Fit mutant with binomial aging model

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```r
rm(list=ls())
library('flexsurv')
```

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

```r
library('stringr')
source("../lifespan.r")
```

The RLS data used here are from Kaeberlein et al 2004, Plos Genetics http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.0020296

The original data set is at https://doi.org/10.1371/journal.pbio.0020296.sd002

```r
tb = read.csv("kaeberlein04_selected_strains.csv")
```

```r
my.strains = names(tb);
report = data.frame(my.strains)
report$samplesize = NA; report$R=NA; report$t0=NA; report$n=NA; report$G=NA; #report$longfilename=NA;
#write.csv(tb, "kaeberlein04_selected_strains.csv", row.names = FALSE, quote = FALSE)
```

Fit all RLS data sets by strains

```r
for( i in 1:length(report[,1])){
  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];
```

```
  nhat = 6;
  t0= (nhat-1)/Ghat;
  fitBinom = optim ( c(Rhat, t0, nhat),  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
```

```
##                        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

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

Overlay histogram with probability density function of binomial aging model

see http://hongqinlab.blogspot.com/2013/12/binomial-mortailty-model.html m = R (1 + t/t0)^(n-1) s = exp((R t0/n)*(1 - (1+t/t0)^n))
$pdf = s$m

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

```r
# (x,y) are legend positions for plots
x = c(0,    0,   0,    0,   40,   55,  50,   5);
y = c(0.06, 0.06, 0.1, 0.1,0.04, 0.03, 0.03, 0.03  );

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, plot = FALSE);
  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', lty=1)

  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", lty=2)

  legend ( x[i], y[i], c("Binomial","Gompertz"), col=c("red","blue"), lty=c(1,2) )
}
```
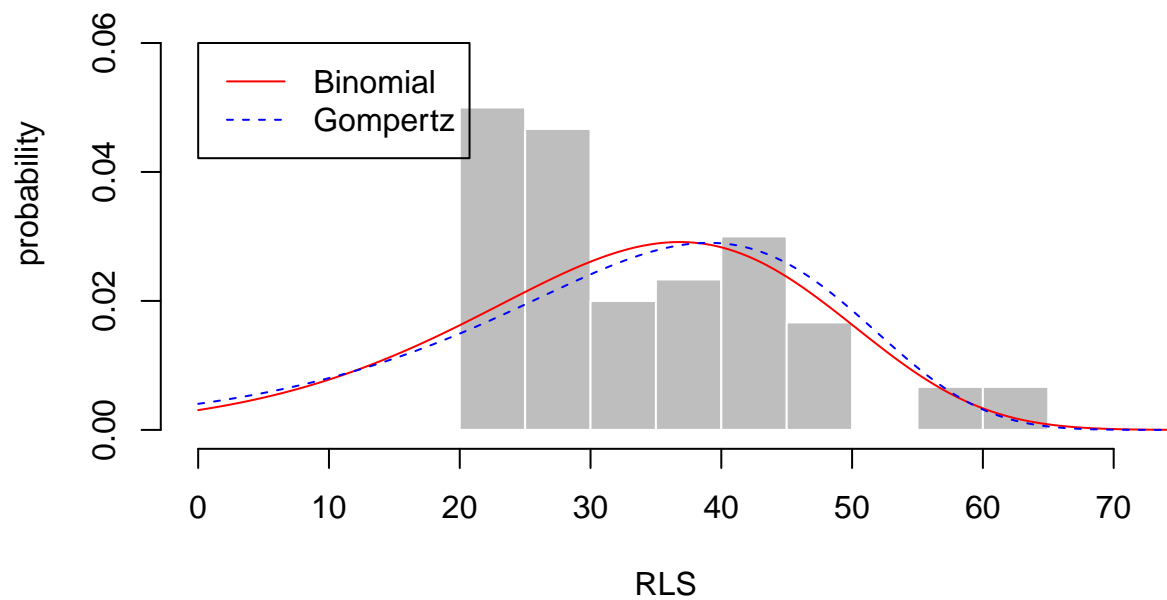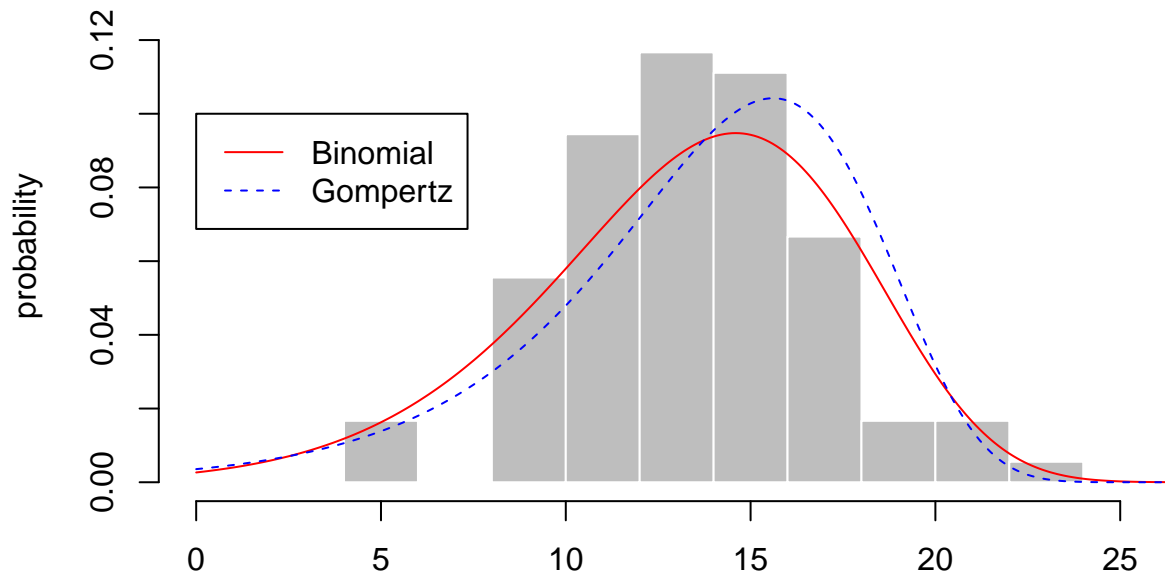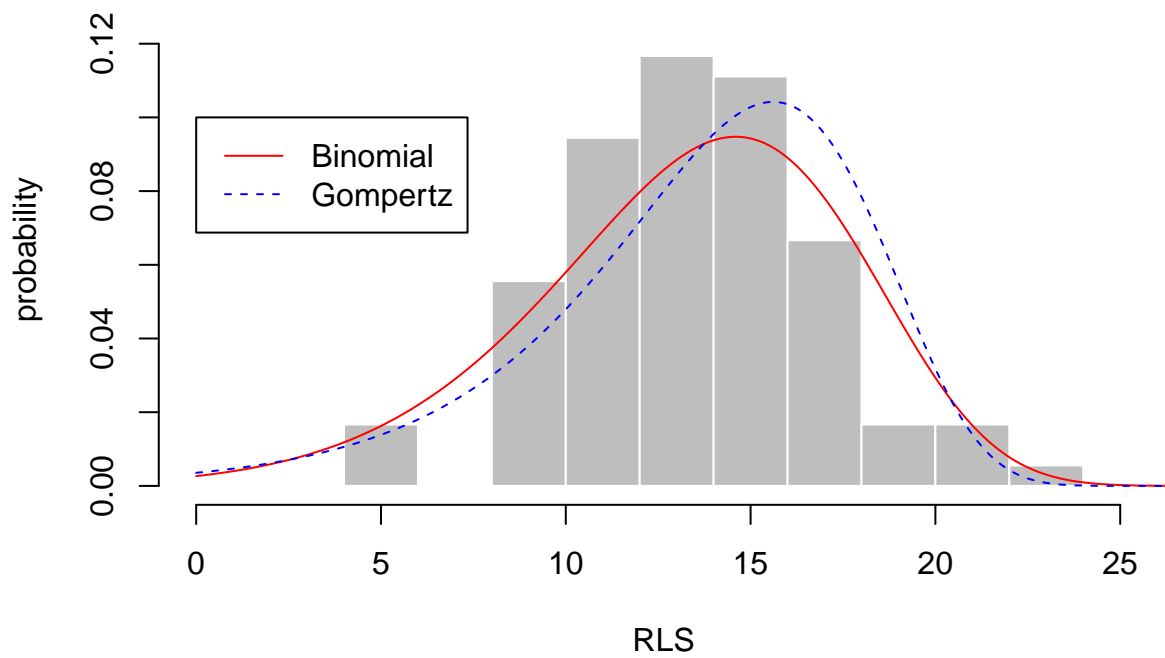
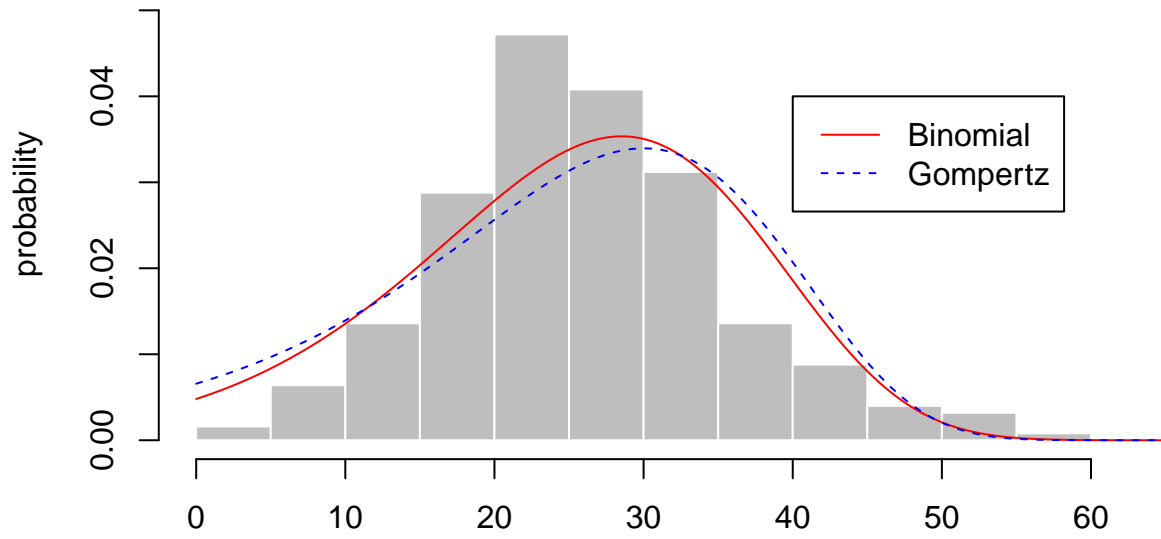## fig4b.BY4742.2glucose
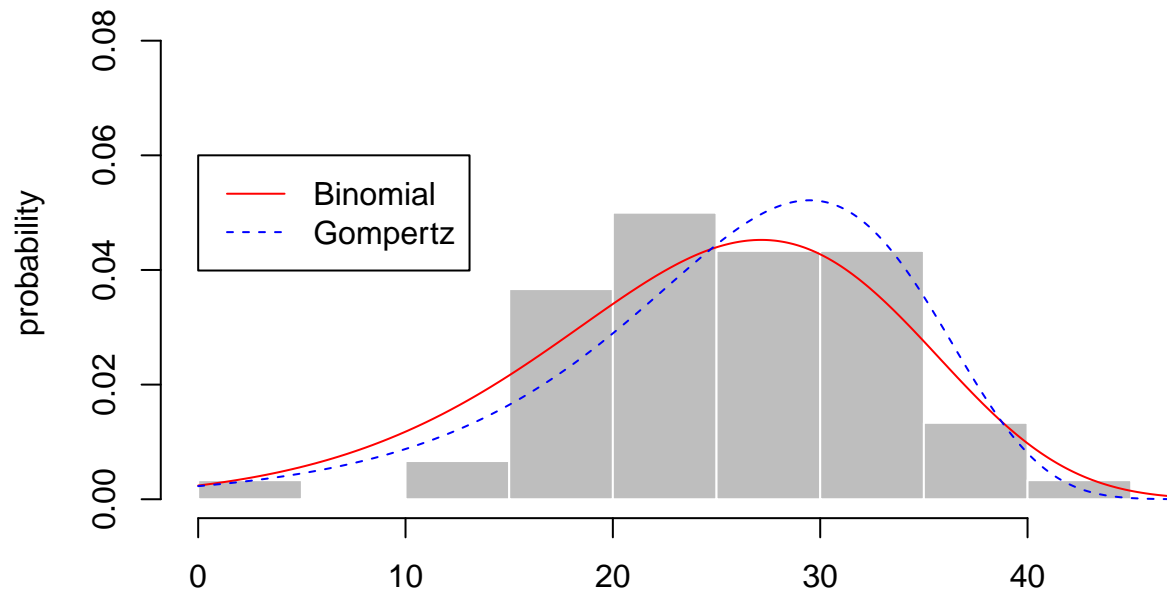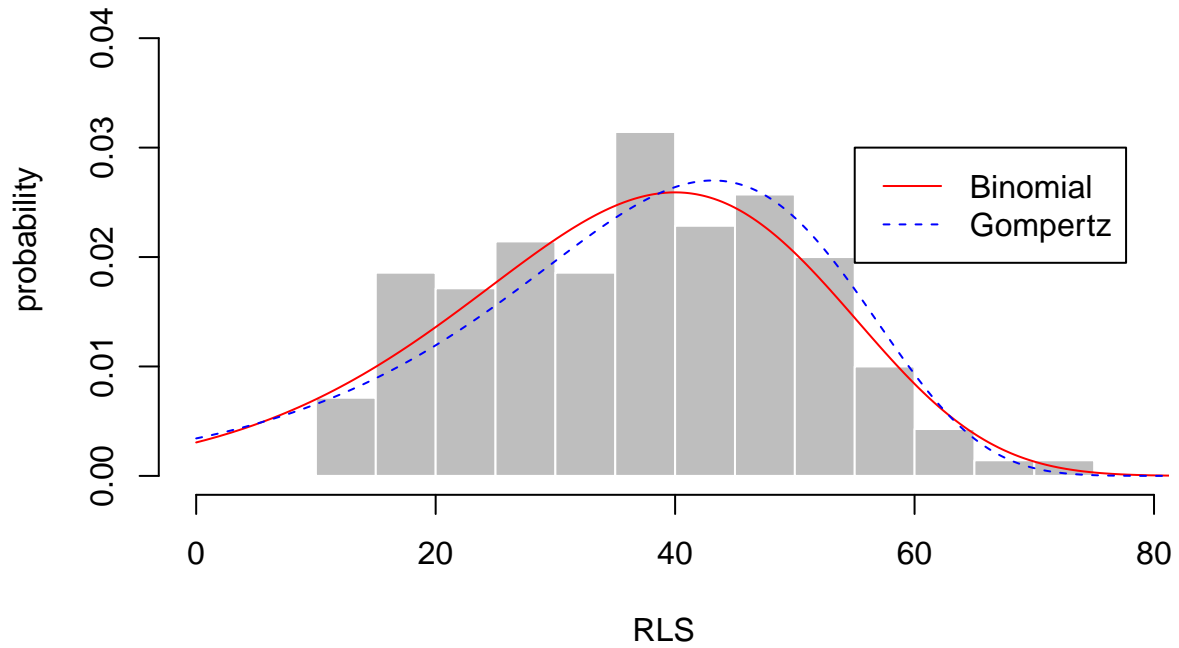

fig4b.by4742.SIR2.ox.2glucose

fig2a.sir2

probability

Binomial
Gompertz

0.12
0.08
0.04
0.00

0   5   10   15   20   25

RLS

fig2b.sir2

probability

Binomial
Gompertz

0.12
0.08
0.04
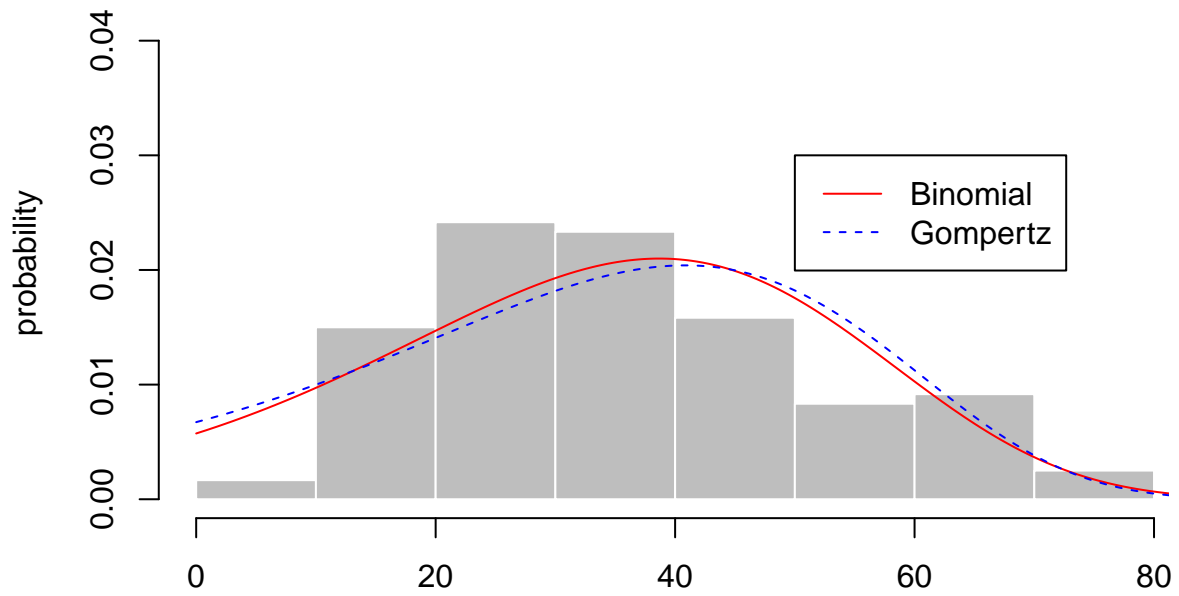0.00

0   5   10   15   20   25

RLS

fig1b.BY4742

fig1b.fob1

fig1b.hxk2

fig1b.fob1.hxk2