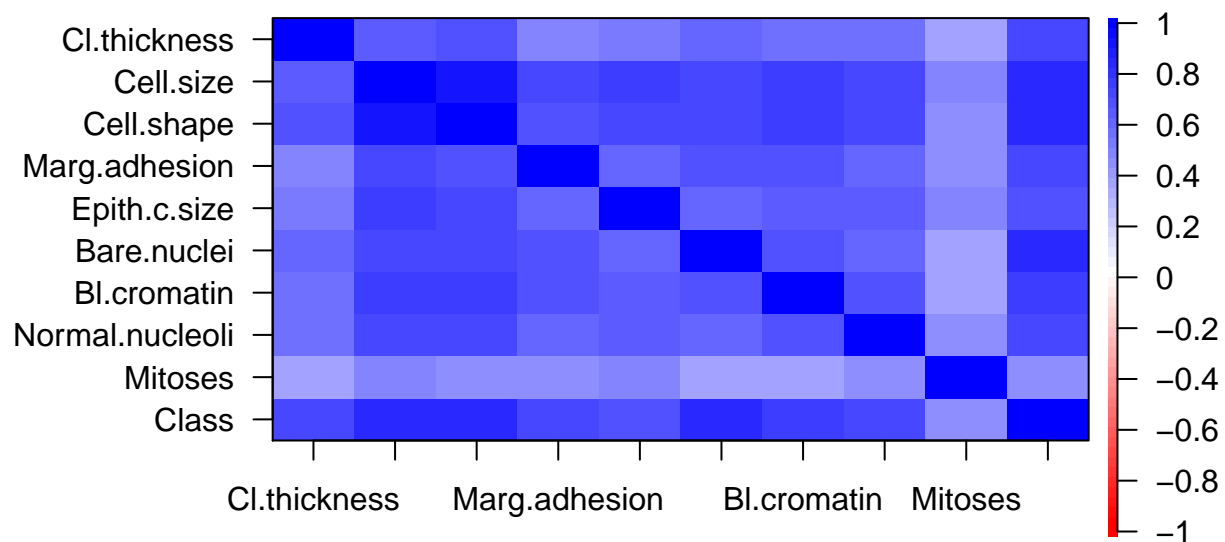
```
library(psych)
cor.plot(BreastCancer[, -10]) # correlation not including response
```

## Correlation plot



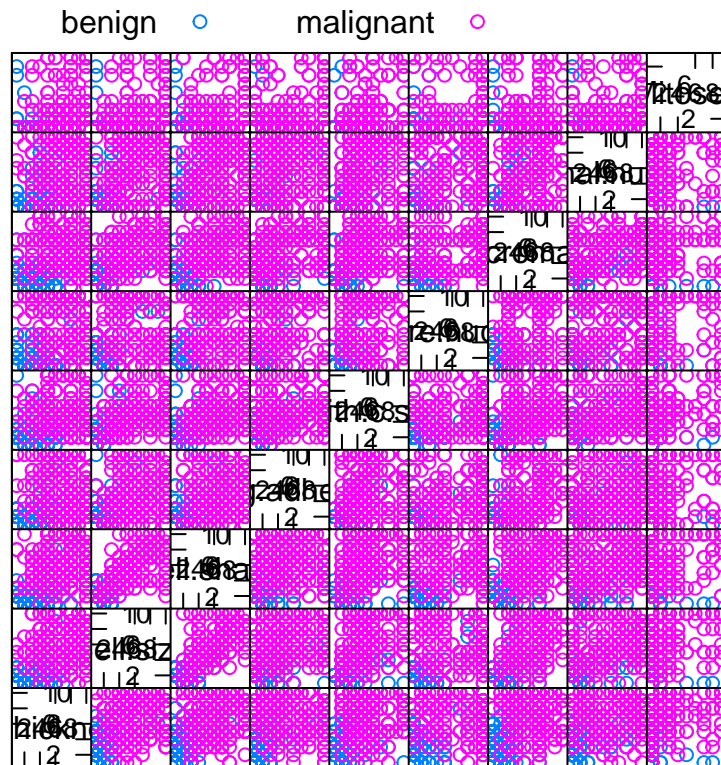
```
BreastCancer_num <- BreastCancer %>%
  mutate(Class = as.numeric(Class)-1) # numeric response
cor.plot(BreastCancer_num[,])
```

## Correlation plot



```
featurePlot(x=BreastCancer[,-10], y=BreastCancer[,10],
  plot="pairs",
  auto.key=list(columns=3))
```

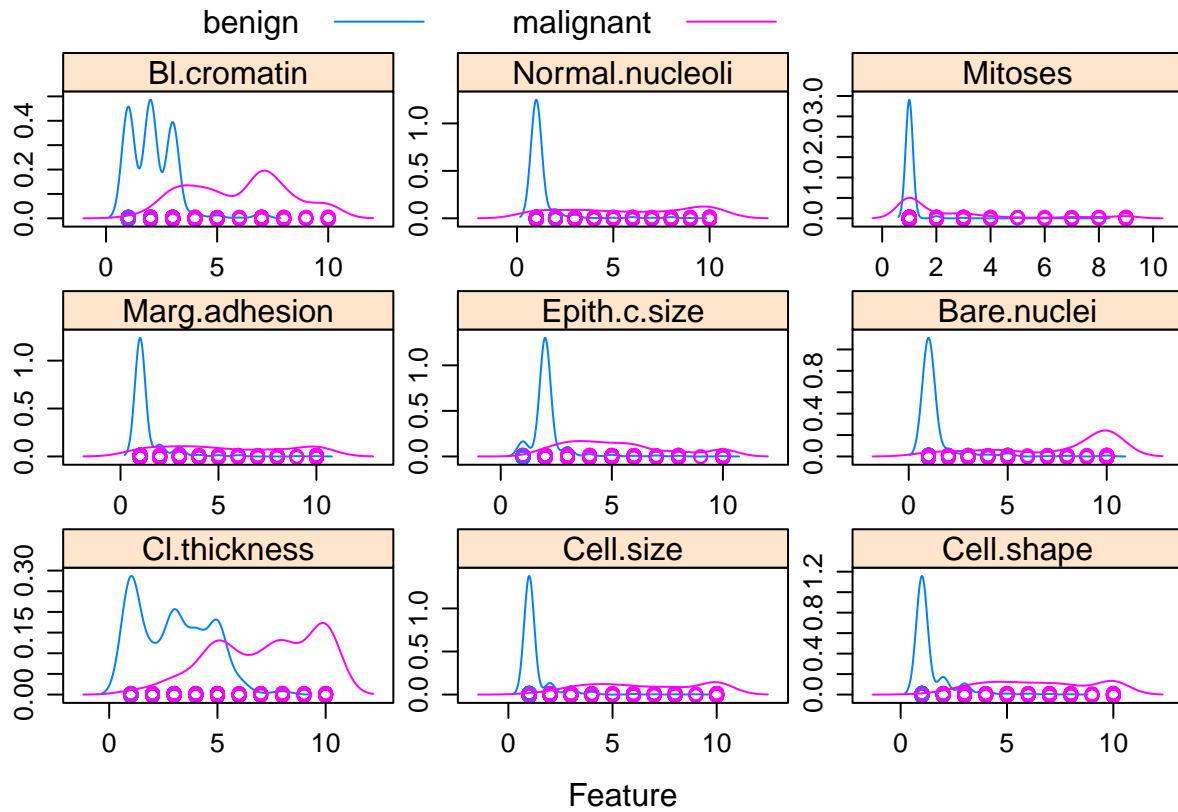
```
## Warning in draw.key(simpleKey(...), draw = FALSE): not enough rows for
## columns
```



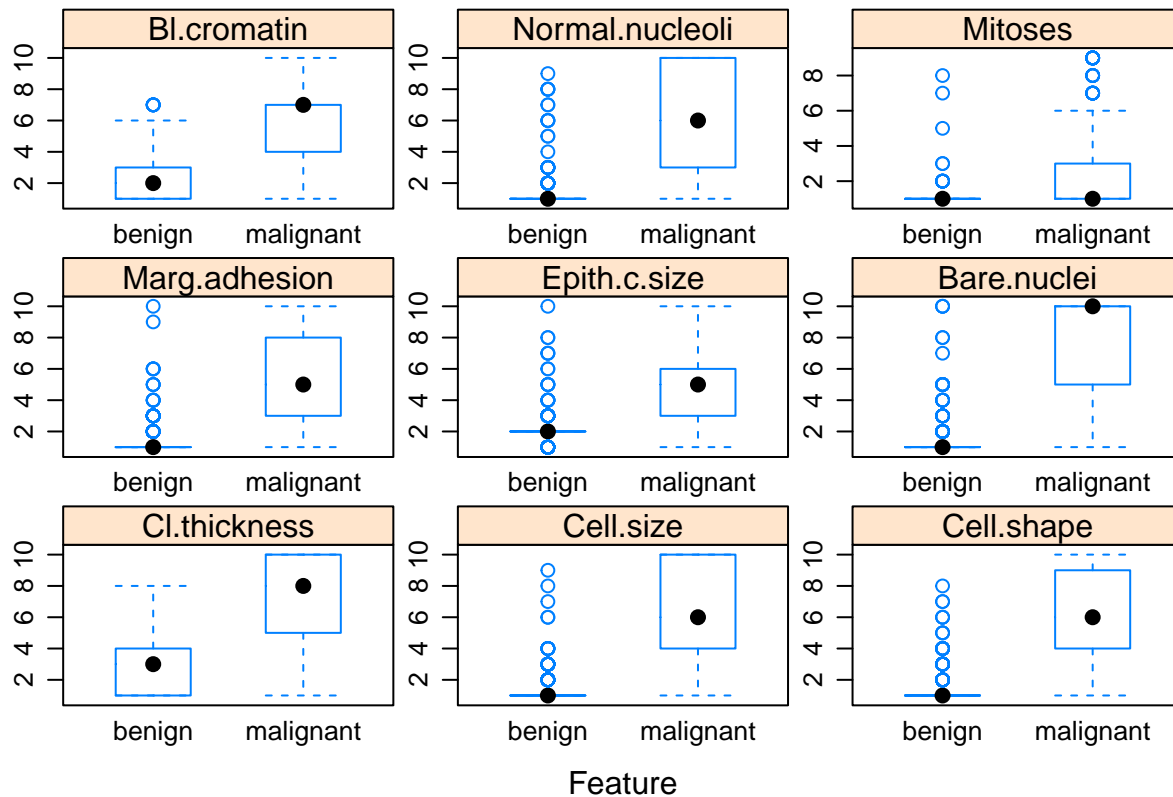
Scatter Plot Matrix

```
featurePlot(x=BreastCancer[,-10], y=BreastCancer[,10],
            plot="density",
            scales=list(x=list(relation="free"),
                        y=list(relation="free")),
            auto.key=list(columns=3),
            layout=c(3,3))
```

```
## Warning in draw.key(simpleKey(...), draw = FALSE): not enough rows for
## columns
```



```
featurePlot(x=BreastCancer[, -10], y=BreastCancer[, 10],
            plot="box",
            scales=list(x=list(relation="free"),
                        y=list(relation="free")),
            auto.key=list(columns=3),
            layout=c(3,3))
```



```
glm1 = glm(Class ~ ., data=BreastCancer_num,family=binomial)
```

```
summary(glm1)
```

```
##
## Call:
## glm(formula = Class ~ ., family = binomial, data = BreastCancer_num)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4855  -0.1152  -0.0619   0.0222   2.4702
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -10.11096   1.173774  -8.613  < 2e-16 ***
## Cl.thickness    0.535256   0.141938   3.771  0.000163 ***
## Cell.size     -0.005943   0.209158  -0.028  0.977332
## Cell.shape     0.322136   0.230644   1.397  0.162510
## Marg.adhesion  0.330694   0.123462   2.679  0.007395 **
## Epith.c.size   0.096797   0.156568   0.618  0.536415
## Bare.nuclei    0.383015   0.093865   4.080  4.49e-05 ***
## Bl.cromatin    0.447401   0.171392   2.610  0.009044 **
## Normal.nucleoli 0.213074   0.112894   1.887  0.059109 .
## Mitoses       0.538551   0.325615   1.654  0.098138 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
```



```
## Null deviance: 884.35 on 682 degrees of freedom
## Residual deviance: 102.90 on 673 degrees of freedom
## (16 observations deleted due to missingness)
## AIC: 122.9
##
## Number of Fisher Scoring iterations: 8
```

At  $\alpha = 0.05$  the following appear significant :

Cl.thickness Marg.adhesion Bare.nuclei Bl.cromatin

```
glm2 = glm(Class ~ Cl.thickness + Marg.adhesion +
            Bare.nuclei + Bl.cromatin,
            data=BreastCancer_num,family=binomial)
```

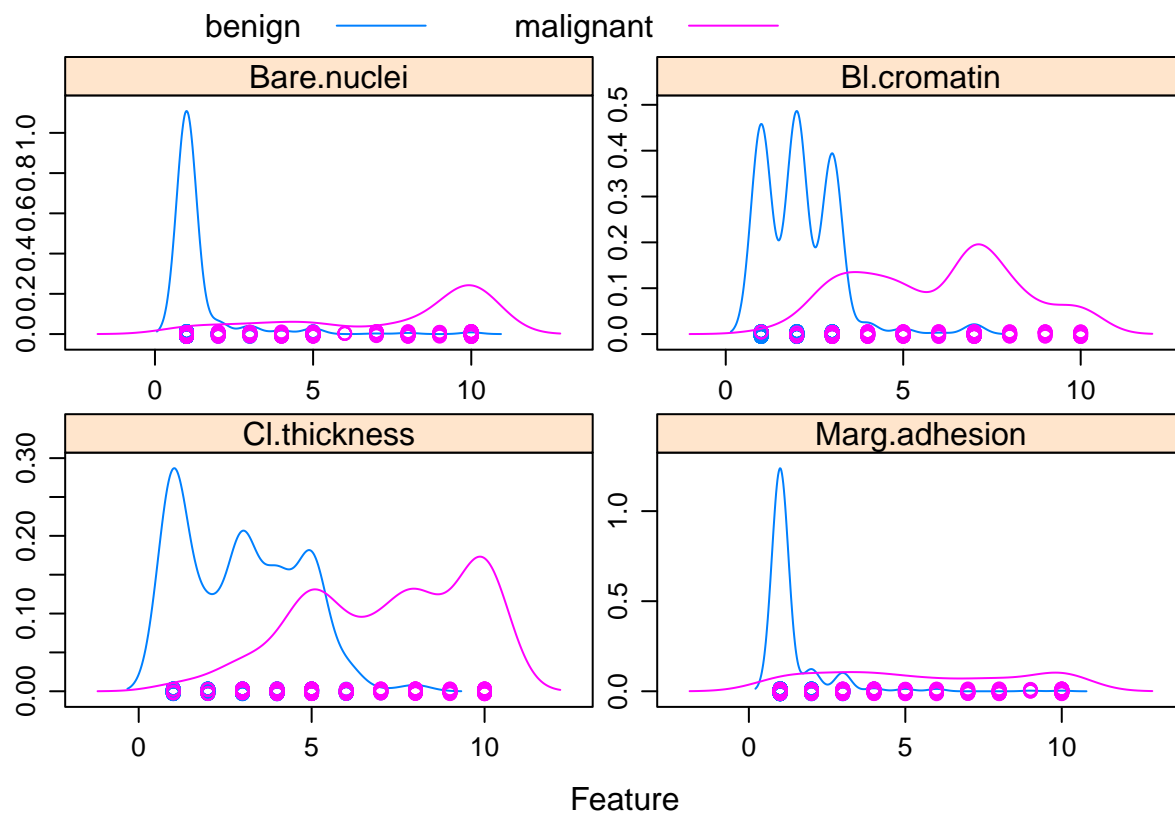
```
summary(glm2)
```

```
##
## Call:
## glm(formula = Class ~ Cl.thickness + Marg.adhesion + Bare.nuclei +
##      Bl.cromatin, family = binomial, data = BreastCancer_num)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.6964  -0.1451  -0.0609   0.0232   2.4476
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -10.11370    1.03264  -9.794 < 2e-16 ***
## Cl.thickness    0.81166    0.12585   6.450 1.12e-10 ***
## Marg.adhesion   0.43412    0.11403   3.807 0.000141 ***
## Bare.nuclei     0.48136    0.08816   5.460 4.76e-08 ***
## Bl.cromatin     0.70154    0.15196   4.616 3.90e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 884.35 on 682 degrees of freedom
## Residual deviance: 125.77 on 678 degrees of freedom
## (16 observations deleted due to missingness)
## AIC: 135.77
##
## Number of Fisher Scoring iterations: 8
```

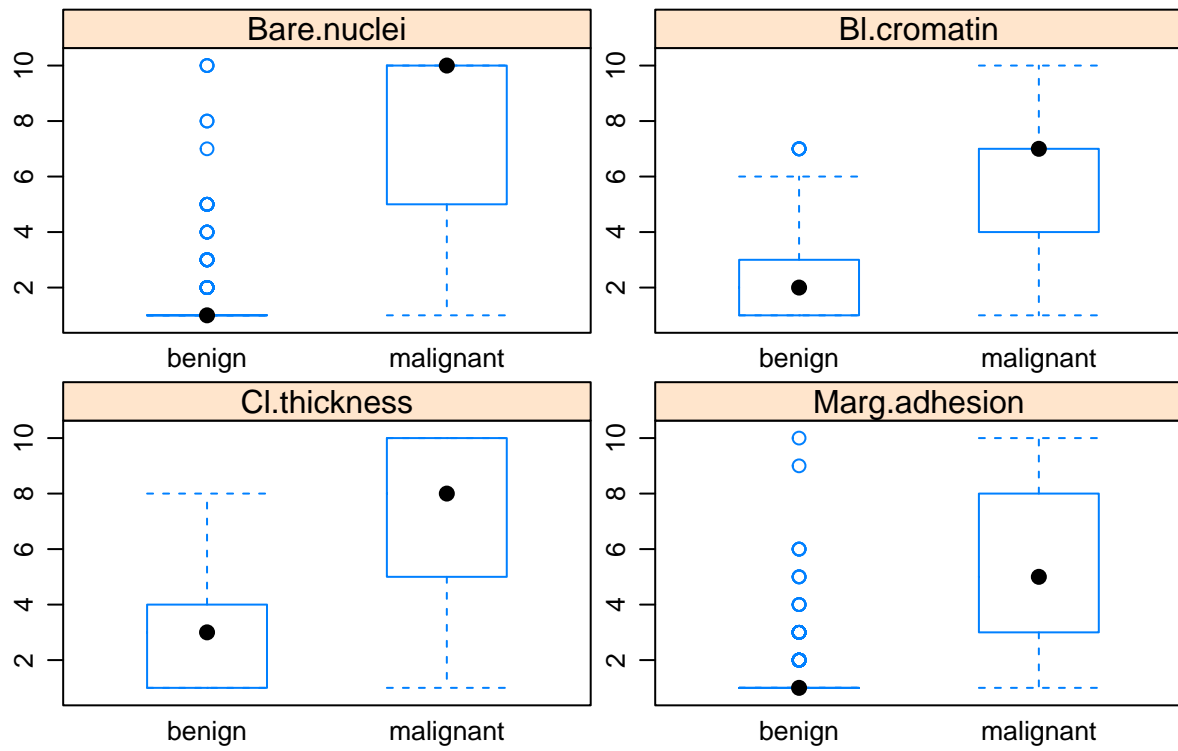
```
library(caret)
```

```
featurePlot(x=BreastCancer[,c(1,4,6,7)], y=BreastCancer[,10],
            plot="density",
            scales=list(x=list(relation="free"),
                          y=list(relation="free")),
            auto.key=list(columns=3))
```

```
## Warning in draw.key(simpleKey(...), draw = FALSE): not enough rows for
## columns
```



```
featurePlot(x=BreastCancer[,c(1,4,6,7)], y=BreastCancer[,10],
  plot="box",
  scales=list(x=list(relation="free"),
    y=list(relation="free")),
  auto.key=list(columns=3))
```



Feature