Initiation à la statistique avec R, code et compléments chapitre 3

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```r
#Chapitre 3
#page 95
library(BioStatR)
Mesures
```

```
##      masse taille          espece
## 1    28.6   19.1  glycine blanche
## 2    20.6   14.8  glycine blanche
## 3    29.2   19.7  glycine blanche
## 4    32.0   21.1  glycine blanche
## 5    24.5   19.4  glycine blanche
## 6    29.0   19.5  glycine blanche
## 7    28.9   18.9  glycine blanche
## 8    18.2   14.6  glycine blanche
## 9     7.9   10.2  glycine blanche
## 10   15.5   14.6  glycine blanche
## 11   22.6   16.4  glycine blanche
## 12   35.5   21.1  glycine blanche
## 13   32.5   20.7  glycine blanche
## 14   28.7   18.7  glycine blanche
## 15   26.0   17.6  glycine blanche
## 16   13.5   13.2  glycine blanche
## 17   16.4   14.0  glycine blanche
## 18   12.5   12.0  glycine blanche
## 19   26.2   18.3  glycine blanche
## 20   22.6   17.8  glycine blanche
## 21    9.7   10.7  glycine blanche
## 22   21.8   16.5  glycine blanche
## 23   17.2   14.5  glycine blanche
## 24   25.2   17.5  glycine blanche
## 25   12.0   12.2  glycine blanche
## 26    6.3    8.6  glycine blanche
## 27    7.0    9.1  glycine blanche
## 28   20.4   17.0  glycine blanche
## 29   18.0   15.3  glycine blanche
## 30   21.1   15.8  glycine blanche
## 31   18.2   15.9  glycine blanche
## 32   15.2   12.2  glycine blanche
## 33   19.8   16.1  glycine blanche
## 34   21.4   16.0  glycine blanche
## 35   15.0   13.8  glycine blanche
## 36   16.4   14.4  glycine blanche
## 37   17.3   14.2  glycine blanche
## 38   16.4   15.7  glycine blanche
## 39   13.5   12.6  glycine blanche
```

```
## 40   13.6   12.0  glycine blanche
## 41   14.6   12.8  glycine blanche
## 42   16.9   15.3  glycine blanche
## 43   11.7   12.4  glycine blanche
## 44   14.0   14.5  glycine blanche
## 45   14.6   12.3  glycine blanche
## 46   10.3   11.8  glycine blanche
## 47   11.3   12.6  glycine blanche
## 48   10.7   11.3  glycine blanche
## 49   10.9   12.5  glycine blanche
## 50   20.0   16.1  glycine blanche
## 51   21.5   16.2  glycine blanche
## 52   12.0   11.3  glycine blanche
## 53    6.1    8.6  glycine blanche
## 54    5.4    8.2  glycine blanche
## 55   40.0   24.5 glycine violette
## 56   49.2   27.0 glycine violette
## 57   46.0   25.8 glycine violette
## 58   26.4   18.7 glycine violette
## 59   42.2   25.2 glycine violette
## 60   48.4   25.8 glycine violette
## 61   23.9   19.2 glycine violette
## 62   31.7   21.4 glycine violette
## 63   16.8   12.0 glycine violette
## 64   21.6   14.0 glycine violette
## 65   24.1   18.5 glycine violette
## 66   13.5   12.8 glycine violette
## 67   22.4   13.8 glycine violette
## 68   26.1   17.3 glycine violette
## 69   12.9   12.4 glycine violette
## 70   26.6   20.0 glycine violette
## 71   29.6   20.5 glycine violette
## 72   22.4   18.2 glycine violette
## 73   17.3   13.3 glycine violette
## 74   16.6   13.5 glycine violette
## 75   12.8   12.0 glycine violette
## 76   19.1   14.5 glycine violette
## 77   12.4   11.6 glycine violette
## 78    8.8    9.2 glycine violette
## 79   13.2   15.1 glycine violette
## 80   15.9   12.2 glycine violette
## 81   13.3   11.2 glycine violette
## 82    6.3    8.4 glycine violette
## 83   12.9   11.5 glycine violette
## 84    6.2    7.8 glycine violette
## 85    8.6    9.8 glycine violette
## 86   14.4   11.6 glycine violette
## 87   11.5    9.8 glycine violette
## 88   11.5   11.0 glycine violette
## 89   12.8   10.6 glycine violette
## 90   11.7   11.1 glycine violette
## 91   15.7   14.0 glycine violette
## 92   12.0   11.4 glycine violette
## 93   13.4   11.1 glycine violette
```

```
## 94    11.3    10.7 glycine violette
## 95     6.6     7.9 glycine violette
## 96    17.8    13.7 glycine violette
## 97     9.6    10.0 glycine violette
## 98    14.3    12.8 glycine violette
## 99    14.0    12.2 glycine violette
## 100   11.3    11.4 glycine violette
## 101   10.2    10.2 glycine violette
## 102   12.2    10.8 glycine violette
## 103   15.9    13.0 glycine violette
## 104   11.7    10.3 glycine violette
## 105   12.4    11.0 glycine violette
## 106   11.5    11.4 glycine violette
## 107   10.6    10.5 glycine violette
## 108    9.4     9.2 glycine violette
## 109    9.2     9.9 glycine violette
## 110    6.1     8.4 glycine violette
## 111   10.9    12.8         bignone
## 112    6.6    10.5         bignone
## 113   22.5    18.0         bignone
## 114   33.7    21.5         bignone
## 115   20.6    17.8         bignone
## 116   16.6    16.3         bignone
## 117   14.2    17.4         bignone
## 118   13.8    15.7         bignone
## 119   14.0    17.3         bignone
## 120    8.7    13.4         bignone
## 121   14.2    13.9         bignone
## 122   10.6    14.6         bignone
## 123   10.9    14.2         bignone
## 124    3.3     8.9         bignone
## 125    9.7    13.0         bignone
## 126    9.3    12.2         bignone
## 127   17.2    16.5         bignone
## 128   10.1    14.7         bignone
## 129    9.0    13.4         bignone
## 130    7.1    11.6         bignone
## 131    7.1    12.9         bignone
## 132    1.5     6.5         bignone
## 133    4.1     9.5         bignone
## 134    8.0    11.8         bignone
## 135    7.4    13.6         bignone
## 136    7.2    12.9         bignone
## 137    6.9    11.6         bignone
## 138    2.9     9.4         bignone
## 139    2.4     9.5         bignone
## 140   10.7    14.0         bignone
## 141   13.8    13.5         bignone
## 142   10.9    12.1         bignone
## 143   10.3    11.6         bignone
## 144    8.8    13.4         bignone
## 145    9.0    10.9         bignone
## 146    8.2    12.2         bignone
## 147    9.6    13.4         bignone
```

```
## 148   9.0   12.5          bignone
## 149   5.3   10.5          bignone
## 150   1.5    7.0          bignone
## 151   6.7   13.2          bignone
## 152   2.9    9.3          bignone
## 153   2.9    7.9          bignone
## 154   3.5   10.3          bignone
## 155   3.4    7.5          bignone
## 156   4.9    8.5          bignone
## 157   4.7   10.1          bignone
## 158   4.7    8.3          bignone
## 159   5.2   10.8          bignone
## 160   2.1    8.3          bignone
## 161   2.2    7.1          bignone
## 162   1.4    6.4          bignone
## 163   2.7    6.5          bignone
## 164   1.0    4.8          bignone
## 165   2.5    7.4          bignone
## 166   5.5    9.3          bignone
## 167   2.7    8.6          bignone
## 168   6.7    9.9          bignone
## 169   7.3   13.9          bignone
## 170   2.9    8.7          bignone
## 171   3.8    9.3          bignone
## 172   7.6   13.7          bignone
## 173   3.6    8.3          bignone
## 174   3.0    8.1          bignone
## 175   5.8   11.2          bignone
## 176   5.3   12.0          bignone
## 177   3.2   11.3          bignone
## 178   4.4    6.7          bignone
## 179   3.4   10.6          bignone
## 180   2.9    8.9          bignone
## 181   4.9   15.3     laurier rose
## 182   6.2   15.9     laurier rose
## 183   4.0   15.0     laurier rose
## 184   3.3   11.0     laurier rose
## 185   4.8   15.1     laurier rose
## 186   5.6   15.6     laurier rose
## 187   4.5   15.3     laurier rose
## 188   6.3   18.4     laurier rose
## 189   4.2   14.0     laurier rose
## 190   3.9   12.6     laurier rose
## 191   5.8   16.8     laurier rose
## 192   4.7   13.6     laurier rose
## 193   6.0   15.1     laurier rose
## 194   6.5   16.7     laurier rose
## 195   5.0   15.3     laurier rose
## 196   5.5   17.1     laurier rose
## 197   4.7   14.6     laurier rose
## 198   5.7   15.0     laurier rose
## 199   3.6   10.4     laurier rose
## 200   5.4   16.5     laurier rose
## 201   5.3   16.6     laurier rose
```

```
## 202    5.0    15.9        laurier rose
## 203    4.5    14.4        laurier rose
## 204    4.4    16.2        laurier rose
## 205    4.8    15.2        laurier rose
## 206    4.5    15.8        laurier rose
## 207    3.2    11.0        laurier rose
## 208    4.7    14.1        laurier rose
## 209    4.0    13.7        laurier rose
## 210    5.8    15.4        laurier rose
## 211    5.5    15.3        laurier rose
## 212    4.4    13.5        laurier rose
## 213    3.5    12.0        laurier rose
## 214    4.4    14.7        laurier rose
## 215    4.3    15.5        laurier rose
## 216    4.1    12.9        laurier rose
## 217    5.3    15.0        laurier rose
## 218    4.7    15.8        laurier rose
## 219    5.3    13.8        laurier rose
## 220    4.7    12.8        laurier rose
## 221    4.9    16.0        laurier rose
## 222    4.1    12.0        laurier rose
## 223    4.6    14.3        laurier rose
## 224    4.8    14.5        laurier rose
## 225    3.4    11.4        laurier rose
## 226    3.4    13.3        laurier rose
## 227    5.8    15.5        laurier rose
## 228    4.8    15.1        laurier rose
## 229    3.9    12.8        laurier rose
## 230    3.4    12.7        laurier rose
## 231    4.5    15.7        laurier rose
## 232    3.3    13.2        laurier rose
## 233    3.3    13.4        laurier rose
## 234    3.6    13.8        laurier rose
## 235    3.5    11.2        laurier rose
## 236    3.8    11.4        laurier rose
## 237    3.2    11.1        laurier rose
## 238    3.8    14.4        laurier rose
## 239    5.3    13.4        laurier rose
## 240    5.8    14.7        laurier rose
## 241    4.6    14.9        laurier rose
## 242    3.2    10.5        laurier rose
## 243    4.3    14.6        laurier rose
## 244    2.7    11.3        laurier rose
## 245    2.6     9.1        laurier rose
## 246    2.4     9.0        laurier rose
## 247    2.6     9.4        laurier rose
## 248    3.2    12.1        laurier rose
## 249    6.4    16.1        laurier rose
## 250    3.4    13.2        laurier rose
## 251    3.4    11.4        laurier rose
## 252    2.7    11.5        laurier rose
```

```r
head(Mesures)
```

```
##    masse taille          espece
```

```
## 1   28.6    19.1 glycine blanche
## 2   20.6    14.8 glycine blanche
## 3   29.2    19.7 glycine blanche
## 4   32.0    21.1 glycine blanche
## 5   24.5    19.4 glycine blanche
## 6   29.0    19.5 glycine blanche
```

```r
#page 96
head(Mesures,10)
```

```
##    masse taille          espece
## 1   28.6   19.1 glycine blanche
## 2   20.6   14.8 glycine blanche
## 3   29.2   19.7 glycine blanche
## 4   32.0   21.1 glycine blanche
## 5   24.5   19.4 glycine blanche
## 6   29.0   19.5 glycine blanche
## 7   28.9   18.9 glycine blanche
## 8   18.2   14.6 glycine blanche
## 9    7.9   10.2 glycine blanche
## 10  15.5   14.6 glycine blanche
```

```r
tail(Mesures)
```

```
##     masse taille        espece
## 247   2.6    9.4 laurier rose
## 248   3.2   12.1 laurier rose
## 249   6.4   16.1 laurier rose
## 250   3.4   13.2 laurier rose
## 251   3.4   11.4 laurier rose
## 252   2.7   11.5 laurier rose
```

```r
#page 97
str(Mesures)
```

```
## 'data.frame':    252 obs. of  3 variables:
##  $ masse : num  28.6 20.6 29.2 32 24.5 29 28.9 18.2 7.9 15.5 ...
##  $ taille: num  19.1 14.8 19.7 21.1 19.4 19.5 18.9 14.6 10.2 14.6 ...
##  $ espece: Factor w/ 4 levels "bignone","glycine blanche",..: 2 2 2 2 2 2 2 2 2 2 ...
```

```r
class(Mesures$espece)
```

```
## [1] "factor"
```

```r
names(Mesures$espece)
```

```
## NULL
```

```r
names(Mesures)
```

```
## [1] "masse"  "taille" "espece"
```

```r
#page 98
levels(Mesures$espece)
```

```
## [1] "bignone"         "glycine blanche"  "glycine violette"
## [4] "laurier rose"
```

```r
?factor
str(Mesures5)
```

```
## 'data.frame':    252 obs. of  5 variables:
##  $ masse    : num  28.6 20.6 29.2 32 24.5 29 28.9 18.2 7.9 15.5 ...
##  $ taille   : num  19.1 14.8 19.7 21.1 19.4 19.5 18.9 14.6 10.2 14.6 ...
##  $ graines  : int  4 3 5 7 4 4 4 2 1 2 ...
##  $ masse_sec: num  9.3 7.7 10.4 11.5 8.4 10.3 10.1 6.3 2.7 5.5 ...
##  $ espece   : Factor w/ 4 levels "bignone","glycine blanche",..: 2 2 2 2 2 2 2 2 2 2 ...
```

Mesures5

```
##     masse taille graines masse_sec          espece
## 1    28.6   19.1       4       9.3  glycine blanche
## 2    20.6   14.8       3       7.7  glycine blanche
## 3    29.2   19.7       5      10.4  glycine blanche
## 4    32.0   21.1       7      11.5  glycine blanche
## 5    24.5   19.4       4       8.4  glycine blanche
## 6    29.0   19.5       4      10.3  glycine blanche
## 7    28.9   18.9       4      10.1  glycine blanche
## 8    18.2   14.6       2       6.3  glycine blanche
## 9     7.9   10.2       1       2.7  glycine blanche
## 10   15.5   14.6       2       5.5  glycine blanche
## 11   22.6   16.4       2       8.3  glycine blanche
## 12   35.5   21.1       6      13.1  glycine blanche
## 13   32.5   20.7       5      11.4  glycine blanche
## 14   28.7   18.7       5      10.5  glycine blanche
## 15   26.0   17.6       3       9.5  glycine blanche
## 16   13.5   13.2       2       4.7  glycine blanche
## 17   16.4   14.0       2       6.0  glycine blanche
## 18   12.5   12.0       3       4.3  glycine blanche
## 19   26.2   18.3       5       9.1  glycine blanche
## 20   22.6   17.8       2       8.2  glycine blanche
## 21    9.7   10.7       1       3.3  glycine blanche
## 22   21.8   16.5       3       7.2  glycine blanche
## 23   17.2   14.5       3       5.9  glycine blanche
## 24   25.2   17.5       4       9.1  glycine blanche
## 25   12.0   12.2       2       4.2  glycine blanche
## 26    6.3    8.6       1       2.2  glycine blanche
## 27    7.0    9.1       1       2.5  glycine blanche
## 28   20.4   17.0       4       7.1  glycine blanche
## 29   18.0   15.3       3       6.3  glycine blanche
## 30   21.1   15.8       4       7.3  glycine blanche
## 31   18.2   15.9       2       5.8  glycine blanche
## 32   15.2   12.2       3       5.2  glycine blanche
## 33   19.8   16.1       4       6.6  glycine blanche
## 34   21.4   16.0       3       7.5  glycine blanche
## 35   15.0   13.8       1       5.1  glycine blanche
## 36   16.4   14.4       2       5.3  glycine blanche
## 37   17.3   14.2       5       5.9  glycine blanche
## 38   16.4   15.7       2       6.1  glycine blanche
## 39   13.5   12.6       2       4.8  glycine blanche
## 40   13.6   12.0       3       4.5  glycine blanche
## 41   14.6   12.8       4       4.6  glycine blanche
## 42   16.9   15.3       3       5.9  glycine blanche
## 43   11.7   12.4       2       4.1  glycine blanche
## 44   14.0   14.5       2       5.0  glycine blanche
## 45   14.6   12.3       2       5.3  glycine blanche
```

```
## 46  10.3  11.8  2   3.8  glycine blanche
## 47  11.3  12.6  2   4.0  glycine blanche
## 48  10.7  11.3  2   3.9  glycine blanche
## 49  10.9  12.5  3   3.6  glycine blanche
## 50  20.0  16.1  4   7.2  glycine blanche
## 51  21.5  16.2  2   7.7  glycine blanche
## 52  12.0  11.3  2   4.3  glycine blanche
## 53   6.1   8.6  1   2.2  glycine blanche
## 54   5.4   8.2  1   2.1  glycine blanche
## 55  40.0  24.5  7  17.4 glycine violette
## 56  49.2  27.0  7  16.2 glycine violette
## 57  46.0  25.8  5  13.9 glycine violette
## 58  26.4  18.7  3   8.3 glycine violette
## 59  42.2  25.2  5  15.5 glycine violette
## 60  48.4  25.8  4  16.2 glycine violette
## 61  23.9  19.2  4   8.0 glycine violette
## 62  31.7  21.4  5  10.9 glycine violette
## 63  16.8  12.0  4   5.3 glycine violette
## 64  21.6  14.0  5   7.2 glycine violette
## 65  24.1  18.5  3   8.1 glycine violette
## 66  13.5  12.8  3   4.5 glycine violette
## 67  22.4  13.8  3   7.5 glycine violette
## 68  26.1  17.3  6   8.8 glycine violette
## 69  12.9  12.4  3   4.6 glycine violette
## 70  26.6  20.0  5   8.9 glycine violette
## 71  29.6  20.5  3   9.7 glycine violette
## 72  22.4  18.2  3   7.0 glycine violette
## 73  17.3  13.3  3   5.8 glycine violette
## 74  16.6  13.5  4   5.6 glycine violette
## 75  12.8  12.0  2   4.5 glycine violette
## 76  19.1  14.5  3   6.7 glycine violette
## 77  12.4  11.6  2   4.3 glycine violette
## 78   8.8   9.2  2   3.3 glycine violette
## 79  13.2  15.1  3   4.1 glycine violette
## 80  15.9  12.2  3   5.3 glycine violette
## 81  13.3  11.2  2   5.0 glycine violette
## 82   6.3   8.4  1   2.3 glycine violette
## 83  12.9  11.5  2   4.5 glycine violette
## 84   6.2   7.8  1   2.2 glycine violette
## 85   8.6   9.8  2   3.0 glycine violette
## 86  14.4  11.6  2   5.1 glycine violette
## 87  11.5   9.8  2   4.0 glycine violette
## 88  11.5  11.0  2   3.9 glycine violette
## 89  12.8  10.6  2   5.0 glycine violette
## 90  11.7  11.1  2   4.2 glycine violette
## 91  15.7  14.0  3   6.1 glycine violette
## 92  12.0  11.4  2   4.3 glycine violette
## 93  13.4  11.1  2   4.2 glycine violette
## 94  11.3  10.7  2   3.7 glycine violette
## 95   6.6   7.9  1   2.5 glycine violette
## 96  17.8  13.7  4   6.3 glycine violette
## 97   9.6  10.0  2   3.2 glycine violette
## 98  14.3  12.8  3   5.3 glycine violette
## 99  14.0  12.2  2   5.2 glycine violette
```

```
## 100   11.3   11.4      3       4.2 glycine violette
## 101   10.2   10.2      3       3.8 glycine violette
## 102   12.2   10.8      3       4.7 glycine violette
## 103   15.9   13.0      4       5.5 glycine violette
## 104   11.7   10.3      2       4.5 glycine violette
## 105   12.4   11.0      2       4.1 glycine violette
## 106   11.5   11.4      2       4.5 glycine violette
## 107   10.6   10.5      2       4.0 glycine violette
## 108    9.4    9.2      2       3.3 glycine violette
## 109    9.2    9.9      2       3.5 glycine violette
## 110    6.1    8.4      1       2.5 glycine violette
## 111   10.9   12.8     NA       3.0         bignone
## 112    6.6   10.5     NA       1.1         bignone
## 113   22.5   18.0     NA       3.4         bignone
## 114   33.7   21.5     NA       6.6         bignone
## 115   20.6   17.8     NA       3.5         bignone
## 116   16.6   16.3     NA       4.3         bignone
## 117   14.2   17.4     NA       2.1         bignone
## 118   13.8   15.7     NA       2.1         bignone
## 119   14.0   17.3     NA       2.4         bignone
## 120    8.7   13.4     NA       2.2         bignone
## 121   14.2   13.9     NA       3.2         bignone
## 122   10.6   14.6     NA       1.7         bignone
## 123   10.9   14.2     NA       1.6         bignone
## 124    3.3    8.9     NA       0.5         bignone
## 125    9.7   13.0     NA       1.5         bignone
## 126    9.3   12.2     NA       1.9         bignone
## 127   17.2   16.5     NA       2.4         bignone
## 128   10.1   14.7     NA       2.3         bignone
## 129    9.0   13.4     NA       2.9         bignone
## 130    7.1   11.6     NA       1.5         bignone
## 131    7.1   12.9     NA       1.6         bignone
## 132    1.5    6.5     NA       0.2         bignone
## 133    4.1    9.5     NA       1.4         bignone
## 134    8.0   11.8     NA       2.2         bignone
## 135    7.4   13.6     NA       1.9         bignone
## 136    7.2   12.9     NA       1.1         bignone
## 137    6.9   11.6     NA       1.3         bignone
## 138    2.9    9.4     NA       0.8         bignone
## 139    2.4    9.5     NA       1.1         bignone
## 140   10.7   14.0     NA       2.3         bignone
## 141   13.8   13.5     NA       3.5         bignone
## 142   10.9   12.1     NA       1.7         bignone
## 143   10.3   11.6     NA       2.0         bignone
## 144    8.8   13.4     NA       1.7         bignone
## 145    9.0   10.9     NA       2.5         bignone
## 146    8.2   12.2     NA       1.7         bignone
## 147    9.6   13.4     NA       1.2         bignone
## 148    9.0   12.5     NA       1.7         bignone
## 149    5.3   10.5     NA       0.9         bignone
## 150    1.5    7.0     NA       0.7         bignone
## 151    6.7   13.2     NA       1.1         bignone
## 152    2.9    9.3     NA       0.6         bignone
## 153    2.9    7.9     NA       1.0         bignone
```

```
## 154   3.5   10.3    NA      1.2        bignone
## 155   3.4    7.5    NA      1.1        bignone
## 156   4.9    8.5    NA      1.5        bignone
## 157   4.7   10.1    NA      1.2        bignone
## 158   4.7    8.3    NA      1.3        bignone
## 159   5.2   10.8    NA      0.9        bignone
## 160   2.1    8.3    NA      0.5        bignone
## 161   2.2    7.1    NA      0.5        bignone
## 162   1.4    6.4    NA      0.6        bignone
## 163   2.7    6.5    NA      0.4        bignone
## 164   1.0    4.8    NA      0.4        bignone
## 165   2.5    7.4    NA      0.8        bignone
## 166   5.5    9.3    NA      0.9        bignone
## 167   2.7    8.6    NA      0.9        bignone
## 168   6.7    9.9    NA      2.0        bignone
## 169   7.3   13.9    NA      1.1        bignone
## 170   2.9    8.7    NA      1.3        bignone
## 171   3.8    9.3    NA      1.0        bignone
## 172   7.6   13.7    NA      2.6        bignone
## 173   3.6    8.3    NA      1.5        bignone
## 174   3.0    8.1    NA      1.0        bignone
## 175   5.8   11.2    NA      2.0        bignone
## 176   5.3   12.0    NA      1.1        bignone
## 177   3.2   11.3    NA      1.5        bignone
## 178   4.4    6.7    NA      1.5        bignone
## 179   3.4   10.6    NA      1.4        bignone
## 180   2.9    8.9    NA      0.9        bignone
## 181   4.9   15.3    NA      1.2     laurier rose
## 182   6.2   15.9    NA      1.1     laurier rose
## 183   4.0   15.0    NA      0.7     laurier rose
## 184   3.3   11.0    NA       NA     laurier rose
## 185   4.8   15.1    NA      0.8     laurier rose
## 186   5.6   15.6    NA      1.0     laurier rose
## 187   4.5   15.3    NA      0.7     laurier rose
## 188   6.3   18.4    NA      1.6     laurier rose
## 189   4.2   14.0    NA      0.8     laurier rose
## 190   3.9   12.6    NA      1.1     laurier rose
## 191   5.8   16.8    NA      0.9     laurier rose
## 192   4.7   13.6    NA      1.0     laurier rose
## 193   6.0   15.1    NA      1.5     laurier rose
## 194   6.5   16.7    NA      1.7     laurier rose
## 195   5.0   15.3    NA      1.0     laurier rose
## 196   5.5   17.1    NA      1.3     laurier rose
## 197   4.7   14.6    NA      1.0     laurier rose
## 198   5.7   15.0    NA      1.5     laurier rose
## 199   3.6   10.4    NA      1.1     laurier rose
## 200   5.4   16.5    NA      1.3     laurier rose
## 201   5.3   16.6    NA      1.1     laurier rose
## 202   5.0   15.9    NA      1.0     laurier rose
## 203   4.5   14.4    NA      1.0     laurier rose
## 204   4.4   16.2    NA      1.1     laurier rose
## 205   4.8   15.2    NA      0.8     laurier rose
## 206   4.5   15.8    NA      0.8     laurier rose
## 207   3.2   11.0    NA      0.6     laurier rose
```

```
## 208   4.7   14.1      NA      0.8     laurier rose
## 209   4.0   13.7      NA      0.8     laurier rose
## 210   5.8   15.4      NA      1.5     laurier rose
## 211   5.5   15.3      NA      1.3     laurier rose
## 212   4.4   13.5      NA      0.7     laurier rose
## 213   3.5   12.0      NA      1.1     laurier rose
## 214   4.4   14.7      NA      0.9     laurier rose
## 215   4.3   15.5      NA      1.2     laurier rose
## 216   4.1   12.9      NA      1.5     laurier rose
## 217   5.3   15.0      NA      1.6     laurier rose
## 218   4.7   15.8      NA      0.9     laurier rose
## 219   5.3   13.8      NA       NA     laurier rose
## 220   4.7   12.8      NA      1.2     laurier rose
## 221   4.9   16.0      NA      1.6     laurier rose
## 222   4.1   12.0      NA      0.6     laurier rose
## 223   4.6   14.3      NA      0.7     laurier rose
## 224   4.8   14.5      NA      0.9     laurier rose
## 225   3.4   11.4      NA      1.1     laurier rose
## 226   3.4   13.3      NA      0.6     laurier rose
## 227   5.8   15.5      NA      1.1     laurier rose
## 228   4.8   15.1      NA      1.0     laurier rose
## 229   3.9   12.8      NA      0.8     laurier rose
## 230   3.4   12.7      NA      0.8     laurier rose
## 231   4.5   15.7      NA      0.9     laurier rose
## 232   3.3   13.2      NA      0.5     laurier rose
## 233   3.3   13.4      NA      0.5     laurier rose
## 234   3.6   13.8      NA      0.6     laurier rose
## 235   3.5   11.2      NA      0.6     laurier rose
## 236   3.8   11.4      NA      1.1     laurier rose
## 237   3.2   11.1      NA      1.0     laurier rose
## 238   3.8   14.4      NA      0.7     laurier rose
## 239   5.3   13.4      NA      1.6     laurier rose
## 240   5.8   14.7      NA      1.7     laurier rose
## 241   4.6   14.9      NA      0.9     laurier rose
## 242   3.2   10.5      NA      1.1     laurier rose
## 243   4.3   14.6      NA      0.8     laurier rose
## 244   2.7   11.3      NA      0.5     laurier rose
## 245   2.6    9.1      NA      0.4     laurier rose
## 246   2.4    9.0      NA       NA     laurier rose
## 247   2.6    9.4      NA      0.9     laurier rose
## 248   3.2   12.1      NA      0.6     laurier rose
## 249   6.4   16.1      NA      1.8     laurier rose
## 250   3.4   13.2      NA      1.2     laurier rose
## 251   3.4   11.4      NA      1.2     laurier rose
## 252   2.7   11.5      NA      0.7     laurier rose
```

```r
#page 101
table_graines<-table(Mesures5$graines)
table_graines
```

```
## 
##  1  2  3  4  5  6  7 
## 11 41 27 16 10  2  3
```

```
effcum_graines<-cumsum(table_graines)
effcum_graines
```

```
##   1   2   3   4   5   6   7
##  11  52  79  95 105 107 110
```

```
#page 102
table(Mesures5$espece)
```

```
##
##         bignone   glycine blanche glycine violette     laurier rose
##              70              54              56               72
```

```
freq_table_graines<-table_graines/sum(table_graines)
options(digits=3)
freq_table_graines
```

```
##
##      1      2      3      4      5      6      7
## 0.1000 0.3727 0.2455 0.1455 0.0909 0.0182 0.0273
```

```
freq_table_graines<-prop.table(table(Mesures5$graines))
freq_table_graines
```

```
##
##      1      2      3      4      5      6      7
## 0.1000 0.3727 0.2455 0.1455 0.0909 0.0182 0.0273
```

```
#page 103
freqcum_table_graines<-cumsum(table_graines/sum(table_graines))
freqcum_table_graines
```

```
##     1     2     3     4     5     6     7
## 0.100 0.473 0.718 0.864 0.955 0.973 1.000
```

```
freqcum_table_graines<-cumsum(prop.table((table(Mesures5$graines))))
freqcum_table_graines
```

```
##     1     2     3     4     5     6     7
## 0.100 0.473 0.718 0.864 0.955 0.973 1.000
```

```
#page 104
?hist
```

```
#page 105
minmax<-c(min(Mesures$masse),max(Mesures$masse))
minmax
```

```
## [1]  1.0 49.2
```

```
histo<-hist(Mesures$masse)
```
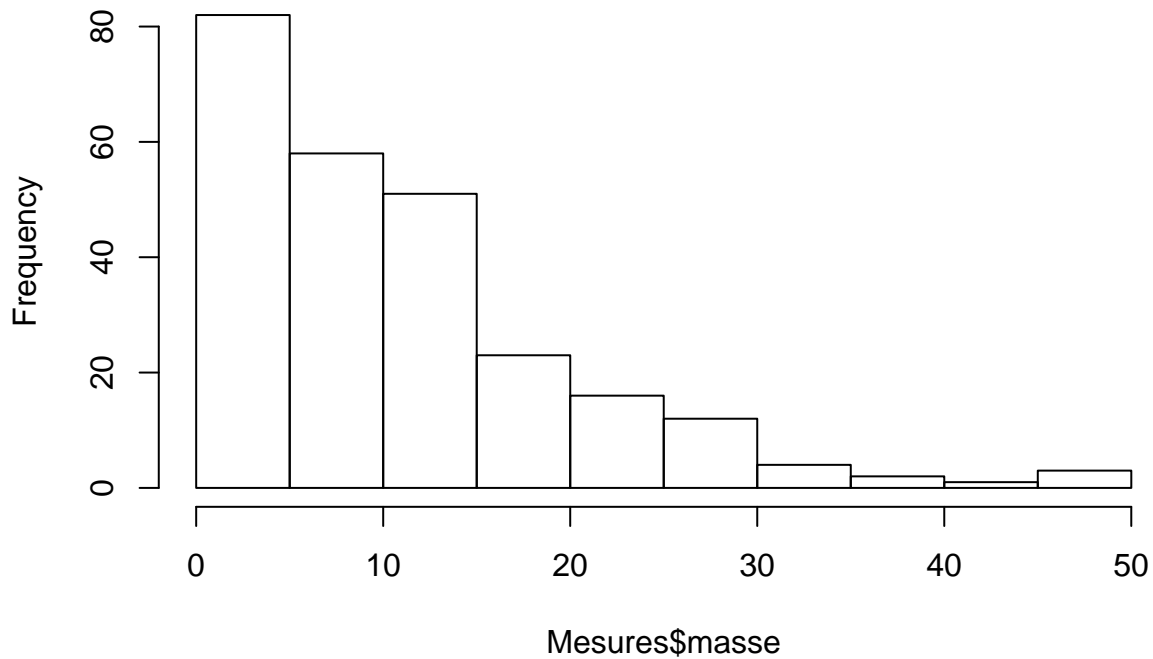
Histogram of Mesures$masse


```
classes<-histo$breaks
classes
```

```
## [1]  0  5 10 15 20 25 30 35 40 45 50
```

```
effectifs<-histo$counts
effectifs
```

```
## [1] 82 58 51 23 16 12  4  2  1  3
```

```
effectifs<-histo$counts
cumsum(effectifs)
```

```
## [1]  82 140 191 214 230 242 246 248 249 252
```

```
frequences<-effectifs/sum(effectifs)
print(frequences,digits=3)
```

```
## [1] 0.32540 0.23016 0.20238 0.09127 0.06349 0.04762 0.01587 0.00794
## [9] 0.00397 0.01190
```

```
sum(frequences)
```

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

```
print(cumsum(frequences),digits=3)
```

```
##  [1] 0.325 0.556 0.758 0.849 0.913 0.960 0.976 0.984 0.988 1.000
```

```
table(Mesures$espece)
```

```
##
##        bignone  glycine blanche glycine violette    laurier rose
```

```
##                    70              54              56              72
```

```
plot(taille~masse,data=Mesures)
```
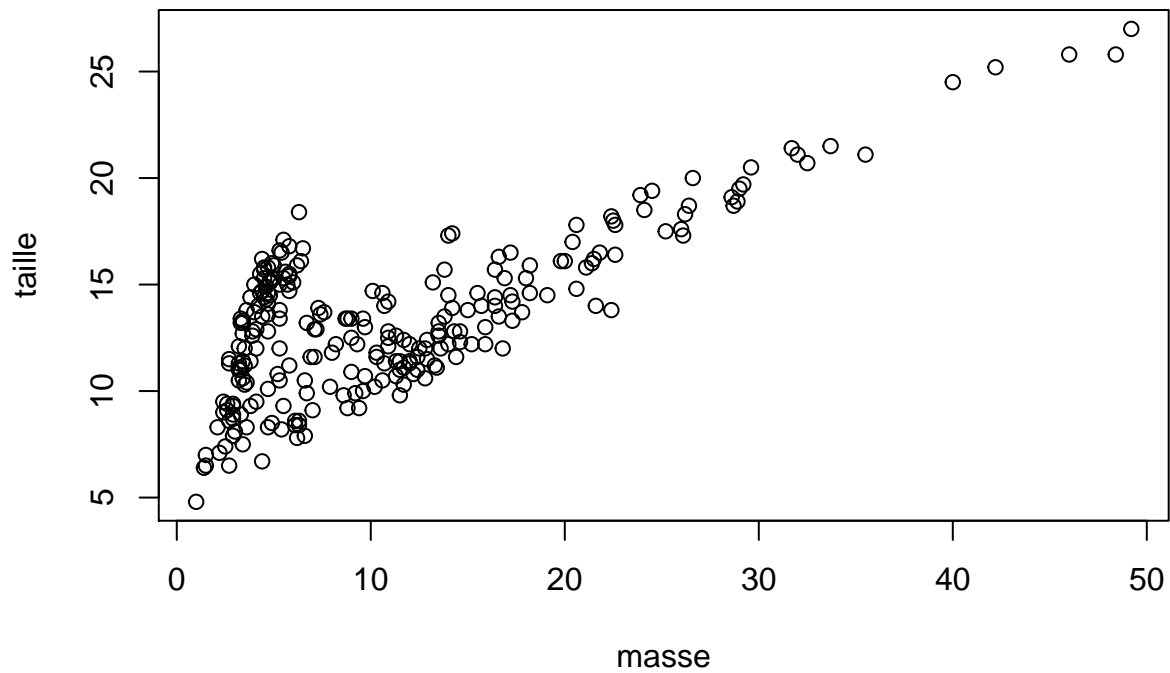


```
#ggplot est une bibliothèque graphique à connaître
if(!("ggplot2" %in%
    rownames(installed.packages())))){install.packages("ggplot2")}
library(ggplot2)
#ggplot(Mesures, aes(x = masse)) + geom_histogram()
#Pas le même calcul de la largeur des classes par défaut. Dans ggplot2, la
#largeur des classes (binwidth) est égale à l'étendue divisée par 30.
ggplot(Mesures,aes(x=masse,y=taille))+geom_point()
```
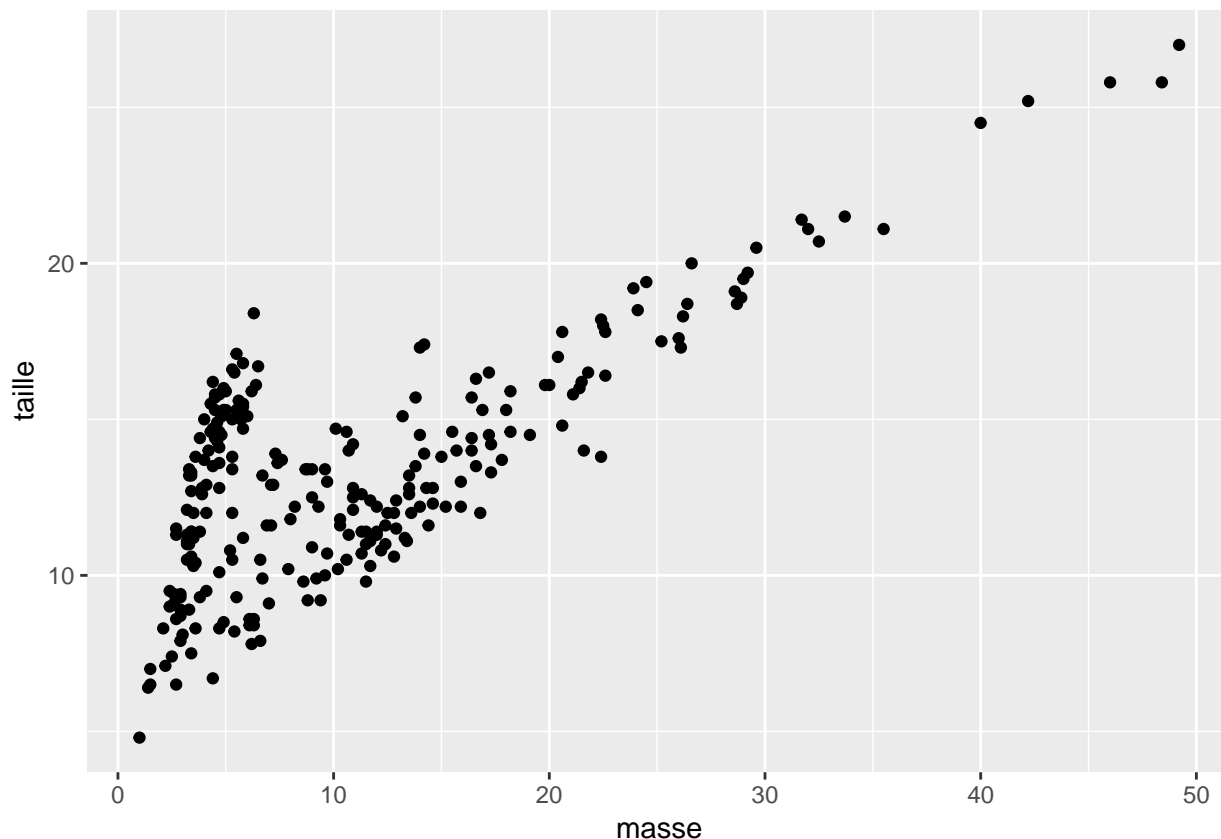
```r
pdf("figure32Bggplot.pdf")
print(ggplot(Mesures, aes(x = masse,y=taille)) + geom_point())
dev.off()
```

```
## pdf
##   2
```

```r
#page 109
args(plot.default)
```

```
## function (x, y = NULL, type = "p", xlim = NULL, ylim = NULL,
##     log = "", main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
##     ann = par("ann"), axes = TRUE, frame.plot = axes, panel.first = NULL,
##     panel.last = NULL, asp = NA, ...)
## NULL
```

```r
names(par())
```

```
##  [1] "xlog"     "ylog"     "adj"      "ann"      "ask"
##  [6] "bg"       "bty"      "cex"      "cex.axis" "cex.lab"
## [11] "cex.main" "cex.sub"  "cin"      "col"      "col.axis"
## [16] "col.lab"  "col.main" "col.sub"  "cra"      "crt"
## [21] "csi"      "cxy"      "din"      "err"      "family"
## [26] "fg"       "fig"      "fin"      "font"     "font.axis"
## [31] "font.lab" "font.main" "font.sub" "lab"      "las"
## [36] "lend"     "lheight"  "ljoin"    "lmitre"   "lty"
## [41] "lwd"      "mai"      "mar"      "mex"      "mfcol"
## [46] "mfg"      "mfrow"    "mgp"      "mkh"      "new"
## [51] "oma"      "omd"      "omi"      "page"     "pch"
```

```
## [56] "pin"         "plt"        "ps"         "pty"        "smo"
## [61] "srt"         "tck"        "tcl"        "usr"        "xaxp"
## [66] "xaxs"        "xaxt"       "xpd"        "yaxp"       "yaxs"
## [71] "yaxt"        "ylbias"
```

```
#page 110
plot(taille~masse,pch=19,main="Taille vs. Masse",xlab="Masse",ylab="Taille",data=Mesures)
```
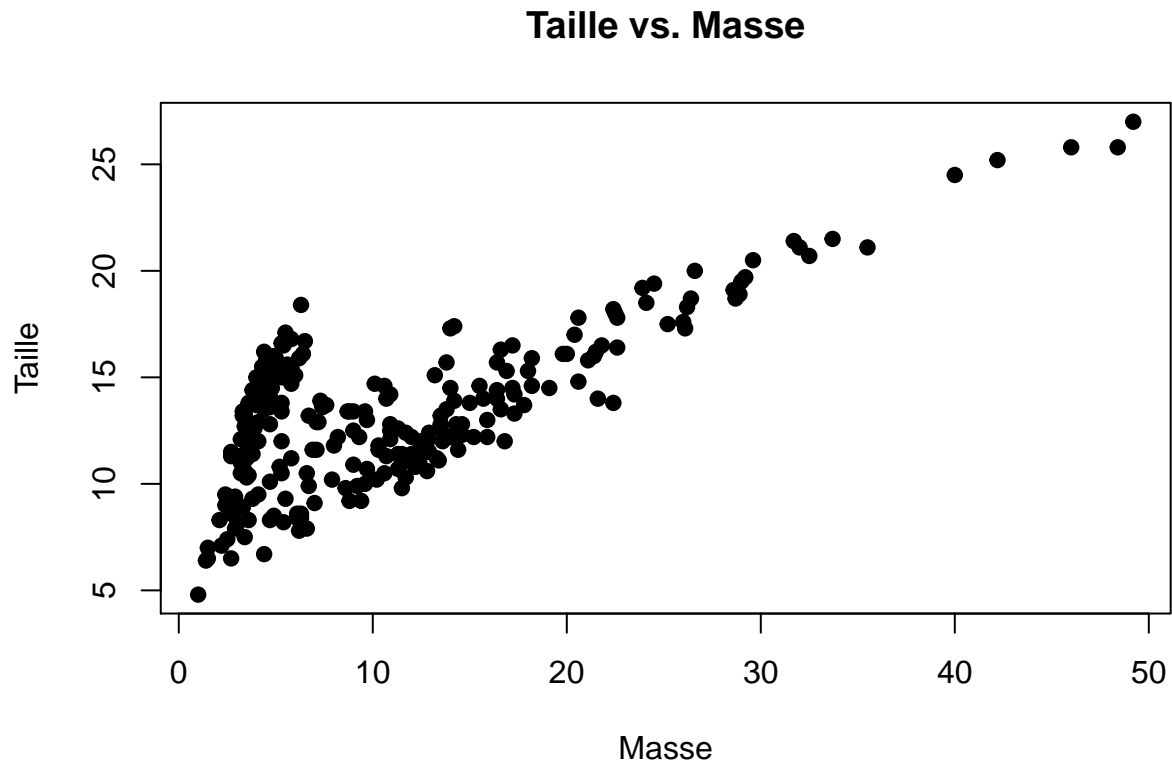
Taille vs. Masse


```
ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) + xlab("Masse") +
  ylab("Taille") + ggtitle("Taille vs. Masse")
```
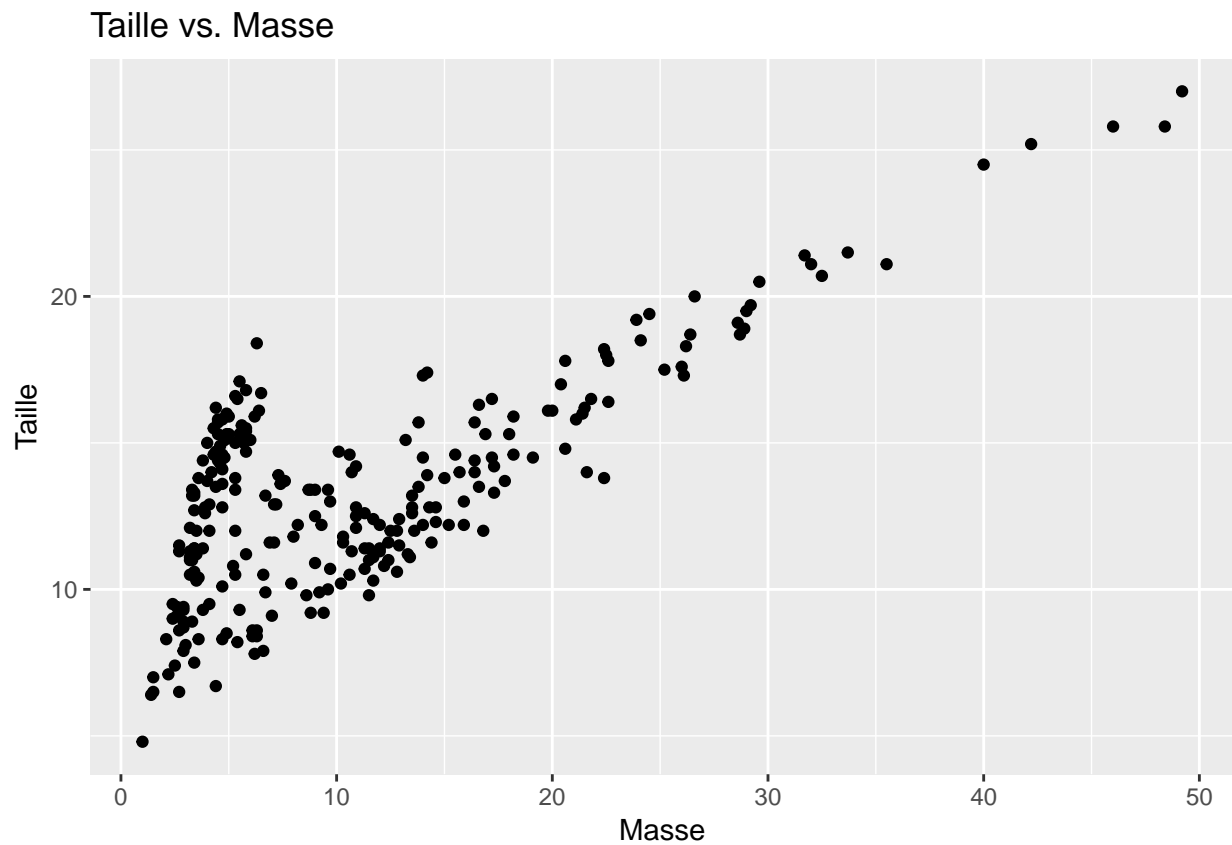
Taille vs. Masse


```r
#Autre manière de spécifier le titre et le noms des axes
ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) + labs(title =
  "Taille vs. Masse", x = "Masse", y = "Taille")
```
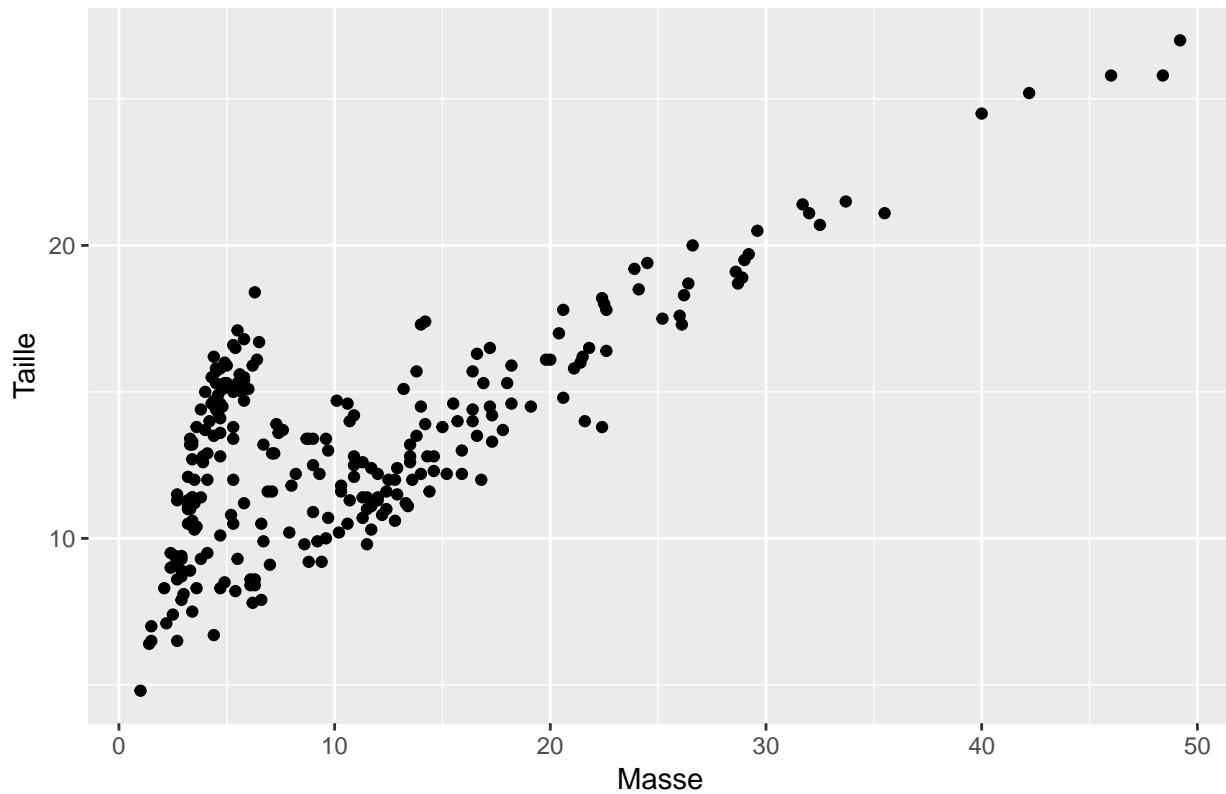
Taille vs. Masse


```
#page 111
pdf("figure33Bggplot.pdf")
print(ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) +
        xlab("Masse") + ylab("Taille") + ggtitle("Taille vs. Masse"))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) + xlab("Masse") +
  ylab("Taille") + ggtitle("Taille vs. Masse")+theme(plot.title=element_text(hjust = 0.5))
```
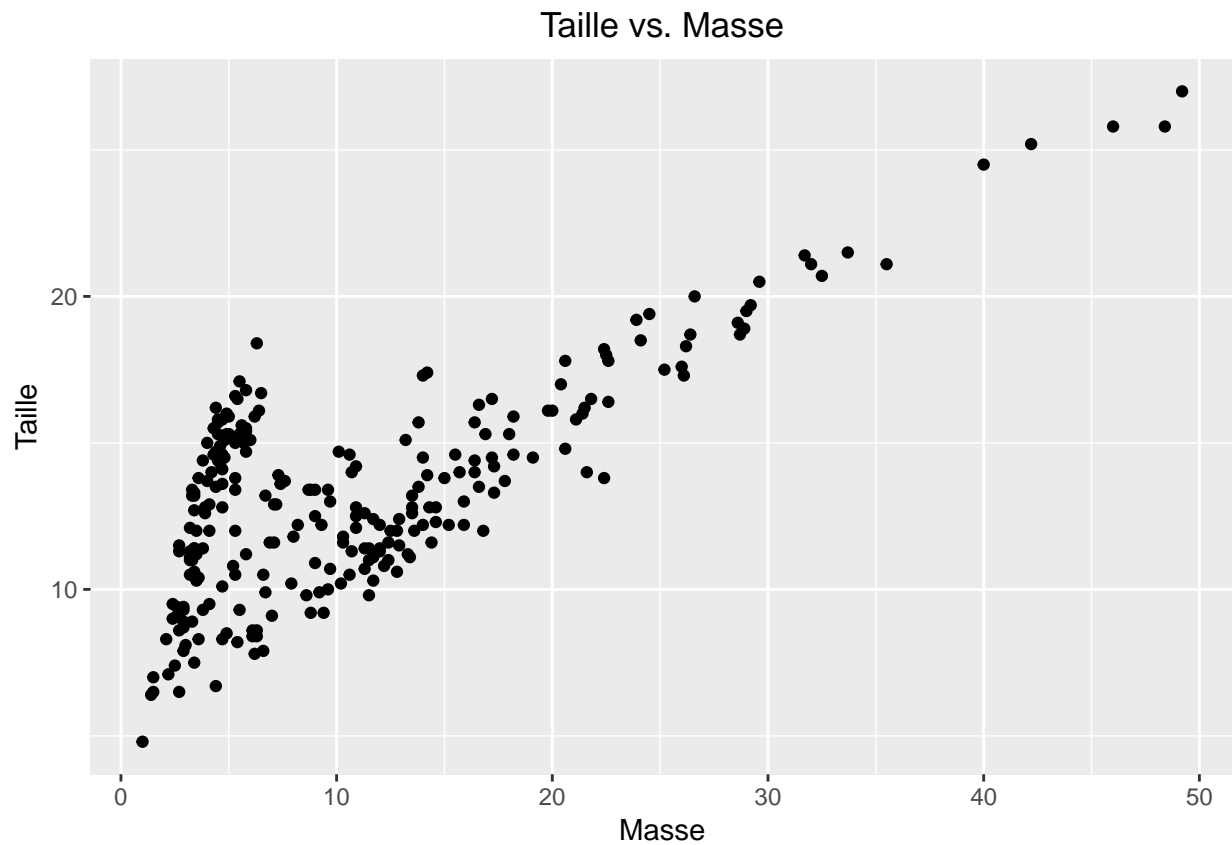
Taille vs. Masse

```
#Titre au centre
theme_update(plot.title = element_text(hjust = 0.5))
ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) + labs(title =
  "Taille vs. Masse", x = "Masse", y = "Taille")
```
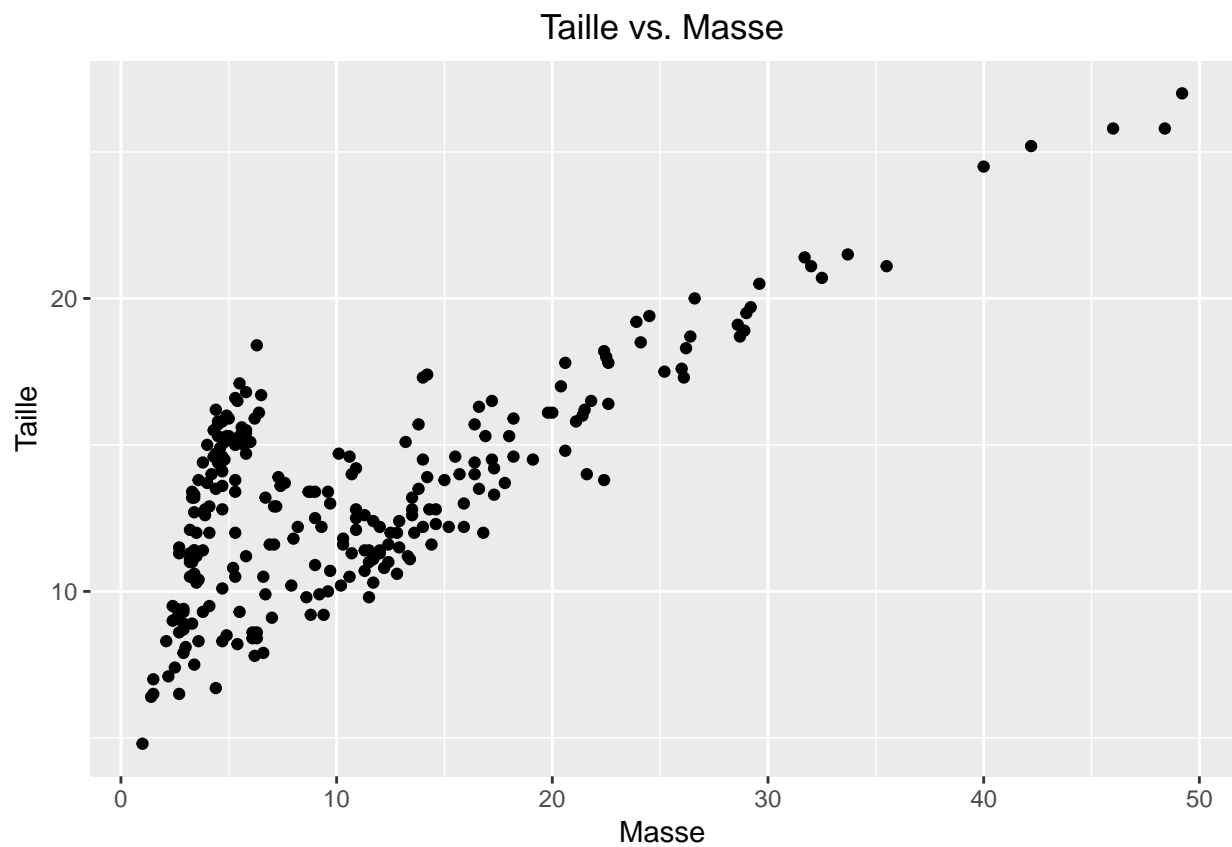
Taille vs. Masse


```r
#Titre à gauche
theme_update(plot.title = element_text(hjust = 0))
ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) + labs(title =
  "Taille vs. Masse", x = "Masse", y = "Taille")
```
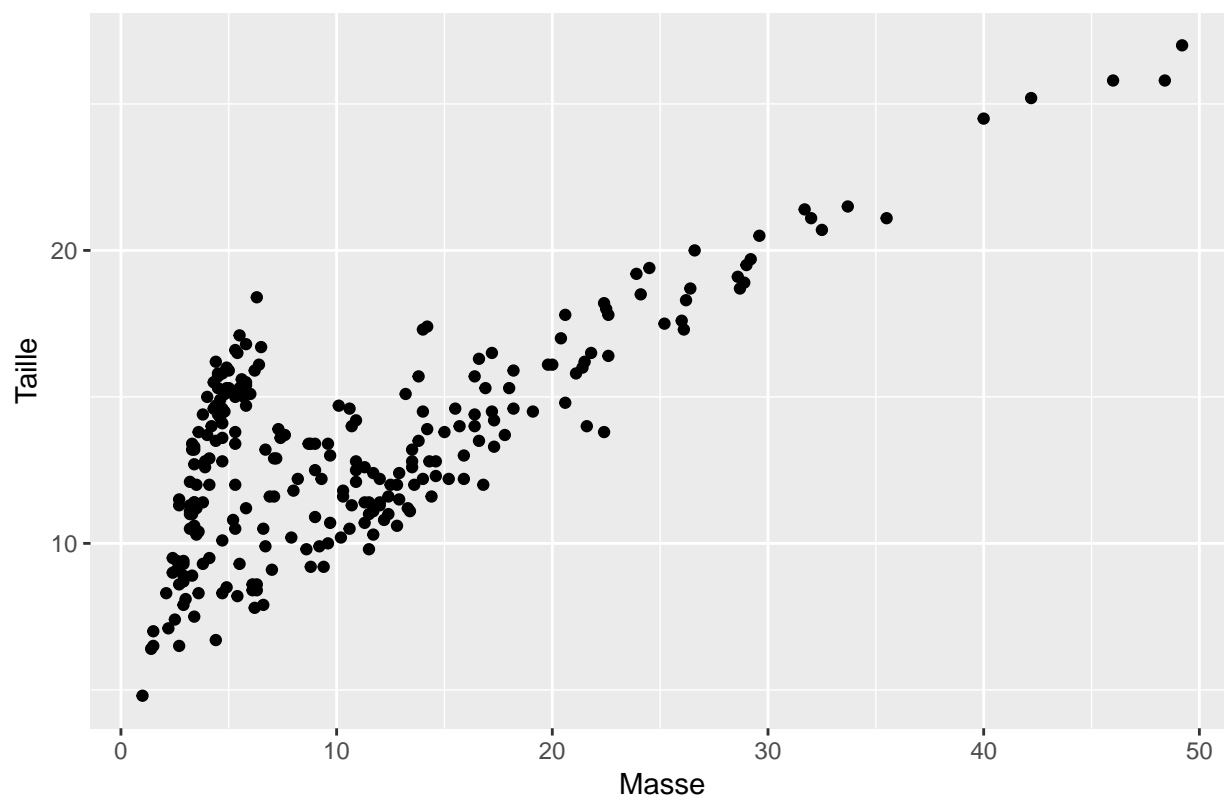
Taille vs. Masse


```
#page 112
#Titre à droite
theme_update(plot.title = element_text(hjust = 1))
ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) + labs(title =
  "Taille vs. Masse", x = "Masse", y = "Taille")
```
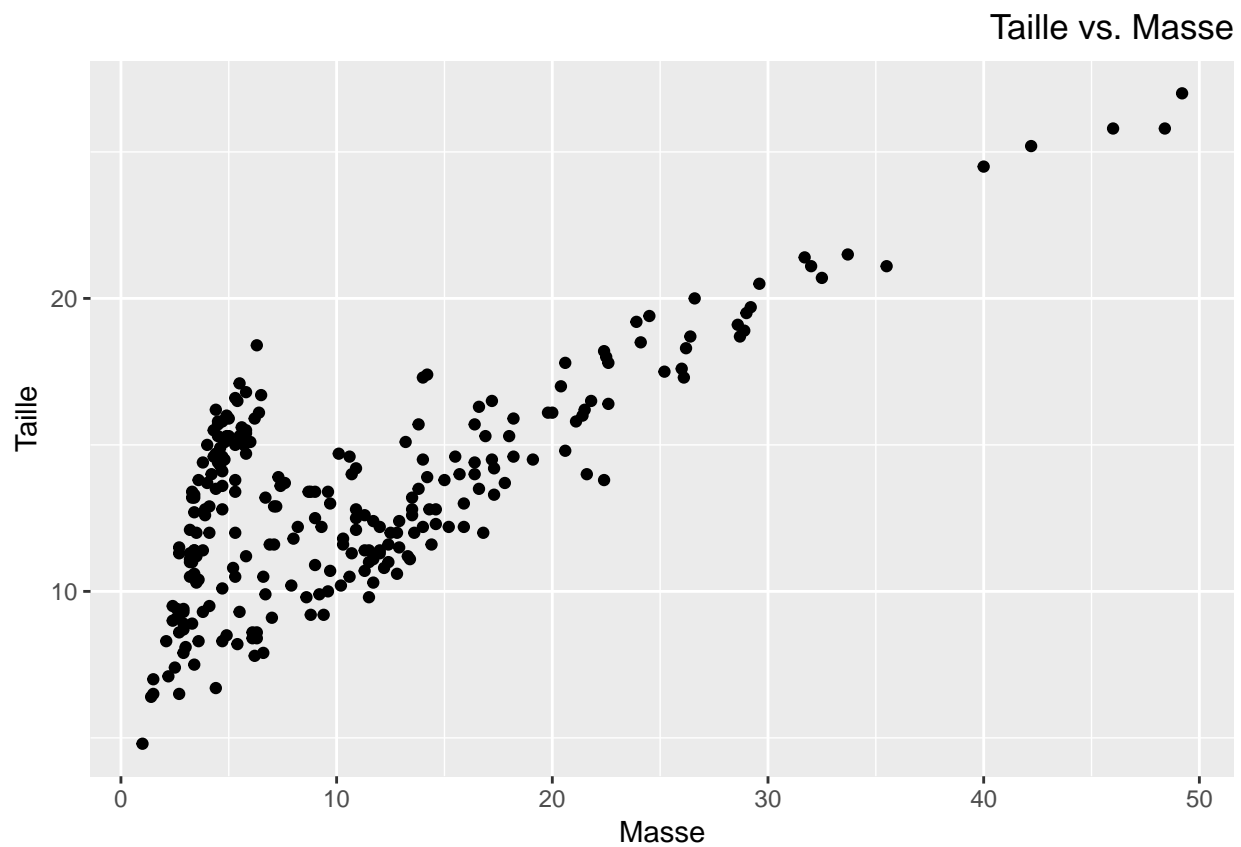
Taille vs. Masse

```
pdf("figure33Cggplot.pdf")
theme_update(plot.title = element_text(hjust = 0.5))
print(ggplot(Mesures, aes(x = masse,y=taille)) + geom_point(pch=19) +
        xlab("Masse") + ylab("Taille") + ggtitle("Taille vs. Masse"))
dev.off()
```

```
## pdf
##   2
```

```
#page 113
pairs(Mesures5)
```
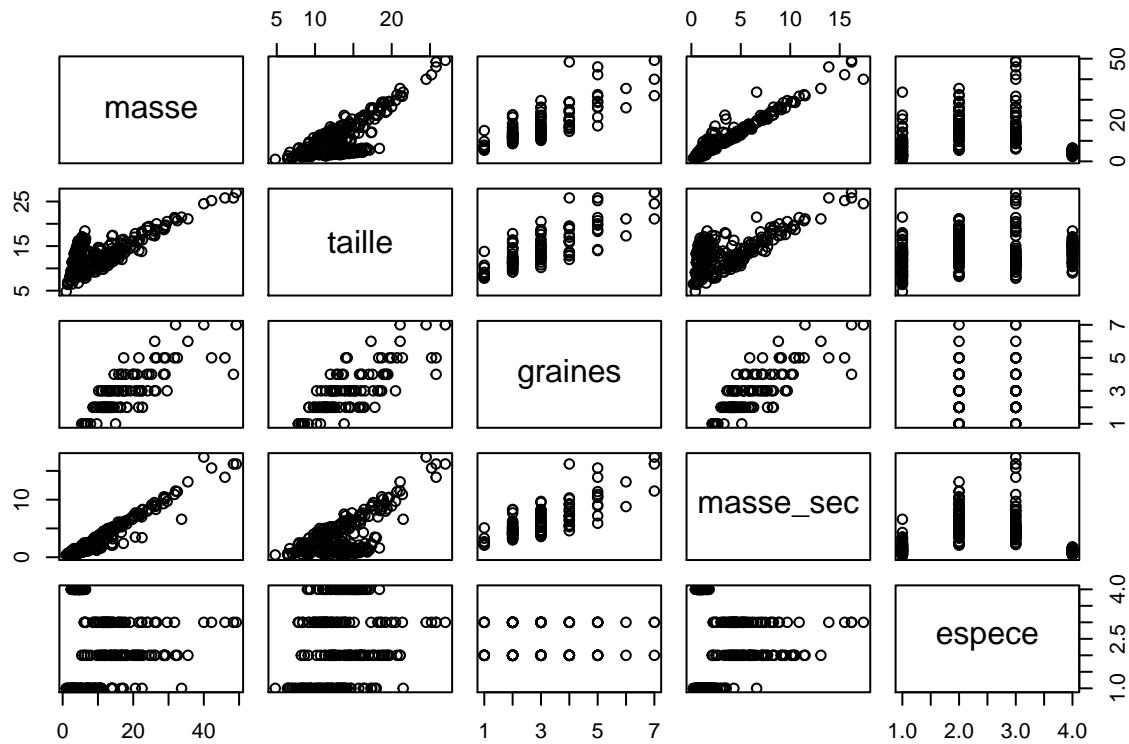
```
pdf("figure34.pdf")
pairs(Mesures5)
dev.off()
```

```
## pdf
##   2
```

```
pairs(Mesures5,diag.panel=panel.hist)
```
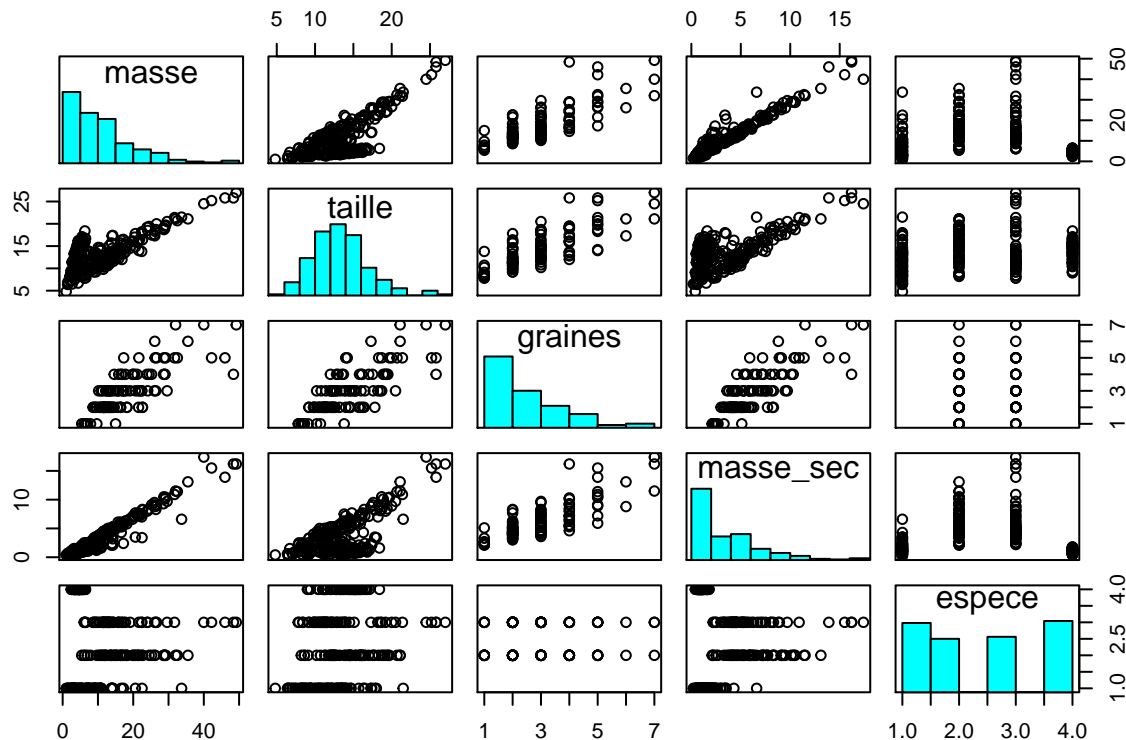
```r
pdf("figure35A.pdf")
pairs(Mesures5,diag.panel=panel.hist)
dev.off()
```

```
## pdf
##   2
```

```r
#page 114
if(!("GGally" %in% rownames(installed.packages()))){install.packages("GGally")}
library(GGally)
#Noir et blanc
ggpairs(Mesures5)
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning: Removed 142 rows containing missing values (geom_point).


## Warning: Removed 142 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning: Removed 142 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing non-finite values (stat_density).

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```r
pdf("figure35Bggplot.pdf")
print(ggpairs(Mesures5))
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning: Removed 142 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_density).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```

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

```
## Warning: Removed 142 rows containing non-finite values (stat_bin).
```

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

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```

```r
dev.off()
```

```
## pdf
##   2
```

```r
#Si besoin, créer des abréviations pour les noms des variables
Mesures5abbr <- Mesures5
Mesures5abbr$espece <- abbreviate(Mesures5$espece)
ggpairs(Mesures5abbr, axisLabels='show')
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning: Removed 142 rows containing non-finite values (stat_boxplot).

## Warning: Removed 3 rows containing missing values (geom_point).


## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing non-finite values (stat_density).

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).
```
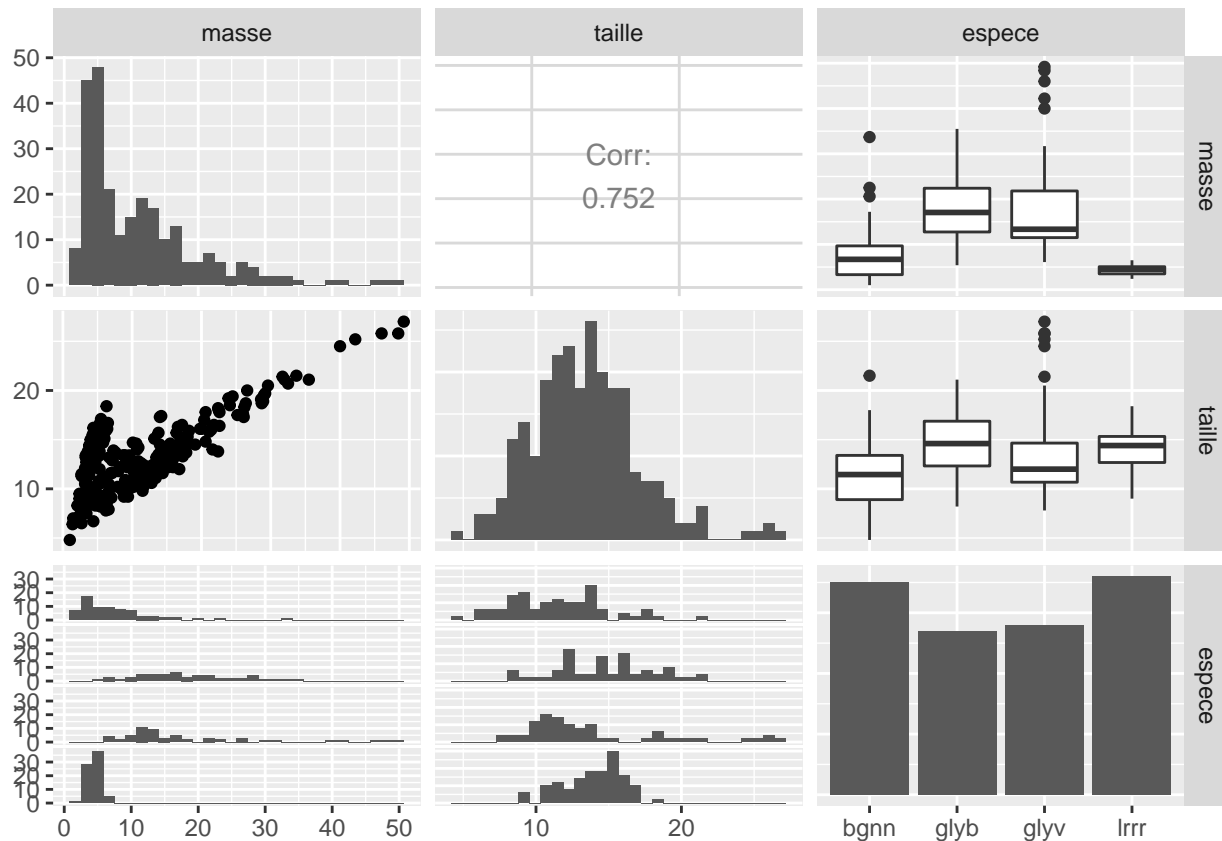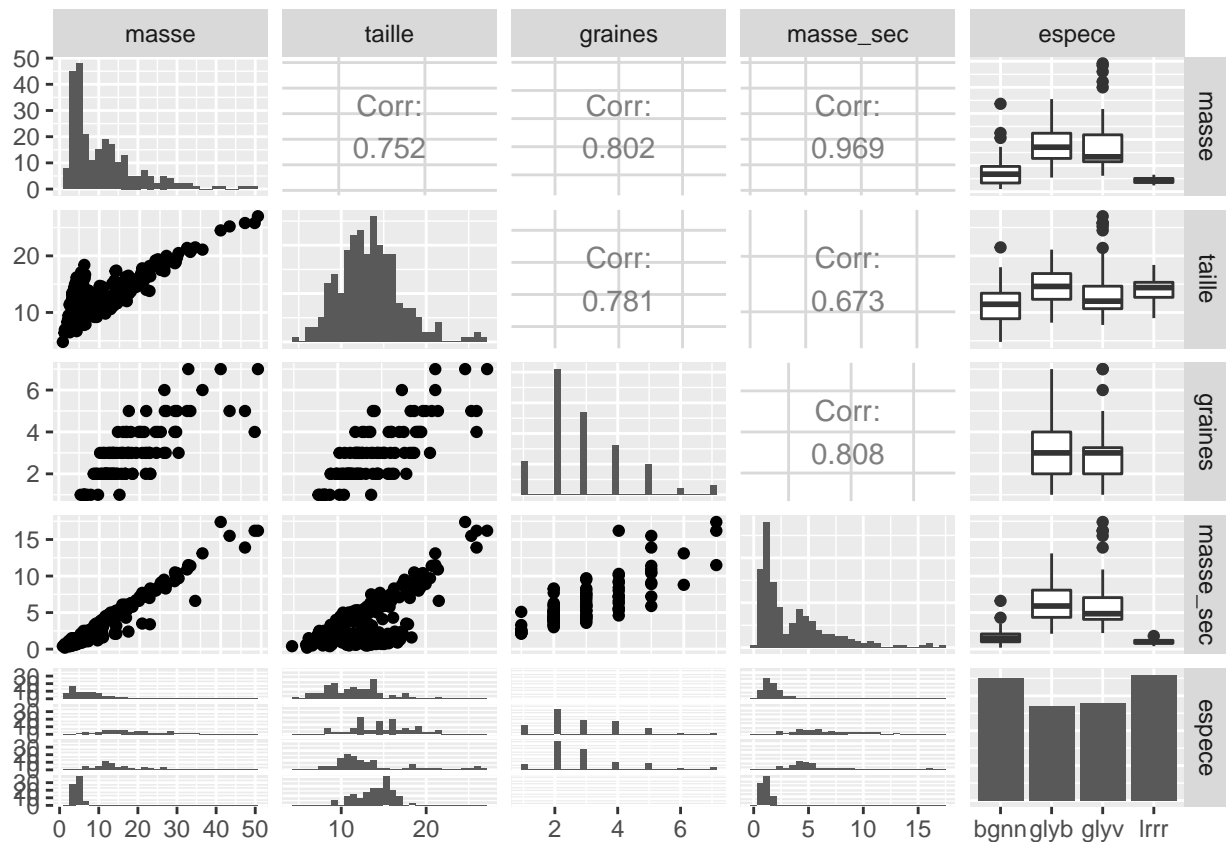


```r
pdf("figure35abbrggplot.pdf")
print(ggpairs(Mesures5abbr, axisLabels='show'))
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning: Removed 142 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_density).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```

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

```
## Warning: Removed 142 rows containing non-finite values (stat_bin).
```

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

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```
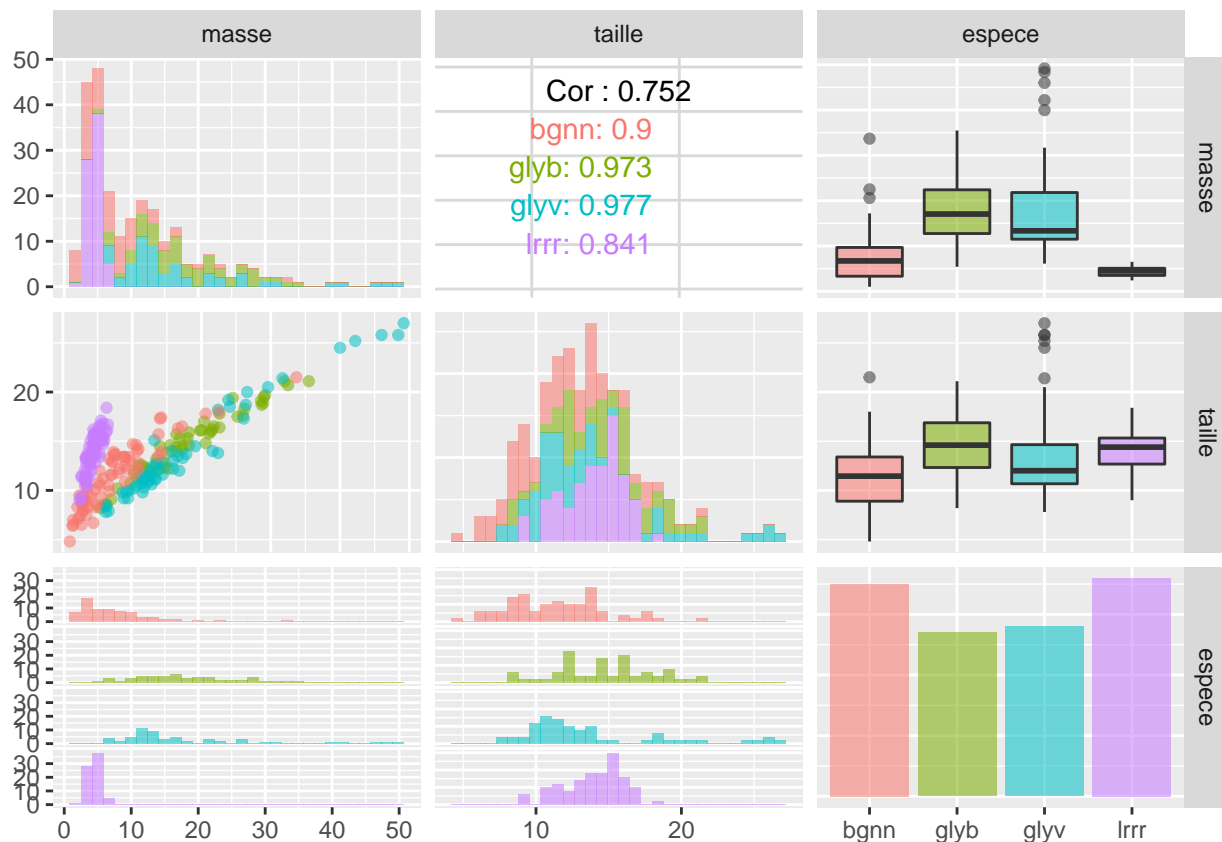
```r
dev.off()
```

```
## pdf
##   2
```

```r
#Couleur et groupes
ggpairs(Mesures5abbr, ggplot2::aes(colour=espece, alpha=0.4), axisLabels='show')
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing non-finite values (stat_density).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning: Removed 142 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing non-finite values (stat_density).

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).
```
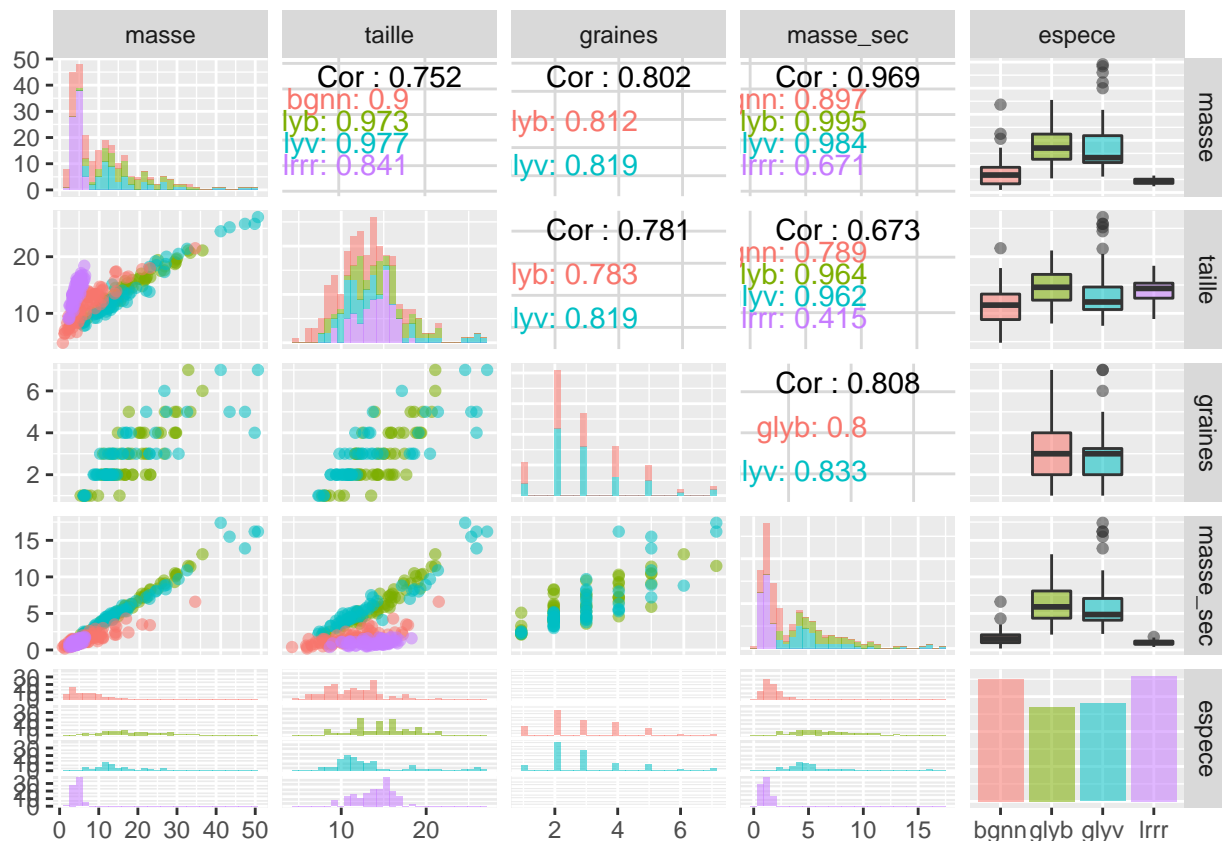


```
pdf("figure35couleurggplot.pdf")
print(ggpairs(Mesures5abbr, ggplot2::aes(colour=espece, alpha=0.4),
              axisLabels='show'))
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning: Removed 142 rows containing missing values (geom_point).


## Warning: Removed 142 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing non-finite values (stat_density).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning: Removed 142 rows containing non-finite values (stat_boxplot).

## Warning: Removed 3 rows containing missing values (geom_point).


## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing non-finite values (stat_density).

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).
```

```r
dev.off()
```

```
## pdf
##   2
```

```r
#En plus
#Noir et blanc
Mesuresabbr <- Mesures
Mesuresabbr$espece <- abbreviate(Mesures$espece)
ggpairs(Mesuresabbr, diag=list(continuous="bar"), axisLabels='show')
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'

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

```
ggpairs(Mesures5abbr, diag=list(continuous="bar"), axisLabels='show')
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'

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

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

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

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning: Removed 142 rows containing missing values (geom_point).


## Warning: Removed 142 rows containing missing values (geom_point).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning: Removed 142 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing missing values (geom_point).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).
```



```
pdf("figure35Mesuresggplot.pdf")
print(ggpairs(Mesuresabbr, diag=list(continuous="bar"), axisLabels='show'))
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'
```

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

```
dev.off()
```

```
## pdf
##    2
```

```
pdf("figure35Mesures5ggplot.pdf")
print(ggpairs(Mesures5abbr, diag=list(continuous="bar"), axisLabels='show'))
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'
```

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

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

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

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

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

```
## Warning: Removed 142 rows containing non-finite values (stat_bin).
```

```
## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values
```

```
## Warning: Removed 142 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## Warning: Removed 3 rows containing missing values (geom_point).
```

```
## Warning: Removed 142 rows containing missing values (geom_point).
```

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

```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```

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

```
## Warning: Removed 142 rows containing non-finite values (stat_bin).
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
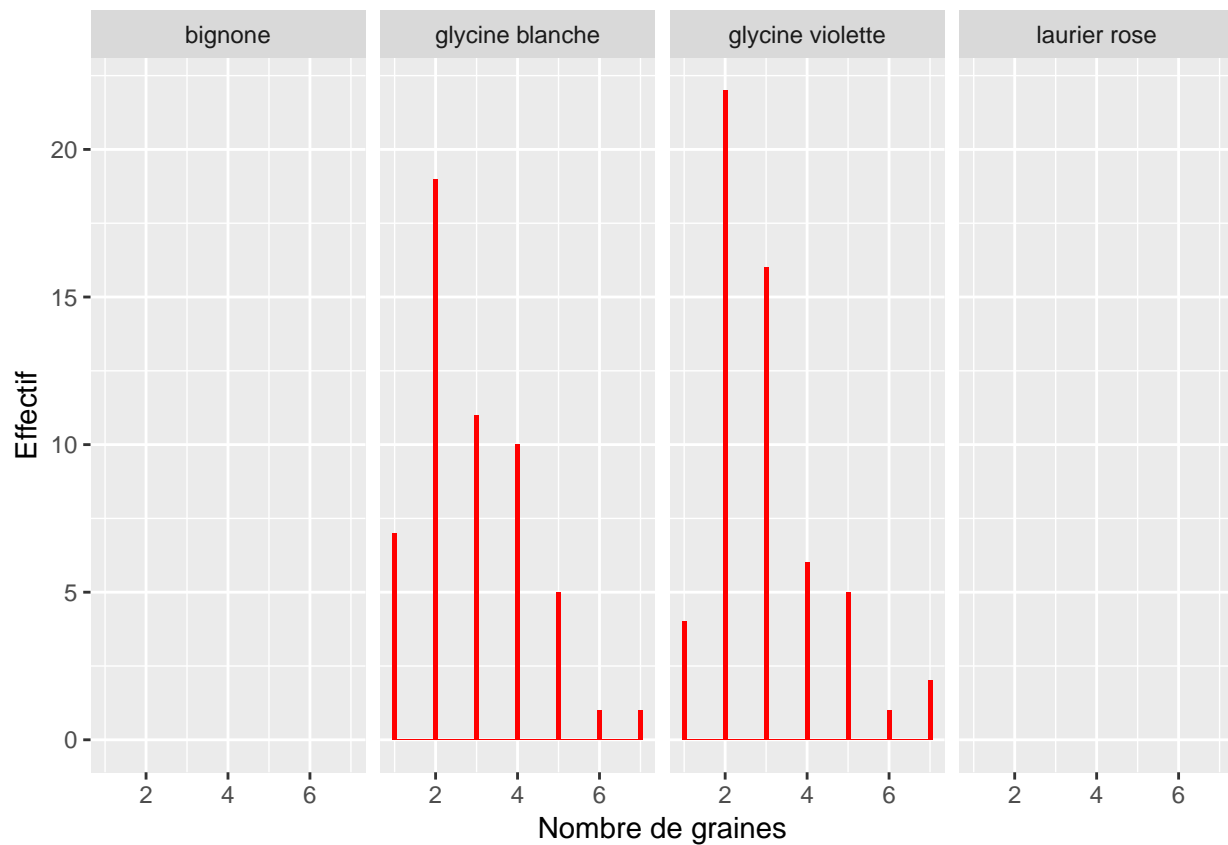
```
## Warning: Removed 3 rows containing non-finite values (stat_bin).
```

```
dev.off()
```

```
## pdf
##    2
```

```r
#Couleur
ggpairs(Mesuresabbr, ggplot2::aes(colour=espece, alpha=0.4),
        diag=list(continuous="bar"), axisLabels='show')
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'
```

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



```r
pdf("figure35MesuresCouleurggplot.pdf")
print(ggpairs(Mesuresabbr, ggplot2::aes(colour=espece, alpha=0.4),
              diag=list(continuous="bar"), axisLabels='show'))
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'
```

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

```r
dev.off()
```

```
## pdf
```

```
##    2
ggpairs(Mesures5abbr, ggplot2::aes(colour=espece, alpha=0.4),
        diag=list(continuous="bar"), axisLabels='show')
```

Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
"densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'

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

Warning in (function (data, mapping, alignPercent = 0.6, method =
"pearson", : Removed 142 rows containing missing values

Warning in (function (data, mapping, alignPercent = 0.6, method =
"pearson", : Removed 3 rows containing missing values

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

Warning in (function (data, mapping, alignPercent = 0.6, method =
"pearson", : Removed 142 rows containing missing values

Warning in (function (data, mapping, alignPercent = 0.6, method =
"pearson", : Removed 3 rows containing missing values

Warning: Removed 142 rows containing missing values (geom_point).

Warning: Removed 142 rows containing missing values (geom_point).

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

Warning: Removed 142 rows containing non-finite values (stat_bin).

Warning in (function (data, mapping, alignPercent = 0.6, method =
"pearson", : Removed 142 rows containing missing values

Warning: Removed 142 rows containing non-finite values (stat_boxplot).

Warning: Removed 3 rows containing missing values (geom_point).

Warning: Removed 3 rows containing missing values (geom_point).

Warning: Removed 142 rows containing missing values (geom_point).

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

Warning: Removed 3 rows containing non-finite values (stat_bin).

Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

Warning: Removed 142 rows containing non-finite values (stat_bin).

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

Warning: Removed 3 rows containing non-finite values (stat_bin).

```r
pdf("figure35Mesures5Couleurggplot.pdf")
print(ggpairs(Mesures5abbr, ggplot2::aes(colour=espece, alpha=0.4),
              diag=list(continuous="bar"), axisLabels='show'))
```

```
## Warning in check_and_set_ggpairs_defaults("diag", diag, continuous =
## "densityDiag", : Changing diag$continuous from 'bar' to 'barDiag'

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

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

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

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 142 rows containing missing values

## Warning in (function (data, mapping, alignPercent = 0.6, method =
## "pearson", : Removed 3 rows containing missing values

## Warning: Removed 142 rows containing missing values (geom_point).


## Warning: Removed 142 rows containing missing values (geom_point).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

## Warning in (function (data, mapping, alignPercent = 0.6, method =
```

36

```
## "pearson", : Removed 142 rows containing missing values

## Warning: Removed 142 rows containing non-finite values (stat_boxplot).

## Warning: Removed 3 rows containing missing values (geom_point).


## Warning: Removed 3 rows containing missing values (geom_point).

## Warning: Removed 142 rows containing missing values (geom_point).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).

## Warning: Removed 3 rows containing non-finite values (stat_boxplot).

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

## Warning: Removed 142 rows containing non-finite values (stat_bin).

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

## Warning: Removed 3 rows containing non-finite values (stat_bin).
```
```r
dev.off()
```
```
## pdf
##   2
```
```r
#page 116
plot(table(Mesures5$graines),type="h",lwd=4,col="red",xlab="Nombre de graines",ylab="Effectif")
```
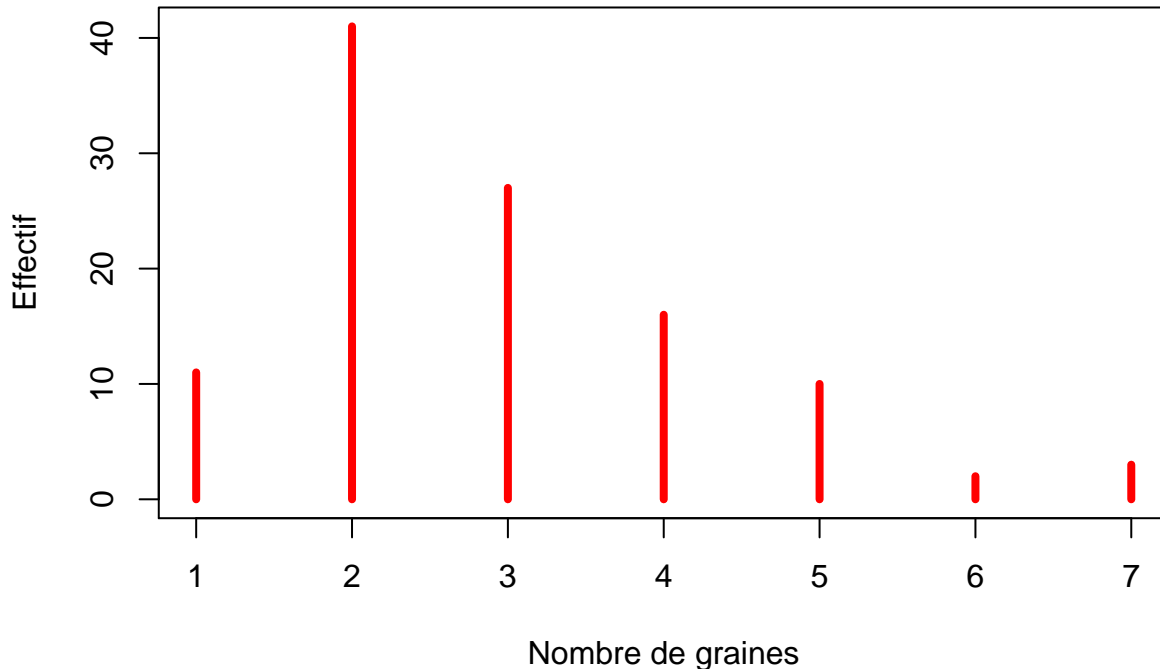


```r
pdf("figure36Aggplot.pdf")
plot(table(Mesures5$graines),type="h",lwd=4,col="red",xlab="Nombre de graines",ylab="Effectif")
dev.off()
```
```
## pdf
```

```
##    2
```

```
table(Mesures5$graines)

##
##  1  2  3  4  5  6  7
## 11 41 27 16 10  2  3
```

```
ggplot(Mesures5, aes(x = graines)) + geom_bar(fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif")
```

```
## Warning: Removed 142 rows containing non-finite values (stat_count).
```
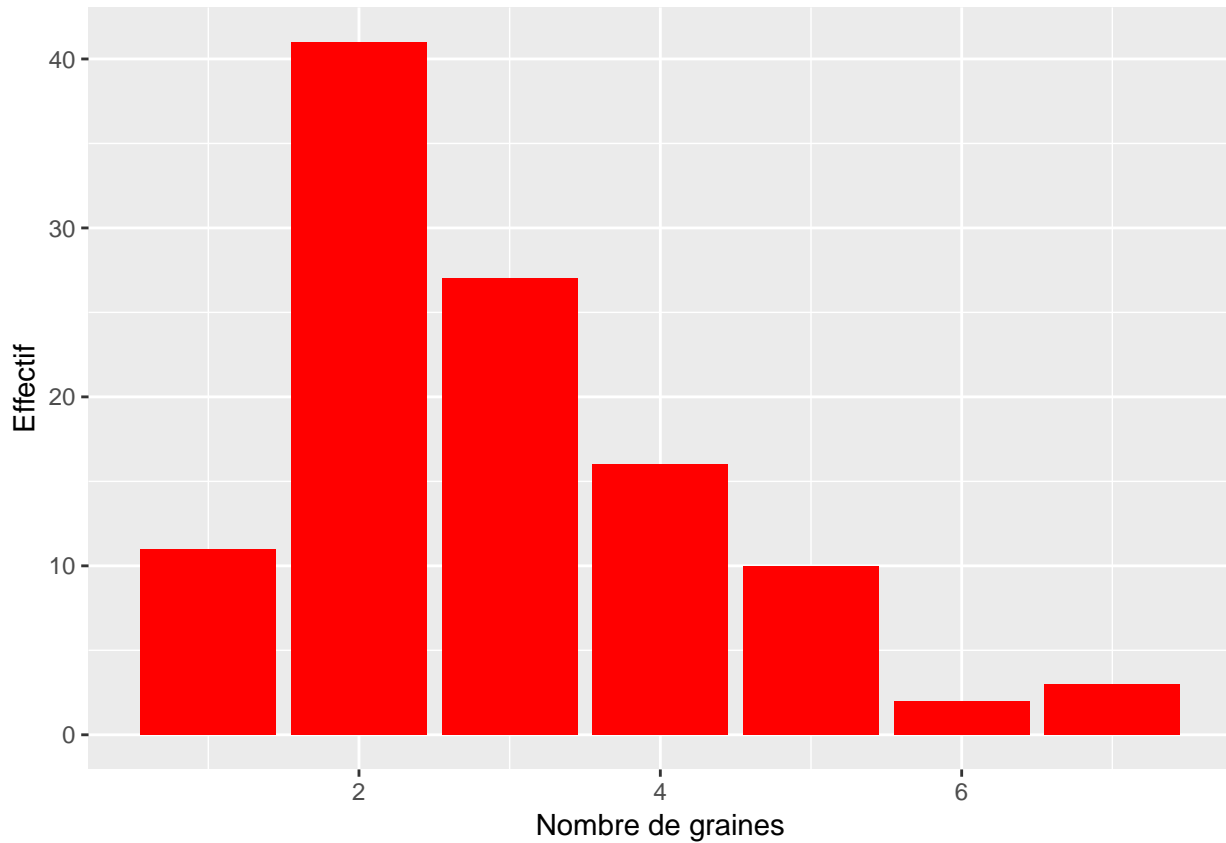
```
ggplot(Mesures5, aes(x = graines)) + geom_histogram(binwidth=.1,fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif")
```

```
## Warning: Removed 142 rows containing non-finite values (stat_bin).
```
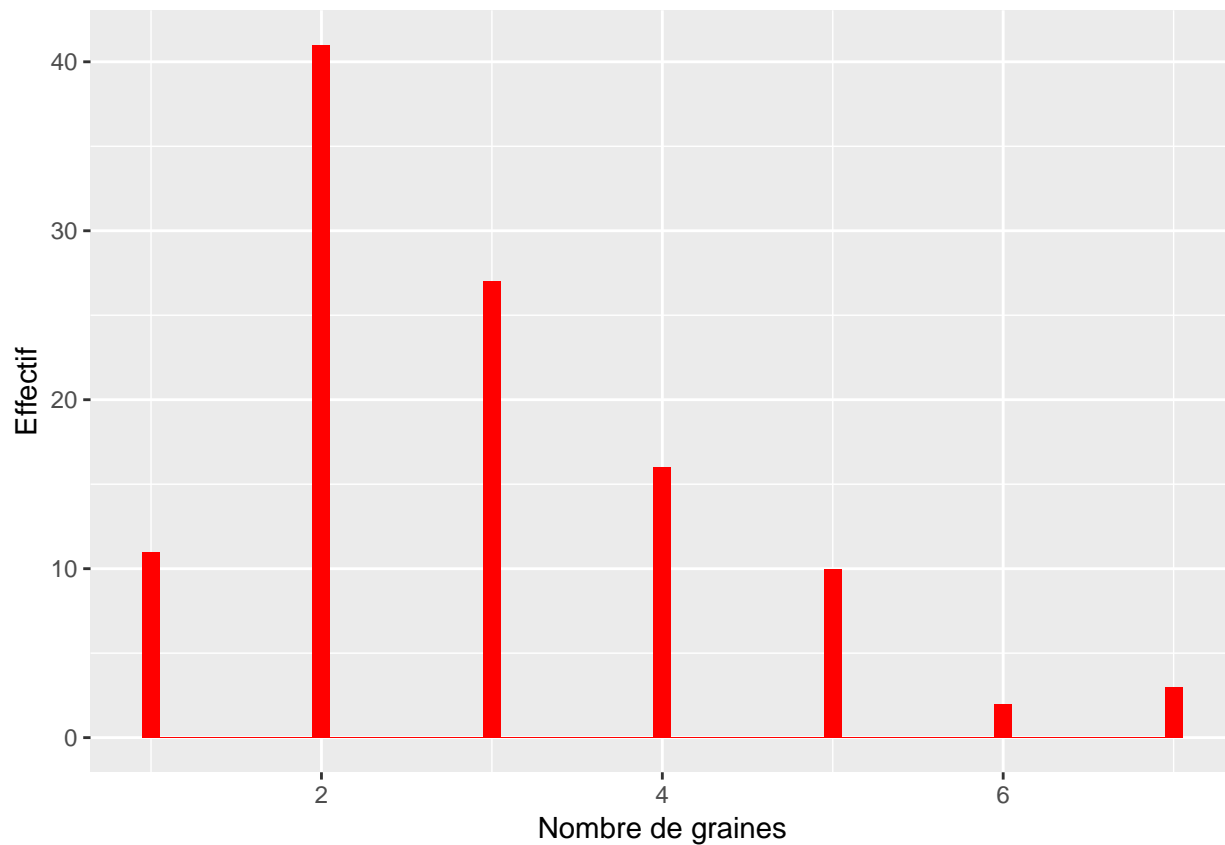
```
pdf("figure36Bggplot.pdf")
ggplot(Mesures5, aes(x = graines)) + geom_histogram(binwidth=.1,fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif")
```

Warning: Removed 142 rows containing non-finite values (stat_bin).

```
dev.off()
```

pdf
2

```
#page 119
ggplot(Mesures5, aes(x = graines)) + geom_histogram(binwidth=.1,fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif") + facet_grid(.~espece)
```

Warning: Removed 142 rows containing non-finite values (stat_bin).

```
ggplot(Mesures5, aes(x = graines)) + geom_histogram(binwidth=.1,fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif") + facet_grid(espece~.)
```

```
## Warning: Removed 142 rows containing non-finite values (stat_bin).
```

```
ggplot(Mesures5, aes(x = graines)) + geom_histogram(binwidth=.1,fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)
```
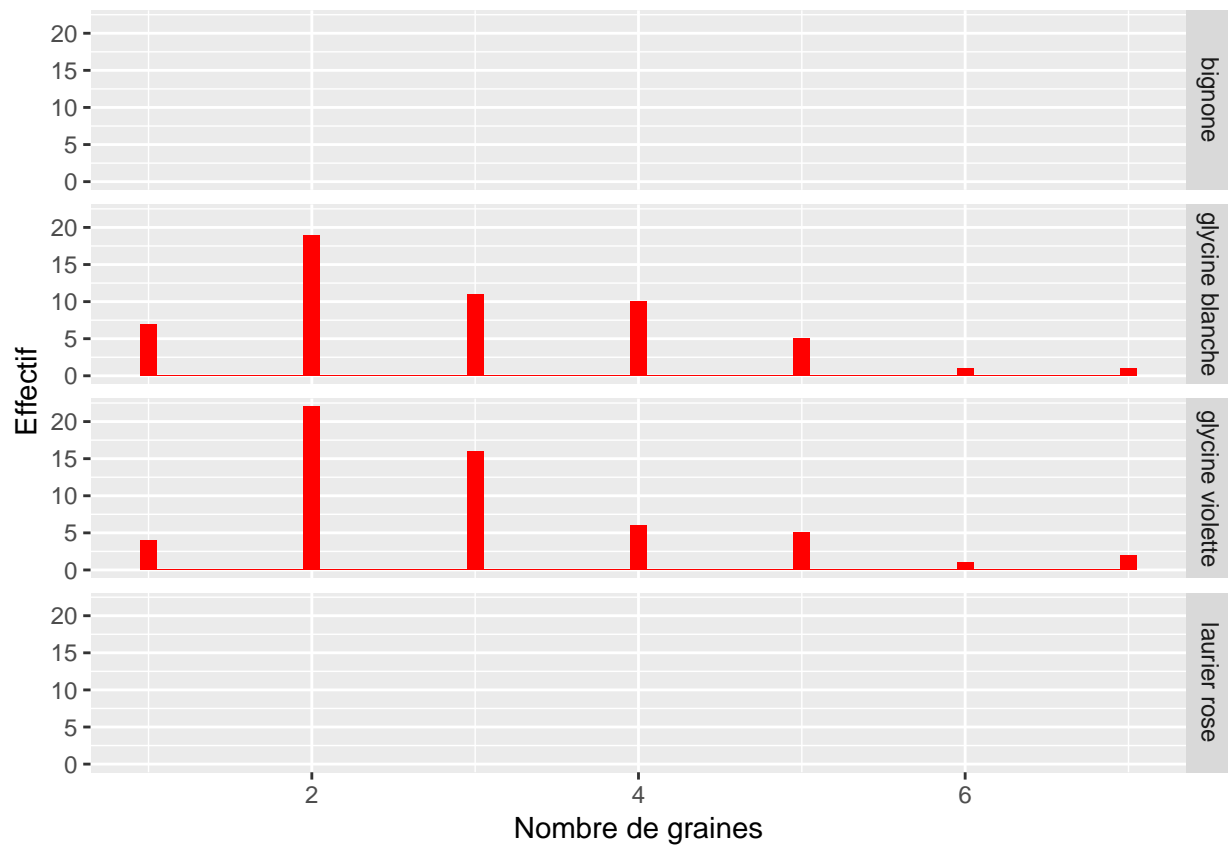
Warning: Removed 142 rows containing non-finite values (stat_bin).

```
pdf("figure36Cggplot.pdf")
ggplot(Mesures5, aes(x = graines)) + geom_histogram(binwidth=.1,fill=I("red")) +
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)
```

Warning: Removed 142 rows containing non-finite values (stat_bin).

```
dev.off()
```

pdf
2

```
tapply(Mesures5$graines,Mesures5$espece,table)
```

$bignone
< table of extent 0 >
##
$`glycine blanche`
##
1 2 3 4 5 6 7
7 19 11 10 5 1 1
##
$`glycine violette`
##
1 2 3 4 5 6 7
4 22 16 6 5 1 2
##
$`laurier rose`
< table of extent 0 >

```
#En plus avec ggplot
data.graines_espece<-as.data.frame(table(Mesures5$graines,Mesures5$espece))
colnames(data.graines_espece)<-c("nbr.graines","espece","effectif")
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines))+geom_bar(stat=
  "identity")+ facet_grid(espece~.)
```



```
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines))+geom_bar(stat=
  "identity")+ facet_grid(~espece)
```

```
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines))+geom_bar(stat=
  "identity")+ facet_wrap(~espece)
```

```
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=espece))+geom_bar(
  stat="identity")+ facet_wrap(~espece)
```

```
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=espece))+geom_bar(
  stat="identity")+ facet_wrap(~espece) + scale_fill_grey() + theme_bw()
```

```r
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))+
  geom_bar(stat="identity")+ facet_wrap(~espece)
```

```
ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))+
  geom_bar(stat="identity")+ facet_wrap(~espece) + scale_fill_grey() + theme_bw()
```

```
pdf("figure36Dggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines))+geom_bar(stat=
  "identity")+ facet_grid(espece~.))
dev.off()
```

```
## pdf
##    2
```

```
pdf("figure36Eggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines))+geom_bar(stat=
  "identity")+ facet_grid(~espece))
dev.off()
```
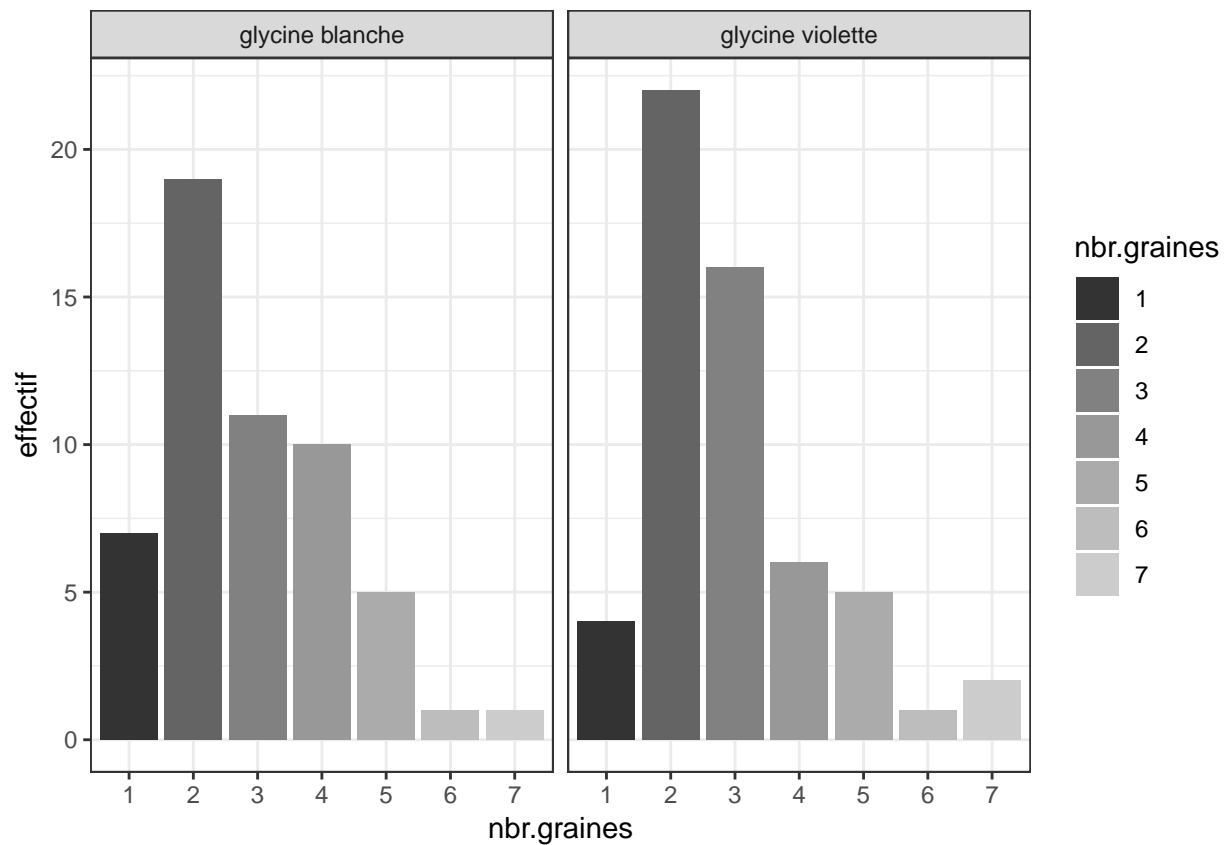
```
## pdf
##    2
```

```
pdf("figure36Fggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines))+geom_bar(stat=
  "identity")+ facet_wrap(~espece))
dev.off()
```

```
## pdf
##    2
```

```
pdf("figure36Gggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=espece))+
        geom_bar(stat="identity")+ facet_wrap(~espece))
dev.off()
```

```
## pdf
```

```
##    2
pdf("figure36Hbwggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=espece))+
        geom_bar(stat="identity")+ facet_wrap(~espece) + scale_fill_grey() + theme_bw())
dev.off()
```

```
## pdf
##    2
```

```
pdf("figure36Iggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_wrap(~espece))
dev.off()
```
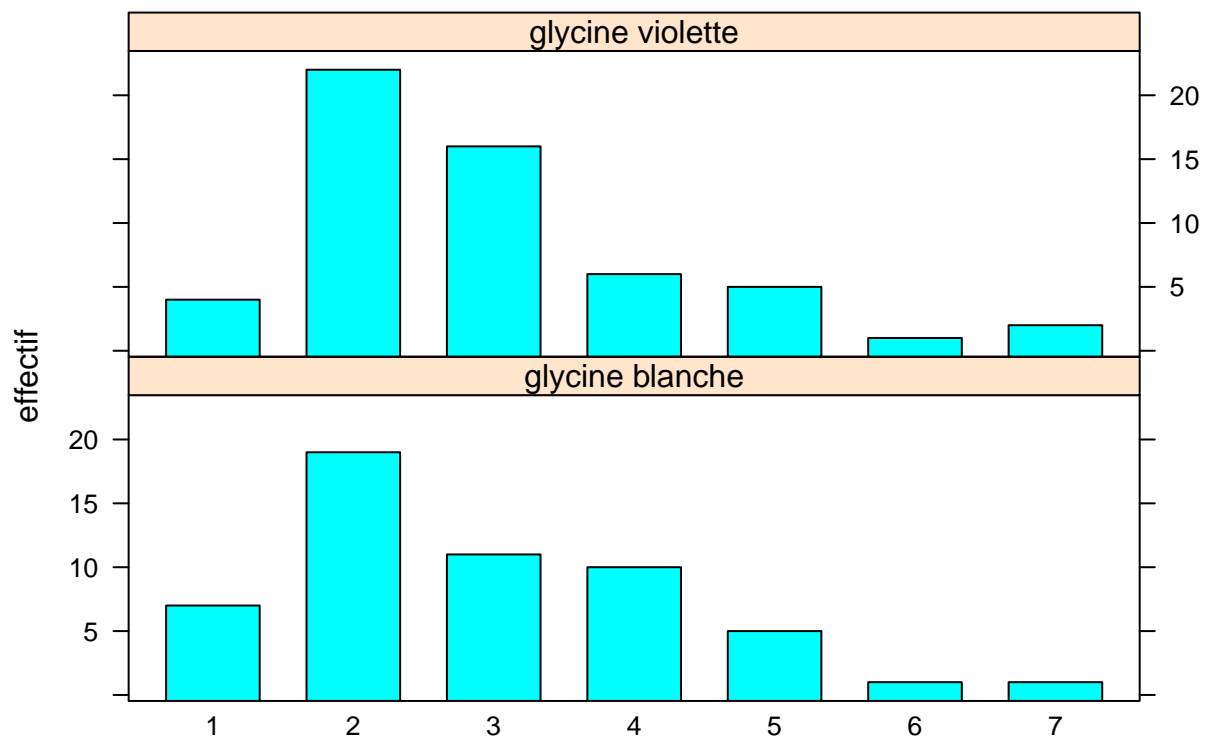
```
## pdf
##    2
```

```
pdf("figure36Jbwggplot.pdf")
print(ggplot(data.graines_espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_wrap(~espece) + scale_fill_grey() +
        theme_bw())
dev.off()
```

```
## pdf
##    2
```

```
#page 120
if(!("lattice" %in%
     rownames(installed.packages())))){install.packages("lattice")}
library("lattice")
data.graines_espece<-as.data.frame(table(Mesures5$graines,Mesures5$espece))
colnames(data.graines_espece)<-c("nbr.graines","espece","effectif")
barchart(effectif~nbr.graines|espece,data=data.graines_espece,layout=c(1,4))
```
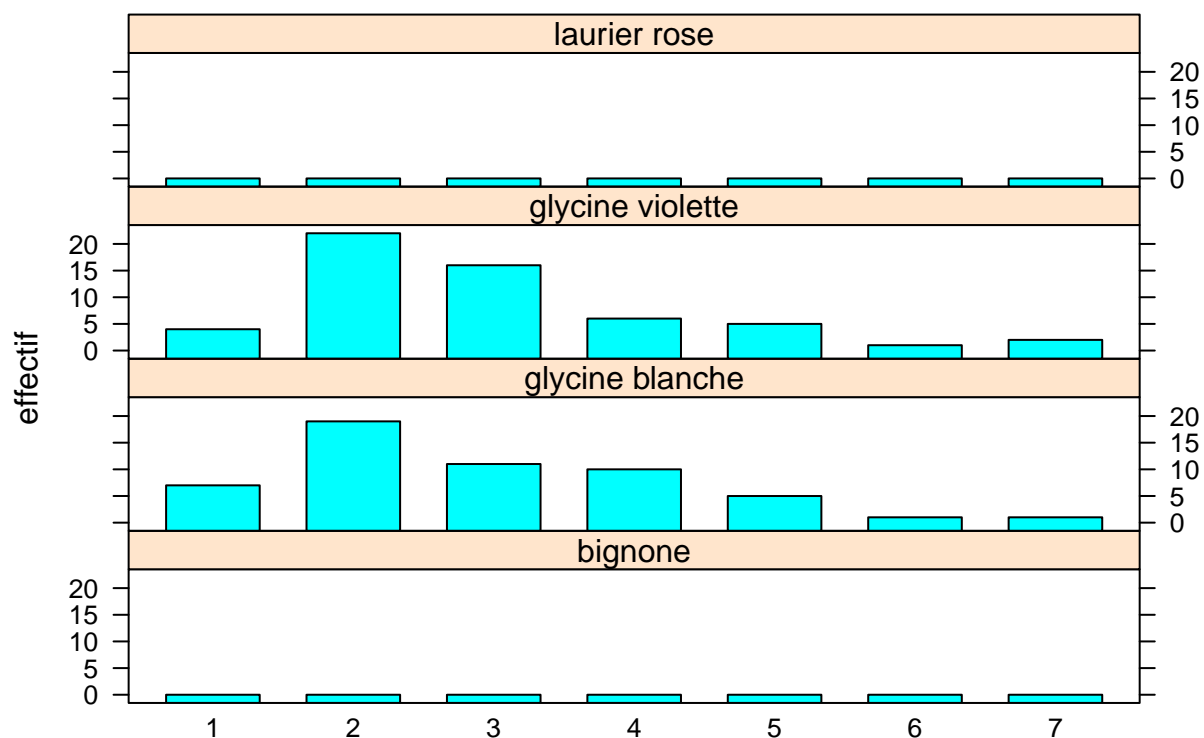
```
#page 121
as.data.frame(table(Mesures5$graines,Mesures5$espece))
```

```
##    Var1              Var2 Freq
## 1     1           bignone    0
## 2     2           bignone    0
## 3     3           bignone    0
## 4     4           bignone    0
## 5     5           bignone    0
## 6     6           bignone    0
## 7     7           bignone    0
## 8     1   glycine blanche    7
## 9     2   glycine blanche   19
## 10    3   glycine blanche   11
## 11    4   glycine blanche   10
## 12    5   glycine blanche    5
## 13    6   glycine blanche    1
## 14    7   glycine blanche    1
## 15    1  glycine violette    4
## 16    2  glycine violette   22
## 17    3  glycine violette   16
## 18    4  glycine violette    6
## 19    5  glycine violette    5
## 20    6  glycine violette    1
## 21    7  glycine violette    2
## 22    1       laurier rose    0
## 23    2       laurier rose    0
## 24    3       laurier rose    0
## 25    4       laurier rose    0
## 26    5       laurier rose    0
## 27    6       laurier rose    0
```

```
## 28    7    laurier rose    0
```

```r
(table.graines.espece <-
    table(Mesures5$graines,Mesures5$espece,dnn=c("nbr.graines","espece")))
```

```
##              espece
## nbr.graines bignone glycine blanche glycine violette laurier rose
##           1       0               7                4            0
##           2       0              19               22            0
##           3       0              11               16            0
##           4       0              10                6            0
##           5       0               5                5            0
##           6       0               1                1            0
##           7       0               1                2            0
```

```r
print(table.graines.espece,zero.print=".")
```

```
##              espece
## nbr.graines bignone glycine blanche glycine violette laurier rose
##           1       .               7                4            .
##           2       .              19               22            .
##           3       .              11               16            .
##           4       .              10                6            .
##           5       .               5                5            .
##           6       .               1                1            .
##           7       .               1                2            .
```

```r
(data.graines.espece <-
    as.data.frame(table.graines.espece,responseName="effectif"))
```

```
##    nbr.graines           espece effectif
## 1            1          bignone        0
## 2            2          bignone        0
## 3            3          bignone        0
## 4            4          bignone        0
## 5            5          bignone        0
## 6            6          bignone        0
## 7            7          bignone        0
## 8            1  glycine blanche        7
## 9            2  glycine blanche       19
## 10           3  glycine blanche       11
## 11           4  glycine blanche       10
## 12           5  glycine blanche        5
## 13           6  glycine blanche        1
## 14           7  glycine blanche        1
## 15           1 glycine violette        4
## 16           2 glycine violette       22
## 17           3 glycine violette       16
## 18           4 glycine violette        6
## 19           5 glycine violette        5
## 20           6 glycine violette        1
## 21           7 glycine violette        2
## 22           1     laurier rose        0
## 23           2     laurier rose        0
## 24           3     laurier rose        0
## 25           4     laurier rose        0
```

```
## 26          5      laurier rose        0
## 27          6      laurier rose        0
## 28          7      laurier rose        0
```

```
barchart(effectif~nbr.graines|espece,data= data.graines.espece)
```
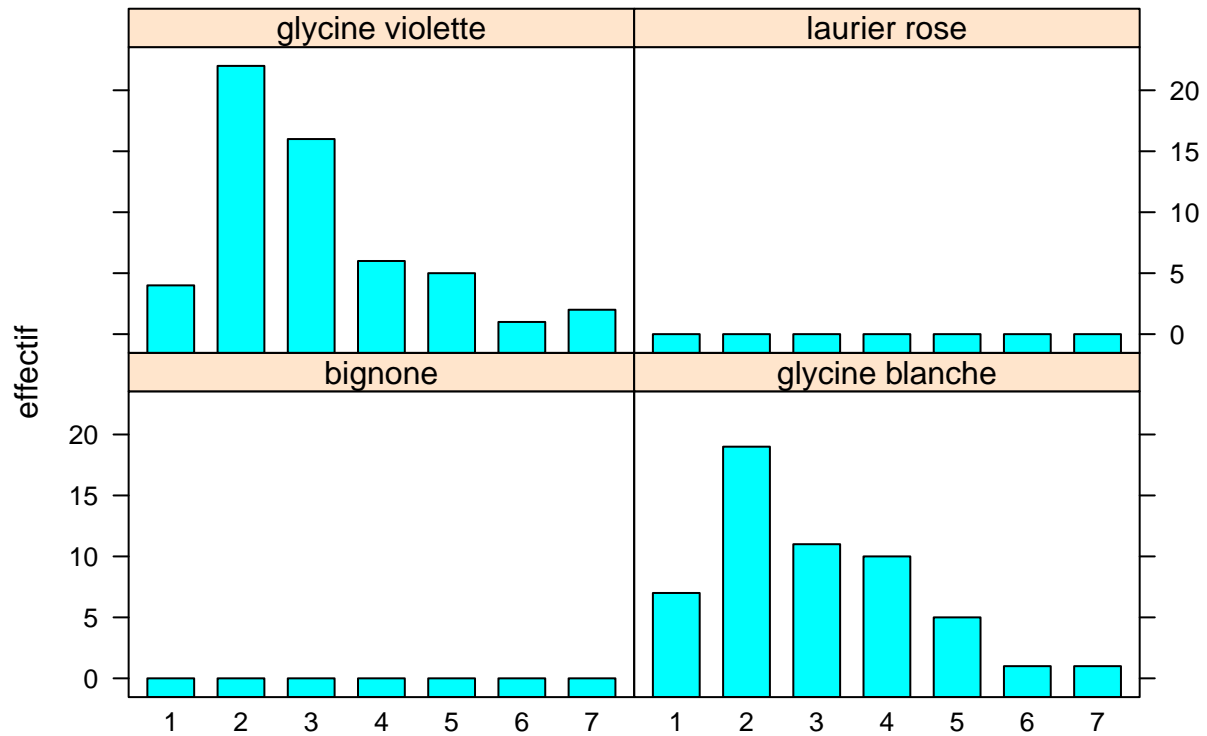


```
pdf("figure38lattice.pdf")
barchart(effectif~nbr.graines|espece,data= data.graines.espece)
dev.off()
```

```
## pdf
##   2
```

```
#En plus avec ggplot2
ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))+
  geom_bar(stat="identity")+ facet_wrap(~espece)
```
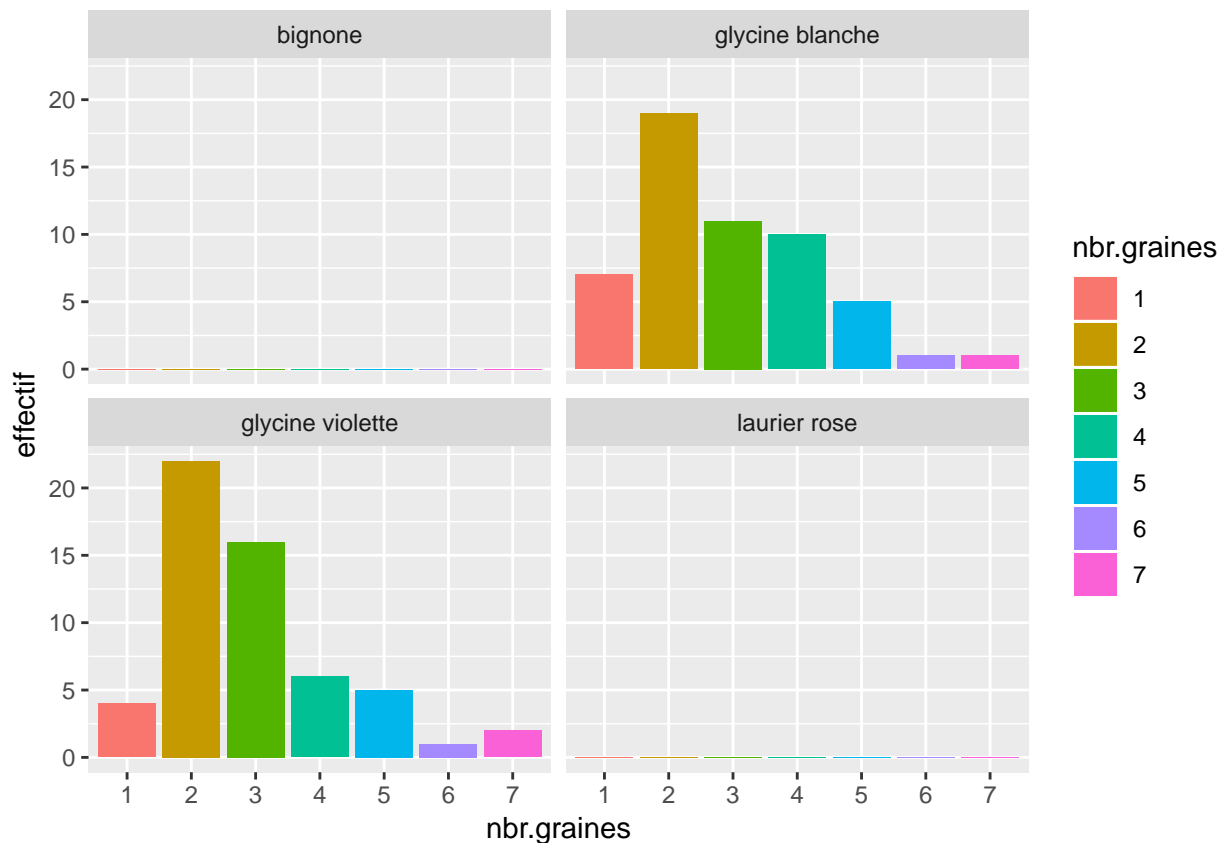
```r
pdf("figure38ggplot.pdf")
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_wrap(~espece))
dev.off()
```

```
## pdf
##   2
```

```r
#page 122
(table.graines.espece <-
    table(factor(Mesures5$graines),Mesures5$espece,dnn=c("nbr.graines","espece"),
        exclude=c("bignone","laurier rose")))
```

```
##              espece
## nbr.graines glycine blanche glycine violette
##       1                   7                4
##       2                  19               22
##       3                  11               16
##       4                  10                6
##       5                   5                5
##       6                   1                1
##       7                   1                2
##       <NA>                0                0
```

```r
#En plus pour supprimer la modalité <NA>
(table.graines.espece <-
    table(factor(Mesures5$graines),Mesures5$espece,dnn=c("nbr.graines","espece"),
        exclude=c("bignone","laurier rose"), useNA="no"))
```

```
##           espece
## nbr.graines glycine blanche glycine violette
##           1               7                 4
##           2              19                22
##           3              11                16
##           4              10                 6
##           5               5                 5
##           6               1                 1
##           7               1                 2
```

```r
#page 123
(data.graines.espece<-as.data.frame(table.graines.espece,responseName="effectif"
))
```

```
##    nbr.graines          espece effectif
## 1            1  glycine blanche        7
## 2            2  glycine blanche       19
## 3            3  glycine blanche       11
## 4            4  glycine blanche       10
## 5            5  glycine blanche        5
## 6            6  glycine blanche        1
## 7            7  glycine blanche        1
## 8            1 glycine violette        4
## 9            2 glycine violette       22
## 10           3 glycine violette       16
## 11           4 glycine violette        6
## 12           5 glycine violette        5
## 13           6 glycine violette        1
## 14           7 glycine violette        2
```

```r
pdf("figure39lattice.pdf")
barchart(effectif~nbr.graines|espece,data=data.graines.espece)
dev.off()
```

```
## pdf
##   2
```

```r
#En plus avec ggplot
ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))+
  geom_bar(stat="identity")+ facet_grid(~espece)
```
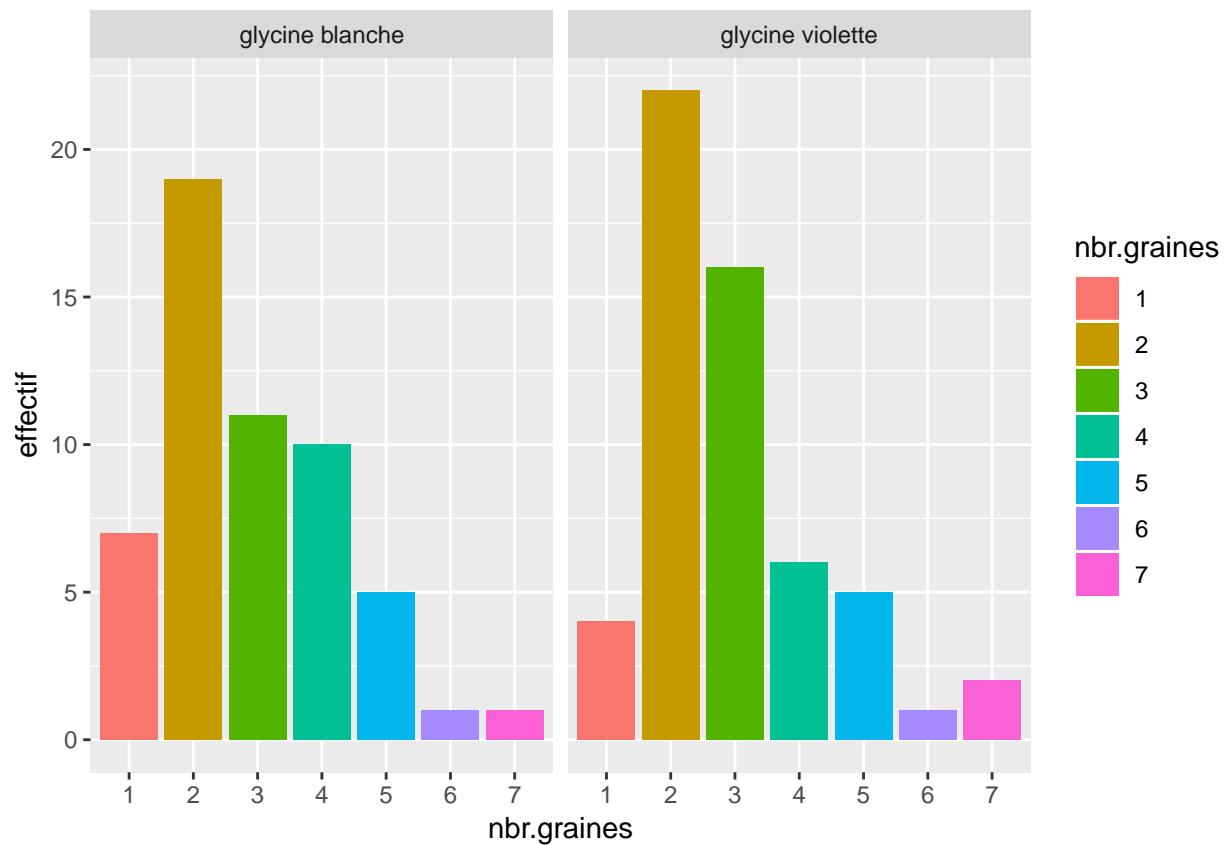
```r
pdf("figure39ggplot.pdf")
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_grid(~espece))
dev.off()
```

```
## pdf
##   2
```

```r
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_grid(~espece) + scale_fill_grey() +
        theme_bw())
```

```
pdf("figure39bwggplot.pdf")
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_grid(~espece) + scale_fill_grey() +
        theme_bw()))
dev.off()
```

```
## pdf
##   2
```

```
barchart(effectif~nbr.graines|espece,data=data.graines.espece,layout=c(1,2))
```

```r
pdf("figure310lattice.pdf")
barchart(effectif~nbr.graines|espece,data=data.graines.espece,layout=c(1,2))
dev.off()
```

```
## pdf
##   2
```

```r
#En plus
ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))+
  geom_bar(stat="identity")+ facet_grid(espece~.)
```
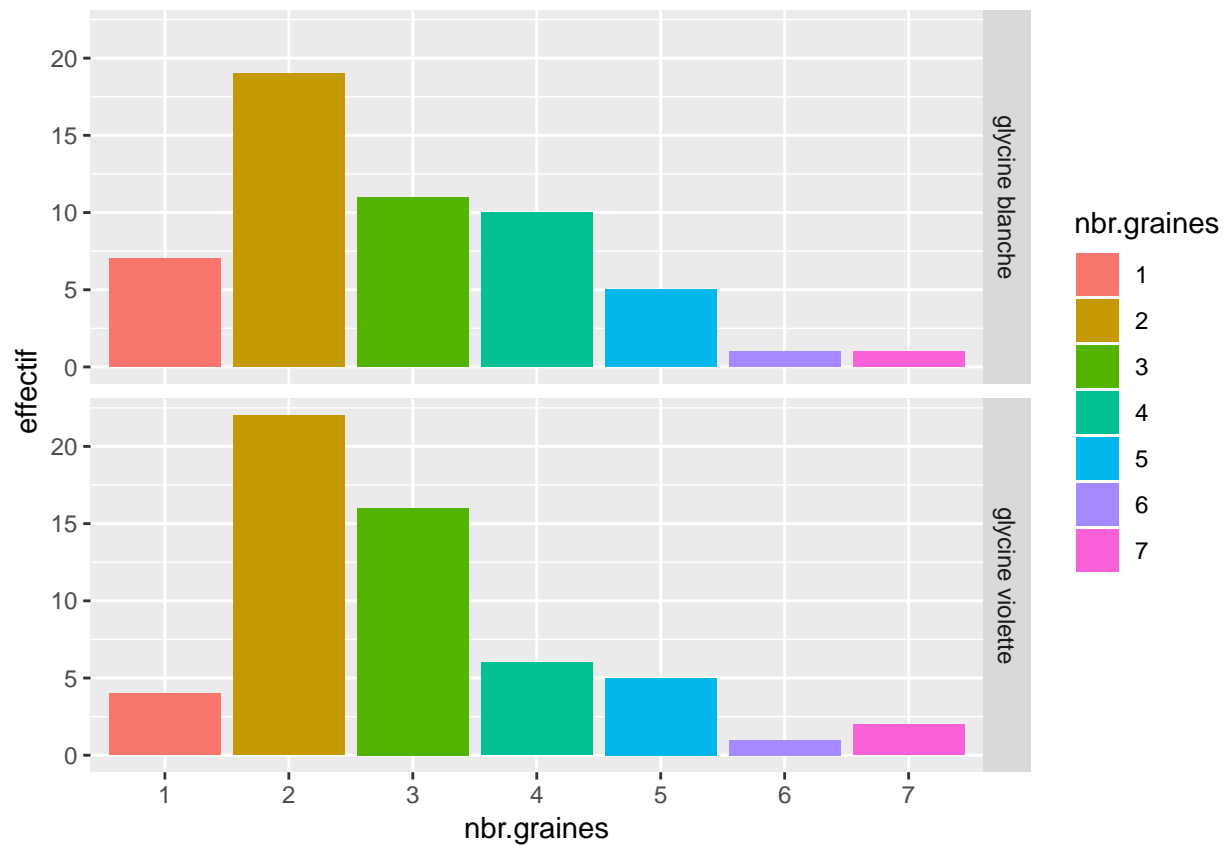
```
pdf("figure310ggplot.pdf")
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_grid(espece~.))
dev.off()
```

```
## pdf
##   2
```

```
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_grid(espece~.) + scale_fill_grey() +
        theme_bw())
```
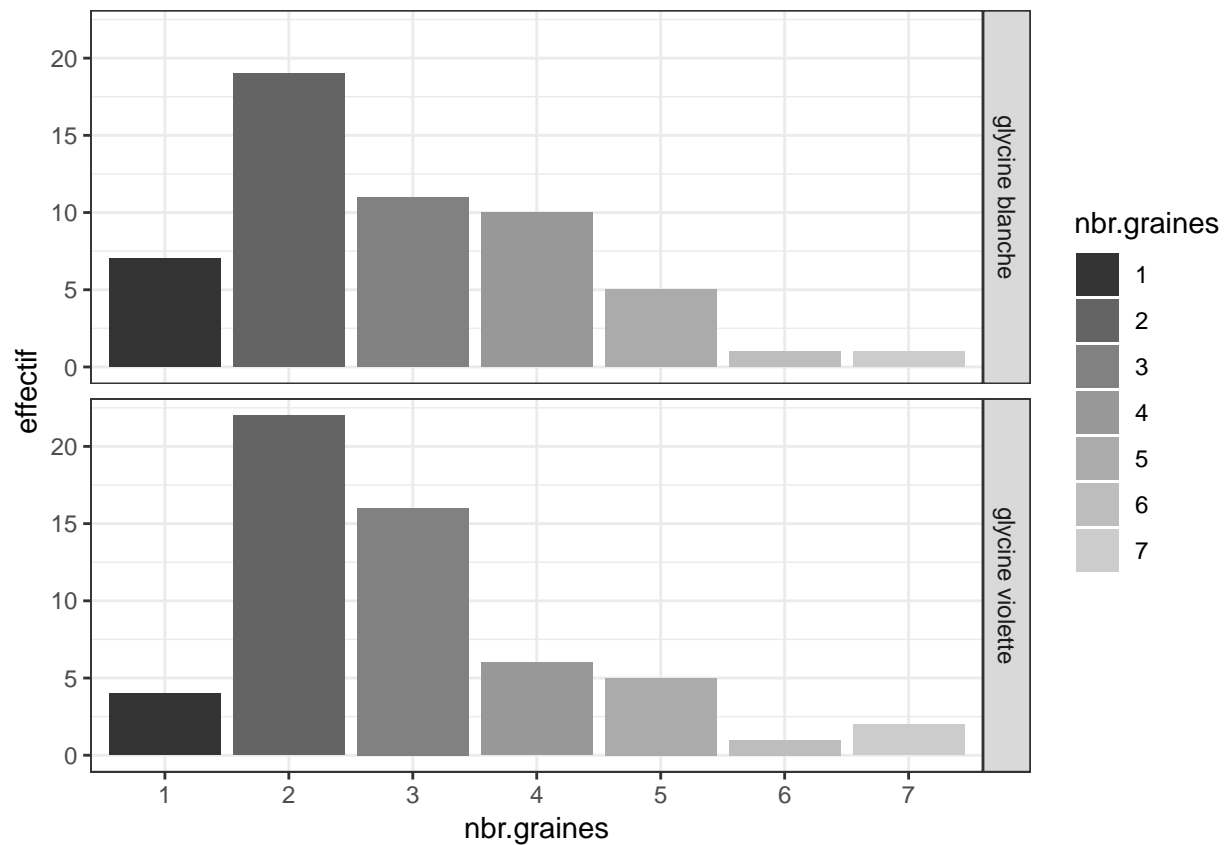
```
pdf("figure310bwggplot.pdf")
print(ggplot(data.graines.espece,aes(y=effectif,x=nbr.graines,fill=nbr.graines))
      +geom_bar(stat="identity")+ facet_grid(espece~.) + scale_fill_grey() +
         theme_bw()))
dev.off()

## pdf
##    2
#page 125
xyplot(effectif~nbr.graines|espece,data=data.graines.espece,type="h",lwd=4)
```
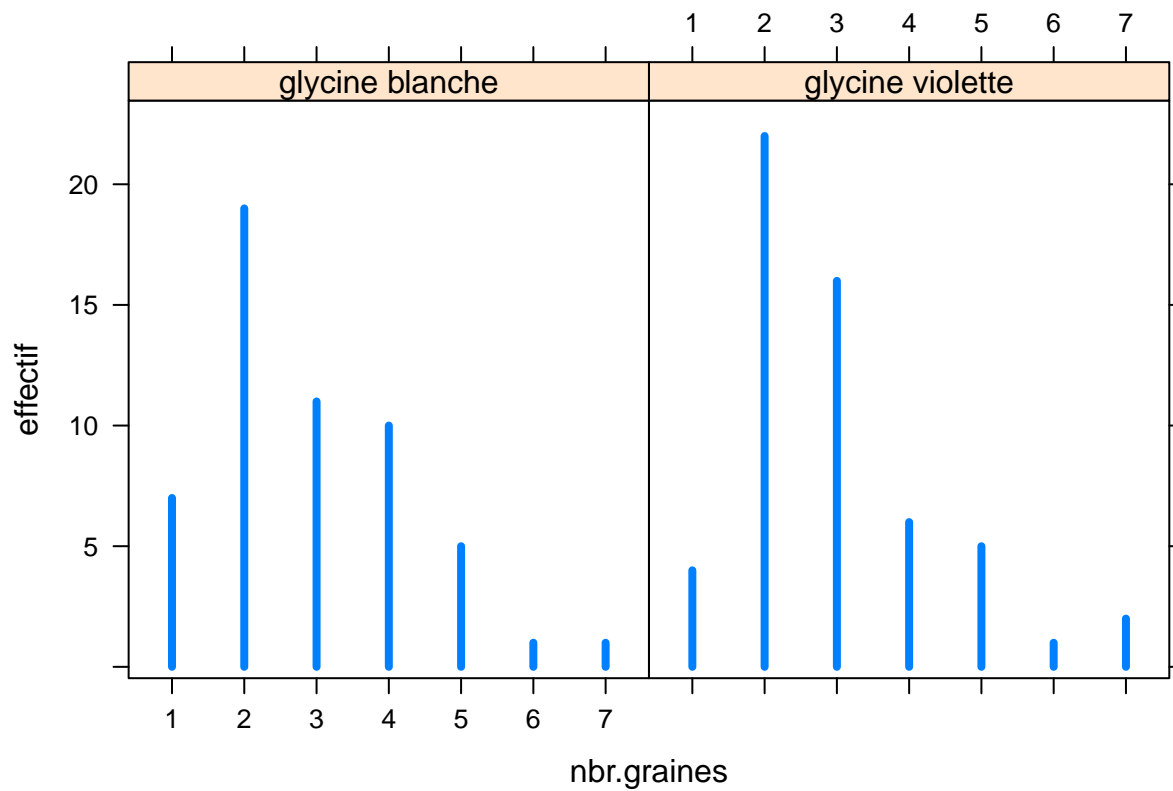
```
pdf("figure311lattice.pdf")
xyplot(effectif~nbr.graines|espece,data=data.graines.espece,type="h",lwd=4)
dev.off()
```

```
## pdf
##   2
```
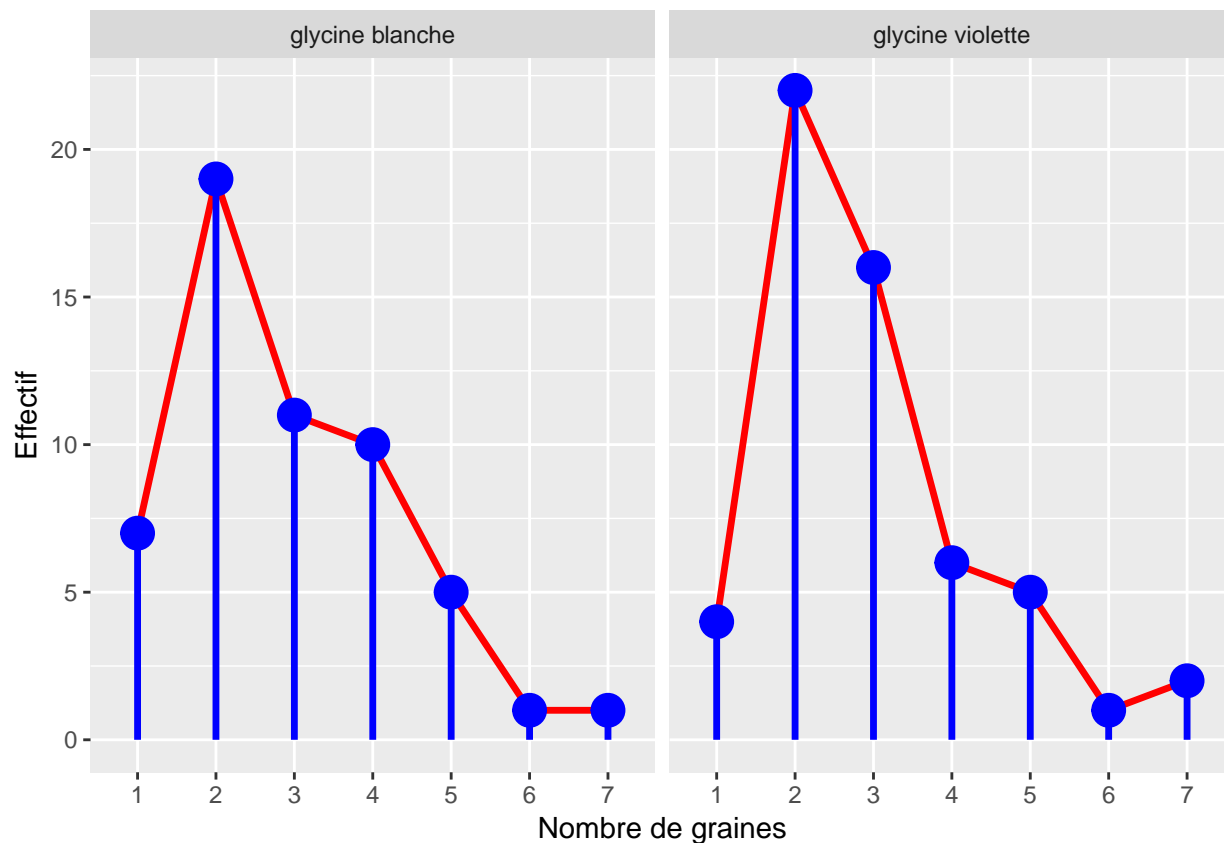
```
#En plus ggplot
ggplot(data.graines.espece, aes(x = nbr.graines)) +
  geom_linerange(aes(ymin=0,ymax=effectif,group=espece),size=1.2,color=I("blue"))+
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)
```
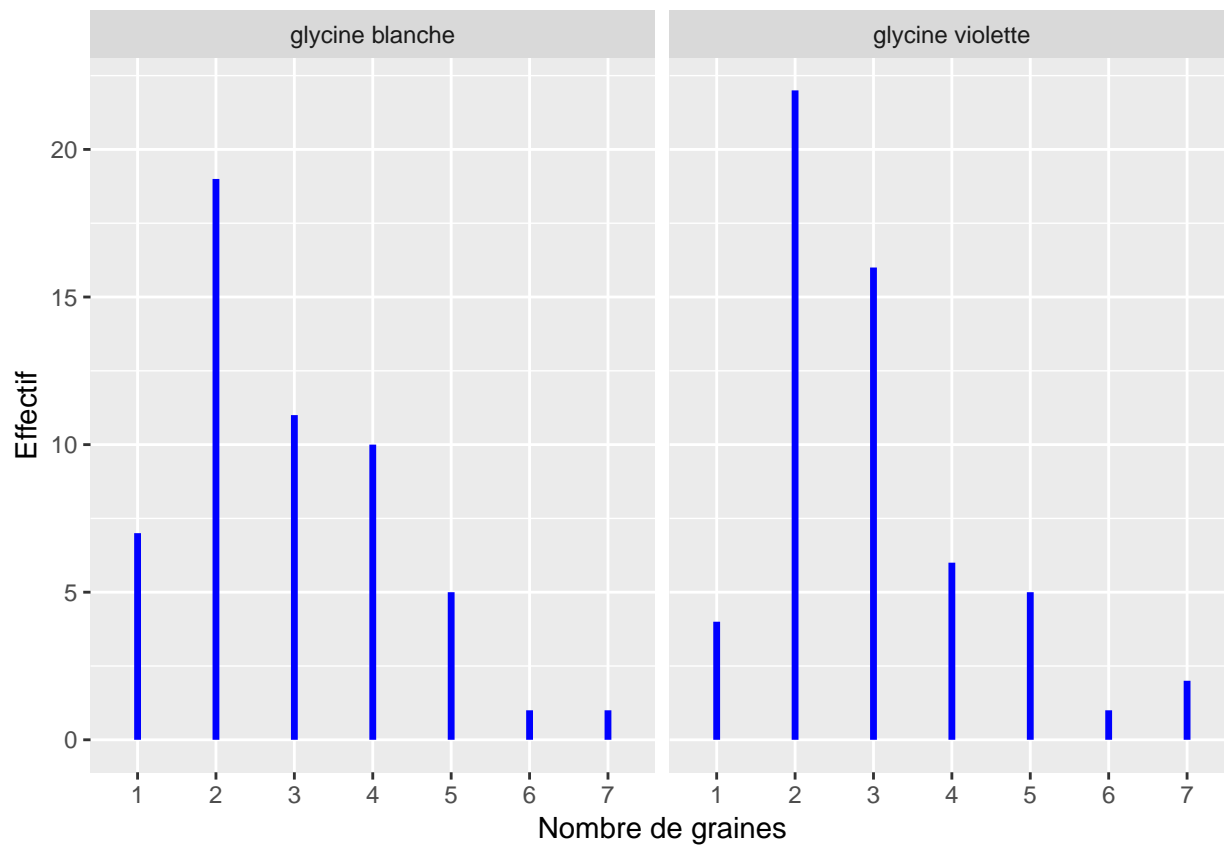
```
pdf("figure311ggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines)) +
        geom_linerange(aes(ymin=0,ymax=effectif,group=espece),size=1.2,color=I("blue"))+
        xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece))
dev.off()
```
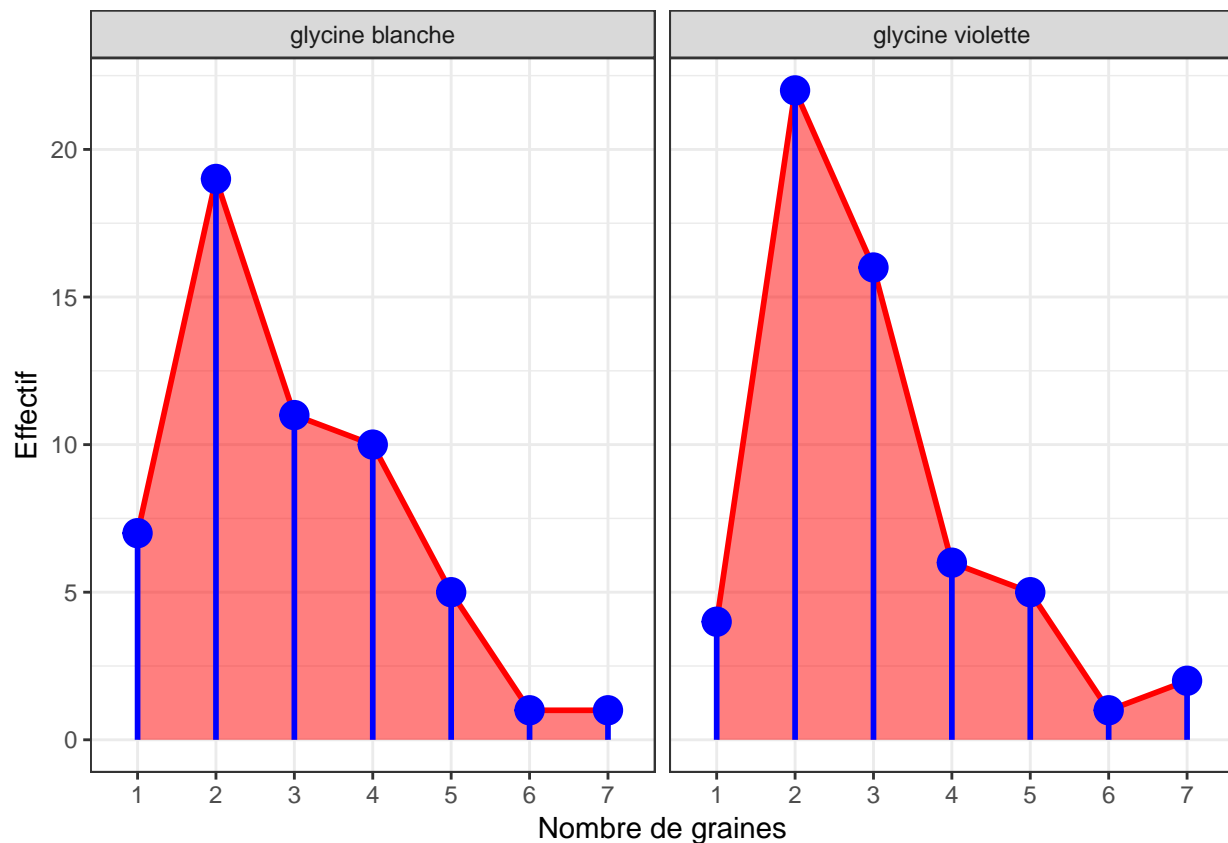
```
## pdf
##   2
```

```
xyplot(effectif~nbr.graines|espece,data=data.graines.espece,type="h",layout=c(1,2),lwd=4)
```
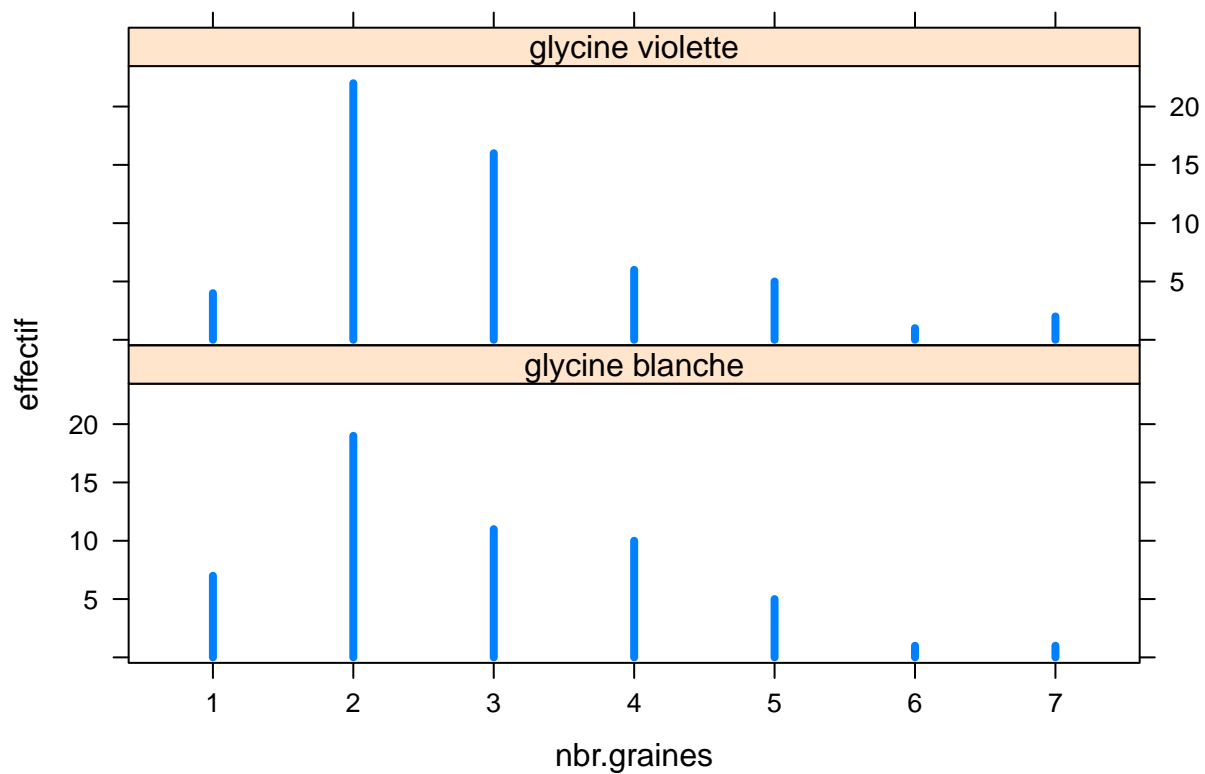
```
pdf("figure312lattice.pdf")
xyplot(effectif~nbr.graines|espece,data=data.graines.espece,type="h",layout=c(1,2),lwd=4)
dev.off()
```

```
## pdf
##   2
```

```
ggplot(data.graines.espece, aes(x = nbr.graines)) +
  geom_linerange(aes(ymin=0,ymax=effectif,group=espece),size=1.2,color=I("blue"))+
  xlab("Nombre de graines") + ylab("Effectif") + facet_grid(espece~.)
```
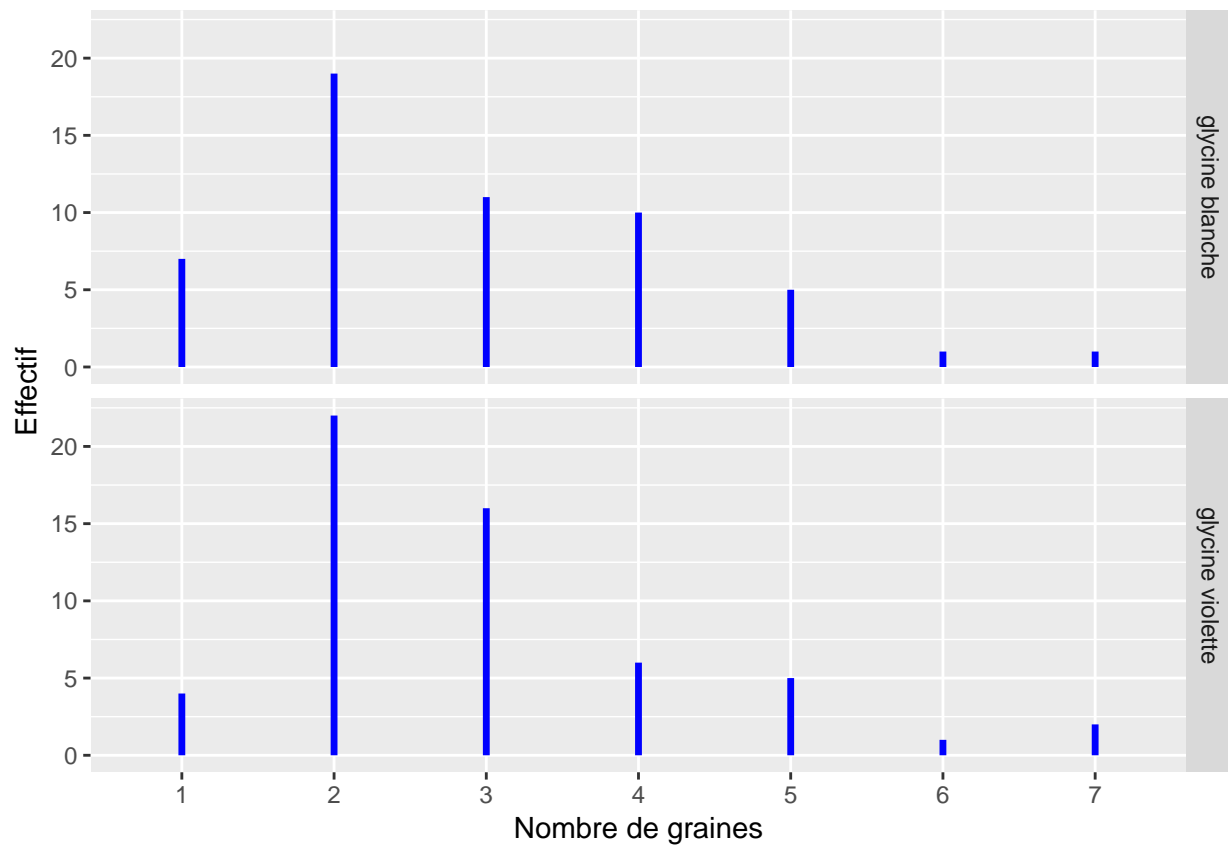
```
pdf("figure312ggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines)) +
        geom_linerange(aes(ymin=0,ymax=effectif,group=espece),size=1.2,color=I("blue"))+
        xlab("Nombre de graines") + ylab("Effectif") + facet_grid(espece~.))
dev.off()
```
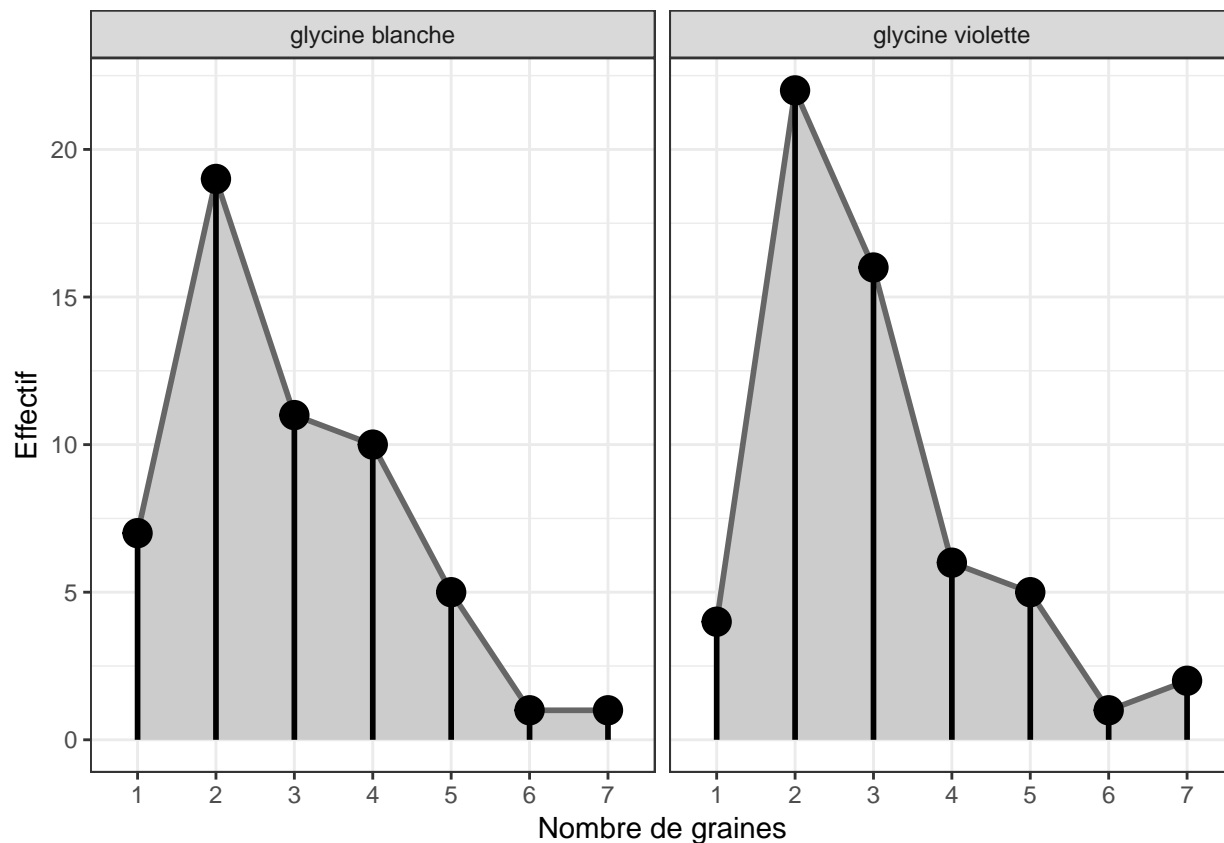
```
## pdf
##    2
```

```
#page 126
barplot(table.graines.espece,beside=TRUE,legend=rownames(table.graines.espece))
```
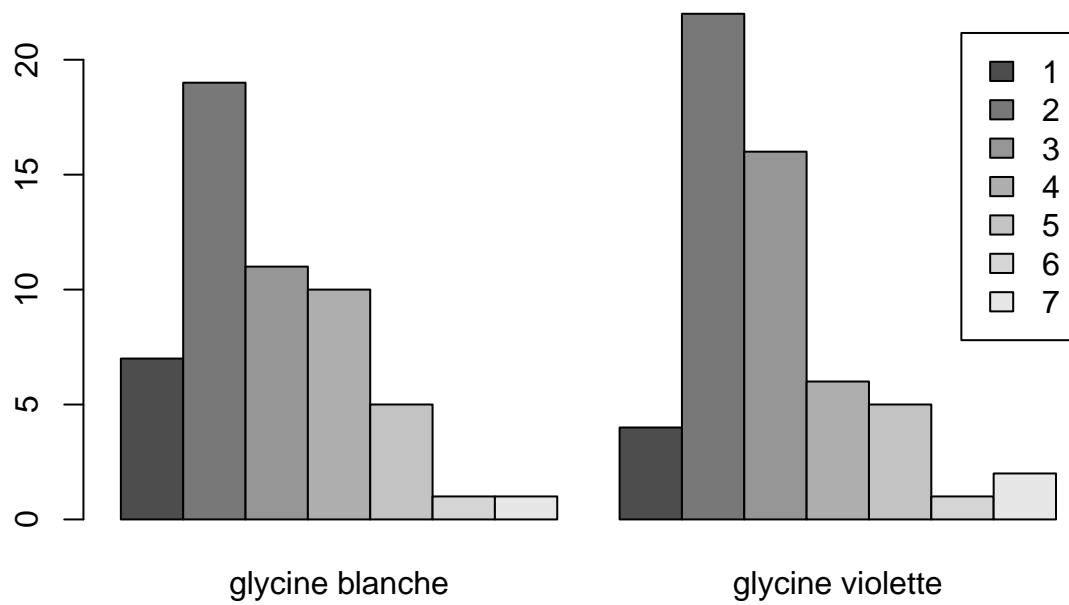
```
pdf("figure313.pdf")
barplot(table.graines.espece,beside=TRUE,legend=rownames(table.graines.espece))
dev.off()
```

```
## pdf
##   2
```

```
#En plus avec ggplot
ggplot(data.graines.espece, aes(x = nbr.graines, y= effectif, fill =
  nbr.graines)) + geom_bar(stat="identity") + xlab("Nombre de graines") +
  ylab("Effectif") + facet_wrap(~espece) + scale_fill_grey() + theme_bw()
```
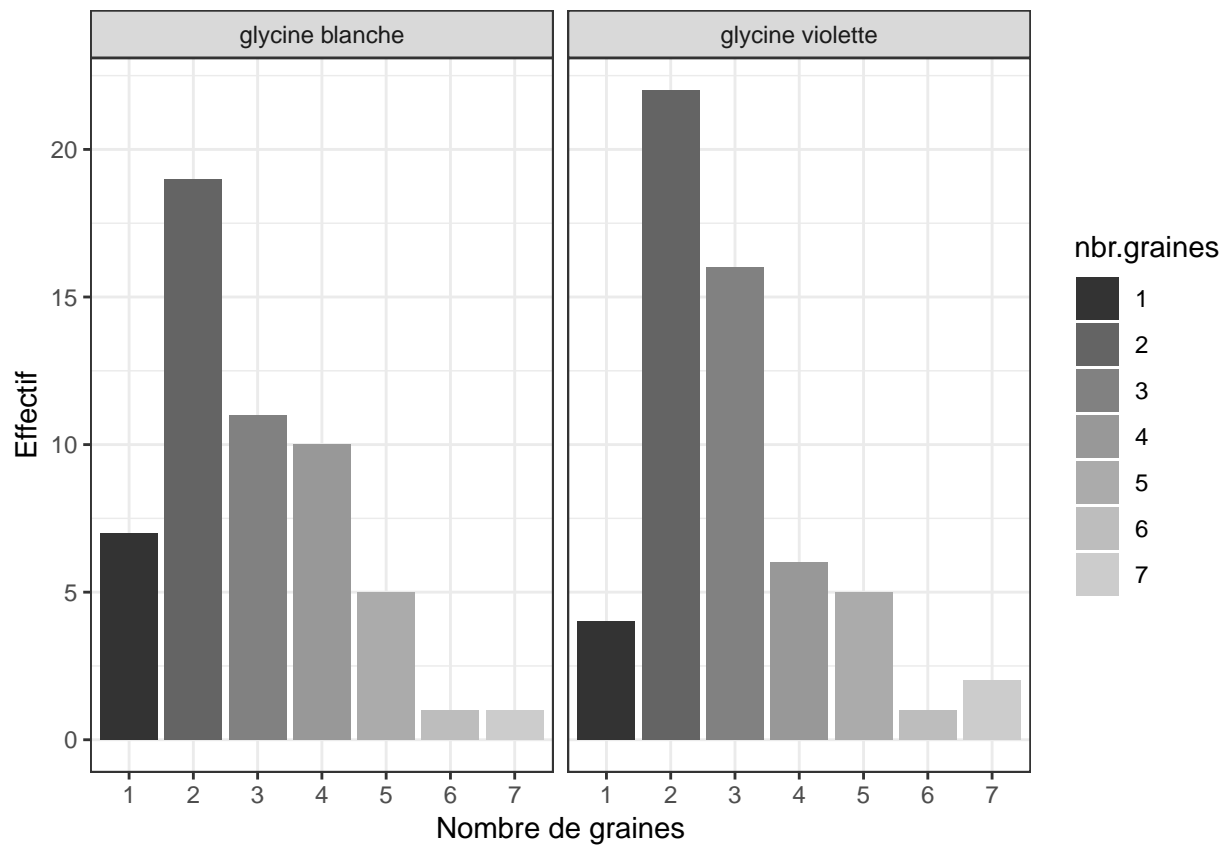
```
pdf("figure313ggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines, y= effectif, fill =
 nbr.graines)) + geom_bar(stat="identity") + xlab("Nombre de graines") +
 ylab("Effectif") + facet_wrap(~espece) + scale_fill_grey() + theme_bw())
dev.off()
```

```
## pdf
##   2
```

```
plot(table(Mesures5$graines),lwd=4,col="red",xlab="Nombre de graines",ylab="Effectif")
lines(table(Mesures5$graines),type="l",lwd=4)
```
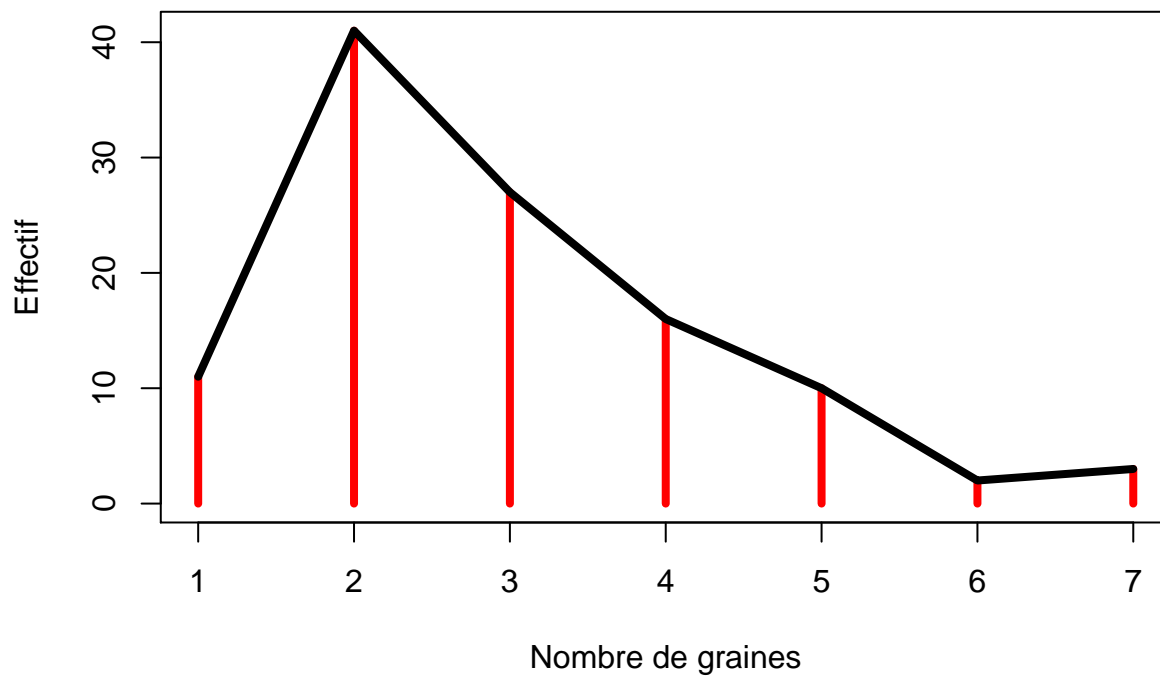
```
pdf("figure314.pdf")
plot(table(Mesures5$graines),lwd=4,col="red",xlab="Nombre de graines",ylab="Effectif")
lines(table(Mesures5$graines),type="l",lwd=4)
dev.off()
```

```
## pdf
##   2
```

```
#En plus avec ggplot
df.table_graines<-as.data.frame(table(Mesures5$graines,dnn="nbr.graines"),
                                responseName="effectif")
ggplot(df.table_graines, aes(x = nbr.graines)) +
  geom_linerange(aes(ymin=0,ymax=effectif),size=1.8,color=I("red"))+
  xlab("Nombre de graines") + ylab("Effectif")
```
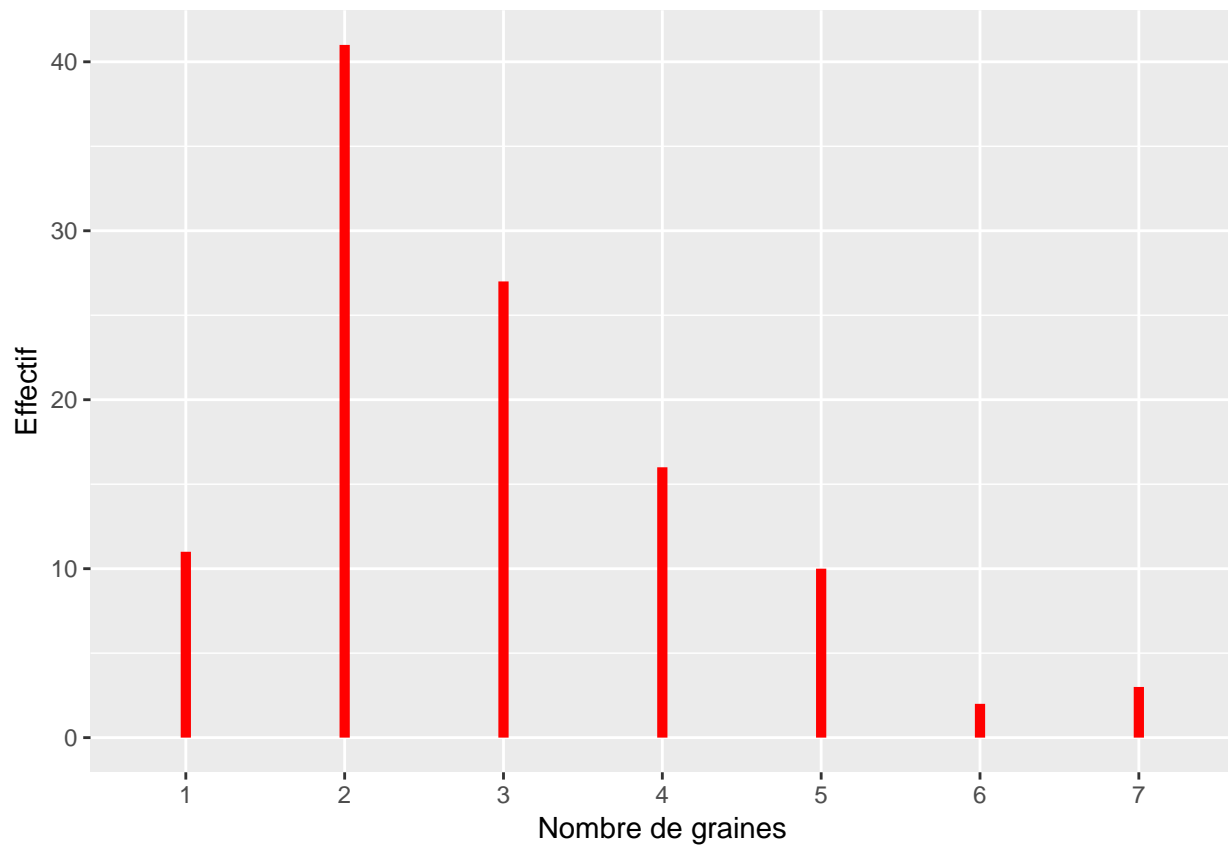
```r
pdf("figure314ggplot.pdf")
ggplot(df.table_graines, aes(x = nbr.graines)) + geom_linerange(aes(ymin=0,ymax=effectif),
  size=1.8,color=I("red"))+ xlab("Nombre de graines") + ylab("Effectif")
dev.off()
```

```
## pdf
##   2
```

```r
ggplot(df.table_graines, aes(x = nbr.graines)) + geom_linerange(aes(ymin=0, ymax=effectif),
  size=1.2,color=I("red"))+ geom_line(aes(y=effectif,group=""),size=1.2,color=I("black"))+
  xlab("Nombre de graines") + ylab("Effectif")
```
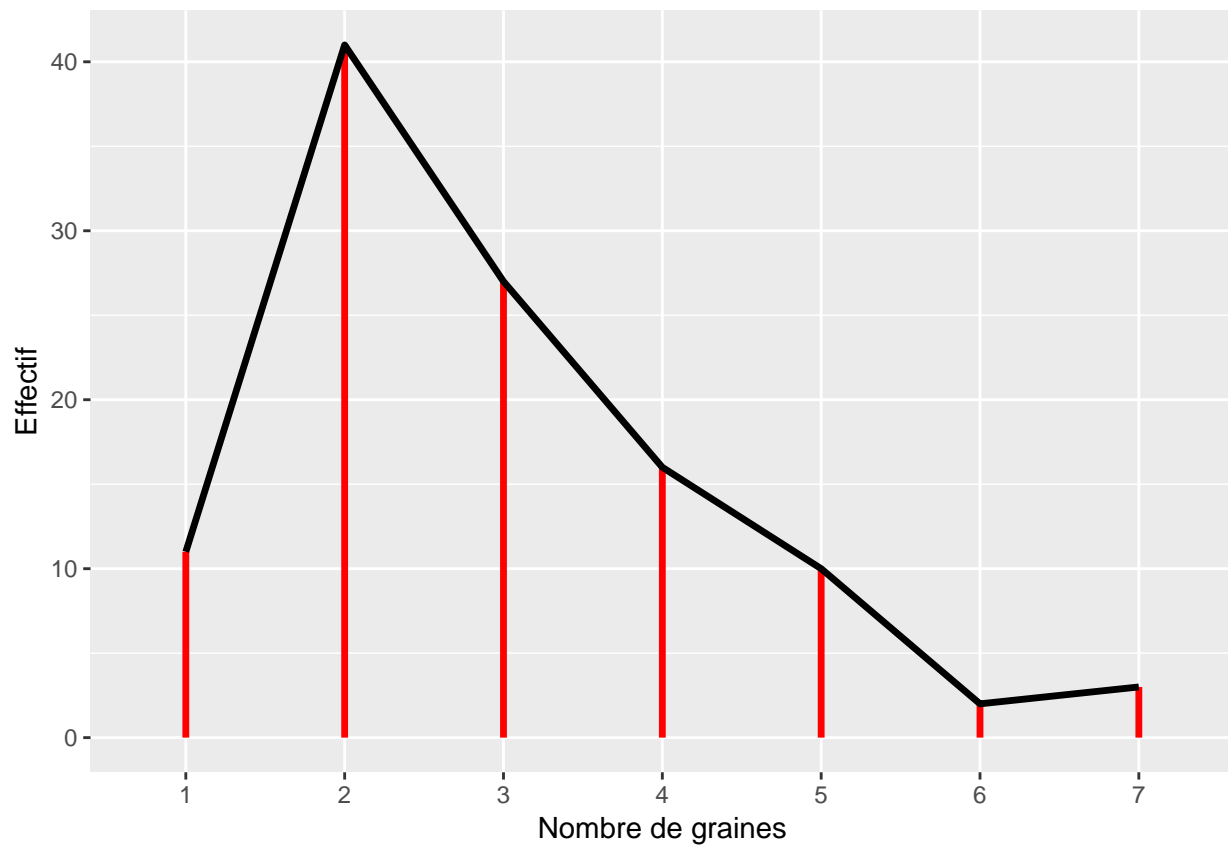
```
pdf("figure314aggplot.pdf")
print(ggplot(df.table_graines, aes(x = nbr.graines)) +
      geom_linerange(aes(ymin=0, ymax=effectif), size=1.2,color=I("red"))+
      geom_line(aes(y=effectif,group=""), size=1.2,color=I("black"))+
      xlab("Nombre de graines") + ylab("Effectif"))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(df.table_graines, aes(x = nbr.graines))+
  geom_line(aes(y=effectif,group=""), size=1.2,color=I("black")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""),
                  size=1.2,color=I("red"))+ xlab("Nombre de graines") + ylab("Effectif")
```
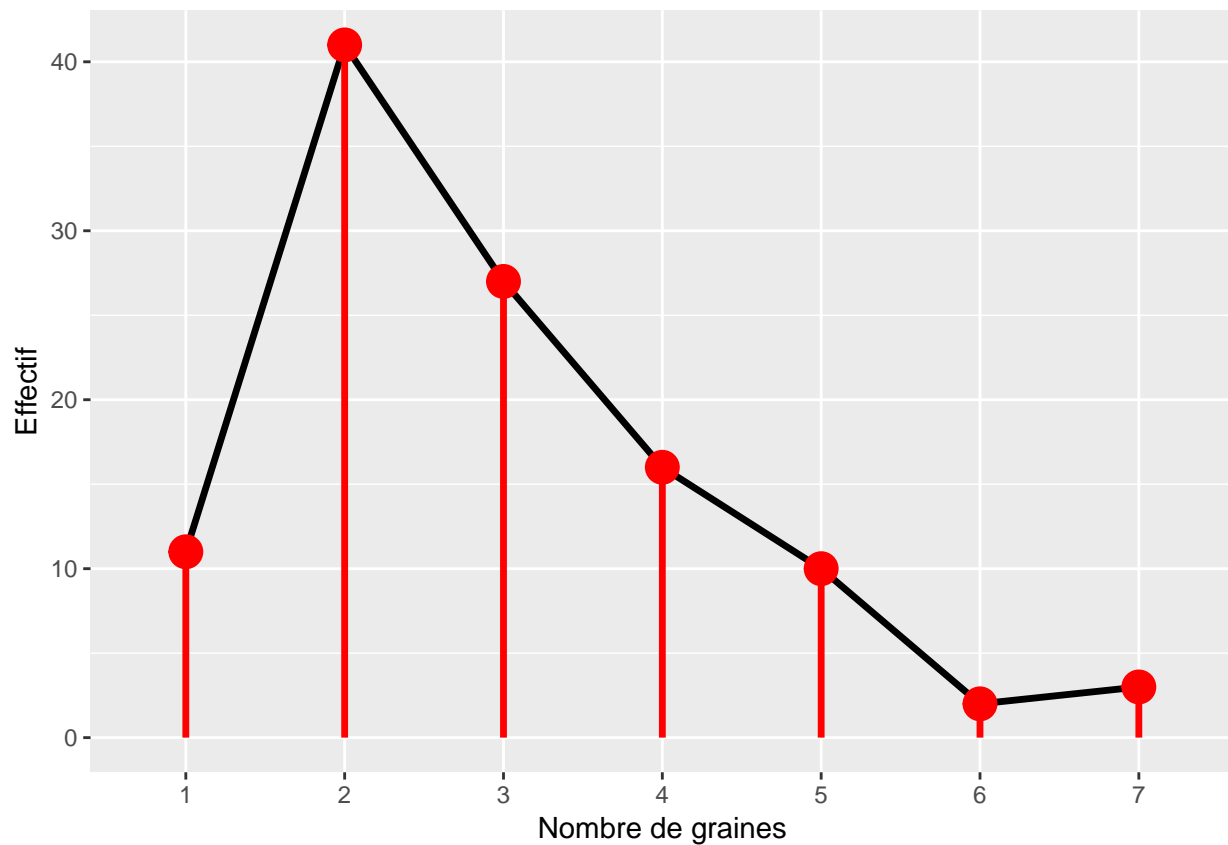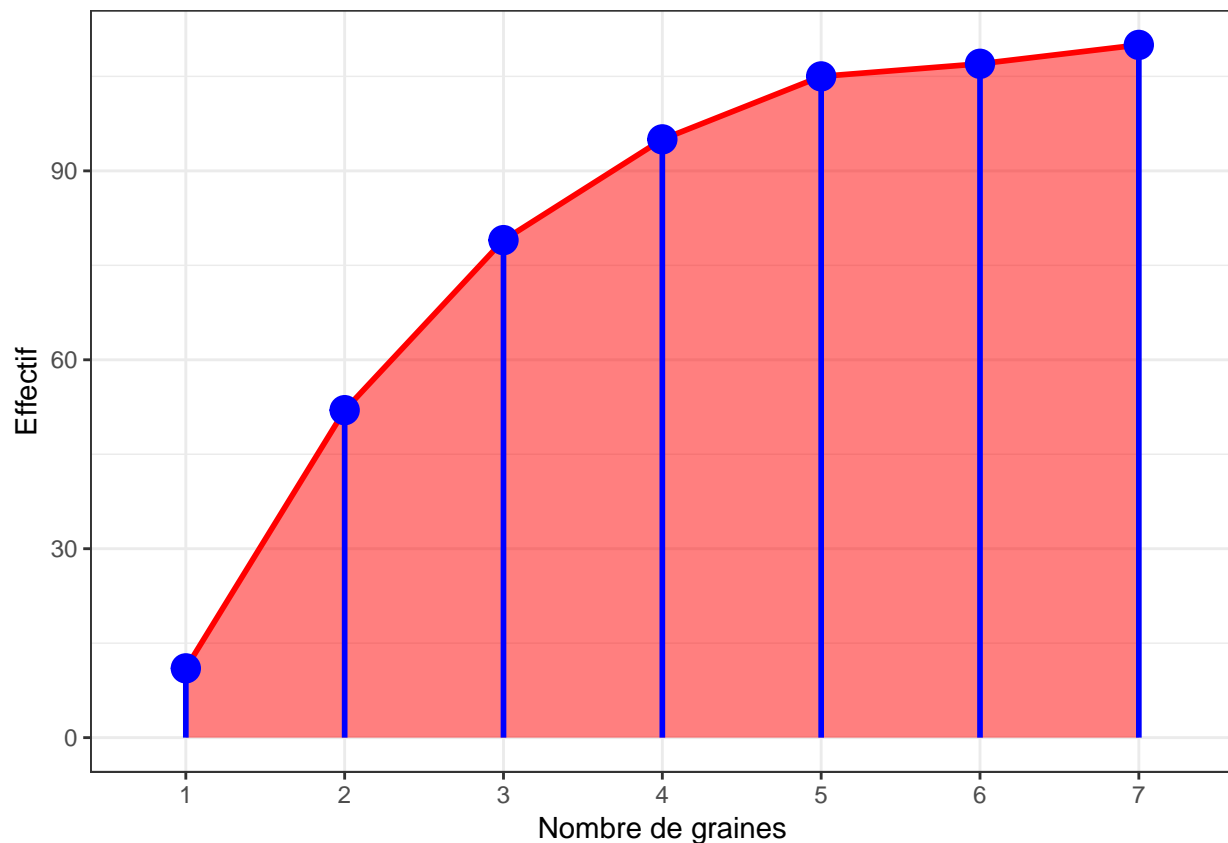
```
pdf("figure314bggplot.pdf")
print(ggplot(df.table_graines, aes(x = nbr.graines))+
        geom_line(aes(y=effectif,group=""), size=1.2,color=I("black")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""),
                        size=1.2,color=I("red"))+ xlab("Nombre de graines") + ylab("Effectif"))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(df.table_graines, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("red"),alpha=.5)+
  geom_line(aes(y=effectif,group=""), size=1, color="red")+
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1,
                  color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +theme_bw()
```
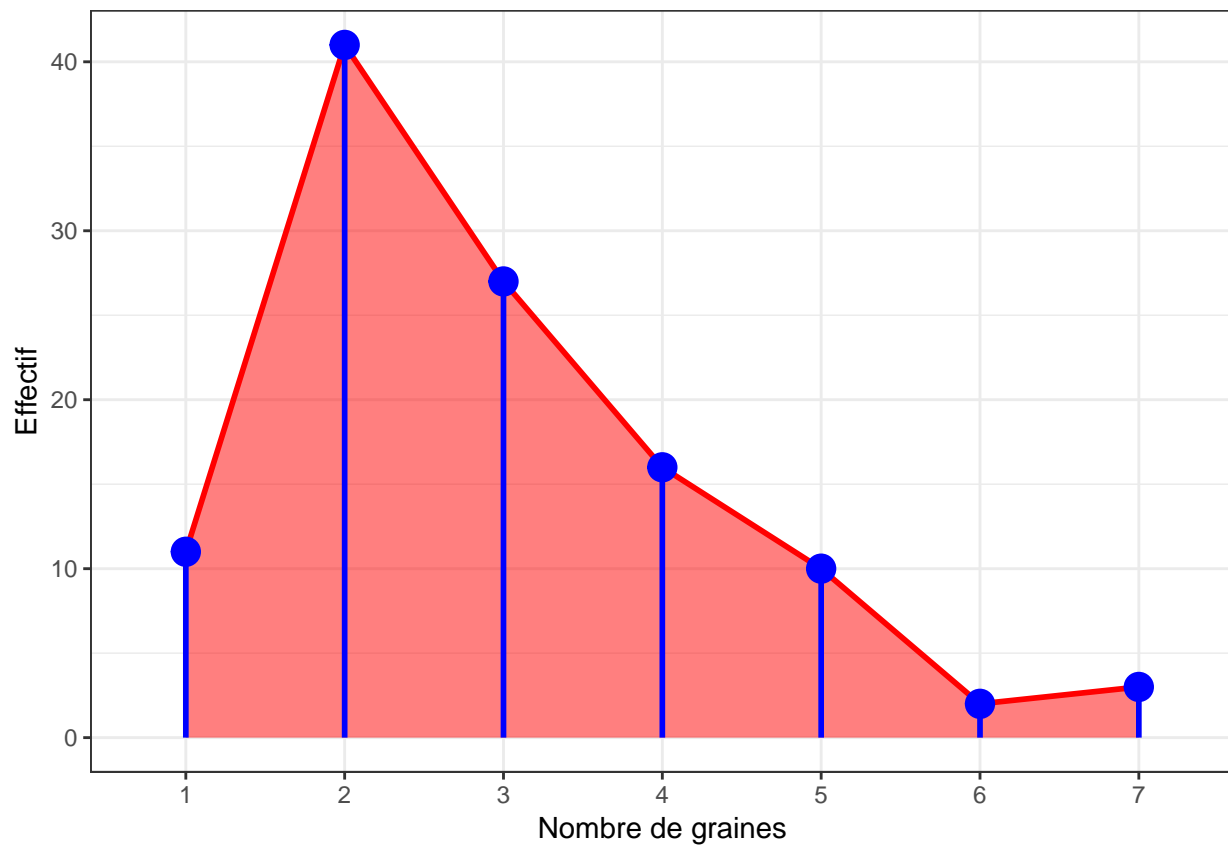
```
pdf("figure314cggplot.pdf")
print(ggplot(df.table_graines, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("red"),alpha=.5)+
        geom_line(aes(y=effectif,group=""), size=1, color="red")+
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1,
                        color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +theme_bw())
dev.off()
```
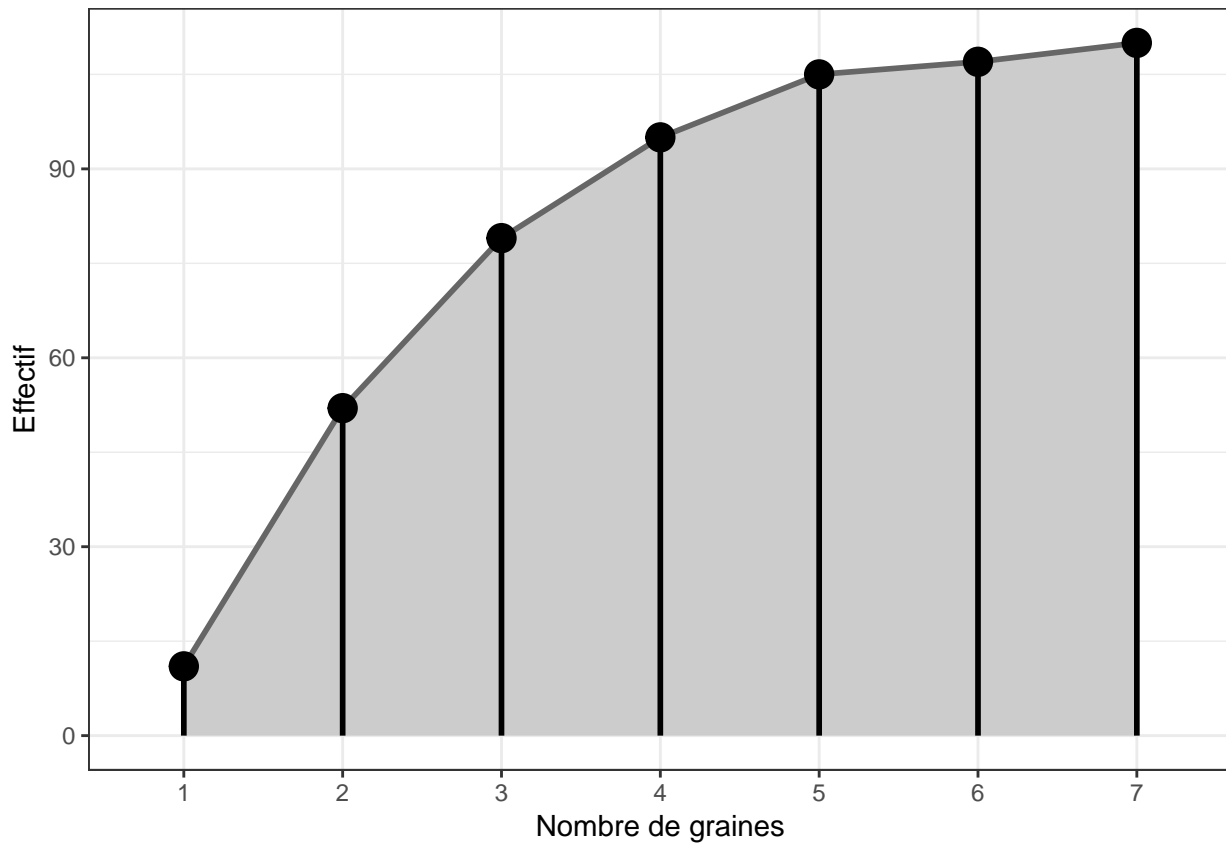
```
## pdf
##   2
```

```
ggplot(df.table_graines, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("gray80"))+
  geom_line(aes(y=effectif,group=""), size=1, color=I("gray40")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1)+
  xlab("Nombre de graines") + ylab("Effectif") +theme_bw()
```

```r
pdf("figure314dggplot.pdf")
print(ggplot(df.table_graines, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("gray80"))+
        geom_line(aes(y=effectif,group=""), size=1, color=I("gray40")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1)+
        xlab("Nombre de graines") + ylab("Effectif") +theme_bw())
dev.off()
```

```
## pdf
##   2
```

```r
#En plus, ggplot par groupes
ggplot(data.graines.espece, aes(x = nbr.graines)) +
  geom_linerange(aes(ymin=0,ymax=effectif,group=espece), size=1.2,color=I("red"))+
  geom_line(aes(y=effectif,group=espece), size=1.2,color=I("black"))+
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)
```

```
pdf("figure314groupeAggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines)) +
        geom_linerange(aes(ymin=0,ymax=effectif,group=espece), size=1.2,color=I("red"))+
        geom_line(aes(y=effectif,group=espece), size=1.2,color=I("black"))+
        xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(data.graines.espece, aes(x = nbr.graines))+
  geom_line(aes(y=effectif,group=espece), size=1.2,color=I("red")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece),
                  size=1.2,color=I("blue"))+ xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece)
```

```r
pdf("figure314groupeAggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines))+
        geom_line(aes(y=effectif,group=espece), size=1.2,color=I("red")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece),
                        size=1.2,color=I("blue"))+ xlab("Nombre de graines") + ylab("Effectif") +
        facet_wrap(~espece))
dev.off()
```
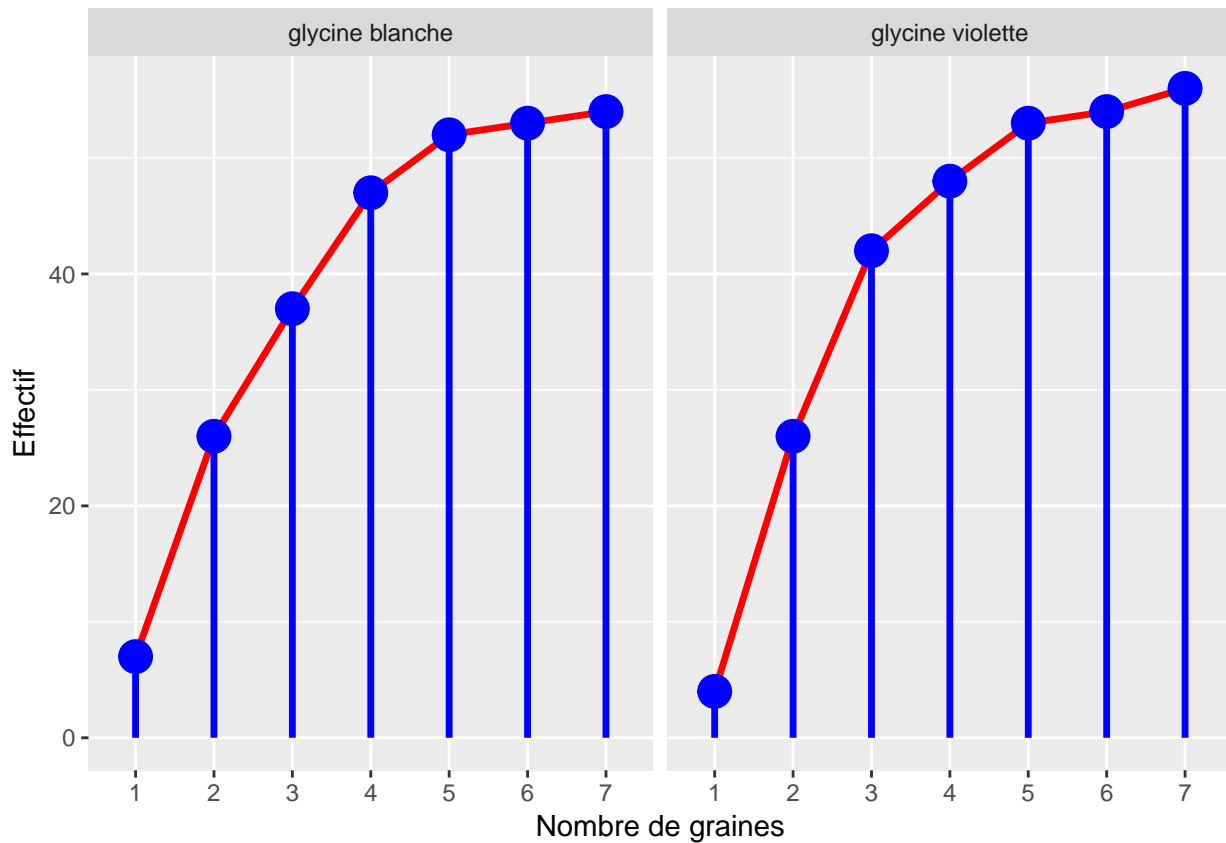
```
## pdf
##   2
```

```r
ggplot(data.graines.espece, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("red"),alpha=.5)+
  geom_line(aes(y=effectif,group=espece), size=1, color="red")+
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1,
                  color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece)+theme_bw()
```

```
pdf("figure314groupeAggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("red"),alpha=.5)+
        geom_line(aes(y=effectif,group=espece), size=1, color="red")+
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1,
                        color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +
        facet_wrap(~espece)+theme_bw())
dev.off()
```
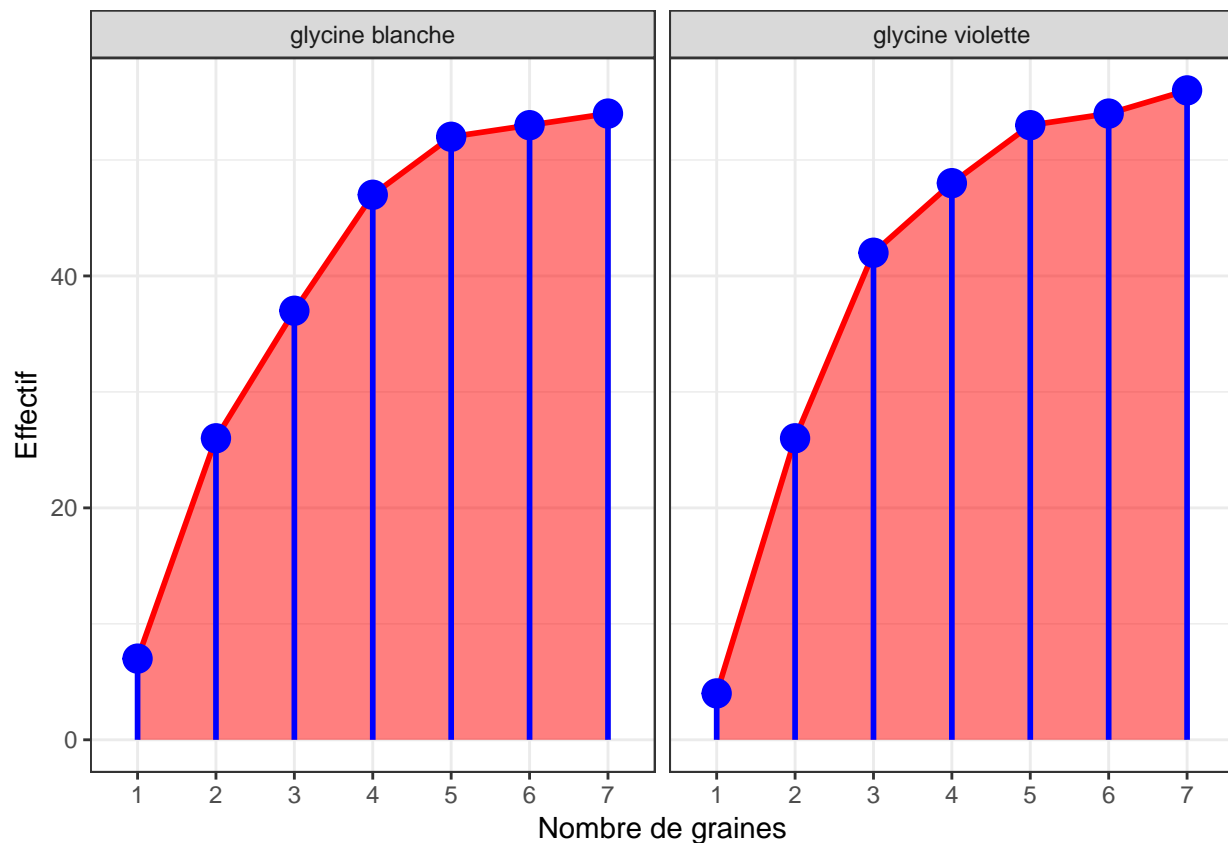
```
## pdf
##   2
```

```
ggplot(data.graines.espece, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("gray80"))+
  geom_line(aes(y=effectif,group=espece), size=1, color=I("gray40")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1)+
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)+theme_bw()
```
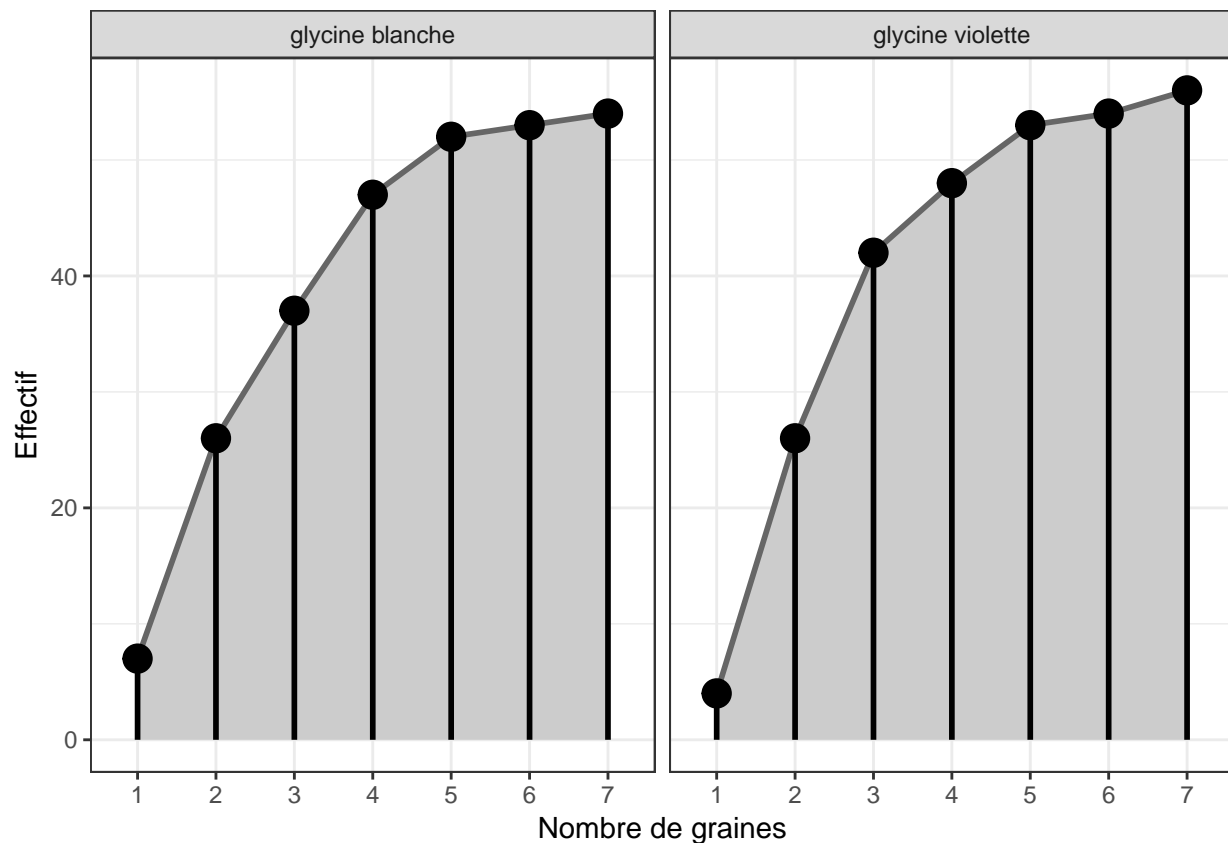
```r
pdf("figure314groupeAggplot.pdf")
print(ggplot(data.graines.espece, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("gray80"))+
        geom_line(aes(y=effectif,group=espece), size=1, color=I("gray40")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1)+
        xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)+theme_bw())
dev.off()
```

```
## pdf
##   2
```

```r
#page 128
plot(cumsum(table(Mesures5$graines)),type="h",lwd=4,col="red",xlab="Nombre de graines",
     ylab="Effectif")
lines(cumsum(table(Mesures5$graines)),lwd=4)
```
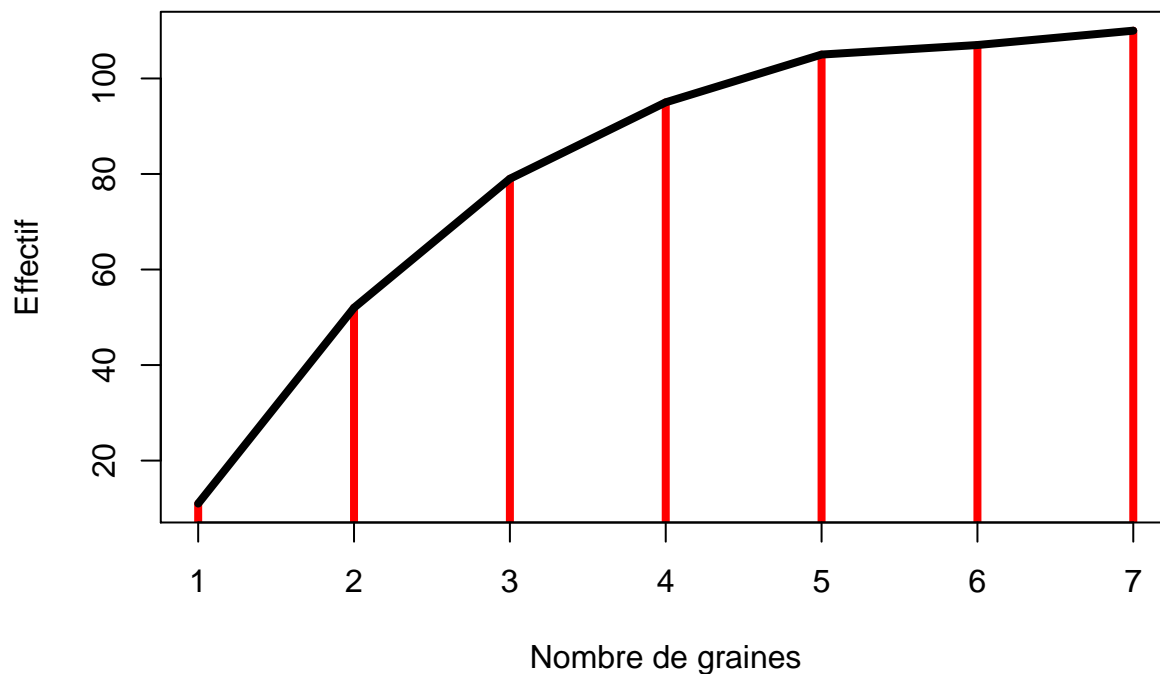
```r
pdf("figure315.pdf")
plot(cumsum(table(Mesures5$graines)),type="h",lwd=4,col="red",xlab="Nombre de graines",
     ylab="Effectif")
lines(cumsum(table(Mesures5$graines)),lwd=4)
dev.off()
```

```
## pdf
##   2
```

```r
df.cumsum.table_graines<-df.table_graines; df.cumsum.table_graines[,2] <-
  cumsum(df.table_graines[,2])
ggplot(df.cumsum.table_graines, aes(x = nbr.graines)) +
  geom_linerange(aes(ymin=0, ymax=effectif), size=1.2,color=I("red"))+
  geom_line(aes(y=effectif,group=""), size=1.2,color=I("black"))+
  xlab("Nombre de graines") + ylab("Effectif")
```
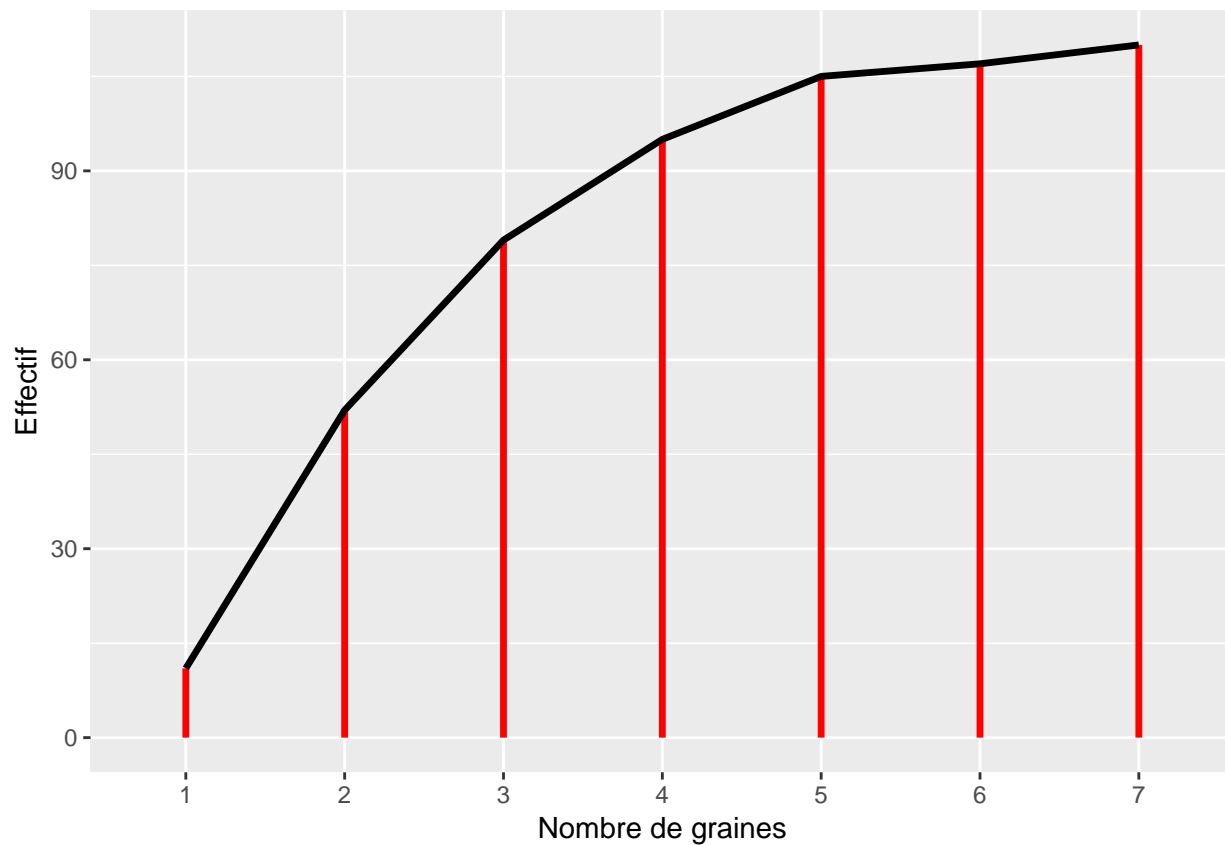
```r
pdf("figure315ggplot.pdf")
print(ggplot(df.cumsum.table_graines, aes(x = nbr.graines)) +
        geom_linerange(aes(ymin=0, ymax=effectif), size=1.2,color=I("red"))+
        geom_line(aes(y=effectif,group=""), size=1.2,color=I("black"))+
        xlab("Nombre de graines") + ylab("Effectif"))
dev.off()
```

```
## pdf
##   2
```

```r
ggplot(df.cumsum.table_graines, aes(x = nbr.graines))+
  geom_line(aes(y=effectif,group=""), size=1.2,color=I("black")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""),
                  size=1.2,color=I("red"))+ xlab("Nombre de graines") + ylab("Effectif")
```

```
pdf("figure315bggplot.pdf")
print(ggplot(df.cumsum.table_graines, aes(x = nbr.graines))+
        geom_line(aes(y=effectif,group=""), size=1.2,color=I("black")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""),
                        size=1.2,color=I("red"))+ xlab("Nombre de graines") + ylab("Effectif"))
dev.off()

## pdf
##    2

ggplot(df.cumsum.table_graines, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("red"),alpha=.5)+
  geom_line(aes(y=effectif,group=""), size=1, color="red")+
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1,
                  color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +theme_bw()
```

```r
pdf("figure315cggplot.pdf")
print(ggplot(df.cumsum.table_graines, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("red"),alpha=.5)+
        geom_line(aes(y=effectif,group=""), size=1, color="red")+
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1,
                        color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +theme_bw())
dev.off()

## pdf
##   2
```

```r
ggplot(df.cumsum.table_graines, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("gray80"))+
  geom_line(aes(y=effectif,group=""), size=1, color=I("gray40")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1)+
  xlab("Nombre de graines") + ylab("Effectif") +theme_bw()
```

```
pdf("figure315dggplot.pdf")
print(ggplot(df.cumsum.table_graines, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=""),fill=I("gray80"))+
        geom_line(aes(y=effectif,group=""), size=1, color=I("gray40")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=""), size=1)+
        xlab("Nombre de graines") + ylab("Effectif") +theme_bw())
dev.off()
```

```
## pdf
##   2
```

```
#Par groupes
data.cumsum.graines.espece<-data.graines.espece
data.cumsum.graines.espece[,3] <- unlist(tapply(data.graines.espece[,3],
                                          data.graines.espece[,2],cumsum))

ggplot(data.cumsum.graines.espece, aes(x = nbr.graines)) +
  geom_linerange(aes(ymin=0,ymax=effectif,group=espece), size=1.2,color=I("red"))+
  geom_line(aes(y=effectif,group=espece), size=1.2,color=I("black"))+
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)
```
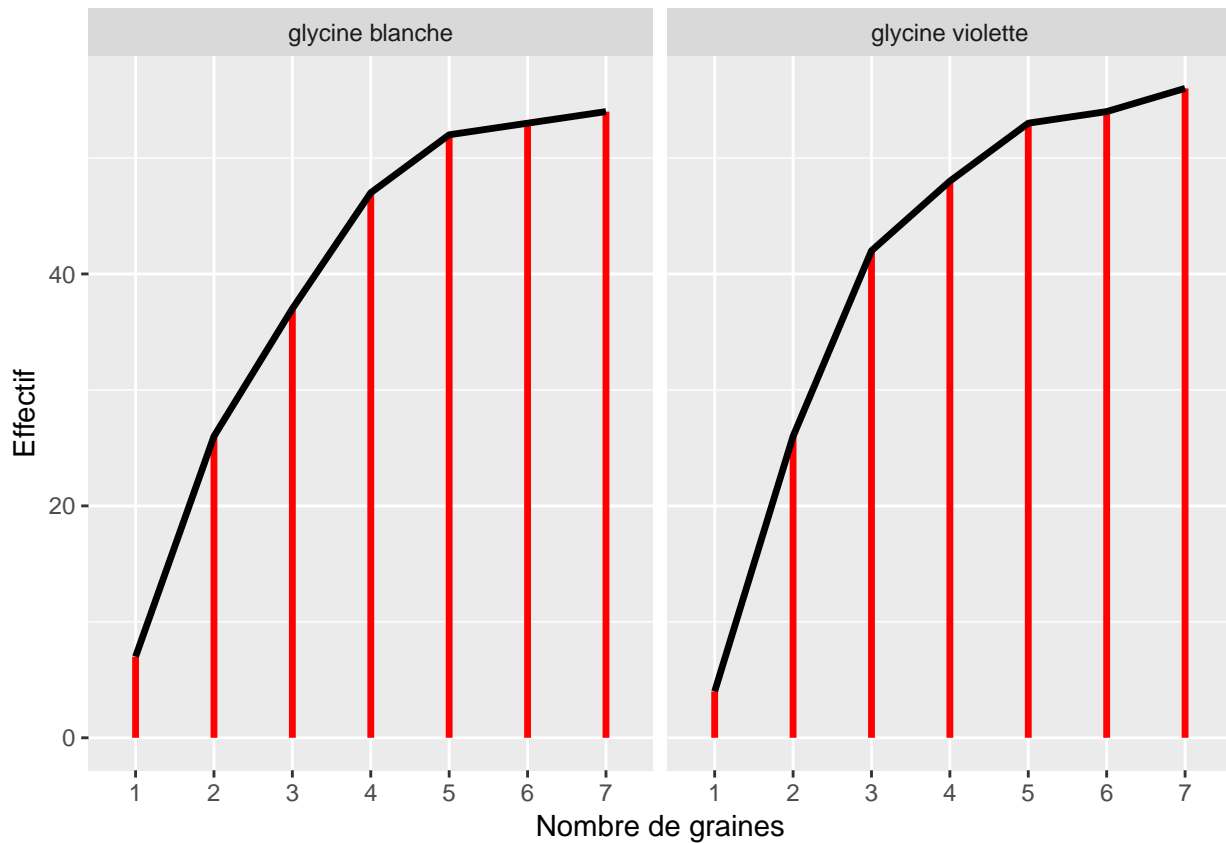
```
pdf("figure315eggplot.pdf")
print(ggplot(data.cumsum.graines.espece, aes(x = nbr.graines)) +
        geom_linerange(aes(ymin=0,ymax=effectif,group=espece), size=1.2,color=I("red"))+
        geom_line(aes(y=effectif,group=espece), size=1.2,color=I("black"))+
        xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(data.cumsum.graines.espece, aes(x = nbr.graines))+
  geom_line(aes(y=effectif,group=espece), size=1.2,color=I("red")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece),
                  size=1.2,color=I("blue"))+ xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece)
```

```r
pdf("figure315fggplot.pdf")
print(ggplot(data.cumsum.graines.espece, aes(x = nbr.graines))+
        geom_line(aes(y=effectif,group=espece), size=1.2,color=I("red")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece),
                        size=1.2,color=I("blue"))+ xlab("Nombre de graines") + ylab("Effectif") +
        facet_wrap(~espece))
dev.off()
```

```
## pdf
##   2
```

```r
ggplot(data.cumsum.graines.espece, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("red"),alpha=.5)+
  geom_line(aes(y=effectif,group=espece), size=1, color="red")+
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1,
                  color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece)+theme_bw()
```

```
pdf("figure315gggplot.pdf")
print(ggplot(data.cumsum.graines.espece, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("red"),alpha=.5)+
        geom_line(aes(y=effectif,group=espece), size=1, color="red")+
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1,
                        color="blue")+  xlab("Nombre de graines") + ylab("Effectif") +
        facet_wrap(~espece)+theme_bw())
dev.off()
```

```
## pdf
##   2
```

```
ggplot(data.cumsum.graines.espece, aes(x = nbr.graines)) +
  geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("gray80"))+
  geom_line(aes(y=effectif,group=espece), size=1, color=I("gray40")) +
  geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1)+
  xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)+theme_bw()
```

```
pdf("figure315hggplot.pdf")
print(ggplot(data.cumsum.graines.espece, aes(x = nbr.graines)) +
        geom_ribbon(aes(ymin=0,ymax=effectif,group=espece),fill=I("gray80"))+
        geom_line(aes(y=effectif,group=espece), size=1, color=I("gray40")) +
        geom_pointrange(aes(ymin=0,ymax=effectif,y=effectif,group=espece), size=1)+
        xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)+theme_bw())
dev.off()
```

```
## pdf
##   2
```

```
pie.graines<-c(0.1000,0.3727,0.2455,0.1455,0.0909,0.0182,0.0273)

#page 129
names(pie.graines)<-c("1 graine","2 graines","3 graines","4 graines","5
                     graines","6 graines","7 graines")
pie(pie.graines,col=c("red","purple","cyan","blue","green","cornsilk","orange"))
```
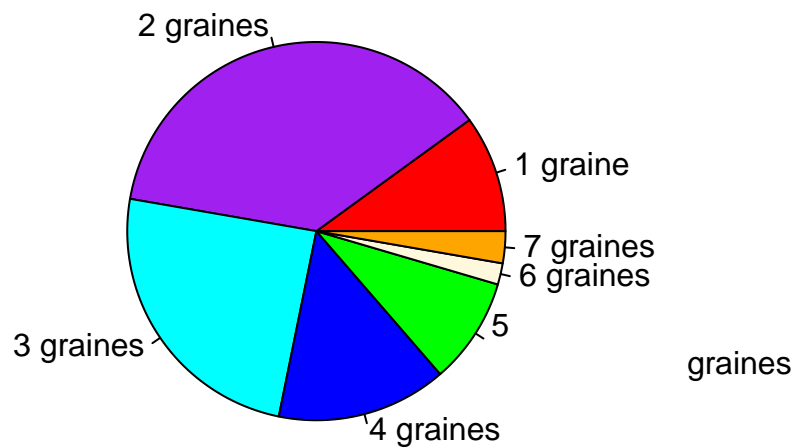
```r
pie(table(Mesures5$graines),labels=c("1 graine",paste(2:7,"
                                      graines")),col=rainbow(7))
```
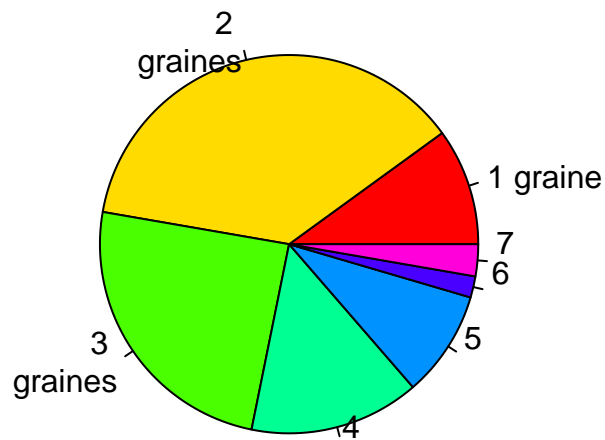


```r
pdf("figure316.pdf")
pie(table(Mesures5$graines),labels=c("1 graine",paste(2:7,"
                                      graines")),col=rainbow(7))
dev.off()
```

```
## pdf
##   2
```

```r
#ggplot pie is only a polar coord change from geom_bar
p=ggplot(data.graines.espece, aes(x="", y= effectif, fill = nbr.graines)) +
  geom_bar(stat="identity",position="fill") + xlab("Nombre de graines") +
  ylab("Effectif") + facet_wrap(~espece) + scale_fill_grey() + theme_bw()
p
```
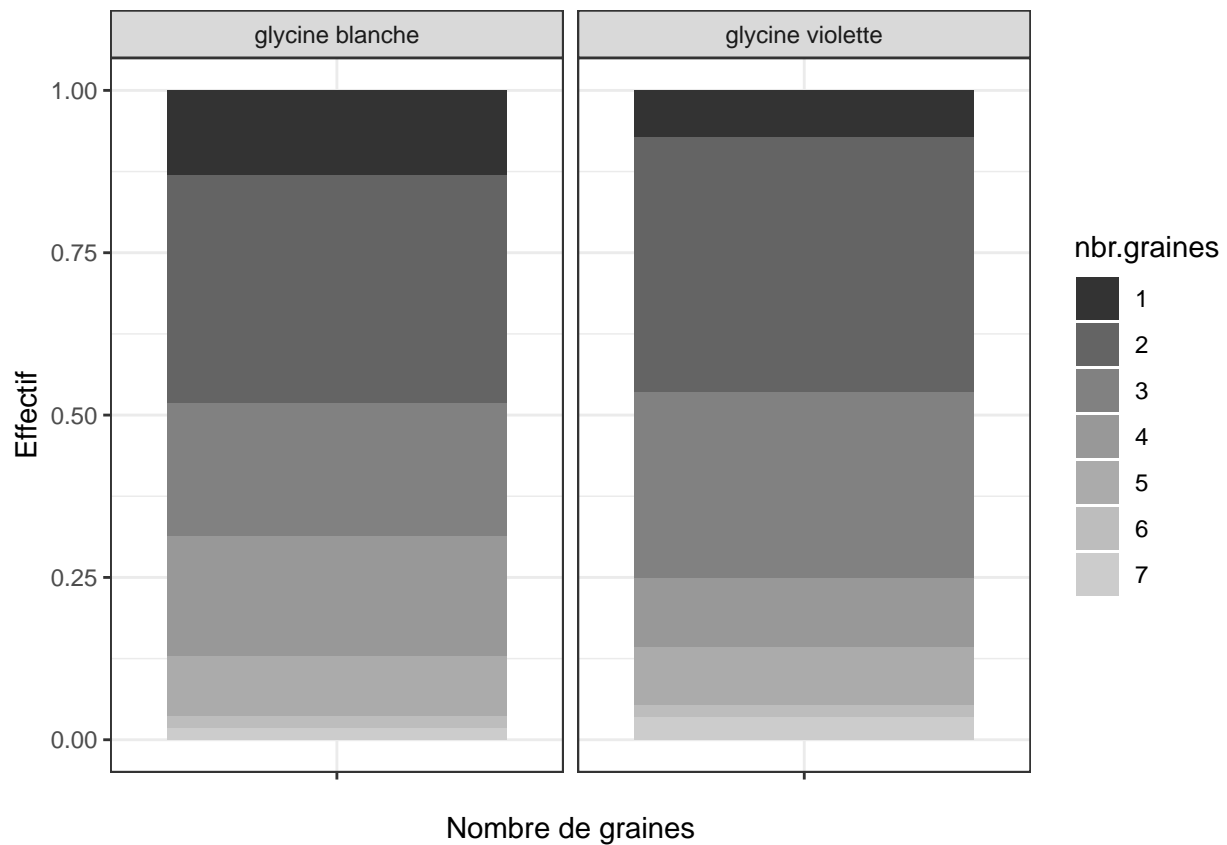
```
q <- p+coord_polar(theta="y")
q
```
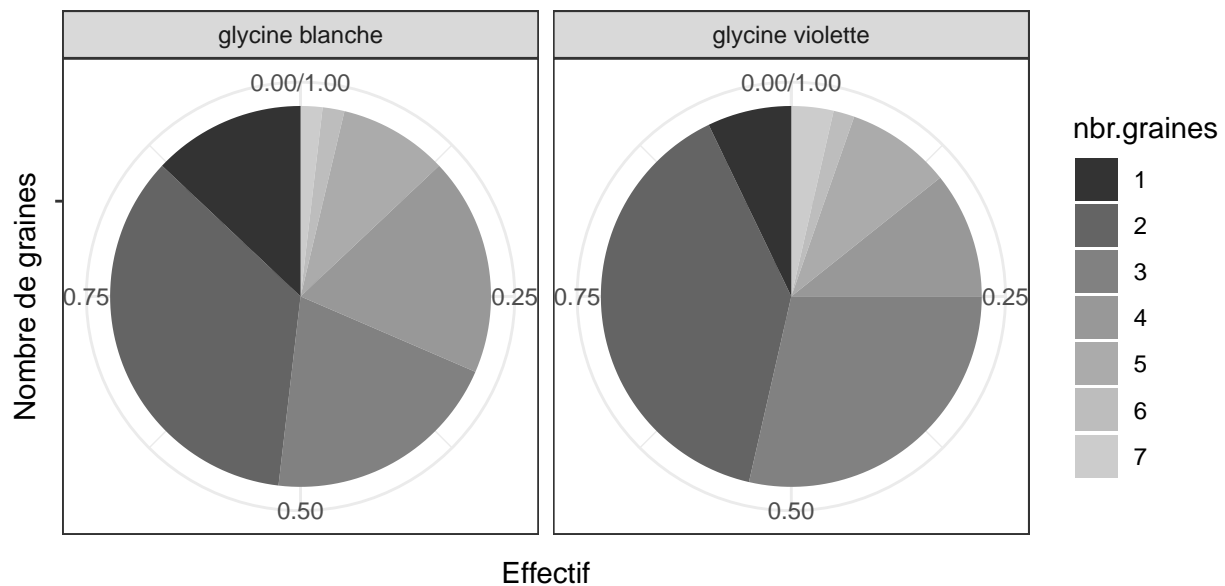


```
q + scale_fill_hue()
```

```
## Scale for 'fill' is already present. Adding another scale for 'fill',
## which will replace the existing scale.
```

```
q + scale_fill_brewer()
```
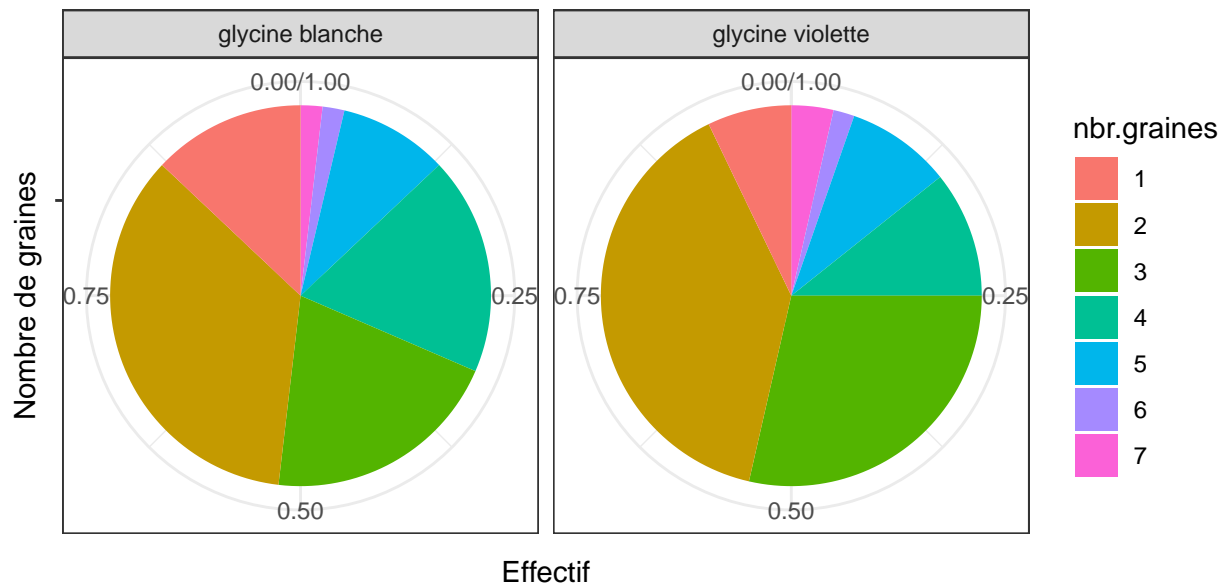
Scale for 'fill' is already present. Adding another scale for 'fill',
which will replace the existing scale.
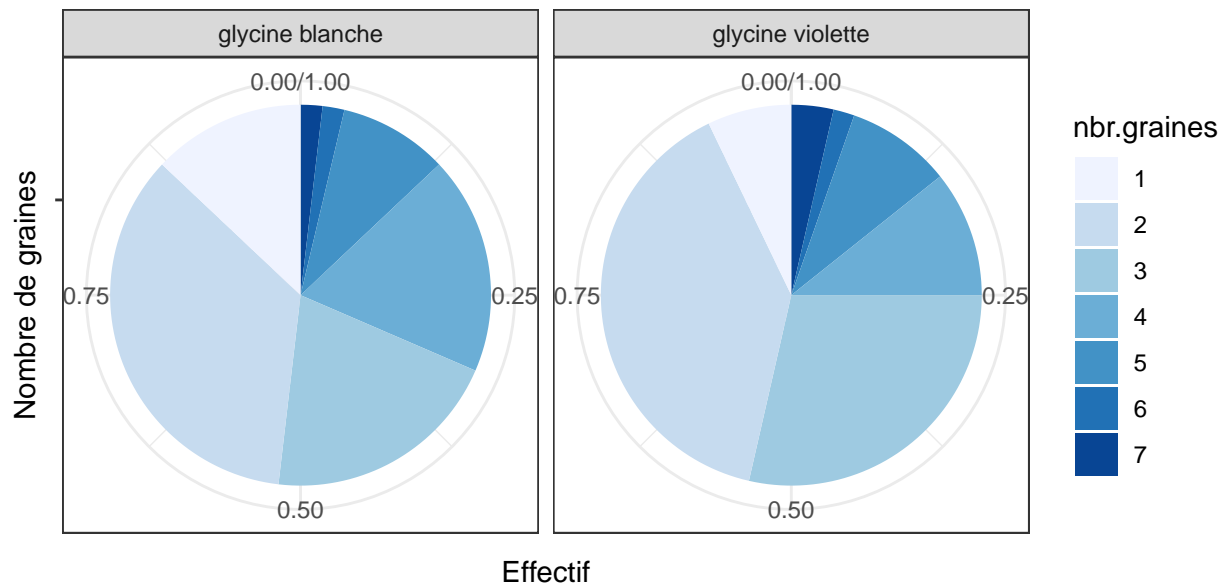

```
pdf("figure316aggplot.pdf")
print(q)
dev.off()
```

pdf
2

```
pdf("figure316bggplot.pdf")
print(q + scale_fill_hue())
```

Scale for 'fill' is already present. Adding another scale for 'fill',
which will replace the existing scale.

```
dev.off()
```

pdf
2

```
pdf("figure316cggplot.pdf")
print(q + scale_fill_brewer())
```

Scale for 'fill' is already present. Adding another scale for 'fill',
which will replace the existing scale.

```
dev.off()
```

pdf
2

```
#page 130
hist(Mesures$masse)
```
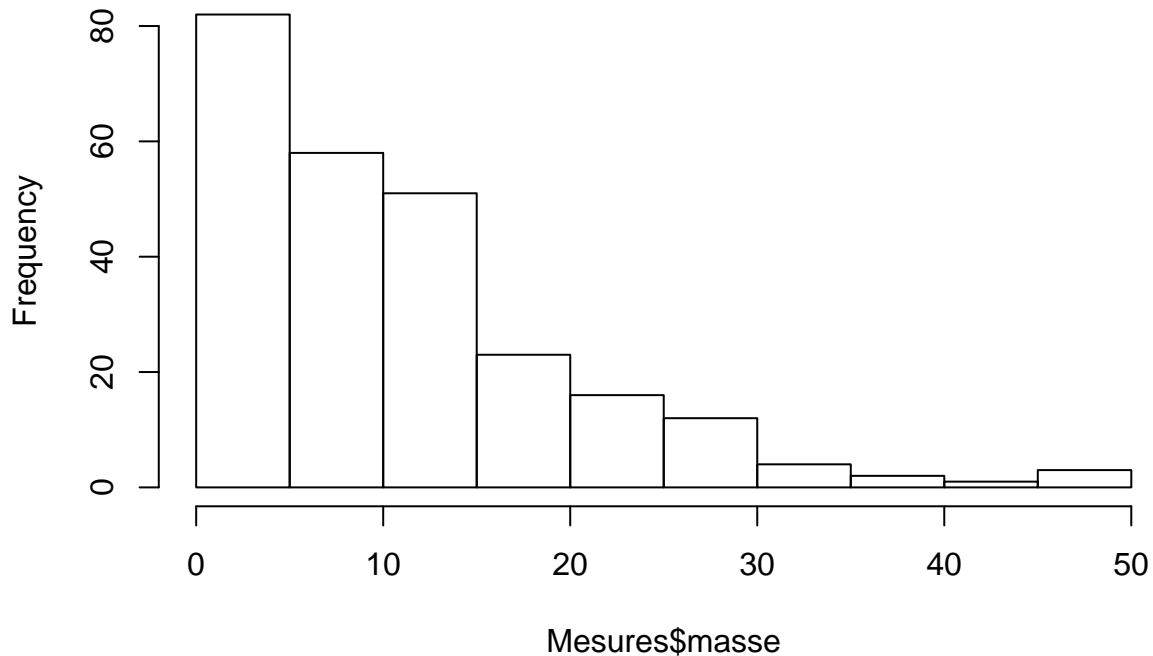
Histogram of Mesures$masse


```
histo<-hist(Mesures$masse,ylab="Effectif",xlab="Masse",main="Histogramme des
          masses")
```

Histogramme des masses
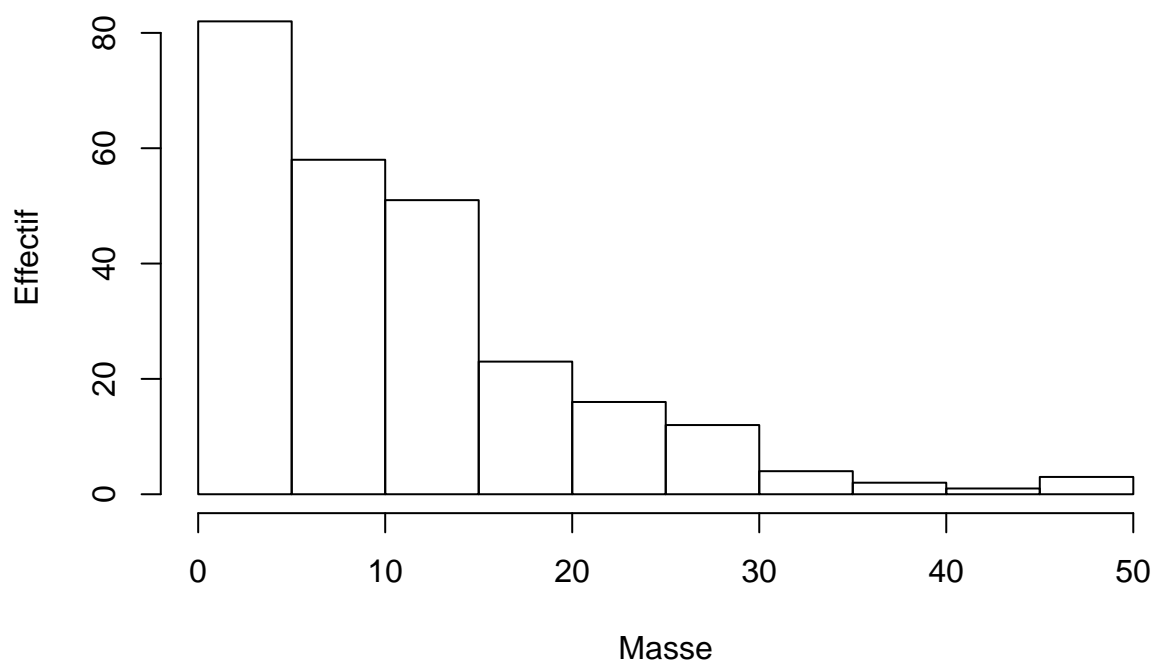

```
#en plus ggplot
g=ggplot(Mesures,aes(x=masse))+geom_histogram()
g
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
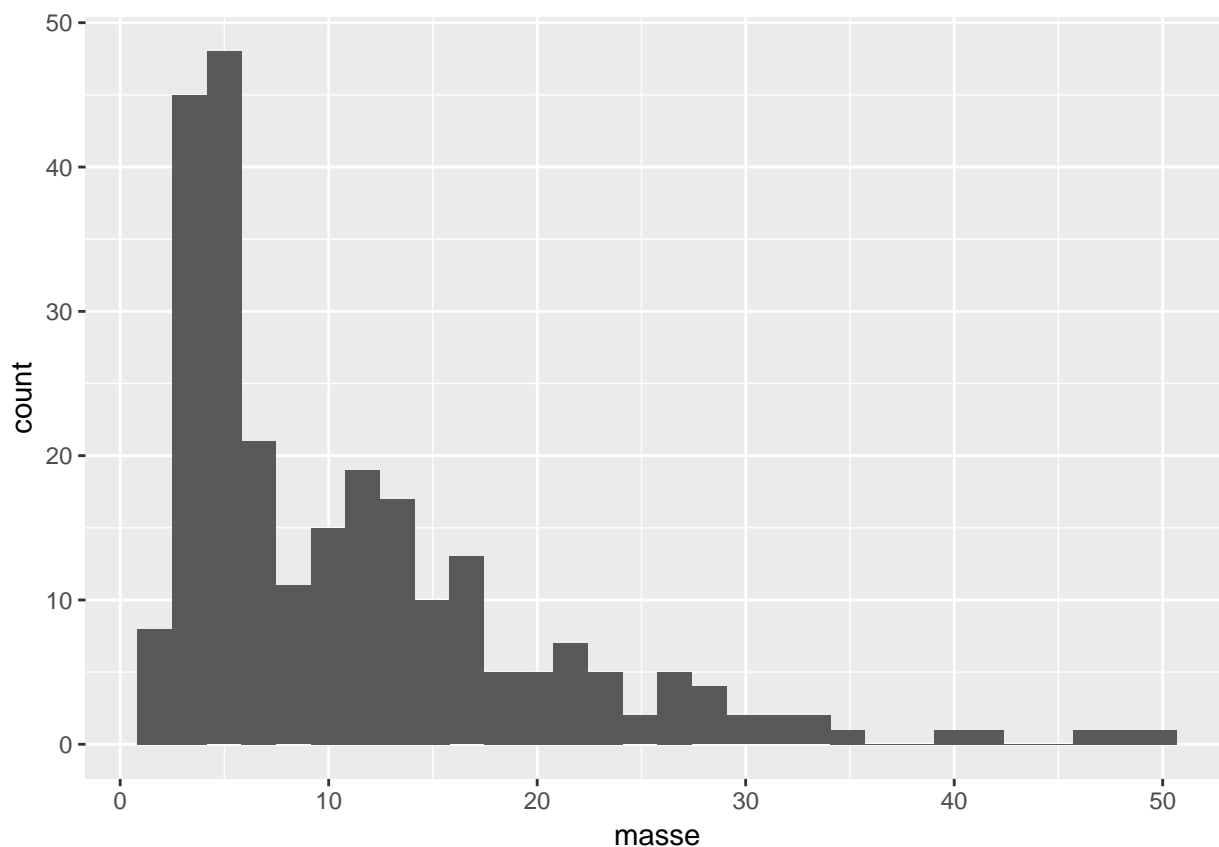
```
pdf("figure317aggplot.pdf")
g
```

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

```
dev.off()
```

pdf
2

```
g1 = g +
  geom_histogram(binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse)
  ) #Règle de Sturges
g1
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
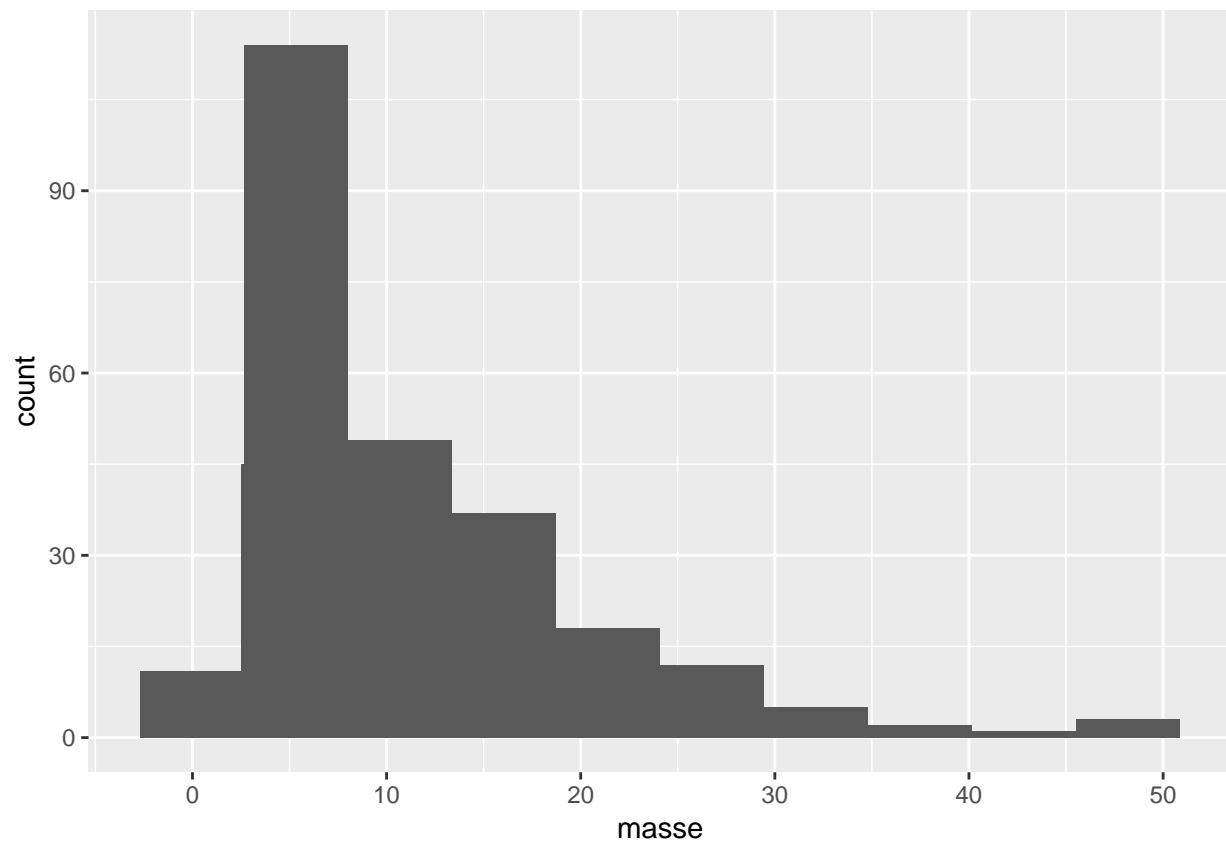
```
pdf("figure317bggplot.pdf")
g1
```

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

```
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures,aes(x=masse))+geom_histogram(aes(fill=..count..))+
  scale_fill_gradient("Count", low = "green", high = "red")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
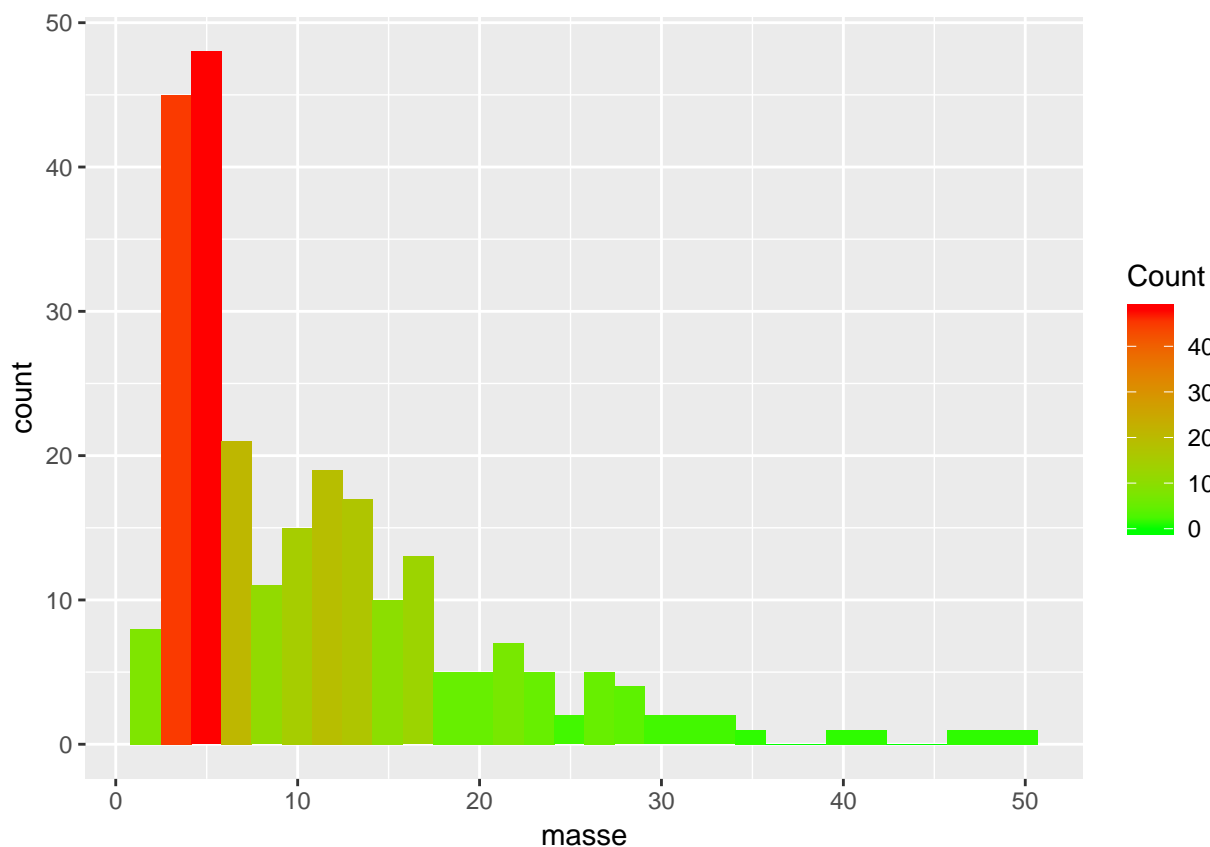
```r
pdf("figure317cggplot.pdf")
print(ggplot(Mesures,aes(x=masse))+geom_histogram(aes(fill=..count..))+
        scale_fill_gradient("Count", low = "green", high = "red"))
```

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

```r
dev.off()
```

```
## pdf
##   2
```

```r
g+geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse))+scale_fill_gradient("Count",low = "green", high ="red")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
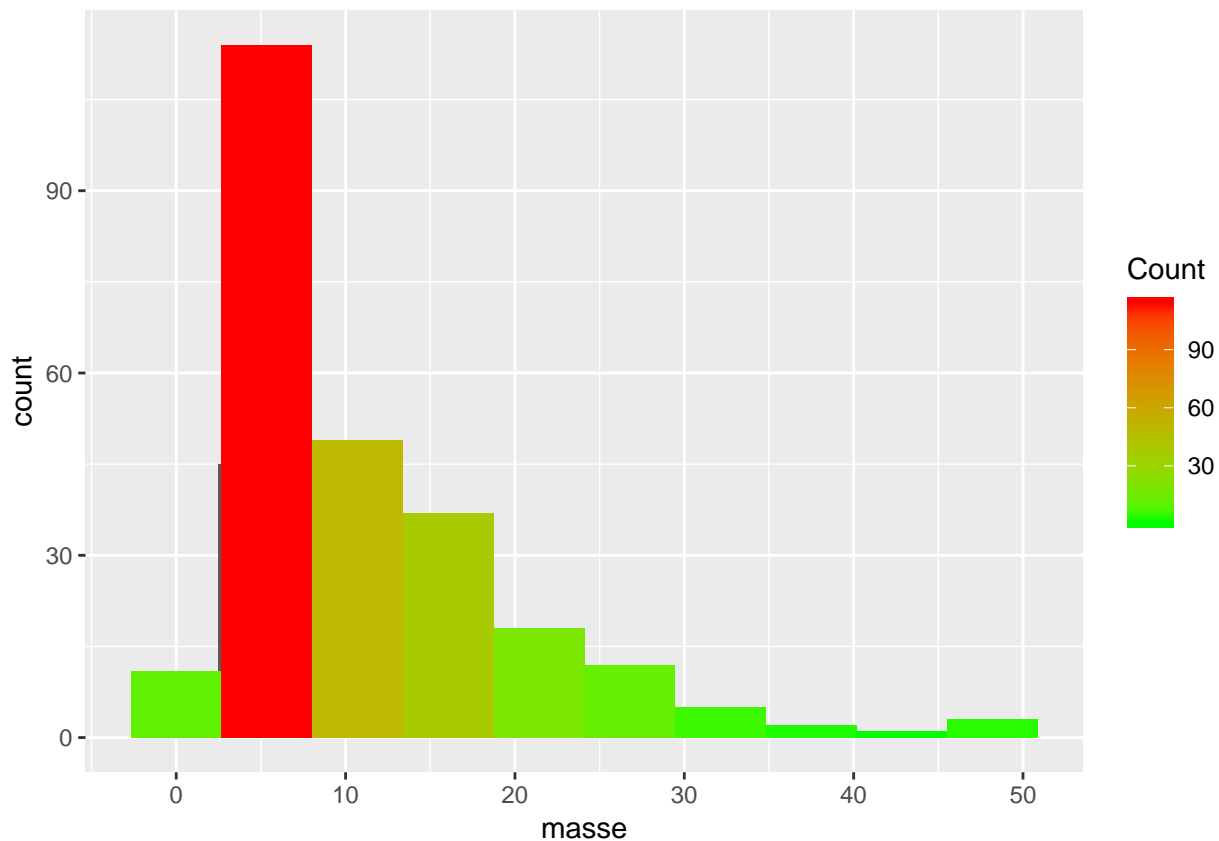
```
pdf("figure317dggplot.pdf")
print(g+geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse))+scale_fill_gradient("Count", low = "green", high = "red"))
```

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

```
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures,aes(x=masse))+geom_histogram(aes(fill=..count..))+
  scale_fill_gradient("Count", low = "grey80", high = "black")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
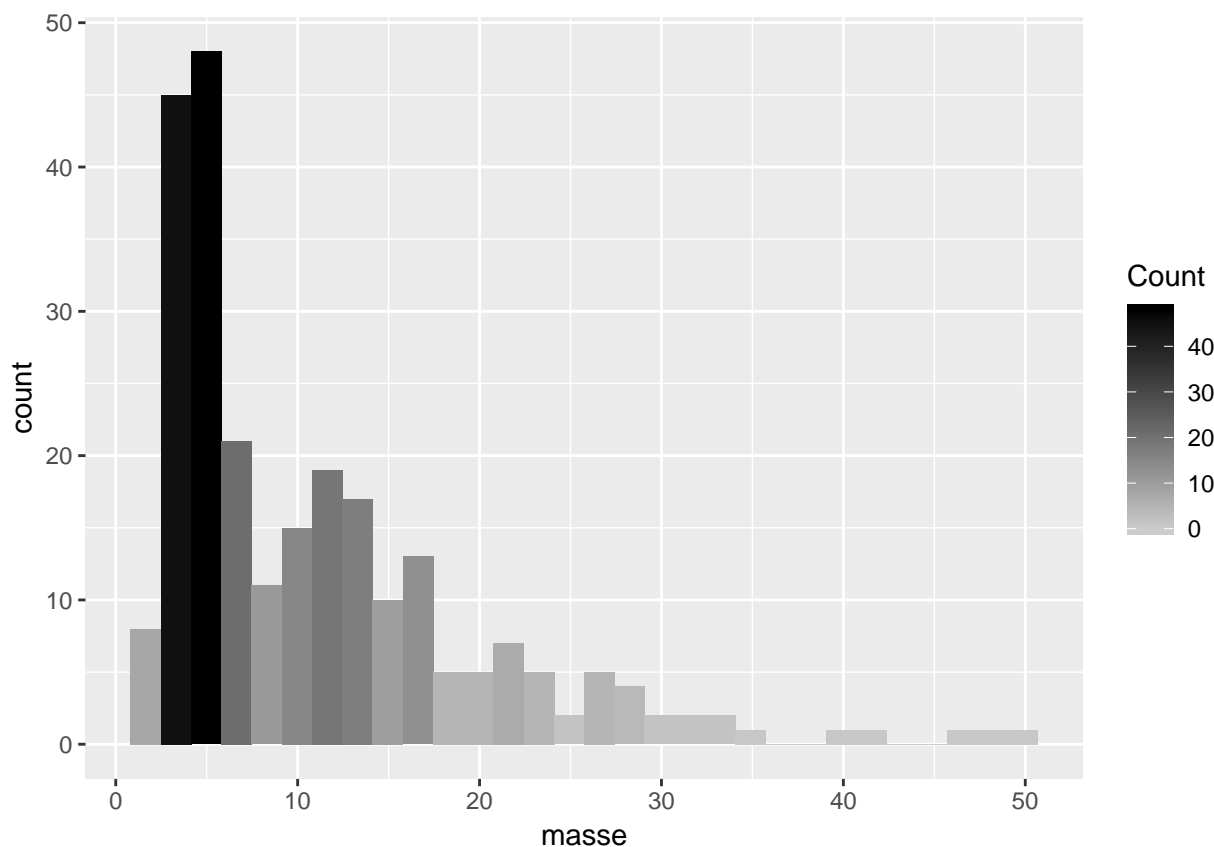
```
pdf("figure317eggplot.pdf")
print(ggplot(Mesures,aes(x=masse))+geom_histogram(aes(fill=..count..))+
        scale_fill_gradient("Count", low = "grey80", high = "black"))
```

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

```
dev.off()
```

pdf
2

```
g+geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse))+scale_fill_gradient("Count", low = "grey80", high = "black")
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
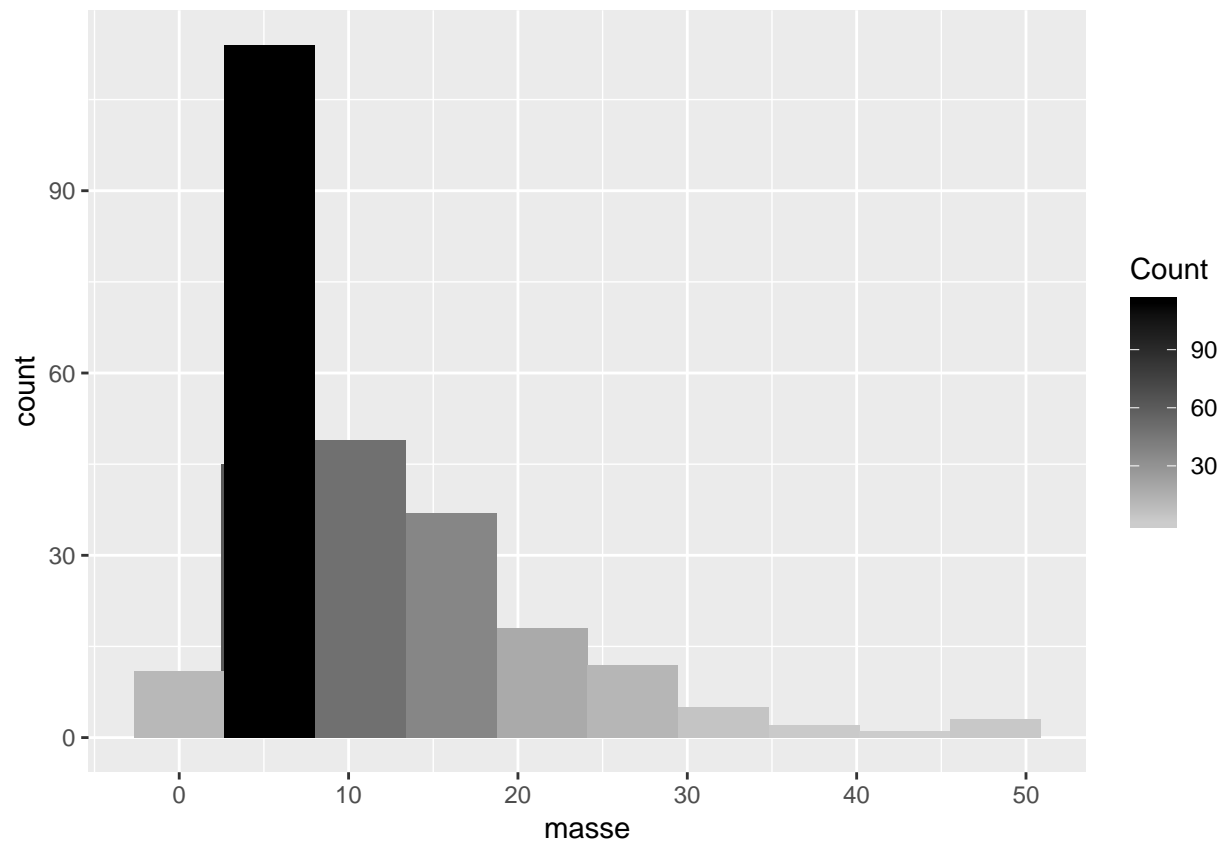
```
pdf("figure317fggplot.pdf")
print(g+geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse))+scale_fill_gradient("Count", low = "grey80", high = "black"))
```

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

```
dev.off()
```

```
## pdf
##    2
#page 131
histo<-hist(Mesures$masse)
```

Histogram of Mesures$masse
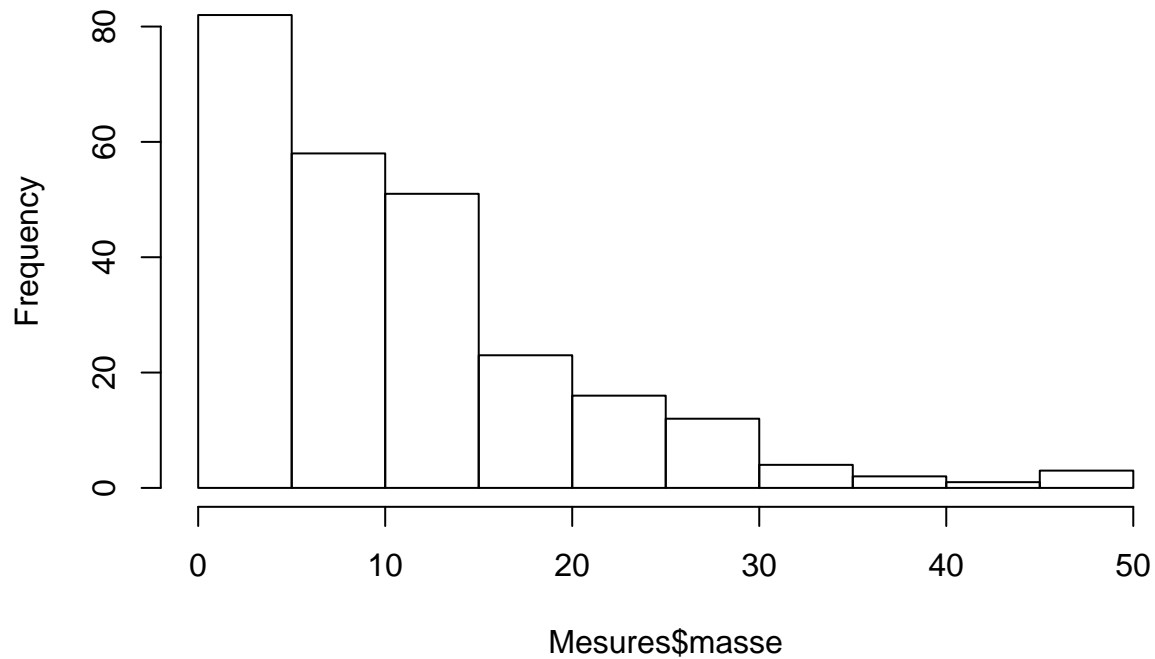

```
histo
```

```
## $breaks
##  [1]  0  5 10 15 20 25 30 35 40 45 50
##
## $counts
##  [1] 82 58 51 23 16 12  4  2  1  3
##
## $density
##  [1] 0.065079 0.046032 0.040476 0.018254 0.012698 0.009524 0.003175
##  [8] 0.001587 0.000794 0.002381
##
## $mids
##  [1]  2.5  7.5 12.5 17.5 22.5 27.5 32.5 37.5 42.5 47.5
##
## $xname
## [1] "Mesures$masse"
##
## $equidist
## [1] TRUE
##
## attr(,"class")
## [1] "histogram"
```

```
#page 133
library(lattice)
histogram(~masse|espece,data=Mesures)
```
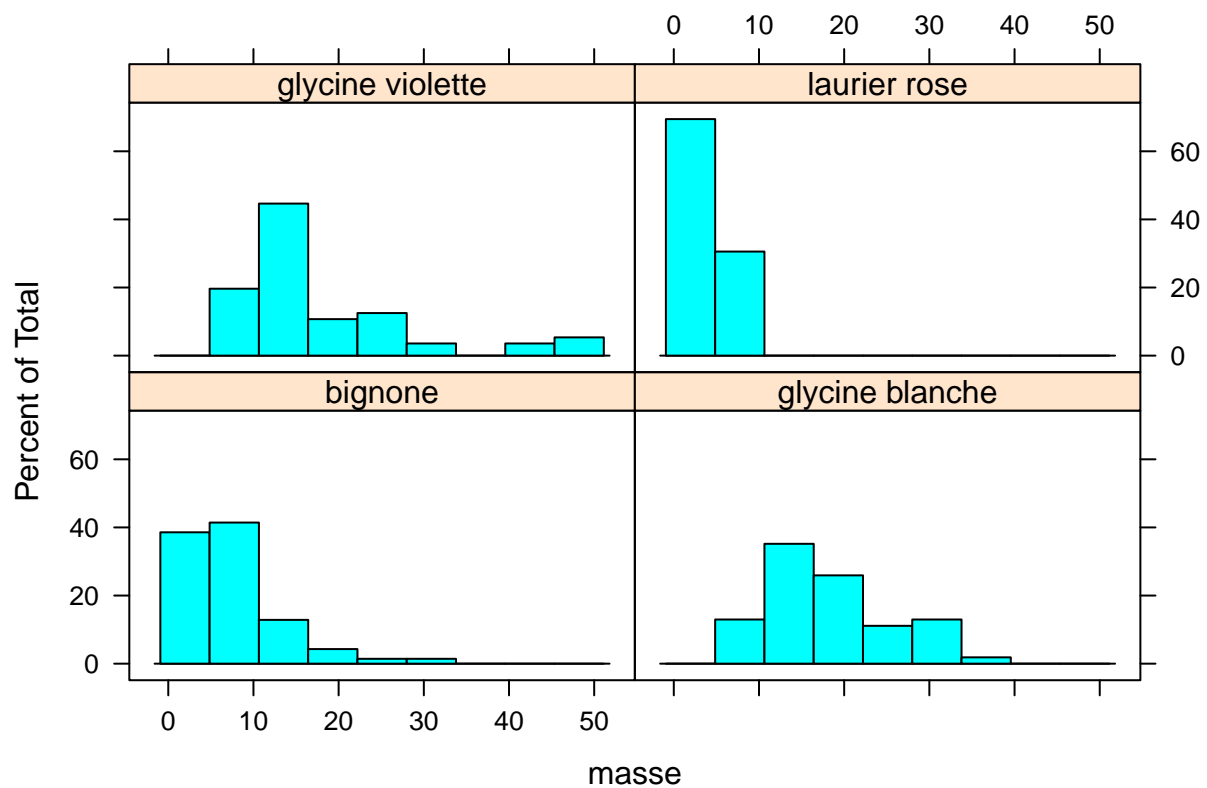
```r
pdf("figure318lattice.pdf")
histogram(~masse|espece,data=Mesures)
dev.off()
```

```
## pdf
##   2
```

```r
#en plus
ggplot(Mesures, aes(x = masse)) +
  geom_histogram(binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse)
  ) + xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece)
```
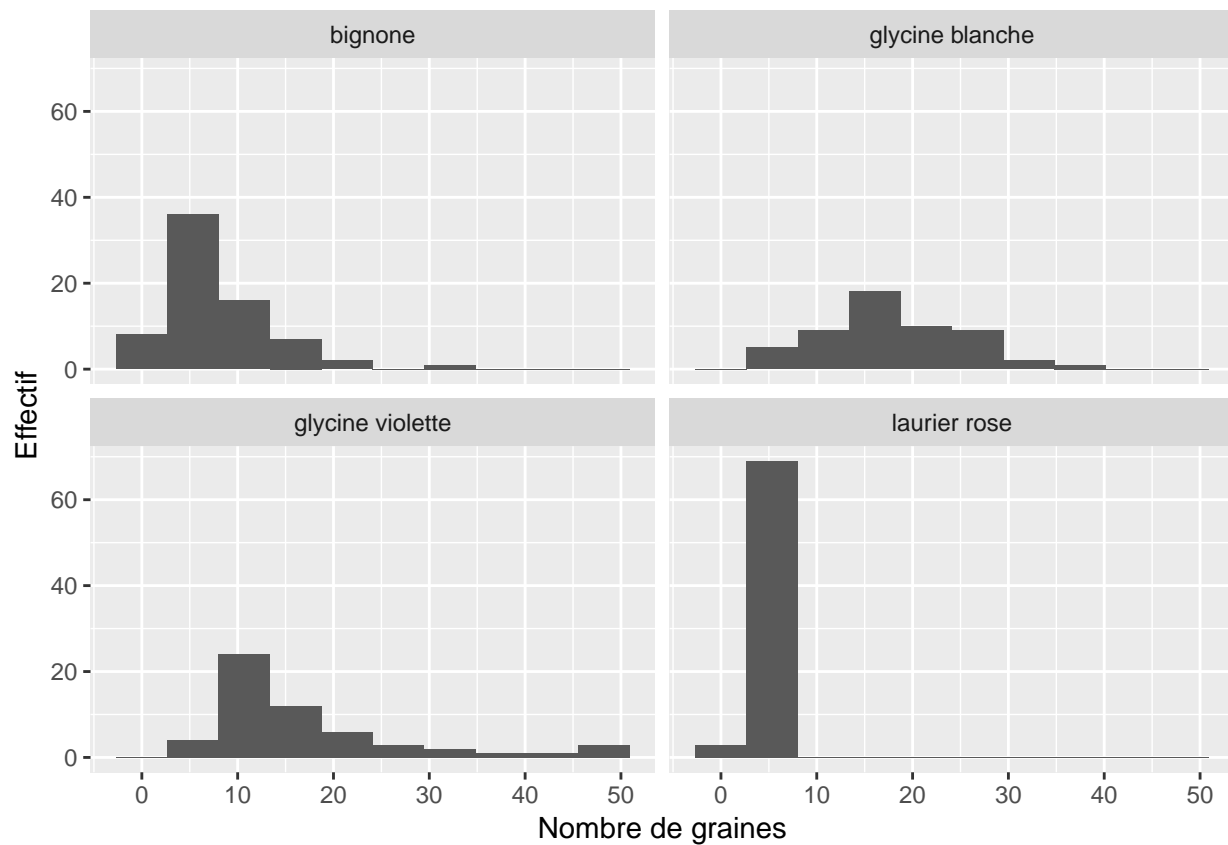
```
pdf("figure318ggplot.pdf")
print(ggplot(Mesures, aes(x = masse)) +
        geom_histogram(binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse)
        ) + xlab("Nombre de graines") + ylab("Effectif") + facet_wrap(~espece))
dev.off()
```

```
## pdf
##    2
```

```
ggplot(Mesures, aes(x = masse)) +
  geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse)) + xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece) + scale_fill_gradient("Count", low = "green", high = "red")
```
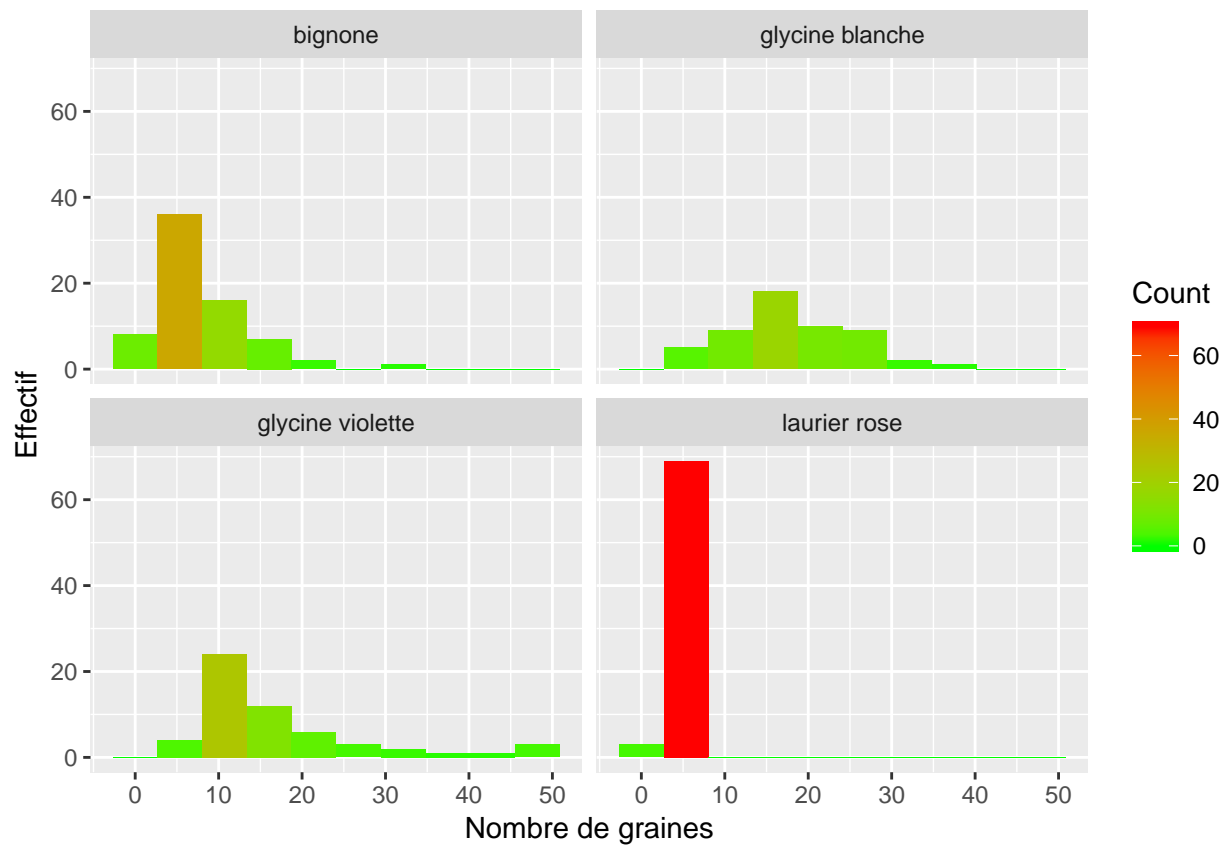
```
pdf("figure318aggplot.pdf")
print(ggplot(Mesures, aes(x = masse)) +
  geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse)) + xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece) + scale_fill_gradient("Count", low = "green", high = "red"))
dev.off()

## pdf
##   2
g=ggplot(Mesures, aes(x = masse)) +
  geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse)) + xlab("Nombre de graines") + ylab("Effectif") +
  facet_wrap(~espece)
g
```
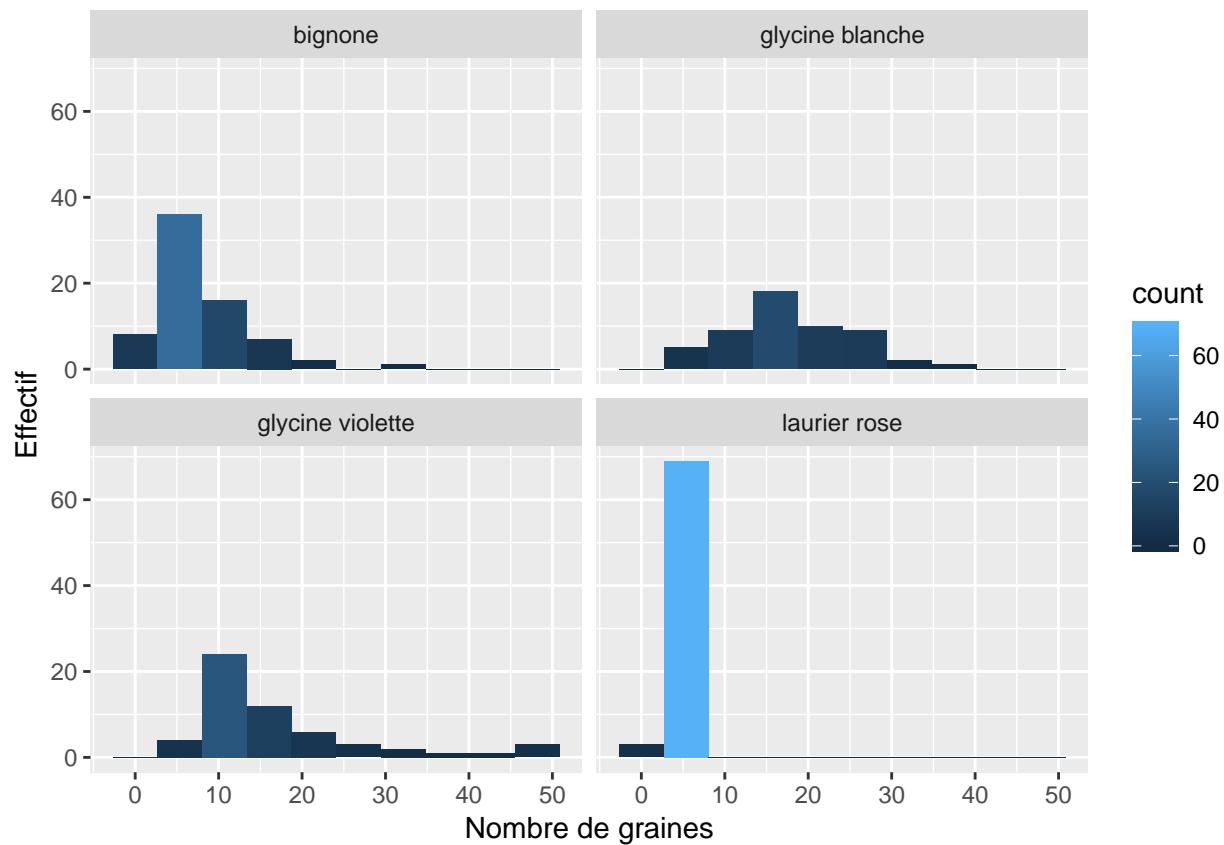
```
pdf("figure318bggplot.pdf")
print(g)
dev.off()
```

```
## pdf
##   2
```

```
histo<-hist(Mesures$masse,ylab="Effectif",xlab="Masse",main="Polygone des
            effectifs des masses")
lines(histo$mids,histo$counts,lwd=2)
points(histo$mids,histo$counts,cex=1.2,pch=19)
```

Polygone des
effectifs des masses
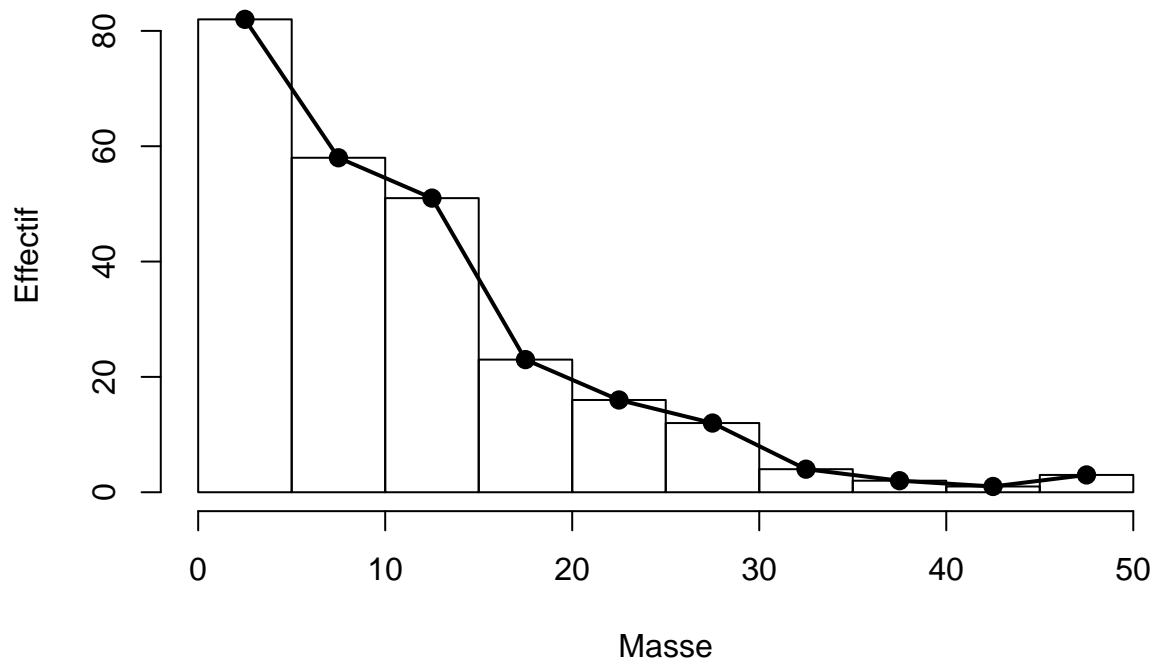

```
pdf("figure319.pdf")
histo<-hist(Mesures$masse,ylab="Effectif",xlab="Masse",main="Polygone des
          effectifs des masses")
lines(histo$mids,histo$counts,lwd=2)
points(histo$mids,histo$counts,cex=1.2,pch=19)
dev.off()
```

```
## pdf
##   2
```

```
#En plus ggplot
g=ggplot(Mesures, aes(x = masse)) +
  geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse),boundary=0) + xlab("Nombre de graines") + ylab("Effectif")
g
```
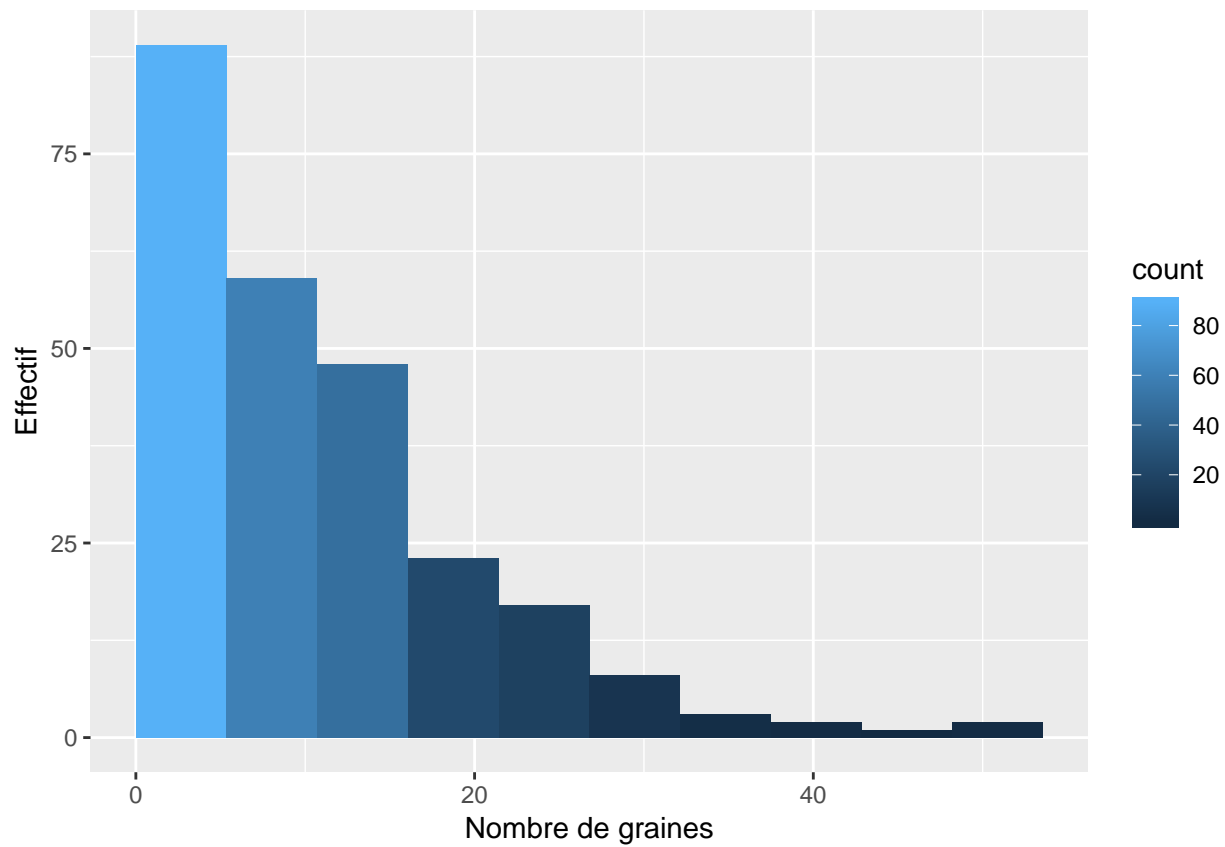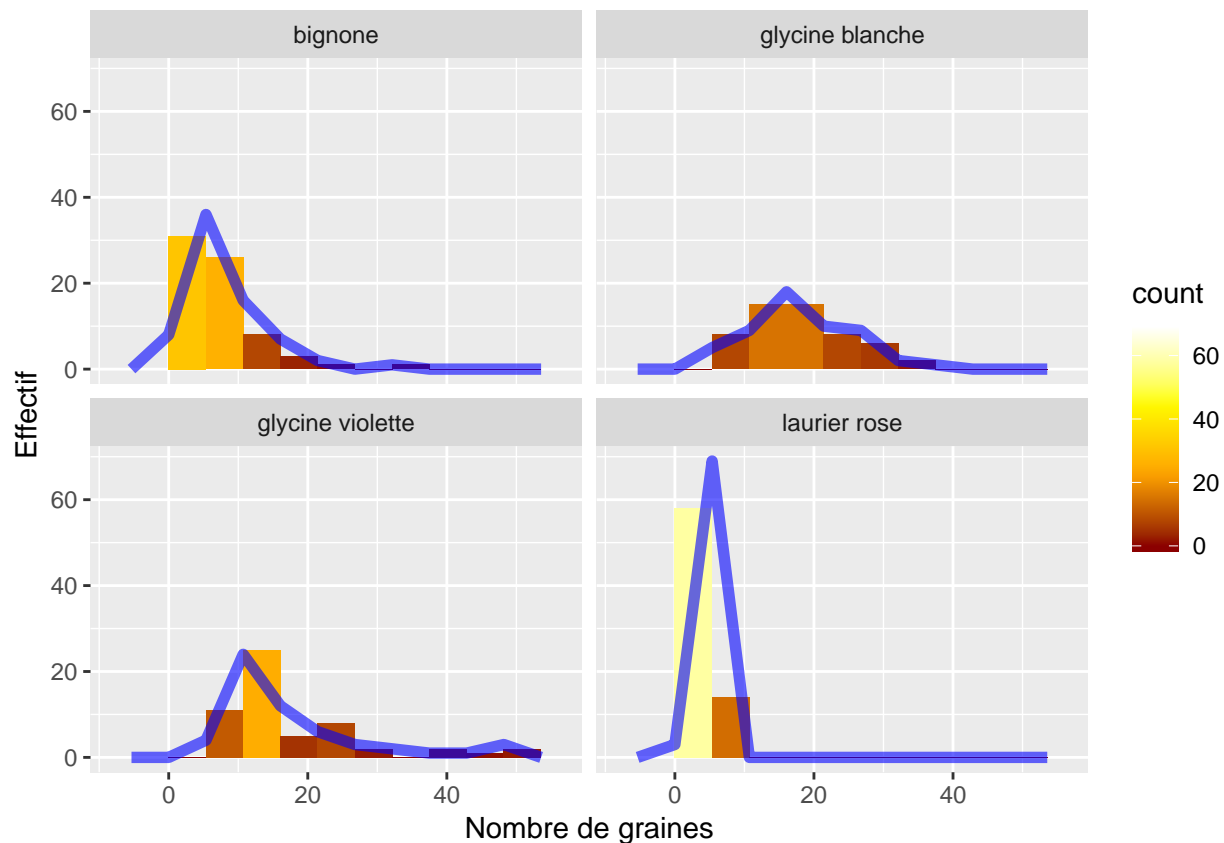
```
pdf("figure319ggplot.pdf")
print(g)
dev.off()
```

```
## pdf
##   2
```

```
g1=g+geom_line(binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
            size=2,alpha=.60,color="blue",stat="bin",boundary=0)
g1
```
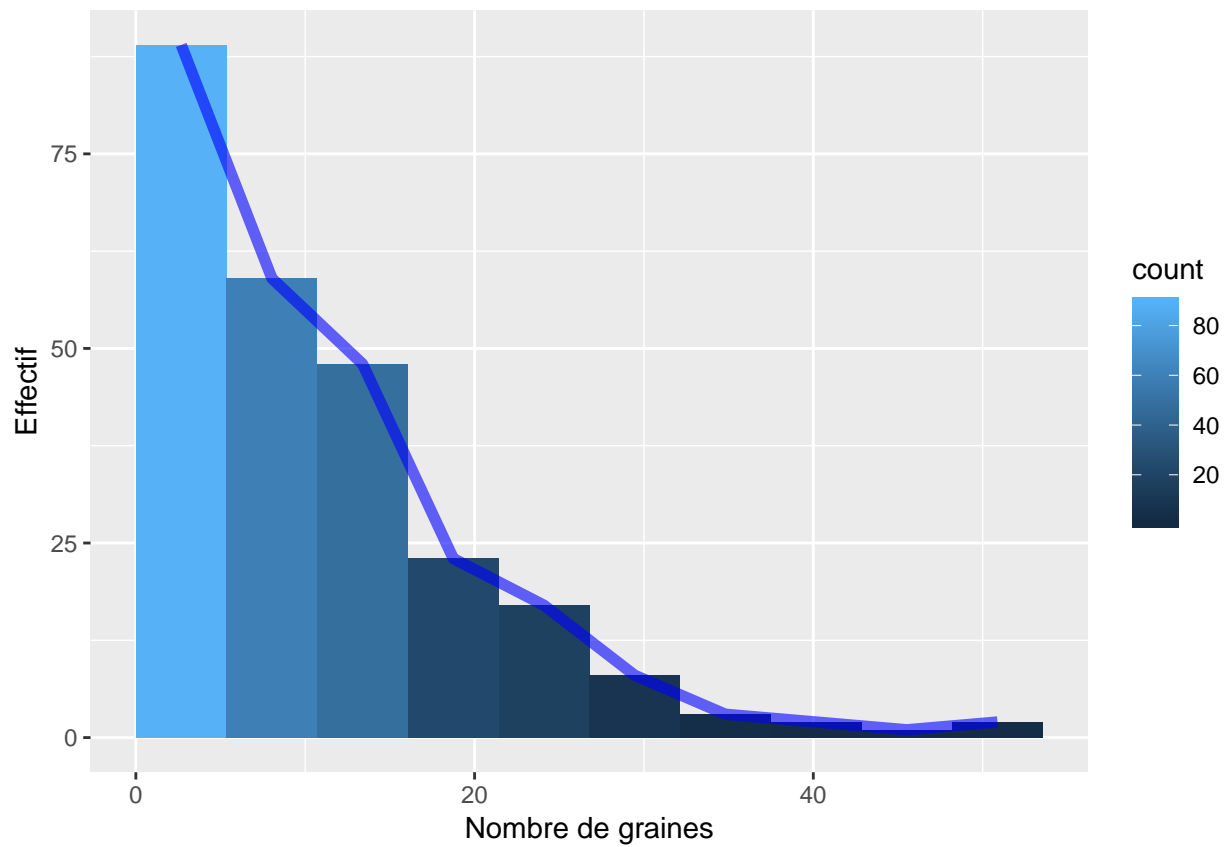
```
pdf("figure319aggplot.pdf")
g1
dev.off()
```

```
## pdf
##   2
```

```
g+stat_bin(binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
          size=2,alpha=.60,color="blue",geom="line",boundary=0)
```
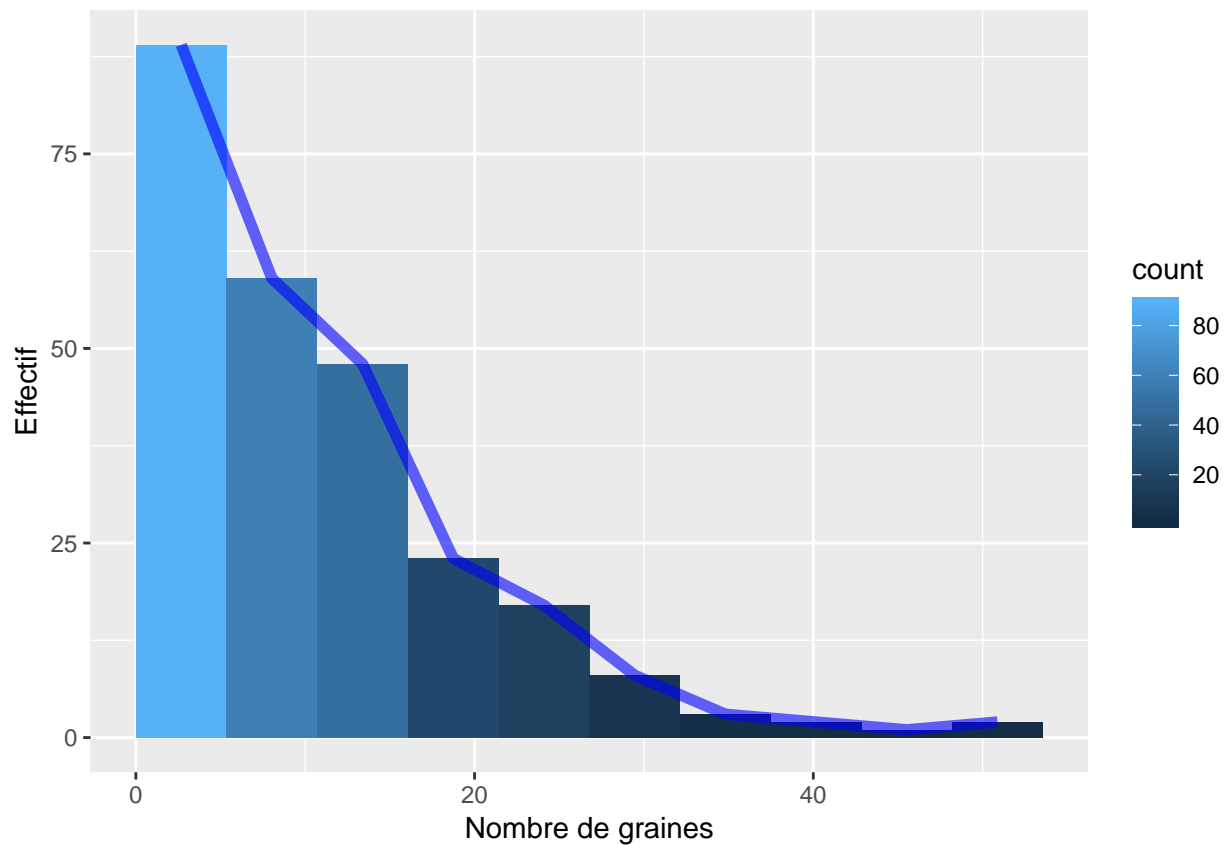
```
pdf("figure319bggplot.pdf")
print(g+stat_bin(binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse),size=2,alpha=.60,color="blue",geom="line",boundary=0))
dev.off()
```

```
## pdf
##   2
```

```
g1+ scale_fill_gradient(low="white", high="black")
```
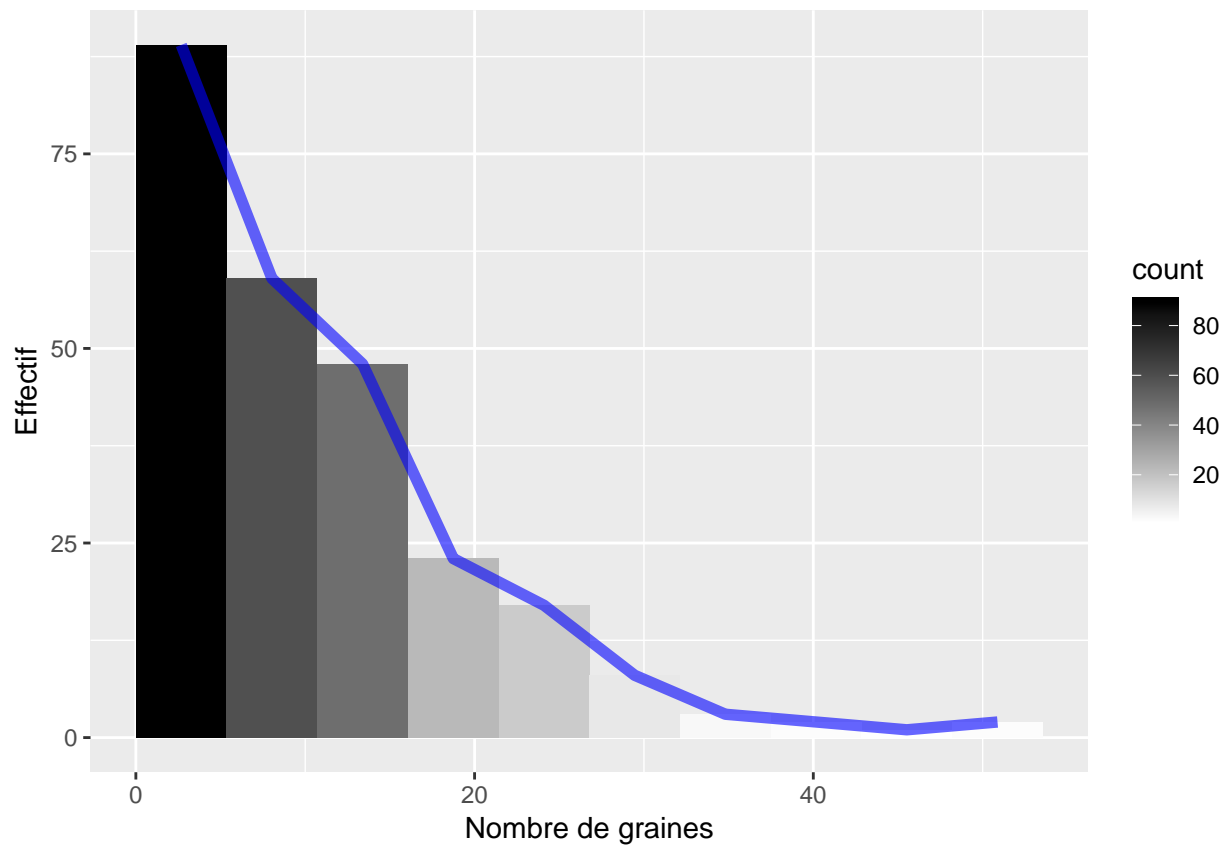
```
pdf("figure319cggplot.pdf")
print(g1+ scale_fill_gradient(low="white", high="black"))
dev.off()
```

```
## pdf
##   2
```

```
if(!("scales" %in% rownames(installed.packages()))){install.packages("scales")}
library(scales)
g1+ scale_fill_gradient2(low=muted("red"), mid="white",
                         high=muted("blue"),midpoint=40)
```
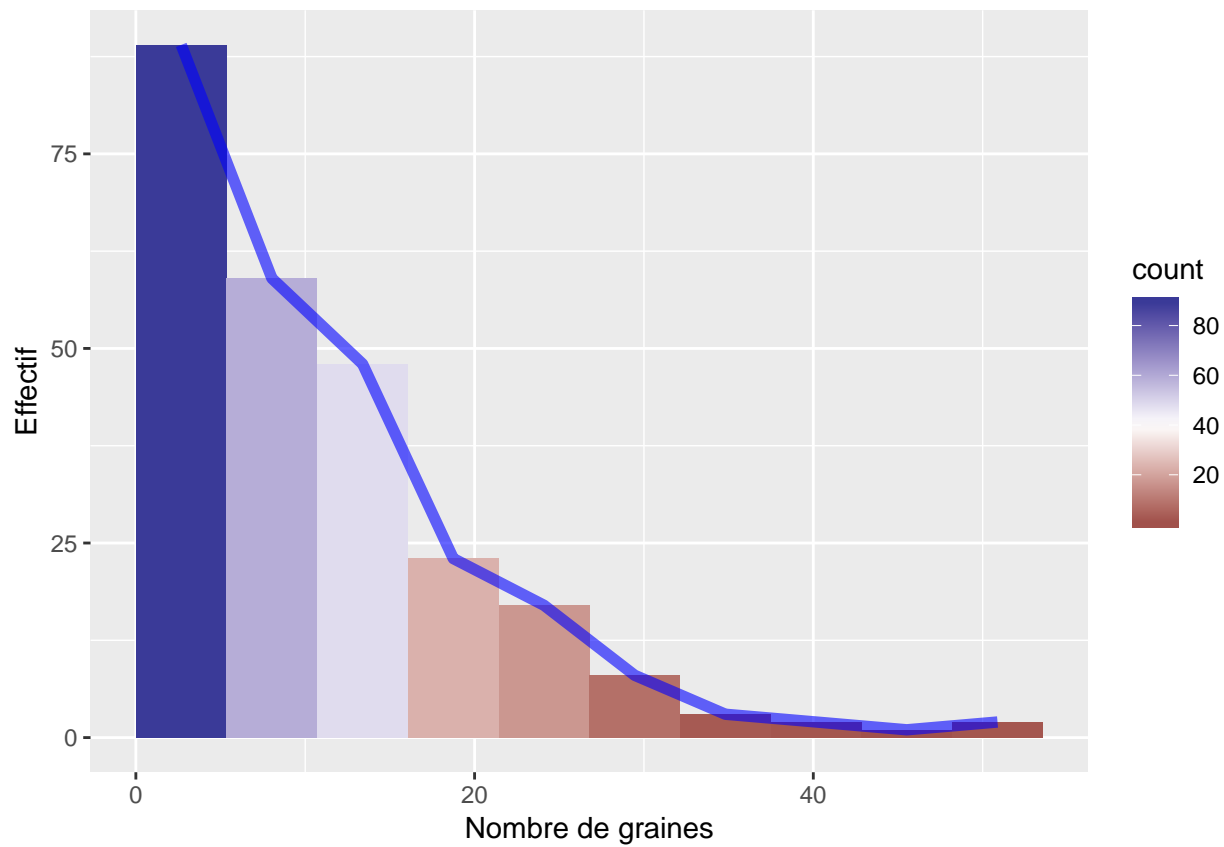
```
pdf("figure319dggplot.pdf")
g1+ scale_fill_gradient2(low=muted("red"), mid="white",
                        high=muted("blue"),midpoint=40)
dev.off()

## pdf
##   2

g1+ scale_fill_gradientn(colours = c("darkred", "orange", "yellow", "white"))
```
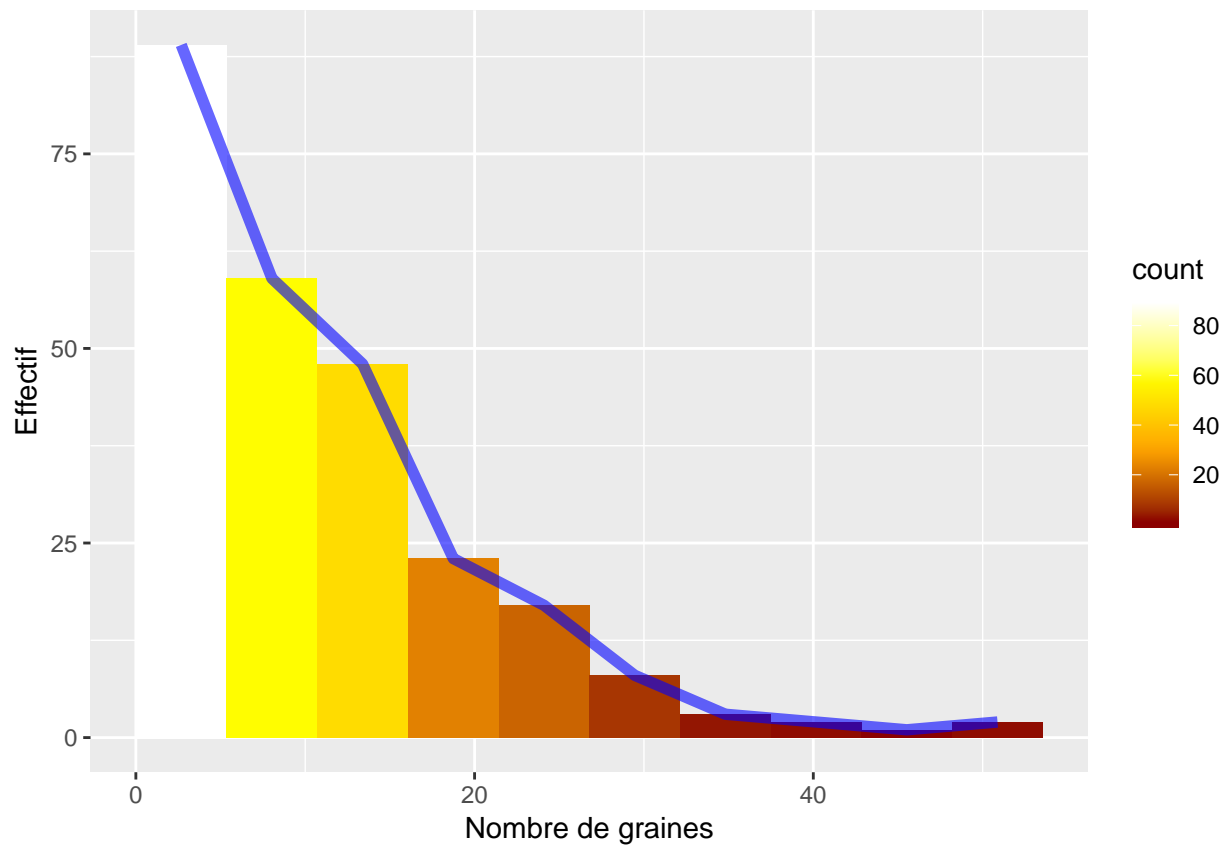
```
pdf("figure319eggplot.pdf")
g1+ scale_fill_gradientn(colours = c("darkred", "orange", "yellow", "white"))
dev.off()
```

```
## pdf
##   2
```

```
#Par groupe
g=ggplot(Mesures, aes(x = masse)) +
  geom_histogram(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse),boundary=0) + xlab("Nombre de graines") +
  ylab("Effectif") + facet_wrap(~espece)
g
```

```r
pdf("figure319fggplot.pdf")
print(g)
dev.off()
```

```
## pdf
##   2
```

```r
g+geom_freqpoly(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse),size=2,alpha=.60,color="blue")+
  scale_fill_gradientn(colours = c("darkred", "orange", "yellow", "white"))
```

```
## Warning: Ignoring unknown aesthetics: fill
```
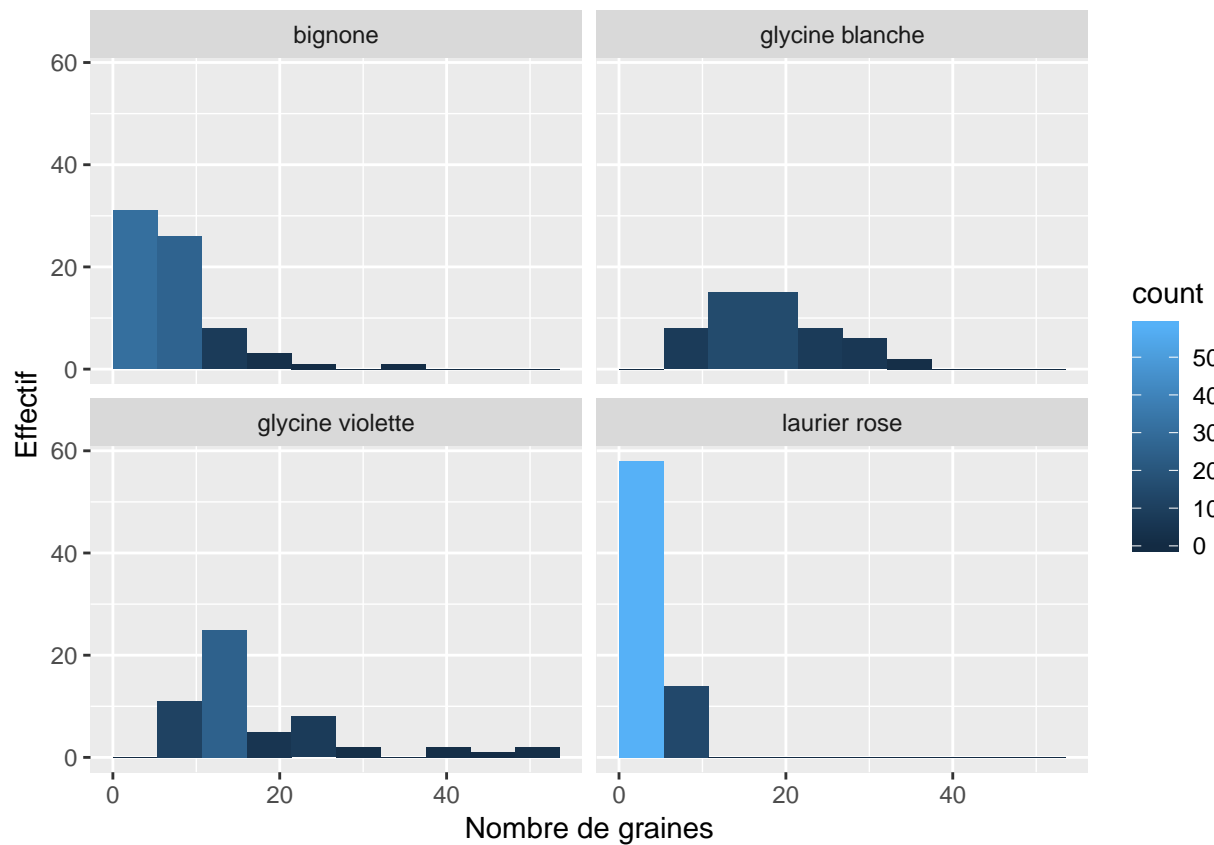
```r
pdf("figure319fggplot.pdf")
print(g+geom_freqpoly(aes(fill=..count..),binwidth=diff(range(Mesures$masse))/
    nclass.Sturges(Mesures$masse),size=2,alpha=.60,color="blue")+
    scale_fill_gradientn(colours = c("darkred", "orange", "yellow", "white")))
```

```
## Warning: Ignoring unknown aesthetics: fill
```

```r
dev.off()
```

```
## pdf
##   2
```

```r
#page 135
histo<-hist(Mesures$masse,plot=FALSE)
barplot<-barplot(cumsum(histo$counts),ylab="Effectif",xlab="Masse",main="
                Polygone des effectifs cumulés des masses")
lines(barplot,cumsum(histo$counts),lwd=2)
points(barplot,cumsum(histo$counts),cex=1.2,pch=19)
```

Polygone des effectifs cumulés des masses
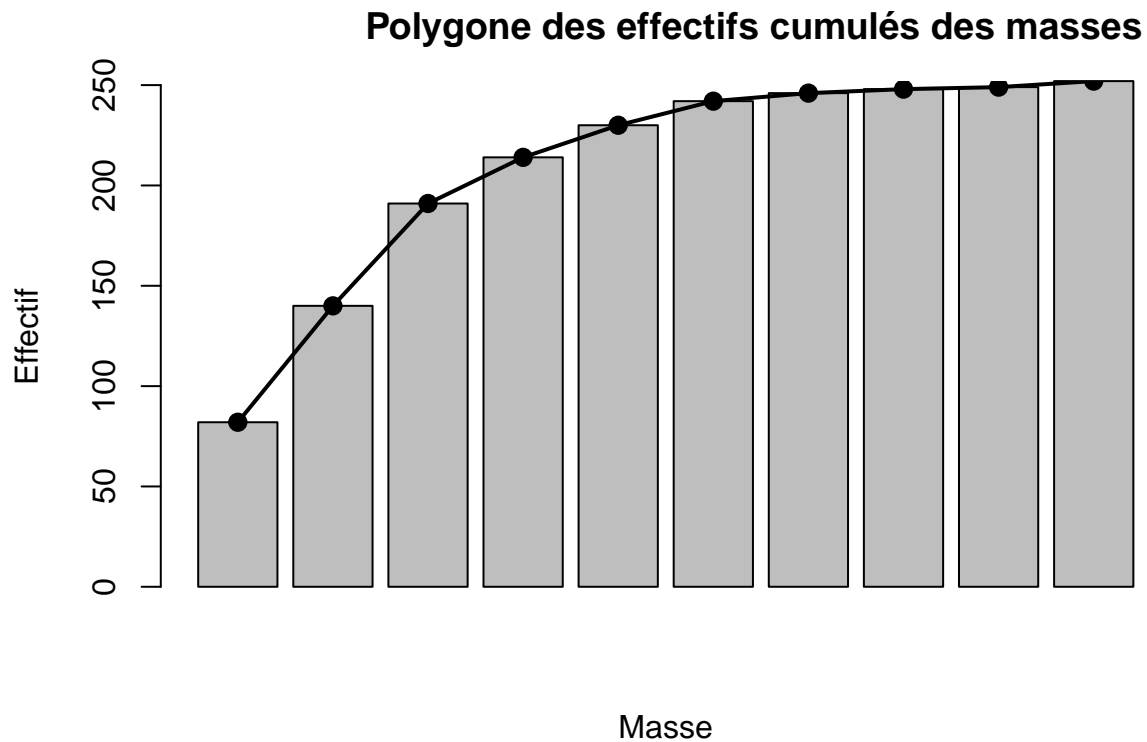

```
pdf("figure320.pdf")
barplot<-barplot(cumsum(histo$counts),ylab="Effectif",xlab="Masse",main="
                Polygone des effectifs cumulés des masses")
lines(barplot,cumsum(histo$counts),lwd=2)
points(barplot,cumsum(histo$counts),cex=1.2,pch=19)
dev.off()
```

```
## pdf
##   2
```

```
#Effectifs et polygone des fréquences cumulées
library(qcc)
```

```
## Package 'qcc' version 2.7
```

```
## Type 'citation("qcc")' for citing this R package in publications.
```

```
pareto.chart(table(Mesures5$graines))
```
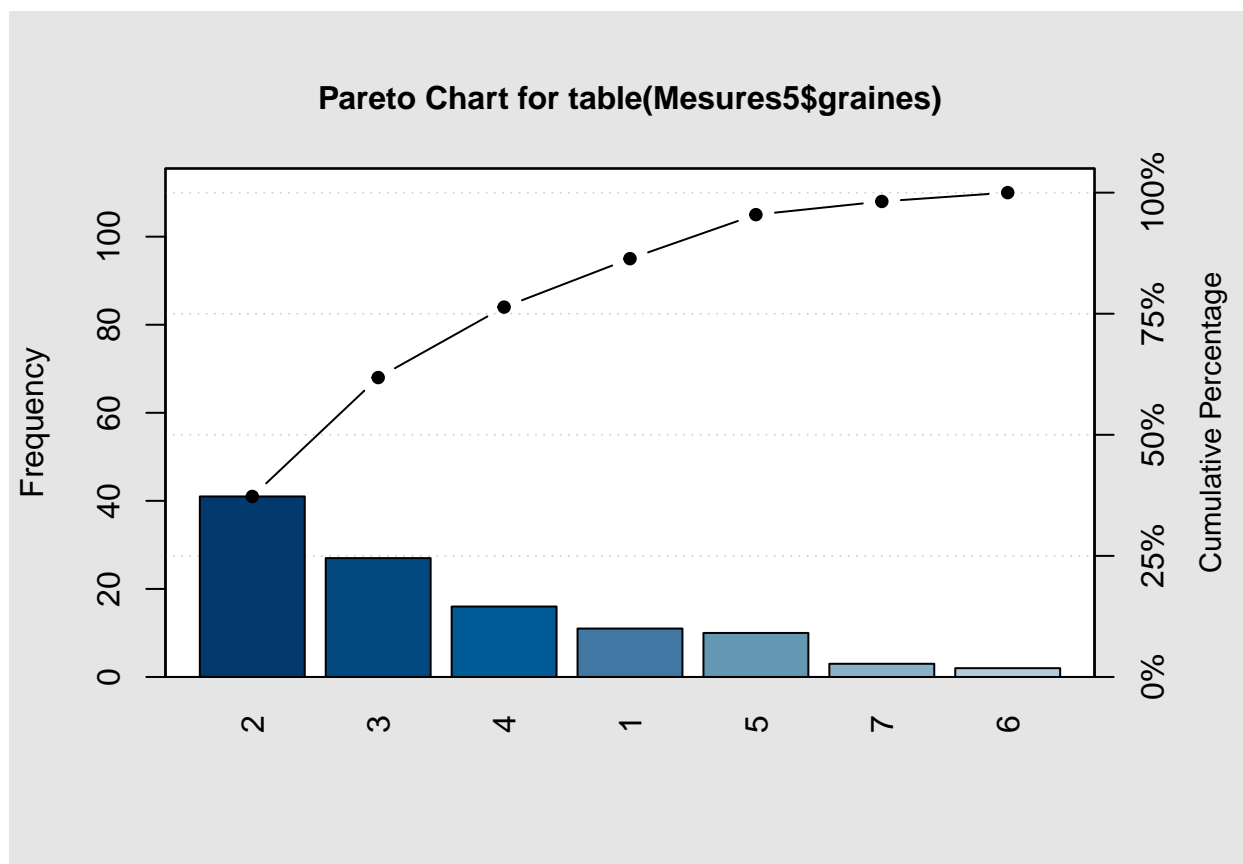
Pareto Chart for table(Mesures5$graines)

```
## 
## Pareto chart analysis for table(Mesures5$graines)
##      Frequency Cum.Freq. Percentage Cum.Percent.
##   2      41.00     41.00      37.27        37.27
##   3      27.00     68.00      24.55        61.82
##   4      16.00     84.00      14.55        76.36
##   1      11.00     95.00      10.00        86.36
##   5      10.00    105.00       9.09        95.45
##   7       3.00    108.00       2.73        98.18
##   6       2.00    110.00       1.82       100.00
```

```r
pdf("figure320qcc.pdf")
pareto.chart(table(Mesures5$graines))
```

```
## 
## Pareto chart analysis for table(Mesures5$graines)
##      Frequency Cum.Freq. Percentage Cum.Percent.
##   2      41.00     41.00      37.27        37.27
##   3      27.00     68.00      24.55        61.82
##   4      16.00     84.00      14.55        76.36
##   1      11.00     95.00      10.00        86.36
##   5      10.00    105.00       9.09        95.45
##   7       3.00    108.00       2.73        98.18
##   6       2.00    110.00       1.82       100.00
```

```r
dev.off()
```

```
## pdf
```

```
##    2
consmw=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse)
consmw
```

```
## [1] 5.36
consmw.espece=cbind(espece=names(unlist(lapply(split(Mesures$masse,Mesures$
  espece),function(xxx) return(diff(range(xxx))/nclass.Sturges(xxx))))),
  consmw.espece=unlist(lapply(split(Mesures$masse,Mesures$espece),function(xxx)
  return(diff(range(xxx))/nclass.Sturges(xxx)))))
consmw.espece
```

```
##                    espece            consmw.espece
## bignone           "bignone"          "4.0875"
## glycine blanche   "glycine blanche"  "4.3"
## glycine violette  "glycine violette" "6.15714285714286"
## laurier rose      "laurier rose"     "0.5125"
Mesures.binw<-merge(cbind(Mesures,consmw=diff(range(Mesures$masse))/
  nclass.Sturges(Mesures$masse)),consmw.espece)
```

```
g=ggplot(Mesures.binw, aes(x = masse))
g +
  geom_histogram(data=Mesures.binw,aes(y=5.355556*..density..,fill=..density..),
  binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),boundary =
  min(Mesures$masse)) + xlab("Masse") + ylab("Fréquence")
```
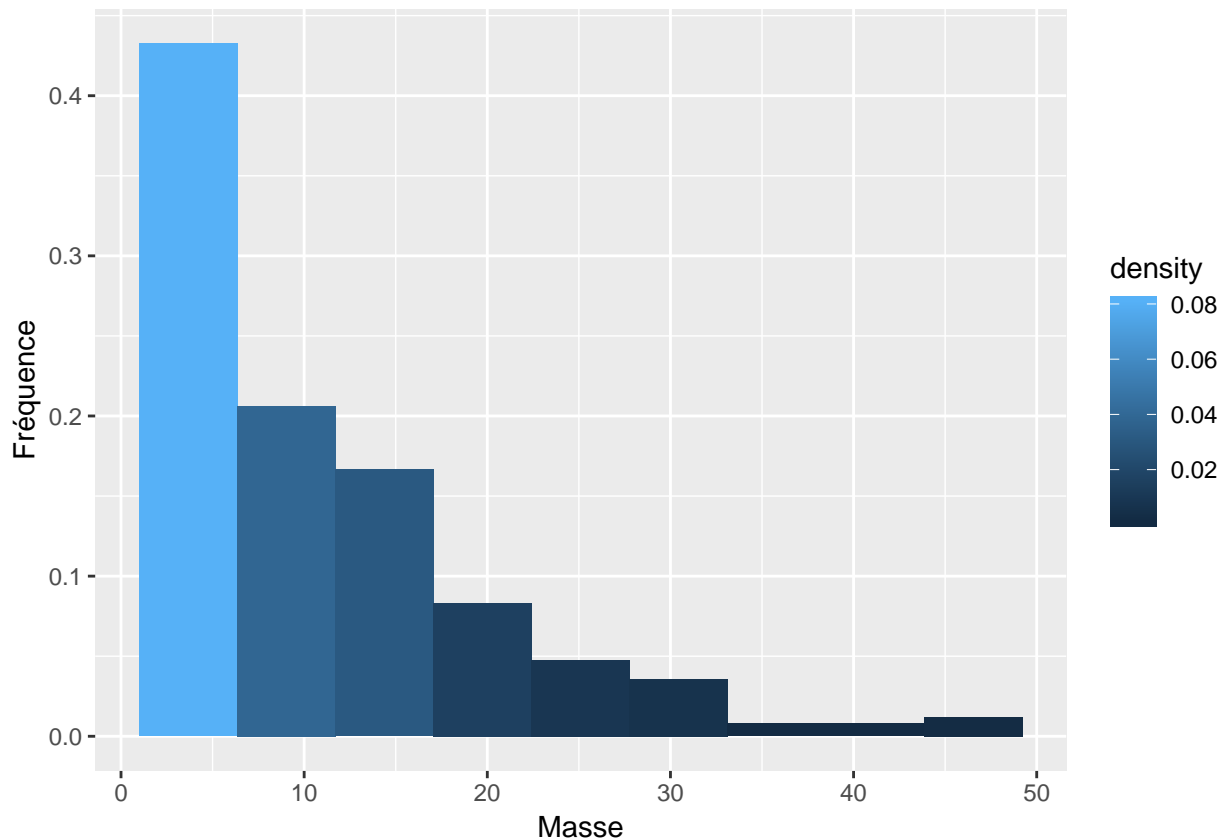


```
pdf("figure320ggplot.pdf")
print(g +
```

```
  geom_histogram(data=Mesures.binw,aes(y=5.355556*..density..,fill=..density..),
  binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),boundary =
  min(Mesures$masse)) + xlab("Masse") + ylab("Fréquence"))
dev.off()
```

```
## pdf
##   2
```

```
g +
  geom_histogram(data=Mesures.binw,aes(y=5.355556*..count..,fill=..count..),
  binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),boundary =
  min(Mesures$masse)) + xlab("Masse") + ylab("Dénombrement")
```
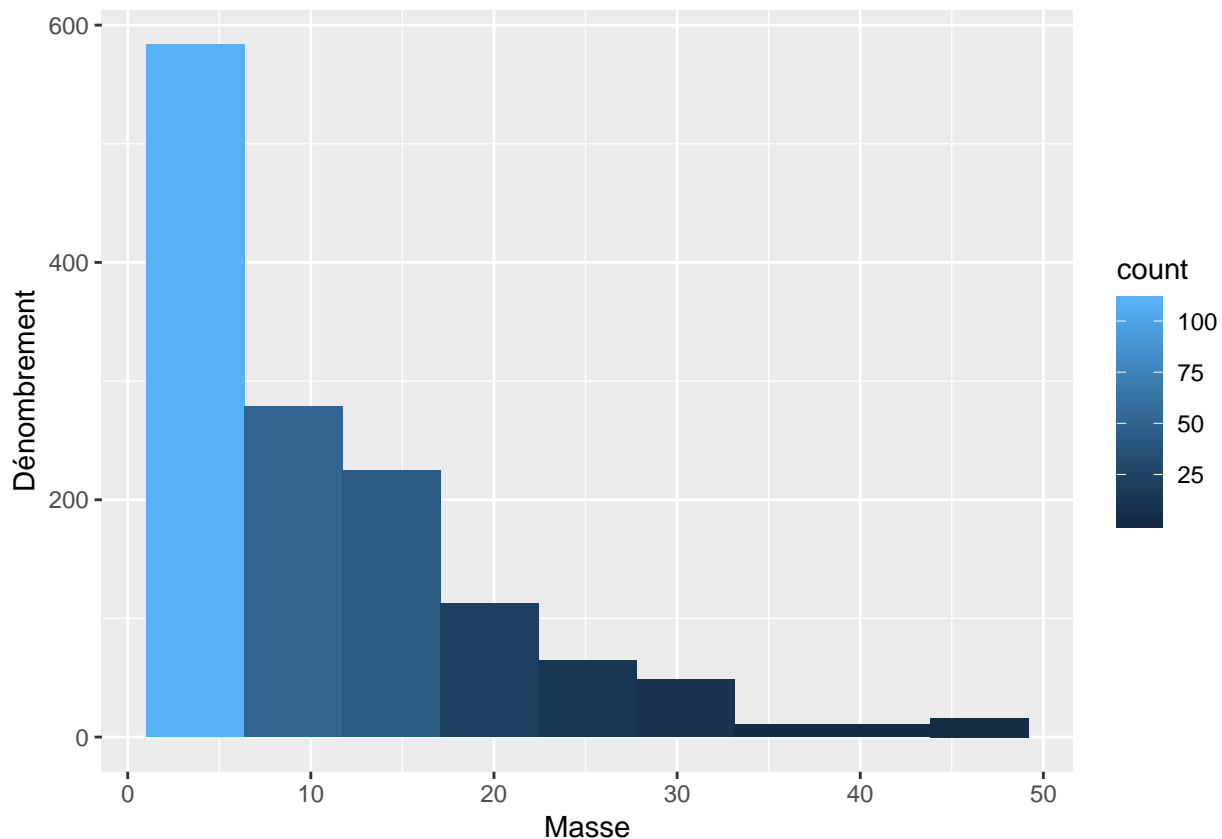


```
pdf("figure320aggplot.pdf")
print(g +
  geom_histogram(data=Mesures.binw,aes(y=5.355556*..count..,fill=..count..),
  binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),boundary =
  min(Mesures$masse)) + xlab("Masse") + ylab("Dénombrement"))
dev.off()
```

```
## pdf
##   2
```

```
g + stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh") +
  stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh",geom="linerange",ymin
  =0,aes(ymax=..y..))
```

```
## Warning: Ignoring unknown parameters: direction
```
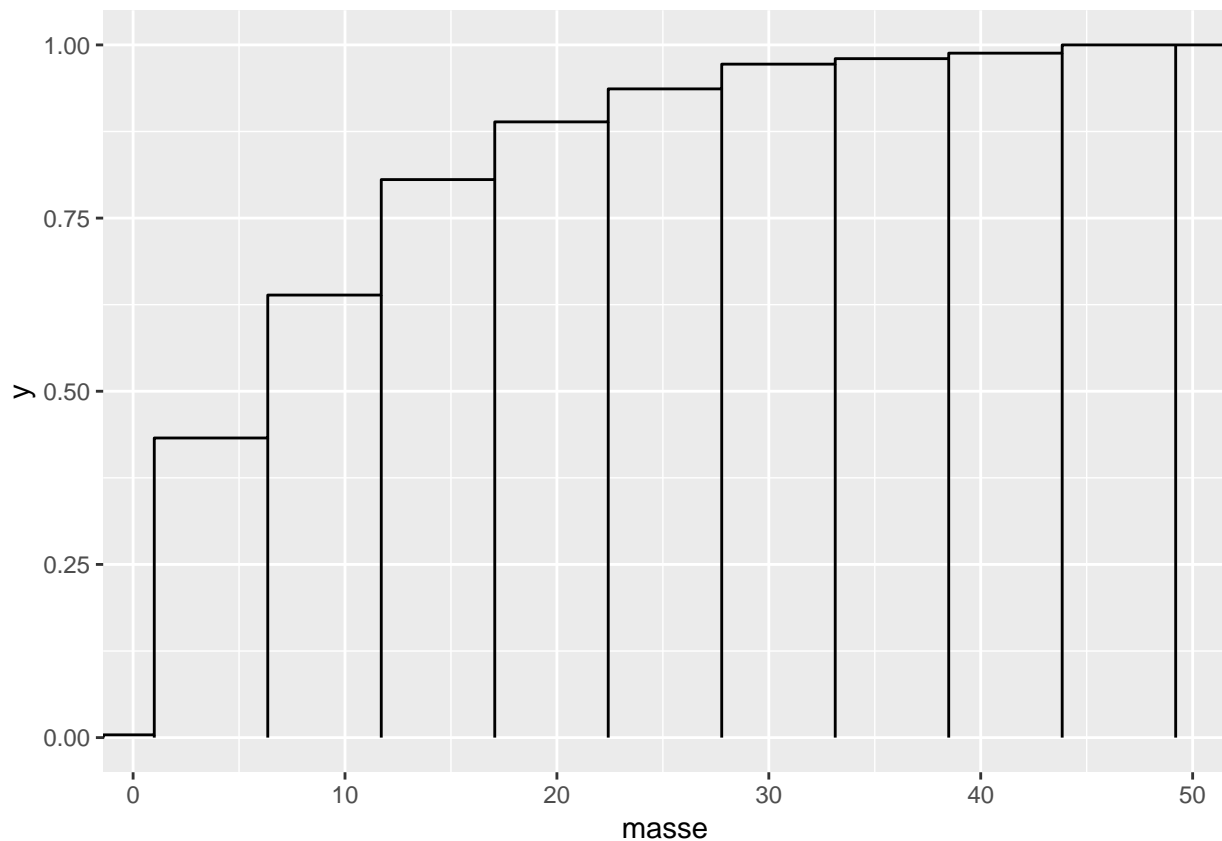
```r
pdf("figure320bggplot.pdf")
print(g + stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh") +
  stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh",geom="linerange",ymin
  =0,aes(ymax=..y..)))
```

```
## Warning: Ignoring unknown parameters: direction
```

```r
dev.off()
```

```
## pdf
##   2
```
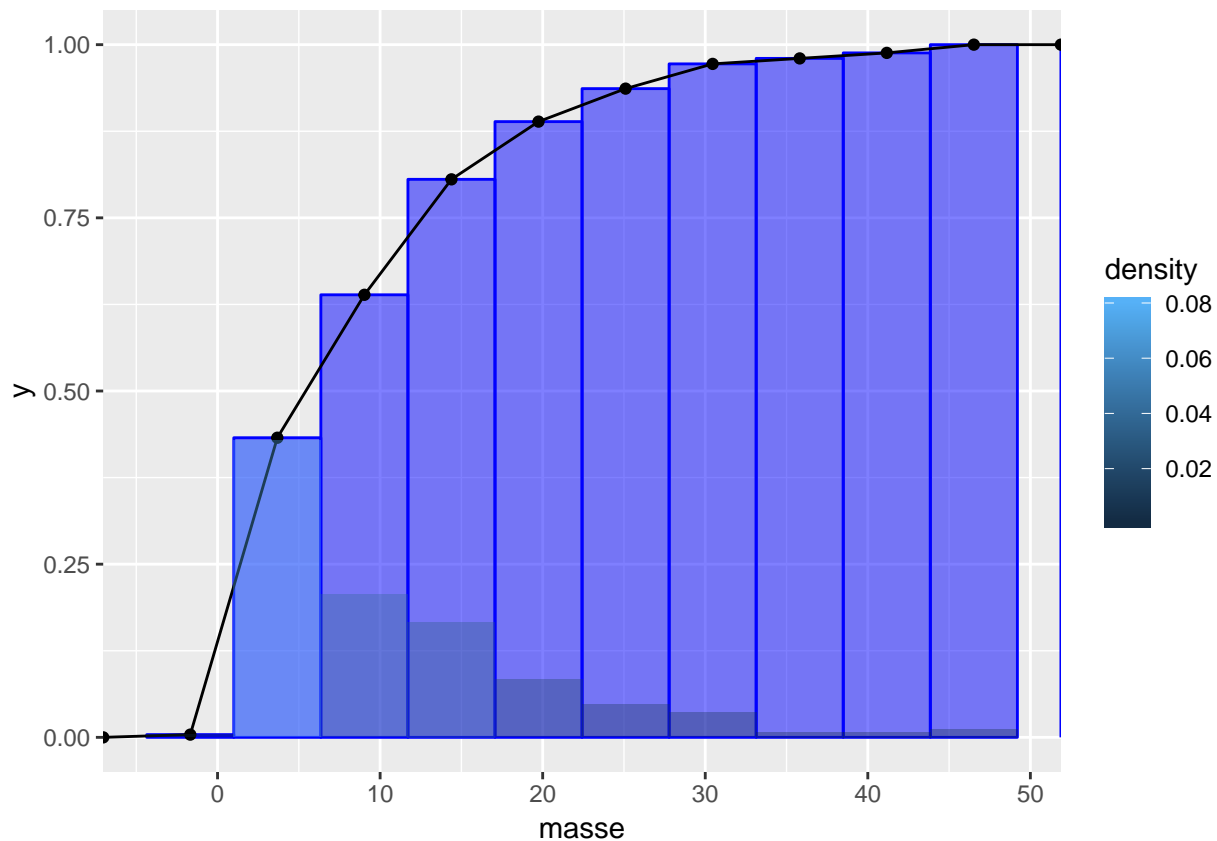
```r
g +
  geom_histogram(aes(y=5.355556*..density..,fill=..density..),binwidth=diff(range(
    Mesures$masse))/nclass.Sturges(Mesures$masse),boundary = min(Mesures$masse)) +
  xlab("Masse") + ylab("Fréquence") +
  stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh") +
  stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh",geom="linerange",ymin
          =0,aes(ymax=..y..))
```

```
## Warning: Ignoring unknown parameters: direction
```

```r
pdf("figure320cggplot.pdf")
print(g +
  geom_histogram(aes(y=5.355556*..density..,fill=..density..),binwidth=diff(range(
  Mesures$masse))/nclass.Sturges(Mesures$masse),boundary = min(Mesures$masse)) +
  xlab("Masse") + ylab("Fréquence") +
  stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh") +
  stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,direction="vh",geom="linerange",ymin
  =0,aes(ymax=..y..)))
```

```
## Warning: Ignoring unknown parameters: direction
```

```r
dev.off()
```

```
## pdf
##   2
```

```r
#depuis ggplot2 2.0 ne freqpoly n'est plus un geom acceptable
#g+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("rect"),fill="blue",aes(
#ymax=..y..,ymin=0,xmax=..x..,xmin=..x..-diff(range(BioStatR::Mesures$masse))/
#grDevices::nclass.Sturges(BioStatR::Mesures$masse)),alpha=.5,colour="blue")+
#stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("freqpoly"),fill="blue",aes(
#x=masse-5.355556/2,y=..y..))+geom_histogram(aes(y=5.355556*..density..,fill=..
#density..),binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
#alpha=.35,boundary = min(Mesures5$masse))
#pdf("figure320dggplot.pdf")
#print(g+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("rect"),fill="blue",
#aes(ymax=..y..,ymin=0,xmax=..x..,xmin=..x..-diff(range(BioStatR::Mesures$masse)
#)/grDevices::nclass.Sturges(BioStatR::Mesures$masse)),alpha=.5,colour="blue")+
#stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("freqpoly"),fill="blue",aes(
```

```
#x=masse-5.355556/2,y=..y..))+geom_histogram(aes(y=5.355556*..density..,fill=..
#density..),binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
#alpha=.35,boundary = min(Mesures5$masse)))
#dev.off()
#
g+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("bar"),fill="blue",
  aes(x=masse-5.355556/2,width=5.355556),alpha=.5,colour="blue")+stat_ecdf(n=
  nclass.Sturges(Mesures$masse)+1,geom=c("line"),fill="blue",aes(x=masse-5.355556/2,
  y=..y..))+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("point"),fill="blue",
  aes(x=masse-5.355556/2,y=..y..))+geom_histogram(aes(y=5.355556*..density..,
  fill=..density..),binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
  alpha=.35,boundary = min(Mesures5$masse))
```
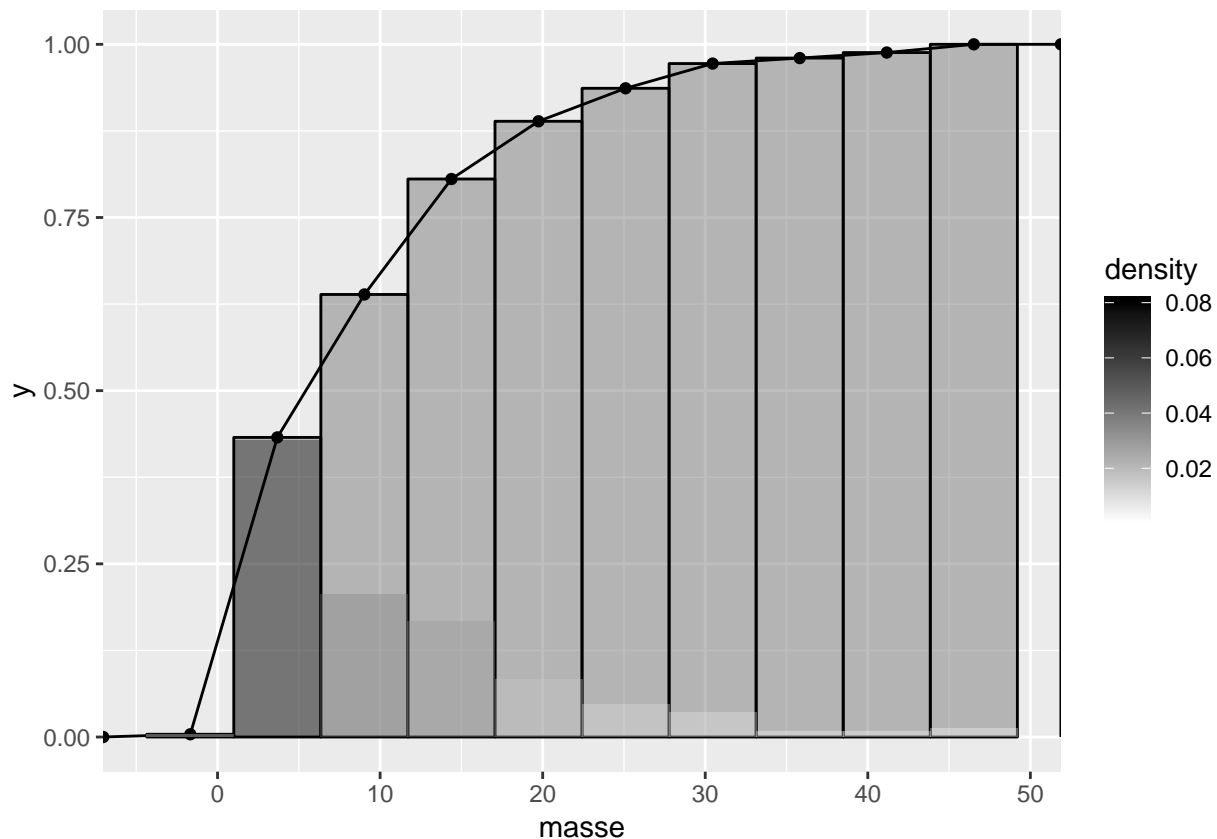
Warning: Ignoring unknown aesthetics: width

Warning: Ignoring unknown parameters: fill


```
pdf("figure320eggplot.pdf")
print(g+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("bar"),fill="blue",
  aes(x=masse-5.355556/2,width=5.355556),alpha=.5,colour="blue")+stat_ecdf(n=
  nclass.Sturges(Mesures$masse)+1,geom=c("line"),fill="blue",aes(x=masse-5.355556/2,
  y=..y..))+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("point"),fill="blue",
  aes(x=masse-5.355556/2,y=..y..))+geom_histogram(aes(y=5.355556*..density..,
  fill=..density..),binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
  alpha=.35,boundary = min(Mesures5$masse)))
```

Warning: Ignoring unknown aesthetics: width

```
## Warning: Ignoring unknown parameters: fill
```

```r
dev.off()
```

```
## pdf
##   2
```

```r
g+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("bar"),fill="grey50",aes(x=masse-
  5.355556/2,width=5.355556),alpha=.5,colour="black")+stat_ecdf(n=
  nclass.Sturges(Mesures$masse)+1,geom=c("line"),fill="grey50",aes(x=masse-5.355556/2,
  y=..y..))+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("point"),fill="black",
  aes(x=masse-5.355556/2,y=..y..))+geom_histogram(aes(y=5.355556*..density..,
  fill=..density..),binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
  alpha=.35,boundary = min(Mesures5$masse))+ scale_fill_gradient(low="white", high="black")
```
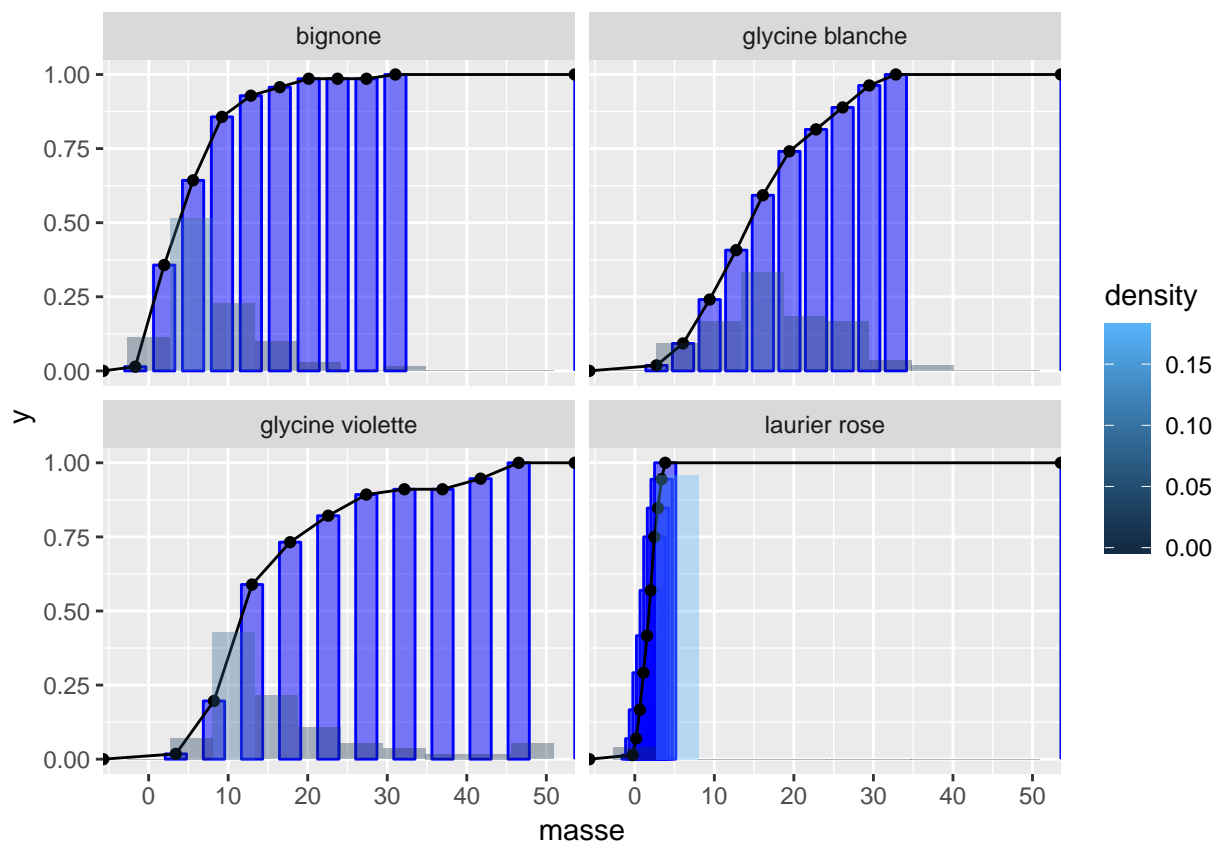
```
## Warning: Ignoring unknown aesthetics: width
```

```
## Warning: Ignoring unknown parameters: fill
```



```r
pdf("figure320fggplot.pdf")
print(g+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("bar"),fill="grey50", aes(x=
  masse-5.355556/2,width=5.355556),alpha=.5,colour="black")+stat_ecdf(n=
  nclass.Sturges(Mesures$masse)+1,geom=c("line"),fill="grey50",aes(x=masse-5.355556/2,
  y=..y..))+stat_ecdf(n=nclass.Sturges(Mesures$masse)+1,geom=c("point"),
  fill="black",aes(x=masse-5.355556/2,y=..y..))+geom_histogram(aes(y=5.355556*..density..,
  fill=..density..),binwidth=diff(range(Mesures$masse))/nclass.Sturges(Mesures$masse),
  alpha=.35,boundary = min(Mesures5$masse))+scale_fill_gradient(low="white", high="black"))
```

```
## Warning: Ignoring unknown aesthetics: width
```

```
## Warning: Ignoring unknown parameters: fill
```

```
dev.off()
```

```
## pdf
##   2
```
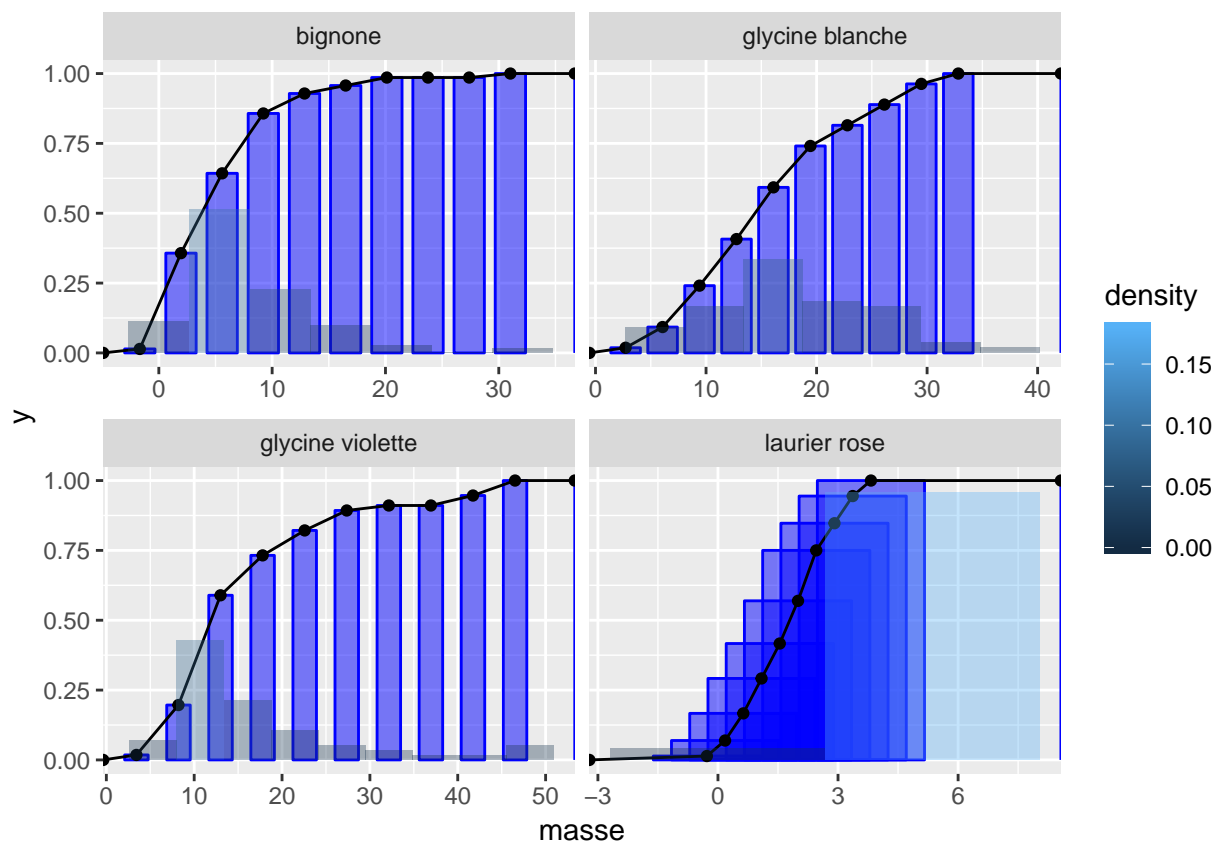
```
#Par groupe
g+stat_ecdf(n=9+1,geom=c("bar"),fill="blue",aes(x=masse-5.355556/2,width=5.355556/2),
alpha=.5,colour="blue",binwidth=5.355556)+stat_ecdf(n=9+1,geom=c("line"),fill="blue",
  aes(x=masse-5.355556/2,y=..y..))+stat_ecdf(n=9+1,geom=c("point"),fill="blue",
  aes(x=masse-5.355556/2,y=..y..))+facet_wrap(~espece)+geom_histogram(aes(y=
  5.355556*..density..,fill=..density..),binwidth=5.355556,alpha=.35)
```

```
## Warning: Ignoring unknown parameters: binwidth
```

```
## Warning: Ignoring unknown aesthetics: width
```

```
## Warning: Ignoring unknown parameters: fill
```



```
pdf("figure320gggplot.pdf")
print(g+stat_ecdf(n=9+1,geom=c("bar"),fill="blue",aes(x=masse-5.355556/2,width=5.355556/2),
alpha=.5,colour="blue",binwidth=5.355556)+stat_ecdf(n=9+1,geom=c("line"),fill="blue",
aes(x=masse-5.355556/2,y=..y..))+stat_ecdf(n=9+1,geom=c("point"),fill="blue",
aes(x=masse-5.355556/2,y=..y..))+facet_wrap(~espece)+geom_histogram(aes(y=5.355556*..density..,
fill=..density..),binwidth=5.355556,alpha=.35))
```

```
## Warning: Ignoring unknown parameters: binwidth
```

```
## Warning: Ignoring unknown aesthetics: width
```

```
## Warning: Ignoring unknown parameters: fill
```

```
dev.off()
```

```
## pdf
##   2
```

```
g+stat_ecdf(n=9+1,geom=c("bar"),fill="blue",aes(x=masse-5.355556/2,width=5.355556/2),
  alpha=.5,colour="blue")+stat_ecdf(n=9+1,geom=c("line"),fill="blue",aes(x=masse-5.355556/2,
  y=..y..))+stat_ecdf(n=9+1,geom=c("point"),fill="blue",aes(x=masse-5.355556/2,y=..y..))+
  facet_wrap(~espece,scales="free_x")+geom_histogram(aes(y=5.355556*..density..,
  fill=..density..),binwidth=5.355556,alpha=.35)
```

```
## Warning: Ignoring unknown aesthetics: width
```

```
## Warning: Ignoring unknown parameters: fill
```



```
pdf("figure320hggplot.pdf")
print(g+stat_ecdf(n=9+1,geom=c("bar"),fill="blue",aes(x=masse-5.355556/2,width=5.355556/2),
  alpha=.5,colour="blue")+stat_ecdf(n=9+1,geom=c("line"),fill="blue",aes(x=masse-5.355556/2,
  y=..y..))+stat_ecdf(n=9+1,geom=c("point"),fill="blue",aes(x=masse-5.355556/2,y=..y..))+
  facet_wrap(~espece,scales="free_x")+geom_histogram(aes(y=5.355556*..density..,
  fill=..density..),binwidth=5.355556,alpha=.35))
```

```
## Warning: Ignoring unknown aesthetics: width
```

```
## Warning: Ignoring unknown parameters: fill
```

```
dev.off()
```

```
## pdf
##   2
```
```
#page 137
boxplot(Mesures$masse)
title("Boîte à moustaches de la variable masse")
```

Boîte à moustaches de la variable masse
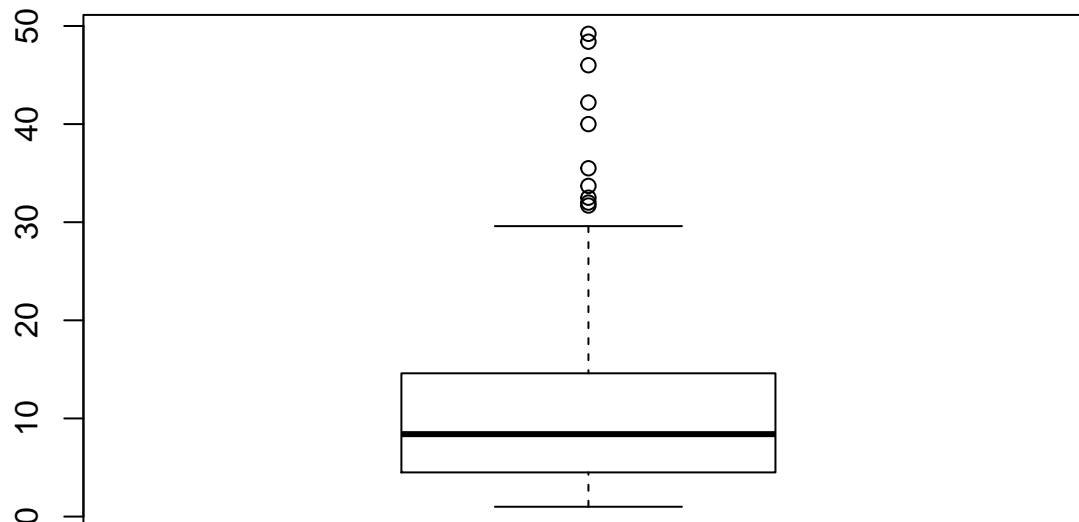

```
pdf("figure321.pdf")
boxplot(Mesures$masse)
title("Boîte à moustaches de la variable masse")
dev.off()
```
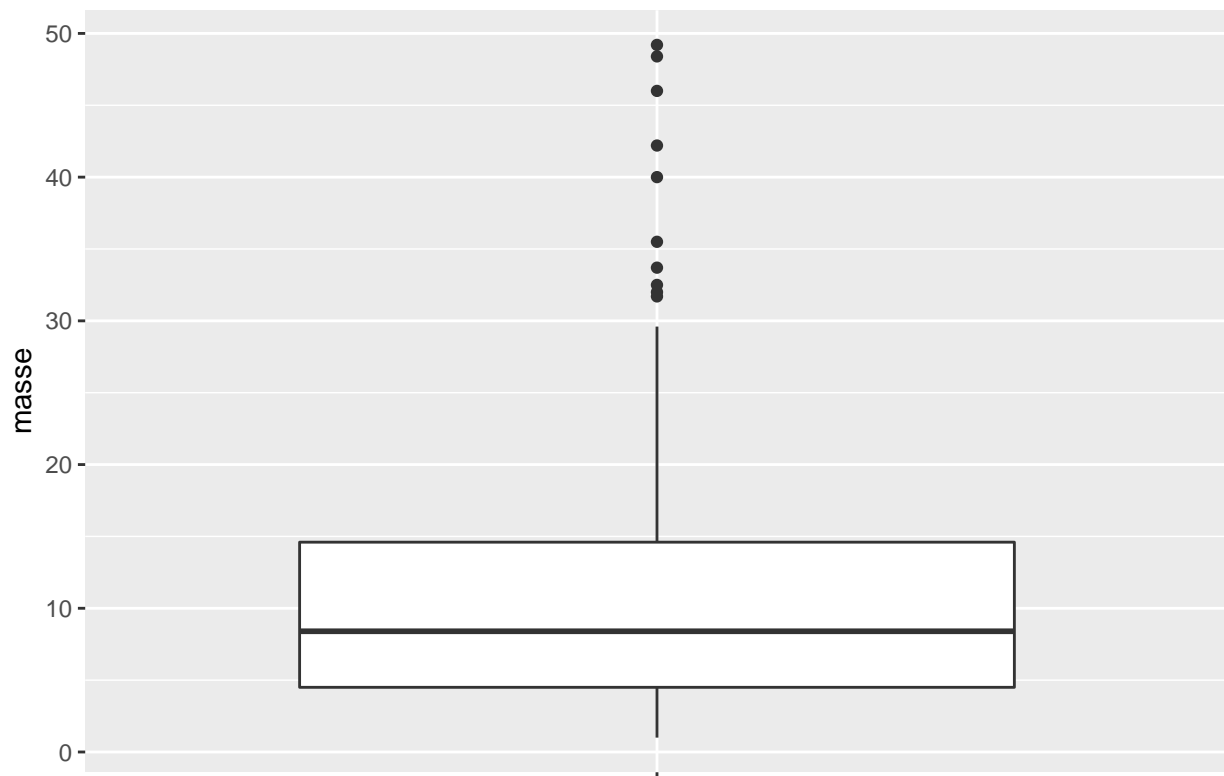
```
## pdf
##   2
```
```
#En plus ggplot
ggplot(Mesures, aes(x="",y=masse)) + geom_boxplot()
```
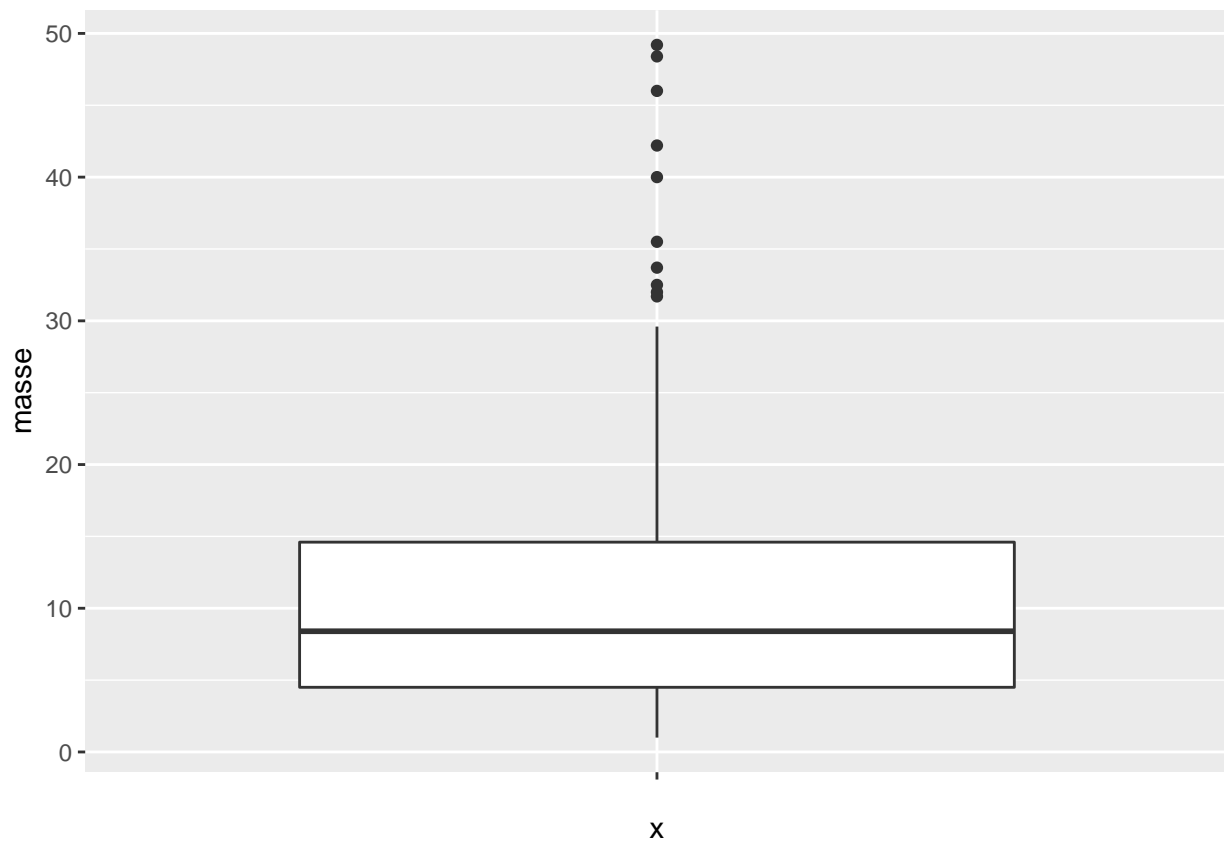
```r
pdf("figure321ggplot.pdf")
print(ggplot(Mesures, aes(x="",y=masse)) + geom_boxplot())
dev.off()
```
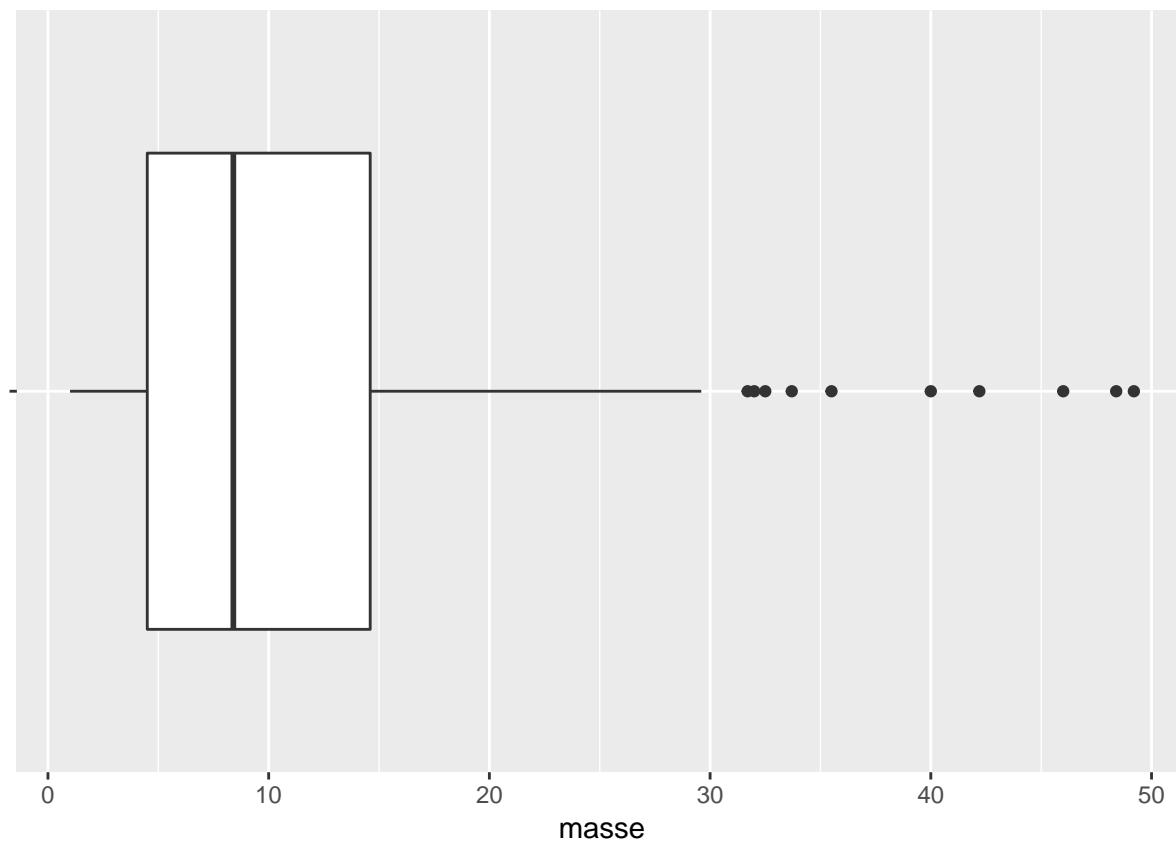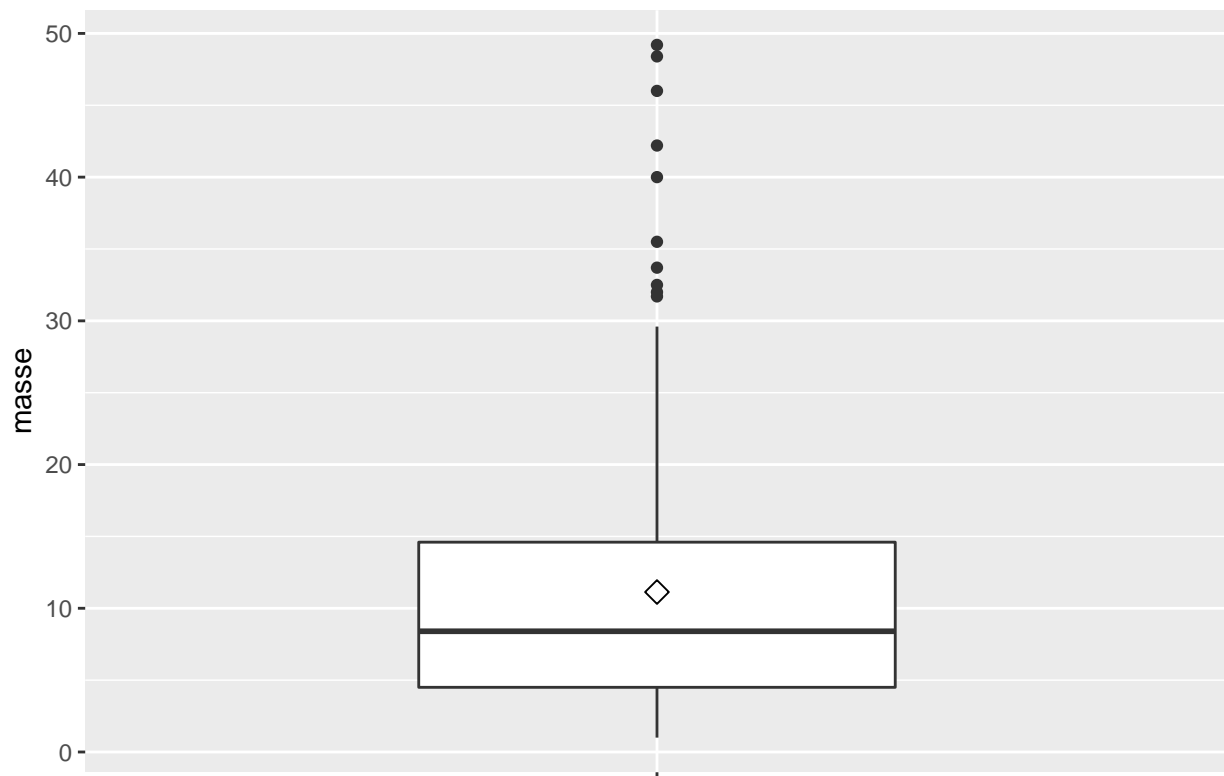
```
## pdf
##   2
```

```r
#remove label axe x
ggplot(Mesures, aes(x="",y=masse)) + geom_boxplot() + xlab("")
```

```
pdf("figure321aggplot.pdf")
print(ggplot(Mesures, aes(x="",y=masse)) + geom_boxplot() + xlab(""))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x="",y=masse)) + geom_boxplot() + coord_flip() + xlab("")
```

```
pdf("figure321bggplot.pdf")
print(ggplot(Mesures, aes(x="",y=masse)) + geom_boxplot() + coord_flip() +
  xlab(""))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x="", y=masse)) + geom_boxplot(width=.5) +
  stat_summary(fun.y="mean", geom="point", shape=23, size=3, fill="white") +
  xlab("")
```

```
pdf("figure321cggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_boxplot(width=.5) +
  stat_summary(fun.y="mean", geom="point", shape=23, size=3, fill="white") +
  xlab(""))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x="", y=masse)) + geom_violin() + geom_boxplot(width=.1,
  fill="black") + stat_summary(fun.y=mean, geom="point", fill="white", shape=21, size=2.5)
```
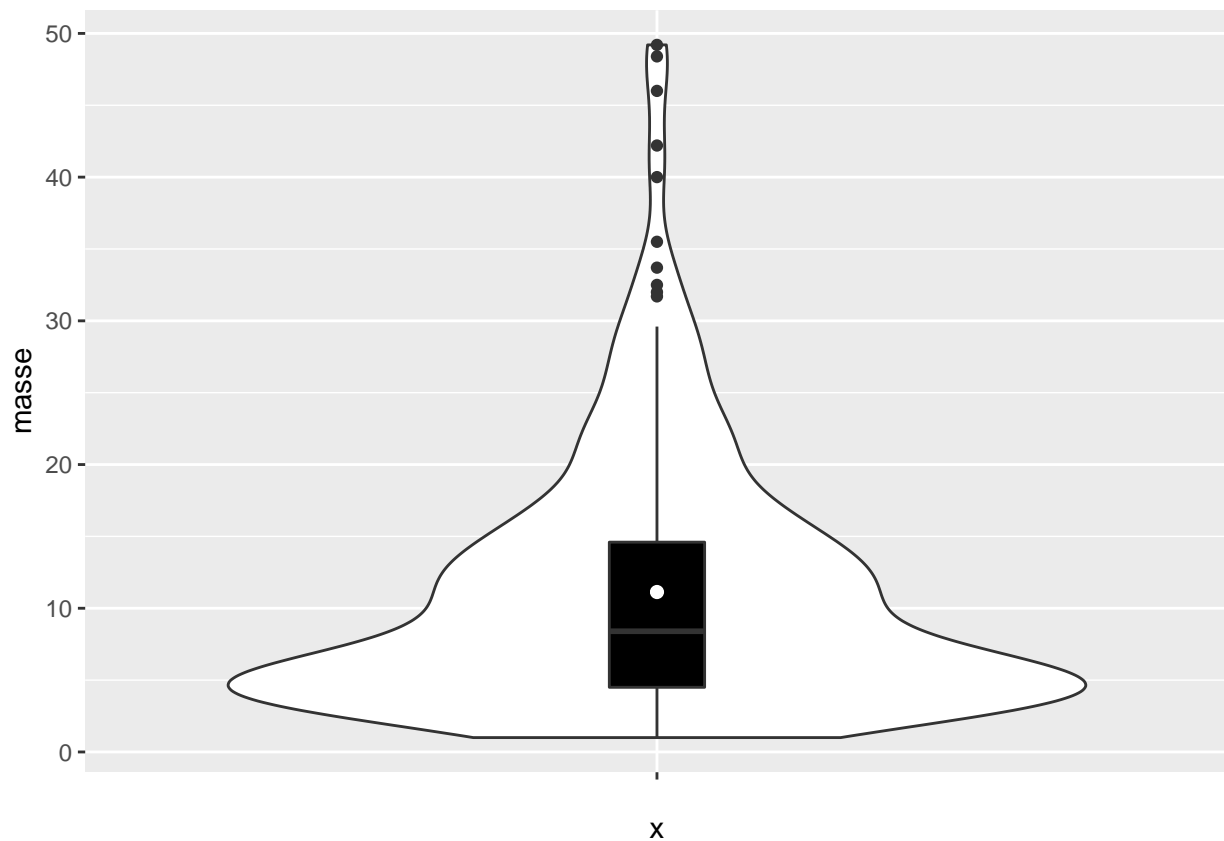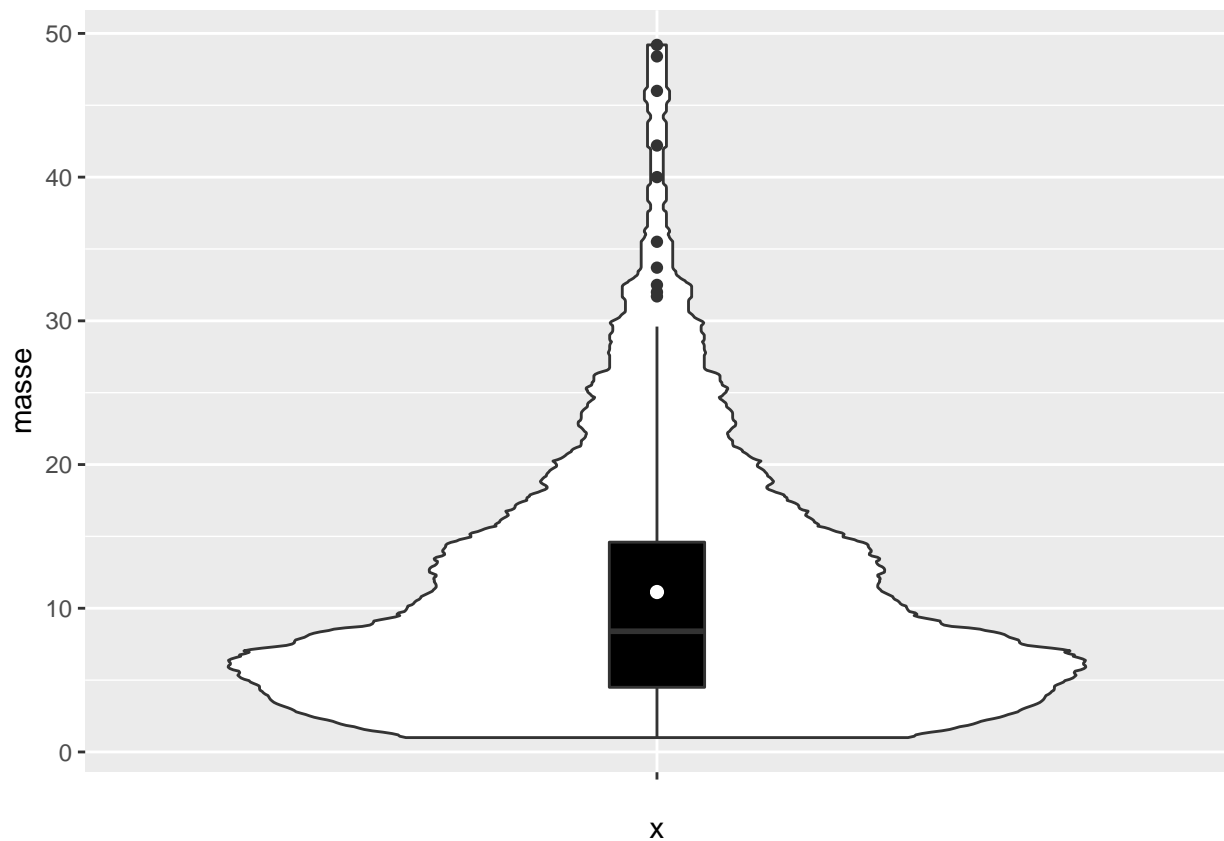
```
pdf("figure321dggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_violin() +
  geom_boxplot(width=.1, fill="black") + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5))
dev.off()
```

```
## pdf
##   2
```

```
#Without extreme values
ggplot(Mesures, aes(x="", y=masse)) + geom_violin() + geom_boxplot(width=.1,
  fill="black", outlier.colour=NA) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)
```
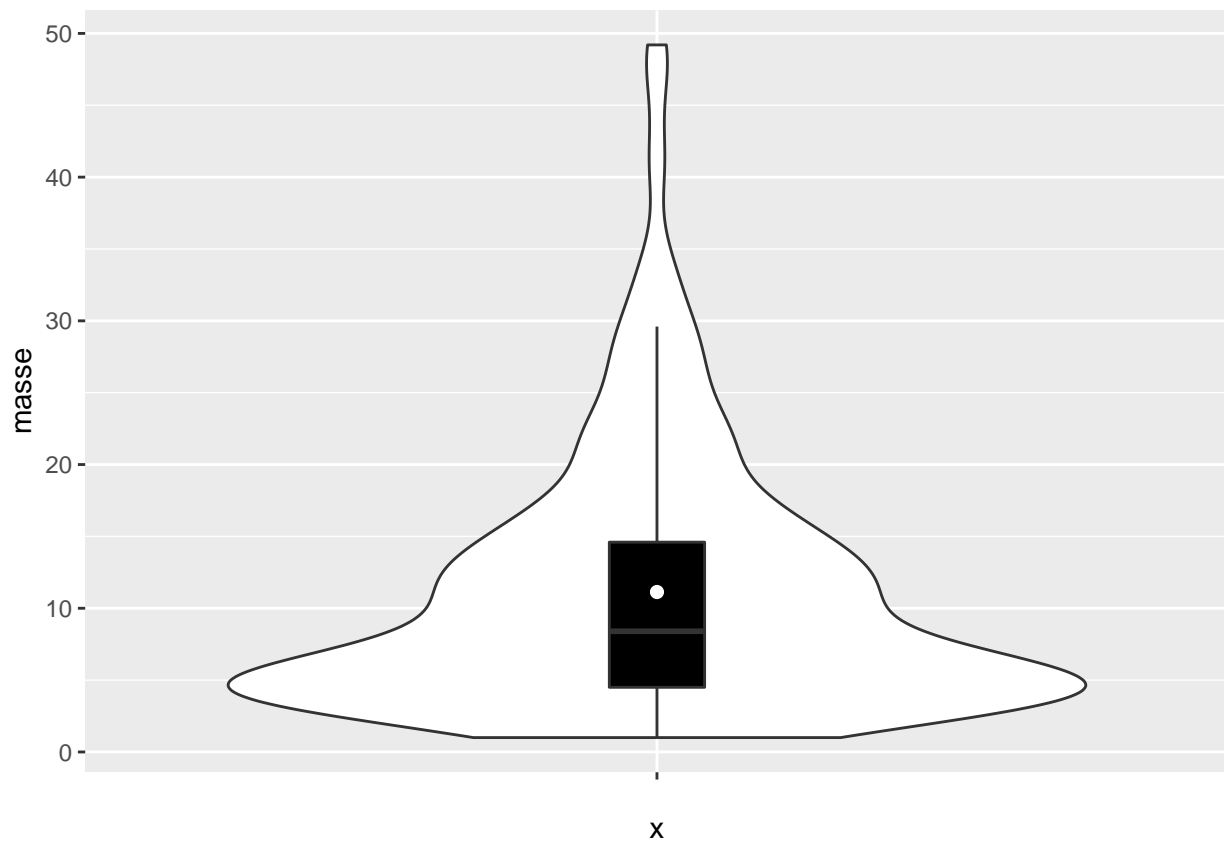
```
pdf("figure321eggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_violin() +
  geom_boxplot(width=.1, fill="black", outlier.colour=NA) +
  stat_summary(fun.y=mean, geom="point", fill="white", shape=21, size=2.5))
dev.off()
```

```
## pdf
##   2
```

```
#Gaussian kernel is the default and very (too) smooth for a finite population
ggplot(Mesures, aes(x="", y=masse)) + geom_violin(kernel="rectangular") +
  geom_boxplot(width=.1, fill="black") + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)
```

```r
pdf("figure321fggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_violin(kernel="rectangular") +
  geom_boxplot(width=.1, fill="black") + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5))
dev.off()
```

```
## pdf
##   2
```

```r
#Without extreme values
ggplot(Mesures, aes(x="", y=masse)) + geom_violin(kernel="rectangular") +
  geom_boxplot(width=.1, fill="black", outlier.colour=NA) +
  stat_summary(fun.y=mean, geom="point", fill="white", shape=21, size=2.5)
```
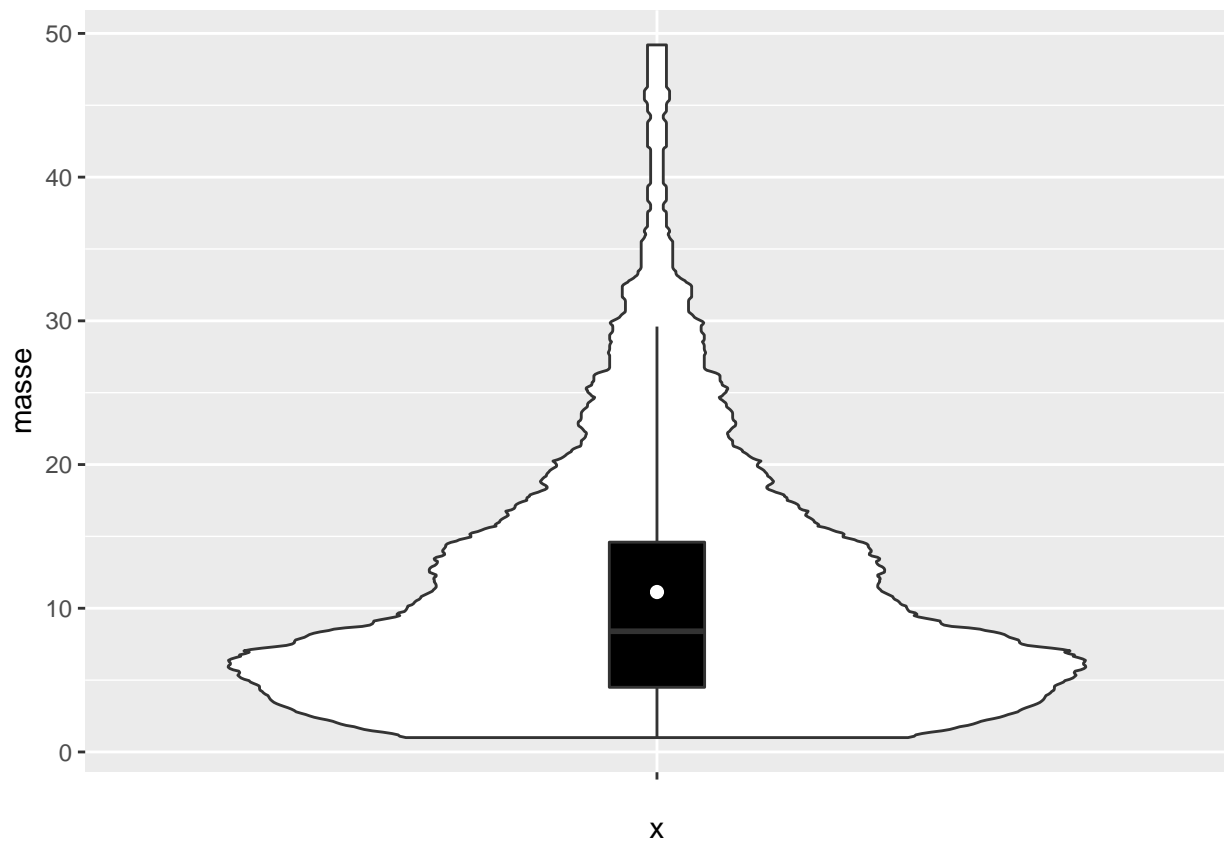
```
pdf("figure321gggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_violin(kernel="rectangular") +
        geom_boxplot(width=.1, fill="black", outlier.colour=NA) +
        stat_summary(fun.y=mean, geom="point", fill="white", shape=21, size=2.5))
dev.off()
```

```
## pdf
##   2
```
```
#page 138
boxplot.stats(Mesures$masse)
```

```
## $stats
## [1]   1.0   4.5   8.4 14.6 29.6
##
## $n
## [1] 252
##
## $conf
## [1] 7.39 9.41
##
## $out
##  [1] 32.0 35.5 32.5 40.0 49.2 46.0 42.2 48.4 31.7 33.7
```
```
boxplot(Mesures$masse~Mesures$espece)
```
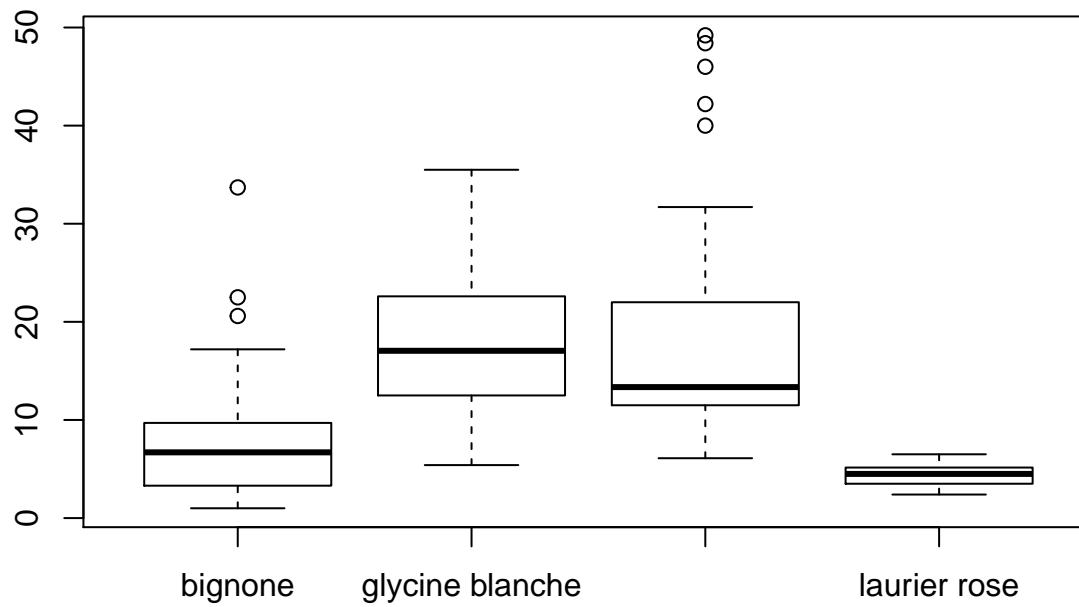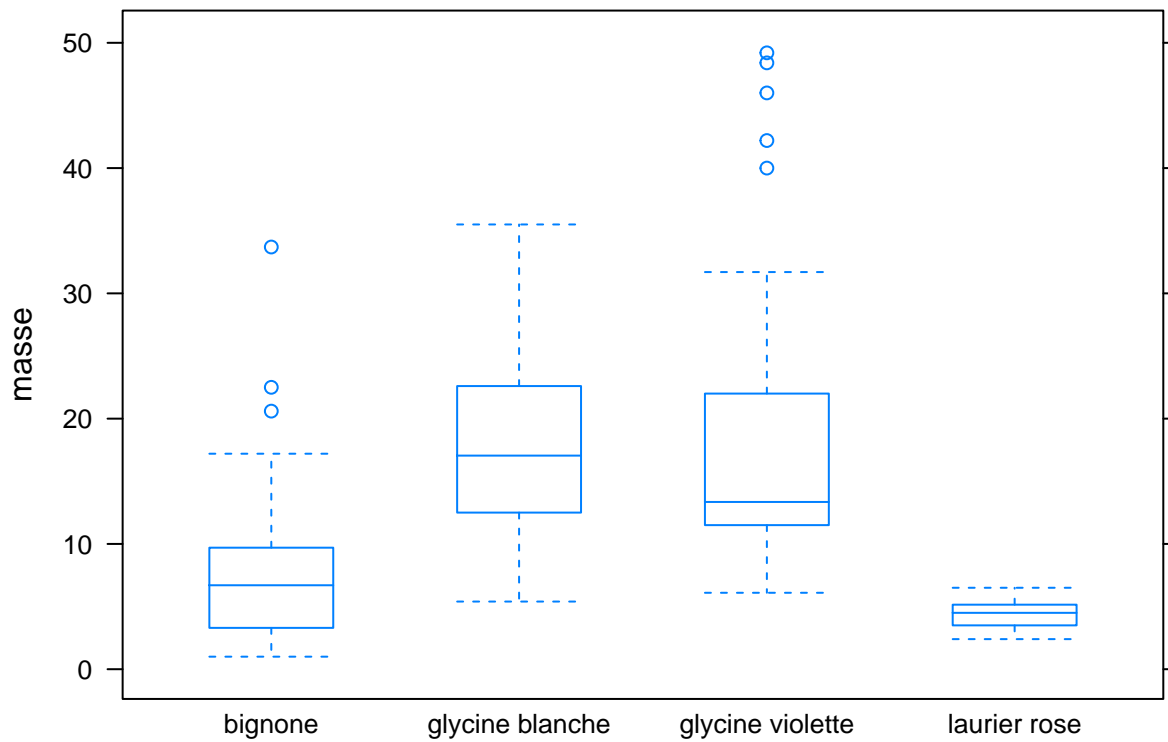
```r
pdf("figure322.pdf")
boxplot(Mesures$masse~Mesures$espece)
dev.off()
```
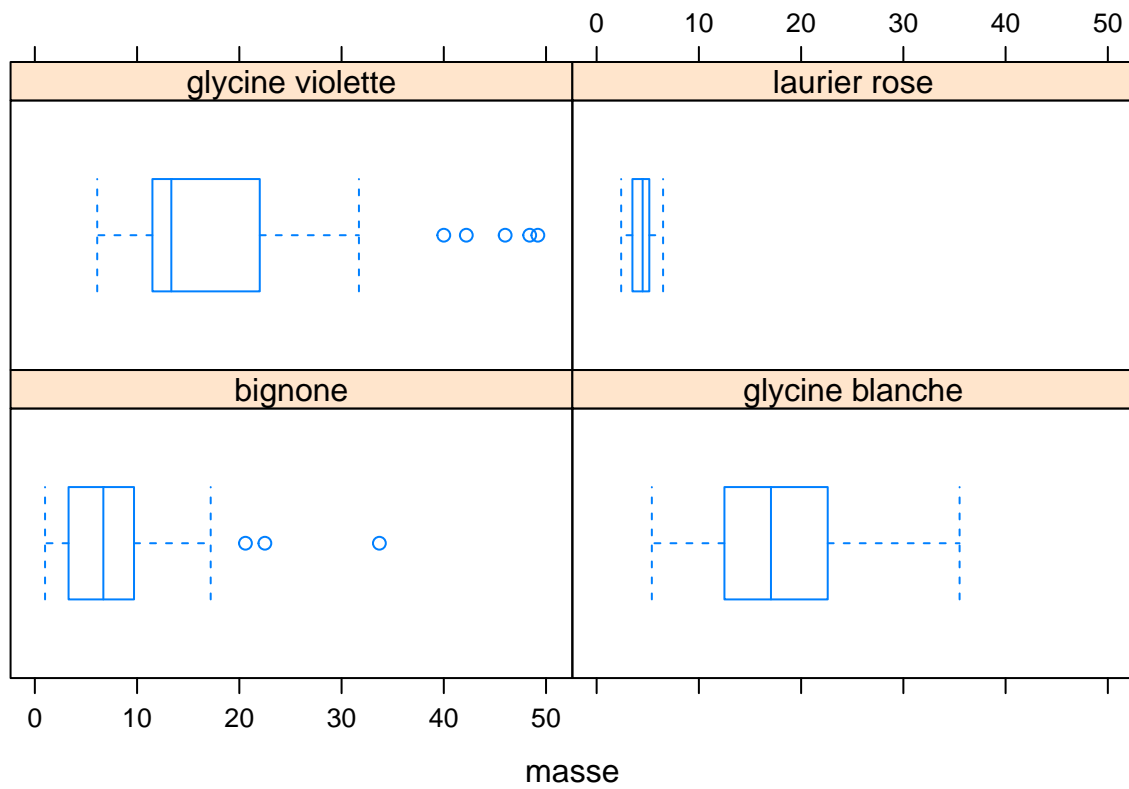
```
## pdf
##   2
```

```r
#page 139
pdf("figure322color.pdf")
boxplot(Mesures$masse~Mesures$espece,col=rainbow(4))
dev.off()
```

```
## pdf
##   2
```

```r
#En plus lattice par groupe
bwplot(masse~espece,data=Mesures,pch="|")
```
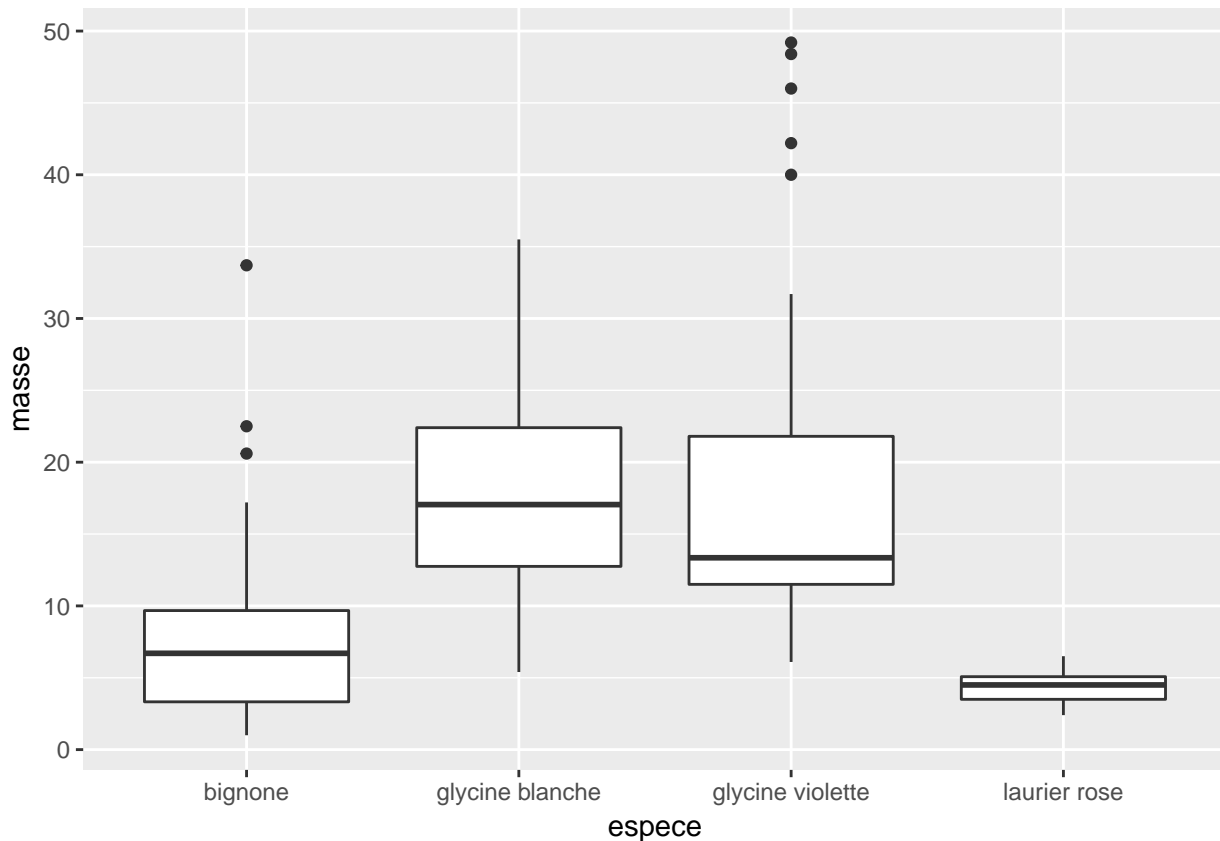
```
bwplot(~masse|espece,data=Mesures,pch="|")
```



```
pdf("figure322lattice.pdf")
bwplot(masse~espece,data=Mesures,pch="|")
dev.off()
```
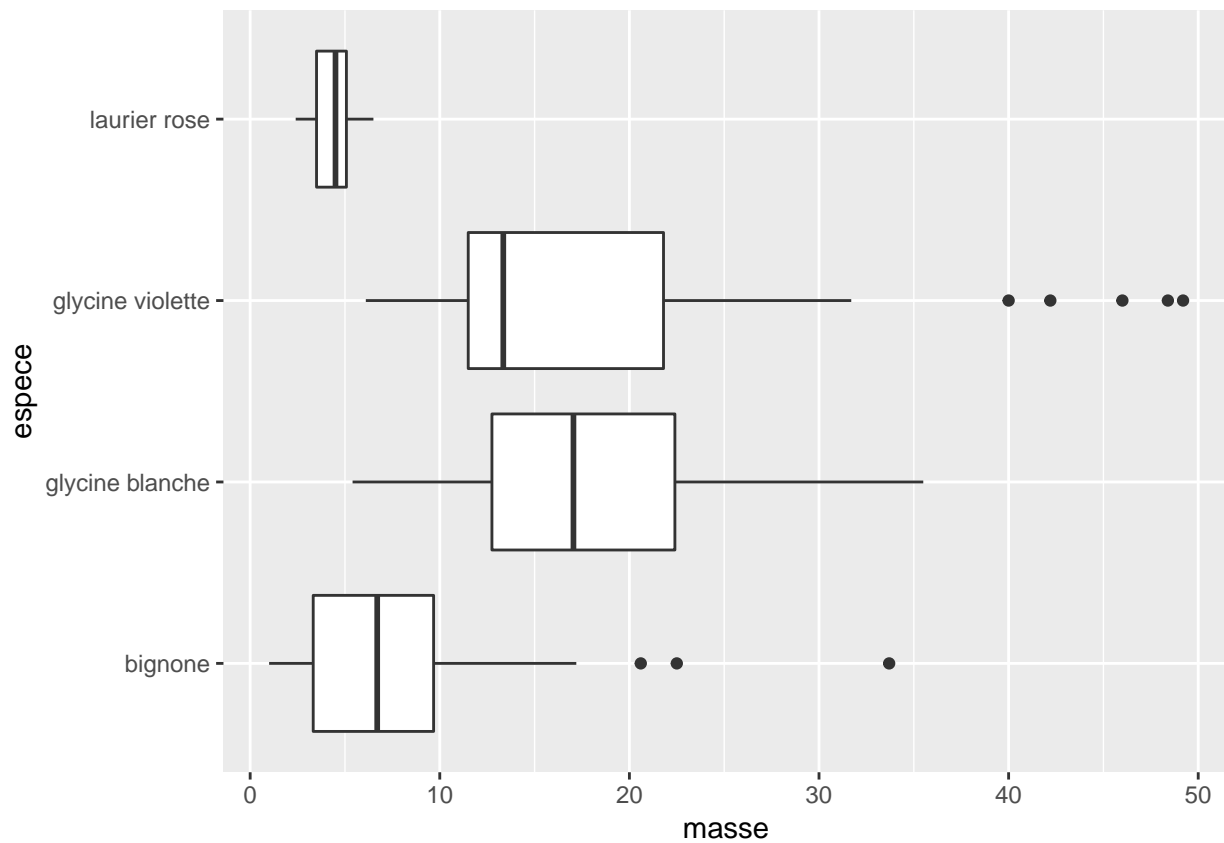
```
## pdf
##   2
```

```r
pdf("figure322latticegroupe.pdf")
bwplot(~masse|espece,data=Mesures,pch="|")
dev.off()
```

```
## pdf
##   2
```

```r
#En plus ggplot par groupe
ggplot(Mesures, aes(x=espece,y=masse)) + geom_boxplot()
```



```r
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x=espece,y=masse)) + geom_boxplot())
dev.off()
```
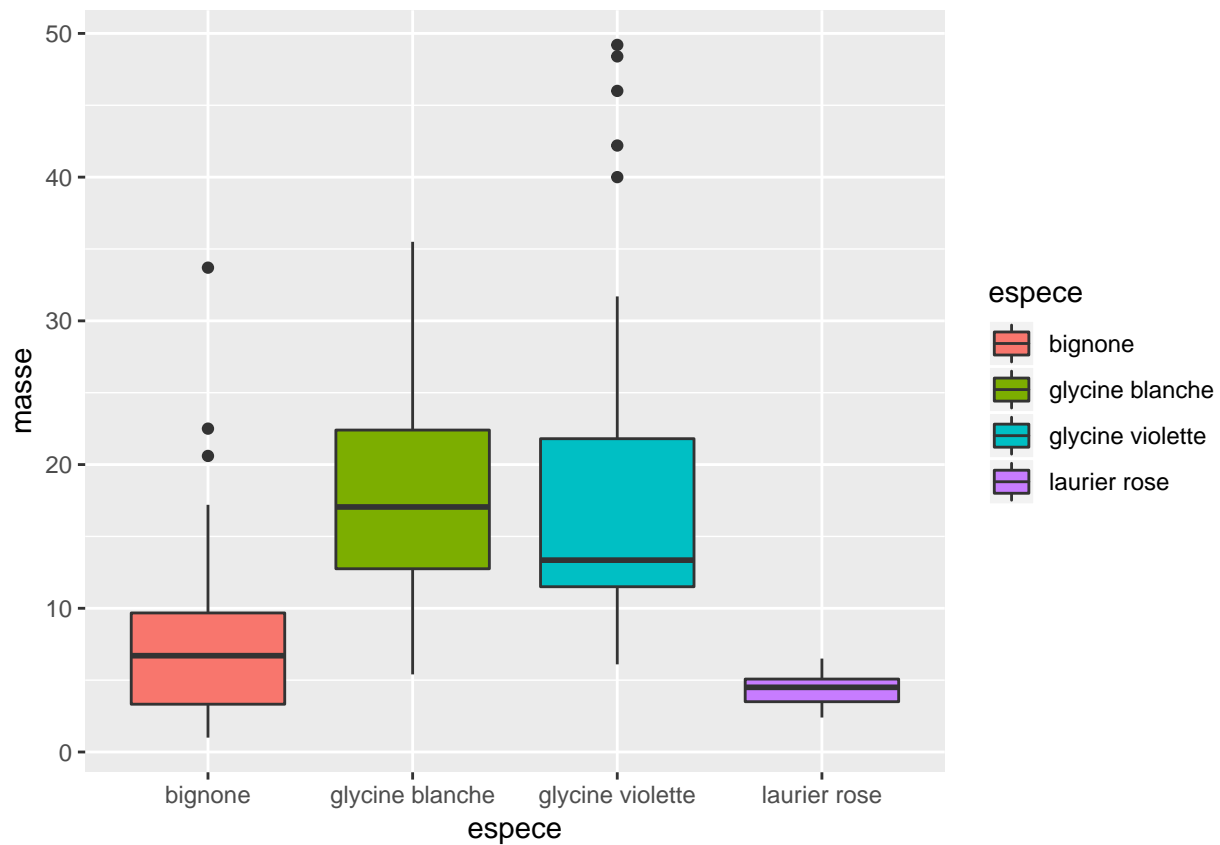
```
## pdf
##   2
```

```r
ggplot(Mesures, aes(x=espece,y=masse)) + geom_boxplot() + coord_flip()
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x=espece,y=masse)) + geom_boxplot() + coord_flip())
dev.off()
```
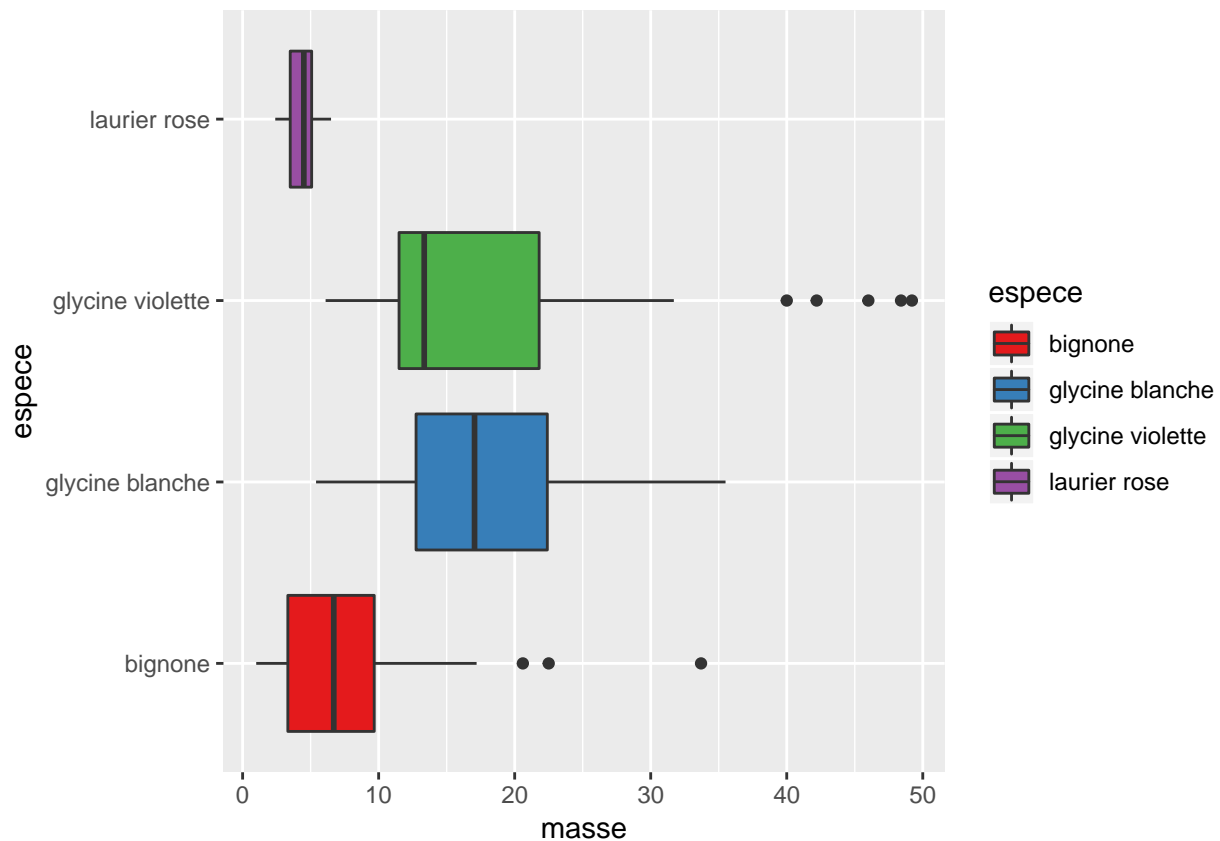
```
## pdf
##   2
```

```
ggplot(Mesures, aes(x=espece,y=masse,fill=espece)) + geom_boxplot()
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x=espece,y=masse,fill=espece)) + geom_boxplot())
dev.off()

## pdf
##   2

ggplot(Mesures, aes(x=espece,y=masse,fill=espece)) + geom_boxplot() +
  coord_flip() + scale_fill_brewer(palette="Set1")
```
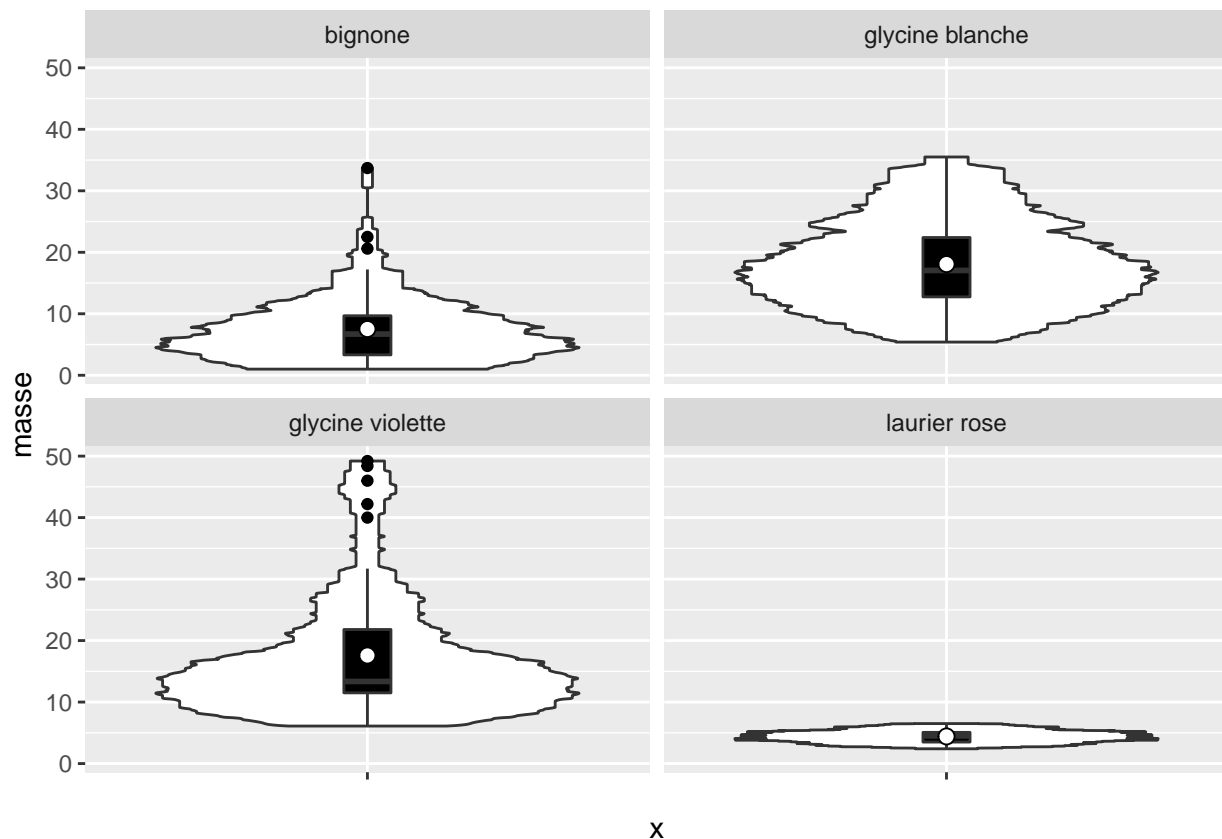
```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x=espece,y=masse,fill=espece)) + geom_boxplot() +
  coord_flip() + scale_fill_brewer(palette="Set1"))
dev.off()
```

```
## pdf
##   2
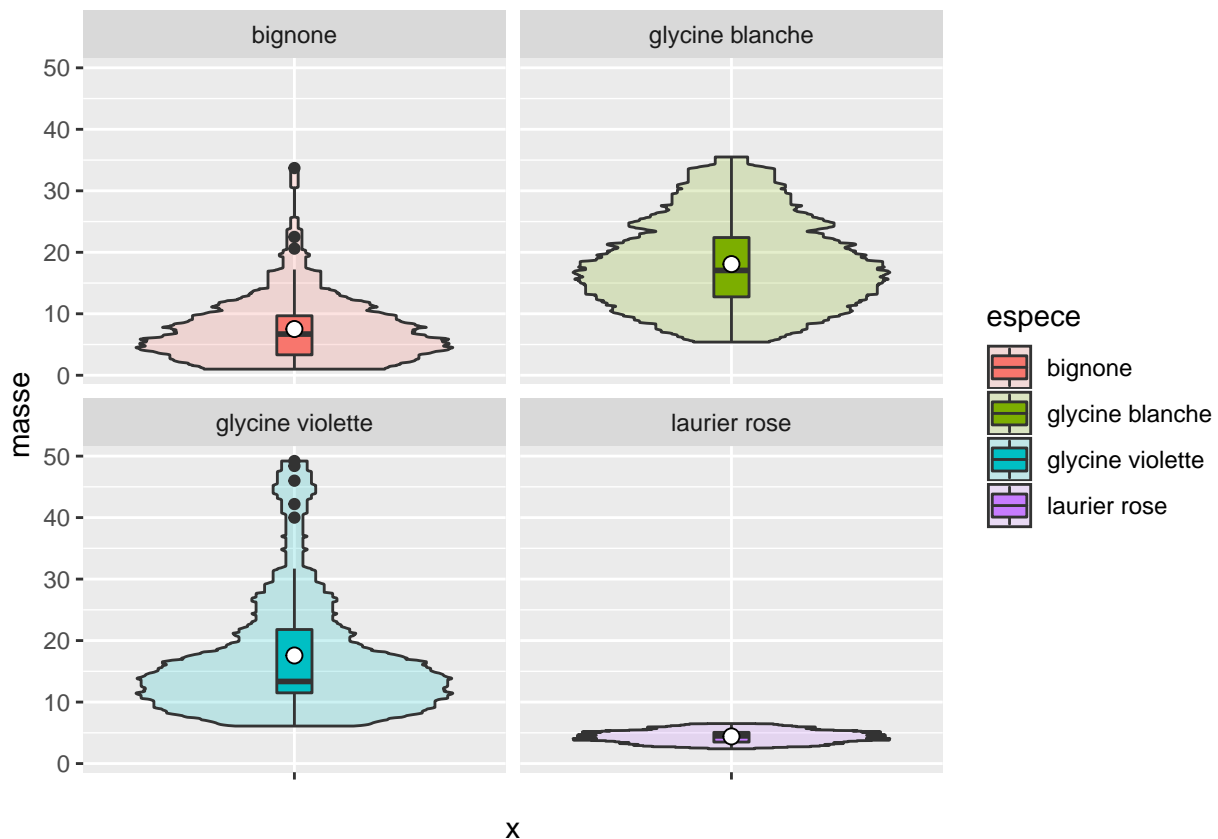```

```
ggplot(Mesures, aes(x="", y=masse)) + geom_violin(kernel="rectangular") +
  geom_boxplot(width=.1, fill="black", outlier.colour="black") +
  stat_summary(fun.y=mean, geom="point", fill="white", shape=21,
  size=2.5)+facet_wrap(~espece)
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_violin(kernel="rectangular") +
  geom_boxplot(width=.1, fill="black", outlier.colour="black") +
  stat_summary(fun.y=mean, geom="point", fill="white", shape=21,
  size=2.5)+facet_wrap(~espece))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece),kernel="rectangular",alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece),kernel="rectangular",alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece))
dev.off()
```
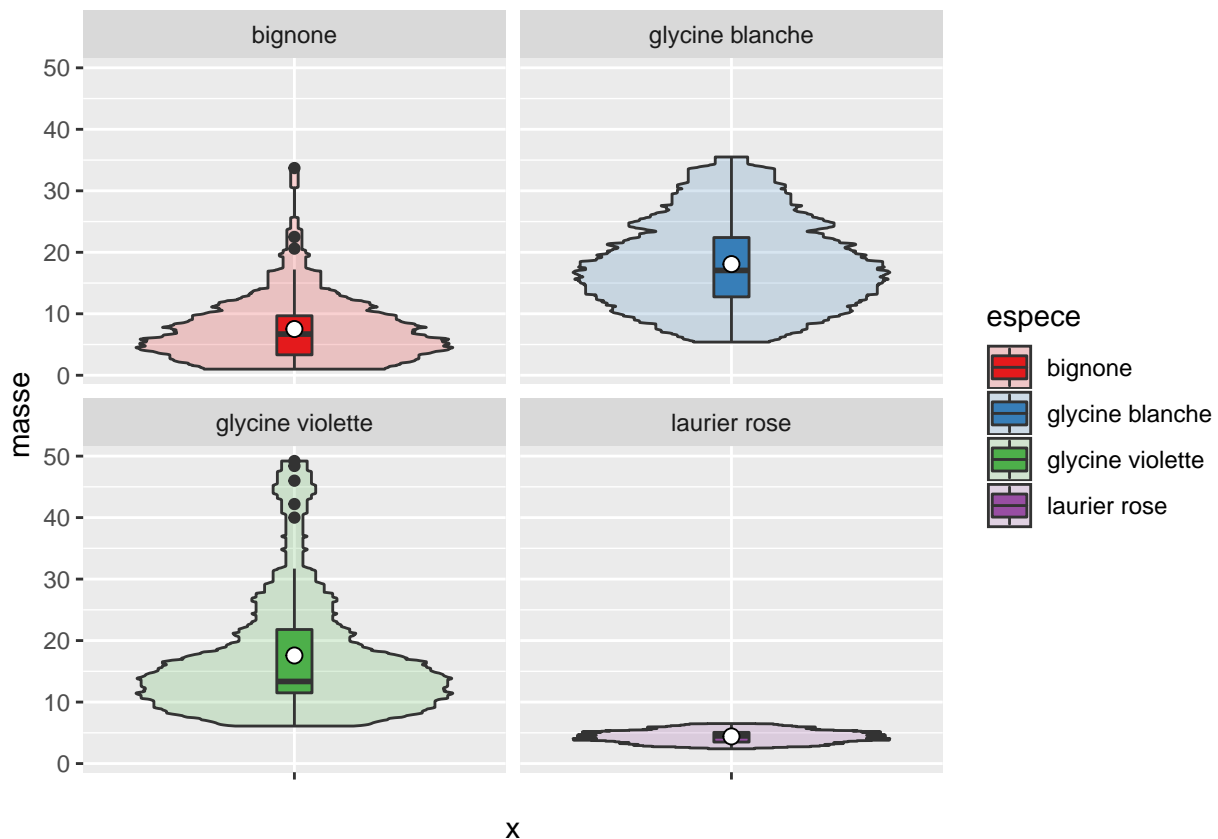
```
## pdf
##    2
```

```
ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece),kernel="rectangular",alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)+scale_fill_brewer(palette="Set1")
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece),kernel="rectangular",alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)+scale_fill_brewer(palette="Set1"))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece,kernel="rectangular"),alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)+scale_fill_brewer(palette="Set2")
```

```
## Warning: Ignoring unknown aesthetics: kernel
```
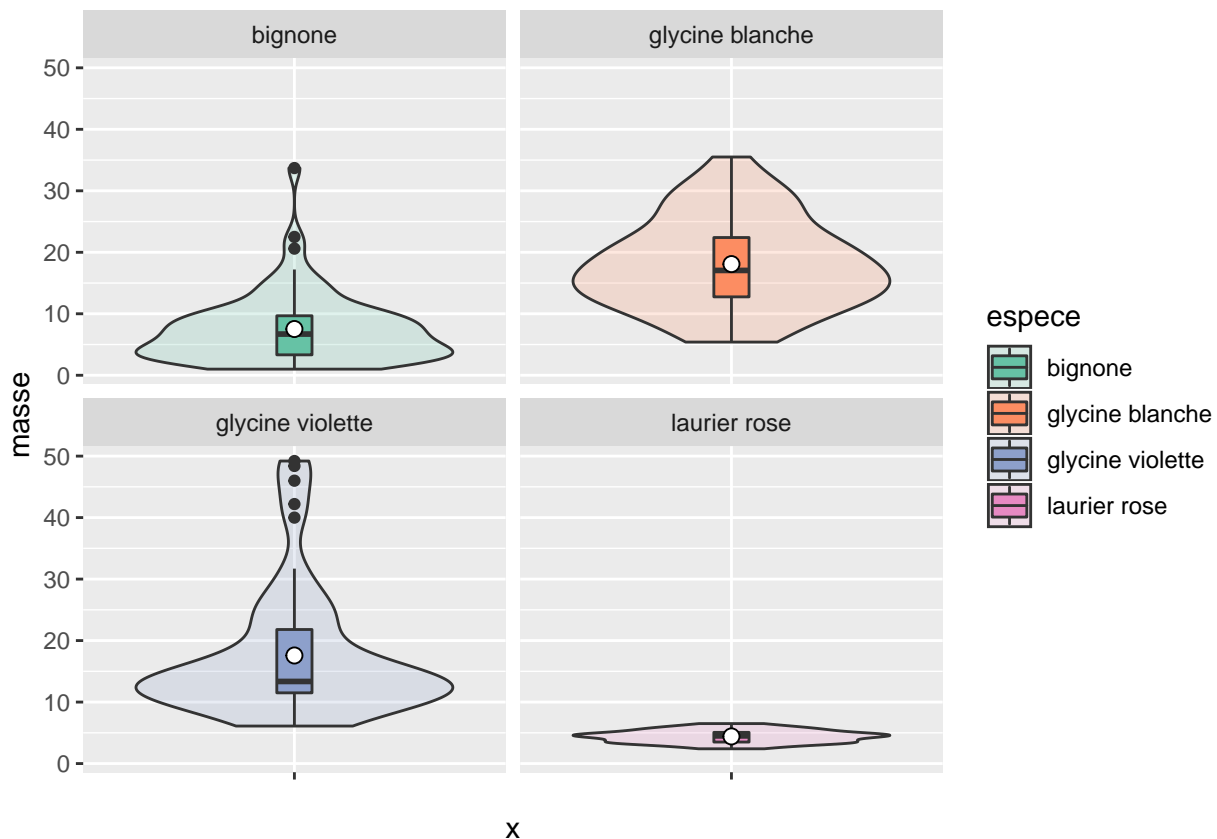
```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece,kernel="rectangular"),alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)+scale_fill_brewer(palette="Set2"))
```

```
## Warning: Ignoring unknown aesthetics: kernel
```

```
dev.off()
```

```
## pdf
##    2
```

```
ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece,kernel="rectangular"),alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)+scale_fill_brewer(palette="Set3")
```

```
## Warning: Ignoring unknown aesthetics: kernel
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) +
  geom_violin(aes(fill=espece,kernel="rectangular"),alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1) + stat_summary(fun.y=mean, geom="point",
  fill="white", shape=21, size=2.5)+facet_wrap(~espece)+scale_fill_brewer(palette="Set3"))
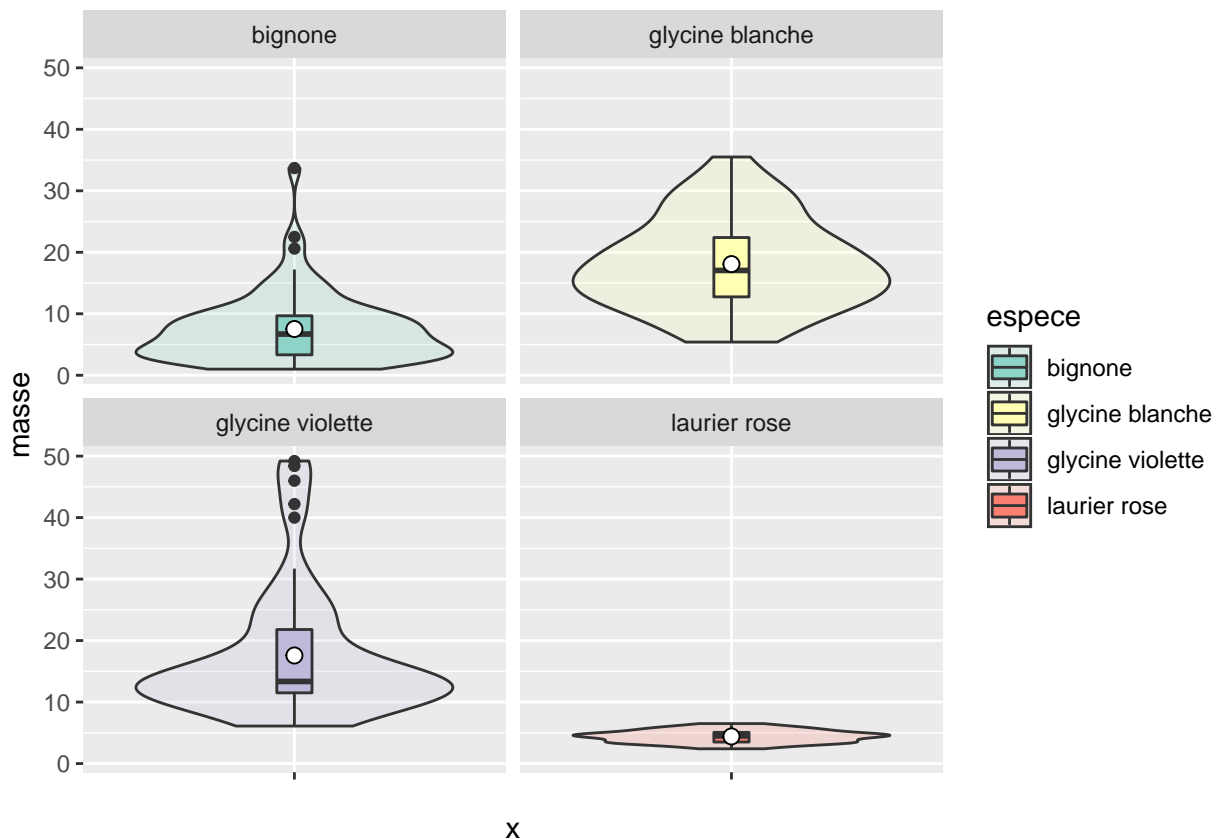```
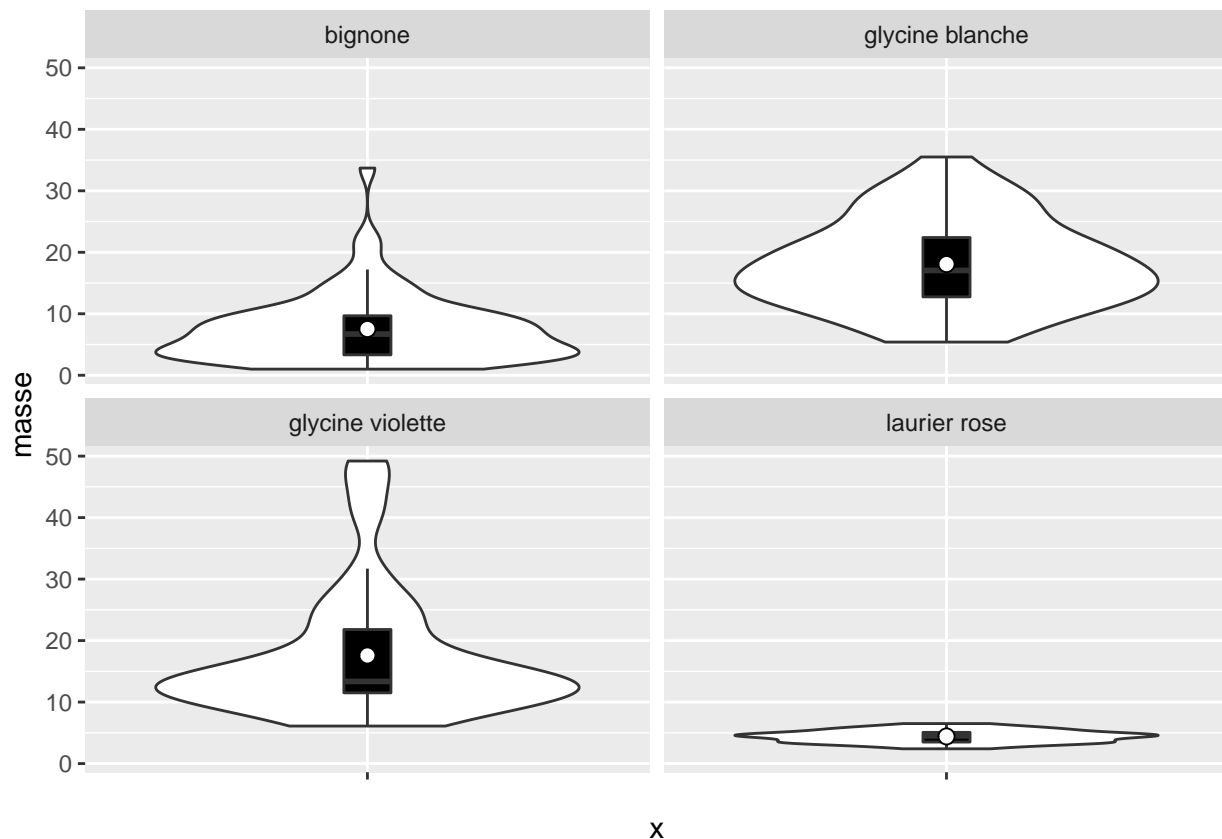
```
Warning: Ignoring unknown aesthetics: kernel
```

```
dev.off()
```

```
## pdf
##    2
```

```
#Without extreme values and with Gaussian kernel
ggplot(Mesures, aes(x="", y=masse)) + geom_violin() + geom_boxplot(width=.1,
 fill="black", outlier.colour=NA) + stat_summary(fun.y=mean, geom="point",
 fill="white", shape=21, size=2.5)+facet_wrap(~espece)
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) + geom_violin() +
        geom_boxplot(width=.1, fill="black", outlier.colour=NA) +
        stat_summary(fun.y=mean, geom="point", fill="white", shape=21,
                        size=2.5)+facet_wrap(~espece))
dev.off()
```

```
## pdf
##   2
```

```
ggplot(Mesures, aes(x="", y=masse)) + geom_violin(aes(fill=espece),alpha=.2) +
  geom_boxplot(aes(fill=espece),width=.1,outlier.color=NA) +
  stat_summary(fun.y=mean, geom="point", fill="white", shape=21,
                size=2.5)+facet_wrap(~espece)+ scale_fill_brewer(palette="Set3")
```

```
pdf("figure322ggplot.pdf")
print(ggplot(Mesures, aes(x="", y=masse)) +
        geom_violin(aes(fill=espece),alpha=.2) +
        geom_boxplot(aes(fill=espece),width=.1,outlier.color=NA) +
        stat_summary(fun.y=mean, geom="point", fill="white", shape=21,
                    size=2.5)+facet_wrap(~espece)+ scale_fill_brewer(palette="Set3"))
dev.off()
```

```
## pdf
##   2
```

```
#page 140
stem(Mesures$masse)
```

```
##
##   The decimal point is at the |
##
##    0 | 0455
##    2 | 1244566777799990222223333444444455566688899
##    4 | 001112334444555566777777788889990023333344555678888
##    6 | 0112233345667790112369
##    8 | 0267880002346677
##   10 | 1233667799993335555777
##   12 | 00024458899234555688
##   14 | 000223466025799
##   16 | 444668922338
##   18 | 02218
##   20 | 046614568
```

```
##   22 | 445669
##   24 | 152
##   26 | 01246
##   28 | 679026
##   30 | 7
##   32 | 057
##   34 | 5
##   36 |
##   38 |
##   40 | 0
##   42 | 2
##   44 |
##   46 | 0
##   48 | 42
```

```
#page 142
hist(Mesures$masse,ylab="Effectif",xlab="Masse",main="Histogramme des masses")
```

Histogramme des masses
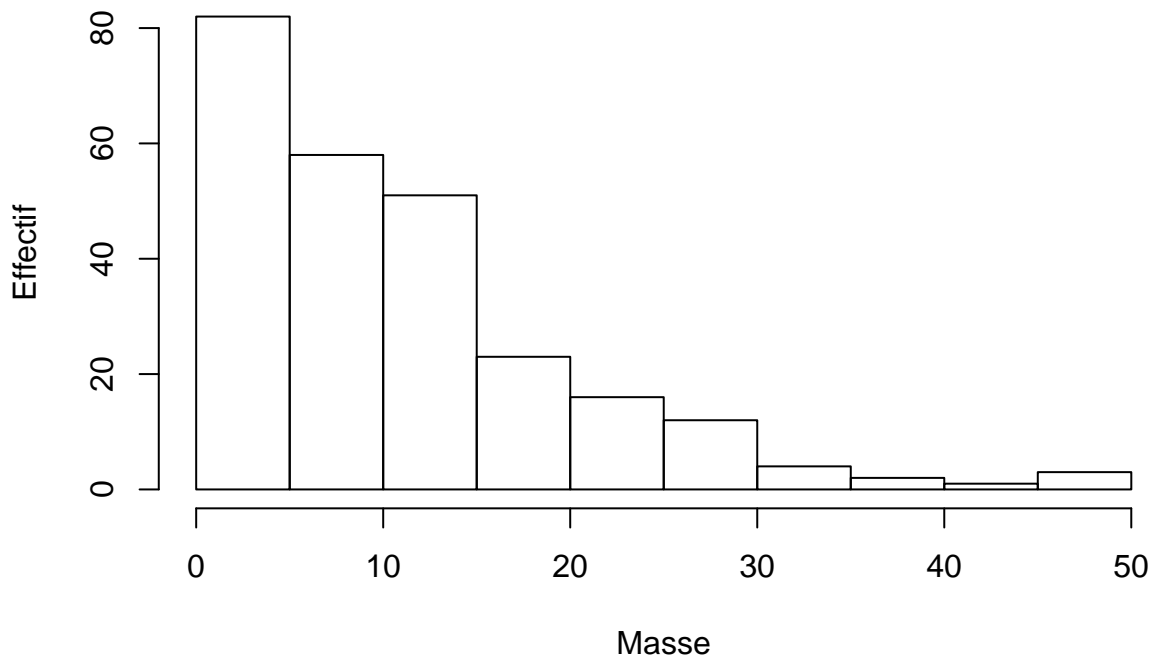

```
histo<-hist(Mesures$masse,plot=FALSE)
classes<-histo$breaks
classes
```

```
##  [1]  0  5 10 15 20 25 30 35 40 45 50
```

```
#page 143
effectifs<-histo$counts
effectifs
```

```
##  [1] 82 58 51 23 16 12  4  2  1  3
```

```
which(histo$density==max(histo$density))
```

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

```r
median(Mesures$masse)
```

```
## [1] 8.4
```

```r
quantile(Mesures$masse,0.5,type=6)
```

```
## 50%
## 8.4
```

```r
quantile(Mesures$masse,0.25,type=6)
```

```
## 25%
## 4.5
```

```r
quantile(Mesures$masse,0.75,type=6)
```

```
##  75%
## 14.6
```

```r
quantile(Mesures$masse,c(0.25,0.5,0.75),type=6)
```

```
##  25%  50%  75%
##  4.5  8.4 14.6
```

```r
quantile(Mesures$masse,type=6)
```

```
##   0%  25%  50%  75% 100%
##  1.0  4.5  8.4 14.6 49.2
```

```r
options(digits=7)
mean(Mesures$masse)
```

```
## [1] 11.13056
```

```r
summary(Mesures$masse)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.00    4.50    8.40   11.13   14.60   49.20
```

```r
max(Mesures$masse)-min(Mesures$masse)
```

```
## [1] 48.2
```

```r
diff(range(Mesures$masse))
```

```
## [1] 48.2
```

```r
IQR(Mesures$masse,type=6)
```

```
## [1] 10.1
```

```r
var(Mesures$masse)
```

```
## [1] 81.02811
```

```r
var(Mesures$masse)*length(Mesures$masse)/(length(Mesures$masse)-1)
```

```
## [1] 81.35093
```

```r
#page 150
sd(Mesures$masse)
```

```
## [1] 9.001561
```

```r
#page 151
mad(Mesures$masse,constant=1)
```

```
## [1] 4.55
```

```r
mad(Mesures$masse,quantile(Mesures$masse,type=1,probs=.5),constant=1)
```

```
## [1] 4.6
```

```r
median(abs(Mesures$masse-quantile(Mesures$masse,type=1,probs=.5)))
```

```
## [1] 4.6
```

```r
mad(Mesures$masse,constant=1,low=TRUE)
```

```
## [1] 4.5
```

```r
#page 152
quantile(abs(Mesures$masse-median(Mesures$masse)),type=1,probs=.5)
```

```
## 50%
## 4.5
```

```r
mad(Mesures$masse,quantile(Mesures$masse,type=1,probs=.5),constant=1,low=TRUE)
```

```
## [1] 4.6
```

```r
quantile(abs(Mesures$masse-quantile(Mesures$masse,type=1,probs=.5)),type=1,probs
        =.5)
```

```
## 50%
## 4.6
```

```r
#mads par rapport à une autre référence
mad(Mesures$masse,quantile(Mesures$masse,type=4,probs=.5),constant=1)
```

```
## [1] 4.6
```

```r
mad(Mesures$masse,quantile(Mesures$masse,type=6,probs=.5),constant=1)
```

```
## [1] 4.55
```

```r
mad(Mesures$masse,quantile(Mesures$masse,type=7,probs=.5),constant=1)
```

```
## [1] 4.55
```

```r
#Autre example de calculs à partir d'un petit échantillon
x <- c(1,2,3,5,7,8)
sort(abs(x - median(x)))
```

```
## [1] 1 1 2 3 3 4
```

```r
c(mad(x, constant = 1),
  mad(x, constant = 1, low = TRUE),
  mad(x, constant = 1, high = TRUE))
```

```
## [1] 2.5 2.0 3.0
```

```r
quantile(x,type=1,probs=.5)
```

```
## 50%
##   3
```

```r
quantile(x,type=2,probs=.5)
```

```
## 50%
##   4
```

```r
mad(x,constant=1,low = TRUE)
```

```
## [1] 2
```

```r
sort(abs(x-quantile(x,type=1,probs=.5)))
```

```
## [1] 0 1 2 2 4 5
```

```r
quantile(abs(x-quantile(x,type=1,probs=.5)),type=1,probs=.5)
```

```
## 50%
##   2
```

```r
library(BioStatR)
cvar(Mesures$masse)
```

```
## [1] 80.87253
```

```r
#page 154
# Asymétrie et aplatissement d'un échantillon
if(!("agricolae" %in%
    rownames(installed.packages())){install.packages("agricolae")}
library(agricolae)
skewness(Mesures$masse)
```

```
## [1] 1.639849
```

```r
kurtosis(Mesures$masse)
```

```
## [1] 3.080963
```

```r
#Pour retirer la bibliothèque agricolae de la mémoire de R avant de charger e1071
detach(package:agricolae)
if(!("e1071" %in% rownames(installed.packages())){install.packages("e1071")}
library(e1071)
# Asymétrie et aplatissement d'une série statistique (=population)
skewness(Mesures$masse,type=1)
```

```
## [1] 1.630072
```

```r
kurtosis(Mesures$masse,type=1)
```

```
## [1] 2.996456
```

```r
# Asymétrie et aplatissement d'un échantillon (comme agricolae)
skewness(Mesures$masse,type=2)
```

```
## [1] 1.639849
```

```r
kurtosis(Mesures$masse,type=2)
```

```
## [1] 3.080963
```

```
detach(package:e1071)

#Exercice 3.1
#page 164
#1)
Variete<-c(rep(1,4),rep(2,4),rep(3,4))
Variete
```

```
##  [1] 1 1 1 1 2 2 2 2 3 3 3 3
```

```
Jutosite<-c(4,6,3,5,7,8,7,6,8,6,5,6)
Jutosite
```

```
##  [1] 4 6 3 5 7 8 7 6 8 6 5 6
```

```
Pommes<-data.frame(Variete,Jutosite)
Pommes
```

```
##    Variete Jutosite
## 1        1        4
## 2        1        6
## 3        1        3
## 4        1        5
## 5        2        7
## 6        2        8
## 7        2        7
## 8        2        6
## 9        3        8
## 10       3        6
## 11       3        5
## 12       3        6
```

```
#page 165
#2)
str(Pommes)
```

```
## 'data.frame':    12 obs. of  2 variables:
##  $ Variete : num  1 1 1 1 2 2 2 2 3 3 ...
##  $ Jutosite: num  4 6 3 5 7 8 7 6 8 6 ...
```

```
class(Pommes$Variete)
```

```
## [1] "numeric"
```

```
#3)
Variete<-factor(Variete)
Pommes<-data.frame(Variete,Jutosite)
rm(Variete)
rm(Jutosite)
str(Pommes)
```

```
## 'data.frame':    12 obs. of  2 variables:
##  $ Variete : Factor w/ 3 levels "1","2","3": 1 1 1 1 2 2 2 2 3 3 ...
##  $ Jutosite: num  4 6 3 5 7 8 7 6 8 6 ...
```

```
#page 166
class(Pommes$Variete)
```

```
## [1] "factor"
```

```
Pommes

##    Variete Jutosite
## 1        1        4
## 2        1        6
## 3        1        3
## 4        1        5
## 5        2        7
## 6        2        8
## 7        2        7
## 8        2        6
## 9        3        8
## 10       3        6
## 11       3        5
## 12       3        6
```

```
#4)
Variete<-factor(c(rep(1,4),rep(2,4),rep(3,4)))
Jutosite<-c(4,6,3,5,7,8,7,6,8,6,5,6)
Pommes<-data.frame(Variete,Jutosite)
str(Pommes)
```

```
## 'data.frame':    12 obs. of  2 variables:
##  $ Variete : Factor w/ 3 levels "1","2","3": 1 1 1 1 2 2 2 2 3 3 ...
##  $ Jutosite: num  4 6 3 5 7 8 7 6 8 6 ...
```

```
#5)
Variete<-factor(c(rep(1,4),rep(2,4),rep(3,4)),labels=c("V1","V2","V3"))
Jutosite<-c(4,6,3,5,7,8,7,6,8,6,5,6)
Pommes<-data.frame(Variete,Jutosite)
Pommes
```

```
##    Variete Jutosite
## 1       V1        4
## 2       V1        6
## 3       V1        3
## 4       V1        5
## 5       V2        7
## 6       V2        8
## 7       V2        7
## 8       V2        6
## 9       V3        8
## 10      V3        6
## 11      V3        5
## 12      V3        6
```

```
#page 167
str(Pommes)
```

```
## 'data.frame':    12 obs. of  2 variables:
##  $ Variete : Factor w/ 3 levels "V1","V2","V3": 1 1 1 1 2 2 2 2 3 3 ...
##  $ Jutosite: num  4 6 3 5 7 8 7 6 8 6 ...
```

```
#6)
Variete<-as.factor(c(rep(1,4),rep(2,4),rep(3,4)))
Jutosite<-c(4,6,3,5,7,8,7,6,8,6,5,6)
Pommes<-data.frame(Variete,Jutosite)
```

```
Pommes
```

```
##    Variete Jutosite
## 1        1        4
## 2        1        6
## 3        1        3
## 4        1        5
## 5        2        7
## 6        2        8
## 7        2        7
## 8        2        6
## 9        3        8
## 10       3        6
## 11       3        5
## 12       3        6
```

```
str(Pommes)
```

```
## 'data.frame':    12 obs. of  2 variables:
##  $ Variete : Factor w/ 3 levels "1","2","3": 1 1 1 1 2 2 2 2 3 3 ...
##  $ Jutosite: num  4 6 3 5 7 8 7 6 8 6 ...
```

```
#page 168
#7)
tapply(Jutosite,Variete,mean)
```

```
##    1    2    3
## 4.50 7.00 6.25
```

```
tapply(Jutosite,Variete,sd)
```

```
##         1         2         3
## 1.2909944 0.8164966 1.2583057
```

```
tapply(Jutosite,Variete,quantile,type=6)
```

```
## $`1`
##   0%  25%  50%  75% 100%
## 3.00 3.25 4.50 5.75 6.00
##
## $`2`
##   0%  25%  50%  75% 100%
## 6.00 6.25 7.00 7.75 8.00
##
## $`3`
##   0%  25%  50%  75% 100%
## 5.00 5.25 6.00 7.50 8.00
```

```
tapply(Jutosite,Variete,summary)
```

```
## $`1`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    3.00    3.75    4.50    4.50    5.25    6.00
##
## $`2`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    6.00    6.75    7.00    7.00    7.25    8.00
##
```

```
## $`3`
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    5.00    5.75    6.00    6.25    6.50    8.00
```

```
#Exercice 3.2
#page 169
#1)
options(digits=3)
hist(Mesures$masse,breaks=5,plot=FALSE)
```

```
## $breaks
## [1]  0 10 20 30 40 50
##
## $counts
## [1] 140  74  28   6   4
##
## $density
## [1] 0.05556 0.02937 0.01111 0.00238 0.00159
##
## $mids
## [1]  5 15 25 35 45
##
## $xname
## [1] "Mesures$masse"
##
## $equidist
## [1] TRUE
##
## attr(,"class")
## [1] "histogram"
```

```
#page 170
#2)
hist(Mesures$masse,breaks=c(0,5,10,15,20,50),plot=FALSE)
```

```
## $breaks
## [1]  0  5 10 15 20 50
##
## $counts
## [1] 82 58 51 23 38
##
## $density
## [1] 0.06508 0.04603 0.04048 0.01825 0.00503
##
## $mids
## [1]  2.5  7.5 12.5 17.5 35.0
##
## $xname
## [1] "Mesures$masse"
##
## $equidist
## [1] FALSE
##
## attr(,"class")
## [1] "histogram"
```

```r
#page 171
#3)
brk <- c(0,5,10,15,20,50)
table(cut(Mesures$masse, brk))
```

```
##
##   (0,5]  (5,10] (10,15] (15,20] (20,50]
##      82      58      51      23      38
```

```r
head(cut(Mesures$masse,brk))
```

```
## [1] (20,50] (20,50] (20,50] (20,50] (20,50] (20,50]
## Levels: (0,5] (5,10] (10,15] (15,20] (20,50]
```

```r
data.frame(table(cut(Mesures$masse, brk)))
```

```
##      Var1 Freq
## 1   (0,5]   82
## 2  (5,10]   58
## 3 (10,15]   51
## 4 (15,20]   23
## 5 (20,50]   38
```

```r
#4)
if(!("Hmisc" %in% rownames(installed.packages()))){install.packages("Hmisc")}
library(Hmisc)
```

```
## Loading required package: survival
```

```
## Loading required package: Formula
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```r
brk <- c(0,5,10,15,20,50)
res <- cut2(Mesures$masse, brk)
head(res)
```

```
## [1] [20,50] [20,50] [20,50] [20,50] [20,50] [20,50]
## Levels: [ 0, 5) [ 5,10) [10,15) [15,20) [20,50]
```

```r
#page 172
table(res)
```

```
## res
## [ 0, 5) [ 5,10) [10,15) [15,20) [20,50]
##      80      60      50      23      39
```

```r
table(cut2(Mesures$masse, g=10))
```

```
##
## [ 1.0, 3.3) [ 3.3, 4.2) [ 4.2, 4.9) [ 4.9, 6.0) [ 6.0, 8.6) [ 8.6,11.3)
##          26          27          24          24          25          26
## [11.3,13.6) [13.6,16.9) [16.9,23.9) [23.9,49.2]
##          26          24          25          25
```

```r
table(cut2(Mesures$masse, m=50))
```

```
##
## [ 1.0, 4.2) [ 4.2, 6.0) [ 6.0,11.3) [11.3,16.9) [16.9,49.2]
##          53          48          51          50          50
```

```r
#Exercice 3.3
#1)
library(BioStatR)
head(Mesures$masse)
```

```
## [1] 28.6 20.6 29.2 32.0 24.5 29.0
```

```r
#head(masse)
#
#page 173
#2)
attach(Mesures)
head(masse)
```

```
## [1] 28.6 20.6 29.2 32.0 24.5 29.0
```

```r
detach(Mesures)
#head(masse)
#
#Exercice 3.4
options(digits=7)
#1)
head(Europe)
```

```
##          Pays Duree
## 1 Allemagne  41.7
## 2  Autriche  44.1
## 3  Belgique  41.0
## 4    Chypre  41.8
## 5  Danemark  40.5
## 6   Espagne  42.2
```

```r
#2)
str(Europe)
```

```
## 'data.frame':    25 obs. of  2 variables:
##  $ Pays : Factor w/ 25 levels "Allemagne","Autriche",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ Duree: num  41.7 44.1 41 41.8 40.5 42.2 41.5 40.5 41 44.1 ...
```

```r
#page 174
#3)
class(Europe)
```

```
## [1] "data.frame"
```

```r
dim(Europe)
```

```
## [1] 25  2
```

```r
#4)
summary(Europe$Duree)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
```
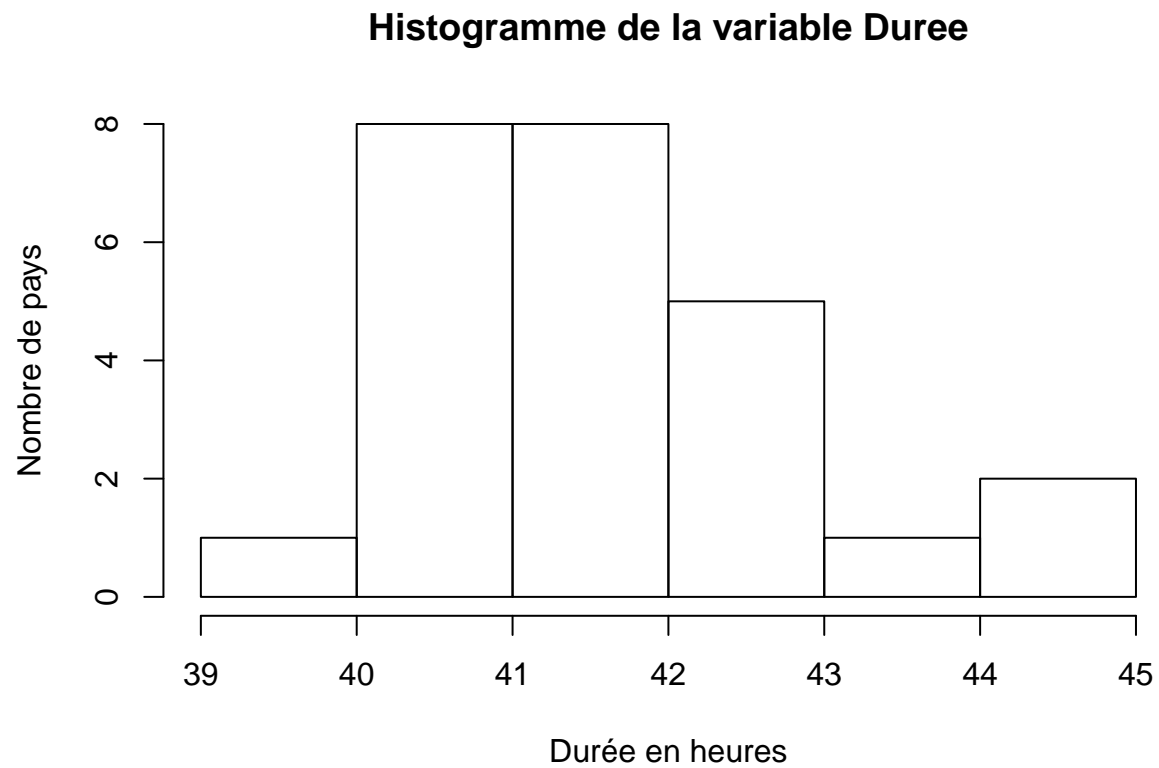
```
##      39.8      41.0      41.5      41.7      42.5      44.1
```
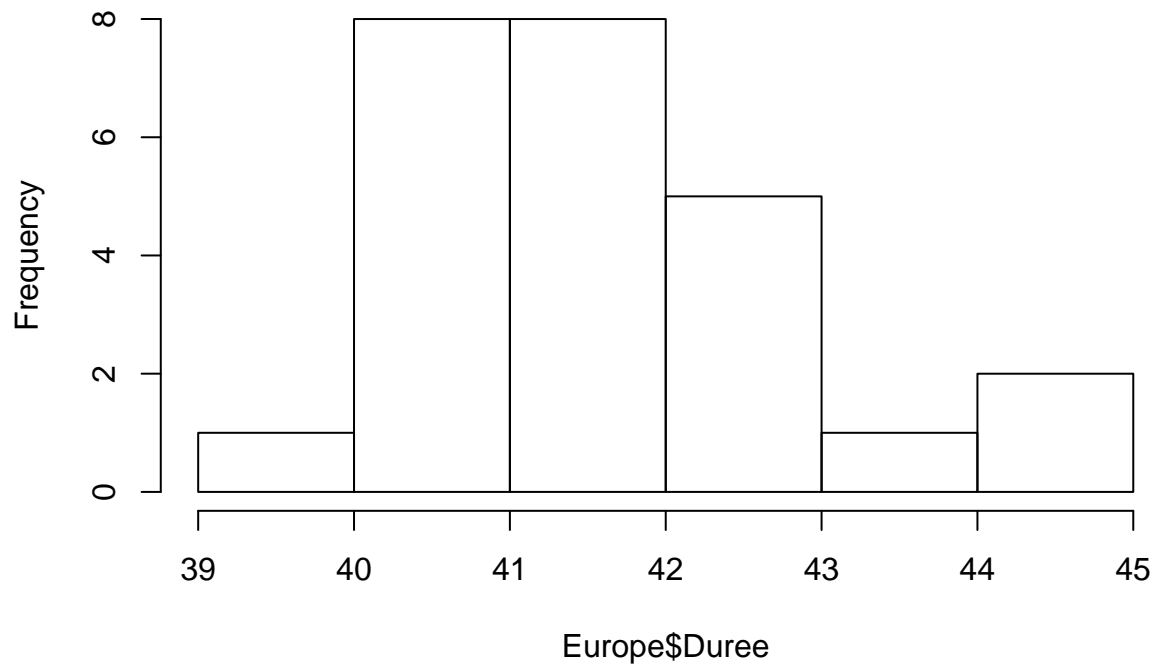
```
histo<-hist(Europe$Duree,xlab="Durée en heures",ylab="Nombre de pays",
            main="Histogramme de la variable Duree")
```

Histogramme de la variable Duree


```
histo<-hist(Europe$Duree)
```

Histogram of Europe$Duree

Europe$Duree

```
classe<-histo$breaks
classe
```

```
## [1] 39 40 41 42 43 44 45
```
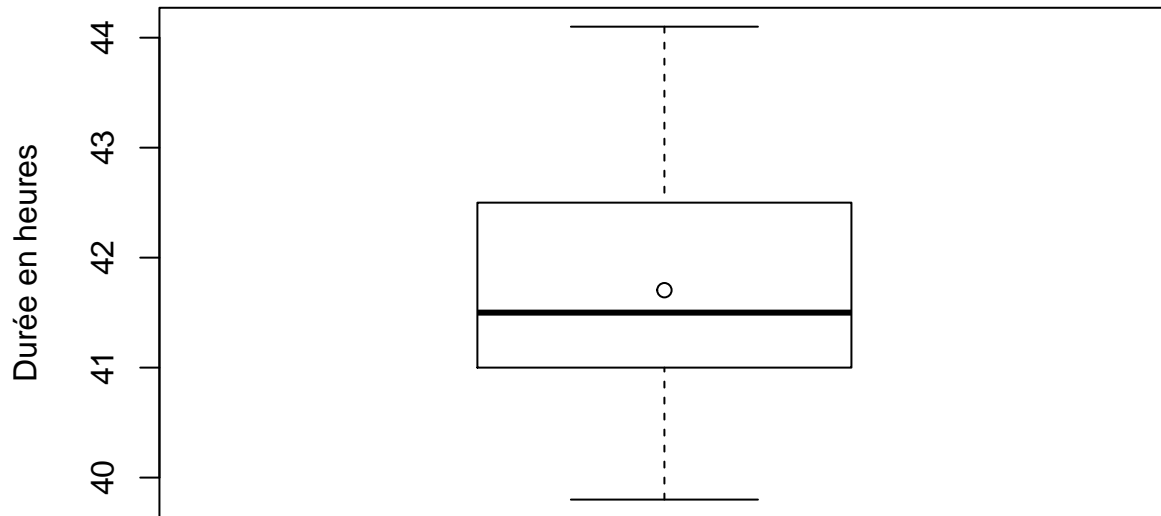```
#page 176
which(histo$density==max(histo$density))
```

```
[1] 2 3
```
```
#5)
sd(Europe$Duree)
```

```
[1] 1.113358
```
```
cvar(Europe$Duree)
```

```
[1] 2.669668
```
```
diff(range(Europe$Duree))
```

```
[1] 4.3
```
```
#6)
boxplot(Europe$Duree,ylab="Durée en heures")
points(1,mean(Europe$Duree),pch=1)
```

```
#page 177
#7)
pdf(file="boxplot.pdf")
boxplot(Europe$Duree,ylab="Durée en heures")
points(1,mean(Europe$Duree),pch=1)
dev.off()
```

```
## pdf
##   2
```

```
#page 178
postscript(file="boxplot.ps")
boxplot(Europe$Duree,ylab="Durée en heures")
points(1,mean(Europe$Duree),pch=1)
dev.off()
```

```
## pdf
##   2
```

```
#Problème 3.1
#1)
Femmes<-c(105,110,112,112,118,119,120,120,125,126,127,128,130,132,133,
          134,135,138,138,138,138,142,145,148,148,150,151,154,154,158)
Femmes
```

```
##  [1] 105 110 112 112 118 119 120 120 125 126 127 128 130 132 133 134 135
## [18] 138 138 138 138 142 145 148 148 150 151 154 154 158
```

```
#page 179
Hommes<-c(141,144,146,148,149,150,150,151,153,153,153,154,155,156,156,
          160,160,160,163,164,164,165,166,168,168,170,172,172,176,179)
Hommes
```

```
##  [1] 141 144 146 148 149 150 150 151 153 153 153 154 155 156 156 160 160
## [18] 160 163 164 164 165 166 168 168 170 172 172 176 179
```

```
#2)
histo.fem<-hist(Femmes,breaks=c(104,114,124,134,144,154,164,174,184))
effectif.fem<-histo.fem$counts
effectif.fem
```

```
## [1] 4 4 8 6 7 1 0 0
```
```r
sum(effectif.fem)
```
```
## [1] 30
```
```r
histo.frm<-hist(Femmes,breaks=c(104,114,124,134,144,154,164,174,184))
```

Histogram of Femmes


```r
frequence.fem<-effectif.fem/sum(effectif.fem)
print(frequence.fem,digits=3)
```
```
## [1] 0.1333 0.1333 0.2667 0.2000 0.2333 0.0333 0.0000 0.0000
```
```r
#page 180
histo.hom<-hist(Hommes,breaks=c(104,114,124,134,144,154,164,174,184))
effectif.hom<-histo.hom$counts
effectif.hom
```
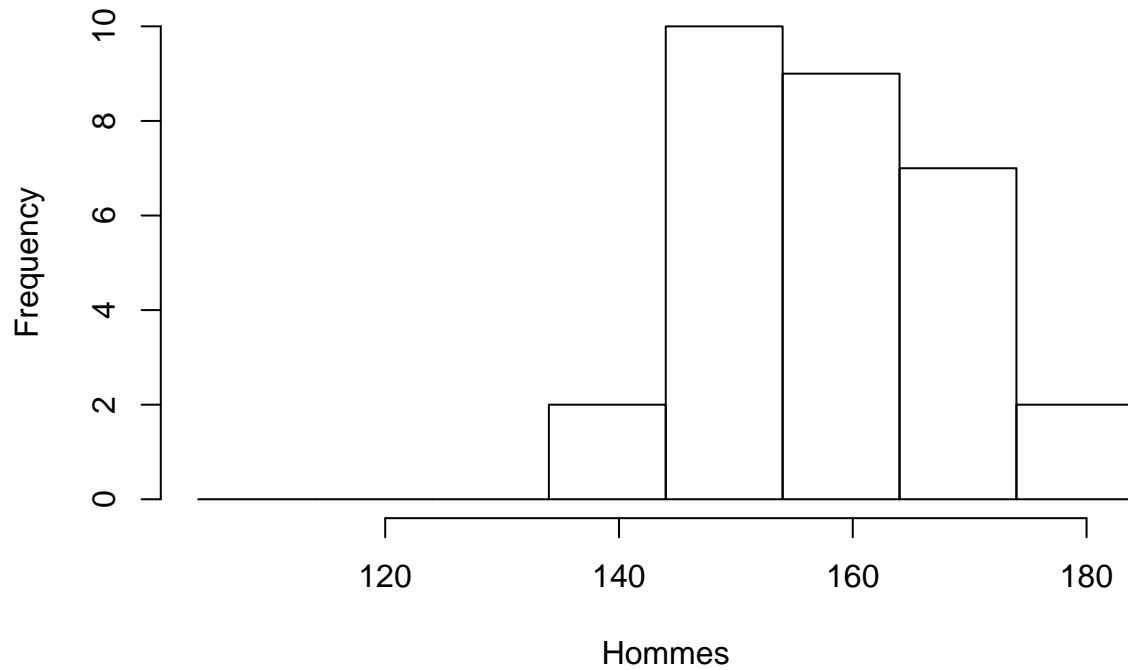```
[1] 0 0 0 2 10 9 7 2
```
```r
histo.hom<-hist(Hommes,breaks=c(104,114,124,134,144,154,164,174,184))
```

Histogram of Hommes


```
frequence.hom<-effectif.hom/sum(effectif.hom)
print(frequence.hom,digits=3)
```
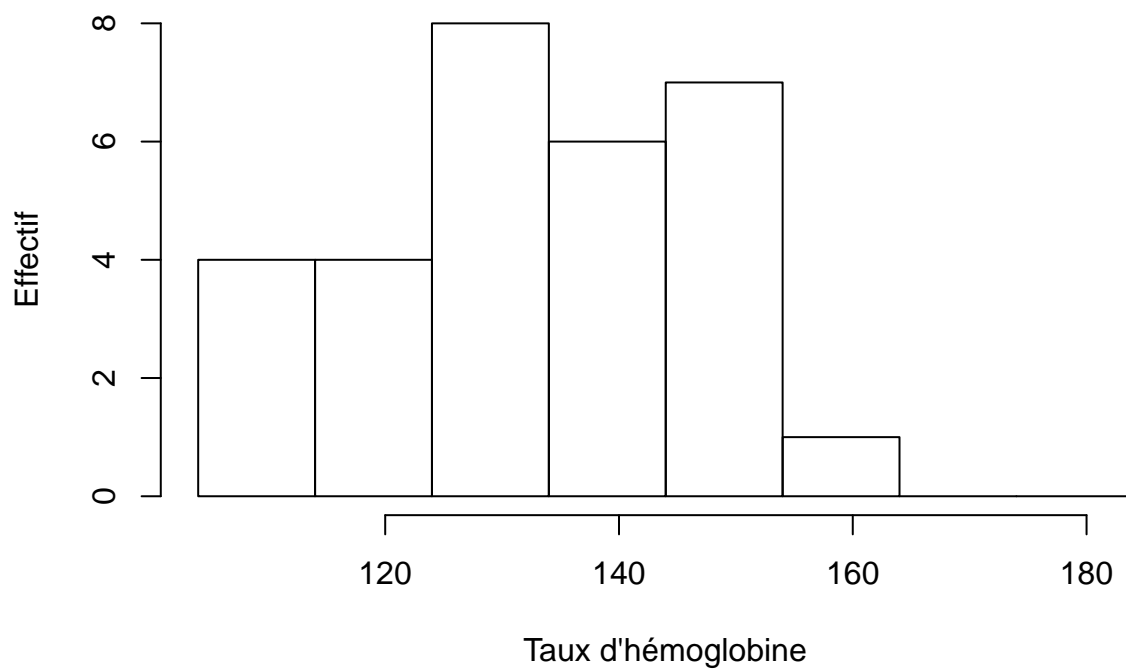
```
## [1] 0.0000 0.0000 0.0000 0.0667 0.3333 0.3000 0.2333 0.0667
```

```
#page 181
#3)
histo<-hist(Femmes,breaks=c(104,114,124,134,144,154,164,174,184),
          main="Histogramme de la variable taux d'hémoglobine pour les
          Femmes",
          xlab="Taux d'hémoglobine",ylab="Effectif")
```
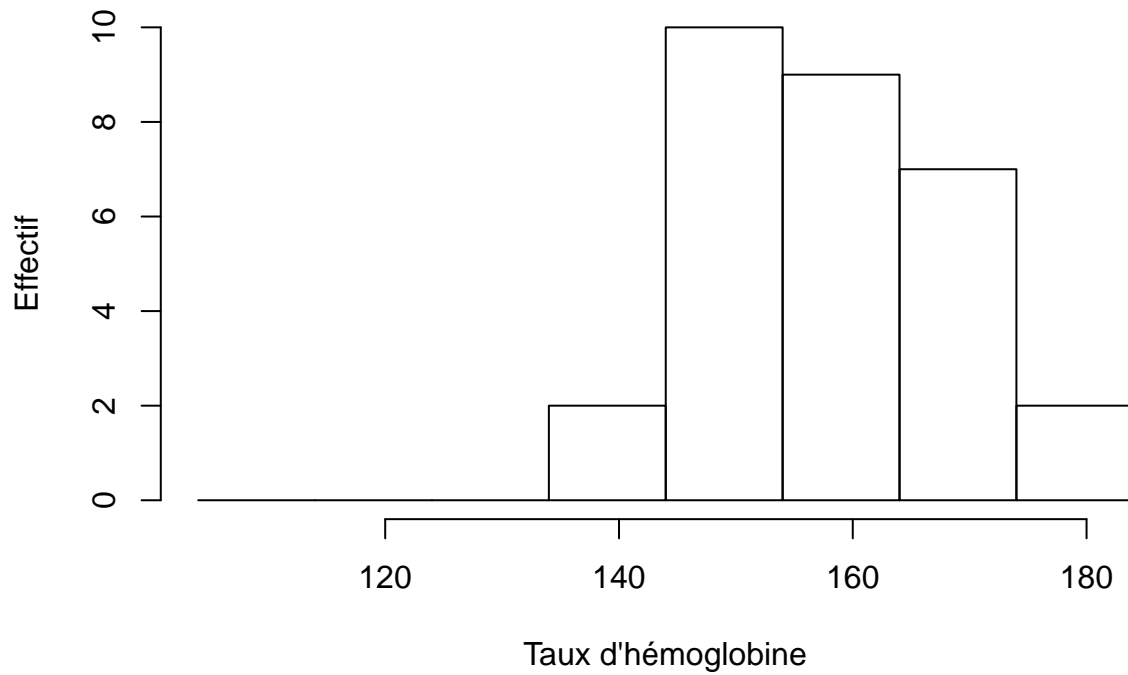
Histogramme de la variable taux d'hémoglobine pour les Femmes
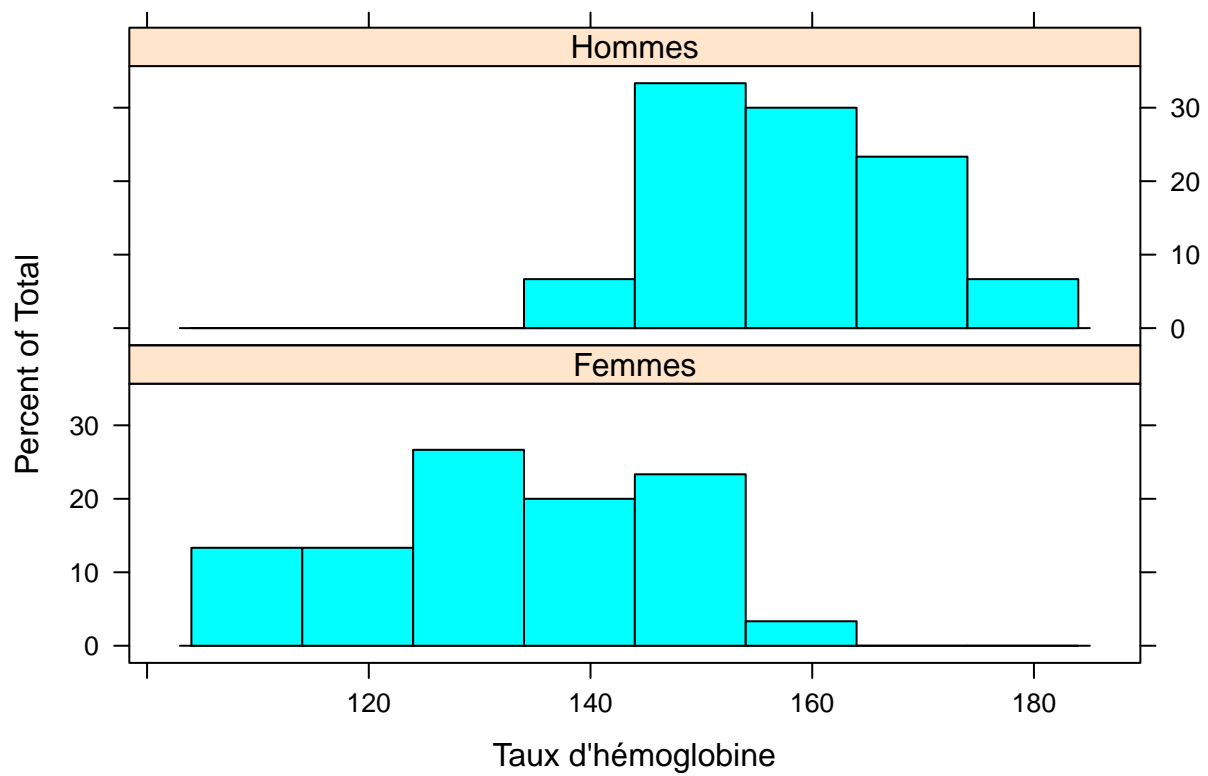

Taux d'hémoglobine

```
#page 182
histo<-hist(Hommes,breaks=c(104,114,124,134,144,154,164,174,184),
          main="Histogramme de la variable taux d'hémoglobine pour les
          Hommes",
          xlab="Taux d'hémoglobine",ylab="Effectif")
```

Histogramme de la variable taux d'hémoglobine pour les Hommes

Taux d'hémoglobine

```
library(lattice)
Ensemble.df <- make.groups(Femmes,Hommes)
colnames(Ensemble.df) <- c("Taux","Sexe")
histogram(~Taux|Sexe,xlab="Taux d'hémoglobine",data=Ensemble.df,
          breaks=c(104,114,124,134,144,154,164,174,184),layout=c(1,2))
```

```
#page 183
histogram(~Taux|Sexe,xlab="Taux d'hémoglobine",data=Ensemble.df,
          breaks=c(104,114,124,134,144,154,164,174,184))
```
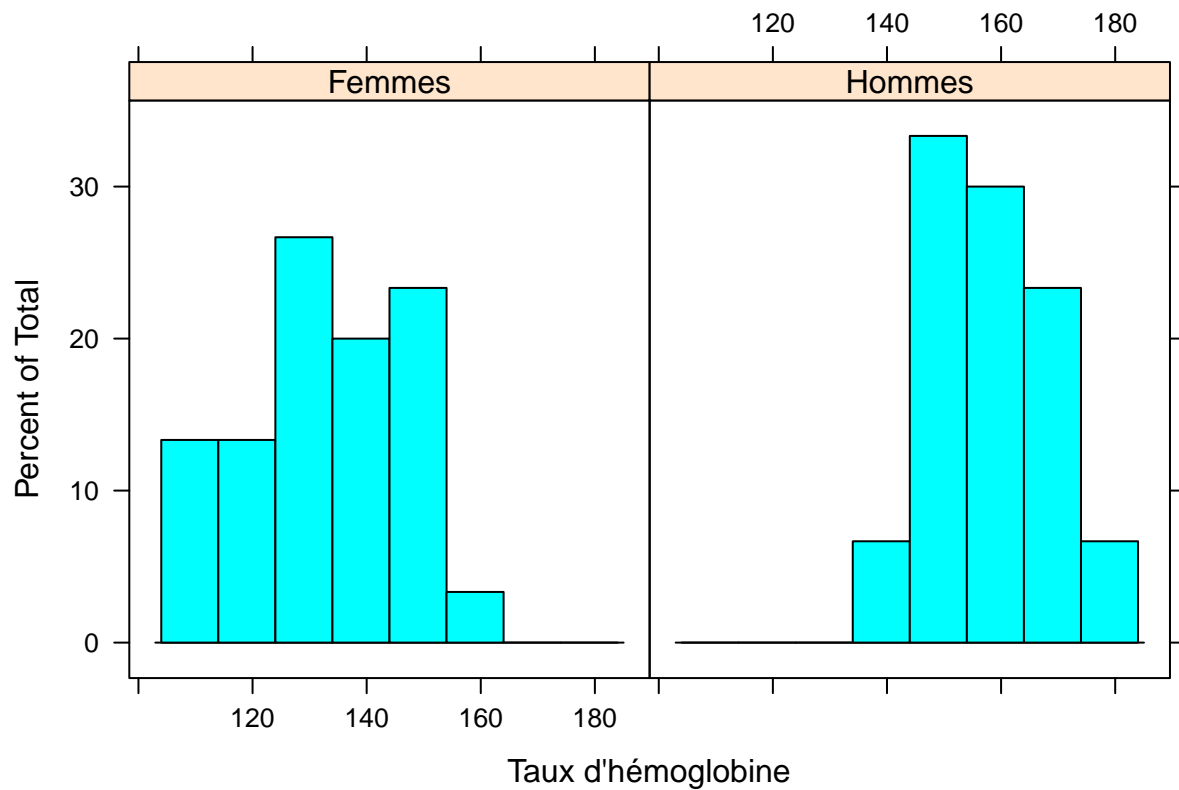
```
#page 184
#4)
Ensemble<-c(Femmes,Hommes)
Ensemble
```

```
##  [1] 105 110 112 112 118 119 120 120 125 126 127 128 130 132 133 134 135
## [18] 138 138 138 138 142 145 148 148 150 151 154 154 158 141 144 146 148
## [35] 149 150 150 151 153 153 153 154 155 156 156 160 160 160 163 164 164
## [52] 165 166 168 168 170 172 172 176 179
```

```
mean(Ensemble)
```

```
## [1] 145.9
```

```
mean(Femmes)
```

```
## [1] 132.9333
```

```
mean(Hommes)
```
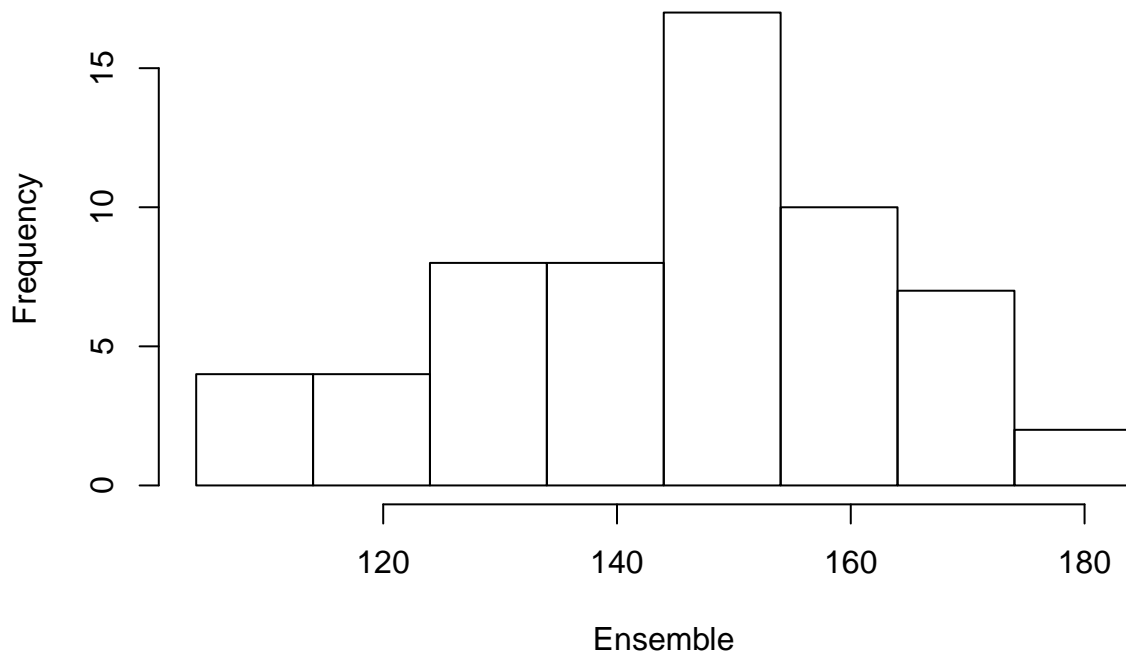
```
## [1] 158.8667
```

```
#5)
histo.ens<-hist(Ensemble,breaks=c(104,114,124,134,144,154,164,174,184))
```

Histogram of Ensemble


```
sum(histo.ens$counts*histo.ens$mids)/length(Ensemble)
```

```
## [1] 145.3333
```

```
#page 185
sum(histo.fem$counts*histo.fem$mids)/length(Femmes)
```

```
## [1] 132.6667
```

```
sum(histo.hom$counts*histo.hom$mids)/length(Hommes)
```

[1] 158

```
#6)
quantile(Ensemble,0.50,type=6)
```

```
##    50%
## 149.5
```

```
quantile(Femmes,0.50,type=6)
```

```
##    50%
## 133.5
```

```
quantile(Hommes,0.50,type=6)
```

```
## 50%
## 158
#Même résultats avec la fonction median
median(Ensemble)
```

[1] 149.5

```
median(Femmes)
```

[1] 133.5

```
median(Hommes)
```

```
## [1] 158
#page 186
#7)
IQR(Ensemble,type=6)
```

[1] 26.25

```
IQR(Femmes,type=6)
```

[1] 25.75

```
IQR(Hommes,type=6)
```

```
## [1] 15.75
#8)
var(Ensemble)*(length(Ensemble)-1)/length(Ensemble)
```

[1] 315.3567

```
var(Femmes)*(length(Femmes)-1)/length(Femmes)
```

[1] 201.2622

```
var(Hommes)*(length(Hommes)-1)/length(Hommes)
```

```
## [1] 93.18222
#page 187
sd(Ensemble)*sqrt((length(Ensemble)-1)/length(Ensemble))
```

[1] 17.75828

```r
sd(Femmes)*sqrt((length(Femmes)-1)/length(Femmes))
```

```
## [1] 14.18669
```

```r
sd(Hommes)*sqrt((length(Hommes)-1)/length(Hommes))
```

```
## [1] 9.653094
```

```r
#9)
# Asymétrie et aplatissement d'une série statistique (=population)
if(!("e1071" %in% rownames(installed.packages()))){install.packages("e1071")}
library(e1071)
```

```
##
## Attaching package: 'e1071'
```

```
## The following object is masked from 'package:Hmisc':
##
##     impute
```

```r
skewness(Femmes,type=1)
```

```
## [1] -0.09996127
```

```r
kurtosis(Femmes,type=1)
```

```
## [1] -0.9140576
```