HW1

AUTHOR
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Problem 1 - Boston housing dataset

Import package and load Boston dataset

```r
library(MASS)
library(ggplot2)
library(dplyr)
library(tidyr)
library(corrplot)
library(epiDisplay)
library(mice)
library(caret)
library(dlookr)
```

```r
data(Boston)
```

Boston dataset data dictionary

```r
 ?Boston
```

```r
nrow(Boston)
```

```
[1] 506
```

```r
ncol(Boston)
```

```
[1] 14
```

1a) How many rows are in this Boston data set? How many columns? What do the rows and columns represent?

Rows: 506
Columns: 14
Column descriptions:
  crim - per capita crime rate by town.
  zn - proportion of residential land zoned for lots over 25,000 sq.ft.
  indus - proportion of non-retail business acres per town.
  chas - Charles River dummy variable (= 1 if tract bounds river; 0 otherwise).
  nox - nitrogen oxides concentration (parts per 10 million).
  rm - average number of rooms per dwelling.
  age - proportion of owner-occupied units built prior to 1940.

dis - weighted mean of distances to five Boston employment centres.

rad - index of accessibility to radial highways.

tax - full-value property-tax rate per $10,000.

ptratio - pupil-teacher ratio by town.

black - 1000(Bk−0.63)² Bk is the proportion of blacks by town.

lstat - lower status of the population (percent).

medv - median value of owner-occupied homes in $1000s.

1b) Make some pairwise scatterplots of the predictors (columns) in this data set. Describe your findings.

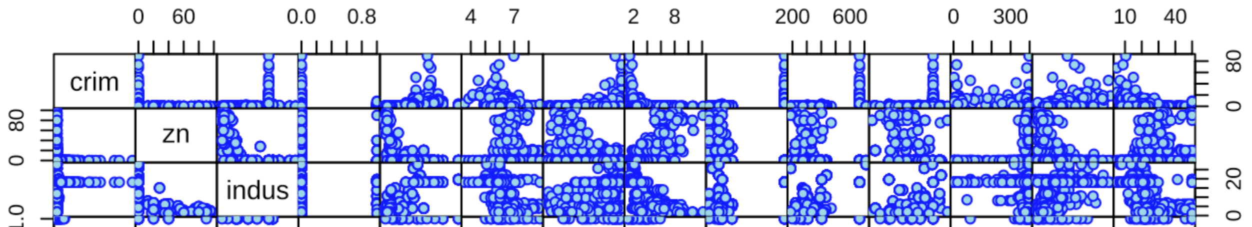
```
str(Boston)
```

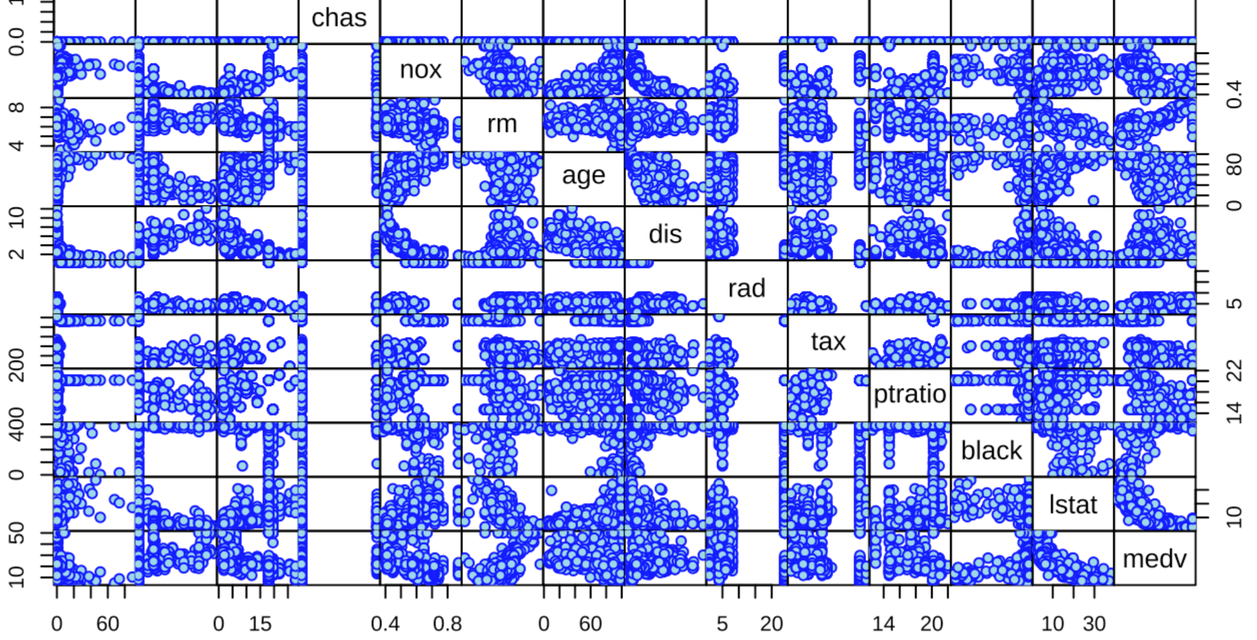
```
'data.frame':	506 obs. of  14 variables:
 $ crim   : num  0.00632 0.02731 0.02729 0.03237 0.06905 ...
 $ zn     : num  18 0 0 0 0 0 12.5 12.5 12.5 12.5 ...
 $ indus  : num  2.31 7.07 7.07 2.18 2.18 2.18 7.87 7.87 7.87 7.87 ...
 $ chas   : int  0 0 0 0 0 0 0 0 0 0 ...
 $ nox    : num  0.538 0.469 0.469 0.458 0.458 0.458 0.524 0.524 0.524 0.524 ...
 $ rm     : num  6.58 6.42 7.18 7 7.15 ...
 $ age    : num  65.2 78.9 61.1 45.8 54.2 58.7 66.6 96.1 100 85.9 ...
 $ dis    : num  4.09 4.97 4.97 6.06 6.06 ...
 $ rad    : int  1 2 2 3 3 3 5 5 5 5 ...
 $ tax    : num  296 242 242 222 222 222 311 311 311 311 ...
 $ ptratio: num  15.3 17.8 17.8 18.7 18.7 18.7 15.2 15.2 15.2 15.2 ...
 $ black  : num  397 397 393 395 397 ...
 $ lstat  : num  4.98 9.14 4.03 2.94 5.33 ...
 $ medv   : num  24 21.6 34.7 33.4 36.2 28.7 22.9 27.1 16.5 18.9 ...
```

```
Boston$chas = as.numeric(Boston$chas)
Boston$rad = as.numeric(Boston$rad)
converted_dtypes = str(subset(Boston, select = c("chas", "rad")))
```

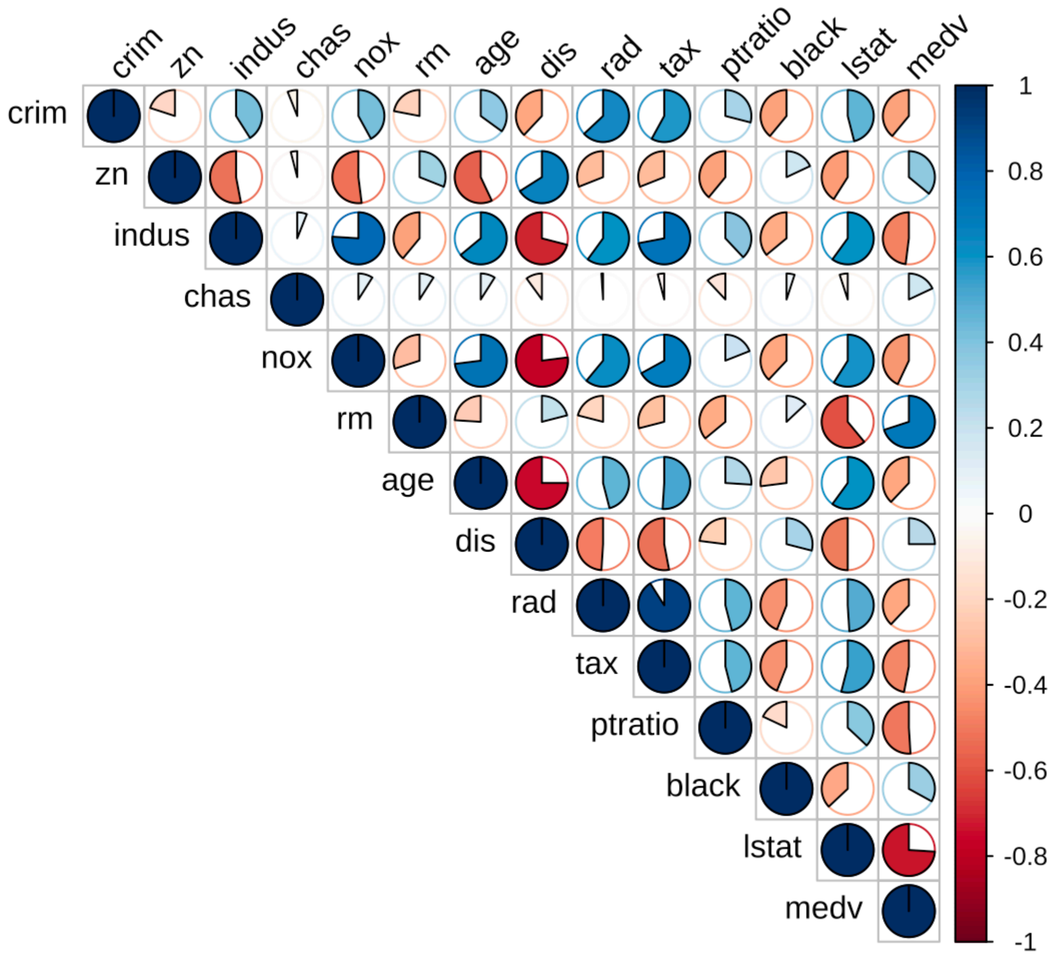
```
'data.frame':	506 obs. of  2 variables:
 $ chas: num  0 0 0 0 0 0 0 0 0 0 ...
 $ rad : num  1 2 2 3 3 3 5 5 5 5 ...
```

```
pairs(Boston,
      pch = 21,
      col = 'blue',
      bg = 'lightblue',
      gap = 0,
      labels = colnames(Boston),
      )
```





```
corrplot(round(cor(Boston),2),
         diag = TRUE,
         sig.level = 0.5,
         method = "pie",
         insig = "blank",
         tl.col = "black",
         tl.srt = 45,
         type = "upper")
```



The scatter and correlation plot help illustrate correlations between two predictors. Our plots identified that predictor indus has been strong positive correlations with other predictors, such as nox, age, rad, tax, and lstat. They also identified that chas has pretty much no correlation to any of the other predictors. Other than these findings, there seems to be no other strong patterns between the relationships of two variables. ### 1c) Are any of the predictors associated with per capita crime rate? If so, explain the relationship.

```
cor(Boston$crim, Boston[-1])
```

```
             zn     indus        chas       nox         rm       age        dis
[1,] -0.2004692 0.4065834 -0.05589158 0.4209717 -0.2192467 0.3527343 -0.3796701
           rad       tax   ptratio      black     lstat       medv
[1,] 0.6255051 0.5827643 0.2899456 -0.3850639 0.4556215 -0.3883046
```

Predictors with a strong positive correlation with per capita crime rate are rad (index of accessibility to radial highways) and tax (property tax rate > $10,000). Moderate positive correlations can be seen for variables indus, nox, age, and lstat. Moderate negative correlations: dis, black, and medv. ### 1d) Do any of the census tracts of Boston appear to have particularly high crime rates? Tax rates? Comment on the range of each predictor.

```
cat("Range crime rates:\n")
```

```
Range crime rates:
```

```
range(Boston$crim)
```

```
[1]  0.00632 88.97620
```

```
cat("Range tax rates:\n")
```

```
Range tax rates:
```

```
range(Boston$tax)
```

```
[1] 187 711
```

```
high_crime_suburbs <- subset(Boston, crim > 40)
cat("Suburbs with high crime rates:\n")
```

```
Suburbs with high crime rates:
```

```
high_crime_suburbs
```

```
       crim zn indus chas   nox    rm   age    dis rad tax ptratio  black lstat
381 88.9762  0  18.1    0 0.671 6.968  91.9 1.4165  24 666    20.2 396.90 17.21
405 41.5292  0  18.1    0 0.693 5.531  85.4 1.6074  24 666    20.2 329.46 27.38
406 67.9208  0  18.1    0 0.693 5.683 100.0 1.4254  24 666    20.2 384.97 22.98
411 51.1358  0  18.1    0 0.597 5.757 100.0 1.4130  24 666    20.2   2.60 10.11
415 45.7461  0  18.1    0 0.693 4.519 100.0 1.6582  24 666    20.2  88.27 36.98
419 73.5341  0  18.1    0 0.679 5.957 100.0 1.8026  24 666    20.2  16.45 20.62
    medv
381 10.4
405  8.5
```

```
405  8.5
406  5.0
411 15.0
415  7.0
419  8.8
```

```
high_tax_suburbs <- subset(Boston, tax > 600)
cat("Suburbs with high tax rates:\n")
```

```
Suburbs with high tax rates:
```

```
high_tax_suburbs
```

```
        crim zn indus chas   nox    rm   age    dis rad tax ptratio  black
357  8.98296  0 18.10    1 0.770 6.212  97.4 2.1222  24 666    20.2 377.73
358  3.84970  0 18.10    1 0.770 6.395  91.0 2.5052  24 666    20.2 391.34
359  5.20177  0 18.10    1 0.770 6.127  83.4 2.7227  24 666    20.2 395.43
360  4.26131  0 18.10    0 0.770 6.112  81.3 2.5091  24 666    20.2 390.74
361  4.54192  0 18.10    0 0.770 6.398  88.0 2.5182  24 666    20.2 374.56
362  3.83684  0 18.10    0 0.770 6.251  91.1 2.2955  24 666    20.2 350.65
363  3.67822  0 18.10    0 0.770 5.362  96.2 2.1036  24 666    20.2 380.79
364  4.22239  0 18.10    1 0.770 5.803  89.0 1.9047  24 666    20.2 353.04
365  3.47428  0 18.10    1 0.718 8.780  82.9 1.9047  24 666    20.2 354.55
366  4.55587  0 18.10    0 0.718 3.561  87.9 1.6132  24 666    20.2 354.70
367  3.69695  0 18.10    0 0.718 4.963  91.4 1.7523  24 666    20.2 316.03
368 13.52220  0 18.10    0 0.631 3.863 100.0 1.5106  24 666    20.2 131.42
369  4.89822  0 18.10    0 0.631 4.970 100.0 1.3325  24 666    20.2 375.52
370  5.66998  0 18.10    1 0.631 6.683  96.8 1.3567  24 666    20.2 375.33
371  6.53876  0 18.10    1 0.631 7.016  97.5 1.2024  24 666    20.2 392.05
372  9.23230  0 18.10    0 0.631 6.216 100.0 1.1691  24 666    20.2 366.15
373  8.26725  0 18.10    1 0.668 5.875  89.6 1.1296  24 666    20.2 347.88
374 11.10810  0 18.10    0 0.668 4.906 100.0 1.1742  24 666    20.2 396.90
375 18.49820  0 18.10    0 0.668 4.138 100.0 1.1370  24 666    20.2 396.90
376 19.60910  0 18.10    0 0.671 7.313  97.9 1.3163  24 666    20.2 396.90
377 15.28800  0 18.10    0 0.671 6.649  93.3 1.3449  24 666    20.2 363.02
378  9.82349  0 18.10    0 0.671 6.794  98.8 1.3580  24 666    20.2 396.90
379 23.64820  0 18.10    0 0.671 6.380  96.2 1.3861  24 666    20.2 396.90
380 17.86670  0 18.10    0 0.671 6.223 100.0 1.3861  24 666    20.2 393.74
381 88.97620  0 18.10    0 0.671 6.968  91.9 1.4165  24 666    20.2 396.90
382 15.87440  0 18.10    0 0.671 6.545  99.1 1.5192  24 666    20.2 396.90
383  9.18702  0 18.10    0 0.700 5.536 100.0 1.5804  24 666    20.2 396.90
384  7.99248  0 18.10    0 0.700 5.520 100.0 1.5331  24 666    20.2 396.90
385 20.08490  0 18.10    0 0.700 4.368  91.2 1.4395  24 666    20.2 285.83
386 16.81180  0 18.10    0 0.700 5.277  98.1 1.4261  24 666    20.2 396.90
387 24.39380  0 18.10    0 0.700 4.652 100.0 1.4672  24 666    20.2 396.90
388 22.59710  0 18.10    0 0.700 5.000  89.5 1.5184  24 666    20.2 396.90
389 14.33370  0 18.10    0 0.700 4.880 100.0 1.5895  24 666    20.2 372.92
390  8.15174  0 18.10    0 0.700 5.390  98.9 1.7281  24 666    20.2 396.90
391  6.96215  0 18.10    0 0.700 5.713  97.0 1.9265  24 666    20.2 394.43
392  5.29305  0 18.10    0 0.700 6.051  82.5 2.1678  24 666    20.2 378.38
393 11.57790  0 18.10    0 0.700 5.036  97.0 1.7700  24 666    20.2 396.90
394  8.64476  0 18.10    0 0.693 6.193  92.6 1.7912  24 666    20.2 396.90
395 13.35980  0 18.10    0 0.693 5.887  94.7 1.7821  24 666    20.2 396.90
396  8.71675  0 18.10    0 0.693 6.471  98.8 1.7257  24 666    20.2 391.98
397  5.87205  0 18.10    0 0.693 6.405  96.0 1.6768  24 666    20.2 396.90
```

```
397  5.87205  0 18.10    0 0.693 6.405  96.0 1.6768  24 666    20.2 396.90
398  7.67202  0 18.10    0 0.693 5.747  98.9 1.6334  24 666    20.2 393.10
399 38.35180  0 18.10    0 0.693 5.453 100.0 1.4896  24 666    20.2 396.90
400  9.91655  0 18.10    0 0.693 5.852  77.8 1.5004  24 666    20.2 338.16
401 25.04610  0 18.10    0 0.693 5.987 100.0 1.5888  24 666    20.2 396.90
402 14.23620  0 18.10    0 0.693 6.343 100.0 1.5741  24 666    20.2 396.90
403  9.59571  0 18.10    0 0.693 6.404 100.0 1.6390  24 666    20.2 376.11
404 24.80170  0 18.10    0 0.693 5.349  96.0 1.7028  24 666    20.2 396.90
405 41.52920  0 18.10    0 0.693 5.531  85.4 1.6074  24 666    20.2 329.46
406 67.92080  0 18.10    0 0.693 5.683 100.0 1.4254  24 666    20.2 384.97
407 20.71620  0 18.10    0 0.659 4.138 100.0 1.1781  24 666    20.2 370.22
408 11.95110  0 18.10    0 0.659 5.608 100.0 1.2852  24 666    20.2 332.09
409  7.40389  0 18.10    0 0.597 5.617  97.9 1.4547  24 666    20.2 314.64
410 14.43830  0 18.10    0 0.597 6.852 100.0 1.4655  24 666    20.2 179.36
411 51.13580  0 18.10    0 0.597 5.757 100.0 1.4130  24 666    20.2   2.60
412 14.05070  0 18.10    0 0.597 6.657 100.0 1.5275  24 666    20.2  35.05
413 18.81100  0 18.10    0 0.597 4.628 100.0 1.5539  24 666    20.2  28.79
414 28.65580  0 18.10    0 0.597 5.155 100.0 1.5894  24 666    20.2 210.97
415 45.74610  0 18.10    0 0.693 4.519 100.0 1.6582  24 666    20.2  88.27
416 18.08460  0 18.10    0 0.679 6.434 100.0 1.8347  24 666    20.2  27.25
417 10.83420  0 18.10    0 0.679 6.782  90.8 1.8195  24 666    20.2  21.57
418 25.94060  0 18.10    0 0.679 5.304  89.1 1.6475  24 666    20.2 127.36
419 73.53410  0 18.10    0 0.679 5.957 100.0 1.8026  24 666    20.2  16.45
420 11.81230  0 18.10    0 0.718 6.824  76.5 1.7940  24 666    20.2  48.45
421 11.08740  0 18.10    0 0.718 6.411 100.0 1.8589  24 666    20.2 318.75
422  7.02259  0 18.10    0 0.718 6.006  95.3 1.8746  24 666    20.2 319.98
423 12.04820  0 18.10    0 0.614 5.648  87.6 1.9512  24 666    20.2 291.55
424  7.05042  0 18.10    0 0.614 6.103  85.1 2.0218  24 666    20.2   2.52
425  8.79212  0 18.10    0 0.584 5.565  70.6 2.0635  24 666    20.2   3.65
426 15.86030  0 18.10    0 0.679 5.896  95.4 1.9096  24 666    20.2   7.68
427 12.24720  0 18.10    0 0.584 5.837  59.7 1.9976  24 666    20.2  24.65
428 37.66190  0 18.10    0 0.679 6.202  78.7 1.8629  24 666    20.2  18.82
429  7.36711  0 18.10    0 0.679 6.193  78.1 1.9356  24 666    20.2  96.73
430  9.33889  0 18.10    0 0.679 6.380  95.6 1.9682  24 666    20.2  60.72
431  8.49213  0 18.10    0 0.584 6.348  86.1 2.0527  24 666    20.2  83.45
432 10.06230  0 18.10    0 0.584 6.833  94.3 2.0882  24 666    20.2  81.33
433  6.44405  0 18.10    0 0.584 6.425  74.8 2.2004  24 666    20.2  97.95
434  5.58107  0 18.10    0 0.713 6.436  87.9 2.3158  24 666    20.2 100.19
435 13.91340  0 18.10    0 0.713 6.208  95.0 2.2222  24 666    20.2 100.63
436 11.16040  0 18.10    0 0.740 6.629  94.6 2.1247  24 666    20.2 109.85
437 14.42080  0 18.10    0 0.740 6.461  93.3 2.0026  24 666    20.2  27.49
438 15.17720  0 18.10    0 0.740 6.152 100.0 1.9142  24 666    20.2   9.32
439 13.67810  0 18.10    0 0.740 5.935  87.9 1.8206  24 666    20.2  68.95
440  9.39063  0 18.10    0 0.740 5.627  93.9 1.8172  24 666    20.2 396.90
441 22.05110  0 18.10    0 0.740 5.818  92.4 1.8662  24 666    20.2 391.45
442  9.72418  0 18.10    0 0.740 6.406  97.2 2.0651  24 666    20.2 385.96
443  5.66637  0 18.10    0 0.740 6.219 100.0 2.0048  24 666    20.2 395.69
444  9.96654  0 18.10    0 0.740 6.485 100.0 1.9784  24 666    20.2 386.73
445 12.80230  0 18.10    0 0.740 5.854  96.6 1.8956  24 666    20.2 240.52
446 10.67180  0 18.10    0 0.740 6.459  94.8 1.9879  24 666    20.2  43.06
447  6.28807  0 18.10    0 0.740 6.341  96.4 2.0720  24 666    20.2 318.01
448  9.92485  0 18.10    0 0.740 6.251  96.6 2.1980  24 666    20.2 388.52
449  9.32909  0 18.10    0 0.713 6.185  98.7 2.2616  24 666    20.2 396.90
450  7.52601  0 18.10    0 0.713 6.417  98.3 2.1850  24 666    20.2 304.21
451  6.71772  0 18.10    0 0.713 6.749  92.6 2.3236  24 666    20.2   0.32
452  5.44114  0 18.10    0 0.713 6.655  98.2 2.3552  24 666    20.2 355.29
```

```
452  5.44114  0 18.10    0 0.713 6.655  98.2 2.3552  24 666    20.2 355.29
453  5.09017  0 18.10    0 0.713 6.297  91.8 2.3682  24 666    20.2 385.09
454  8.24809  0 18.10    0 0.713 7.393  99.3 2.4527  24 666    20.2 375.87
455  9.51363  0 18.10    0 0.713 6.728  94.1 2.4961  24 666    20.2   6.68
456  4.75237  0 18.10    0 0.713 6.525  86.5 2.4358  24 666    20.2  50.92
457  4.66883  0 18.10    0 0.713 5.976  87.9 2.5806  24 666    20.2  10.48
458  8.20058  0 18.10    0 0.713 5.936  80.3 2.7792  24 666    20.2   3.50
459  7.75223  0 18.10    0 0.713 6.301  83.7 2.7831  24 666    20.2 272.21
460  6.80117  0 18.10    0 0.713 6.081  84.4 2.7175  24 666    20.2 396.90
461  4.81213  0 18.10    0 0.713 6.701  90.0 2.5975  24 666    20.2 255.23
462  3.69311  0 18.10    0 0.713 6.376  88.4 2.5671  24 666    20.2 391.43
463  6.65492  0 18.10    0 0.713 6.317  83.0 2.7344  24 666    20.2 396.90
464  5.82115  0 18.10    0 0.713 6.513  89.9 2.8016  24 666    20.2 393.82
465  7.83932  0 18.10    0 0.655 6.209  65.4 2.9634  24 666    20.2 396.90
466  3.16360  0 18.10    0 0.655 5.759  48.2 3.0665  24 666    20.2 334.40
467  3.77498  0 18.10    0 0.655 5.952  84.7 2.8715  24 666    20.2  22.01
468  4.42228  0 18.10    0 0.584 6.003  94.5 2.5403  24 666    20.2 331.29
469 15.57570  0 18.10    0 0.580 5.926  71.0 2.9084  24 666    20.2 368.74
470 13.07510  0 18.10    0 0.580 5.713  56.7 2.8237  24 666    20.2 396.90
471  4.34879  0 18.10    0 0.580 6.167  84.0 3.0334  24 666    20.2 396.90
472  4.03841  0 18.10    0 0.532 6.229  90.7 3.0993  24 666    20.2 395.33
473  3.56868  0 18.10    0 0.580 6.437  75.0 2.8965  24 666    20.2 393.37
474  4.64689  0 18.10    0 0.614 6.980  67.6 2.5329  24 666    20.2 374.68
475  8.05579  0 18.10    0 0.584 5.427  95.4 2.4298  24 666    20.2 352.58
476  6.39312  0 18.10    0 0.584 6.162  97.4 2.2060  24 666    20.2 302.76
477  4.87141  0 18.10    0 0.614 6.484  93.6 2.3053  24 666    20.2 396.21
478 15.02340  0 18.10    0 0.614 5.304  97.3 2.1007  24 666    20.2 349.48
479 10.23300  0 18.10    0 0.614 6.185  96.7 2.1705  24 666    20.2 379.70
480 14.33370  0 18.10    0 0.614 6.229  88.0 1.9512  24 666    20.2 383.32
481  5.82401  0 18.10    0 0.532 6.242  64.7 3.4242  24 666    20.2 396.90
482  5.70818  0 18.10    0 0.532 6.750  74.9 3.3317  24 666    20.2 393.07
483  5.73116  0 18.10    0 0.532 7.061  77.0 3.4106  24 666    20.2 395.28
484  2.81838  0 18.10    0 0.532 5.762  40.3 4.0983  24 666    20.2 392.92
485  2.37857  0 18.10    0 0.583 5.871  41.9 3.7240  24 666    20.2 370.73
486  3.67367  0 18.10    0 0.583 6.312  51.9 3.9917  24 666    20.2 388.62
487  5.69175  0 18.10    0 0.583 6.114  79.8 3.5459  24 666    20.2 392.68
488  4.83567  0 18.10    0 0.583 5.905  53.2 3.1523  24 666    20.2 388.22
489  0.15086  0 27.74    0 0.609 5.454  92.7 1.8209   4 711    20.1 395.09
490  0.18337  0 27.74    0 0.609 5.414  98.3 1.7554   4 711    20.1 344.05
491  0.20746  0 27.74    0 0.609 5.093  98.0 1.8226   4 711    20.1 318.43
492  0.10574  0 27.74    0 0.609 5.983  98.8 1.8681   4 711    20.1 390.11
493  0.11132  0 27.74    0 0.609 5.983  83.5 2.1099   4 711    20.1 396.90
    lstat medv
357 17.60 17.8
358 13.27 21.7
359 11.48 22.7
360 12.67 22.6
361  7.79 25.0
362 14.19 19.9
363 10.19 20.8
364 14.64 16.8
365  5.29 21.9
366  7.12 27.5
367 14.00 21.9
368 13.33 23.1
```

```
369  3.26 50.0
370  3.73 50.0
371  2.96 50.0
372  9.53 50.0
373  8.88 50.0
374 34.77 13.8
375 37.97 13.8
376 13.44 15.0
377 23.24 13.9
378 21.24 13.3
379 23.69 13.1
380 21.78 10.2
381 17.21 10.4
382 21.08 10.9
383 23.60 11.3
384 24.56 12.3
385 30.63  8.8
386 30.81  7.2
387 28.28 10.5
388 31.99  7.4
389 30.62 10.2
390 20.85 11.5
391 17.11 15.1
392 18.76 23.2
393 25.68  9.7
394 15.17 13.8
395 16.35 12.7
396 17.12 13.1
397 19.37 12.5
398 19.92  8.5
399 30.59  5.0
400 29.97  6.3
401 26.77  5.6
402 20.32  7.2
403 20.31 12.1
404 19.77  8.3
405 27.38  8.5
406 22.98  5.0
407 23.34 11.9
408 12.13 27.9
409 26.40 17.2
410 19.78 27.5
411 10.11 15.0
412 21.22 17.2
413 34.37 17.9
414 20.08 16.3
415 36.98  7.0
416 29.05  7.2
417 25.79  7.5
418 26.64 10.4
419 20.62  8.8
420 22.74  8.4
421 15.02 16.7
422 15.70 14.2
423 14.10 20.8
```

```
424 23.29 13.4
425 17.16 11.7
426 24.39  8.3
427 15.69 10.2
428 14.52 10.9
429 21.52 11.0
430 24.08  9.5
431 17.64 14.5
432 19.69 14.1
433 12.03 16.1
434 16.22 14.3
435 15.17 11.7
436 23.27 13.4
437 18.05  9.6
438 26.45  8.7
439 34.02  8.4
440 22.88 12.8
441 22.11 10.5
442 19.52 17.1
443 16.59 18.4
444 18.85 15.4
445 23.79 10.8
446 23.98 11.8
447 17.79 14.9
448 16.44 12.6
449 18.13 14.1
450 19.31 13.0
451 17.44 13.4
452 17.73 15.2
453 17.27 16.1
454 16.74 17.8
455 18.71 14.9
456 18.13 14.1
457 19.01 12.7
458 16.94 13.5
459 16.23 14.9
460 14.70 20.0
461 16.42 16.4
462 14.65 17.7
463 13.99 19.5
464 10.29 20.2
465 13.22 21.4
466 14.13 19.9
467 17.15 19.0
468 21.32 19.1
469 18.13 19.1
470 14.76 20.1
471 16.29 19.9
472 12.87 19.6
473 14.36 23.2
474 11.66 29.8
475 18.14 13.8
476 24.10 13.3
477 18.68 16.7
478 24.91 12.0
```

```
479 18.03 14.6
480 13.11 21.4
481 10.74 23.0
482  7.74 23.7
483  7.01 25.0
484 10.42 21.8
485 13.34 20.6
486 10.58 21.2
487 14.98 19.1
488 11.45 20.6
489 18.06 15.2
490 23.97  7.0
491 29.68  8.1
492 18.07 13.6
493 13.35 20.1
```

1e) How many of the census tracts in this data set bound the Charles river?

```
charles_river_suburbs <- sum(Boston$chas == 1)
cat("Number of suburbs bound to Charles River:", charles_river_suburbs, "\n")
```

```
Number of suburbs bound to Charles River: 35
```

```
charles_river_suburbs
```

```
[1] 35
```

1f) What is the median pupil-teacher ratio among the towns in this data set?

```
median_ptratio <- median(Boston$ptratio)
cat("Median pupil-teacher ratio:", median_ptratio, "\n")
```

```
Median pupil-teacher ratio: 19.05
```

```
median_ptratio
```

```
[1] 19.05
```

Problem 2 - Soybean data

Import packages and data

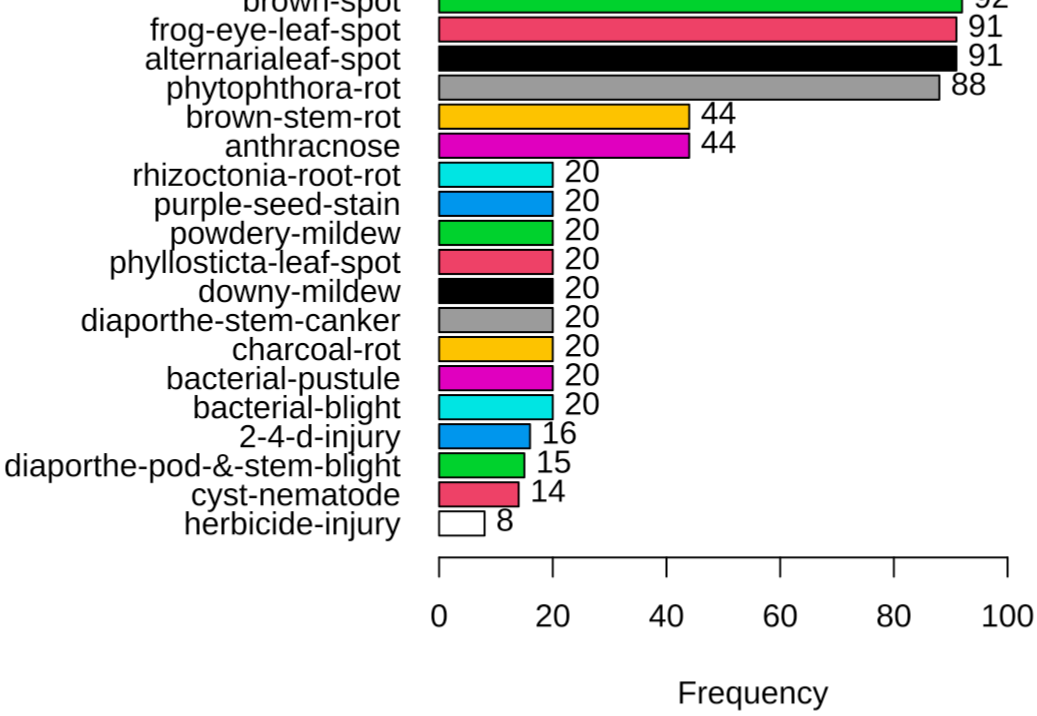
```
library(mlbench)
data(Soybean)
```

```
str(Soybean)
```

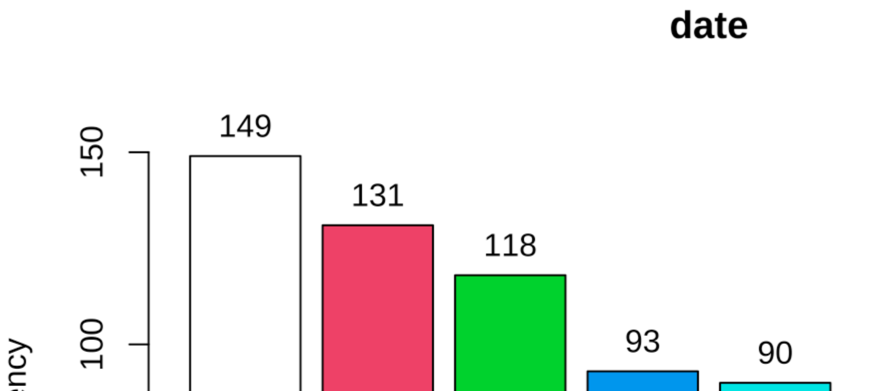
```
'data.frame':	683 obs. of  36 variables:
 $ Class          : Factor w/ 19 levels "2-4-d-injury",..: 11 11 11 11 11 11 11 11 11 11 ...
 $ date           : Factor w/ 7 levels "0","1","2","3",..: 7 5 4 4 7 6 6 5 7 5 ...
 $ plant.stand    : Ord.factor w/ 2 levels "0"<"1": 1 1 1 1 1 1 1 1 1 1 ...
 $ precip         : 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 ...
```

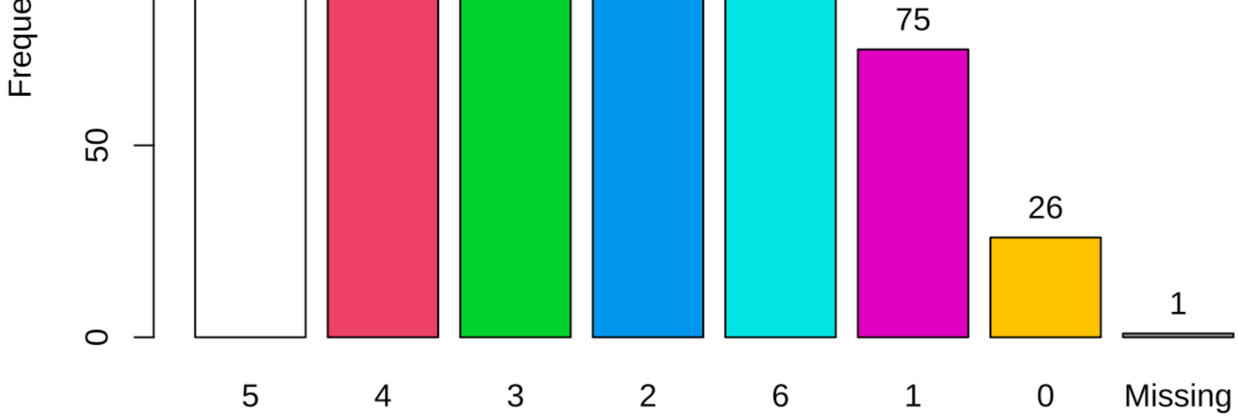
2a) Investigate the frequency distributions for the categorical predictors. Are any of the distributions degenerate in the ways discussed earlier in this chapter?

```
for (i in 1:35) {
  predictor <- Soybean[, i]
  predictor_info <- tab1(predictor,
                         main = colnames(Soybean[i]),
                         sort.group = "decreasing",
                         cum.percent = TRUE,
                         )
  print(predictor_info)
}
```



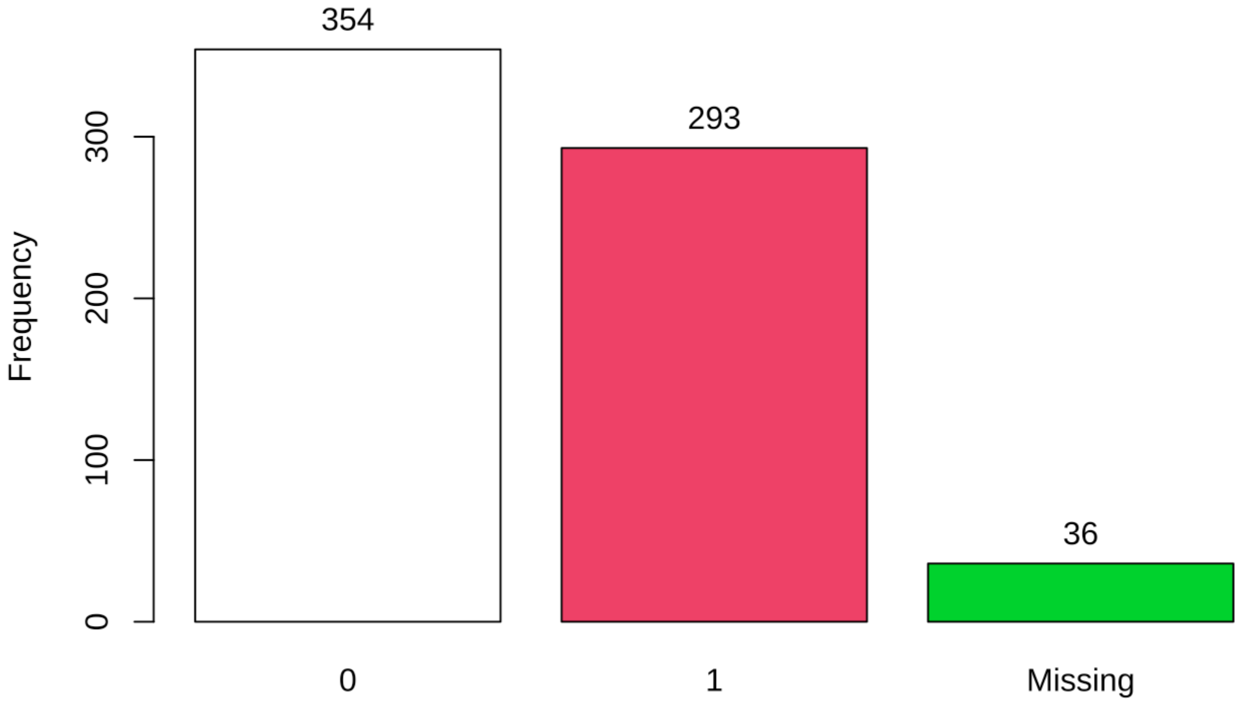
```
predictor :
                            Frequency Percent Cum. percent
brown-spot                         92    13.5         13.5
frog-eye-leaf-spot                 91    13.3         26.8
alternarialeaf-spot                91    13.3         40.1
phytophthora-rot                   88    12.9         53.0
brown-stem-rot                     44     6.4         59.4
anthracnose                        44     6.4         65.9
rhizoctonia-root-rot               20     2.9         68.8
purple-seed-stain                  20     2.9         71.7
powdery-mildew                     20     2.9         74.7
phyllosticta-leaf-spot             20     2.9         77.6
downy-mildew                       20     2.9         80.5
diaporthe-stem-canker              20     2.9         83.5
charcoal-rot                       20     2.9         86.4
bacterial-pustule                  20     2.9         89.3
bacterial-blight                   20     2.9         92.2
2-4-d-injury                       16     2.3         94.6
diaporthe-pod-&-stem-blight        15     2.2         96.8
cyst-nematode                      14     2.0         98.8
herbicide-injury                    8     1.2        100.0
  Total                           683   100.0        100.0
```





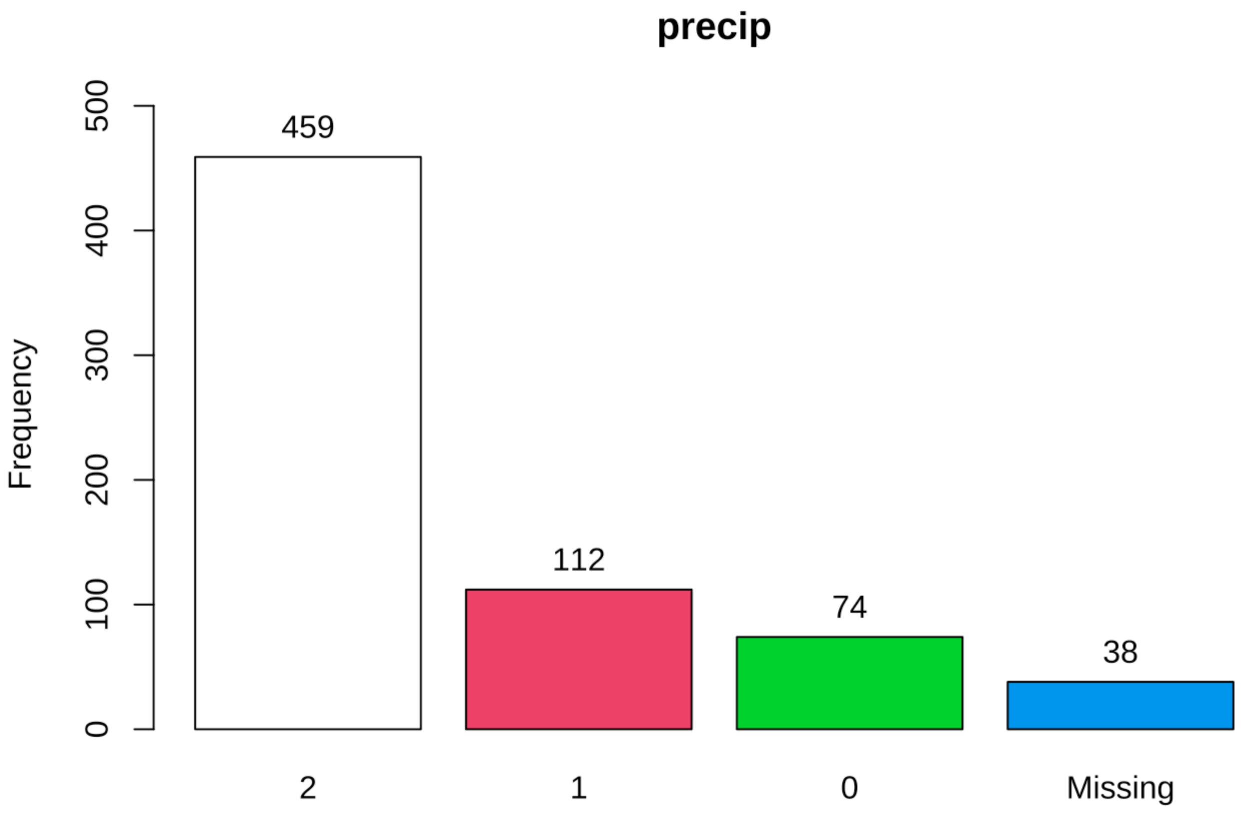
```
predictor :
          Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
5               149     21.8       86.7     21.8       86.8
4               131     19.2       64.9     19.2       65.0
3               118     17.3       45.7     17.3       45.7
2                93     13.6       28.4     13.6       28.4
6                90     13.2       99.9     13.2      100.0
1                75     11.0       14.8     11.0       14.8
0                26      3.8        3.8      3.8        3.8
NA's              1      0.1      100.0      0.0      100.0
  Total         683    100.0      100.0    100.0      100.0
```

plant.stand

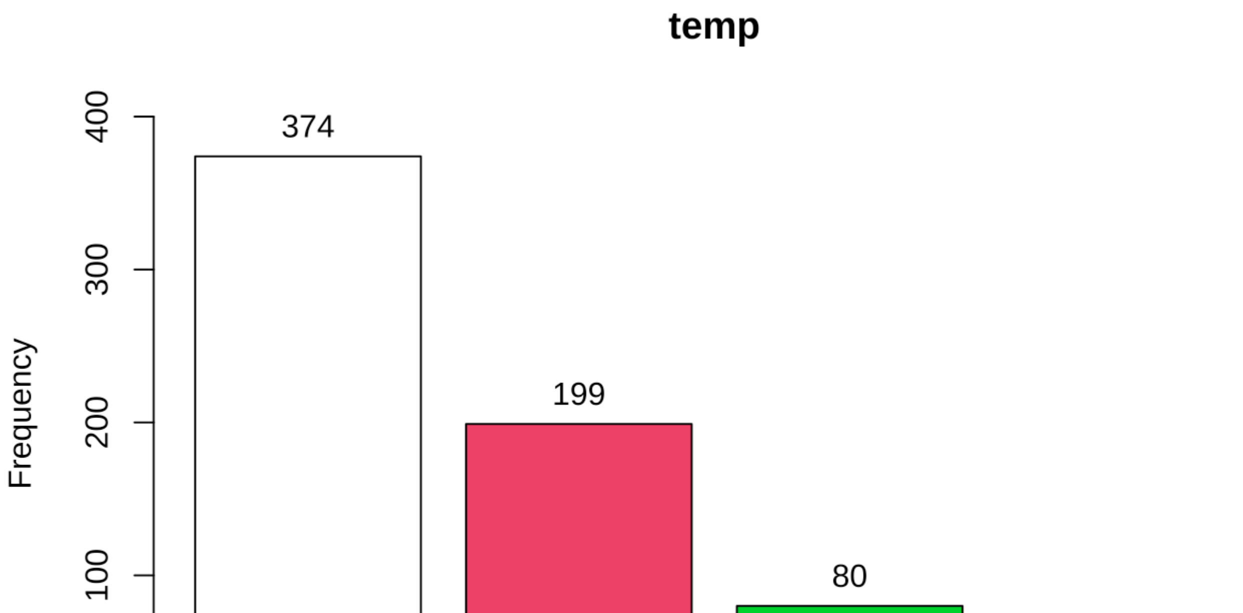


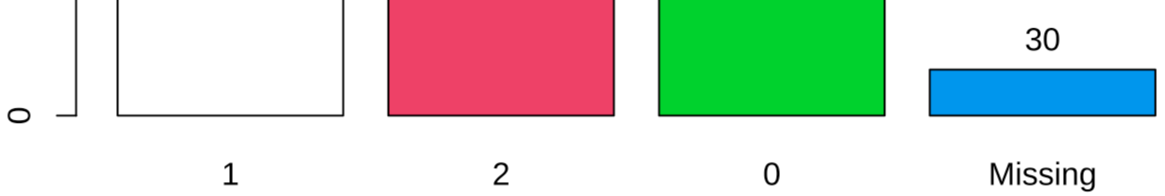
```
predictor :
          Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0               354     51.8       51.8     54.7       54.7
```

```
1              293     42.9       94.7     45.3      100.0
NA's            36      5.3      100.0      0.0      100.0
  Total        683    100.0      100.0    100.0      100.0
```

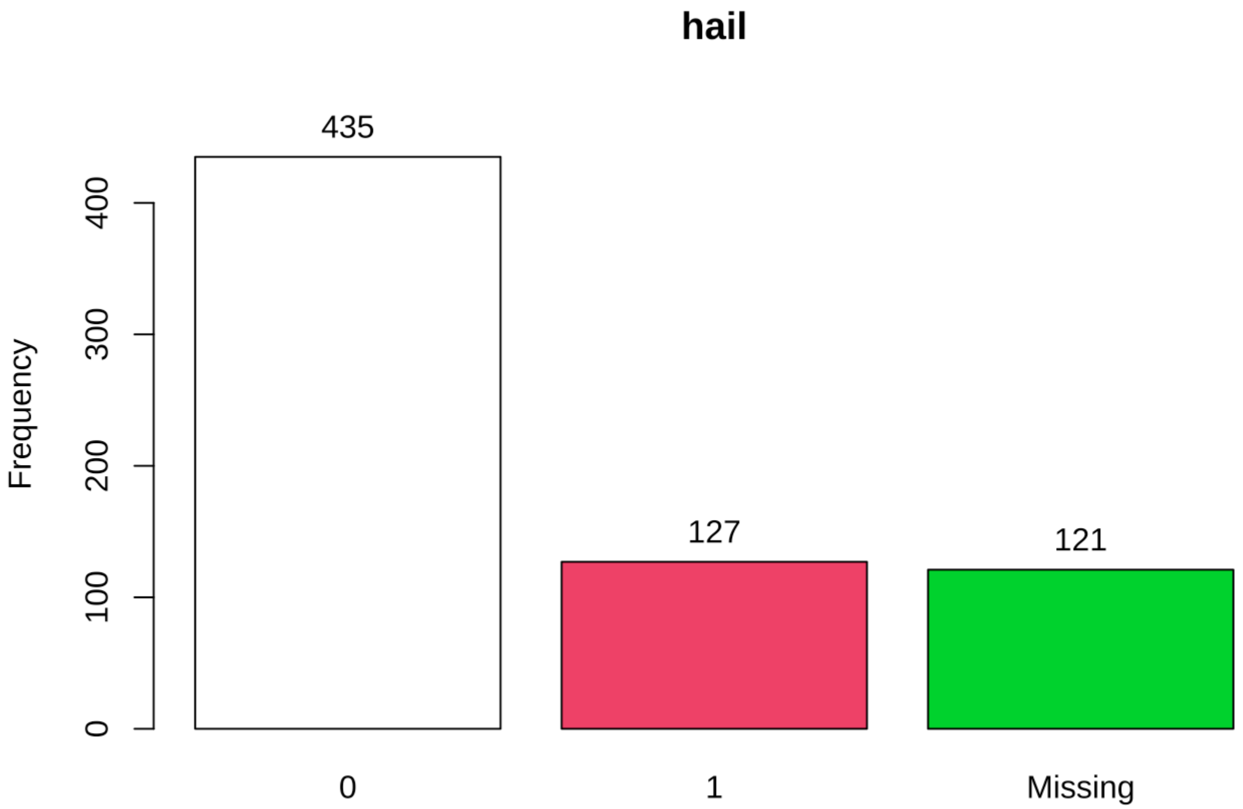


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
2              459     67.2       94.4     71.2      100.0
1              112     16.4       27.2     17.4       28.8
0               74     10.8       10.8     11.5       11.5
NA's            38      5.6      100.0      0.0      100.0
  Total        683    100.0      100.0    100.0      100.0
```

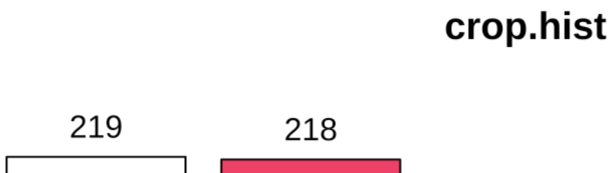


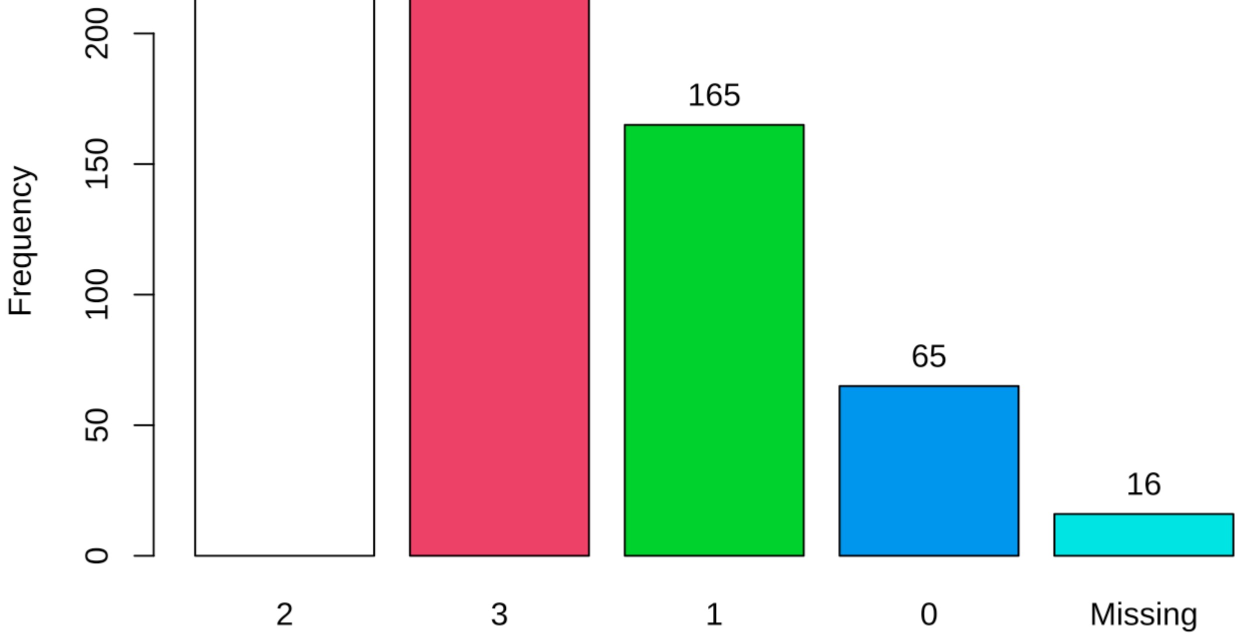


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
1             374     54.8       66.5     57.3       69.5
2             199     29.1       95.6     30.5      100.0
0              80     11.7       11.7     12.3       12.3
NA's           30      4.4      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```



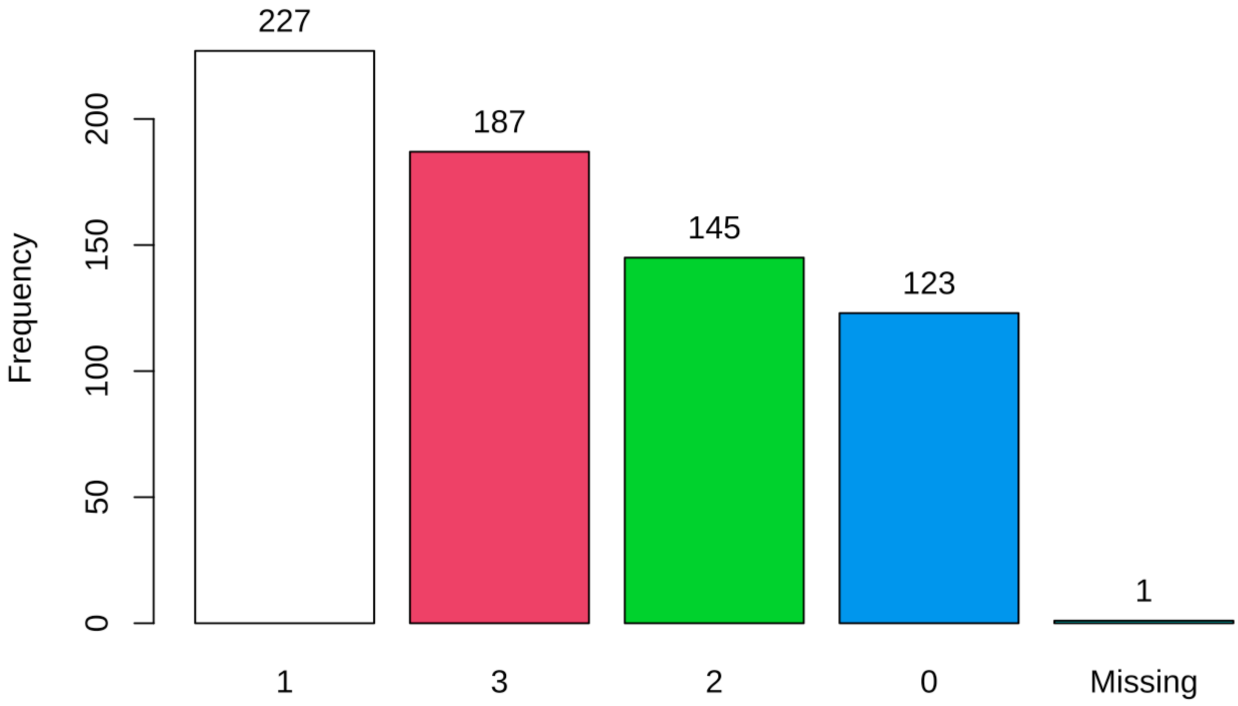
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             435     63.7       63.7     77.4       77.4
1             127     18.6       82.3     22.6      100.0
NA's          121     17.7      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```



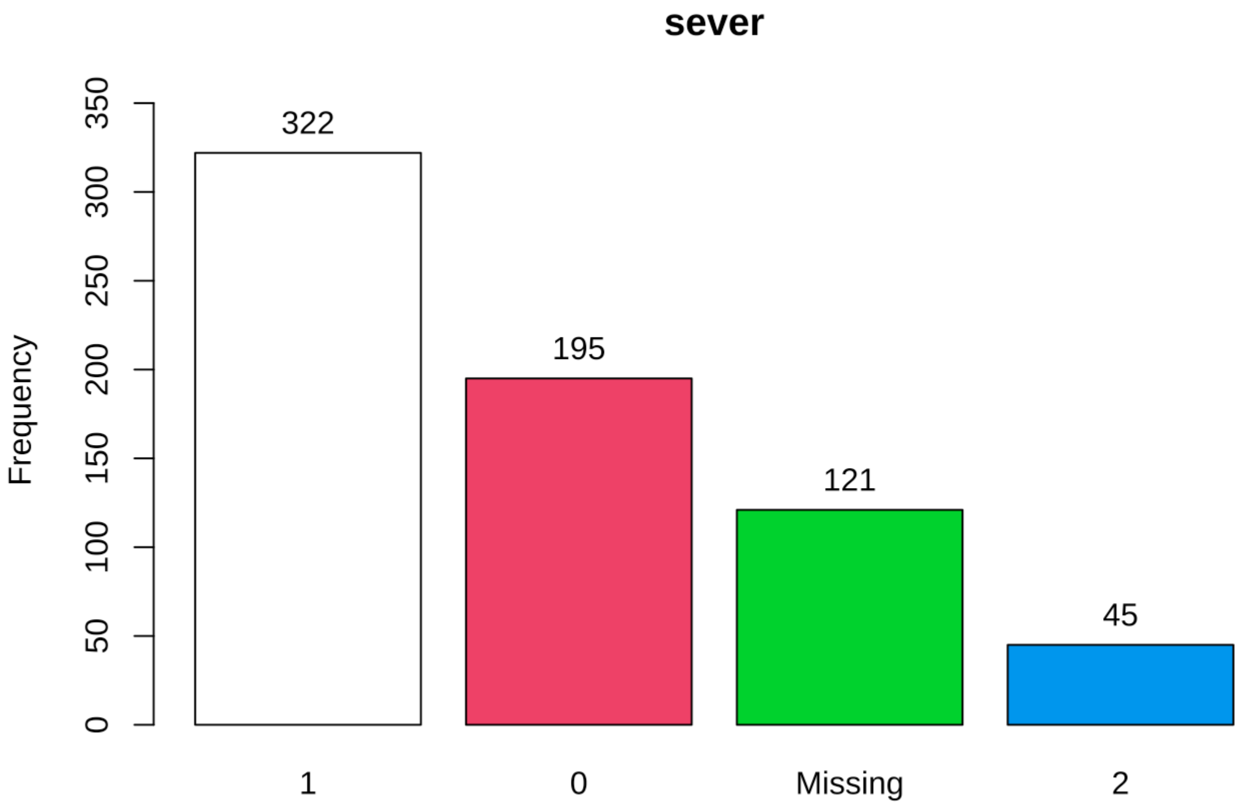


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
2             219     32.1       65.7     32.8       67.3
3             218     31.9       97.7     32.7      100.0
1             165     24.2       33.7     24.7       34.5
0              65      9.5        9.5      9.7        9.7
NA's           16      2.3      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```

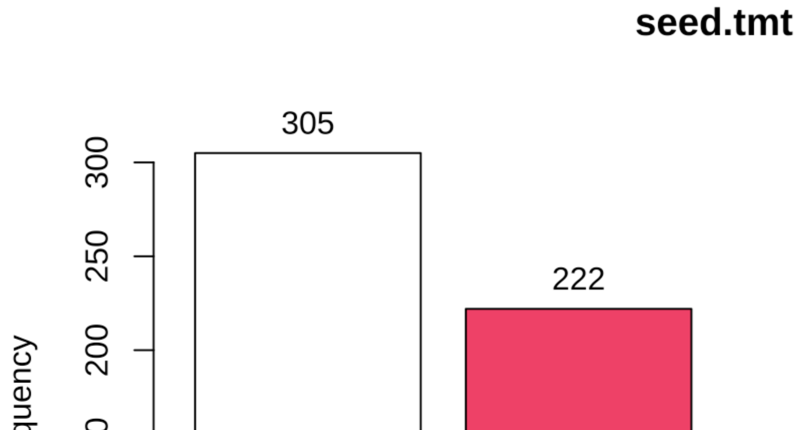
area.dam

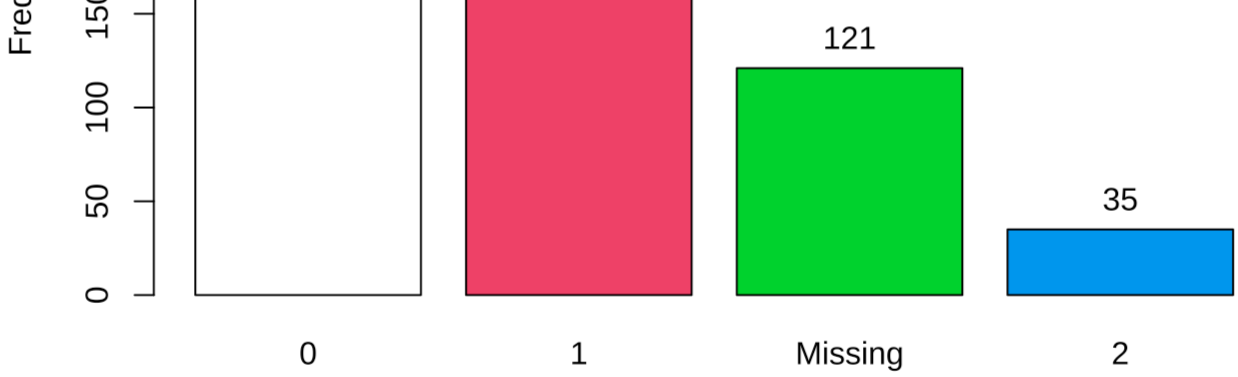


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
1             227     33.2       51.2     33.3       51.3
3             187     27.4       99.9     27.4      100.0
2             145     21.2       72.5     21.3       72.6
0             123     18.0       18.0     18.0       18.0
NA's            1      0.1      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```

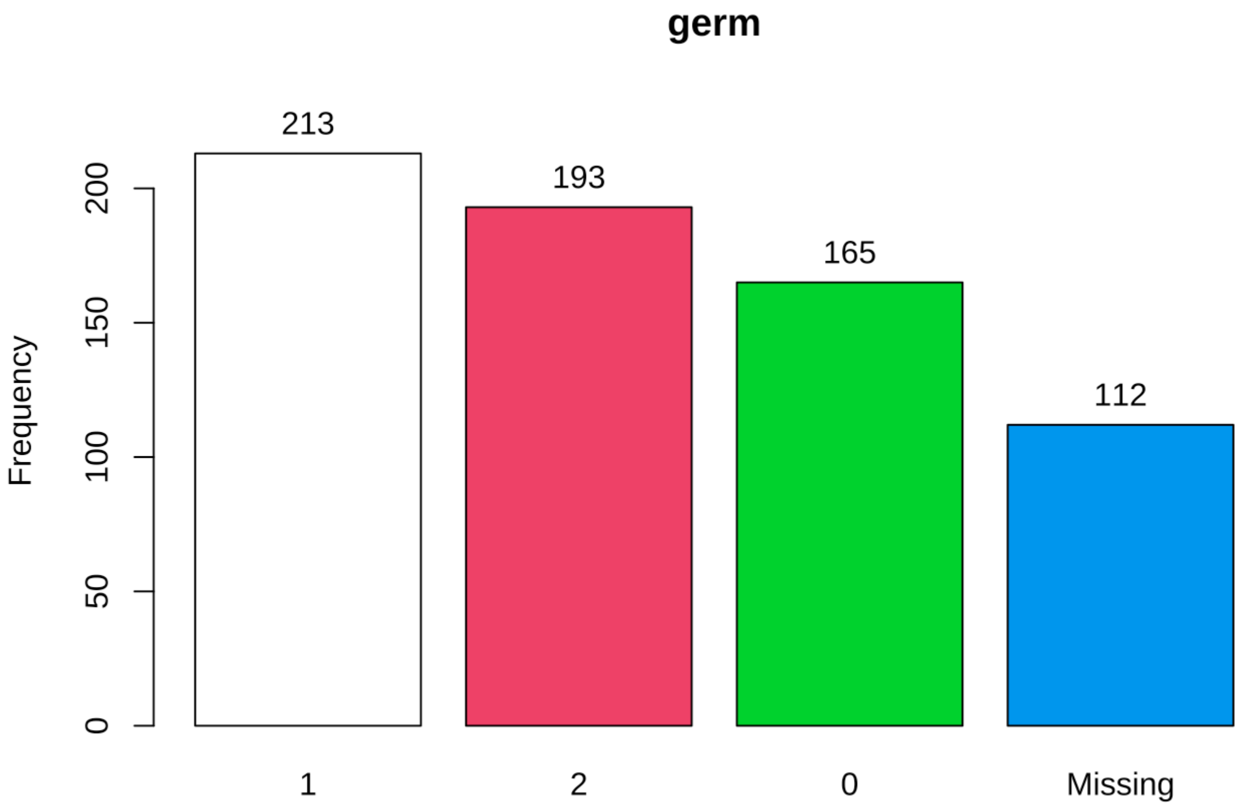


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
1             322     47.1       75.7     57.3       92.0
0             195     28.6       28.6     34.7       34.7
NA's          121     17.7      100.0      0.0      100.0
2              45      6.6       82.3      8.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```

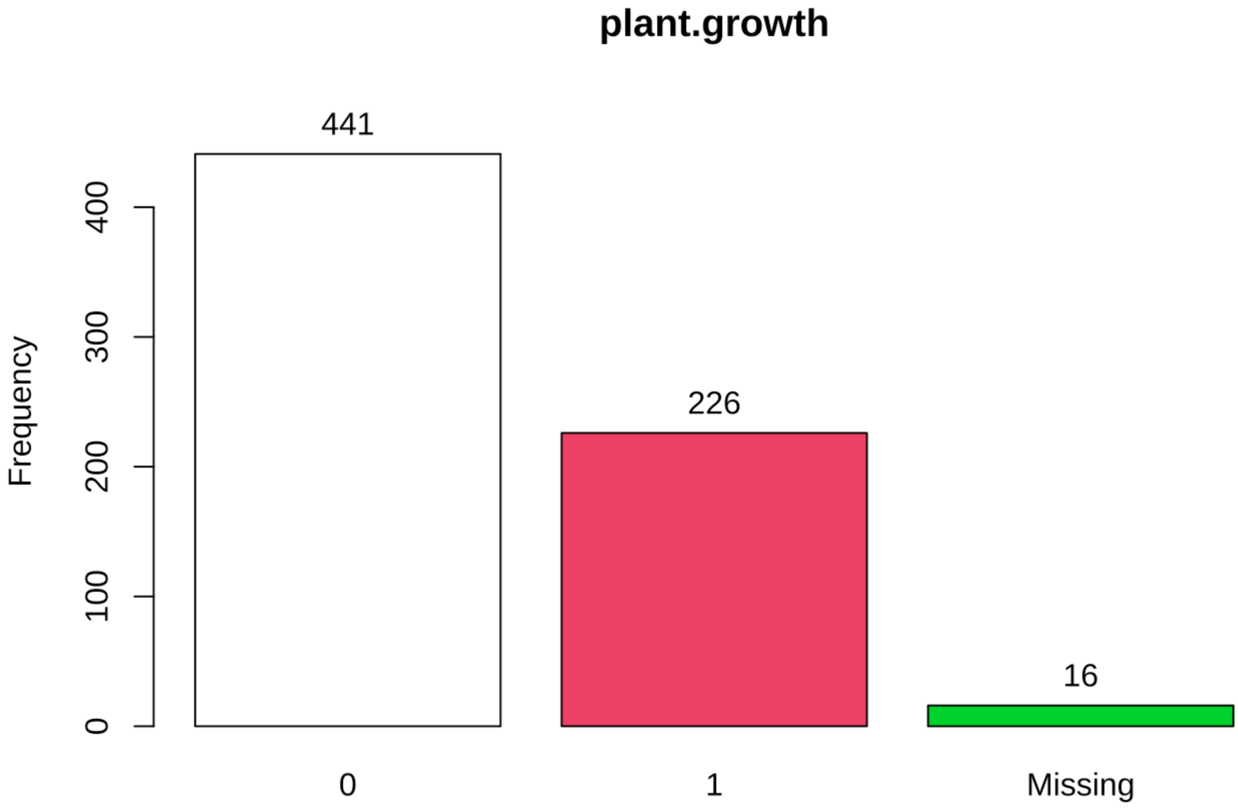




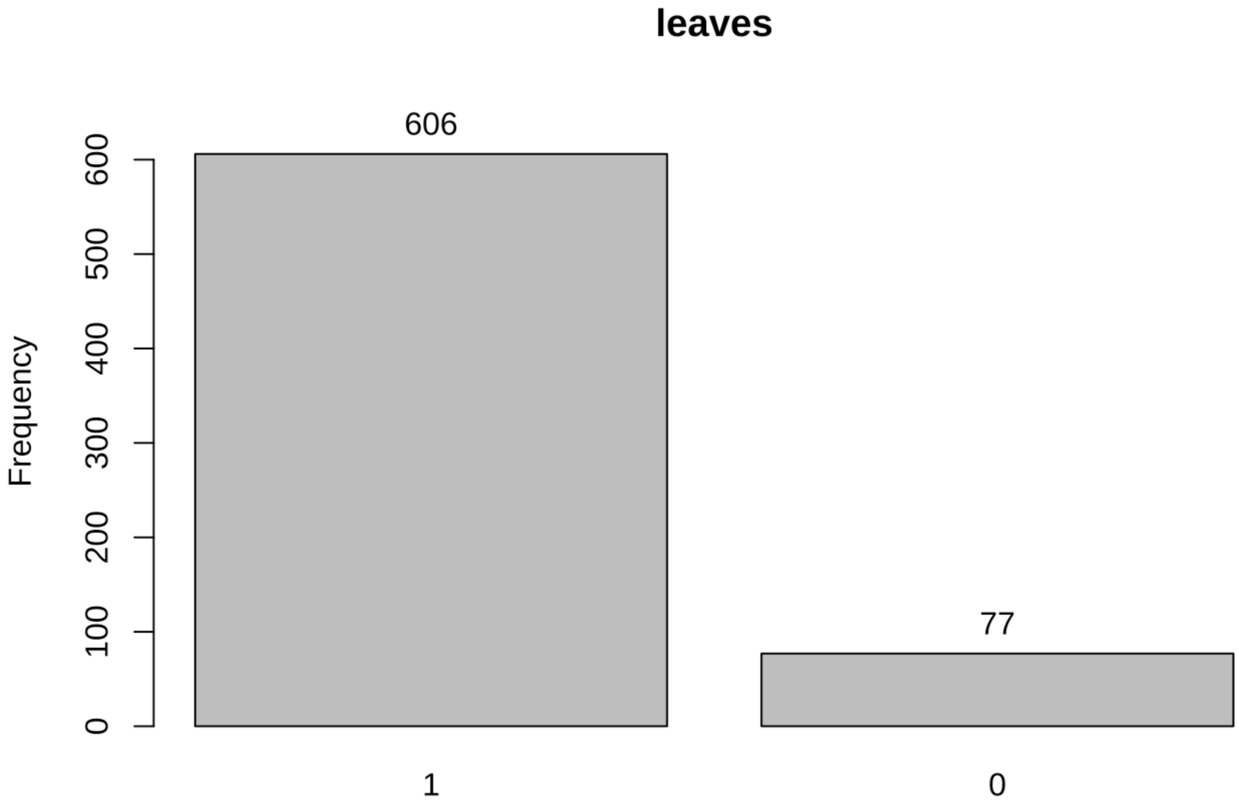
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             305     44.7       44.7     54.3       54.3
1             222     32.5       77.2     39.5       93.8
NA's          121     17.7      100.0      0.0      100.0
2              35      5.1       82.3      6.2      100.0
  Total       683    100.0      100.0    100.0      100.0
```



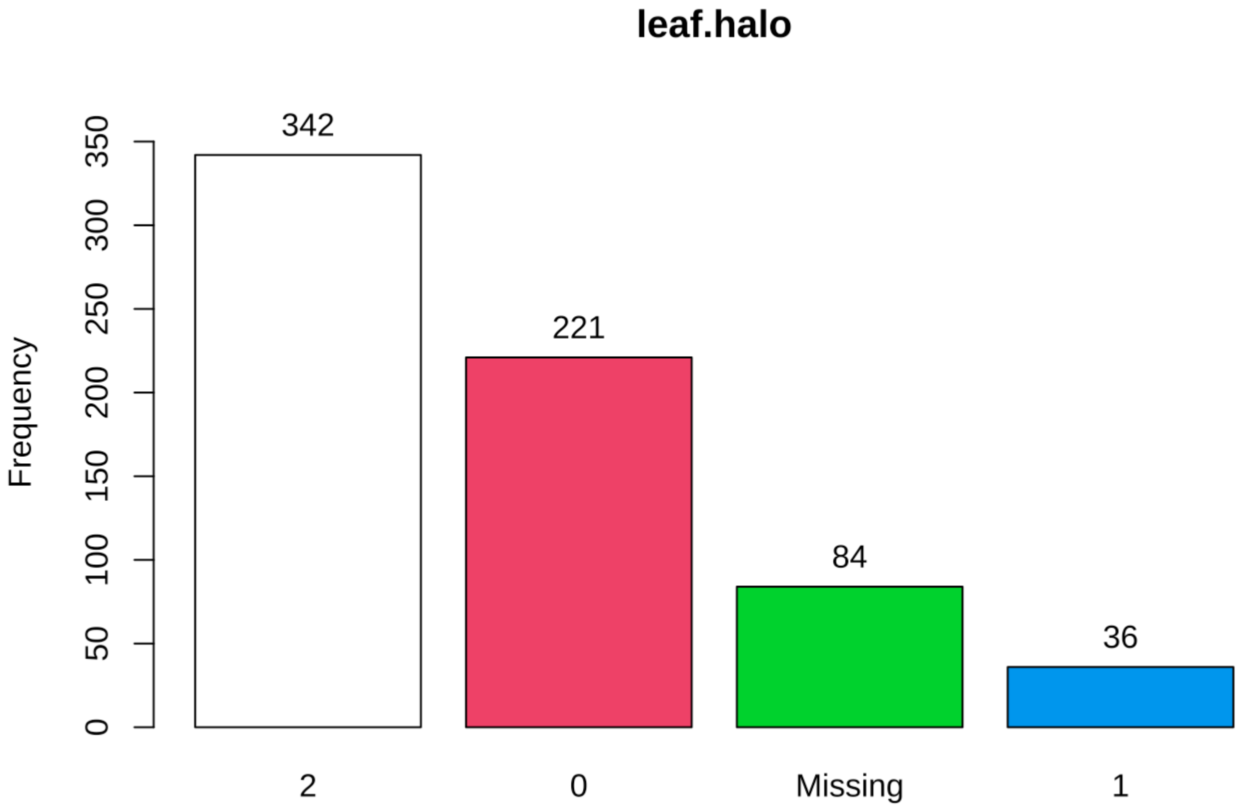
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
1             213     31.2       55.3     37.3       66.2
2             193     28.3       83.6     33.8      100.0
0             165     24.2       24.2     28.9       28.9
NA's          112     16.4      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```



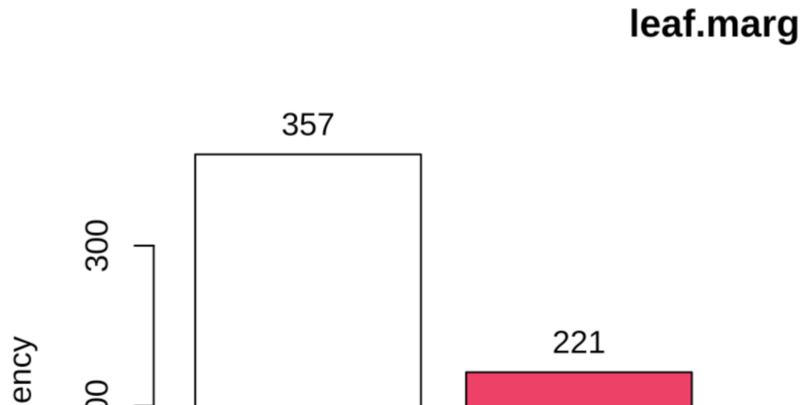
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             441     64.6       64.6     66.1       66.1
1             226     33.1       97.7     33.9      100.0
NA's           16      2.3      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```

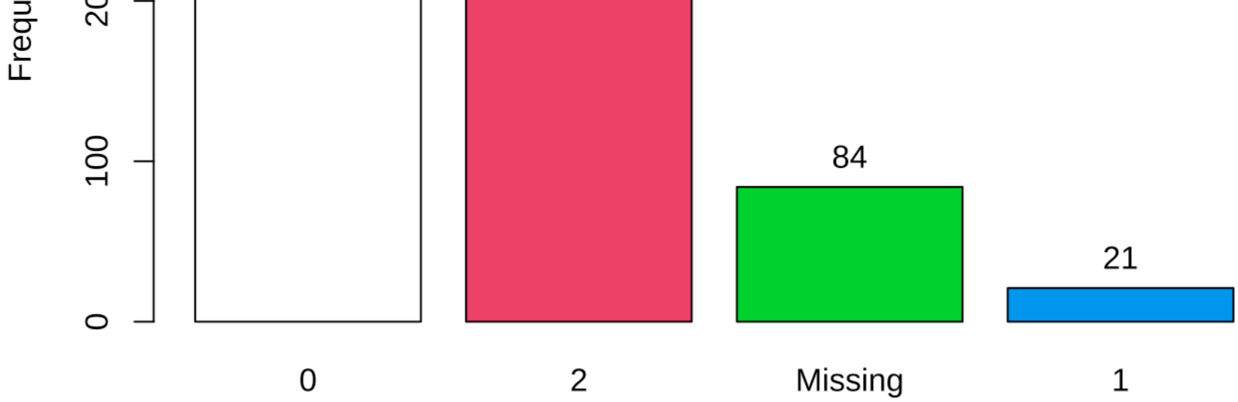


```
predictor :
        Frequency Percent Cum. percent
1             606    88.7         88.7
0              77    11.3        100.0
  Total       683   100.0        100.0
```



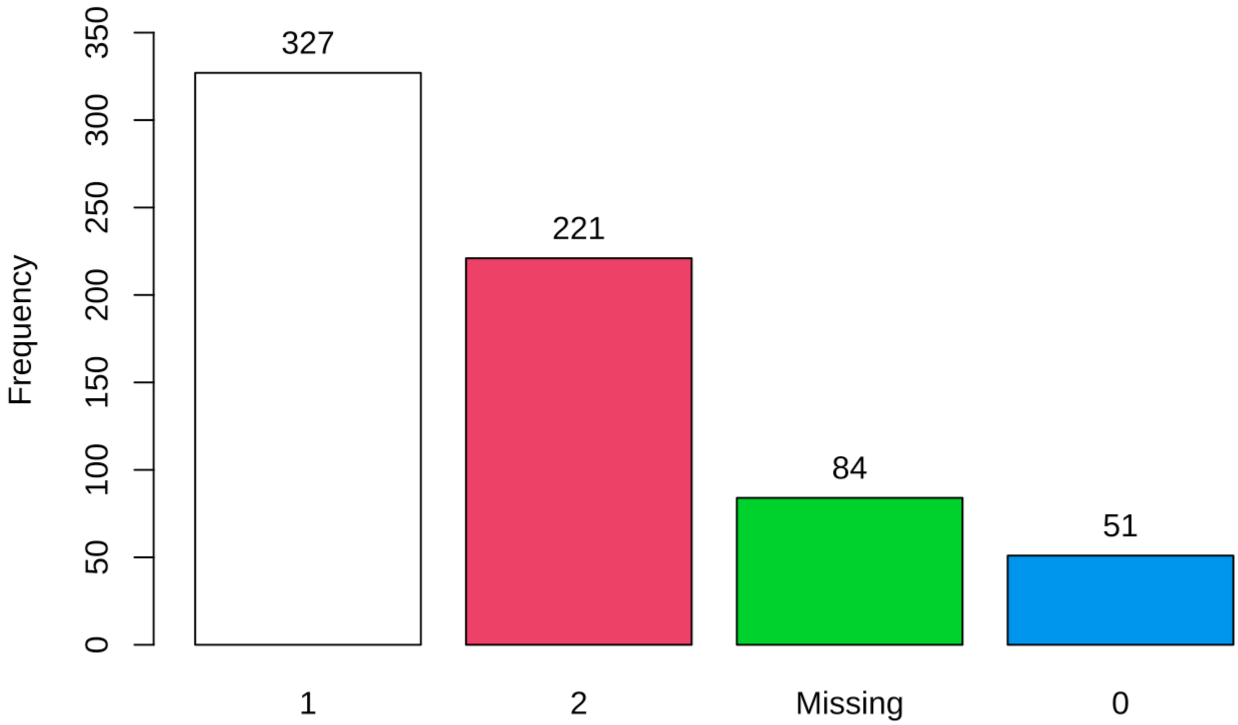
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
2             342     50.1       87.7     57.1      100.0
0             221     32.4       32.4     36.9       36.9
NA's           84     12.3      100.0      0.0      100.0
1              36      5.3       37.6      6.0       42.9
  Total       683    100.0      100.0    100.0      100.0
```



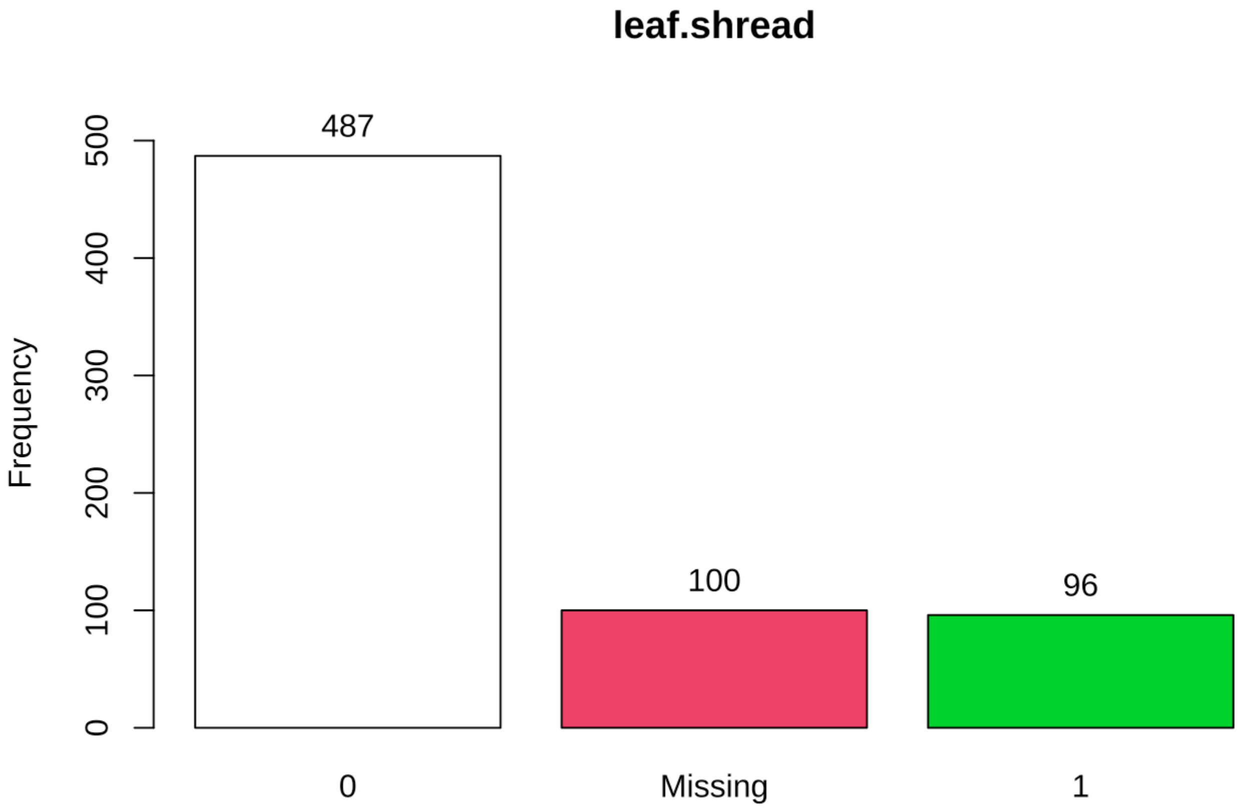


```
predictor :
         Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0              357     52.3       52.3     59.6       59.6
2              221     32.4       87.7     36.9      100.0
NA's            84     12.3      100.0      0.0      100.0
1               21      3.1       55.3      3.5       63.1
  Total        683    100.0      100.0    100.0      100.0
```

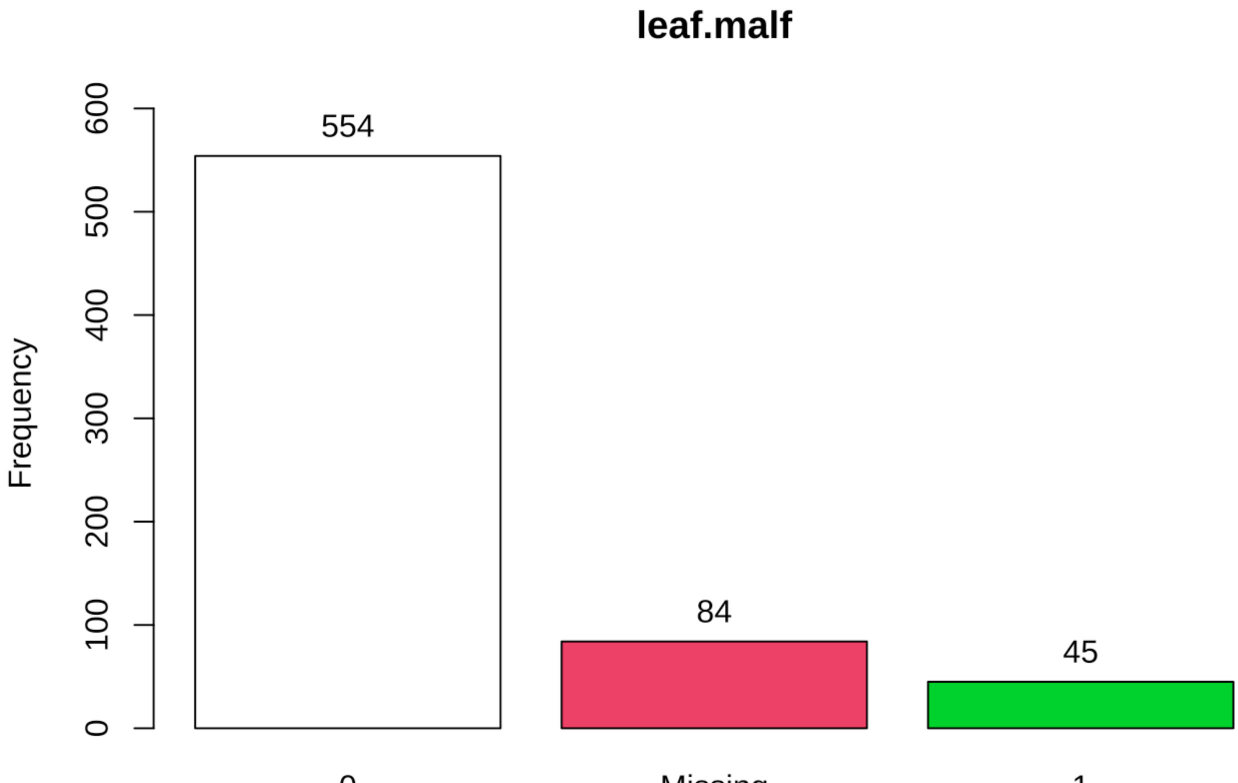
leaf.size



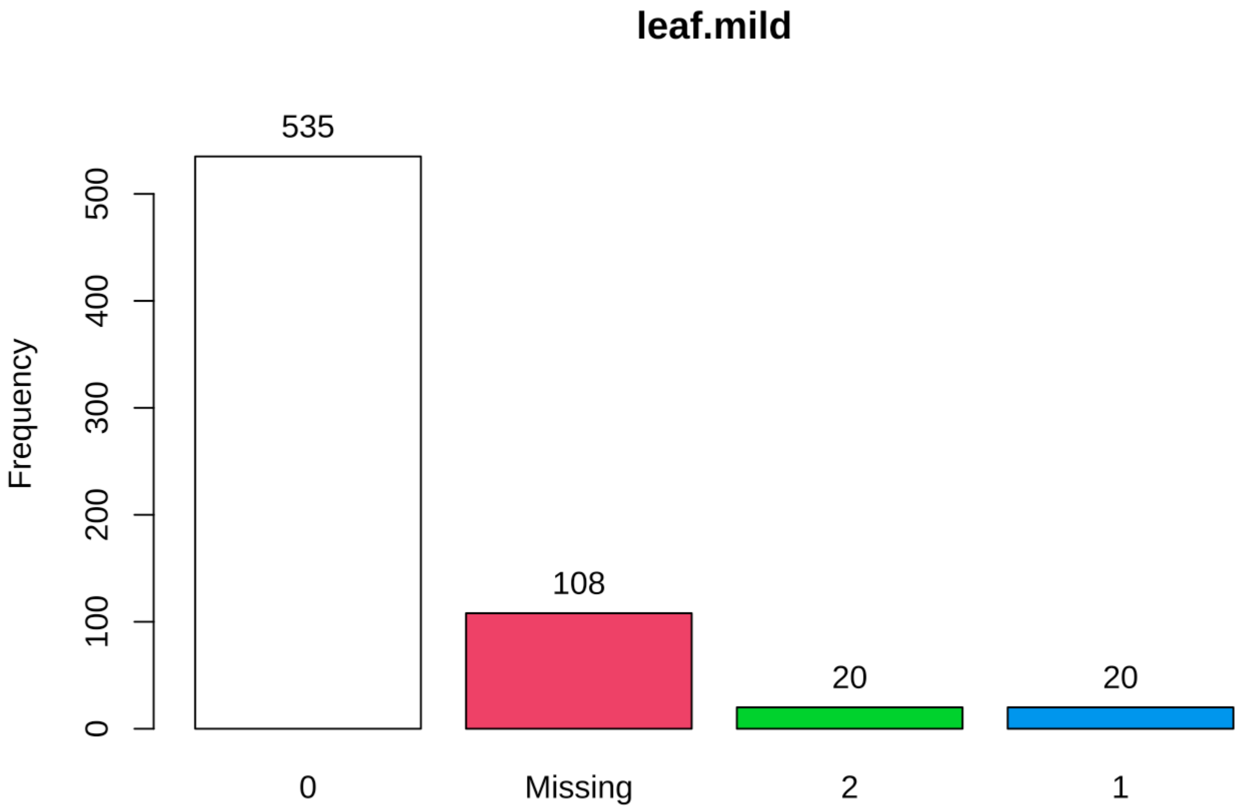
```
predictor :
         Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
1              327     47.9       55.3     54.6       63.1
2              221     32.4       87.7     36.9      100.0
NA's            84     12.3      100.0      0.0      100.0
0               51      7.5        7.5      8.5        8.5
  Total        683    100.0      100.0    100.0      100.0
```



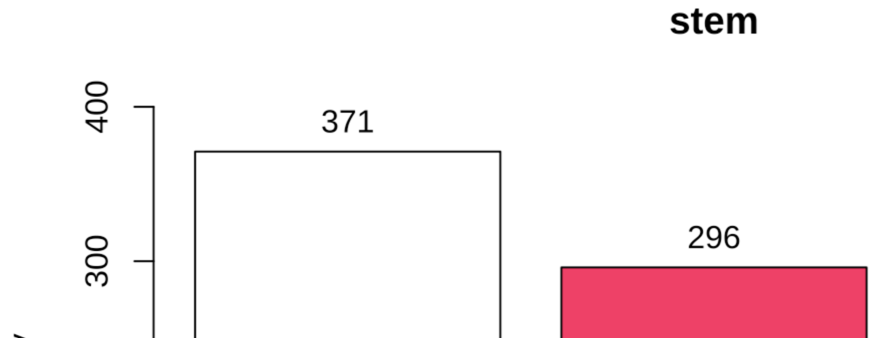
```
predictor :
          Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0               487     71.3       71.3     83.5       83.5
NA's            100     14.6      100.0      0.0      100.0
1                96     14.1       85.4     16.5      100.0
  Total         683    100.0      100.0    100.0      100.0
```

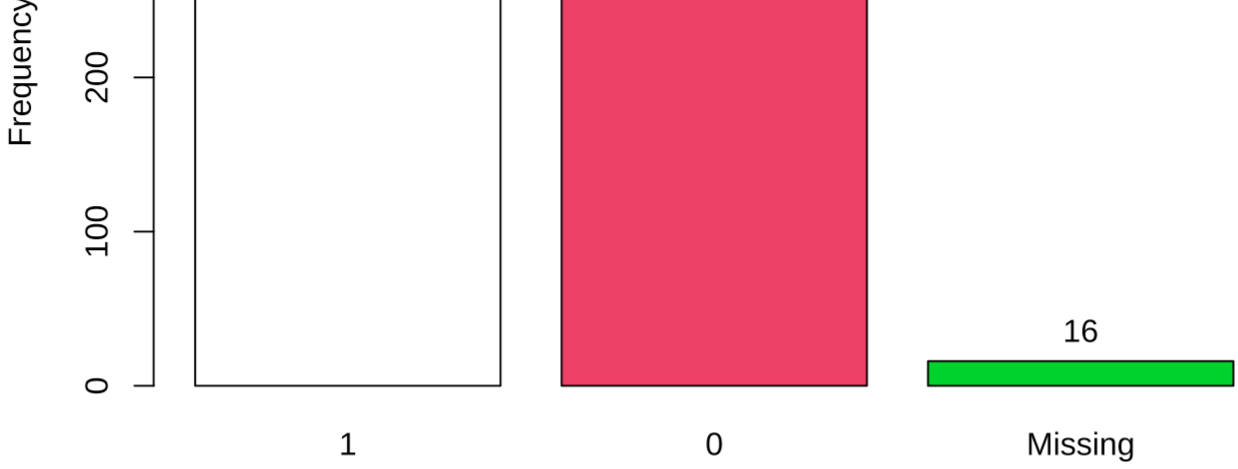


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             554     81.1       81.1     92.5       92.5
NA's           84     12.3      100.0      0.0      100.0
1              45      6.6       87.7      7.5      100.0
  Total       683    100.0      100.0    100.0      100.0
```

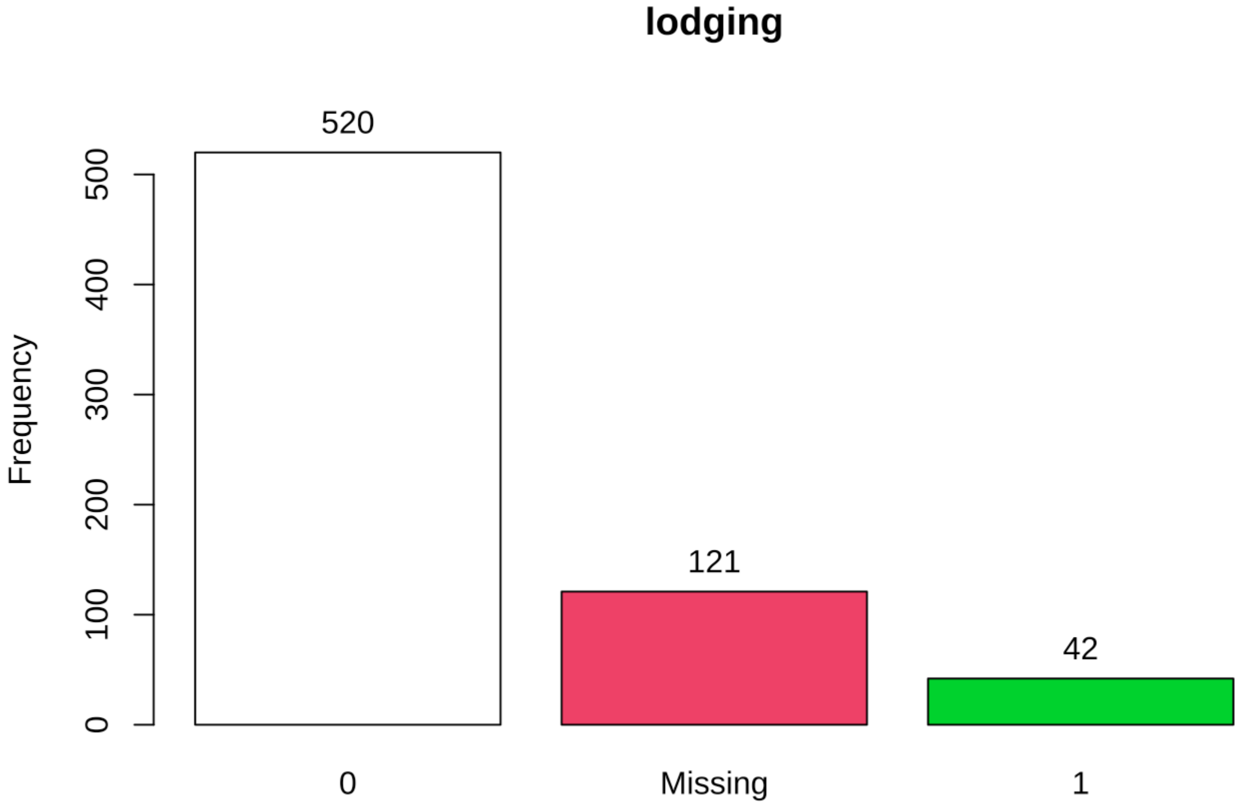


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             535     78.3       78.3     93.0       93.0
NA's          108     15.8      100.0      0.0      100.0
1              20      2.9       81.3      3.5       96.5
2              20      2.9       84.2      3.5      100.0
  Total       683    100.0      100.0    100.0      100.0
```

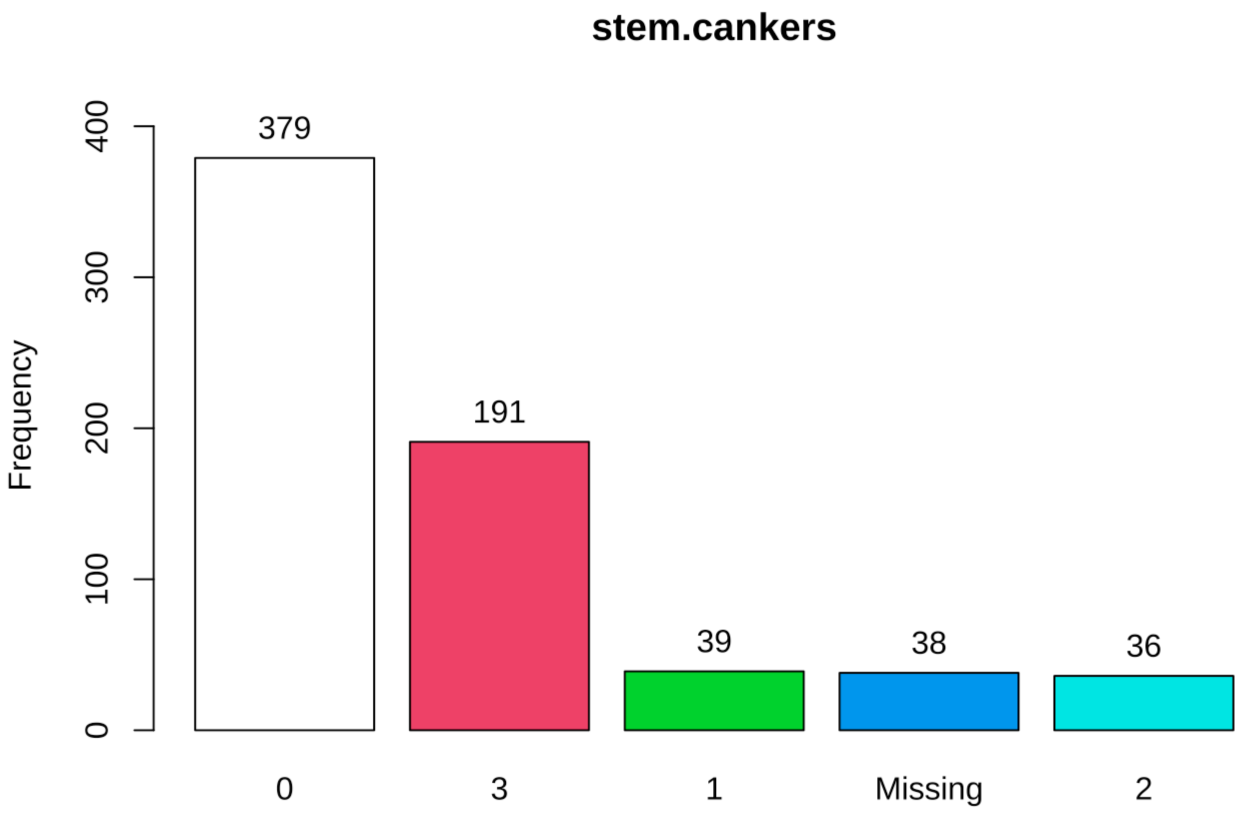




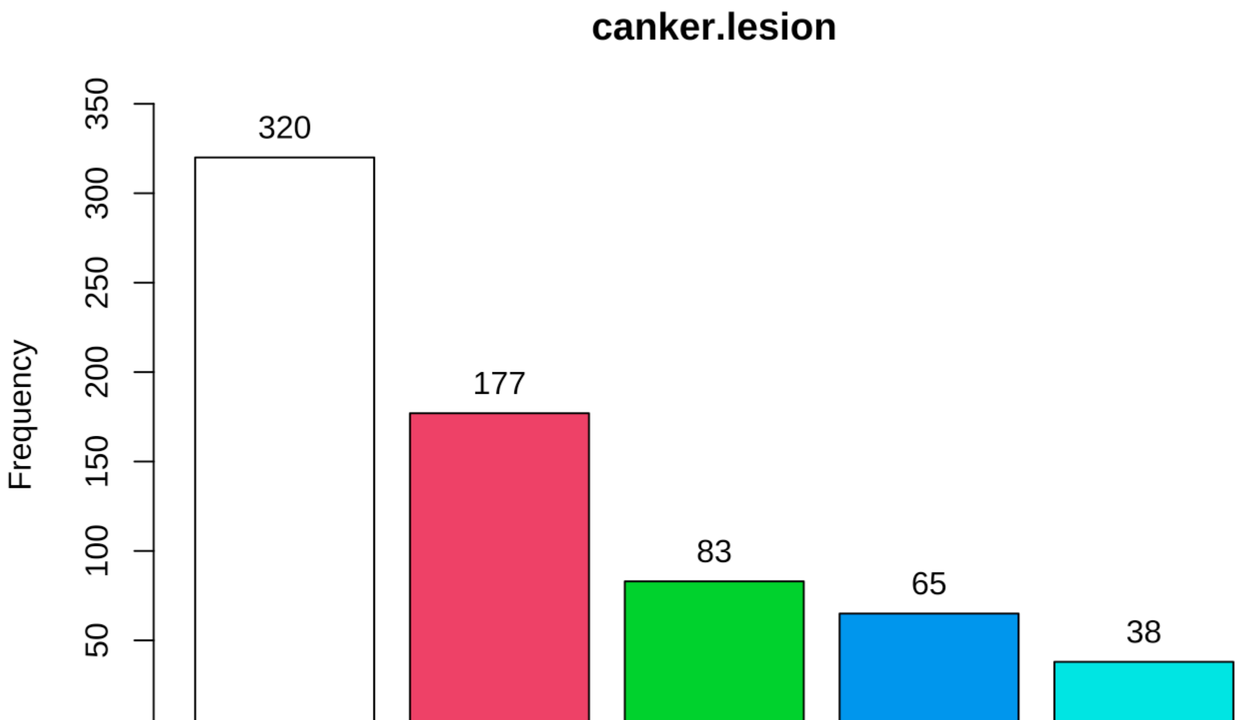
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
1             371     54.3       97.7     55.6      100.0
0             296     43.3       43.3     44.4       44.4
NA's           16      2.3      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```



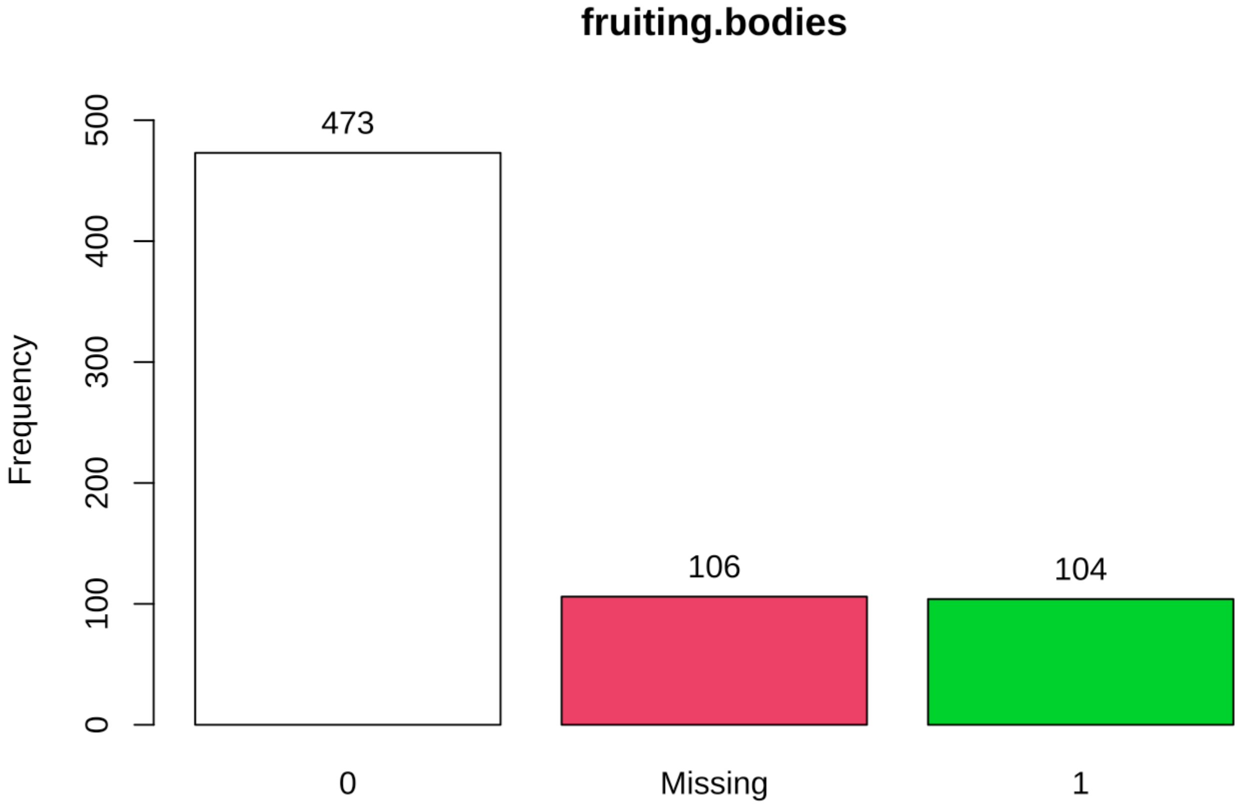
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             520     76.1       76.1     92.5       92.5
NA's          121     17.7      100.0      0.0      100.0
1              42      6.1       82.3      7.5      100.0
  Total       683    100.0      100.0    100.0      100.0
```



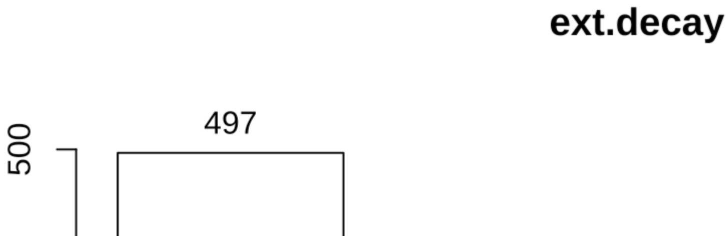
```
predictor :
         Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0              379     55.5       55.5     58.8       58.8
3              191     28.0       94.4     29.6      100.0
1               39      5.7       61.2      6.0       64.8
NA's            38      5.6      100.0      0.0      100.0
2               36      5.3       66.5      5.6       70.4
  Total        683    100.0      100.0    100.0      100.0
```

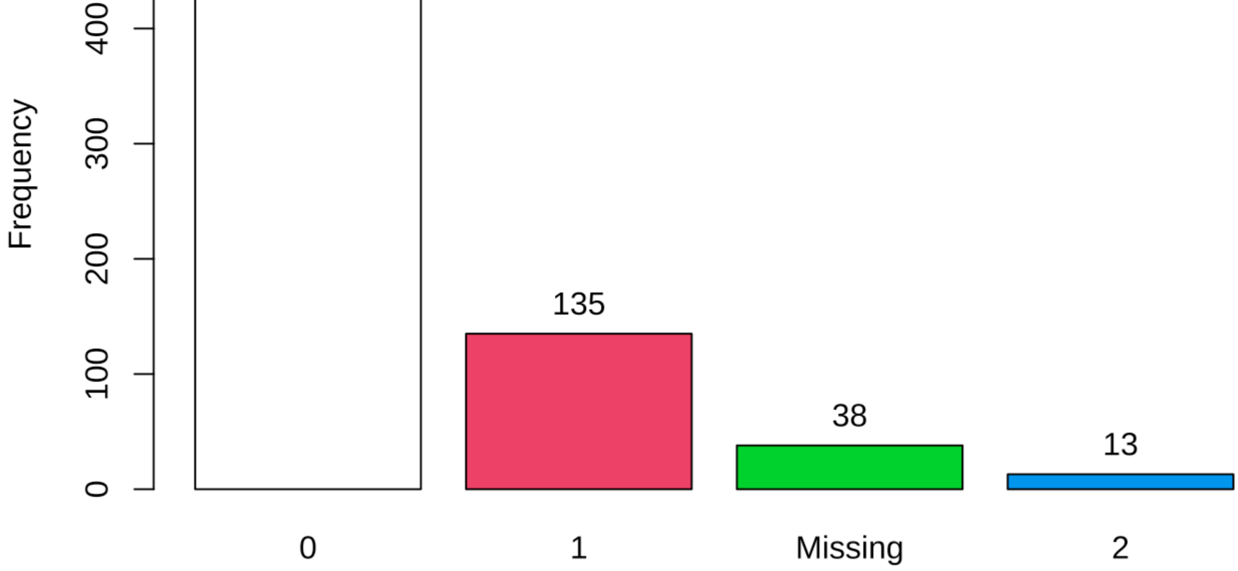


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             320     46.9       46.9     49.6       49.6
2             177     25.9       84.9     27.4       89.9
1              83     12.2       59.0     12.9       62.5
3              65      9.5       94.4     10.1      100.0
NA's           38      5.6      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```

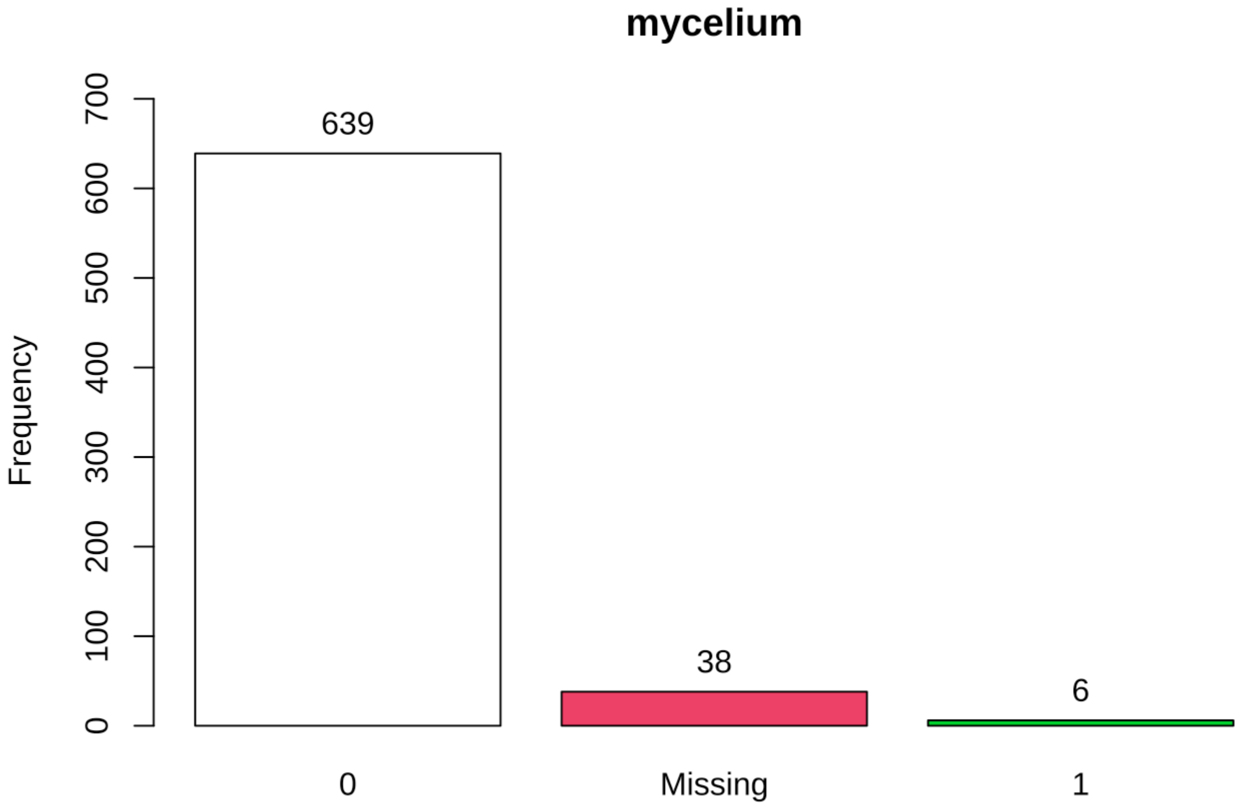

fruiting.bodies

```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             473     69.3       69.3       82         82
NA's          106     15.5      100.0        0        100
1             104     15.2       84.5       18        100
  Total       683    100.0      100.0      100        100
```


ext.decay

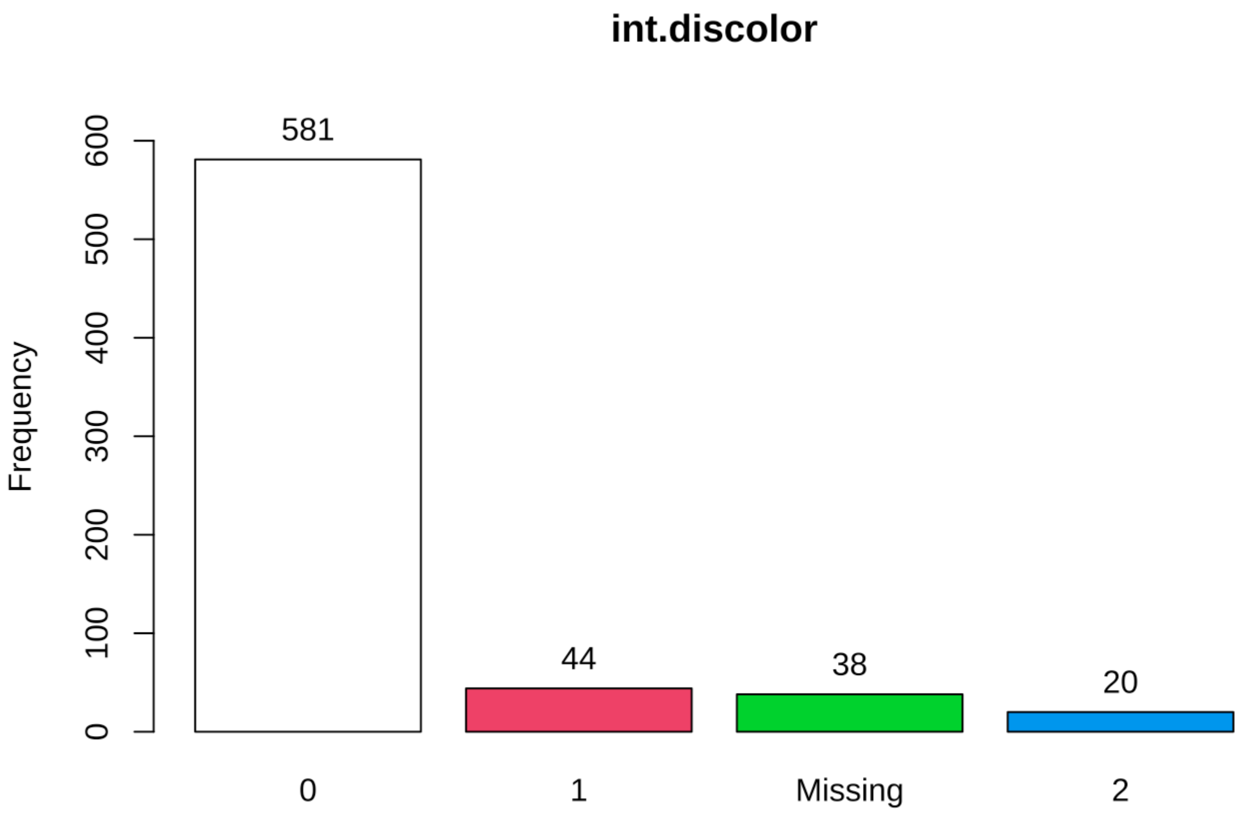


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             497     72.8       72.8     77.1       77.1
1             135     19.8       92.5     20.9       98.0
NA's           38      5.6      100.0      0.0      100.0
2              13      1.9       94.4      2.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```

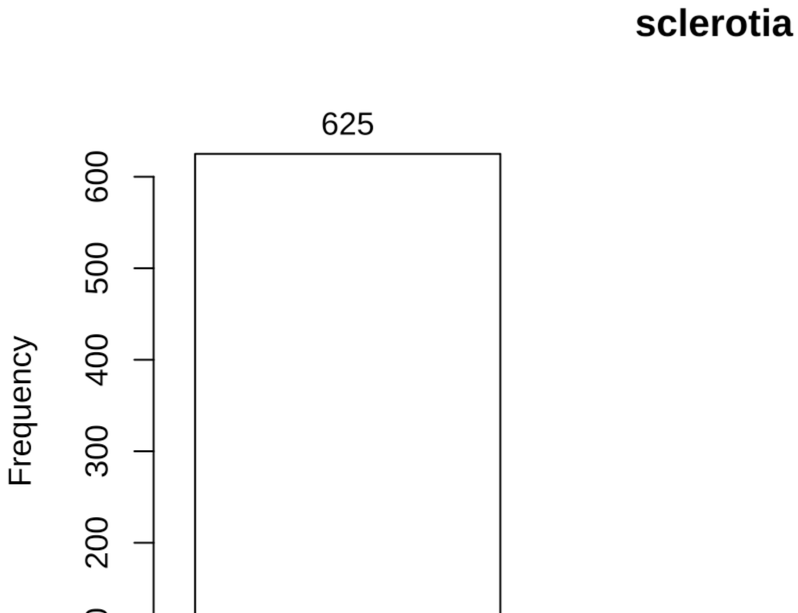


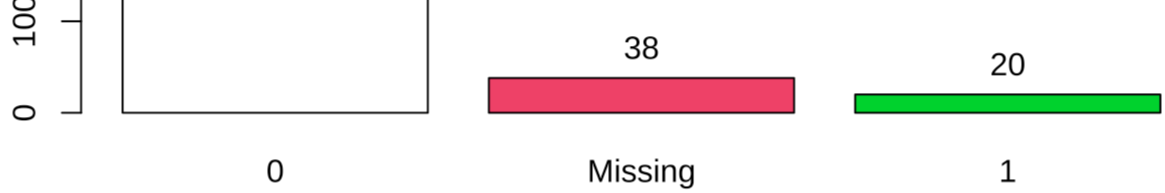
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             639     93.6       93.6     99.1       99.1
```

```
NA's            38      5.6      100.0      0.0      100.0
1                6      0.9       94.4      0.9      100.0
  Total        683    100.0      100.0    100.0      100.0
```



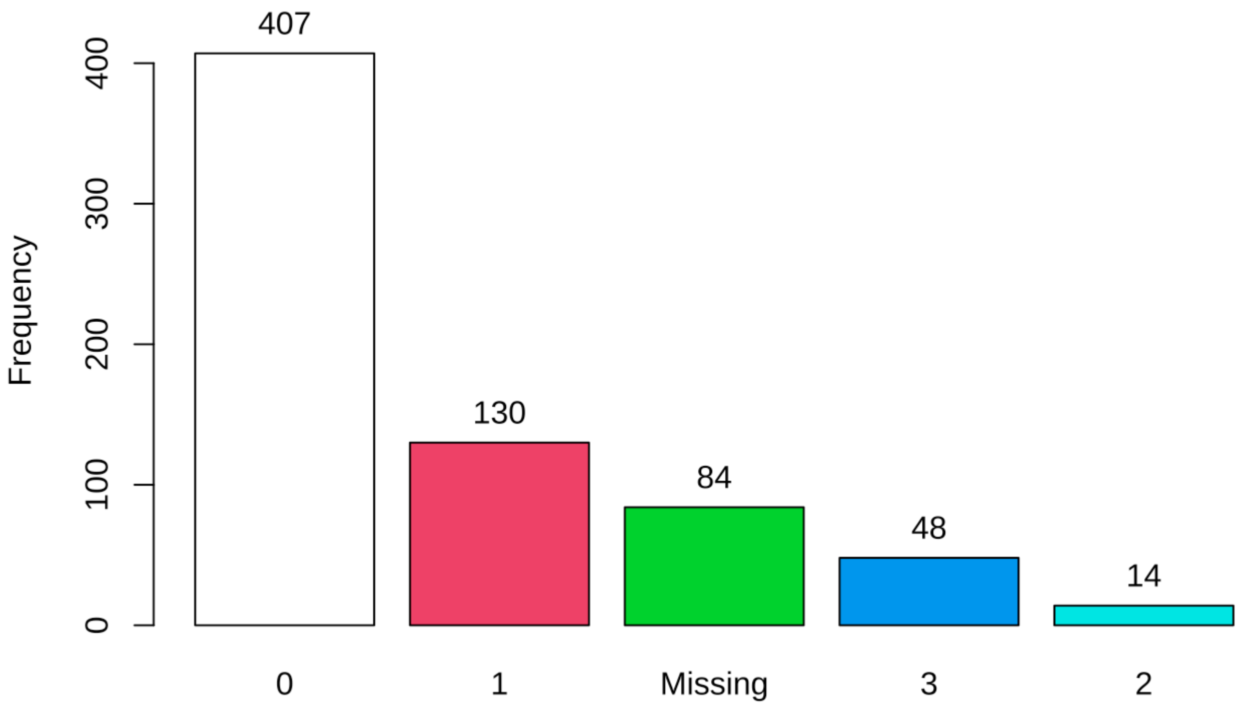
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             581     85.1       85.1     90.1       90.1
1              44      6.4       91.5      6.8       96.9
NA's           38      5.6      100.0      0.0      100.0
2              20      2.9       94.4      3.1      100.0
  Total       683    100.0      100.0    100.0      100.0
```





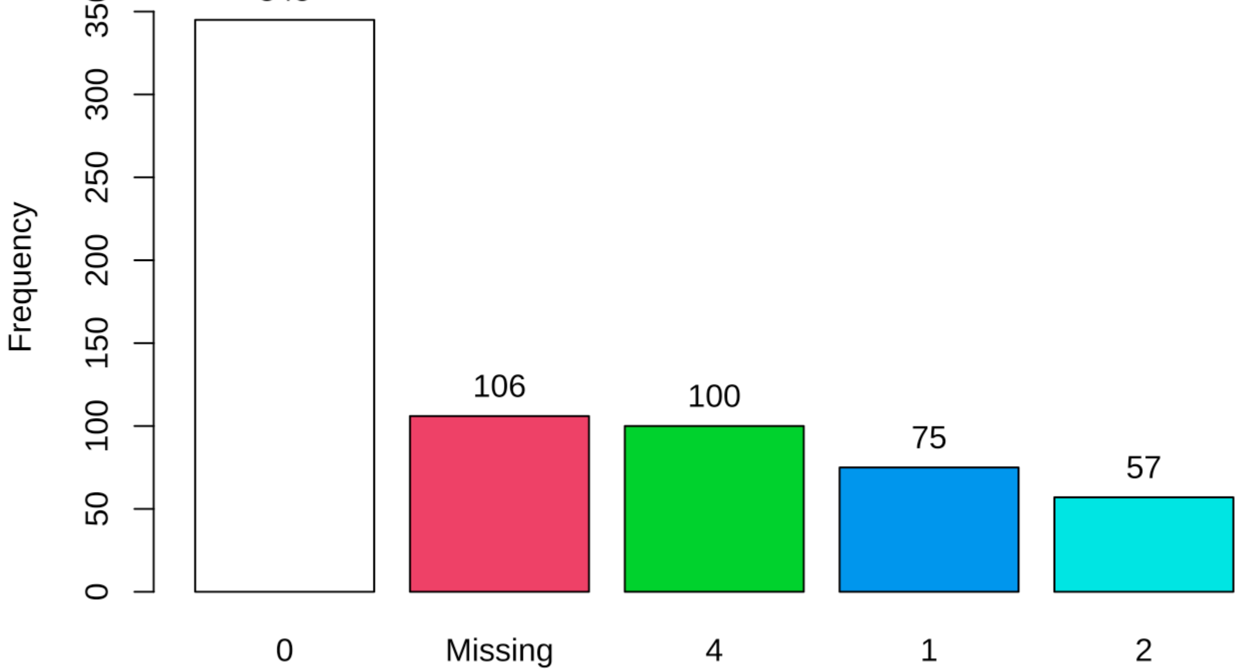
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             625     91.5       91.5     96.9       96.9
NA's           38      5.6      100.0      0.0      100.0
1              20      2.9       94.4      3.1      100.0
  Total       683    100.0      100.0    100.0      100.0
```

fruit.pods

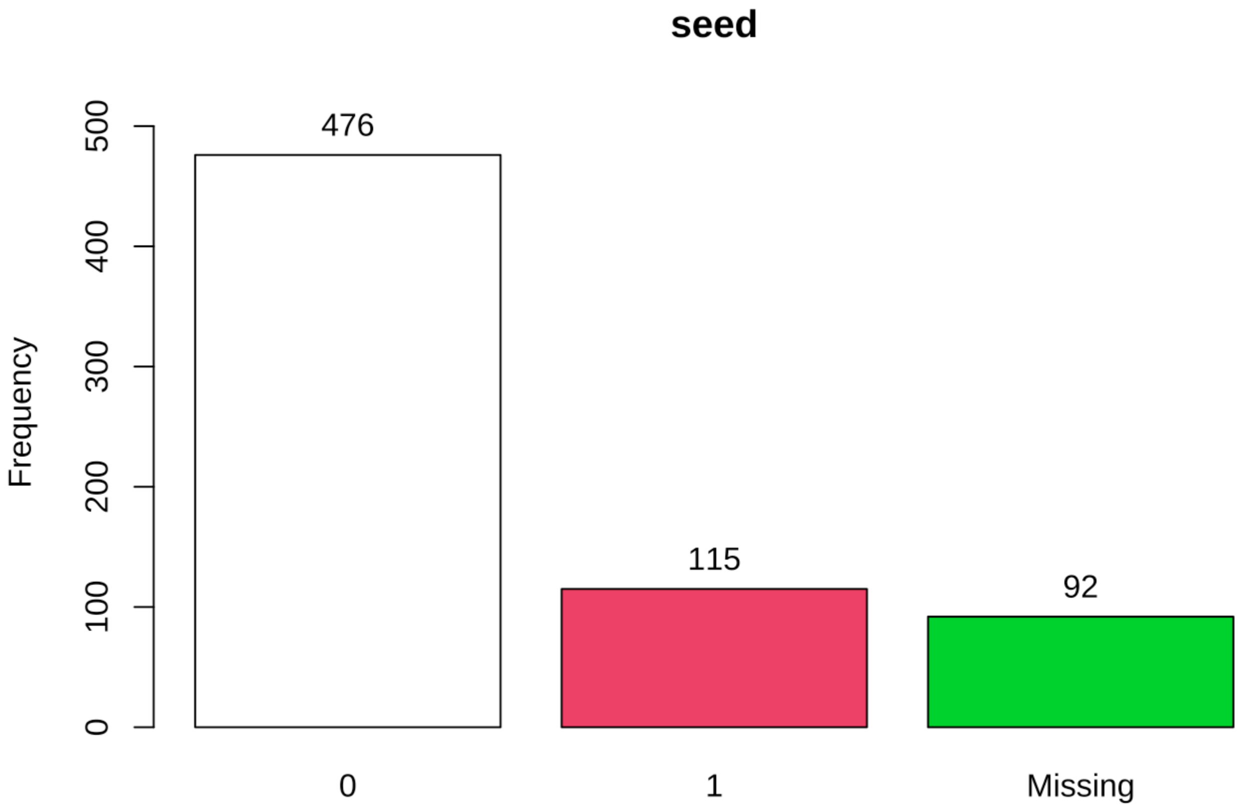


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             407     59.6       59.6     67.9       67.9
1             130     19.0       78.6     21.7       89.6
NA's           84     12.3      100.0      0.0      100.0
3              48      7.0       87.7      8.0      100.0
2              14      2.0       80.7      2.3       92.0
  Total       683    100.0      100.0    100.0      100.0
```

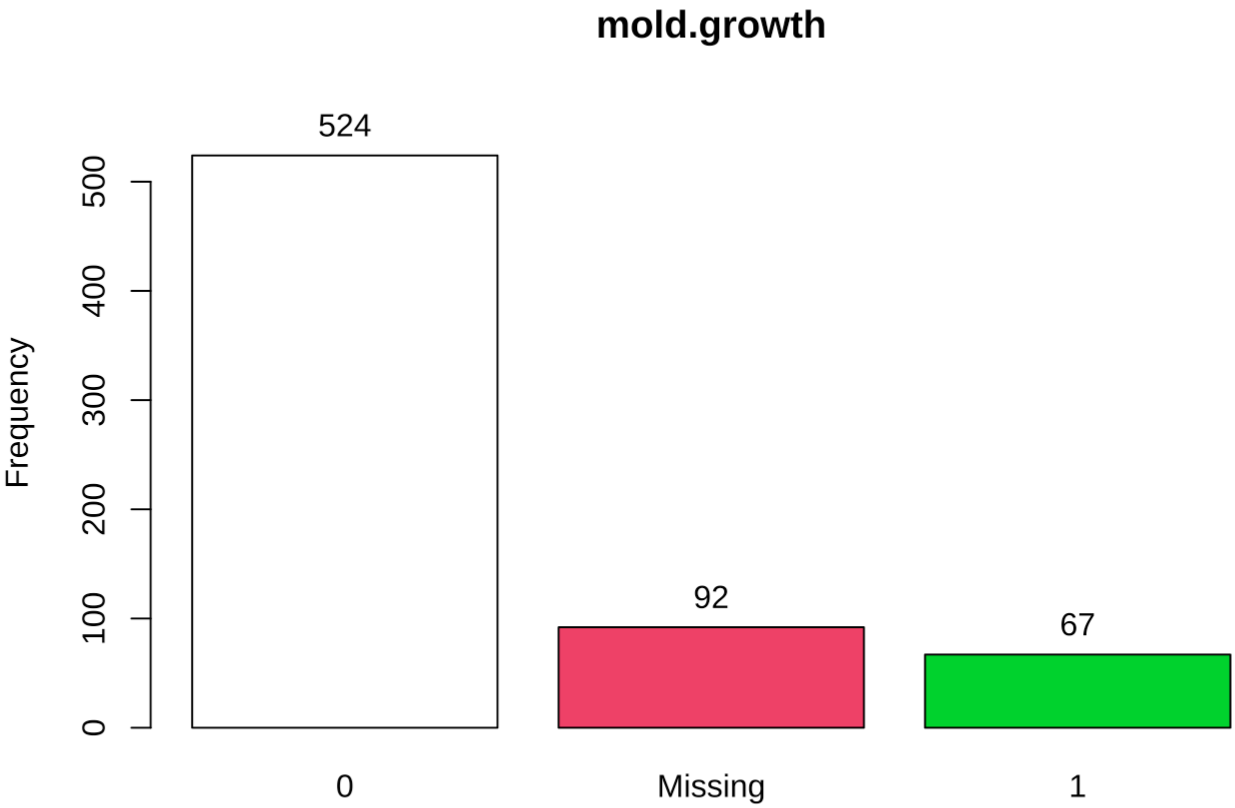
fruit.spots



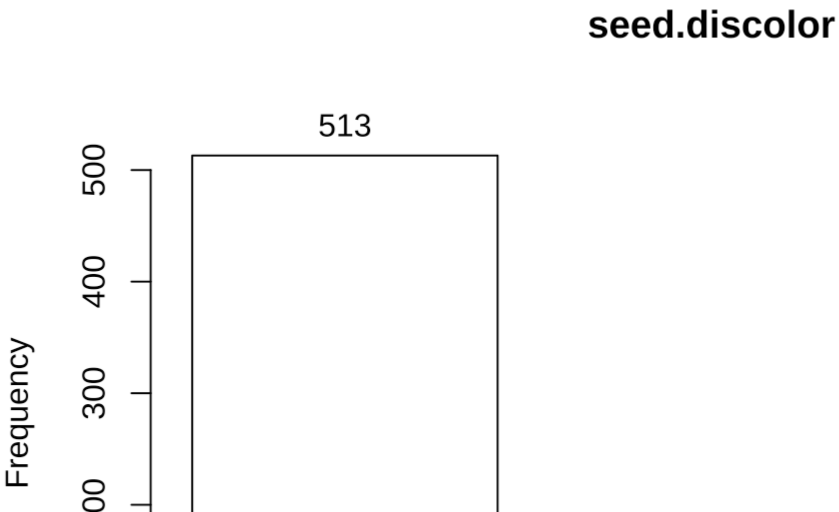
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             345     50.5       50.5     59.8       59.8
NA's          106     15.5      100.0      0.0      100.0
4             100     14.6       84.5     17.3      100.0
1              75     11.0       61.5     13.0       72.8
2              57      8.3       69.8      9.9       82.7
  Total       683    100.0      100.0    100.0      100.0
```

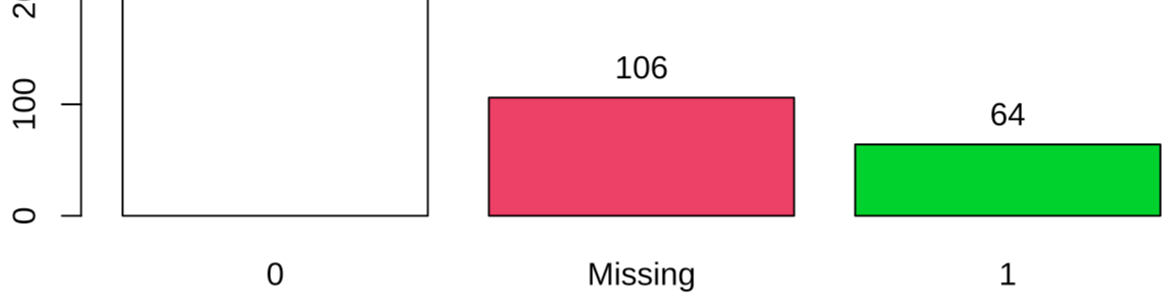


```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             476     69.7       69.7     80.5       80.5
1             115     16.8       86.5     19.5      100.0
NA's           92     13.5      100.0      0.0      100.0
  Total       683    100.0      100.0    100.0      100.0
```



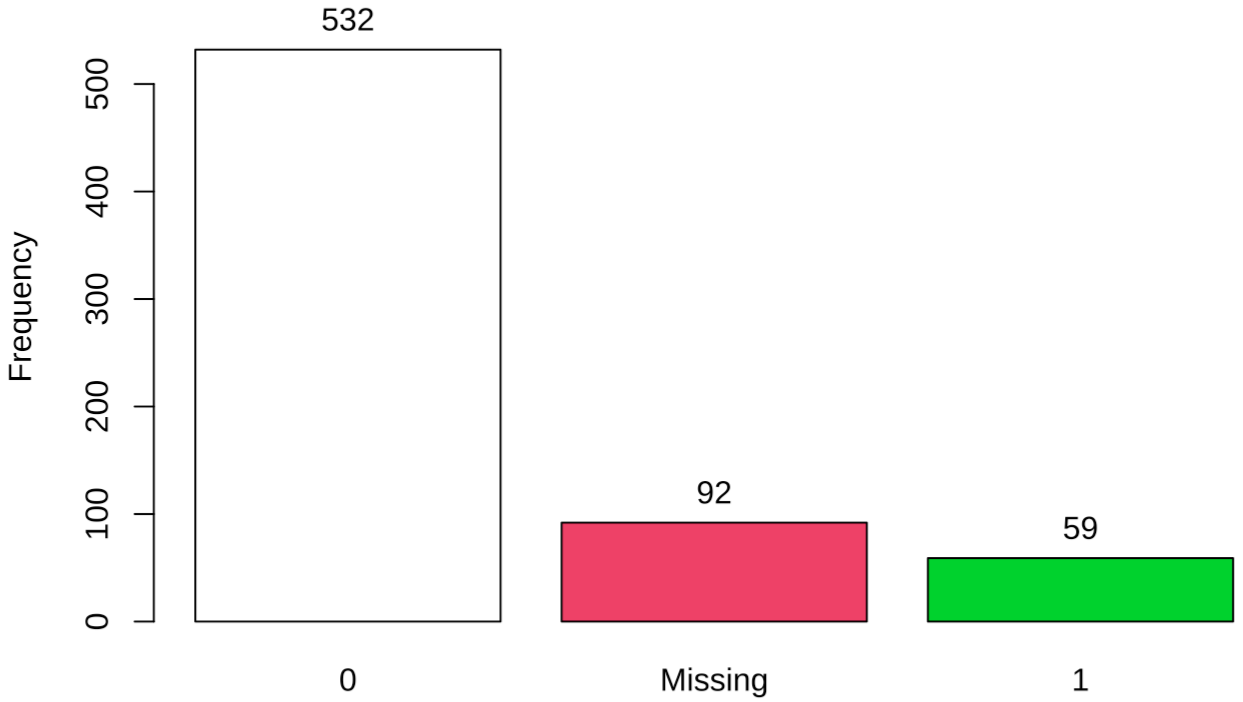
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             524     76.7       76.7     88.7       88.7
NA's           92     13.5      100.0      0.0      100.0
1              67      9.8       86.5     11.3      100.0
  Total       683    100.0      100.0    100.0      100.0
```





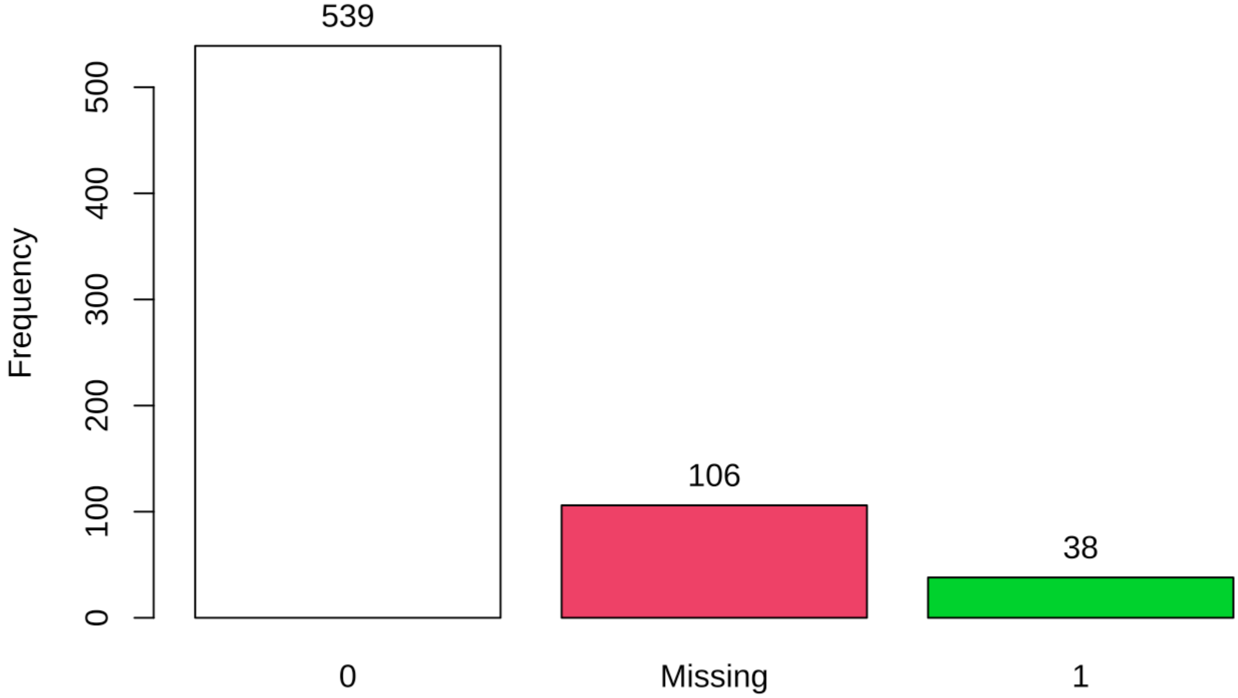
```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             513     75.1       75.1     88.9       88.9
NA's          106     15.5      100.0      0.0      100.0
1              64      9.4       84.5     11.1      100.0
  Total       683    100.0      100.0    100.0      100.0
```

seed.size



```
predictor :
        Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0             532     77.9       77.9       90         90
NA's           92     13.5      100.0        0        100
1              59      8.6       86.5       10        100
  Total       683    100.0      100.0      100        100
```

shriveling

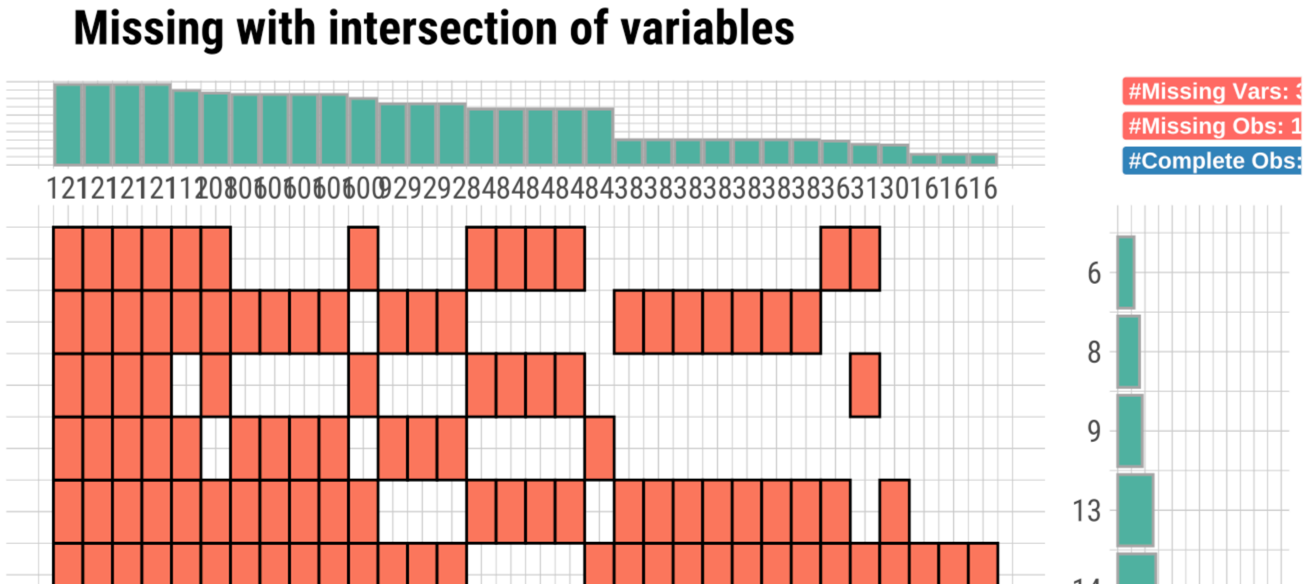


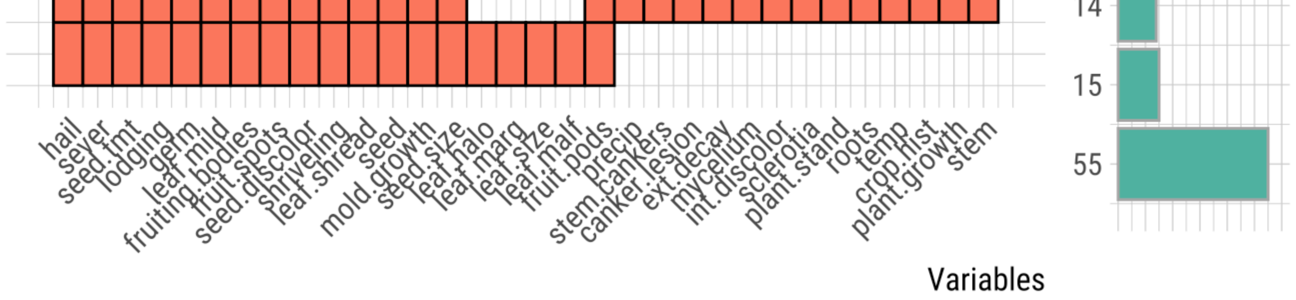
```
predictor :
          Frequency   %(NA+) cum.%(NA+)   %(NA-) cum.%(NA-)
0               539     78.9       78.9     93.4       93.4
NA's            106     15.5      100.0      0.0      100.0
1                38      5.6       84.5      6.6      100.0
  Total         683    100.0      100.0    100.0      100.0
```

Problematic distributions can be seen for variables: int.discolor, leaf.malf, leaf.mild, leaves, lodging, mycelium, mold.growth, roots, sclerotia, seed.discolor, seed.size, and shriveling. Many of these variables only have two factors that is dominated by a single factor.

2b) 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?

```
Soybean %>%
  plot_na_intersect(only_na = TRUE, typographic = TRUE, n_intersacts = 7)
```





34 variables have missing data. Hail, server, seed.tmt, and lodging are all missing from the 121 incomplete cases. These predictors are more likely to be missing. In 55 cases, we identified that the first 16 variables are missing from left to right, indicating a potential pattern of missing data related to classes.

```
missing_total <- colSums(is.na(Soybean))
missing_total
```

```
          Class            date     plant.stand          precip            temp 
              0               1              36              38              30 
           hail       crop.hist        area.dam           sever        seed.tmt 
            121              16               1             121             121 
           germ    plant.growth          leaves       leaf.halo       leaf.marg 
            112              16               0              84              84 
      leaf.size     leaf.shread       leaf.malf       leaf.mild            stem 
             84             100              84             108              16 
        lodging    stem.cankers   canker.lesion fruiting.bodies       ext.decay 
            121              38              38             106              38 
       mycelium    int.discolor       sclerotia      fruit.pods     fruit.spots 
             38              38              38              84             106 
           seed     mold.growth   seed.discolor       seed.size      shriveling 
             92              92             106              92             106 
          roots 
             31 
```

```
missing_pct <- missing_total / nrow(Soybean) * 100
missing_pct
```

```
          Class            date     plant.stand          precip            temp 
      0.0000000       0.1464129       5.2708638       5.5636896       4.3923865 
           hail       crop.hist        area.dam           sever        seed.tmt 
     17.7159590       2.3426061       0.1464129      17.7159590      17.7159590 
           germ    plant.growth          leaves       leaf.halo       leaf.marg 
     16.3982430       2.3426061       0.0000000      12.2986823      12.2986823 
      leaf.size     leaf.shread       leaf.malf       leaf.mild            stem 
     12.2986823      14.6412884      12.2986823      15.8125915       2.3426061 
        lodging    stem.cankers   canker.lesion fruiting.bodies       ext.decay 
     17.7159590       5.5636896       5.5636896      15.5197657       5.5636896 
       mycelium    int.discolor       sclerotia      fruit.pods     fruit.spots 
      5.5636896       5.5636896       5.5636896      12.2986823      15.5197657 
           seed     mold.growth   seed.discolor       seed.size      shriveling 
     13.4699854      13.4699854      15.5197657      13.4699854      15.5197657 
          roots 
      4.5387994 
```

```
sorted_missing <- sort(missing_pct, decreasing = TRUE)
sorted_missing
```

```
           hail           sever        seed.tmt         lodging            germ
     17.7159590      17.7159590      17.7159590      17.7159590      16.3982430
      leaf.mild fruiting.bodies     fruit.spots    seed.discolor      shriveling
     15.8125915      15.5197657      15.5197657      15.5197657      15.5197657
    leaf.shread            seed     mold.growth       seed.size       leaf.halo
     14.6412884      13.4699854      13.4699854      13.4699854      12.2986823
      leaf.marg       leaf.size       leaf.malf      fruit.pods          precip
     12.2986823      12.2986823      12.2986823      12.2986823       5.5636896
   stem.cankers   canker.lesion       ext.decay        mycelium    int.discolor
      5.5636896       5.5636896       5.5636896       5.5636896       5.5636896
     sclerotia     plant.stand           roots            temp       crop.hist
      5.5636896       5.2708638       4.5387994       4.3923865       2.3426061
   plant.growth            stem            date        area.dam           Class
      2.3426061       2.3426061       0.1464129       0.1464129       0.0000000
         leaves
      0.0000000
```

```
missing_preds <- names(sorted_missing)[sorted_missing > 0]
missing_preds
```

```
 [1] "hail"            "sever"           "seed.tmt"        "lodging"
 [5] "germ"            "leaf.mild"       "fruiting.bodies" "fruit.spots"
 [9] "seed.discolor"   "shriveling"      "leaf.shread"     "seed"
[13] "mold.growth"     "seed.size"       "leaf.halo"       "leaf.marg"
[17] "leaf.size"       "leaf.malf"       "fruit.pods"      "precip"
[21] "stem.cankers"    "canker.lesion"   "ext.decay"       "mycelium"
[25] "int.discolor"    "sclerotia"       "plant.stand"     "roots"
[29] "temp"            "crop.hist"       "plant.growth"    "stem"
[33] "date"            "area.dam"
```

2c) Develop a strategy for handling missing data, either by eliminating predictors or imputation.

To handle missing data, my strategy would drop variables with degenerate distributions and impute missing values using the k-nearest neighbors algorithm. The algorithm would determine what observations are normally grouped together based on complete observations in the dataset.

Problem 3 - Oil dataset

Import Data

```
data(oil)
```

Examine data structure

```
str(oilType)
```

```
 Factor w/ 7 levels "A","B","C","D",..: 1 1 1 1 1 1 1 1 1 1 ...
```

Oil Type data table

```
table(oilType)
```

```
oilType
 A  B  C  D  E  F  G 
37 26  3  7 11 10  2 
```

3a) Use the sample function in base R to create a completely random sample of 60 oils. How closely do the frequencies of the random sample match the original samples? Repeat this procedure several times of understand the variation in the sampling process.

```
samp1 <- sample(oilType, 60, replace = FALSE, prob = NULL)
table(samp1)
```

```
samp1
 A  B  C  D  E  F  G 
24 17  3  4  6  6  0 
```

```
samp2 <- sample(oilType, 60, replace = FALSE, prob = NULL)
table(samp2)
```

```
samp2
 A  B  C  D  E  F  G 
24 18  2  5  6  4  1 
```

```
samp3 <- sample(oilType, 60, replace = FALSE, prob = NULL)
table(samp3)
```

```
samp3
 A  B  C  D  E  F  G 
20 18  3  7  6  5  1 
```

```
samp4 <- sample(oilType, 60, replace = FALSE, prob = NULL)
table(samp4)
```

```
samp4
 A  B  C  D  E  F  G 
22 16  2  4  9  6  1 
```

The sampling function produces accurate random samples, and the frequencies of these samples closely match the original, but there is some minor variation that is insignificant.

3b) Use the caret package function createDataPartition to create a stratified random sample. How does this compare to completely random samples?

```
set.seed(318)
```

```r
strat_samp <- createDataPartition(oilType, p = .70, times = 20)
strat_samp <- lapply(strat_samp, function(x, y) table(y[x]), y = oilType)
head(strat_samp, 3)
```

```
$Resample01

 A  B  C  D  E  F  G 
26 19  3  5  8  7  2 

$Resample02

 A  B  C  D  E  F  G 
26 19  3  5  8  7  2 

$Resample03

 A  B  C  D  E  F  G 
26 19  3  5  8  7  2 
```

This sampling technique allocates the equal samples to each class for every round of sampling to minimize the variance of each sample.

3c) With such a small samples size, what are the options for determining performance of the model? Should a test set be used?

Leave one out cross validation is the best option for assessing the performance of a model when the dataset is small and unbalanced. This method uses every data point as a test set once with the rest as the training set. This provides the same number of performance estimates as data points that can be averaged to get a more precise measure. This method uses a test set.

3d) Try different samples sizes and accuracy rates to understand the trade-off between the uncertainty in the results, the model performance, and the test set size.

```r
binom.test(20, 76)
```

```

	Exact binomial test

data:  20 and 76
number of successes = 20, number of trials = 76, p-value = 4.369e-05
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.1687394 0.3767601
sample estimates:
probability of success 
             0.2631579 
```

```r
binom.test(45, 76)
```

```

	Exact binomial test

data:  45 and 76
```

```
data:  45 and 76
number of successes = 45, number of trials = 76, p-value = 0.1354
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.4732913 0.7035155
sample estimates:
probability of success 
             0.5921053 
```

```
binom.test(15, 76)
```

```

	Exact binomial test

data:  15 and 76
number of successes = 15, number of trials = 76, p-value = 9.843e-08
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.1148853 0.3045513
sample estimates:
probability of success 
             0.1973684 
```

As we increase the number of sample sizes, the accuracy of our model increases. The width of our 95% confidence interval and our p-value also increases, indicating that more samples can decrease the significance of our predictor.

4) Briefly discuss what is the bias-variance tradeoff in statistics and predictive modeling.

Bias and variance are the two main components of prediction errors in a model. Bias errors are the difference between a model's predictions and actual values. These errors arise when the model does not adequately learn the patterns of our data. The model is oversimplified and not accounting for all features, underfitting the data. Variance errors occur when the model memorizes the data rather than learn, causing the target function's estimate to substantially change with different training data. The model fails to make generalizations about data it hasn't seen, overfitting the data. The bias-variance trade-off is the attempt to balance between errors caused from bias vs. variance.