Mediation test on natural isolates. short version

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```
rm(list=ls())
#setwd("~/github/0.network.aging.prj.bmc/0a.rls.fitting")
setwd("~/github/bmc_netwk_aging_manuscript/R1/0.nat.rls.fitting")
library('flexsurv')

## Loading required package: survival
source("../lifespan.r")
```

Parse strains from files

```
files = list.files(path="../qinlab_rls/", pattern="rls.tab")
tmp1 = gsub("\d{6}.", "", files)
redundant_strains = gsub(".rls.tab", "", tmp1)
strains = sort( unique( redundant_strains ))
strains
## [1] "101S"
                                            "BY4741"
                                                             "BY4742"
                          "BY4716"
## [5] "BY4743"
                          "JSBY4741"
                                            "M1-2"
                                                             "M13"
## [9] "M14"
                          "M2-8"
                                            "M22"
                                                             "M32"
## [13] "M34"
                          "M5"
                                            "8M"
                                                             "RM112N"
## [17] "S288c"
                          "SGU57"
                                            "sir2D.4741a"
                                                             "sir2D.4742"
                                           "W303"
                                                             "YPS128"
## [21] "sir2DSIR2.4742" "SK1"
## [25] "YPS163"
Take files from natural isolates
my.strains=c("101S", "M1-2", "M13", "M14", "M2-8", "M22", "M32", "M34", "M5", "M8", "RM112N", "S288c", "SGU57", "Y.
files2=c();
for( i in 1:length(my.strains)){
files2 = c( files2, files[grep(my.strains[i], files)]);
report = data.frame(cbind(my.strains))
report$samplesize = NA; report$R=NA; report$t0=NA; report$n=NA; report$G=NA; report$longfilename=NA;
files = files2;
strains = my.strains;
```

Now, fit all RLS data sets by strains

```
for( i in 1:length(report[,1])){
#for( i in 3:4){
  my.files = files[grep(strains[i], files)]
```

```
report$longfilename[i] = paste(my.files, collapse = "::");
  tb = read.table( paste("../qinlab_rls/",my.files[1],sep=''), sep="\t")
  if( length(my.files)> 1){
   for( fi in 2:length(my.files)) {
      tmp.tb = read.table( paste("../qinlab_rls/",my.files[fi],sep="'), sep="\t")
      tb = rbind( tb, tmp.tb)
  }
  report$samplesize[i] = length(tb[,1])
  GompFlex = flexsurvreg(formula = Surv(tb[,1]) ~ 1, dist = 'gompertz')
  WeibFlex = flexsurvreg(formula = Surv(tb[,1]) ~ 1, dist = 'weibull')
  report$avgLS[i] = mean(tb[,1])
  report$stdLS[i] = sd(tb[,1])
  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$GompGFlex[i];
  nhat = 6;
  t0= (nhat-1)/Ghat;
  fitBinom = optim (c(Rhat, t0, nhat), llh.binomialMortality.single.run,
                     lifespan=tb[,1],
                     #method='SANN') #SANN needs control
                     method="L-BFGS-B",
                     lower=c(1E-10, 1, 4), upper=c(1,200,20));
  report[i, c("R", "t0", "n")] = fitBinom$par[1:3]
  report$G[i] = (report$n[i] - 1)/report$t0[i]
report2 = report;
```

Mediation test on Gflex <-t0 <- RFlex

Hong thinks the results indicate the t0 is the mediator from Flex to GFlex, but not sure.

```
library(mediation)
## Loading required package: MASS
```

```
## Loading required package: Matrix
## Loading required package: mvtnorm
## Loading required package: sandwich
## mediation: Causal Mediation Analysis
## Version: 4.4.5
set.seed(20170801)
report2$log10GompRFlex = log10(report2$GompRFlex)
med.fit = lm(t0 \sim log10GompRFlex, data=report2)
summary(med.fit)
##
## Call:
## lm(formula = t0 ~ log10GompRFlex, data = report2)
##
## Residuals:
##
       Min
                1Q
                     Median
                                 3Q
                                         Max
## -10.2238 -7.6956 -0.6106
                              1.5195 22.5871
## Coefficients:
                Estimate Std. Error t value Pr(>|t|)
##
                  99.564
                             20.269
                                    4.912 0.000284 ***
## (Intercept)
## log10GompRFlex
                  19.967
                             7.429
                                     2.688 0.018617 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.928 on 13 degrees of freedom
## Multiple R-squared: 0.3572, Adjusted R-squared: 0.3078
## F-statistic: 7.225 on 1 and 13 DF, p-value: 0.01862
out.fit = lm(GompGFlex ~ t0 + log10GompRFlex, data=report2)
summary(out.fit)
##
## lm(formula = GompGFlex ~ t0 + log10GompRFlex, data = report2)
## Residuals:
        Min
                  1Q
                        Median
                                     3Q
                                              Max
## -0.008037 -0.004385 -0.001282 0.001773 0.012763
## Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
                 ## (Intercept)
                ## log10GompRFlex -0.0095046 0.0063994 -1.485
                                                0.163
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.006857 on 12 degrees of freedom
## Multiple R-squared: 0.9447, Adjusted R-squared: 0.9355
## F-statistic: 102.5 on 2 and 12 DF, p-value: 2.861e-08
```

```
med.out <- mediate(med.fit, out.fit, treat = "log10GompRFlex", mediator = "t0", robustSE = TRUE, sims =</pre>
summary(med.out)
##
## Causal Mediation Analysis
## Quasi-Bayesian Confidence Intervals
##
##
                 Estimate 95% CI Lower 95% CI Upper p-value
## ACME
                 -0.04383
                              -0.08096
                                              -0.01 <2e-16 ***
## ADE
                 -0.00718
                              -0.02469
                                               0.01
                                                       0.46
## Total Effect
                 -0.05101
                              -0.08276
                                              -0.02 <2e-16 ***
## Prop. Mediated 0.86767
                                              1.23 <2e-16 ***
                               0.46191
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Sample Size Used: 15
##
## Simulations: 100
```

Mediation test 2 on Rflex <-t0 < - GFlex

Hong thinks this is negative result, which means to works only in one direction.

```
med.fit = lm(t0 ~ GompGFlex, data=report2)
summary(med.fit)
##
## lm(formula = t0 ~ GompGFlex, data = report2)
## Residuals:
               1Q Median
                               3Q
                                      Max
## -2.6401 -1.9424 -0.8670 -0.0658 8.1513
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) 94.999
                         3.723
                                    25.52 1.72e-12 ***
## GompGFlex
             -427.325
                           31.369 -13.62 4.50e-09 ***
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 3.168 on 13 degrees of freedom
## Multiple R-squared: 0.9345, Adjusted R-squared: 0.9295
## F-statistic: 185.6 on 1 and 13 DF, p-value: 4.503e-09
out.fit = lm(log10GompRFlex ~ t0 + GompGFlex, data=report2)
summary(out.fit)
```

```
##
## Call:
## lm(formula = log10GompRFlex ~ t0 + GompGFlex, data = report2)
## Residuals:
##
                     Median
       Min
                  1Q
                                    3Q
                                            Max
## -0.52342 -0.24509 0.04331 0.22083 0.34492
##
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.002954
                            2.387477 -0.001
                            0.024884 -0.717
                                                0.487
                -0.017838
## GompGFlex
               -16.337520 10.999937 -1.485
                                                0.163
##
## Residual standard error: 0.2843 on 12 degrees of freedom
## Multiple R-squared: 0.457, Adjusted R-squared: 0.3666
## F-statistic: 5.051 on 2 and 12 DF, p-value: 0.02562
med.out <- mediate(med.fit, out.fit, treat = "GompGFlex", mediator = "t0", robustSE = TRUE, sims = 100)</pre>
summary(med.out)
##
## Causal Mediation Analysis
##
## Quasi-Bayesian Confidence Intervals
##
##
                  Estimate 95% CI Lower 95% CI Upper p-value
## ACME
                     6.454
                                -14.468
                                               31.46
                                                        0.74
## ADE
                   -15.052
                                -45.810
                                               8.83
                                                        0.18
## Total Effect
                    -8.598
                                -18.553
                                               -1.06
                                                        0.04 *
## Prop. Mediated
                   -0.526
                                 -9.794
                                                3.54
                                                        0.74
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Sample Size Used: 15
##
##
## Simulations: 100
```