Data624 - Homework4

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Contents


```r
library(mlbench)
library(DataExplorer)
library(GGally)
library(psych)
library(caret)
library(summarytools)
library(naniar)
```

3.1

The UC Irvine Machine Learning Repository6 contains a data set related to glass identification. The data consist of 214 glass samples labeled as one of seven class categories. There are nine predictors, including the refractive index and percentages of eight elements: Na, Mg, Al, Si, K, Ca, Ba, and Fe.

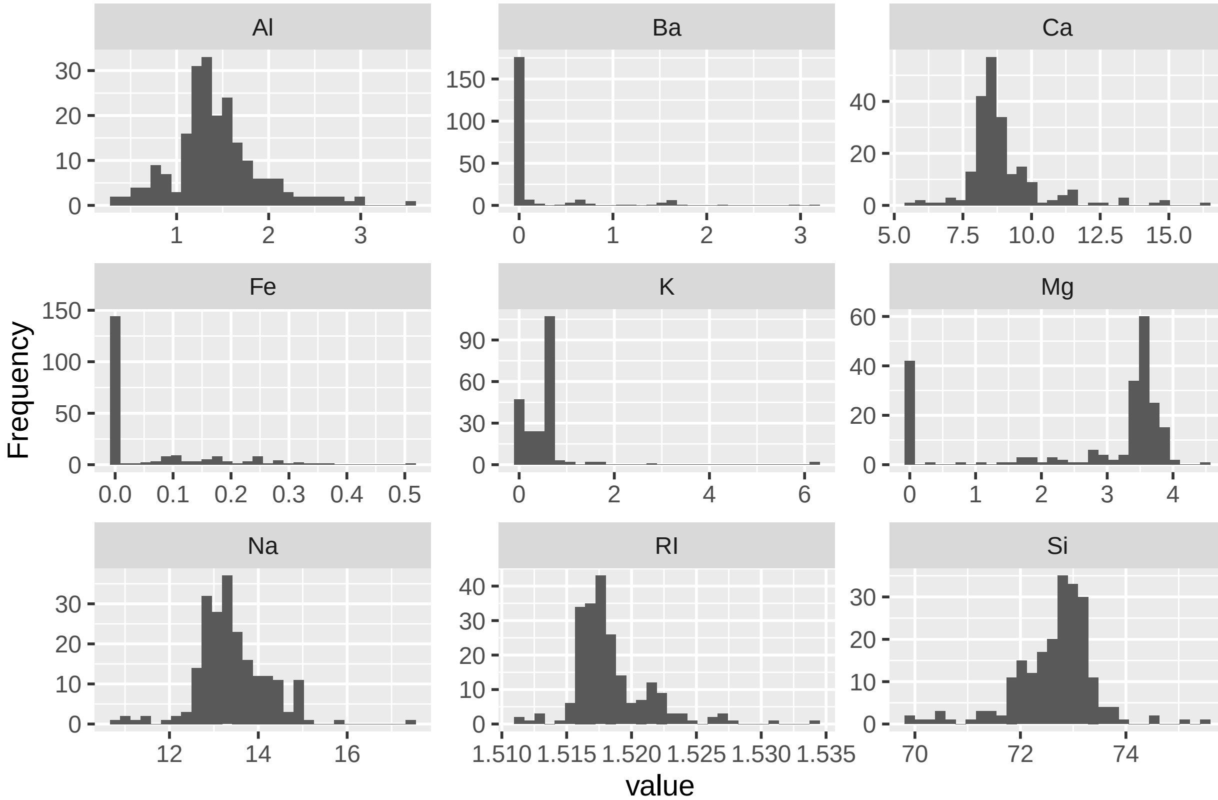
The data can be accessed via:

```r
data(Glass)
str(Glass)
```

```
## 'data.frame':    214 obs. of  10 variables:
##  $ RI  : num  1.52 1.52 1.52 1.52 1.52 ...
##  $ Na  : num  13.6 13.9 13.5 13.2 13.3 ...
##  $ Mg  : num  4.49 3.6 3.55 3.69 3.62 3.61 3.6 3.61 3.58 3.6 ...
##  $ Al  : num  1.1 1.36 1.54 1.29 1.24 1.62 1.14 1.05 1.37 1.36 ...
##  $ Si  : num  71.8 72.7 73 72.6 73.1 ...
##  $ K   : num  0.06 0.48 0.39 0.57 0.55 0.64 0.58 0.57 0.56 0.57 ...
##  $ Ca  : num  8.75 7.83 7.78 8.22 8.07 8.07 8.17 8.24 8.3 8.4 ...
##  $ Ba  : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Fe  : num  0 0 0 0 0 0.26 0 0 0 0.11 ...
##  $ Type: Factor w/ 6 levels "1","2","3","5",..: 1 1 1 1 1 1 1 1 1 1 ...
```

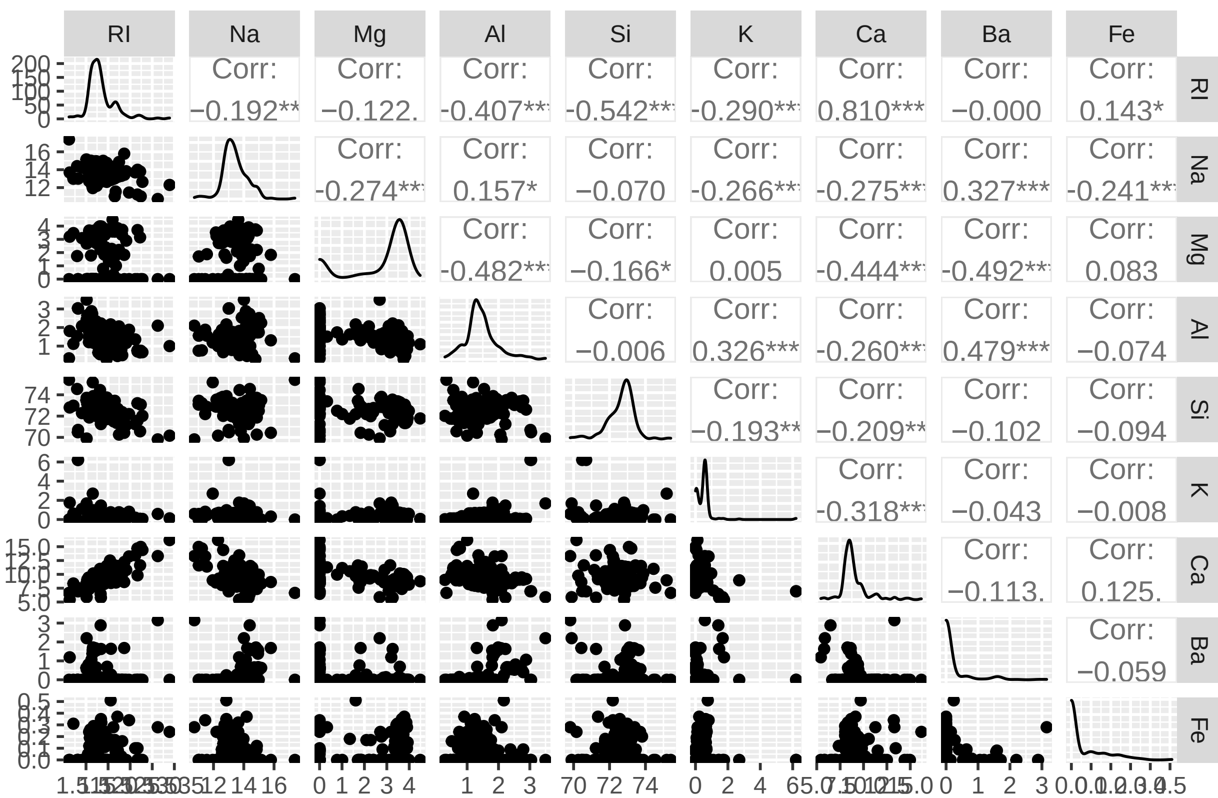
(a) Using visualizations, explore the predictor variables to understand their distributions as well as the relationships between predictors.

```r
# predictors distribution
plot_histogram(Glass,
               geom_histogram_args = list(bins = 30L),
               nrow = 3L,
               ncol = 3L)
```

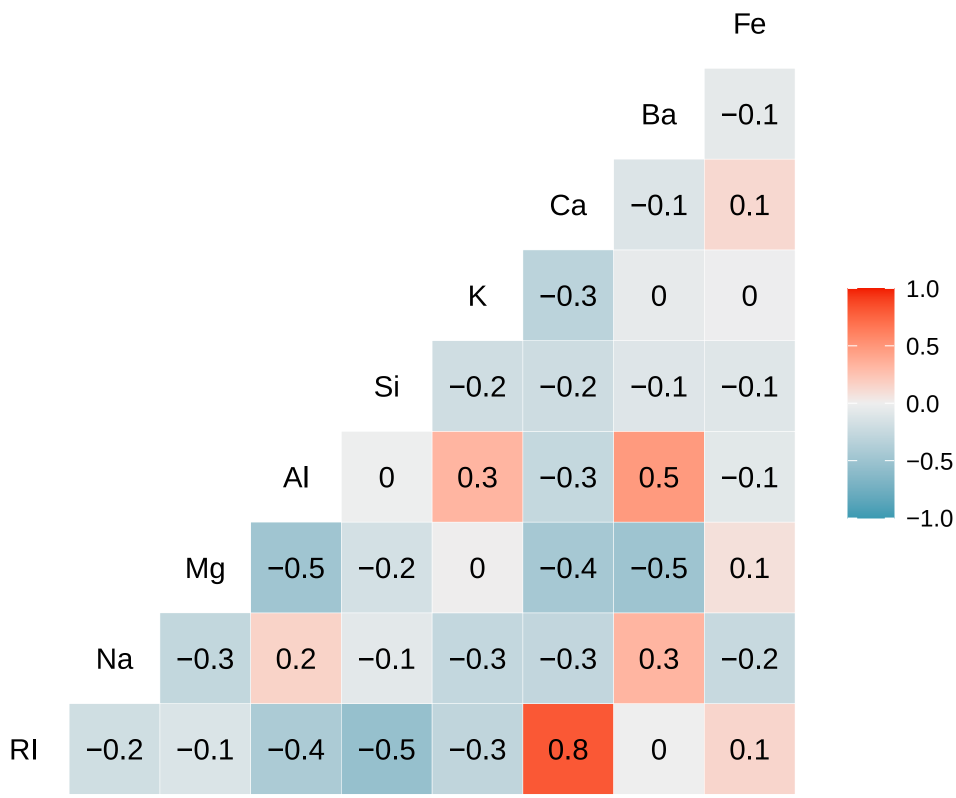



```r
# scatterplot matrix
Glass %>%
  dplyr::select(-Type) %>%
  ggpairs(title = "Paiwise scatter plots") %>%
  print(progress = F)
```

Paiwise scatter plots




```r
# correlation
Glass %>%
  dplyr::select(-Type) %>%
  ggcorr(label = TRUE)
```



(b) Do there appear to be any outliers in the data? Are any predictors skewed?

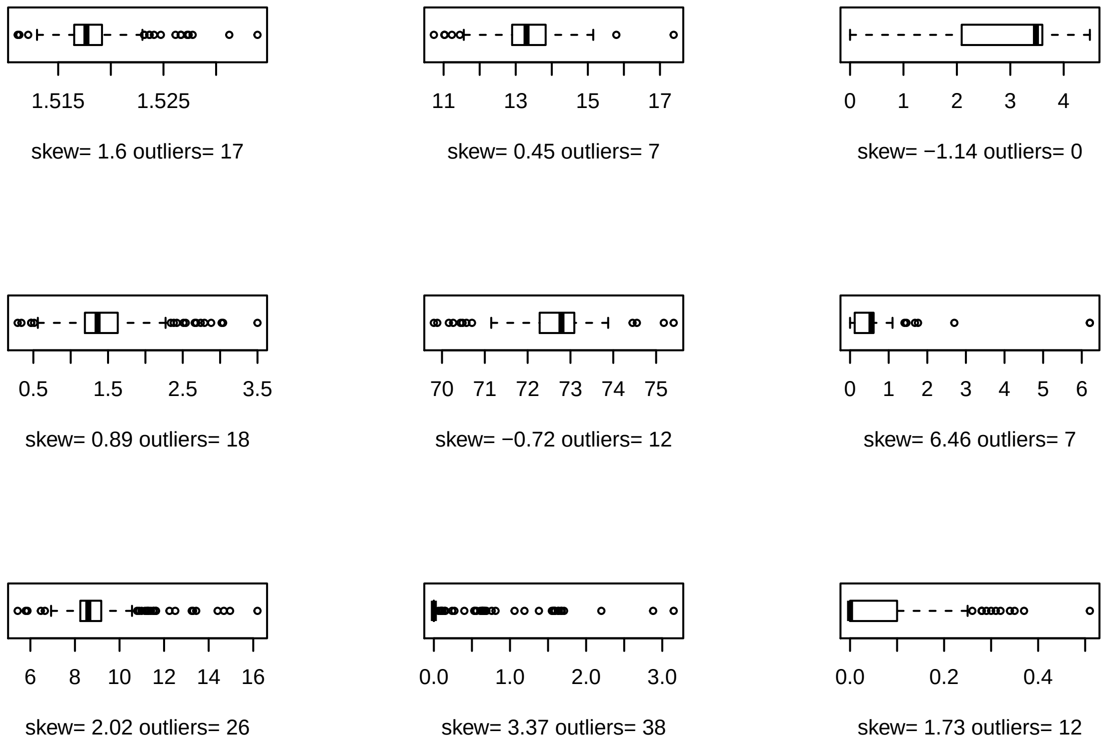
```r
describe(Glass)
```

```
##       vars   n  mean   sd median trimmed  mad   min   max range  skew kurtosis
## RI       1 214  1.52 0.00   1.52    1.52 0.00  1.51  1.53  0.02  1.60     4.72
## Na       2 214 13.41 0.82  13.30   13.38 0.64 10.73 17.38  6.65  0.45     2.90
## Mg       3 214  2.68 1.44   3.48    2.87 0.30  0.00  4.49  4.49 -1.14    -0.45
## Al       4 214  1.44 0.50   1.36    1.41 0.31  0.29  3.50  3.21  0.89     1.94
## Si       5 214 72.65 0.77  72.79   72.71 0.57 69.81 75.41  5.60 -0.72     2.82
## K        6 214  0.50 0.65   0.56    0.43 0.17  0.00  6.21  6.21  6.46    52.87
## Ca       7 214  8.96 1.42   8.60    8.74 0.66  5.43 16.19 10.76  2.02     6.41
## Ba       8 214  0.18 0.50   0.00    0.03 0.00  0.00  3.15  3.15  3.37    12.08
## Fe       9 214  0.06 0.10   0.00    0.04 0.00  0.00  0.51  0.51  1.73     2.52
## Type*   10 214  2.54 1.71   2.00    2.31 1.48  1.00  6.00  5.00  1.04    -0.29
##         se
## RI    0.00
## Na    0.06
## Mg    0.10
## Al    0.03
## Si    0.05
## K     0.04
## Ca    0.10
## Ba    0.03
## Fe    0.01
## Type* 0.12
```

```r
# function to get skewness and number of outliers
label <- function(var) {
  return( paste("skew=" , round(describe(var)$skew,2) , "outliers=" , length(boxplot(var, plot=FALSE)$ou
```

```
}

par(mfrow=c(3,3))
for (i in 1:9){
  boxplot(
    Glass[i], color='green', horizontal = T,
    xlab = label(Glass[i])
    )
}
```



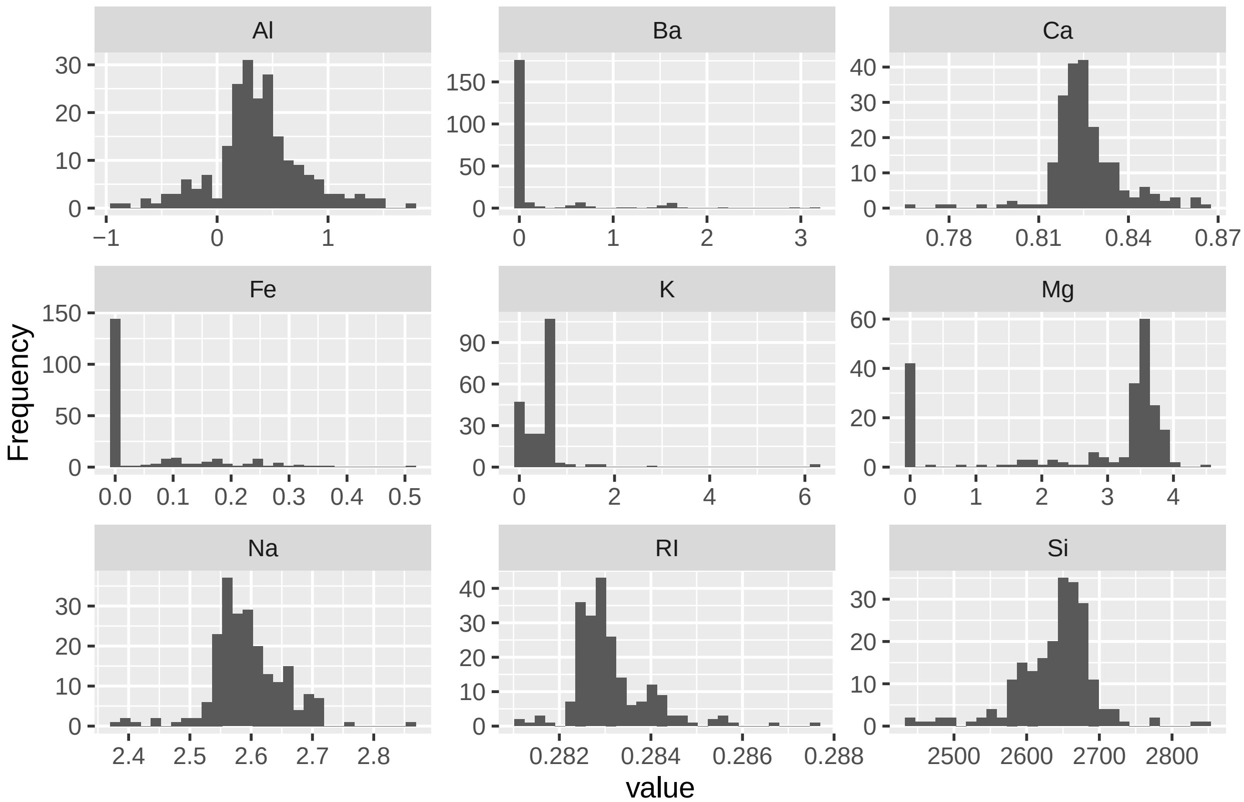
(c) Are there any relevant transformations of one or more predictors that might improve the classification model?

```
glass_boxcox_t <- preProcess(Glass, method = c("BoxCox"))
glass_boxcox_t
```

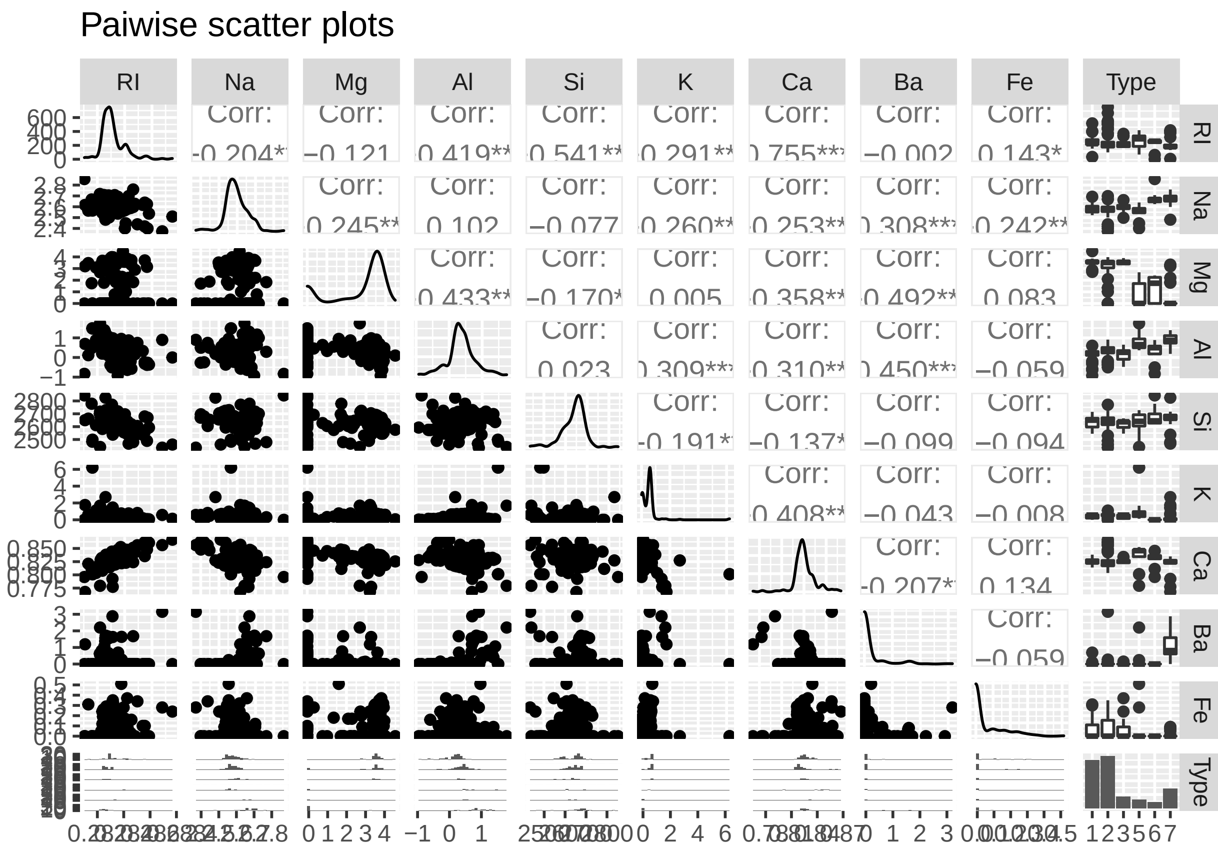
```
## Created from 214 samples and 6 variables
##
## Pre-processing:
##   - Box-Cox transformation (5)
##   - ignored (1)
##
## Lambda estimates for Box-Cox transformation:
## -2, -0.1, 0.5, 2, -1.1
```

```
trans_boxcox <- predict(glass_boxcox_t, Glass)
```

```
plot_histogram(trans_boxcox,
               geom_histogram_args = list(bins = 30L),
               nrow = 3L,
               ncol = 3L)
```




```
# scatterplot matrix
trans_boxcox %>%
  #dplyr::select(-Type) %>%
  ggpairs(title = "Paiwise scatter plots") %>%
  print(progress = F)
```

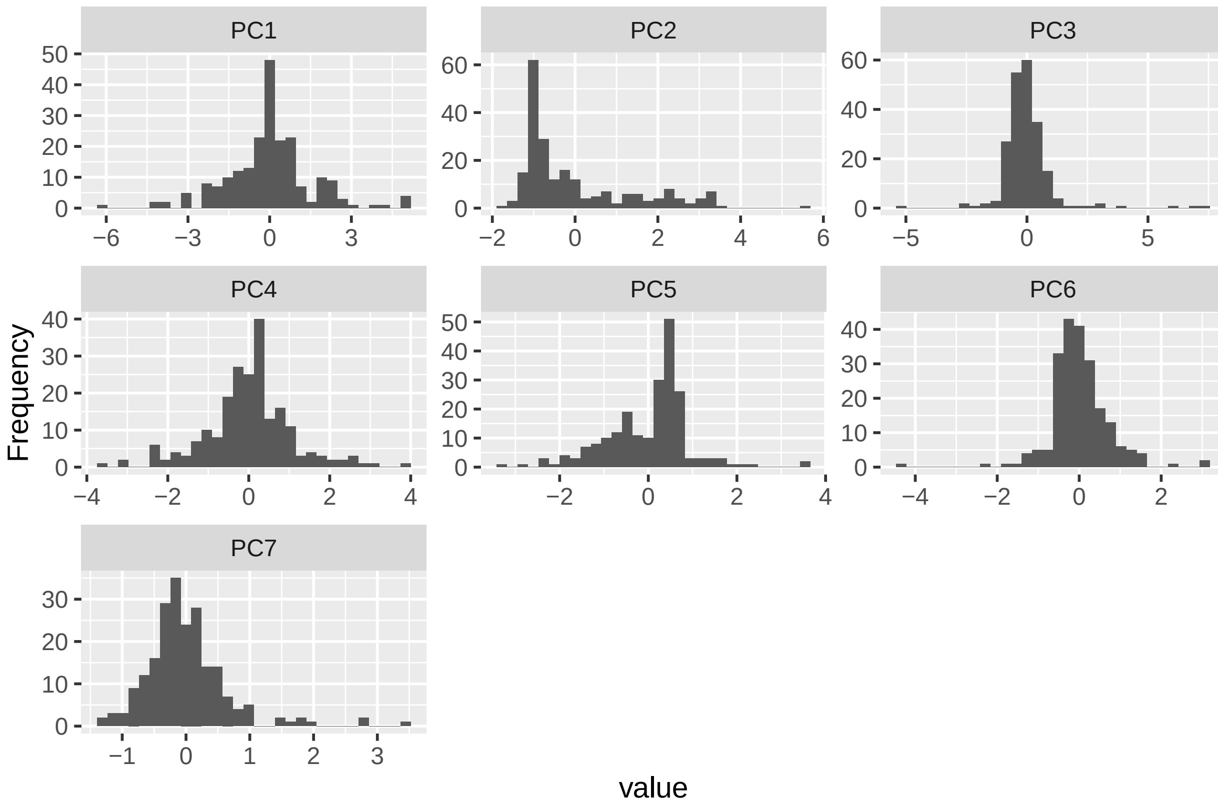



```r
glass_bcpca_t <- preProcess(Glass, method = c("BoxCox", "pca"))
glass_bcpca_t
```

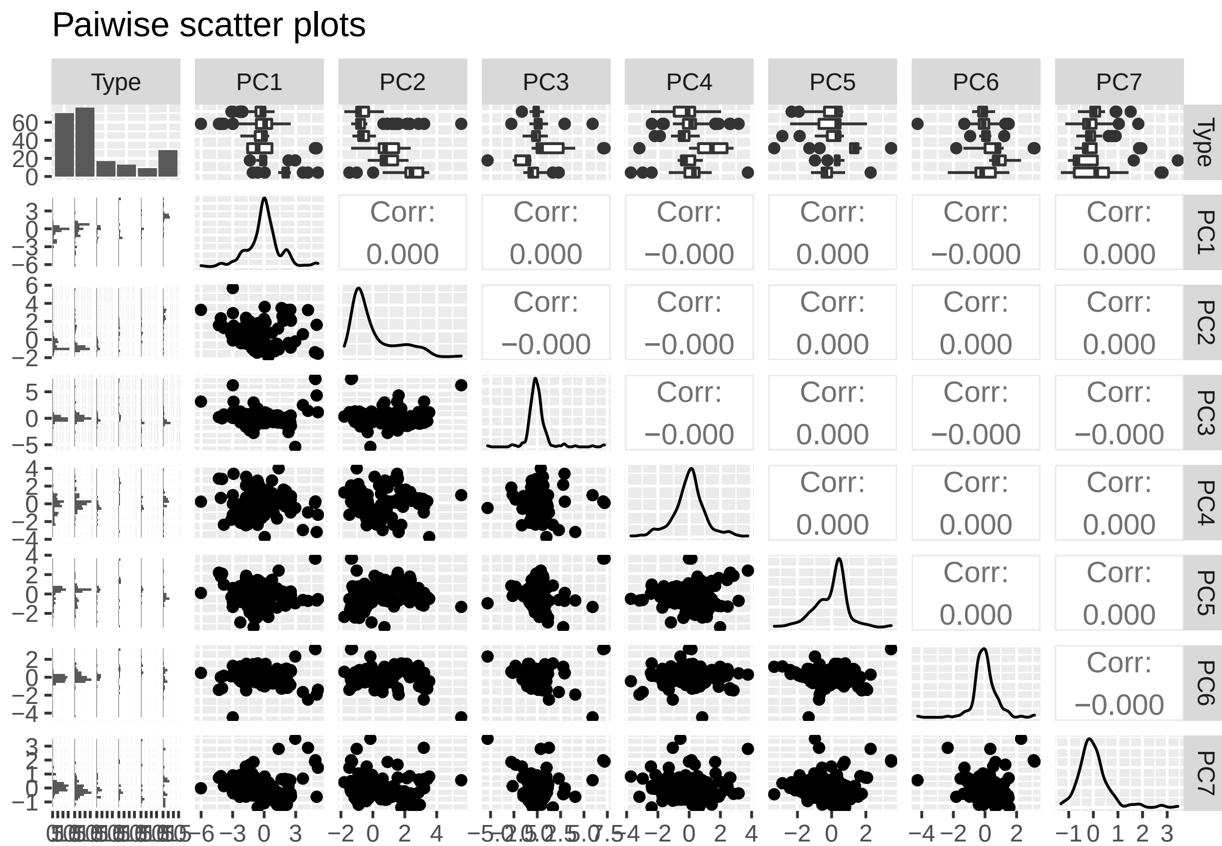
```
## Created from 214 samples and 10 variables
##
## Pre-processing:
##   - Box-Cox transformation (5)
##   - centered (9)
##   - ignored (1)
##   - principal component signal extraction (9)
##   - scaled (9)
##
## Lambda estimates for Box-Cox transformation:
## -2, -0.1, 0.5, 2, -1.1
## PCA needed 7 components to capture 95 percent of the variance
```

```r
trans_bcpca <- predict(glass_bcpca_t, Glass)
```

```r
plot_histogram(trans_bcpca,
               geom_histogram_args = list(bins = 30L),
               nrow = 3L,
               ncol = 3L)
```




```
# scatterplot matrix
trans_bcpca %>%
  #dplyr::select(-Type) %>%
  ggpairs(title = "Paiwise scatter plots") %>%
  print(progress = F)
```



3.2

The soybean data can also be found at the UC Irvine Machine Learning Repository. Data were collected to predict disease in 683 soybeans. The 35 predictors are mostly categorical and include information on the environmental conditions (e.g., temperature, precipitation) and plant conditions (e.g., left spots, mold growth). The outcome labels consist of 19 distinct classes.

The data can be loaded via:

```r
data(Soybean)
str(Soybean)
```

```
## 'data.frame':    683 obs. of  36 variables:
##  $ Class          : Factor w/ 19 levels "2-4-d-injury",..: 11 11 11 11 11 11 11 11 11 11 ...
##  $ date           : Factor w/ 7 levels "0","1","2","3",..: 7 5 4 4 7 6 6 5 7 5 ...
##  $ plant.stand    : Ord.factor w/ 2 levels "0"<"1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ precip         : Ord.factor w/ 3 levels "0"<"1"<"2": 3 3 3 3 3 3 3 3 3 3 ...
##  $ temp           : Ord.factor w/ 3 levels "0"<"1"<"2": 2 2 2 2 2 2 2 2 2 2 ...
##  $ hail           : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 2 1 1 ...
##  $ crop.hist      : Factor w/ 4 levels "0","1","2","3": 2 3 2 2 3 4 3 2 4 3 ...
##  $ area.dam       : Factor w/ 4 levels "0","1","2","3": 2 1 1 1 1 1 1 1 1 1 ...
##  $ sever          : Factor w/ 3 levels "0","1","2": 2 3 3 3 2 2 2 2 2 3 ...
##  $ seed.tmt       : Factor w/ 3 levels "0","1","2": 1 2 2 1 1 1 2 1 2 1 ...
##  $ germ           : Ord.factor w/ 3 levels "0"<"1"<"2": 1 2 3 2 3 2 1 3 2 3 ...
##  $ plant.growth   : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ leaves         : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ leaf.halo      : Factor w/ 3 levels "0","1","2": 1 1 1 1 1 1 1 1 1 1 ...
```

```
##  $ leaf.marg      : Factor w/ 3 levels "0","1","2": 3 3 3 3 3 3 3 3 3 3 ...
##  $ leaf.size      : Ord.factor w/ 3 levels "0"<"1"<"2": 3 3 3 3 3 3 3 3 3 3 ...
##  $ leaf.shread    : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ leaf.malf      : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ leaf.mild      : Factor w/ 3 levels "0","1","2": 1 1 1 1 1 1 1 1 1 1 ...
##  $ stem           : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ lodging        : Factor w/ 2 levels "0","1": 2 1 1 1 1 1 2 1 1 1 ...
##  $ stem.cankers   : Factor w/ 4 levels "0","1","2","3": 4 4 4 4 4 4 4 4 4 4 ...
##  $ canker.lesion  : Factor w/ 4 levels "0","1","2","3": 2 2 1 1 2 1 2 2 2 2 ...
##  $ fruiting.bodies: Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 2 ...
##  $ ext.decay      : Factor w/ 3 levels "0","1","2": 2 2 2 2 2 2 2 2 2 2 ...
##  $ mycelium       : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ int.discolor   : Factor w/ 3 levels "0","1","2": 1 1 1 1 1 1 1 1 1 1 ...
##  $ sclerotia      : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ fruit.pods     : Factor w/ 4 levels "0","1","2","3": 1 1 1 1 1 1 1 1 1 1 ...
##  $ fruit.spots    : Factor w/ 4 levels "0","1","2","4": 4 4 4 4 4 4 4 4 4 4 ...
##  $ seed           : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ mold.growth    : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ seed.discolor  : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ seed.size      : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ shriveling     : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ roots          : Factor w/ 3 levels "0","1","2": 1 1 1 1 1 1 1 1 1 1 ...
```

(a) Investigate the frequency distributions for the categorical predictors. Are any of the distributions degenerate in the ways discussed earlier in this chapter?

```r
dfSummary(Soybean, graph.col = F)
```

```
## Data Frame Summary
## Soybean
## Dimensions: 683 x 36
## Duplicates: 52
##
## -----------------------------------------------------------------------------------------------------
## No   Variable            Stats / Values                   Freqs (% of Valid)   Valid      Missing
## ---- ------------------- -------------------------------- -------------------- ---------- ----------
## 1    Class               1. 2-4-d-injury                   16 ( 2.3%)          683        0
##      [factor]            2. alternarialeaf-spot            91 (13.3%)          (100.0%)   (0.0%)
##                          3. anthracnose                    44 ( 6.4%)
##                          4. bacterial-blight               20 ( 2.9%)
##                          5. bacterial-pustule              20 ( 2.9%)
##                          6. brown-spot                     92 (13.5%)
##                          7. brown-stem-rot                 44 ( 6.4%)
##                          8. charcoal-rot                   20 ( 2.9%)
##                          9. cyst-nematode                  14 ( 2.0%)
##                          10. diaporthe-pod-&-stem-blig     15 ( 2.2%)
##                          [ 9 others ]                     307 (44.9%)
##
## 2    date                1. 0                              26 ( 3.8%)          682        1
##      [factor]            2. 1                              75 (11.0%)          (99.9%)    (0.1%)
##                          3. 2                              93 (13.6%)
##                          4. 3                             118 (17.3%)
##                          5. 4                             131 (19.2%)
##                          6. 5                             149 (21.8%)
##                          7. 6                              90 (13.2%)
```

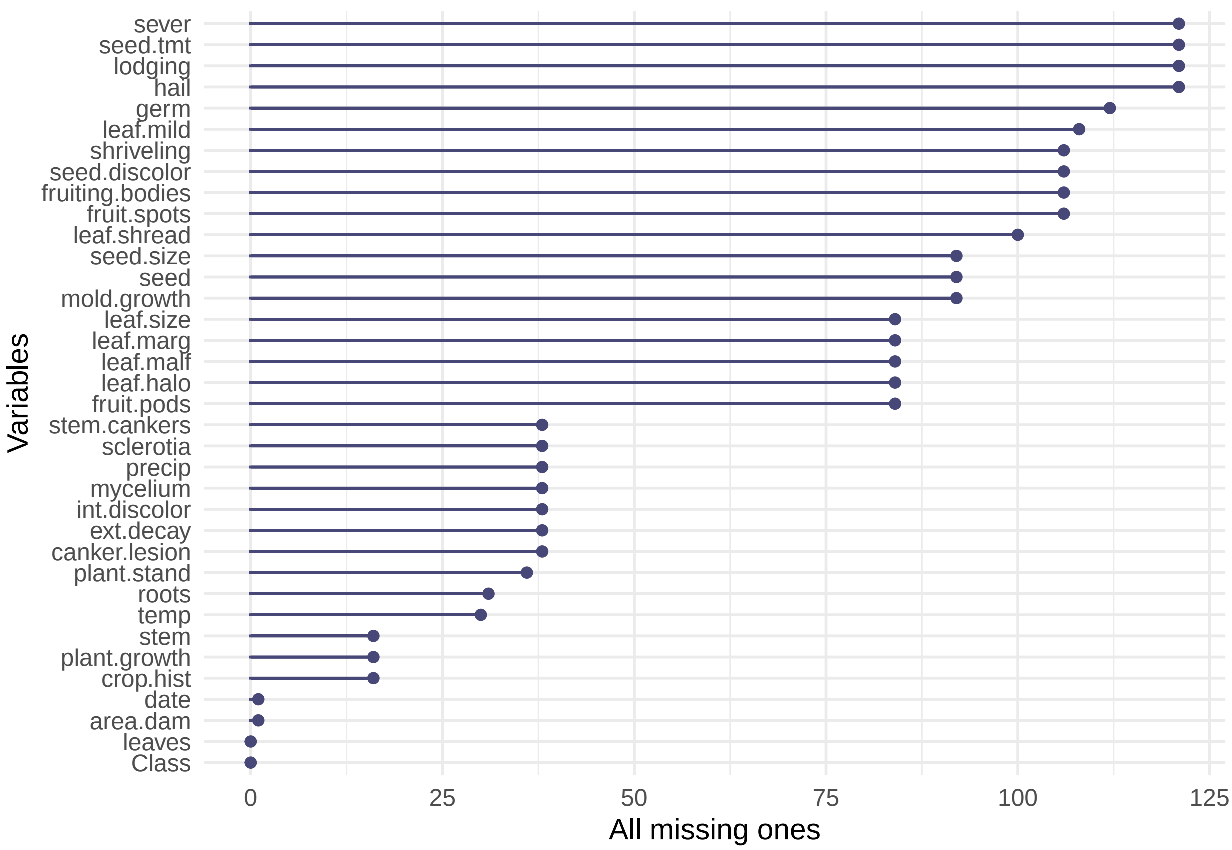
```
##
## 3    plant.stand         1. 0                              354 (54.7%)          647        36
##      [ordered, factor]   2. 1                              293 (45.3%)          (94.7%)    (5.3%)
##
## 4    precip              1. 0                               74 (11.5%)          645        38
##      [ordered, factor]   2. 1                              112 (17.4%)          (94.4%)    (5.6%)
##                          3. 2                              459 (71.2%)
##
## 5    temp                1. 0                               80 (12.3%)          653        30
##      [ordered, factor]   2. 1                              374 (57.3%)          (95.6%)    (4.4%)
##                          3. 2                              199 (30.5%)
##
## 6    hail                1. 0                              435 (77.4%)          562        121
##      [factor]            2. 1                              127 (22.6%)          (82.3%)    (17.7%)
##
## 7    crop.hist           1. 0                               65 ( 9.7%)          667        16
##      [factor]            2. 1                              165 (24.7%)          (97.7%)    (2.3%)
##                          3. 2                              219 (32.8%)
##                          4. 3                              218 (32.7%)
##
## 8    area.dam            1. 0                              123 (18.0%)          682        1
##      [factor]            2. 1                              227 (33.3%)          (99.9%)    (0.1%)
##                          3. 2                              145 (21.3%)
##                          4. 3                              187 (27.4%)
##
## 9    sever               1. 0                              195 (34.7%)          562        121
##      [factor]            2. 1                              322 (57.3%)          (82.3%)    (17.7%)
##                          3. 2                               45 ( 8.0%)
##
## 10   seed.tmt            1. 0                              305 (54.3%)          562        121
##      [factor]            2. 1                              222 (39.5%)          (82.3%)    (17.7%)
##                          3. 2                               35 ( 6.2%)
##
## 11   germ                1. 0                              165 (28.9%)          571        112
##      [ordered, factor]   2. 1                              213 (37.3%)          (83.6%)    (16.4%)
##                          3. 2                              193 (33.8%)
##
## 12   plant.growth        1. 0                              441 (66.1%)          667        16
##      [factor]            2. 1                              226 (33.9%)          (97.7%)    (2.3%)
##
## 13   leaves              1. 0                               77 (11.3%)          683        0
##      [factor]            2. 1                              606 (88.7%)          (100.0%)   (0.0%)
##
## 14   leaf.halo           1. 0                              221 (36.9%)          599        84
##      [factor]            2. 1                               36 ( 6.0%)          (87.7%)    (12.3%)
##                          3. 2                              342 (57.1%)
##
## 15   leaf.marg           1. 0                              357 (59.6%)          599        84
##      [factor]            2. 1                               21 ( 3.5%)          (87.7%)    (12.3%)
##                          3. 2                              221 (36.9%)
##
## 16   leaf.size           1. 0                               51 ( 8.5%)          599        84
##      [ordered, factor]   2. 1                              327 (54.6%)          (87.7%)    (12.3%)
##                          3. 2                              221 (36.9%)
```

```
##
## 17   leaf.shread        1. 0                             487 (83.5%)        583        100
##      [factor]           2. 1                              96 (16.5%)        (85.4%)    (14.6%)
##
## 18   leaf.malf          1. 0                             554 (92.5%)        599        84
##      [factor]           2. 1                              45 ( 7.5%)        (87.7%)    (12.3%)
##
## 19   leaf.mild          1. 0                             535 (93.0%)        575        108
##      [factor]           2. 1                              20 ( 3.5%)        (84.2%)    (15.8%)
##                         3. 2                              20 ( 3.5%)
##
## 20   stem               1. 0                             296 (44.4%)        667        16
##      [factor]           2. 1                             371 (55.6%)        (97.7%)    (2.3%)
##
## 21   lodging            1. 0                             520 (92.5%)        562        121
##      [factor]           2. 1                              42 ( 7.5%)        (82.3%)    (17.7%)
##
## 22   stem.cankers       1. 0                             379 (58.8%)        645        38
##      [factor]           2. 1                              39 ( 6.0%)        (94.4%)    (5.6%)
##                         3. 2                              36 ( 5.6%)
##                         4. 3                             191 (29.6%)
##
## 23   canker.lesion      1. 0                             320 (49.6%)        645        38
##      [factor]           2. 1                              83 (12.9%)        (94.4%)    (5.6%)
##                         3. 2                             177 (27.4%)
##                         4. 3                              65 (10.1%)
##
## 24   fruiting.bodies    1. 0                             473 (82.0%)        577        106
##      [factor]           2. 1                             104 (18.0%)        (84.5%)    (15.5%)
##
## 25   ext.decay          1. 0                             497 (77.1%)        645        38
##      [factor]           2. 1                             135 (20.9%)        (94.4%)    (5.6%)
##                         3. 2                              13 ( 2.0%)
##
## 26   mycelium           1. 0                             639 (99.1%)        645        38
##      [factor]           2. 1                               6 ( 0.9%)        (94.4%)    (5.6%)
##
## 27   int.discolor       1. 0                             581 (90.1%)        645        38
##      [factor]           2. 1                              44 ( 6.8%)        (94.4%)    (5.6%)
##                         3. 2                              20 ( 3.1%)
##
## 28   sclerotia          1. 0                             625 (96.9%)        645        38
##      [factor]           2. 1                              20 ( 3.1%)        (94.4%)    (5.6%)
##
## 29   fruit.pods         1. 0                             407 (67.9%)        599        84
##      [factor]           2. 1                             130 (21.7%)        (87.7%)    (12.3%)
##                         3. 2                              14 ( 2.3%)
##                         4. 3                              48 ( 8.0%)
##
## 30   fruit.spots        1. 0                             345 (59.8%)        577        106
##      [factor]           2. 1                              75 (13.0%)        (84.5%)    (15.5%)
##                         3. 2                              57 ( 9.9%)
##                         4. 4                             100 (17.3%)
##
```

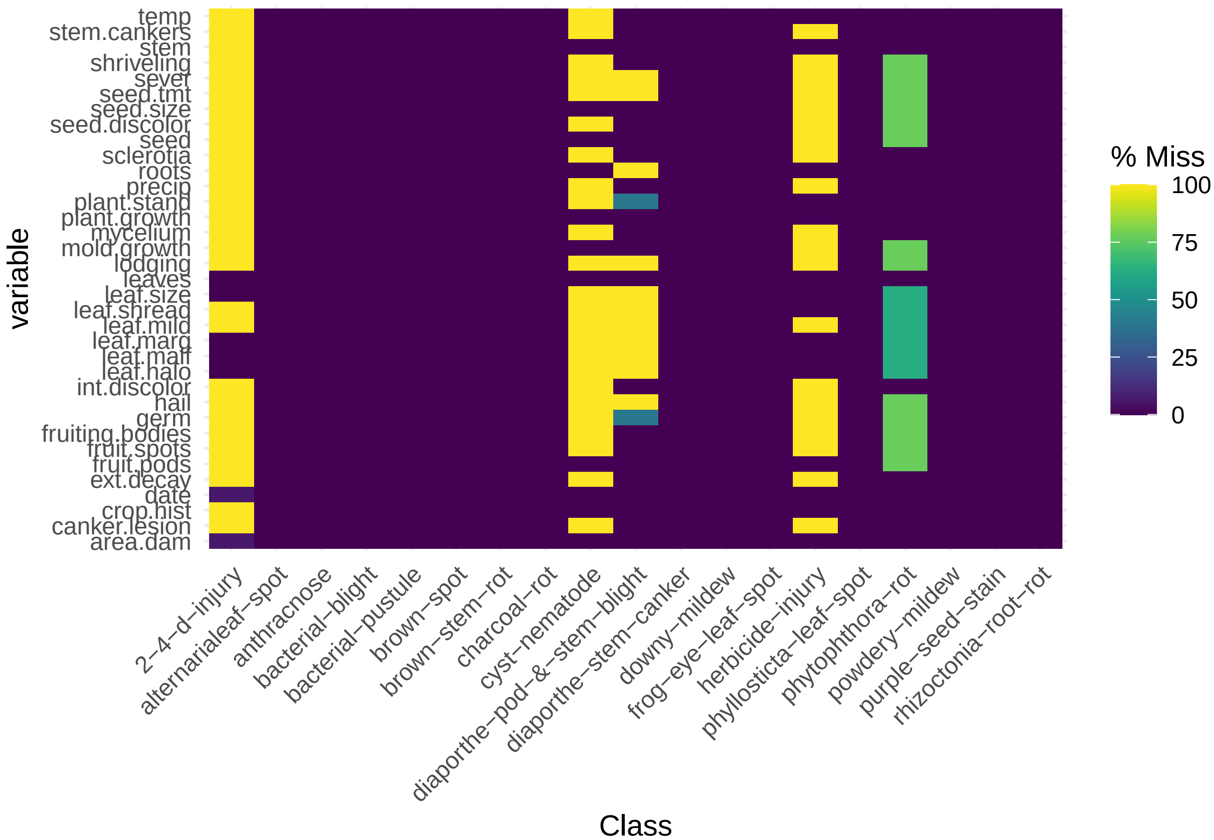
```
## 31    seed              1. 0          476 (80.5%)     591       92
##       [factor]          2. 1          115 (19.5%)     (86.5%)   (13.5%)
##
## 32    mold.growth       1. 0          524 (88.7%)     591       92
##       [factor]          2. 1           67 (11.3%)     (86.5%)   (13.5%)
##
## 33    seed.discolor     1. 0          513 (88.9%)     577       106
##       [factor]          2. 1           64 (11.1%)     (84.5%)   (15.5%)
##
## 34    seed.size         1. 0          532 (90.0%)     591       92
##       [factor]          2. 1           59 (10.0%)     (86.5%)   (13.5%)
##
## 35    shriveling        1. 0          539 (93.4%)     577       106
##       [factor]          2. 1           38 ( 6.6%)     (84.5%)   (15.5%)
##
## 36    roots             1. 0          551 (84.5%)     652       31
##       [factor]          2. 1           86 (13.2%)     (95.5%)   (4.5%)
##                         3. 2           15 ( 2.3%)
## ----------------------------------------------------------------------------------------------------
```

(b) Roughly 18% of the data are missing. Are there particular predictors that are more likely to be missing? Is the pattern of missing data related to the classes?

```r
gg_miss_var(Soybean) + labs(y = "All missing ones")
```




```r
gg_miss_fct(x=Soybean, fct=Class)
```



(c) Develop a strategy for handling missing data, either by eliminating predictors or imputation.