Litter size and fertility: Learning from the data

Data

Parsing (PDF –> table)

See here for PDF to table conversion and parcing.

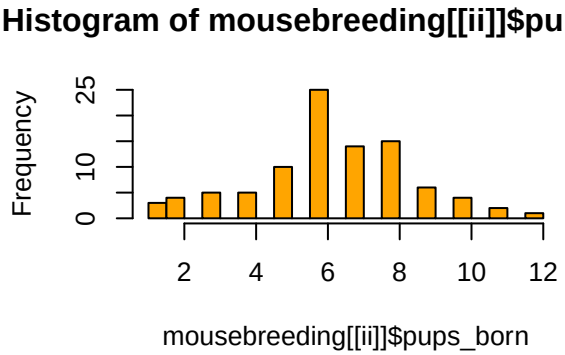
Load and clean the data

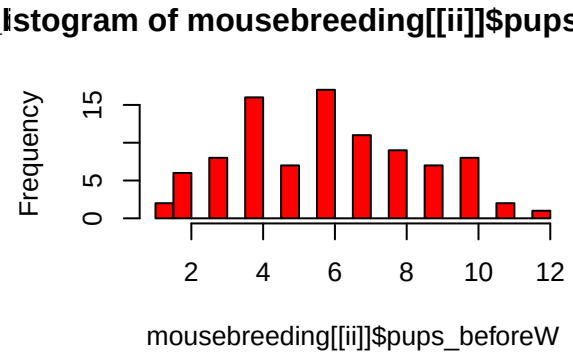
First of all, we load the litter size data (the number of pups born etc.) per strain from the already generated txt files, and then do a small quality check: Look at the distributions of the litter size (it should look like a Poisson, or at least be one-modal).

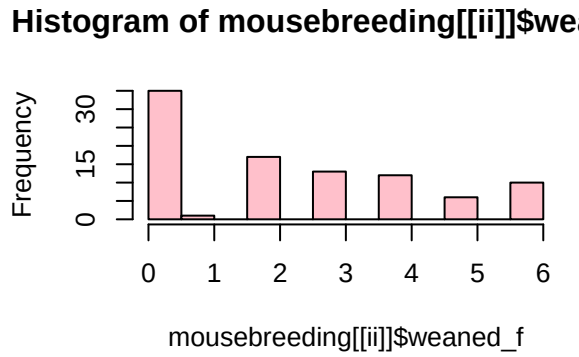
```
names(mousebreeding)
```

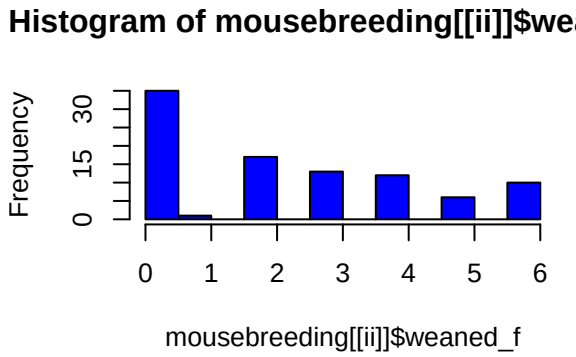
```
##  [1] "B6cBrd"        "B6D2F1"        "B6J_CrlF"      "B6J_Fue"
##  [5] "Balbc"         "Card9_KO"      "CD1_1999_2010" "CD1_2010_2020"
##  [9] "DBA2_J_Fue"    "FcRn"          "NMRI"
```

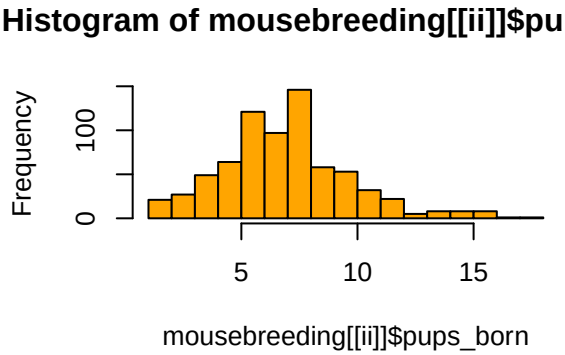
```
for (ii in 1:length(mousebreeding)){
  par(mfrow=c(2,2))
  hist(mousebreeding[[ii]]$pups_born, breaks = 20, col = "orange")
  hist(mousebreeding[[ii]]$pups_beforeW, breaks = 20, col = "red")
  hist(mousebreeding[[ii]]$weaned_f, breaks = 20, col = "pink")
  hist(mousebreeding[[ii]]$weaned_f, breaks = 20, col = "blue")
}
```

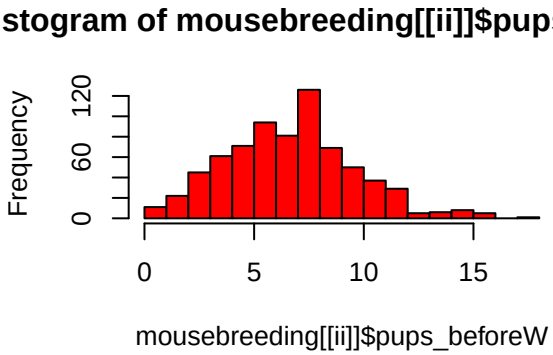

Histogram of mousebreeding[[ii]]$pups_born
Frequency
0
10
25
2
4
6
8
10
12
mousebreeding[[ii]]$pups_born

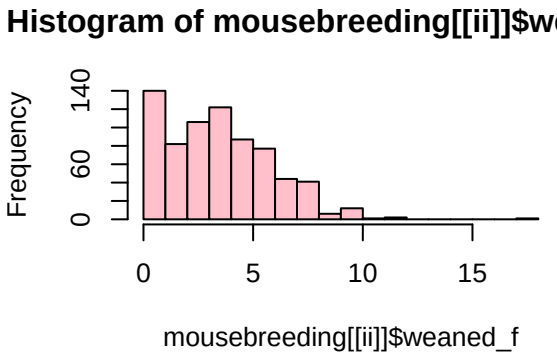

Histogram of mousebreeding[[ii]]$pups_be
Frequency
0
5
15
2
4
6
8
10
12
mousebreeding[[ii]]$pups_beforeW

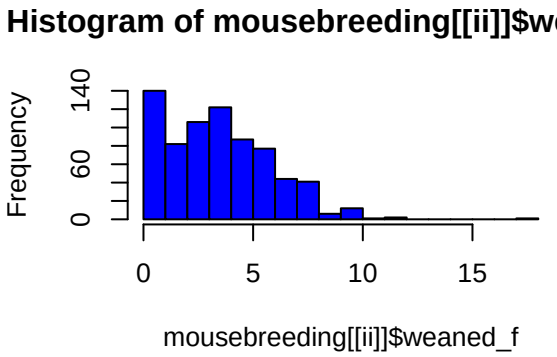

Histogram of mousebreeding[[ii]]$weane
Frequency
0
15
30
0
1
2
3
4
5
6
mousebreeding[[ii]]$weaned_f


Histogram of mousebreeding[[ii]]$weane
Frequency
0
15
30
0
1
2
3
4
5
6
mousebreeding[[ii]]$weaned_f


Histogram of mousebreeding[[ii]]$pups_born
Frequency
0
100
5
10
15
mousebreeding[[ii]]$pups_born


Histogram of mousebreeding[[ii]]$pups_be
Frequency
0
60
120
0
5
10
15
mousebreeding[[ii]]$pups_beforeW


Histogram of mousebreeding[[ii]]$weane
Frequency
0
60
140
0
5
10
15
mousebreeding[[ii]]$weaned_f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0
5
10
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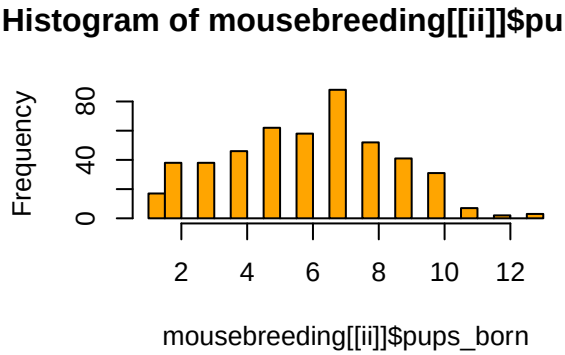
Histogram of mousebreeding[[ii]]$pups_born
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6
8
10
12
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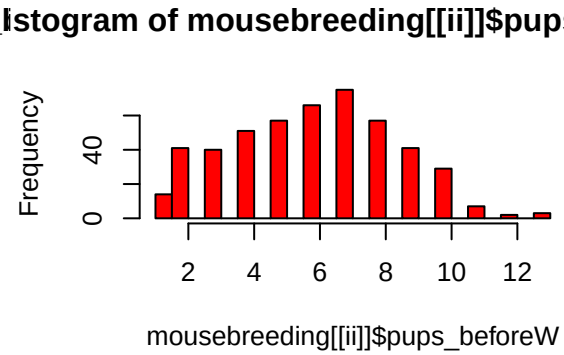
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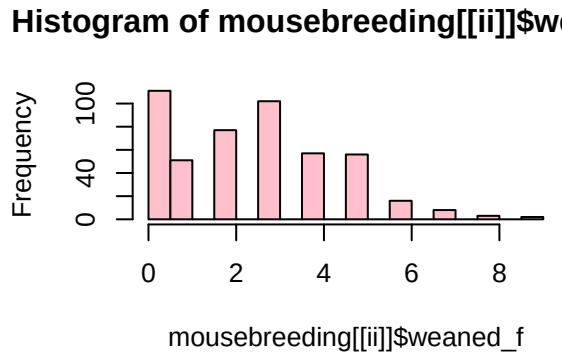
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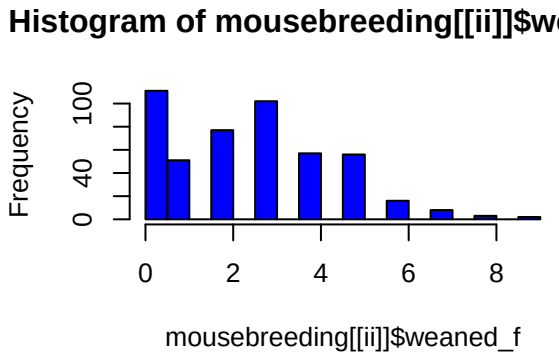
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0
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4
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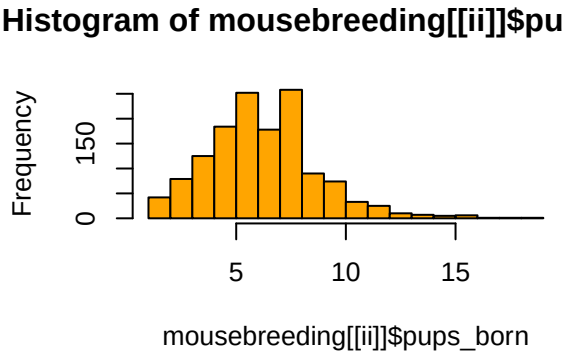
8
mousebreeding[[ii]]$weaned_f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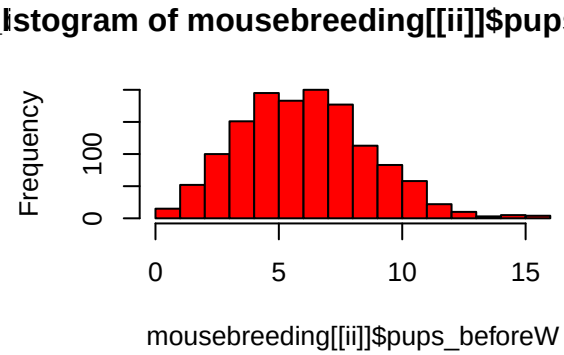
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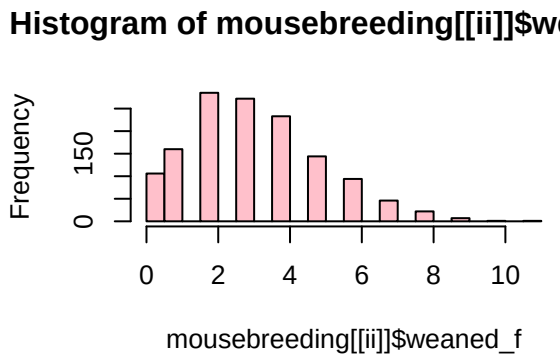
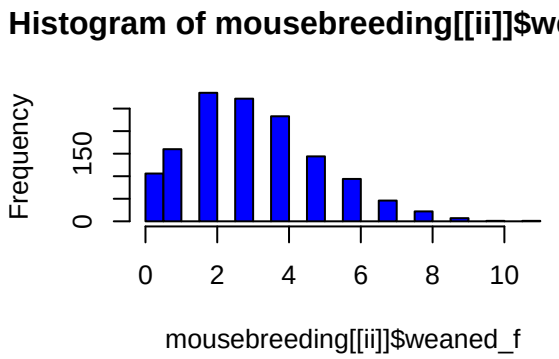
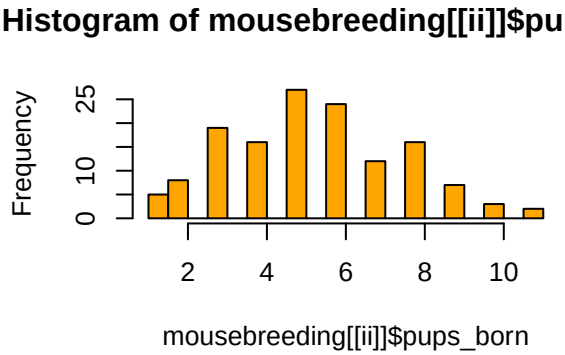
mousebreeding[[ii]]$pups_beforeW


Histogram of mousebreeding[[ii]]$weane
Frequency
0
150
0
2
4
6
8
10
mousebreeding[[ii]]$weaned_f


Histogram of mousebreeding[[ii]]$weane
Frequency
0
150
0
2
4
6
8
10
mousebreeding[[ii]]$weaned_f


Histogram of mousebreeding[[ii]]$pups_born
Frequency
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10
25
2
4
6
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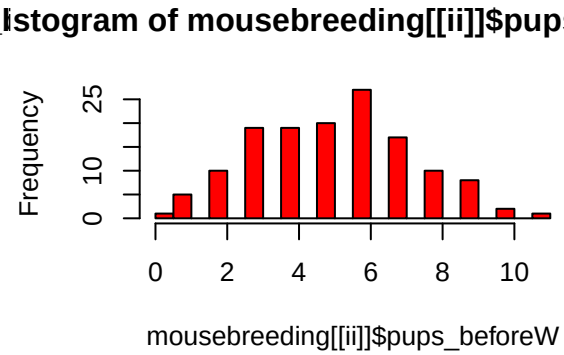
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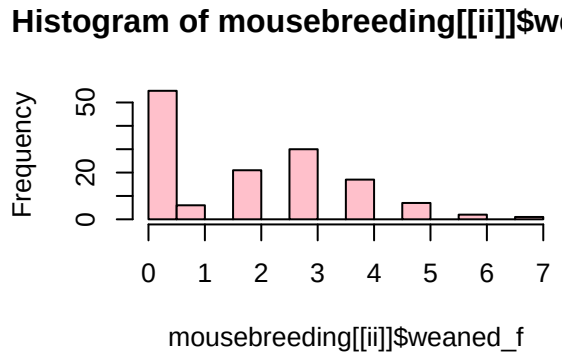
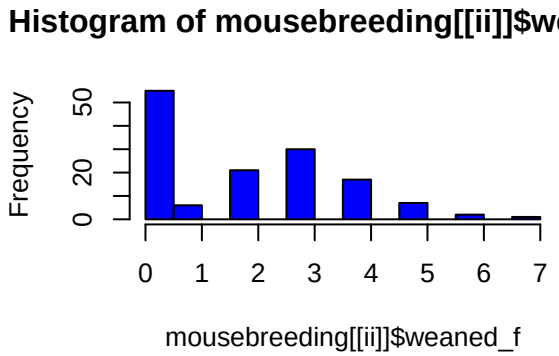

Histogram of mousebreeding[[ii]]$weane
Frequency
0
20
50
0
1
2
3
4
5
6
7
mousebreeding[[ii]]$weaned_f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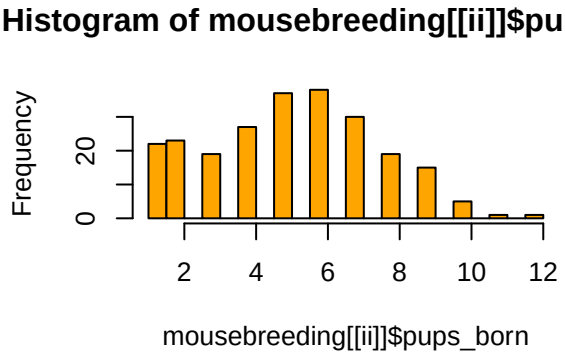
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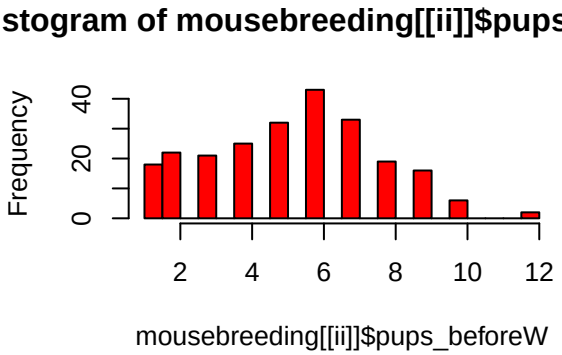
Histogram of mousebreeding[[ii]]$pups_be
Frequency
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40
2
4
6
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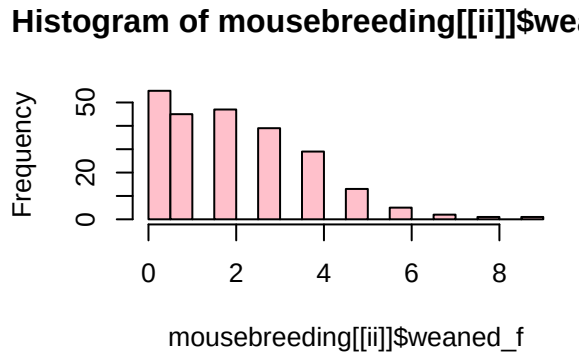
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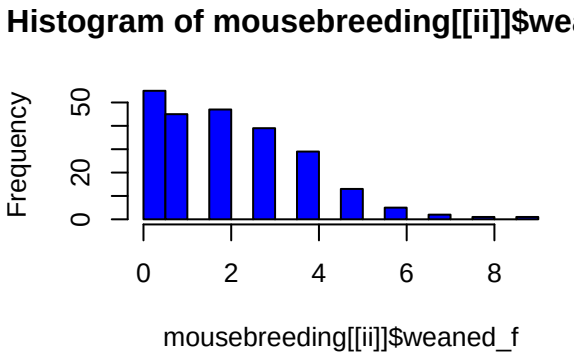
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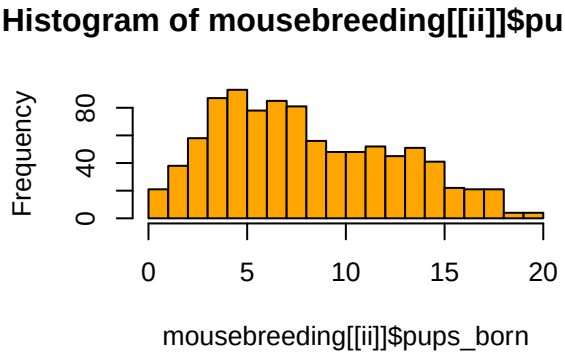
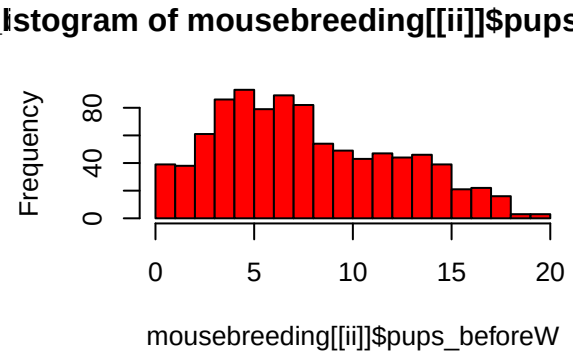

Histogram of mousebreeding[[ii]]$pups_born
Frequency
0
40
80
0
5
10
15
20
mousebreeding[[ii]]$pups_born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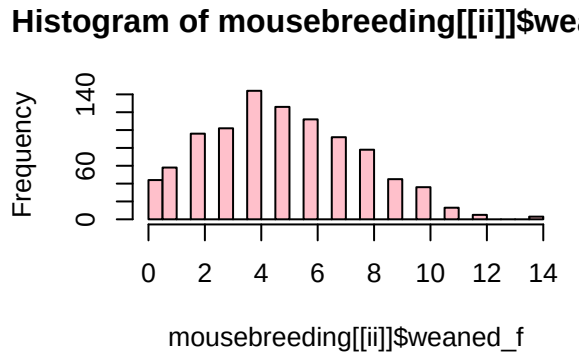
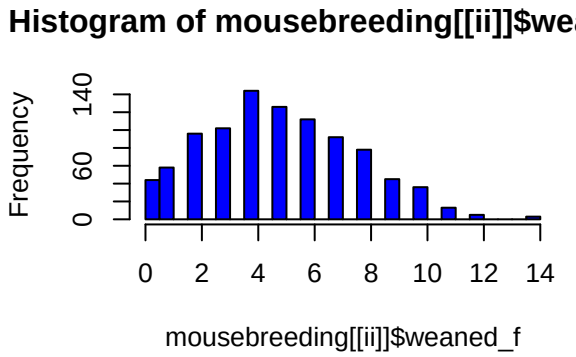

Histogram of mousebreeding[[ii]]$weane
Frequency
0
60
140
0
2
4
6
8
10
12
14
mousebreeding[[ii]]$weaned_f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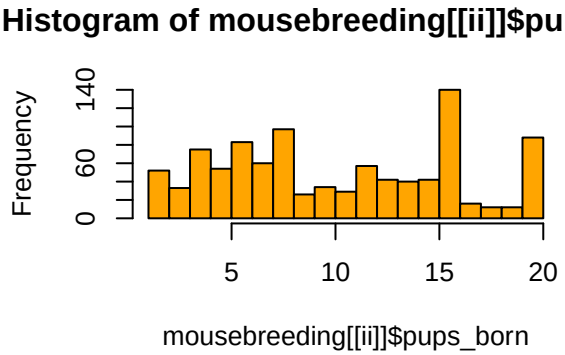
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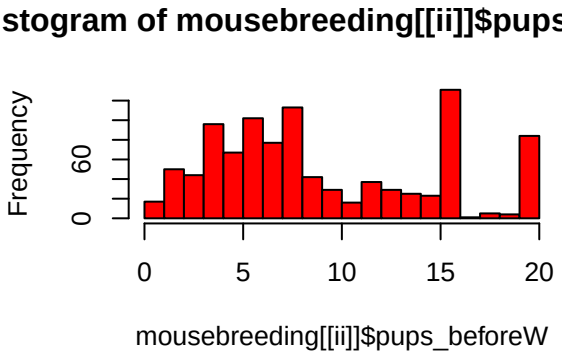
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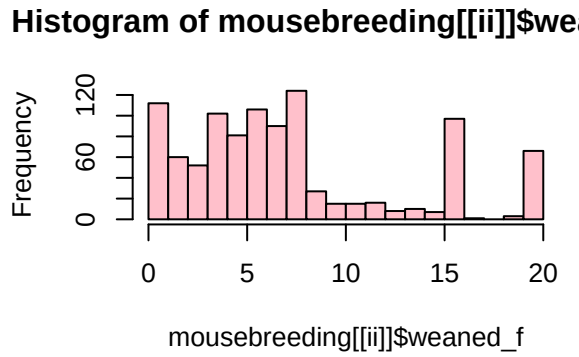
Histogram of mousebreeding[[ii]]$weane
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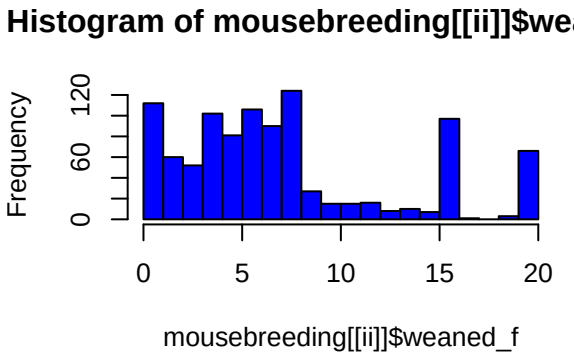
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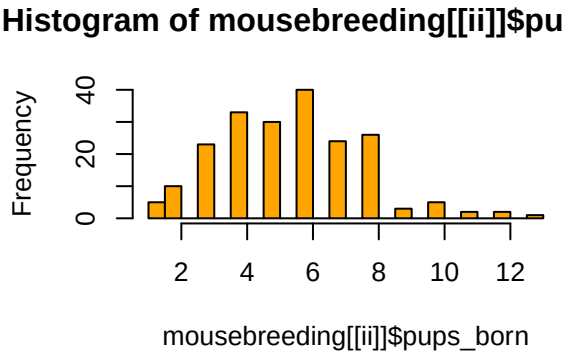
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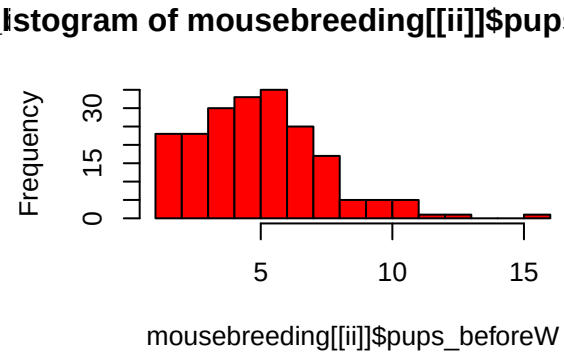
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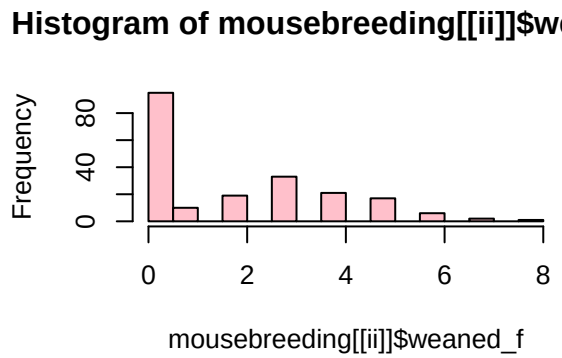
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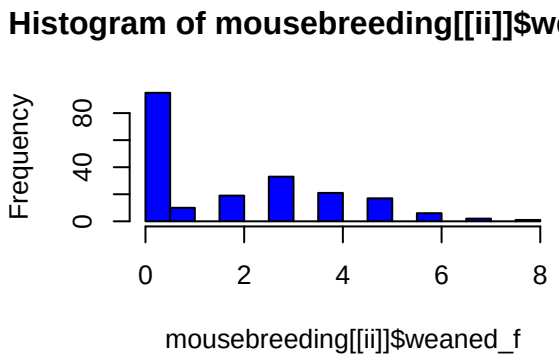
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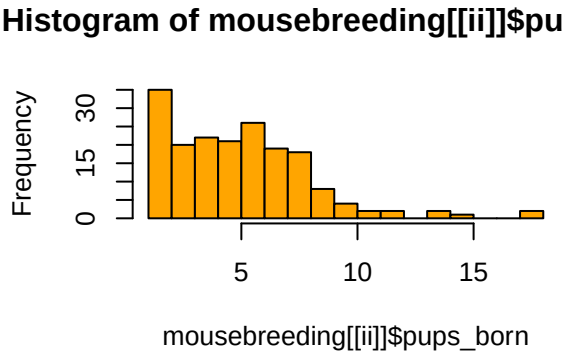
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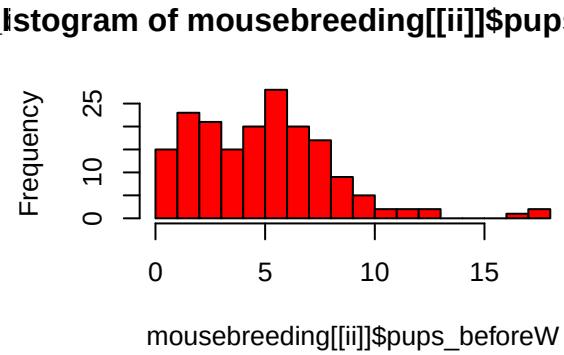
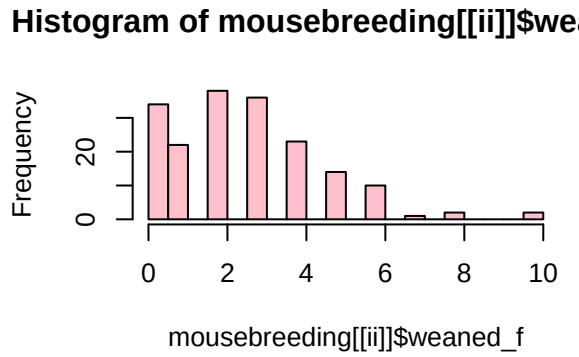
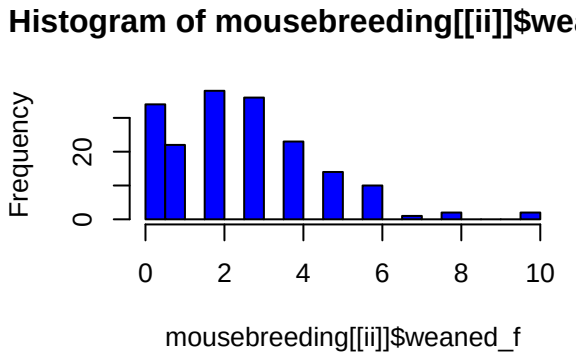
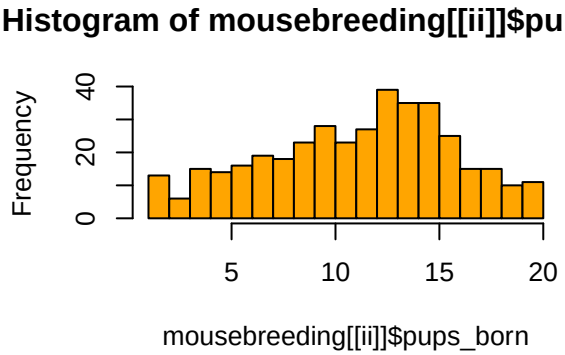
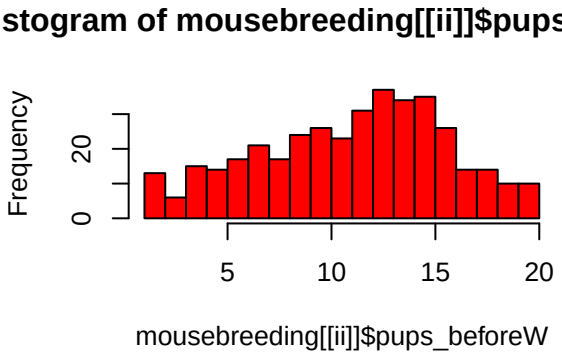
15
mousebreeding[[ii]]$pups_born

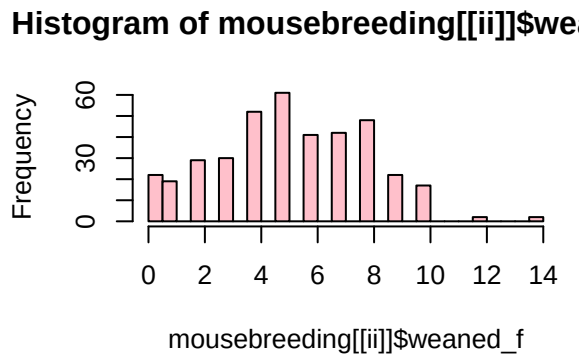

Histogram of mousebreeding[[ii]]$pups_be
Frequency
0
10
25
0
5
10
15
mousebreeding[[ii]]$pups_beforeW

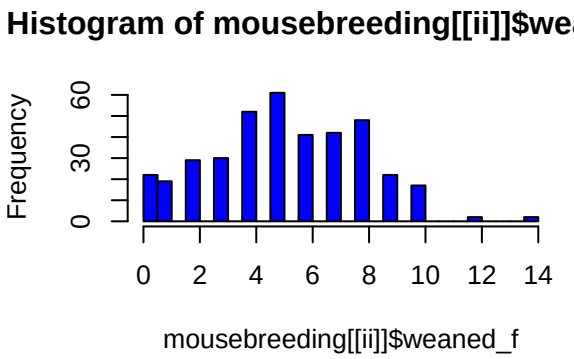

Histogram of mousebreeding[[ii]]$weane
Frequency
0
20
0
2
4
6
8
10
mousebreeding[[ii]]$weaned_f


Histogram of mousebreeding[[ii]]$weane
Frequency
0
20
0
2
4
6
8
10
mousebreeding[[ii]]$weaned_f









Quite often, only pups of one particular gender are required for the experiment. Therefore, all pups of the other gender are killed - and this is usually not stated in the data. Therefore, I filter all these cases out. Here is the number of litters per strain before (left) and after cleaning (right).

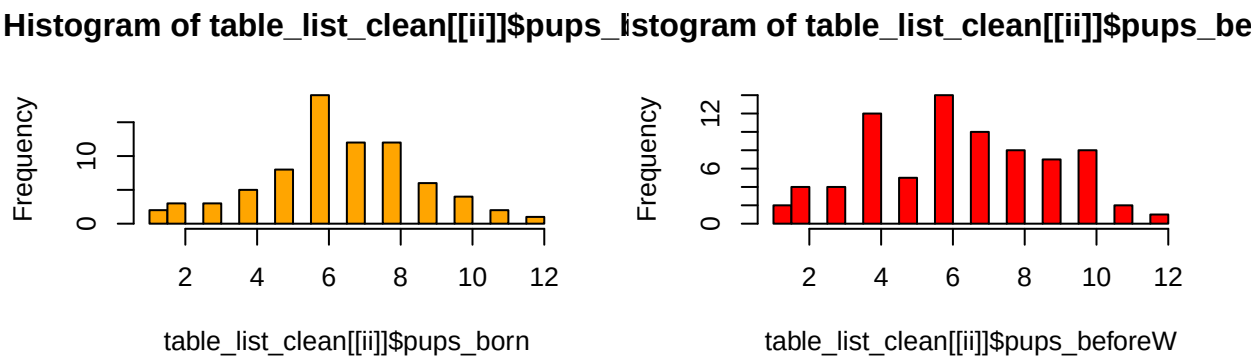
```
nlitters
```

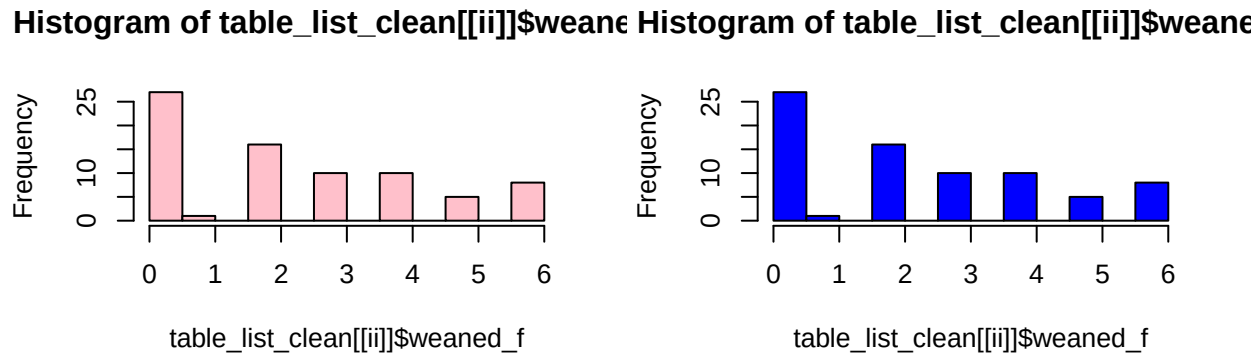
```
##                before after
## B6cBrd             94    77
## B6D2F1            721   565
## B6J_CrlF          483   444
## B6J_Fue          1371  1219
## Balbc             139   116
## Card9_KO          237   211
## CD1_1999_2010     954   593
## CD1_2010_2020     992   280
## DBA2_J_Fue        204   178
## FcRn              182   145
## NMRI              387   375
```

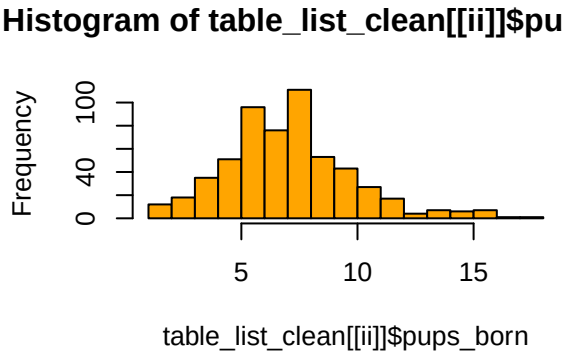
```
names(table_list_clean)
```

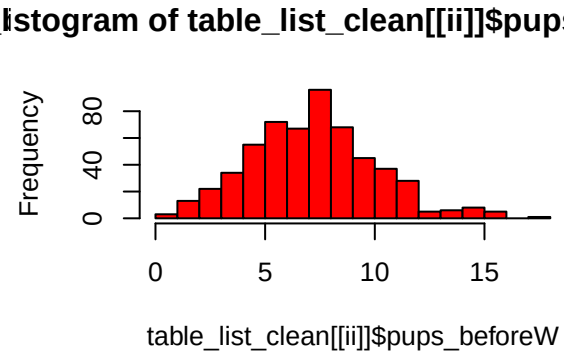
```
##  [1] "B6cBrd"        "B6D2F1"        "B6J_CrlF"      "B6J_Fue"
##  [5] "Balbc"         "Card9_KO"      "CD1_1999_2010" "CD1_2010_2020"
##  [9] "DBA2_J_Fue"    "FcRn"          "NMRI"
```

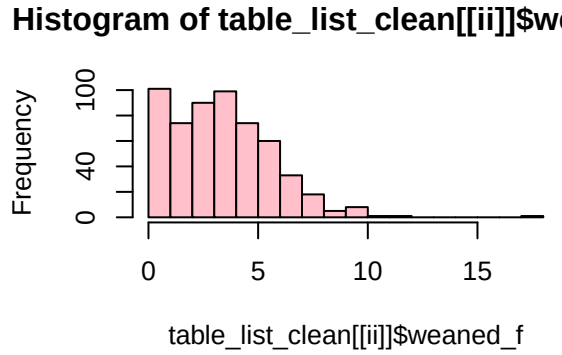
```r
for (ii in 1:length(table_list_clean)){
  par(mfrow=c(2,2))
  hist(table_list_clean[[ii]]$pups_born, breaks = 20, col = "orange")
  hist(table_list_clean[[ii]]$pups_beforeW, breaks = 20, col = "red")
  hist(table_list_clean[[ii]]$weaned_f, breaks = 20, col = "pink")
  hist(table_list_clean[[ii]]$weaned_f, breaks = 20, col = "blue")
}
```

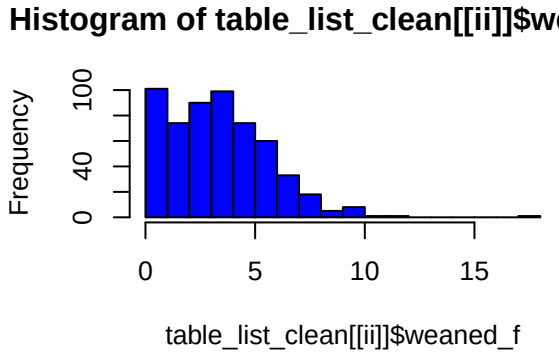


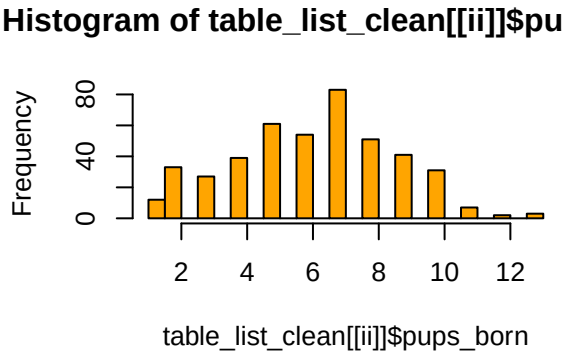


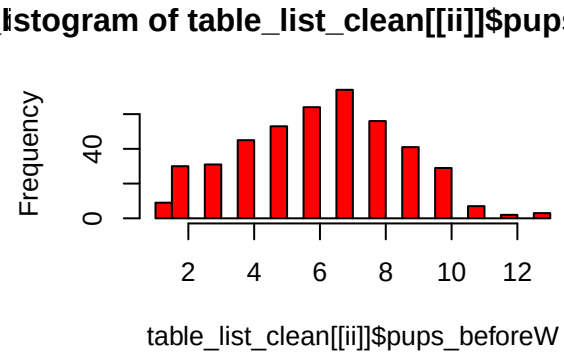

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
40
100
5
10
15
table_list_clean[[ii]]$pups_born

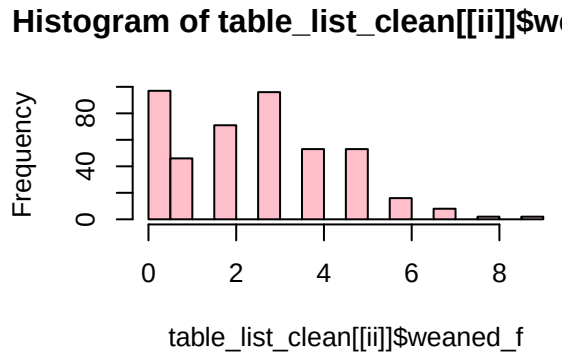

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
40
80
0
5
10
15
table_list_clean[[ii]]$pups_beforeW

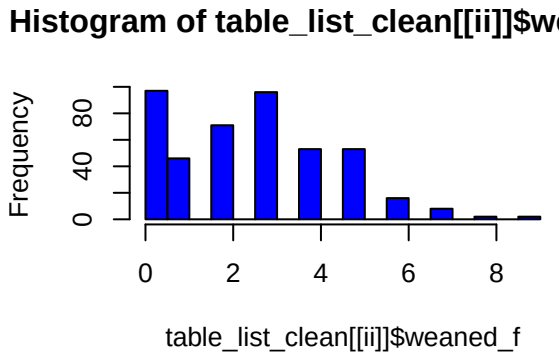

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
100
0
5
10
15
table_list_clean[[ii]]$weaned_f

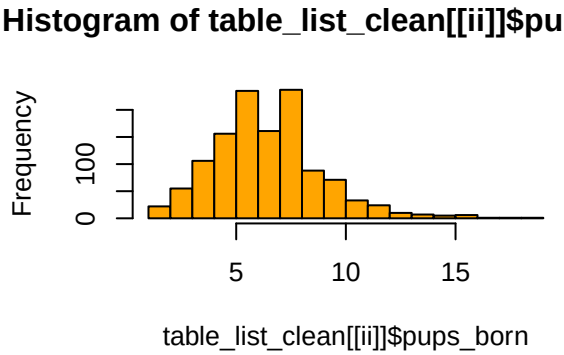

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
100
0
5
10
15
table_list_clean[[ii]]$weaned_f

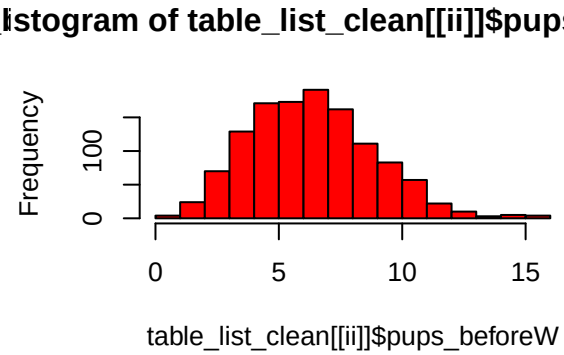

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
40
80
2
4
6
8
10
12
table_list_clean[[ii]]$pups_born

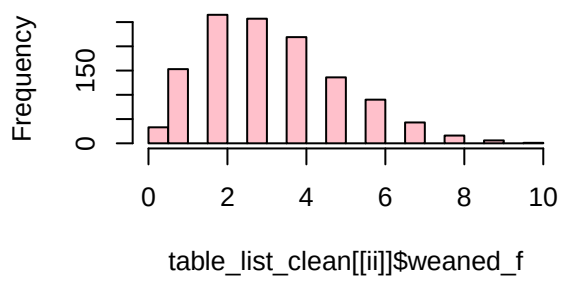

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
40
2
4
6
8
10
12
table_list_clean[[ii]]$pups_beforeW

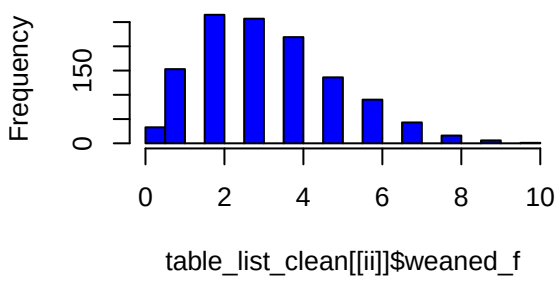

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
80
0
2
4
6
8
table_list_clean[[ii]]$weaned_f

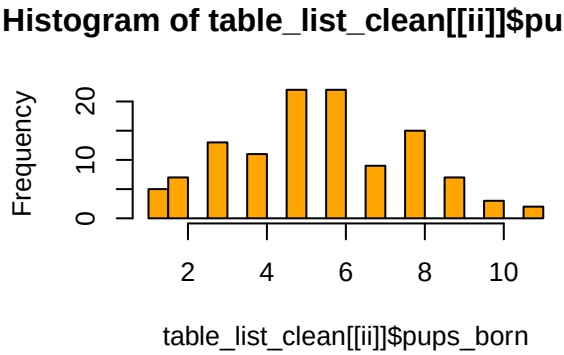

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
80
0
2
4
6
8
table_list_clean[[ii]]$weaned_f

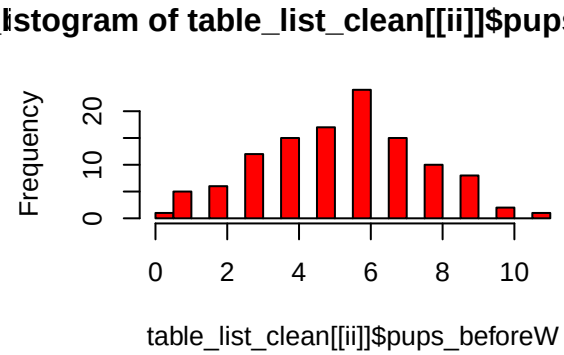

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
100
5
10
15
table_list_clean[[ii]]$pups_born

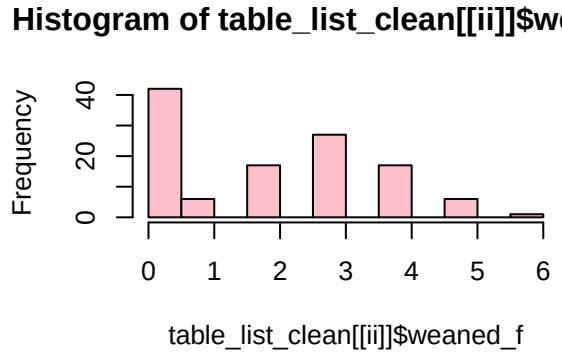

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
100
0
5
10
15
table_list_clean[[ii]]$pups_beforeW

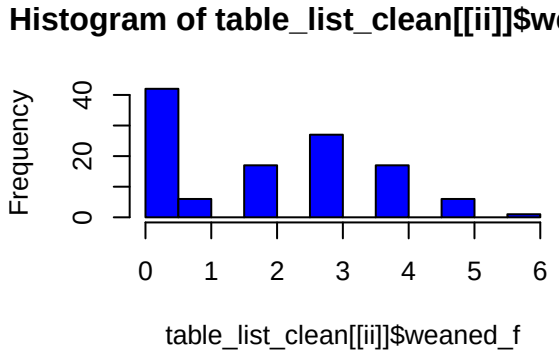

Histogram of table_list_clean[[ii]]$weane
Frequency
0
150
0
2
4
6
8
10
table_list_clean[[ii]]$weaned_f

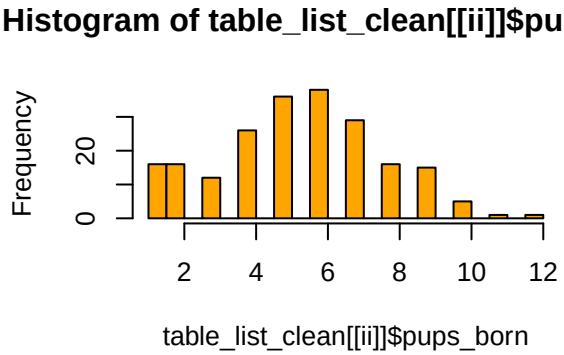

Histogram of table_list_clean[[ii]]$weane
Frequency
0
150
0
2
4
6
8
10
table_list_clean[[ii]]$weaned_f

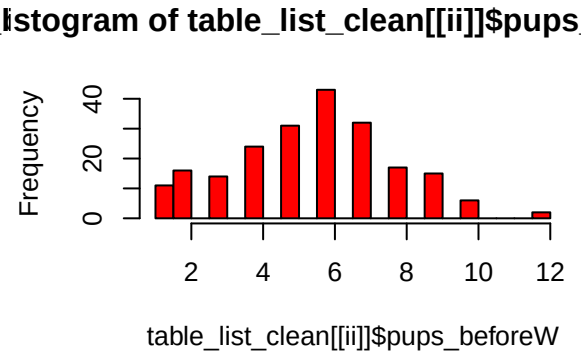

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
10
20
2
4
6
8
10
table_list_clean[[ii]]$pups_born

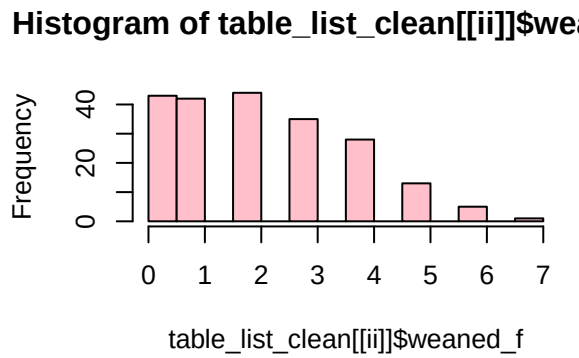

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
10
20
0
2
4
6
8
10
table_list_clean[[ii]]$pups_beforeW

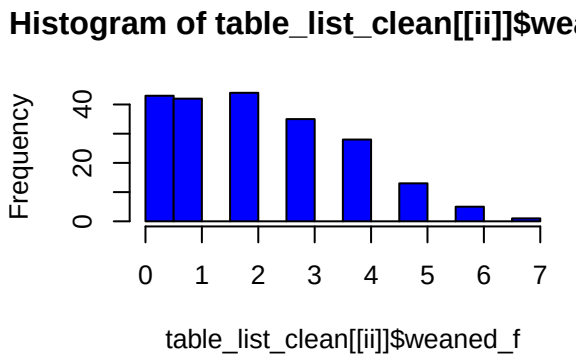

Histogram of table_list_clean[[ii]]$weane
Frequency
0
20
40
0
1
2
3
4
5
6
table_list_clean[[ii]]$weaned_f

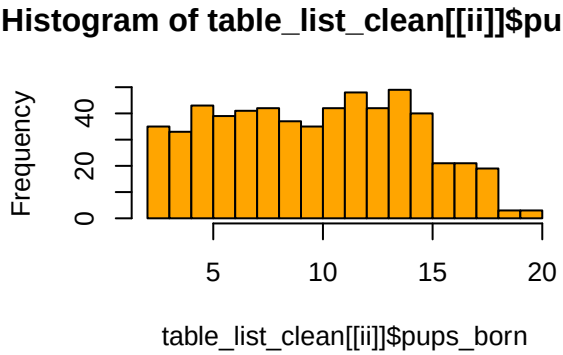

Histogram of table_list_clean[[ii]]$weane
Frequency
0
20
40
0
1
2
3
4
5
6
table_list_clean[[ii]]$weaned_f

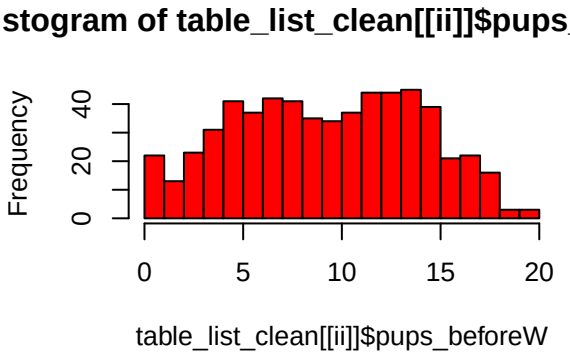

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
20
2
4
6
8
10
12
table_list_clean[[ii]]$pups_born

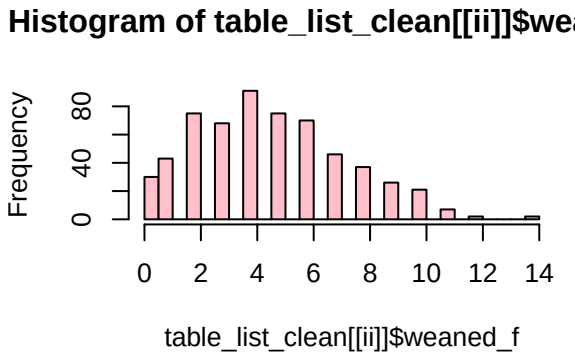

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
20
40
2
4
6
8
10
12
table_list_clean[[ii]]$pups_beforeW

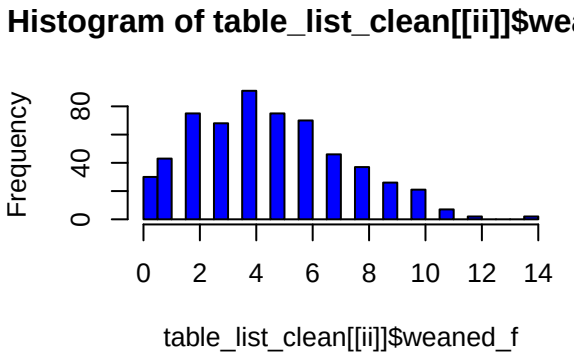

Histogram of table_list_clean[[ii]]$weane
Frequency
0
20
40
0
1
2
3
4
5
6
7
table_list_clean[[ii]]$weaned_f

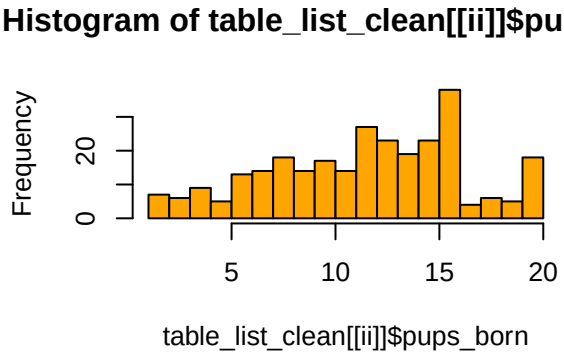

Histogram of table_list_clean[[ii]]$weane
Frequency
0
20
40
0
1
2
3
4
5
6
7
table_list_clean[[ii]]$weaned_f

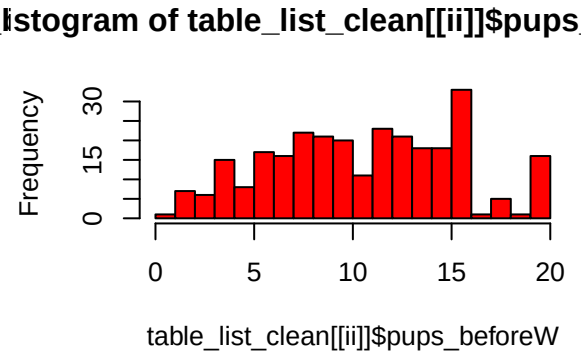

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
20
40
5
10
15
20
table_list_clean[[ii]]$pups_born

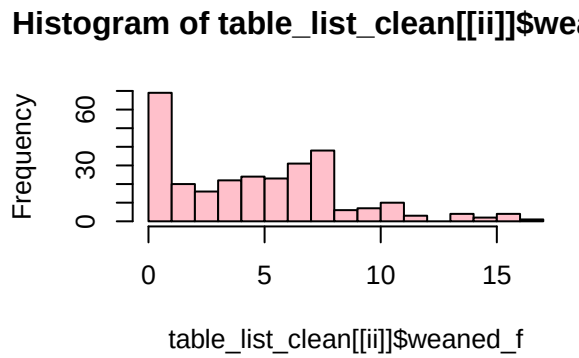

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
20
40
0
5
10
15
20
table_list_clean[[ii]]$pups_beforeW

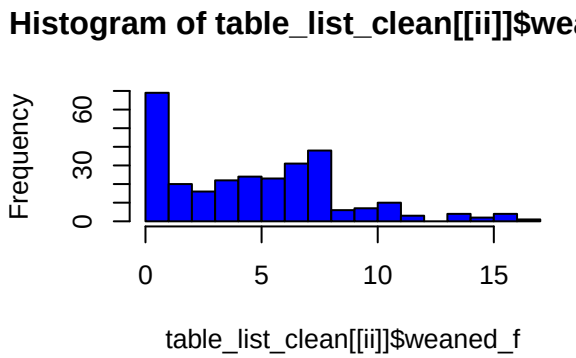

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
80
0
2
4
6
8
10
12
14
table_list_clean[[ii]]$weaned_f

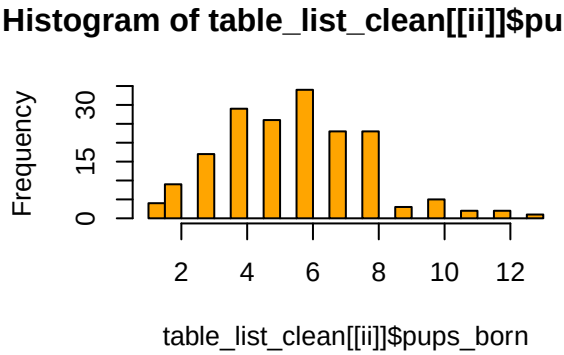

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
80
0
2
4
6
8
10
12
14
table_list_clean[[ii]]$weaned_f

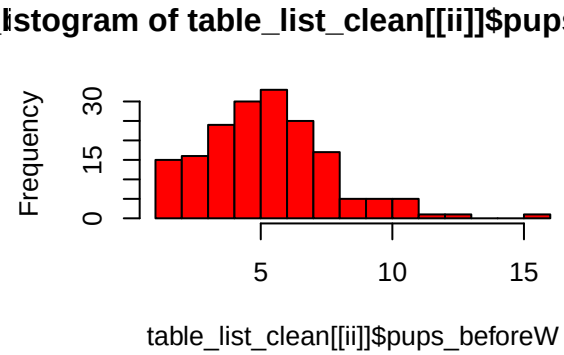

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
20
5
10
15
20
table_list_clean[[ii]]$pups_born

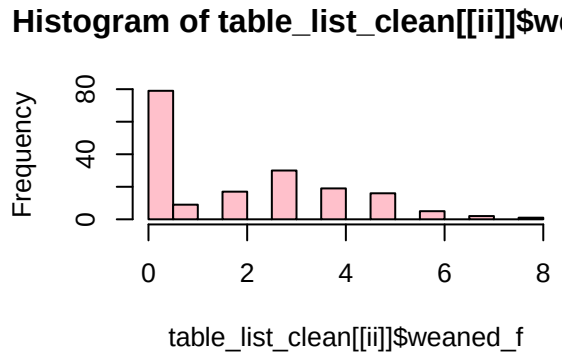

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
15
30
0
5
10
15
20
table_list_clean[[ii]]$pups_beforeW

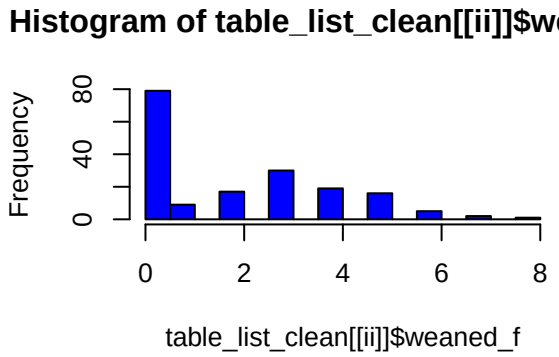

Histogram of table_list_clean[[ii]]$weane
Frequency
0
30
60
0
5
10
15
table_list_clean[[ii]]$weaned_f

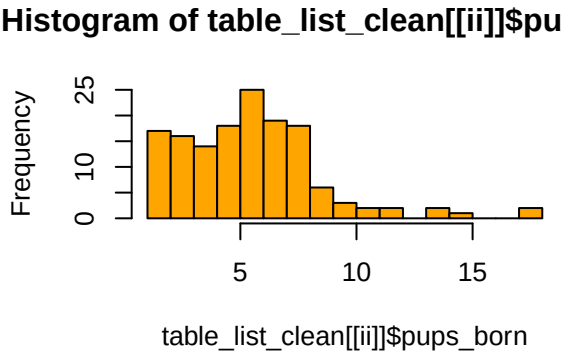

Histogram of table_list_clean[[ii]]$weane
Frequency
0
30
60
0
5
10
15
table_list_clean[[ii]]$weaned_f

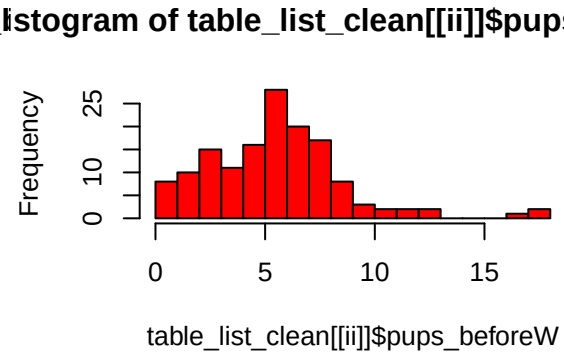

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
15
30
2
4
6
8
10
12
table_list_clean[[ii]]$pups_born

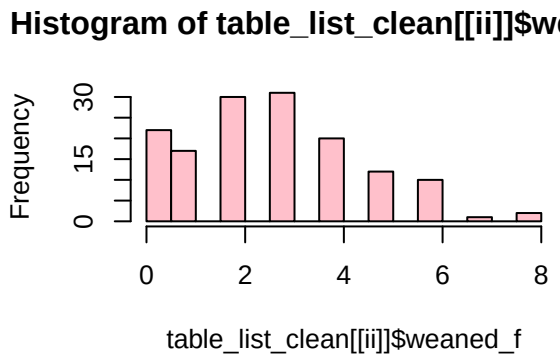

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
15
30
5
10
15
table_list_clean[[ii]]$pups_beforeW

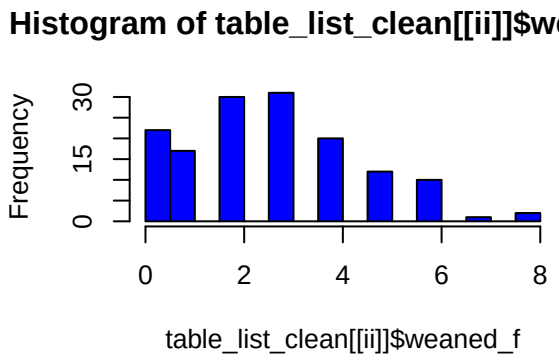

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
80
0
2
4
6
8
table_list_clean[[ii]]$weaned_f

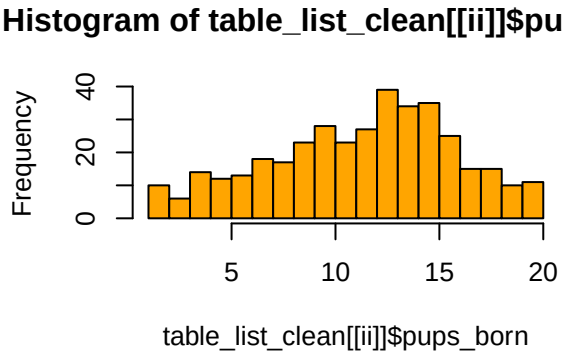

Histogram of table_list_clean[[ii]]$weane
Frequency
0
40
80
0
2
4
6
8
table_list_clean[[ii]]$weaned_f

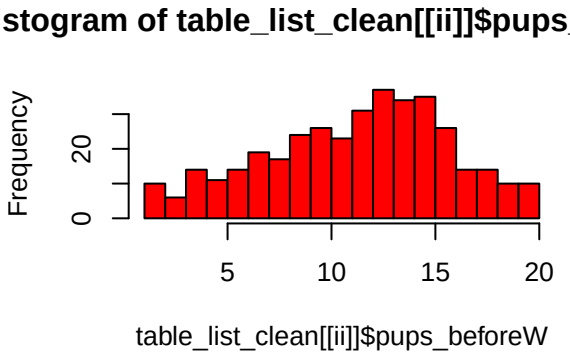

Histogram of table_list_clean[[ii]]$pups_born
Frequency
0
10
25
5
10
15
table_list_clean[[ii]]$pups_born

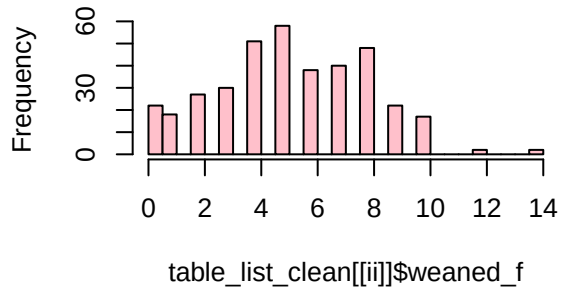

Histogram of table_list_clean[[ii]]$pups_be
Frequency
0
10
25
0
5
10
15
table_list_clean[[ii]]$pups_beforeW

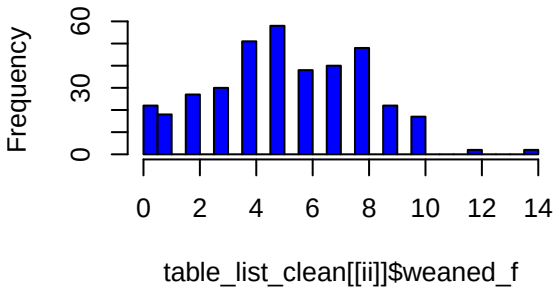

Histogram of table_list_clean[[ii]]$weane
Frequency
0
15
30
0
2
4
6
8
table_list_clean[[ii]]$weaned_f


Histogram of table_list_clean[[ii]]$weane
Frequency
0
15
30
0
2
4
6
8
table_list_clean[[ii]]$weaned_f





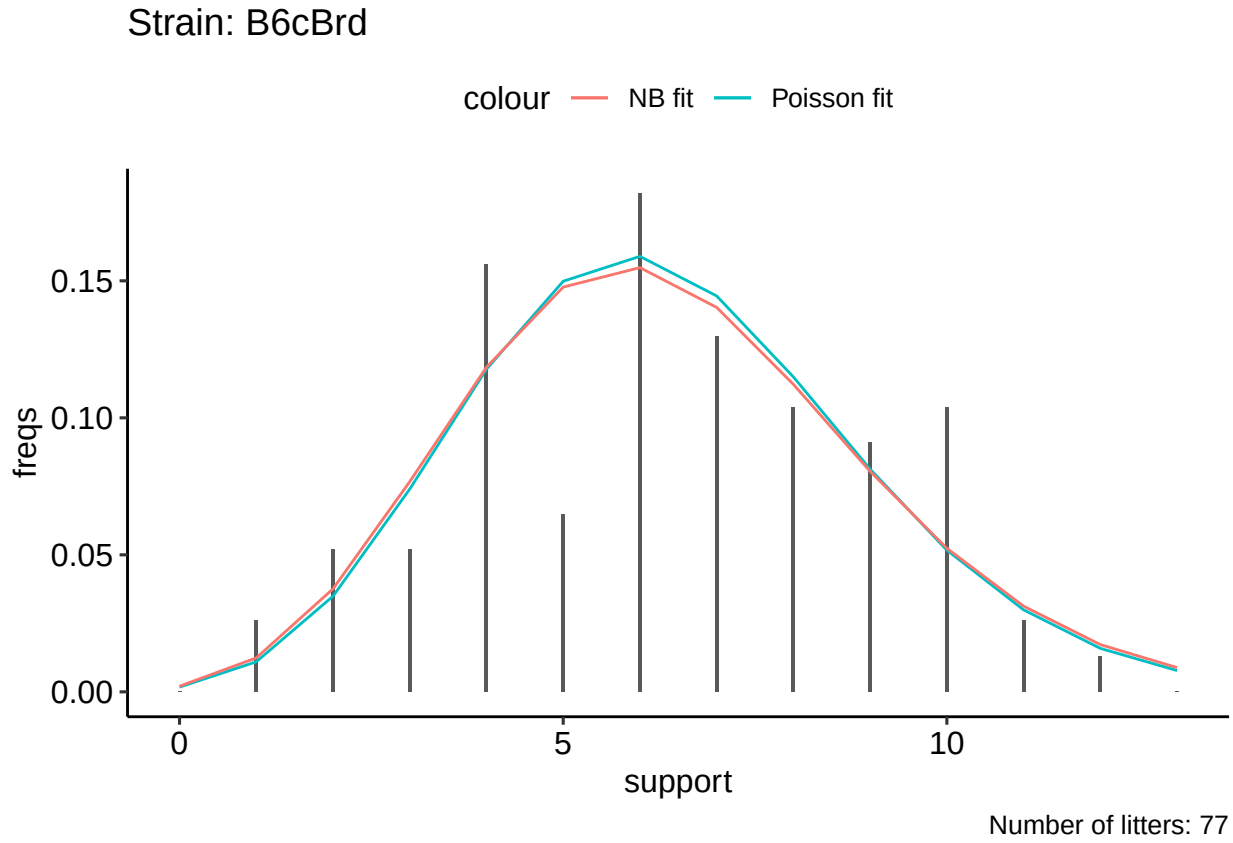




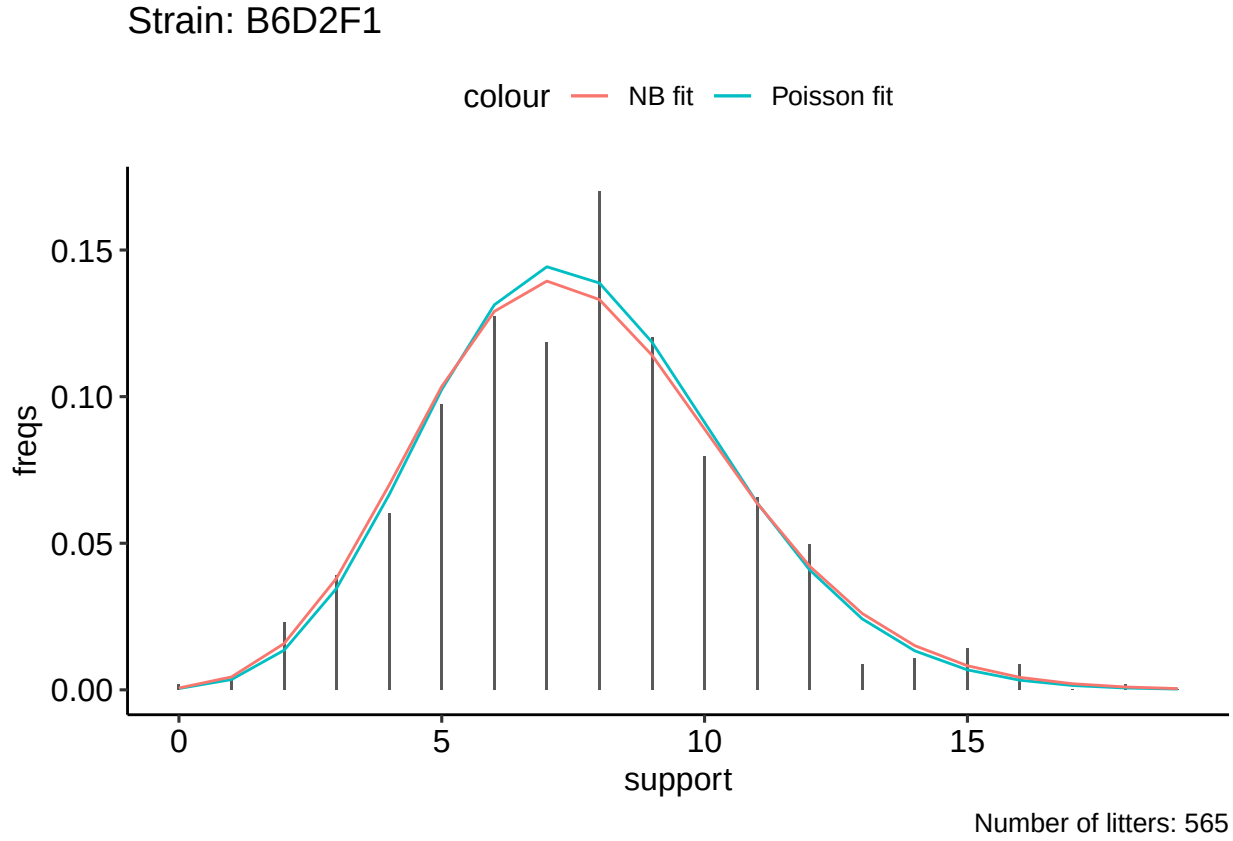
Histograms with a Pois and NB fit for each strain

```
hists_list
```

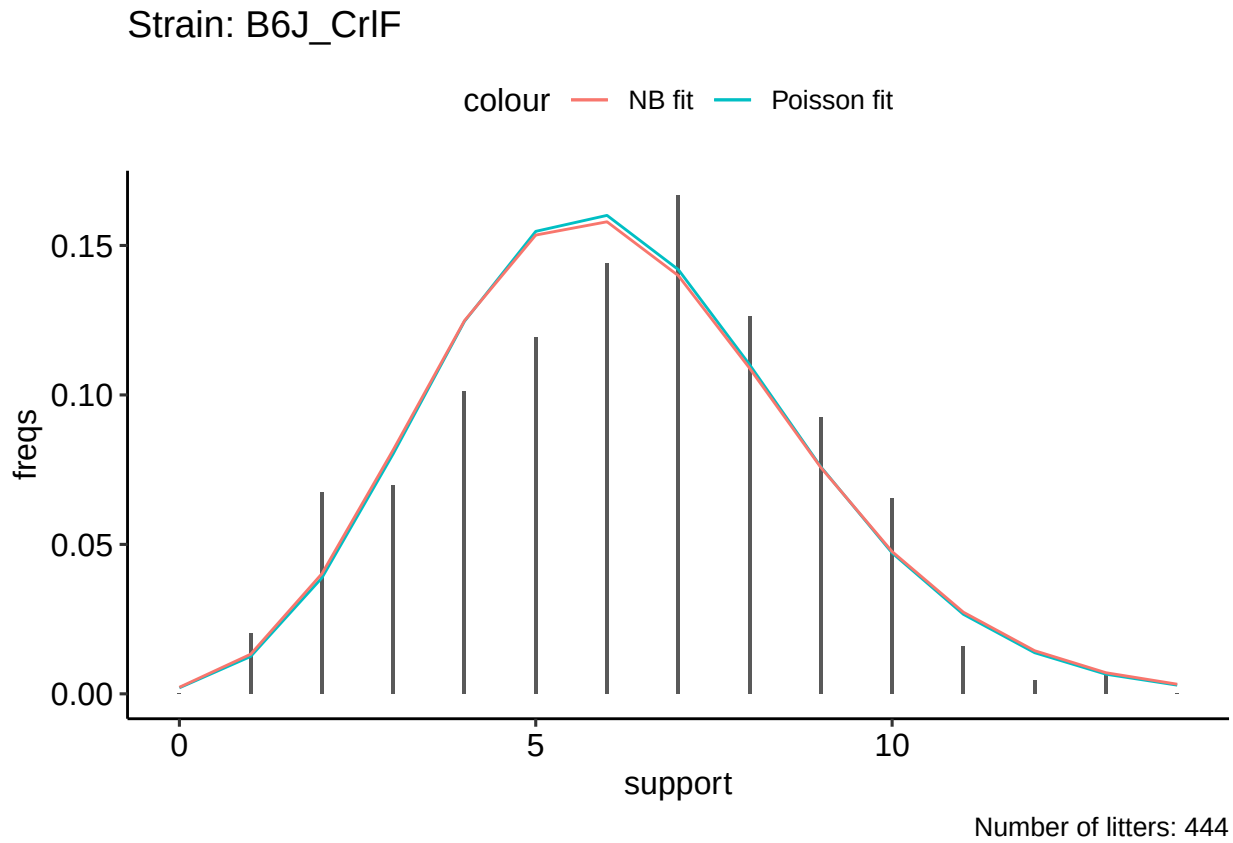
```
## [[1]]
```


Strain: B6cBrd
colour
NB fit
Poisson fit
freqs
0.15
0.10
0.05
0.00
0
5
10
support
Number of litters: 77

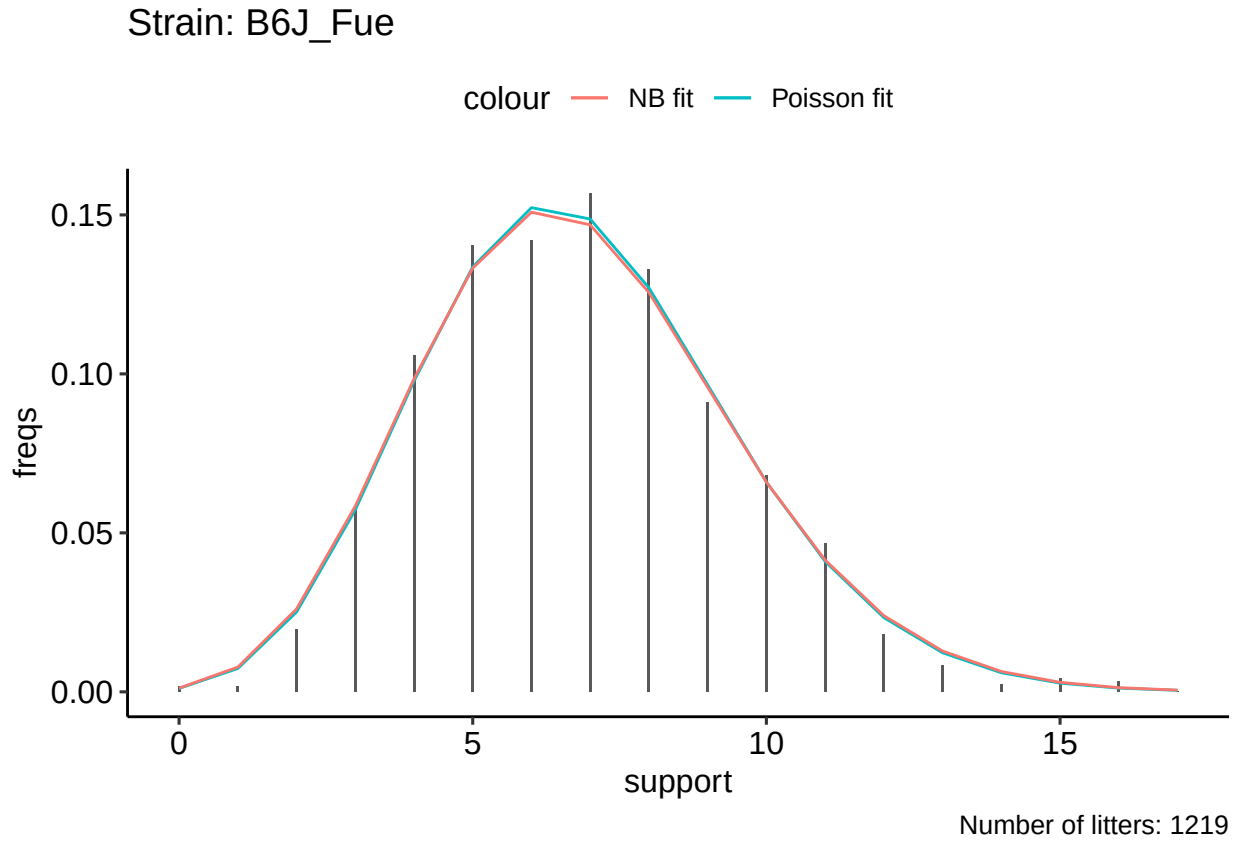
```
##
## [[2]]
```


Strain: B6D2F1
colour
NB fit
Poisson fit
0.15
0.10
0.05
0.00
freqs
0
5
10
15
support
Number of litters: 565

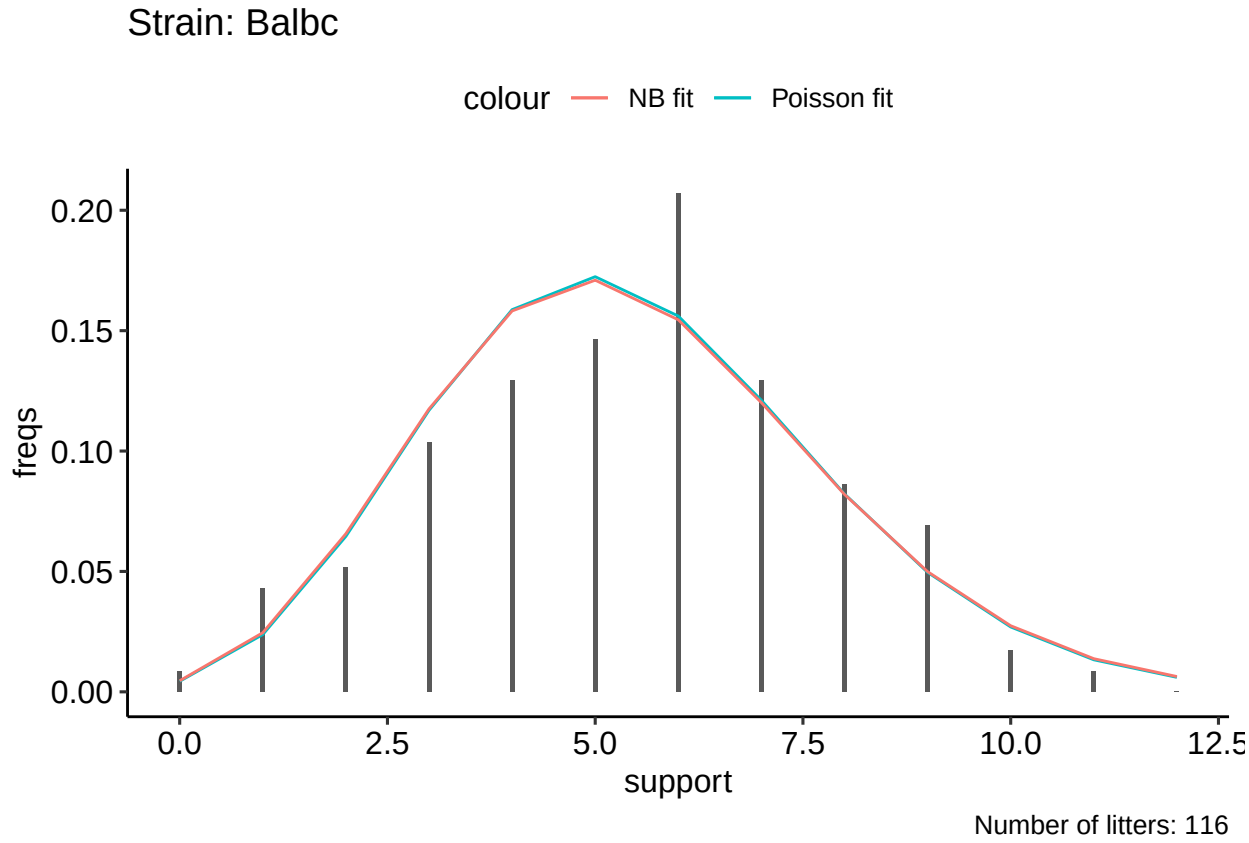
```
##
## [[3]]
```


Strain: B6J_CrlF
colour
NB fit
Poisson fit
0.15
0.10
0.05
0.00
freqs
0
5
10
support
Number of litters: 444

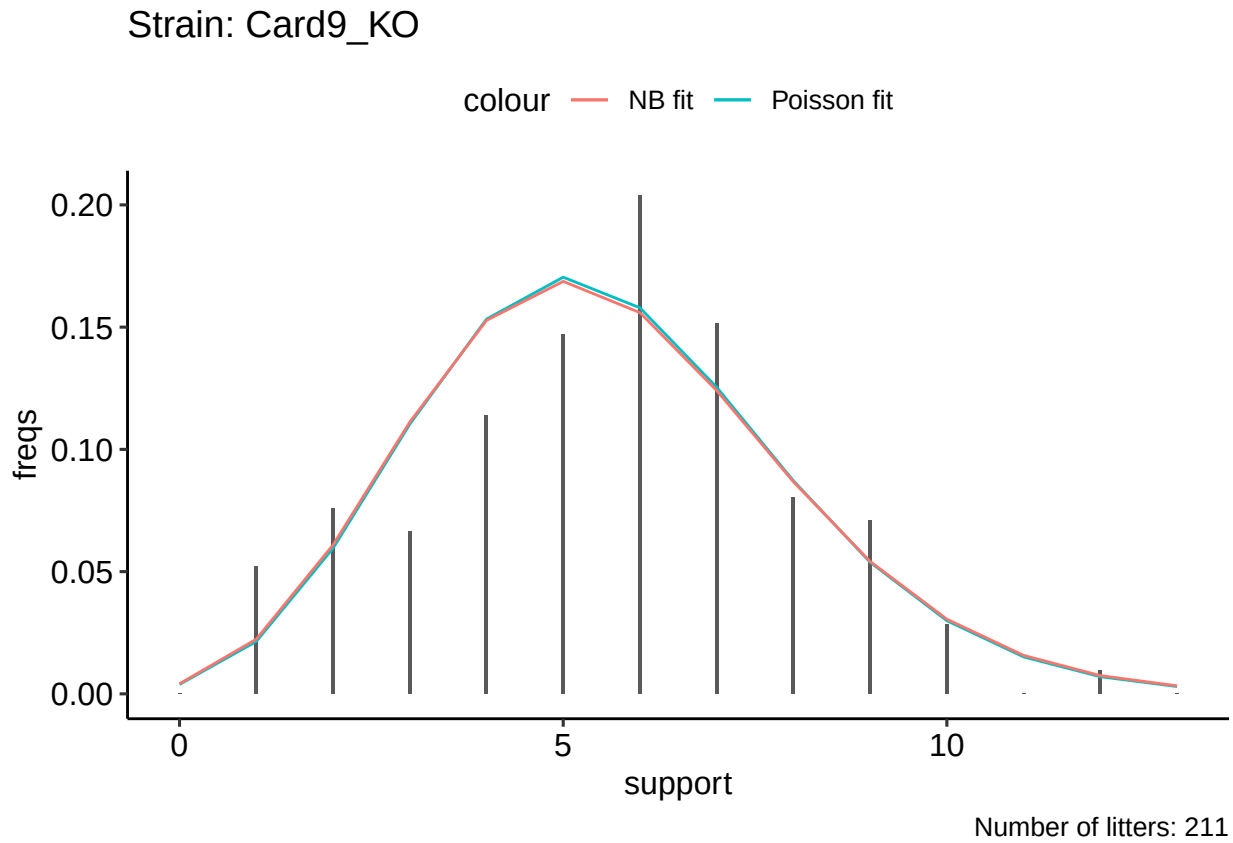
```
##
## [[4]]
```


Strain: B6J_Fue
colour
NB fit
Poisson fit
0.15
0.10
0.05
0.00
freqs
0
5
10
15
support
Number of litters: 1219

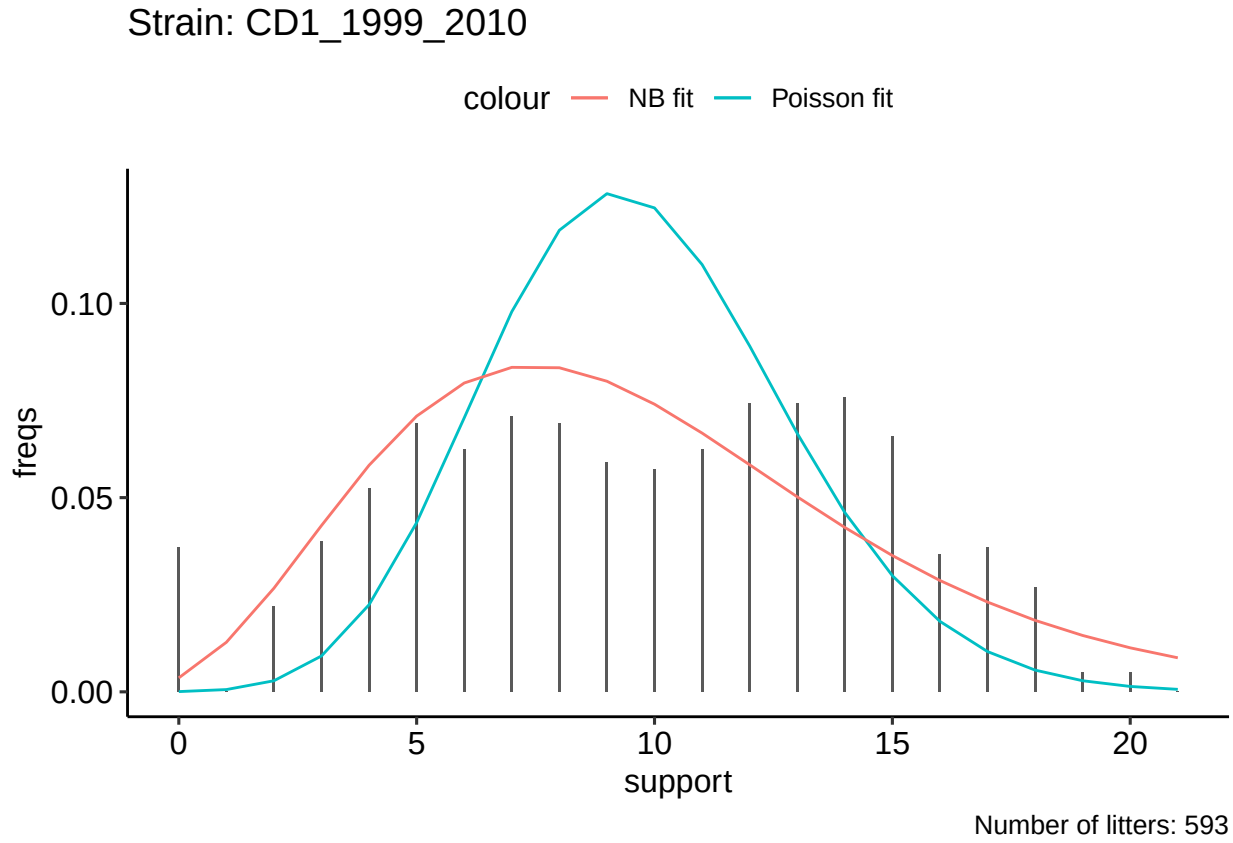
```
##
## [[5]]
```


Strain: Balbc
colour
NB fit
Poisson fit
0.20
0.15
0.10
0.05
0.00
freqs
0.0
2.5
5.0
7.5
10.0
12.5
support
Number of litters: 116

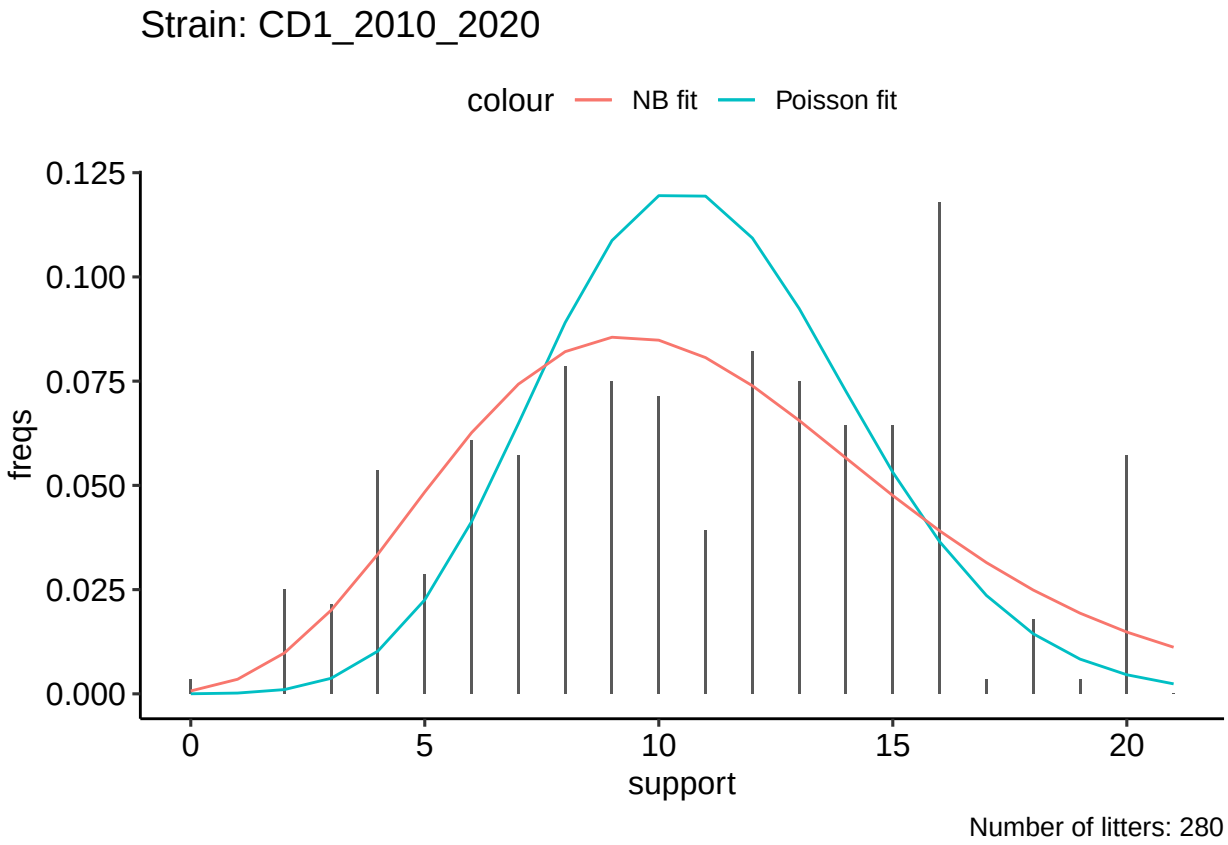
```
##
## [[6]]
```


Strain: Card9_KO
colour
NB fit
Poisson fit
0.20
0.15
0.10
0.05
0.00
freqs
0
5
10
support
Number of litters: 211

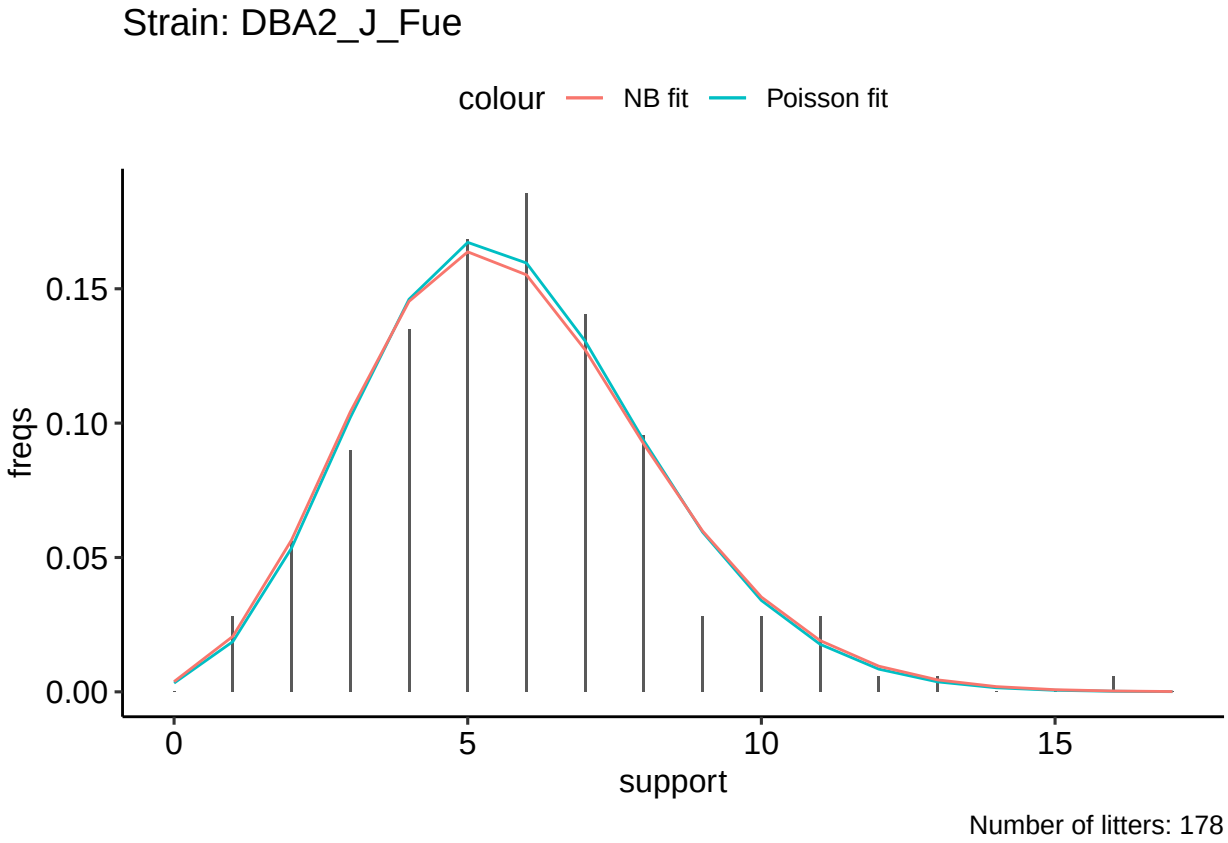
```
##
## [[7]]
```


Strain: CD1_1999_2010
colour
NB fit
Poisson fit
0.10
0.05
0.00
freqs
0
5
10
15
20
support
Number of litters: 593

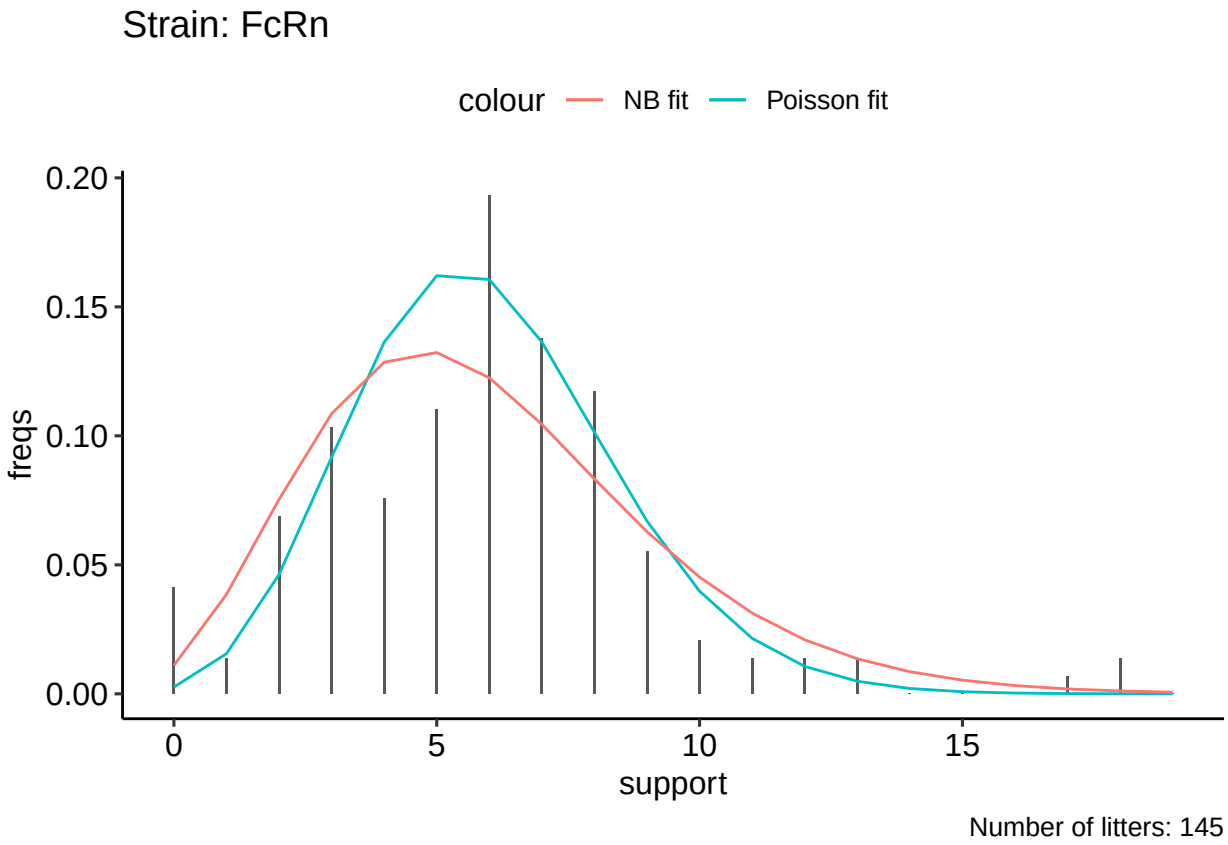
```
##
## [[8]]
```


Strain: CD1_2010_2020
colour
NB fit
Poisson fit
0.125
0.100
0.075
0.050
0.025
0.000
freqs
0
5
10
15
20
support
Number of litters: 280

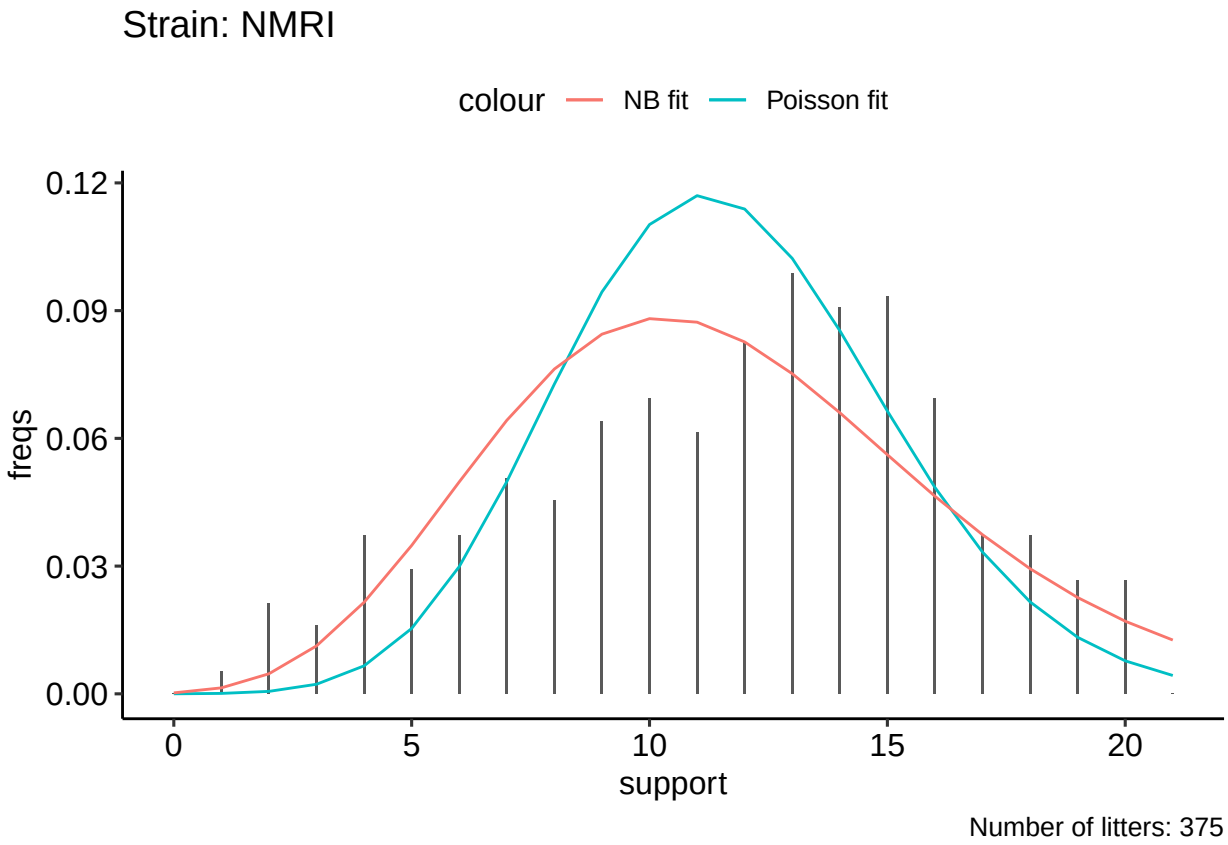
```
##
## [[9]]
```


Strain: DBA2_J_Fue
colour
NB fit
Poisson fit
freqs
0.15
0.10
0.05
0.00
0
5
10
15
support
Number of litters: 178

```
##
## [[10]]
```


Strain: FcRn
colour
NB fit
Poisson fit
0.20
0.15
0.10
0.05
0.00
freqs
0
5
10
15
support
Number of litters: 145

```
##
## [[11]]
```



Litter means etc. by strain

```
names(table_list_clean)
```

```
##  [1] "B6cBrd"        "B6D2F1"        "B6J_CrlF"      "B6J_Fue"
##  [5] "Balbc"         "Card9_KO"      "CD1_1999_2010" "CD1_2010_2020"
##  [9] "DBA2_J_Fue"    "FcRn"          "NMRI"
```

```
mousebreeding_by_strain_clean <- c(
  table_list_clean[c('B6cBrd', 'B6D2F1', 'B6J_CrlF', 'B6J_Fue',
                     'Balbc',
                     'Card9_KO', 'DBA2_J_Fue', 'FcRn', 'NMRI')],
  list(rbind(table_list_clean[["CD1_1999_2010"]],
        table_list_clean[["CD1_2010_2020"]]))
  )
names(mousebreeding_by_strain_clean)[length(mousebreeding_by_strain_clean)] <- "CD1"

str(mousebreeding_by_strain_clean)
```

```
## List of 10
##  $ B6cBrd    :'data.frame':  77 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:77] "13.03.2014" "02.12.2014" "02.11.2014" "07.08.2014" ...
```

```
##   ..$ pups_born   : num [1:77] 8 3 4 5 8 8 8 6 4 6 ...
##   ..$ pups_beforeW: num [1:77] 8 3 4 4 8 8 4 4 4 6 ...
##   ..$ weaned_f    : num [1:77] 6 2 2 2 4 0 2 2 0 3 ...
##   ..$ weaned_m    : num [1:77] 2 1 2 2 4 0 2 2 0 3 ...
##  $ B6D2F1    :'data.frame':  565 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:565] "26.06.2014" "15.05.2014" "19.04.2014" "01.04.2014" ...
##   ..$ pups_born   : num [1:565] 8 6 8 5 7 10 17 2 1 7 ...
##   ..$ pups_beforeW: num [1:565] 8 6 8 7 11 10 14 2 1 6 ...
##   ..$ weaned_f    : num [1:565] 4 4 4 3 6 7 6 1 0 2 ...
##   ..$ weaned_m    : num [1:565] 4 2 4 4 5 3 8 1 0 4 ...
##  $ B6J_CrlF  :'data.frame':  444 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:444] "30.08.2017" "17.07.2017" "01.06.2017" "19.04.2017" ...
##   ..$ pups_born   : num [1:444] 4 4 5 5 2 4 4 2 5 5 ...
##   ..$ pups_beforeW: num [1:444] 4 4 5 5 2 3 4 2 5 5 ...
##   ..$ weaned_f    : num [1:444] 2 2 2 4 1 2 1 0 1 3 ...
##   ..$ weaned_m    : num [1:444] 2 2 2 1 0 1 3 0 4 2 ...
##  $ B6J_Fue   :'data.frame':  1219 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:1219] "15.09.2014" "01.08.2014" "19.06.2014" "24.04.2014" ...
##   ..$ pups_born   : num [1:1219] 4 8 9 4 6 8 8 6 8 4 ...
##   ..$ pups_beforeW: num [1:1219] 4 5 6 7 6 8 8 4 9 9 ...
##   ..$ weaned_f    : num [1:1219] 2 4 5 4 2 4 0 2 5 8 ...
##   ..$ weaned_m    : num [1:1219] 2 1 1 3 4 4 0 2 4 1 ...
##  $ Balbc     :'data.frame':  116 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:116] "05.08.2014" "19.06.2014" "15.05.2014" "17.07.2015" ...
##   ..$ pups_born   : num [1:116] 7 8 5 4 3 4 5 3 7 3 ...
##   ..$ pups_beforeW: num [1:116] 7 7 5 4 3 4 5 3 7 3 ...
##   ..$ weaned_f    : num [1:116] 3 4 3 0 1 2 0 2 0 1 ...
##   ..$ weaned_m    : num [1:116] 4 3 2 0 2 2 0 1 0 2 ...
##  $ Card9_KO  :'data.frame':  211 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:211] "24.08.2019" "11.06.2019" "13.05.2019" "22.04.2019" ...
##   ..$ pups_born   : num [1:211] 10 4 10 1 4 5 5 2 2 4 ...
##   ..$ pups_beforeW: num [1:211] 10 4 10 1 4 5 5 2 2 4 ...
##   ..$ weaned_f    : num [1:211] 4 1 0 0 2 3 1 1 1 3 ...
##   ..$ weaned_m    : num [1:211] 6 3 0 0 2 2 4 1 1 1 ...
##  $ DBA2_J_Fue:'data.frame':  178 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:178] "11.06.2020" "01.05.2020" "04.04.2015" "02.02.2015" ...
##   ..$ pups_born   : num [1:178] 5 5 4 8 2 6 3 3 7 5 ...
##   ..$ pups_beforeW: num [1:178] 5 5 4 8 2 6 2 3 7 5 ...
##   ..$ weaned_f    : num [1:178] 0 1 3 4 0 4 1 0 2 0 ...
##   ..$ weaned_m    : num [1:178] 0 4 1 4 0 2 1 0 5 0 ...
##  $ FcRn      :'data.frame':  145 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:145] "24.07.2019" "17.05.2019" "03.02.2020" "07.01.2020" ...
##   ..$ pups_born   : num [1:145] 5 3 7 7 7 6 4 3 3 6 ...
##   ..$ pups_beforeW: num [1:145] 5 3 7 7 7 4 4 3 3 6 ...
##   ..$ weaned_f    : num [1:145] 3 2 1 4 4 2 2 2 0 3 ...
##   ..$ weaned_m    : num [1:145] 2 0 6 3 3 2 2 0 0 3 ...
##  $ NMRI      :'data.frame':  375 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:375] "26.11.2017" "03.10.2017" "10.09.2017" "13.08.2017" ...
##   ..$ pups_born   : num [1:375] 8 13 4 14 16 12 11 14 10 4 ...
##   ..$ pups_beforeW: num [1:375] 7 13 4 14 16 12 11 14 10 4 ...
##   ..$ weaned_f    : num [1:375] 6 7 3 5 4 8 4 4 6 2 ...
##   ..$ weaned_m    : num [1:375] 0 0 0 0 0 0 0 2 3 0 ...
##  $ CD1       :'data.frame':  873 obs. of  5 variables:
##   ..$ bitrh_dates : chr [1:873] "06.03.2007" "07.03.2007" "06.03.2007" "06.03.2007" ...
```

```
##   ..$ pups_born   : num [1:873] 7 3 3 5 3 7 5 5 5 8 ...
##   ..$ pups_beforeW: num [1:873] 7 3 3 5 3 7 5 5 5 8 ...
##   ..$ weaned_f    : num [1:873] 3 2 1 3 2 4 2 3 1 6 ...
##   ..$ weaned_m    : num [1:873] 4 1 2 2 1 3 3 2 4 2 ...
```

Fertility

```
load("../external/mouse_data/mouse3/fertility/nfemales.Rdata")
pre_tab_list <- lapply(
  names(table_list_clean), FUN = function(df_name){
    df <- table_list_clean[[df_name]]
    originalPDF_file <- summaryDF$originalPDF[which(
        summaryDF$strainNameShort == df_name)]
    df_clean <- as.data.frame(
      apply(data.frame(df[,2:3]),
          c(1,2),
          as.numeric))
    rowmax <- apply(df_clean, 1, max)
    c(
      round(mean(rowmax),1),
      median(rowmax),
      max(rowmax),
      length(rowmax),
      nrow(mousebreeding[[df_name]]),
      nfemales[originalPDF_file],
      df_name)
})
```

```
sum(mousebreeding[[4]]$pups_born==0)
```

```
## [1] 0
```

```
pre_tab_df <- data.frame(do.call(rbind, pre_tab_list))
colnames(pre_tab_df) <- c("mean", "median", "max", "n_trust_breedings", "n_tot_breedings","n_fertile",

#fertility <- round(
#  as.numeric(pre_tab_df$n_fertile)/as.numeric(pre_tab_df$n_tot_breedings)*100,
#  digits = 1)

strain_stats <- data.frame(
            strain = pre_tab_df[,c("strain")],
            #fertility = fertility,
            litter_mean = as.numeric(pre_tab_df[,c("mean")]),
            litter_median = as.numeric(pre_tab_df[,c("median")]),
            litter_max = as.numeric(pre_tab_df[,c("max")]),
            n_trust_breedings = as.numeric(pre_tab_df[,c("n_trust_breedings")]),
            n_tot_breedings = as.numeric(pre_tab_df[,c("n_tot_breedings")])
            #n_fertile = as.numeric(pre_tab_df[,c("n_fertile")])
          )
```

```r
save(strain_stats, file = "strain_stats.Rdata")
write.table(strain_stats, file = "strain_stats.txt",
            quote = FALSE, sep = "\t", row.names = F, col.names = T)
```