

# Fit mutant with binomial aging model

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*June 28 2017 - 13 January, 2018*

```
rm(list=ls())
host = "Applejack" #"Ridgeside"
if (host == "AppleJack") {
  setwd("~/github/bmc_netwk_aging_manuscript/R1/1.kaeberlein04plos")
}
if (host == "Ridgeside") {
}

library('flexsurv')

## Loading required package: survival
library('stringr')
source("../lifespan.r")
list.files()

## [1] "0.example.histogram.density.overlay.Rmd"
## [2] "0.fit.kaeberlein04.html"
## [3] "0.fit.kaeberlein04.pdf"
## [4] "0.fit.kaeberlein04.Rmd"
## [5] "0.histogram.density.overlay.html"
## [6] "0.histogram.density.overlay.Rmd"
## [7] "092304.merged.rls.csv"
## [8] "1.bootstrap.kaeblein04.html"
## [9] "1.bootstrap.kaeblein04.pdf"
## [10] "1.bootstrap.kaeblein04.Rmd"
## [11] "2009"
## [12] "bootstrap"
## [13] "Kerberlein04PLoS.pdf"
## [14] "lifespan.20160926.r"
## [15] "lifespan.r"
## [16] "sandbox"

tb.ori = read.table("092304.merged.rls.csv", header = T, sep="\t")
#summary(tb.ori)
```

## Explore the fitting outcomes of ‘flexsurv’.

```
strains = names(tb.ori)
strains

## [1] "X031104.BY2N.RLS.tab"      "X031104.SK1.RLS.tab"
## [3] "X042204.KLBY4716.RLS.tab"  "X052604.sir2D.rls.tab"
## [5] "X052604.W303.rls.tab"      "X053104.BY4741.rls.tab"
## [7] "X053104.BY4742.rls.tab"    "X053104.JSBY4741.rls.tab"
## [9] "X061004.srp1ts.rls.tab"    "fig1a.BY4742"
```

```

## [11] "fig1a.fob1"                "fig1a.gpa2"
## [13] "fig1a.gpr1"                "fig1a.hxk2"
## [15] "fig1b.BY4742"              "fig1b.fob1"
## [17] "fig1b.hxk2"                "fig1b.fob1.hxk2"
## [19] "fig1c.BY4742"              "fig1c.fob1"
## [21] "fig1c.gpa2"                "fig1c.fob1.gpa2"
## [23] "fig2a.BY4742"              "fig2a.sir2"
## [25] "fig2a.hxk2.sir2"           "fig2a.gpa2.sir2"
## [27] "fig2b.BY4742"              "fig2b.sir2"
## [29] "fig2b.sir2.fob1"           "fig2c.BY4742"
## [31] "fig2c.sir2.fob1"           "fig2c.sir2.fob1.hxk2"
## [33] "fig2d.BY4742"              "fig2d.sir2.fob1"
## [35] "fig2d.gpa2.sir2.fob1"      "fig3.by4742.2glucose"
## [37] "fig3.sir2.fob1.2glucose"    "fig3.by4742.05glucose"
## [39] "fig3.sir2.fob1.05glucose"    "fig3.WT.01glucose"
## [41] "fig3.sir2.fob1.01glucose"    "fig3.by4742.005glucose"
## [43] "fig3.sir2.fob1.005glucose"    "fig4a.PSY316"
## [45] "fig4a.PSY316.fob1"          "fig4a.PSY316.sir2ox"
## [47] "fig4b.BY4742.2glucose"       "fig4b.BY4742.005glucose"
## [49] "fig4b.by4742.SIR2.ox.2glucose" "fig4b.by4742.SIR2.ox.005glucose"

my.strains = c("fig4b.BY4742.2glucose", "fig4b.by4742.SIR2.ox.2glucose", "fig2a.sir2", "fig2b.sir2",
#my.strains = strains
tb = tb.ori[, my.strains]

report = data.frame(my.strains)
report$samplesize = NA; report$R=NA; report$t0=NA; report$n=NA; report$G=NA; #report$longfilename=NA;

```

## Now, fit all RLS data sets by strains

```

for( i in 1:length(report[,1])){
  #report$samplesize[i] = length(tb[,i])
  my.data = tb[,i]
  my.data = my.data[! is.na(my.data)]
  report$samplesize[i] = length(my.data)

  GompFlex = flexsurvreg(formula = Surv(tb[,i]) ~ 1, dist = 'gompertz')
  WeibFlex = flexsurvreg(formula = Surv(tb[,i]) ~ 1, dist = 'weibull')

  report$avgLS[i] = mean(tb[,i], na.rm=T)
  report$stdLS[i] = sd(tb[,i], na.rm = T)
  report$CV[i] = report$stdLS[i] / report$avgLS[i]

  report$GompGFlex[i] = GompFlex$res[1,1]
  report$GompRFlex[i] = GompFlex$res[2,1]
  report$GompLogLikFlex[i] = round(GompFlex$loglik, 1)
  report$GompAICFlex[i] = round(GompFlex$AIC)

  report$WeibShapeFlex[i] = WeibFlex$res[1,1]
  report$WeibRateFlex[i] = WeibFlex$res[2,1]
  report$WeibLogLikFlex[i] = round(WeibFlex$loglik, 1)
  report$WeibAICFlex[i] = round(WeibFlex$AIC)
}

```

```

#set initial values
Rhat = report$GompRFlex[i]; # 'i' was missing. a bug costed HQ a whole afternoon.
Ghat = report$GompGFlex[i];
nhath = 6;
t0= (nhath-1)/Ghat;
fitBinom = optim ( c(Rhat, t0, nhath), llh.binomialMortality.single.run,
                    lifespan=tb[,i],
                    #method='SANN') #SANN needs control
                    method="L-BFGS-B",
                    lower=c(1E-10, 1, 1), upper=c(1,200,20) );
report[i, c("R", "t0", "n")] = fitBinom$par[1:3]
report$G[i] = (report$n[i] - 1)/report$t0[i]
}

```

Show the results

```

#report[ grep("tBY", report$strains), ]
report

```

```

##              my.strains samplesize          R          t0          n
## 1      fig4b.BY4742.2glucose          60 0.002388227 35.59111 7.703055
## 2 fig4b.by4742.SIR2.ox.2glucose          60 0.003068054 66.82089 8.067874
## 3              fig2a.sir2          90 0.002656909 16.80162 8.109348
## 4              fig2b.sir2          90 0.002656909 16.80162 8.109348
## 5              fig1b.BY4742          250 0.004796452 58.10834 8.109395
## 6              fig1b.fob1          140 0.003056547 71.37470 7.695271
## 7              fig1b.hxk2          120 0.005736777 103.59300 7.578456
## 8      fig1b.fob1.hxk2          160 0.005902597 120.65937 6.023612
##              G      avgLS      stdLS      CV GompGFlex GompRFlex
## 1 0.18833511 26.06667 7.557389 0.2899254 0.13946781 0.002283890
## 2 0.10577341 34.60000 10.834972 0.3131495 0.07468834 0.004042203
## 3 0.42313480 13.96667 3.491402 0.2499810 0.27970246 0.003555048
## 4 0.42313480 13.96667 3.491402 0.2499810 0.27970246 0.003555048
## 5 0.12234725 26.62400 9.418144 0.3537464 0.08544660 0.006577615
## 6 0.09380453 37.75000 13.405746 0.3551191 0.06987148 0.003424637
## 7 0.06350290 36.73333 16.338197 0.4447785 0.04823602 0.006725196
## 8 0.04163466 48.28125 21.337707 0.4419460 0.04143860 0.004249514
## GompLogLikFlex GompAICFlex WeibShapeFlex WeibRateFlex WeibLogLikFlex
## 1      -206.8          418      3.925269      28.75636      -206.2
## 2      -235.6          475      3.369961      38.51039      -227.8
## 3      -246.0          496      4.431406      15.29449      -240.4
## 4      -246.0          496      4.431406      15.29449      -240.4
## 5      -937.3         1879      3.024640      29.77138      -914.0
## 6      -565.5         1135      3.139805      42.25834      -559.6
## 7      -507.6         1019      2.397501      41.42400      -502.2
## 8      -713.6         1431      2.441562      54.41078      -714.3
## WeibAICFlex
## 1          416
## 2          460
## 3          485
## 4          485
## 5         1832
## 6         1123
## 7         1008

```

## 8 1433

Output

```
write.csv(report, file = 'sandbox/_report_kaeberlein04_fit.csv', row.names = FALSE)
```

## Overlay the binomial aging model with observation.

see <http://hongqinlab.blogspot.com/2013/12/binomial-mortality-model.html>  $m = R ( 1 + t/t_0 )^{(n-1)}$   $s = \exp( (R t_0/n) * (1 - (1+t/t_0)^n ) )$

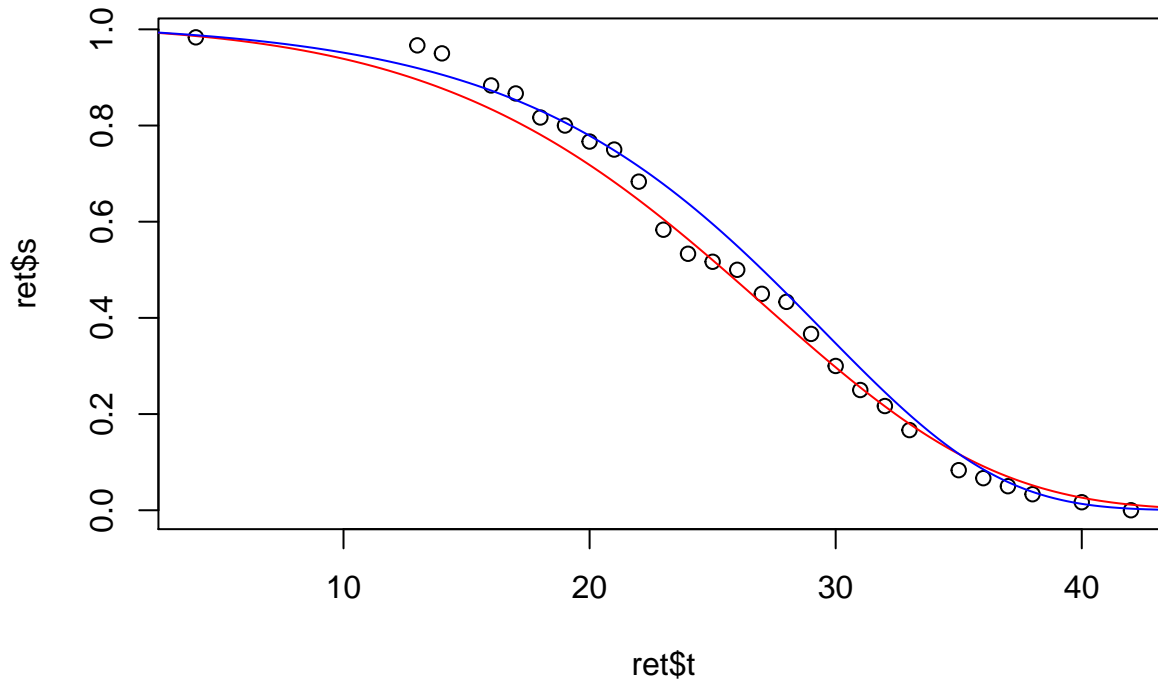
```
for( i in 1:length(report[,1])){
  #report$samplesize[i] = length(tb[,i])
  my.data = tb[,i]
  my.data = my.data[! is.na(my.data)]

  ret = calculate.s(my.data)
  plot( ret$s ~ ret$t, main=my.strains[i]);
  print (report[i, ]);

  #overlay binomial aging viability
  print (report[i, c("R", "t0", "n", "G")] );
  t = seq(0,max(ret$t*1.1), by=0.1);
  # s = exp( (R t0/n)*(1 - (1+t/t0)^n ) )
  s = exp( (report$R[i]* report$t0[i]/report$n[i])*(1 - (1+t/report$t0[i])^report$n[i] ) ) ;
  lines(s ~ t, col='red')

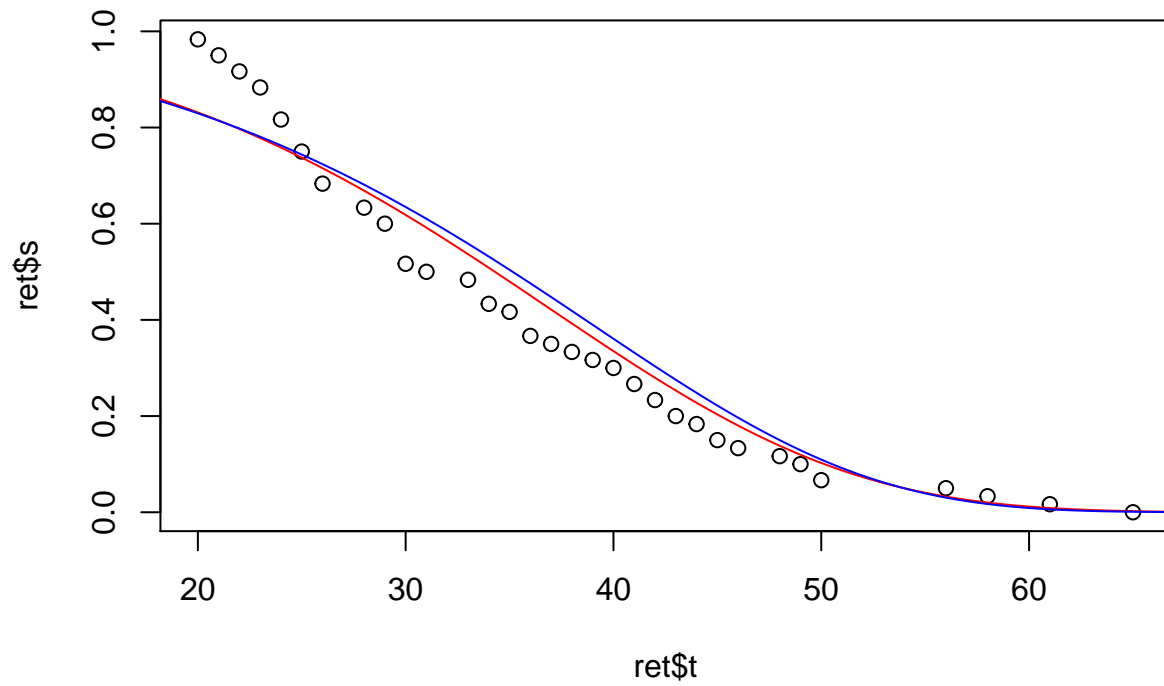
  #overlay gompertz viability
  s.g = G.s( c(report$GompRFlex[i], report$GompGFlex[i], 0), t )
  lines(s.g ~ t, col='blue')
}
```

**fig4b.BY4742.2glucose**



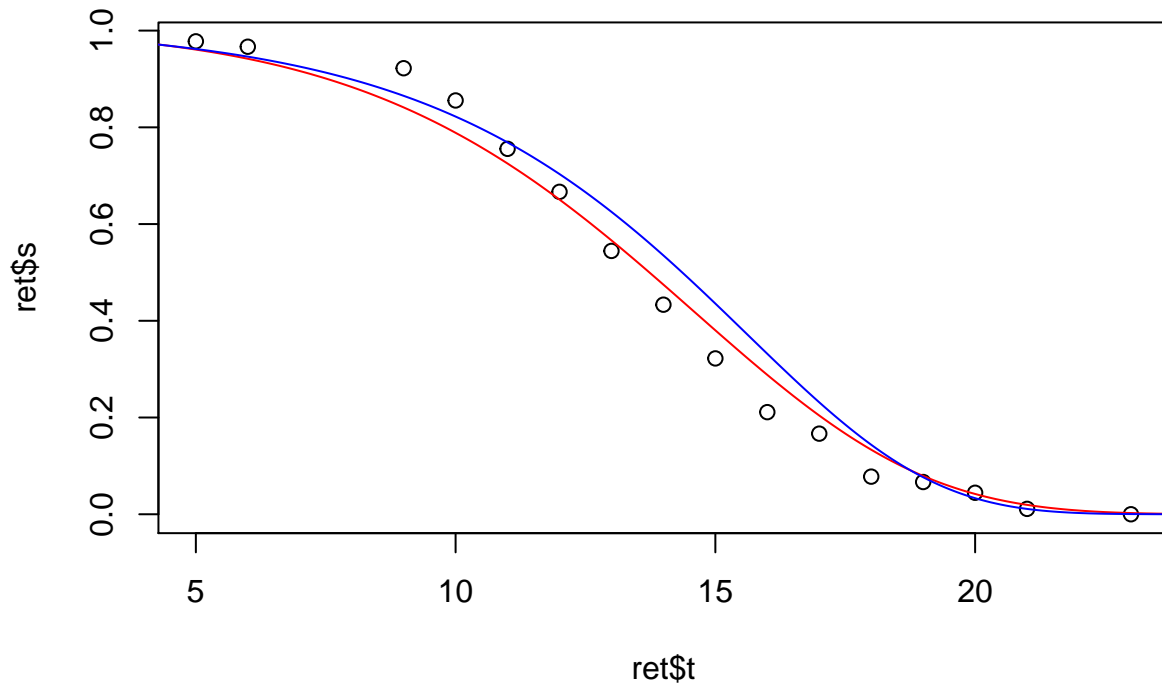
```
##          my.strains samplesize      R      t0      n      G
## 1 fig4b.BY4742.2glucose      60 0.002388227 35.59111 7.703055 0.1883351
##      avgLS      stdLS      CV GompGFlex  GompRFlex  GompLogLikFlex
## 1 26.06667 7.557389 0.2899254 0.1394678 0.00228389      -206.8
##      GompAICFlex WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 1      418      3.925269      28.75636      -206.2      416
##      R      t0      n      G
## 1 0.002388227 35.59111 7.703055 0.1883351
```

**fig4b.by4742.SIR2.ox.2glucose**



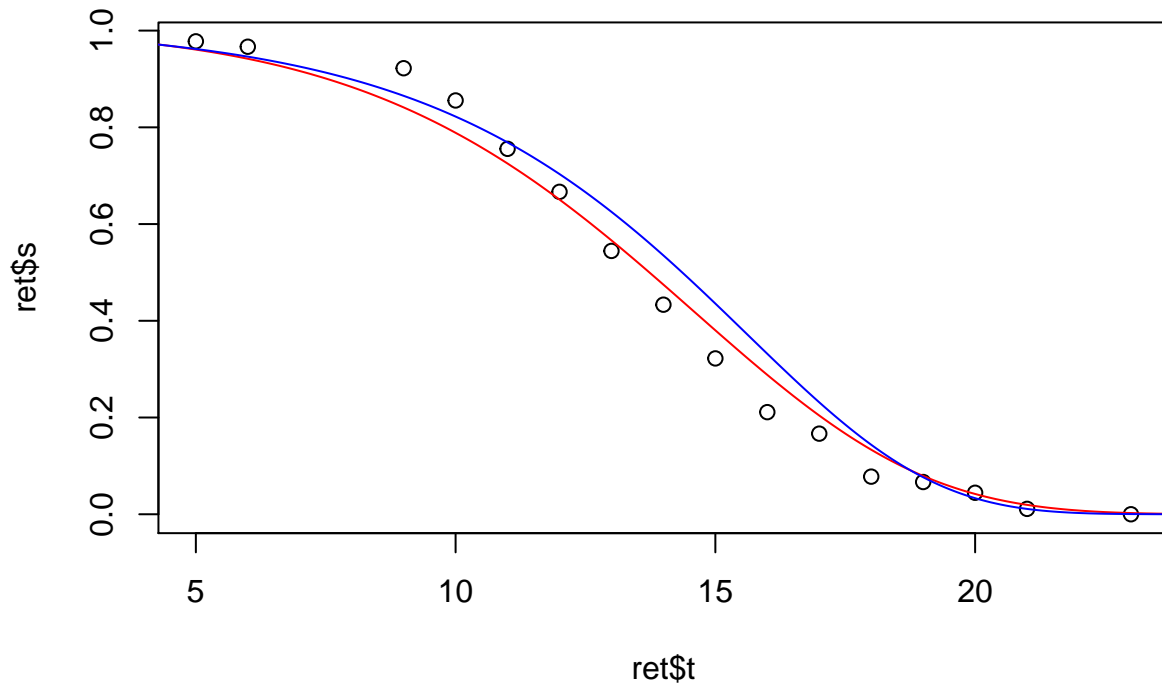
```
##          my.strains samplesize      R      t0      n
## 2 fig4b.by4742.SIR2.ox.2glucose      60 0.003068054 66.82089 8.067874
##          G avgLS   stdLS      CV GompGFlex  GompRFlex GompLogLikFlex
## 2 0.1057734 34.6 10.83497 0.3131495 0.07468834 0.004042203      -235.6
##  GompAICFlex WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 2          475      3.369961      38.51039      -227.8      460
##          R      t0      n      G
## 2 0.003068054 66.82089 8.067874 0.1057734
```

**fig2a.sir2**



```
## my.strains samplesize      R      t0      n      G      avgLS
## 3 fig2a.sir2          90 0.002656909 16.80162 8.109348 0.4231348 13.96667
##      stdLS      CV GompGFlex  GompRFlex GompLogLikFlex GompAICFlex
## 3 3.491402 0.249981 0.2797025 0.003555048          -246          496
##      WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 3      4.431406      15.29449          -240.4          485
##      R      t0      n      G
## 3 0.002656909 16.80162 8.109348 0.4231348
```

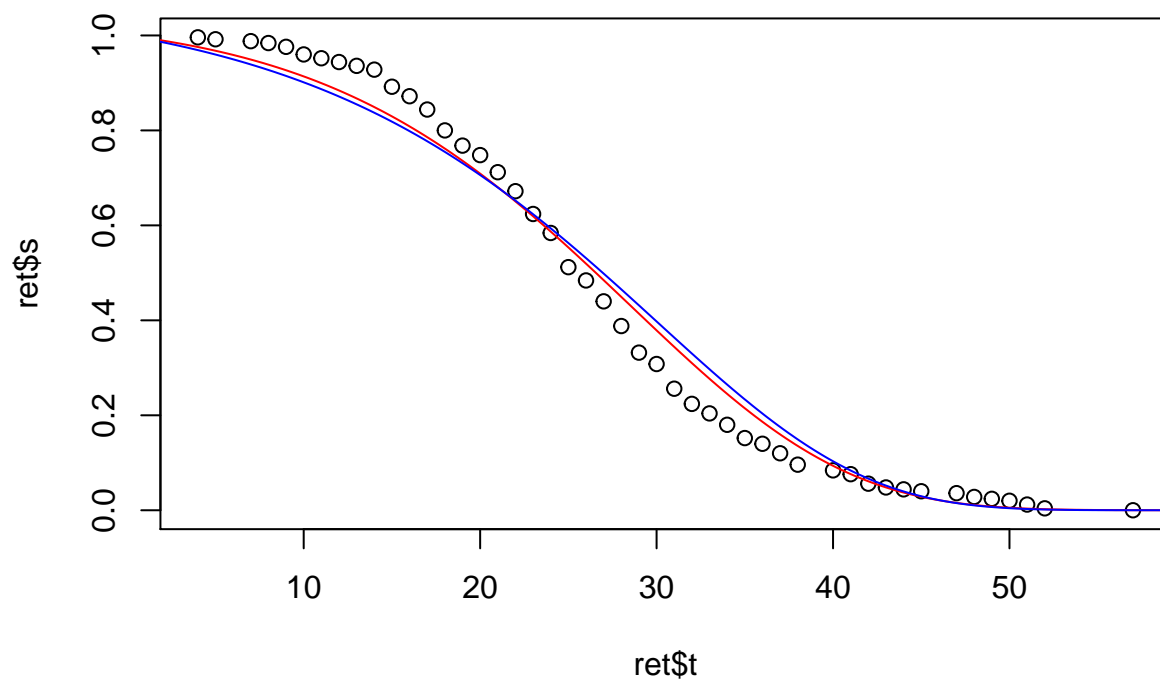
**fig2b.sir2**



```
## my.strains samplesize      R      t0      n      G      avgLS
## 4 fig2b.sir2          90 0.002656909 16.80162 8.109348 0.4231348 13.96667
##      stdLS      CV GompGFlex  GompRFlex GompLogLikFlex GompAICFlex
## 4 3.491402 0.249981 0.2797025 0.003555048          -246          496
##      WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 4      4.431406      15.29449          -240.4          485
##      R      t0      n      G
## 4 0.002656909 16.80162 8.109348 0.4231348
```

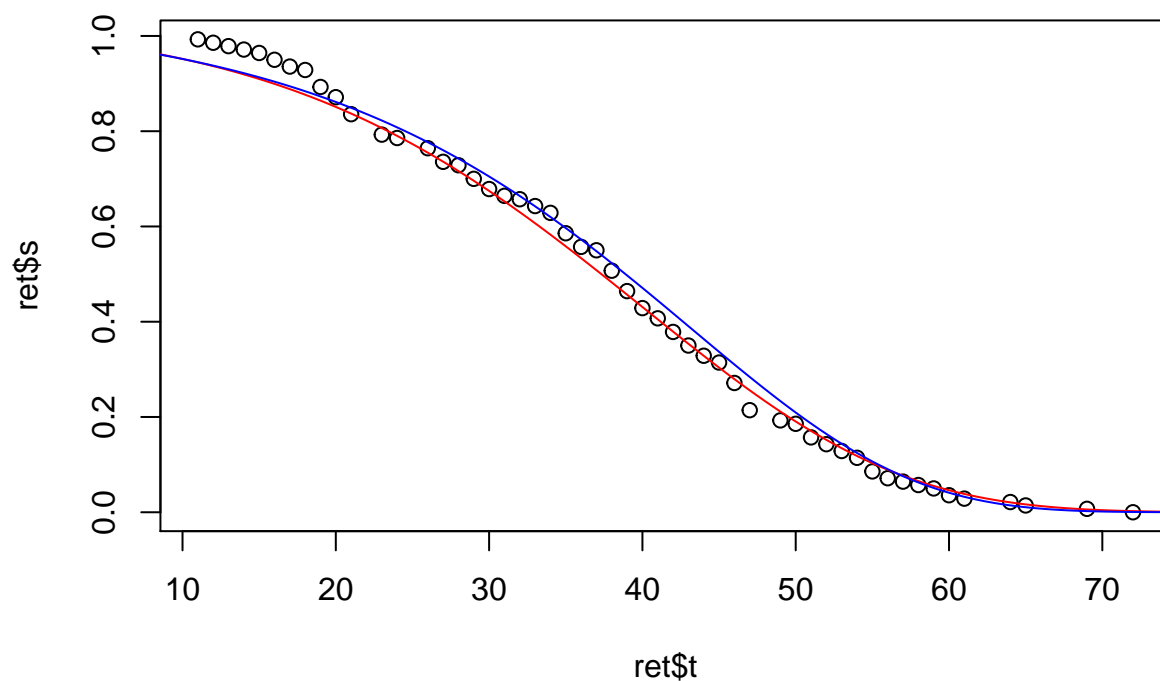


**fig1b.BY4742**



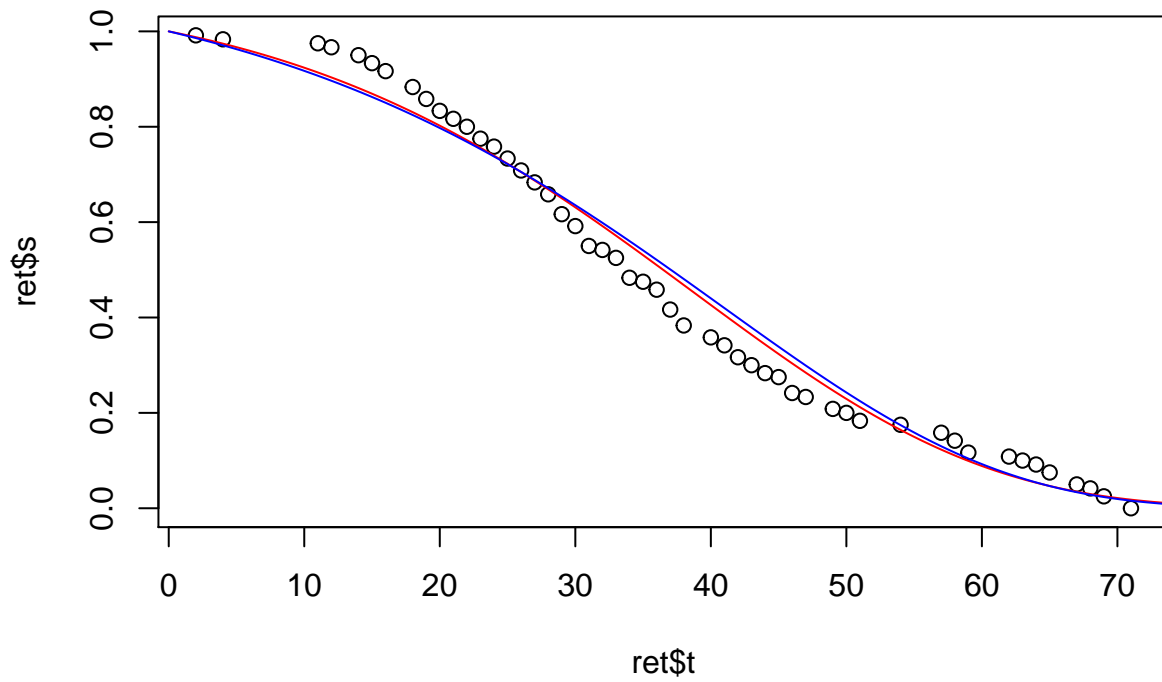
```
##      my.strains samplesize      R      t0      n      G avgLS
## 5 fig1b.BY4742          250 0.004796452 58.10834 8.109395 0.1223473 26.624
##      stdLS      CV GompGFlex  GompRFlex GompLogLikFlex GompAICFlex
## 5 9.418144 0.3537464 0.0854466 0.006577615      -937.3      1879
##      WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 5      3.02464      29.77138      -914      1832
##      R      t0      n      G
## 5 0.004796452 58.10834 8.109395 0.1223473
```

**fig1b.fob1**



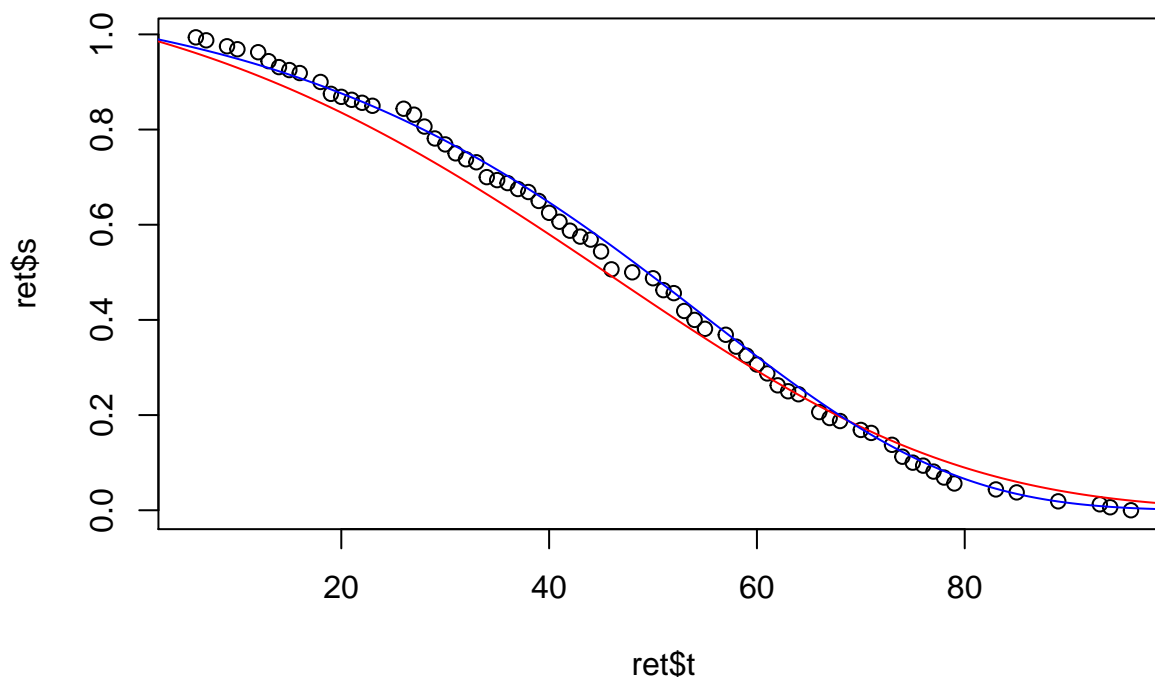
```
## my.strains samplesize      R      t0      n      G avgLS
## 6 fig1b.fob1      140 0.003056547 71.3747 7.695271 0.09380453 37.75
##      stdLS      CV GompGFlex  GompRFlex GompLogLikFlex GompAICFlex
## 6 13.40575 0.3551191 0.06987148 0.003424637      -565.5      1135
##      WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 6      3.139805      42.25834      -559.6      1123
##      R      t0      n      G
## 6 0.003056547 71.3747 7.695271 0.09380453
```

fig1b.hxk2



```
## my.strains samplesize      R      t0      n      G      avgLS
## 7 fig1b.hxk2          120 0.005736777 103.593 7.578456 0.0635029 36.73333
##      stdLS          CV  GompGFlex  GompRFlex GompLogLikFlex GompAICFlex
## 7 16.3382 0.4447785 0.04823602 0.006725196      -507.6      1019
##      WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 7      2.397501      41.424      -502.2      1008
##              R      t0      n      G
## 7 0.005736777 103.593 7.578456 0.0635029
```

fig1b.fob1.hxk2



```
##      my.strains samplesize      R      t0      n      G
## 8 fig1b.fob1.hxk2      160 0.005902597 120.6594 6.023612 0.04163466
##      avgLS      stdLS      CV GompGFlex  GompRFlex GompLogLikFlex
## 8 48.28125 21.33771 0.441946 0.0414386 0.004249514      -713.6
##      GompAICFlex WeibShapeFlex WeibRateFlex WeibLogLikFlex WeibAICFlex
## 8      1431      2.441562      54.41078      -714.3      1433
##      R      t0      n      G
## 8 0.005902597 120.6594 6.023612 0.04163466
```

## over probability mass function with binomial model

see <http://hongqinlab.blogspot.com/2013/12/binomial-mortality-model.html>  $m = R ( 1 + t/t_0 )^{(n-1)}$   $s = \exp( (R t_0/n)(1 - (1+t/t_0)^n ) )$   
 $pdf = sm$

```
for( i in 1:length(report[,1])){
  #report$samplesize[i] = length(tb[,i])
  my.data = tb[,i]
  my.data = my.data[! is.na(my.data)]

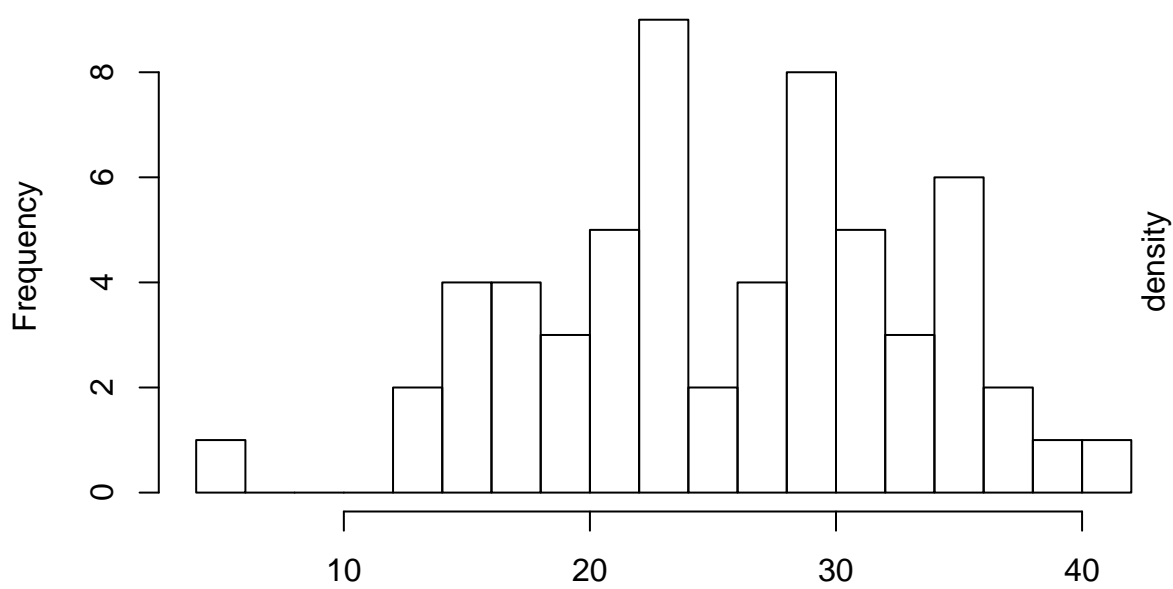
  h= hist(my.data, br=max(my.data)/2)
  plot( h$density ~ h$mids, main=my.strains[i], xlab="RLS",ylab="density")
  t= seq(0, max(h$mids), by=0.1)
  s = exp( (report$R[i]* report$t0[i]/report$n[i])*(1 - (1+t/report$t0[i])^report$n[i] ) ) ;
  m = report$R[i]*(1 + t/ report$t0[i])^(report$n[i] -1 )
  pdf = s*m
  lines( pdf ~ t, col='red')
```

```

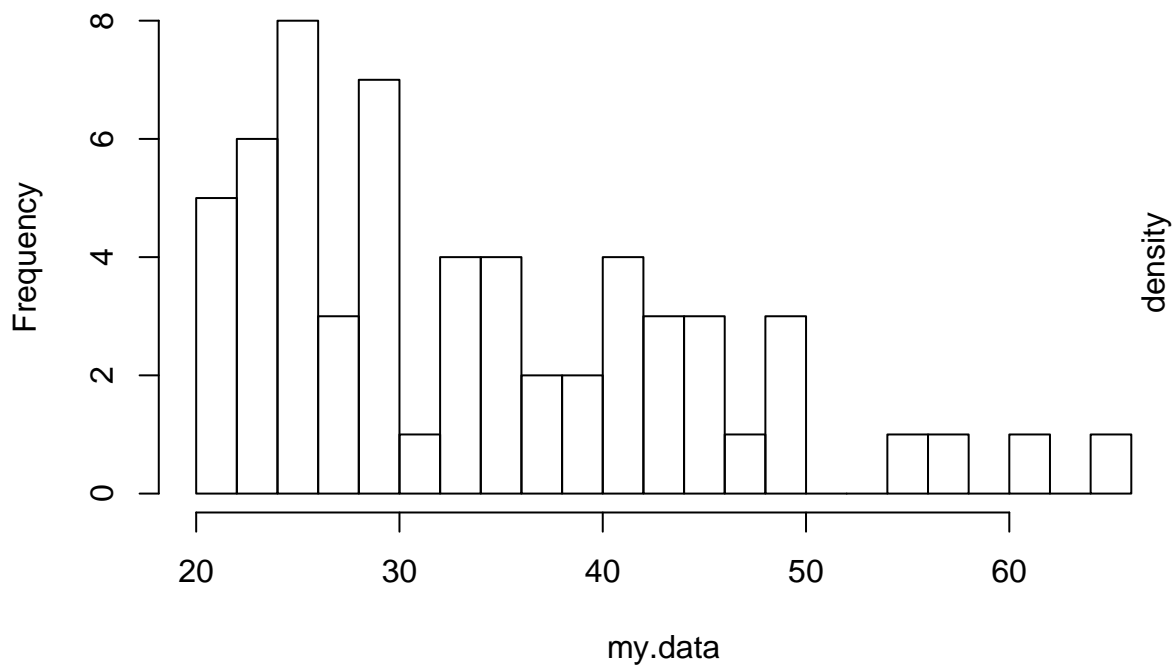
s.g = G.s( c(report$GompRFlex[i], report$GompGFlex[i]), t );
m.g = report$GompRFlex[i]*exp(report$GompGFlex[i]*t)
pdf.g = s.g * m.g
lines( pdf.g ~ t, col="blue")
}

```

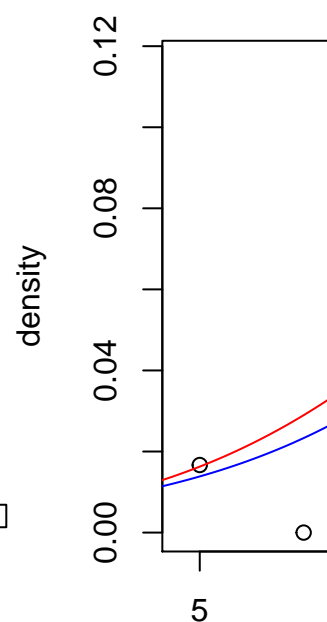
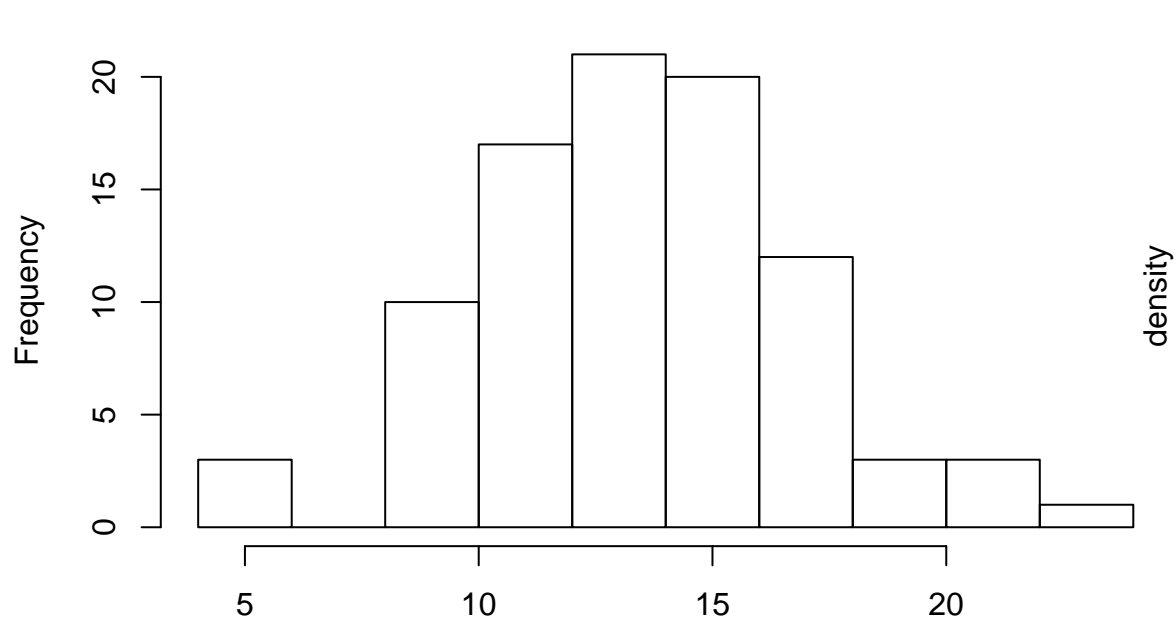
**Histogram of my.data**



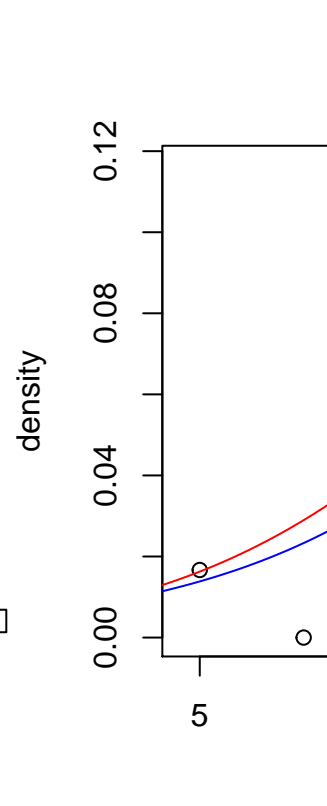
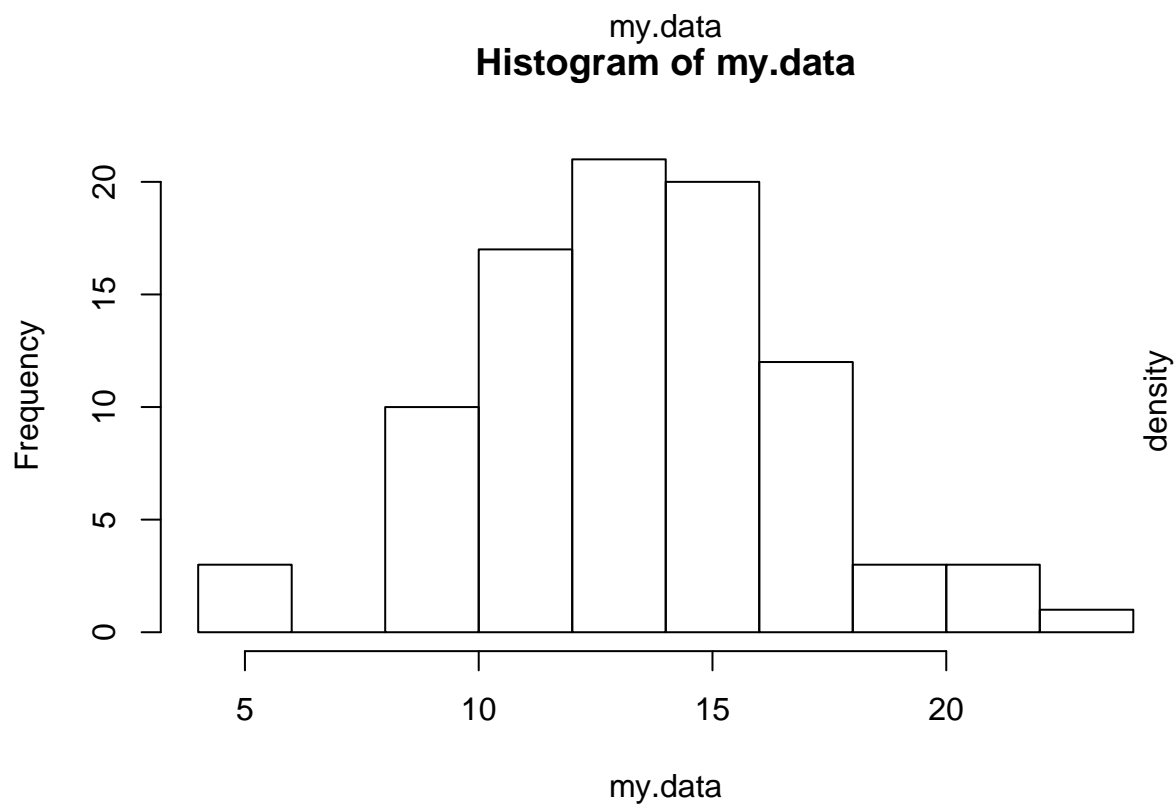
**Histogram of my.data**



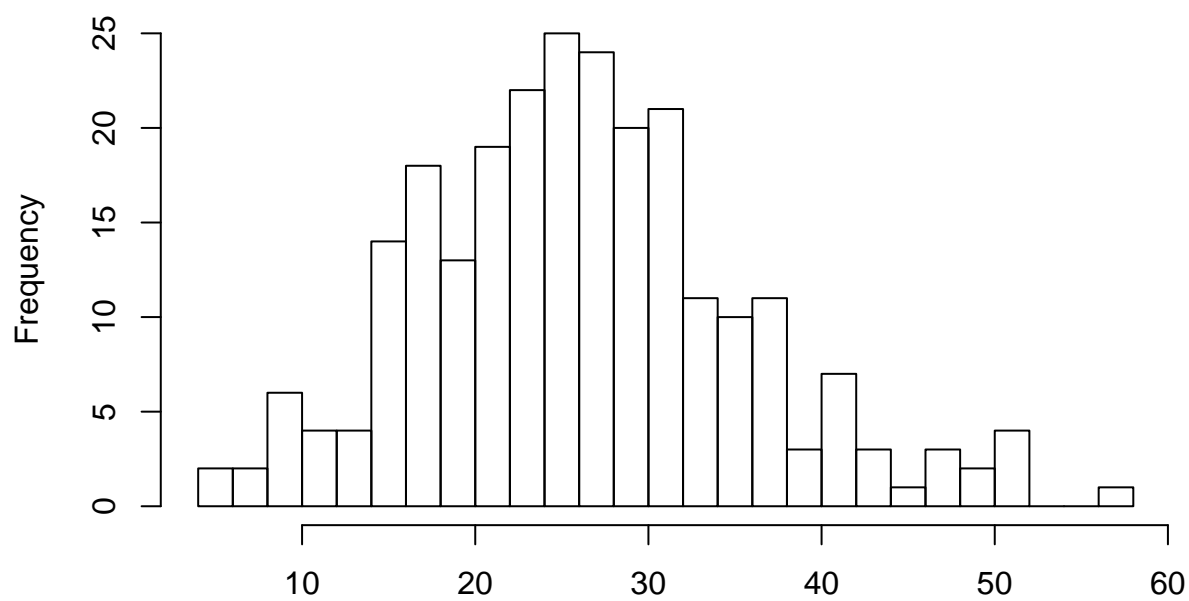
**Histogram of my.data**



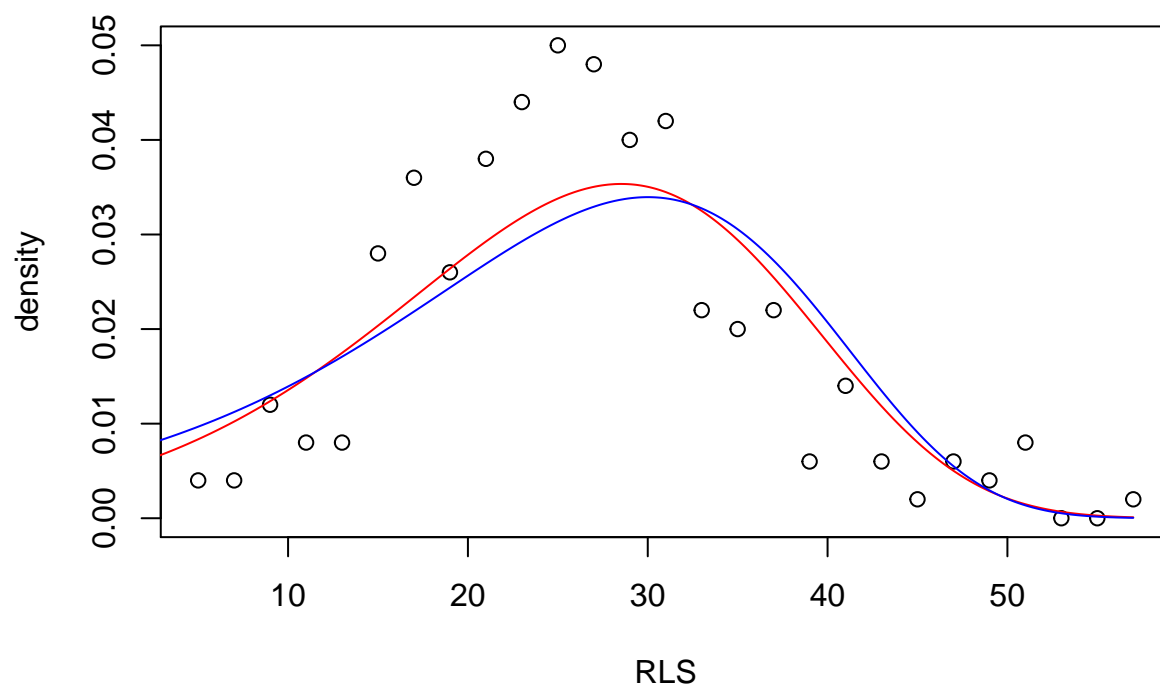
**Histogram of my.data**



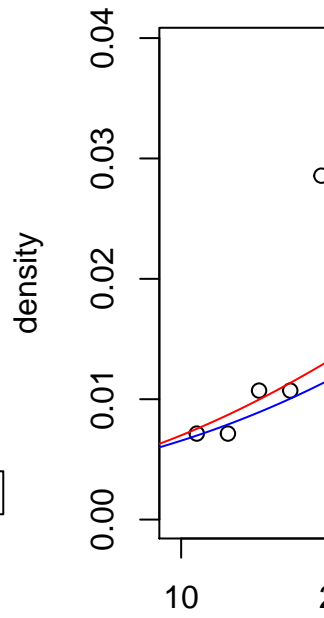
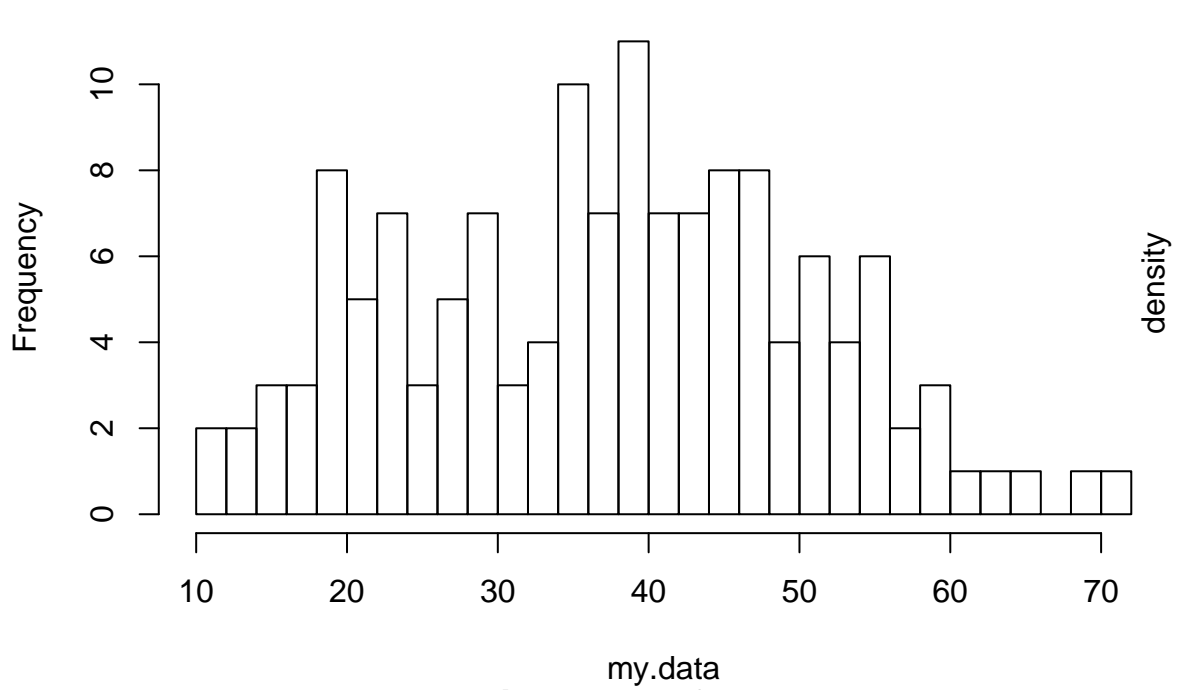
**Histogram of my.data**



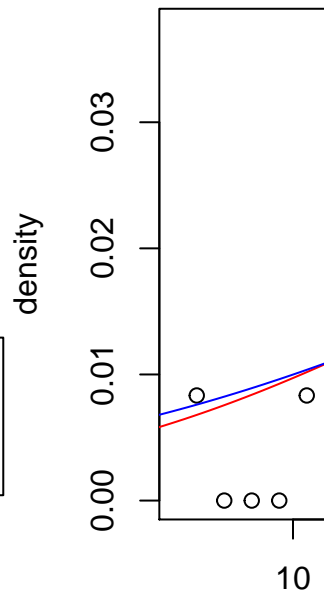
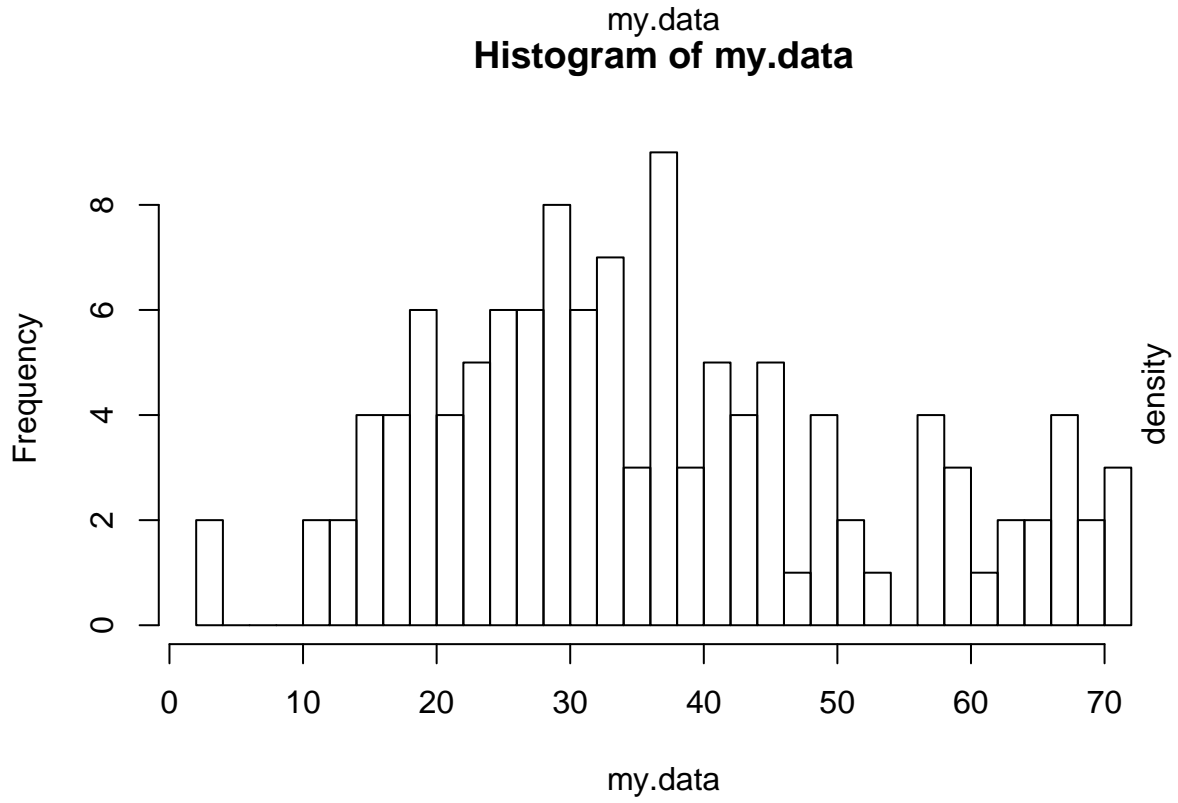
my.data  
**fig1b.BY4742**



**Histogram of my.data**

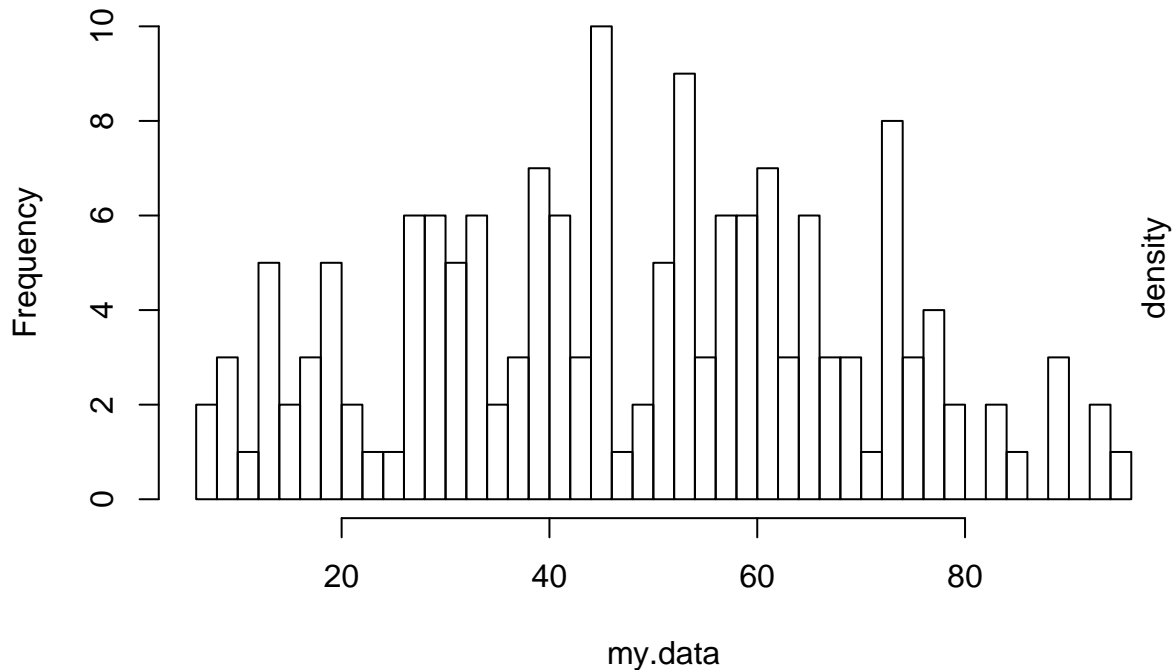


**Histogram of my.data**





## Histogram of my.data



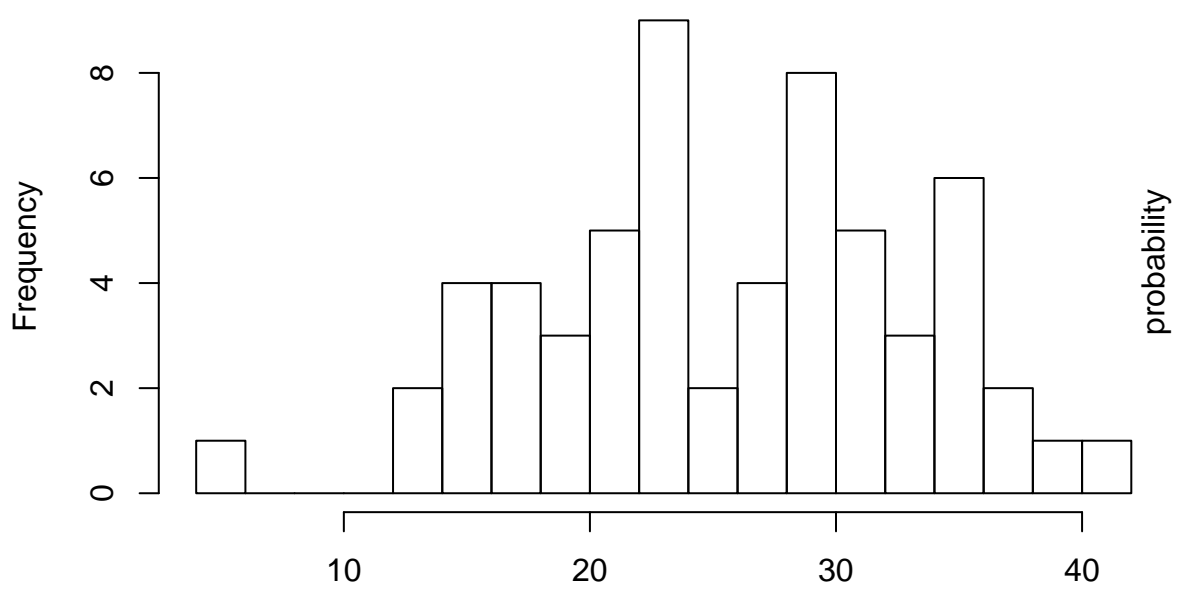
It seems binomial model aging is a reasonable fit whenevern Gompertz model is a reasonable fit.

```
for( i in 1:length(report[,1])){
  my.data = tb[,i]
  my.data = my.data[! is.na(my.data)]

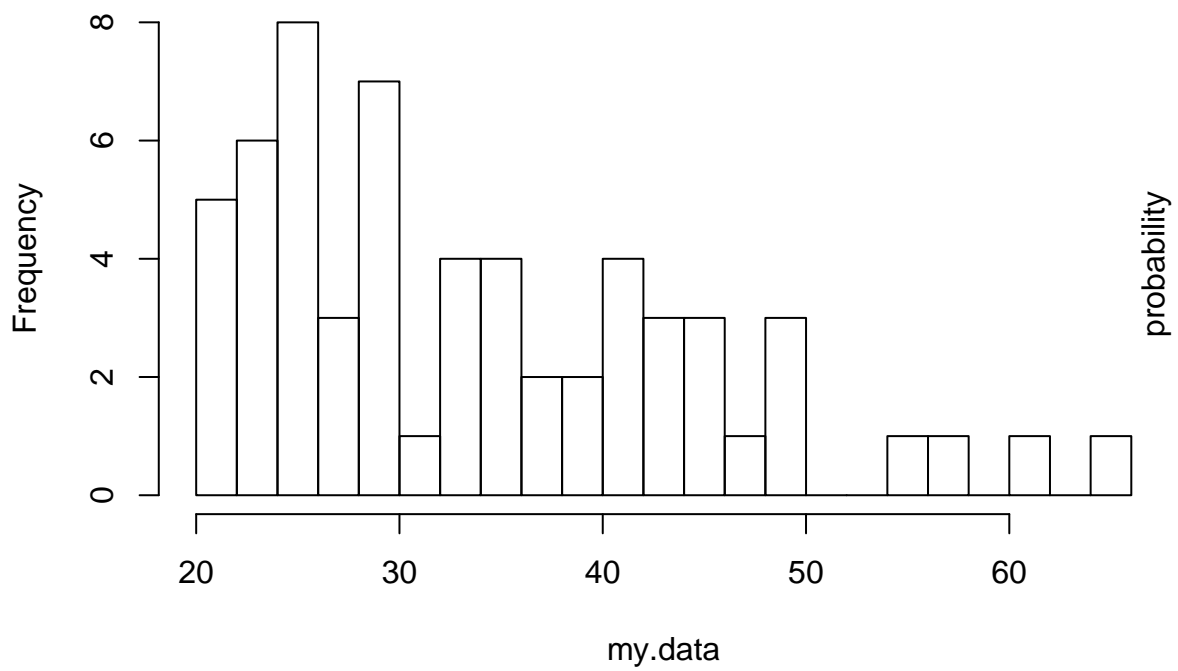
  h= hist(my.data, br=max(my.data)/2);
  hist(my.data, probability = TRUE, col='gray', border='white', xlab='RLS', ylab='probability',
        main=my.strains[i], ylim=c(0, max(h$density)*1.1), xlim=c(0, max(h$mids)*1.1))
  #plot( h$density ~ h$mids, main=my.strains[i], xlab="RLS",ylab="density")
  #par(new=TRUE);
  t= seq(0, max(h$mids)*1.2, by=0.1)
  s = exp( (report$R[i]* report$t0[i]/report$n[i])*(1 - (1+t/report$t0[i])^report$n[i] ) ) );
  m = report$R[i]*(1 + t/ report$t0[i])^(report$n[i] -1 )
  pdf = s*m
  lines( pdf ~ t, col='red')

  s.g = G.s( c(report$GompRFlex[i], report$GompGFlex[i]), t );
  m.g = report$GompRFlex[i]*exp(report$GompGFlex[i]*t)
  pdf.g = s.g * m.g
  lines( pdf.g ~ t, col="blue")
}
```

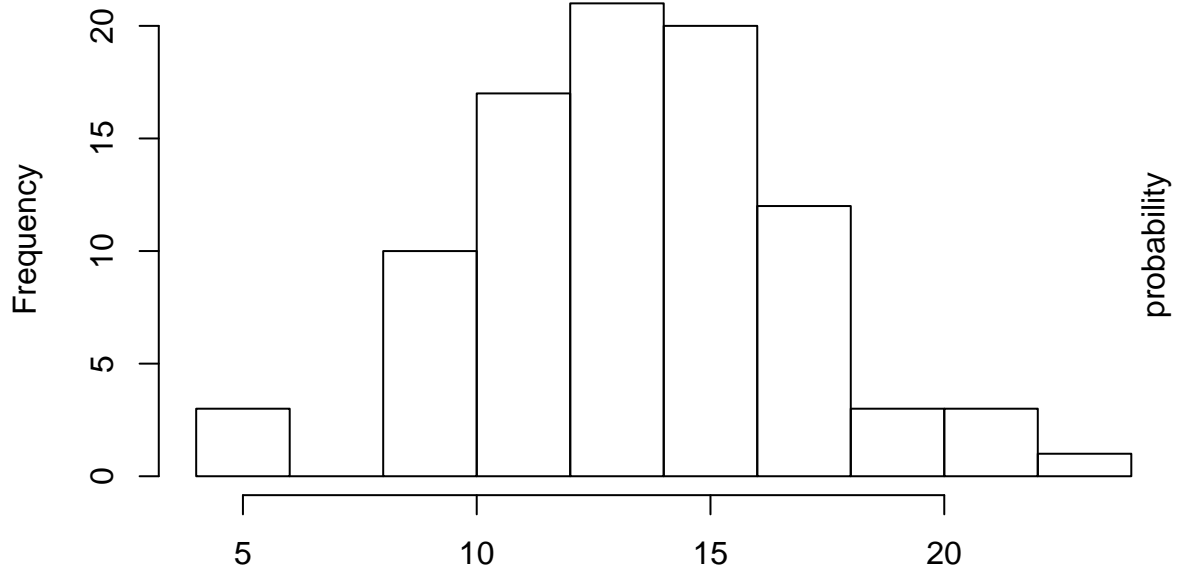
**Histogram of my.data**



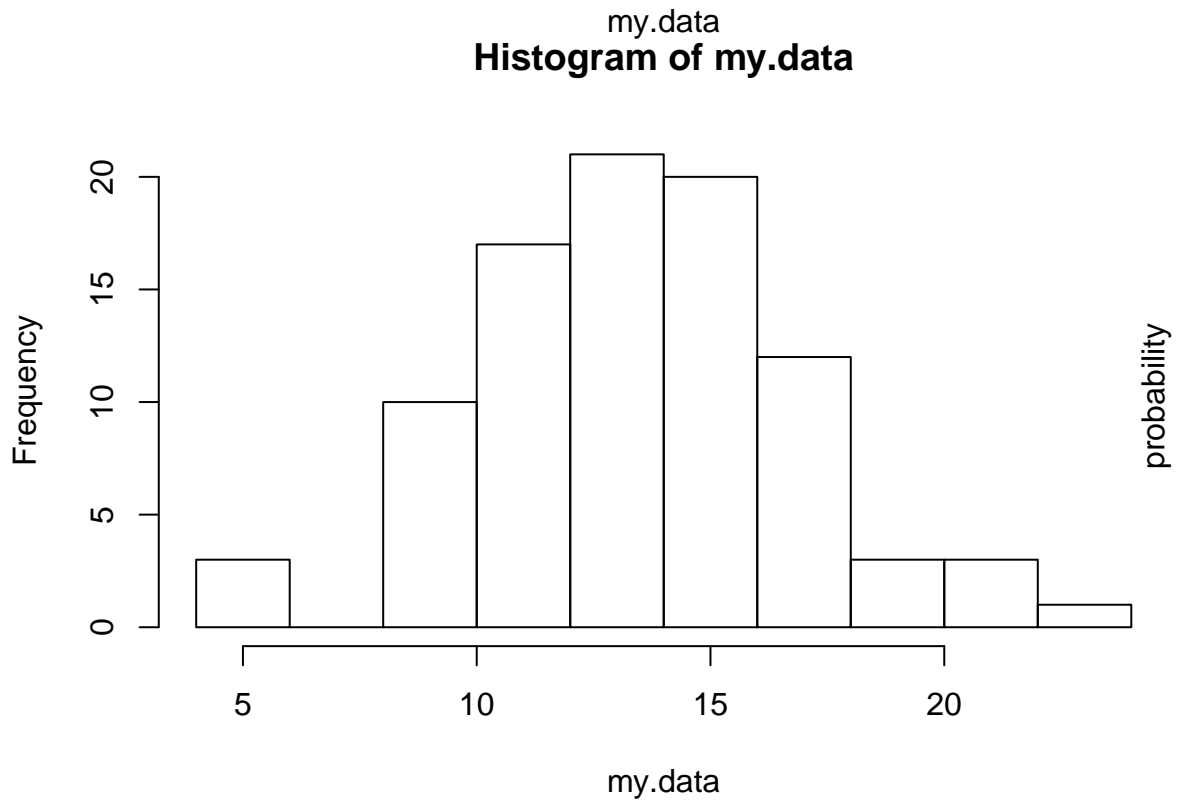
**Histogram of my.data**



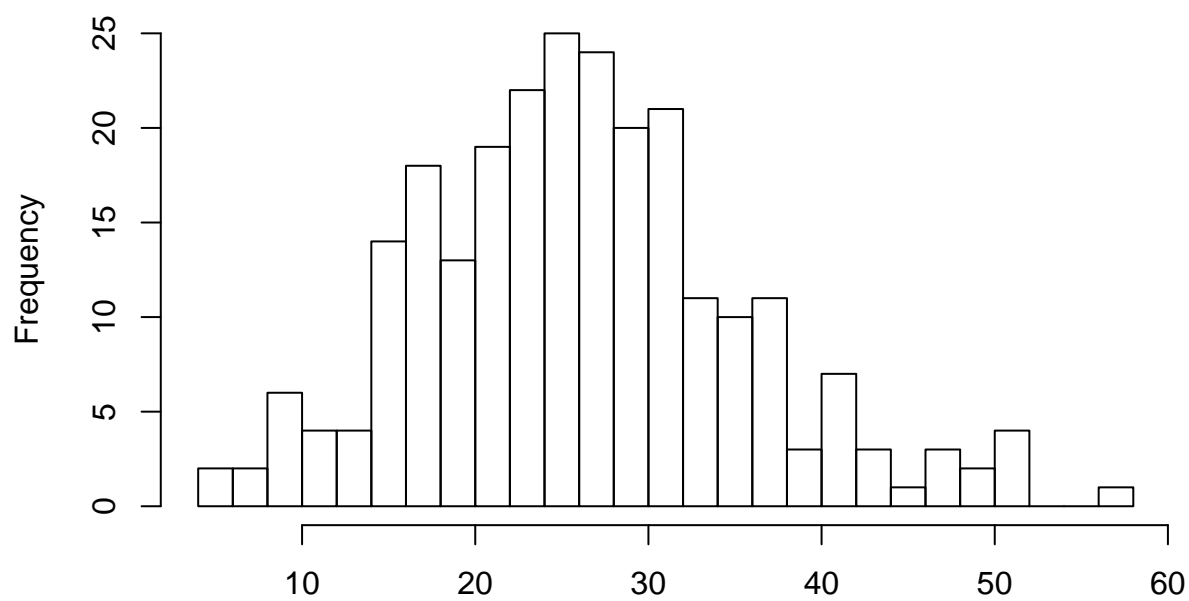
**Histogram of my.data**



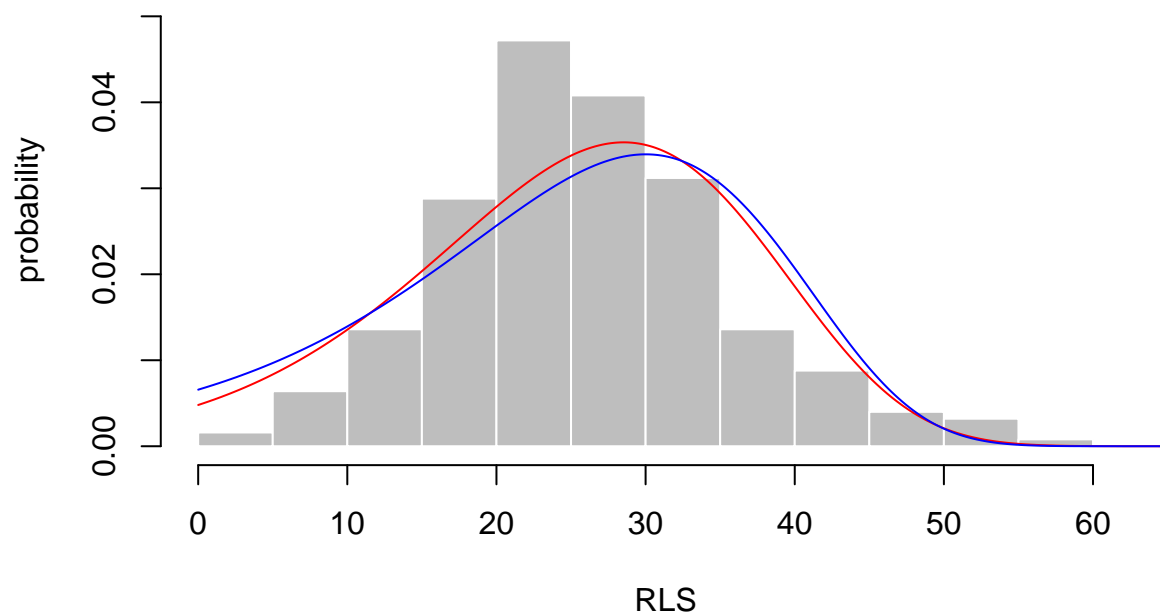
**Histogram of my.data**



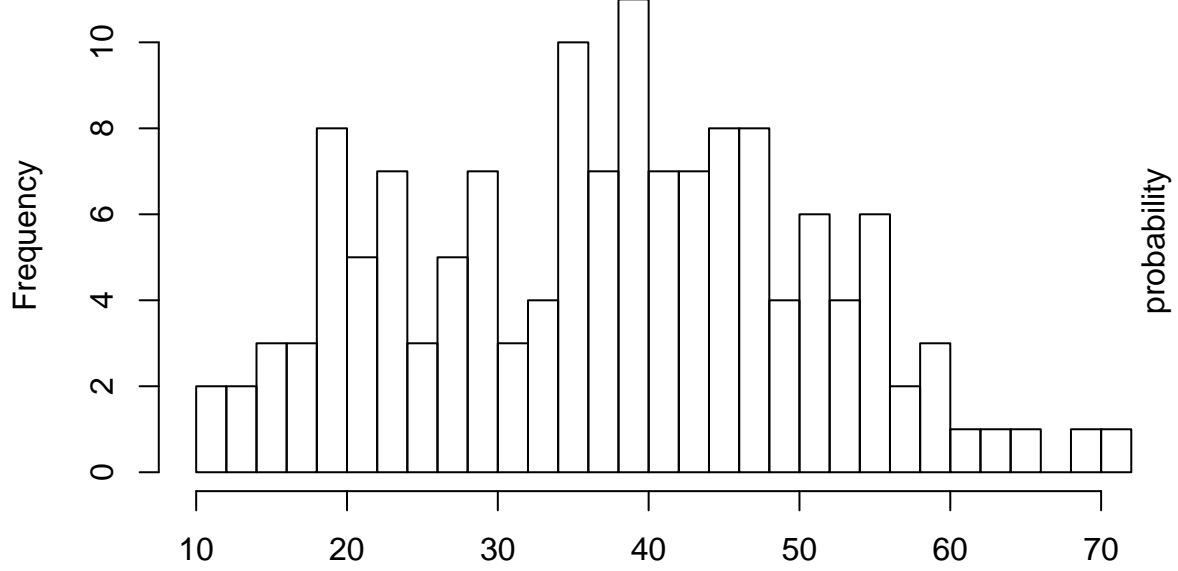
**Histogram of my.data**



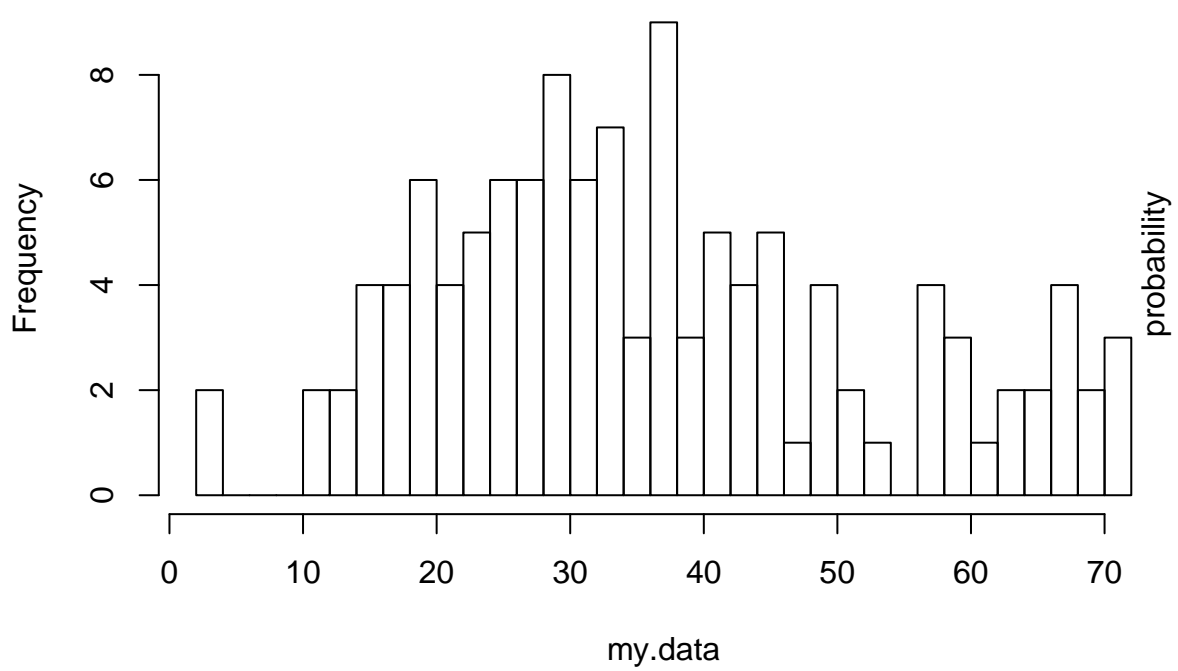
my.data  
**fig1b.BY4742**



**Histogram of my.data**



**Histogram of my.data**



**Histogram of my.data**

