Pfenning-ButterworthFiguresandStats

```
withCallingHandlers(
    expr   = as.numeric(c("1", "A")),
    warning = function(w) warn <<- paste("** warning:", w$message, "**\n\n")
)
```
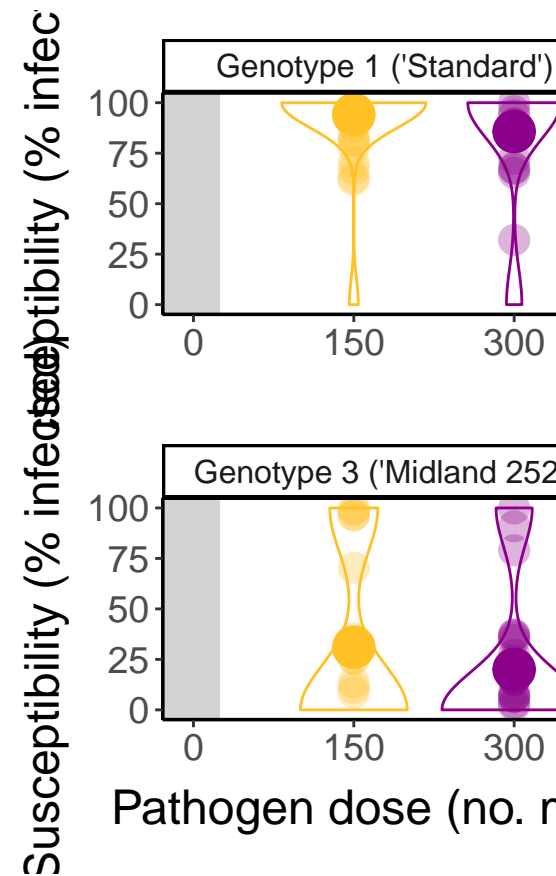
```
## [1]  1 NA
```

```
## ** warning: NAs introduced by coercion **
```
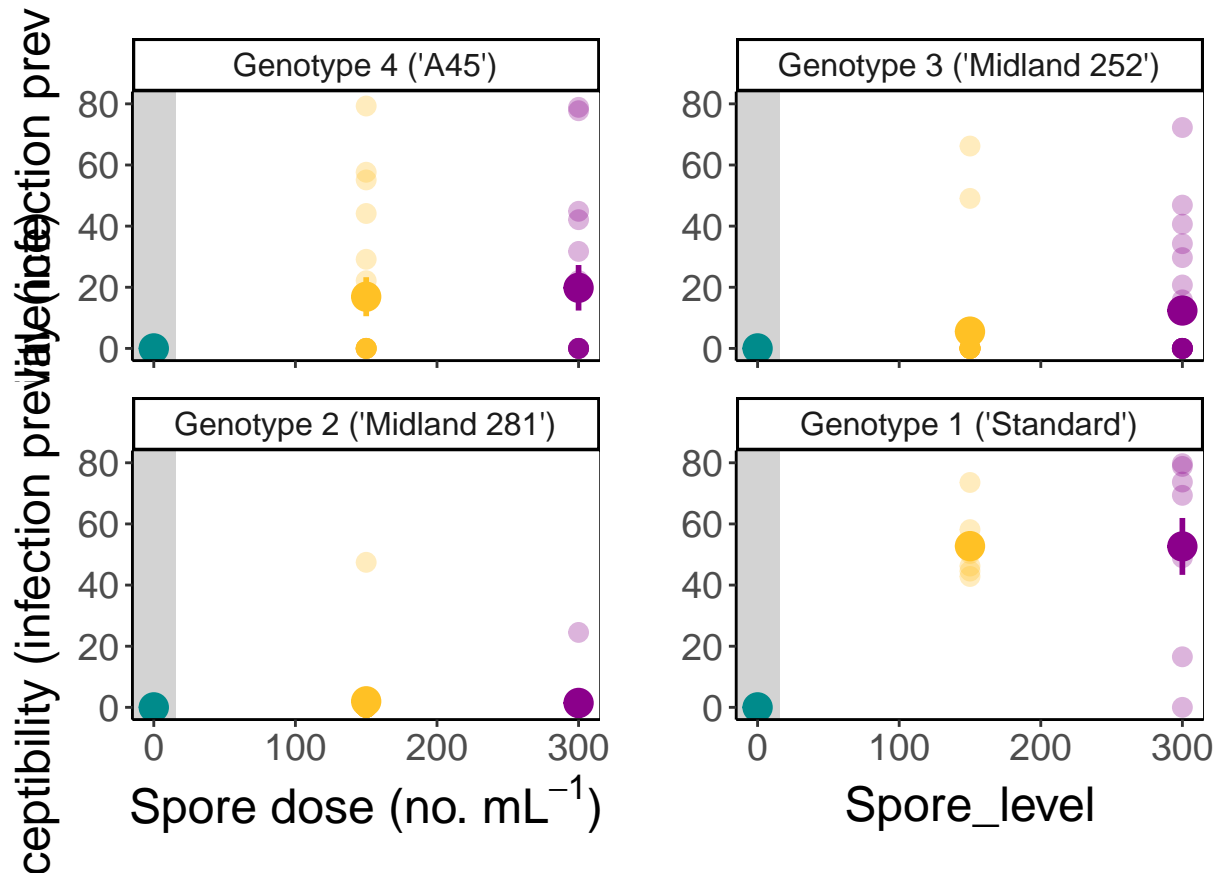
Load libraries

PLOT MEAN Feeding WITH MEAN SPORES set the y-axis for each genotype separately: M281 eats much more than everyone else adjusting scale so differences among spore levels for other genotypes are easily seen.

Alternative options considered for plot 2

**Multi-panel (8 total) with susceptibility first and then spore yield**

Plot 2 A Hosts differ in their immune-mediated changes in feeding behavior

Showing results in this layout to emphasize the difference among the genotypes

Note, this requires adjusting the y-axis since one genotype consumes much more relative

to the others

Grey shading emphasizes the comparison to pathogen-free environments

The focus here is on animals that were either unexposed or infected, thus we will exclude animals that were exposed but where infections were either cleared or too low to detect.
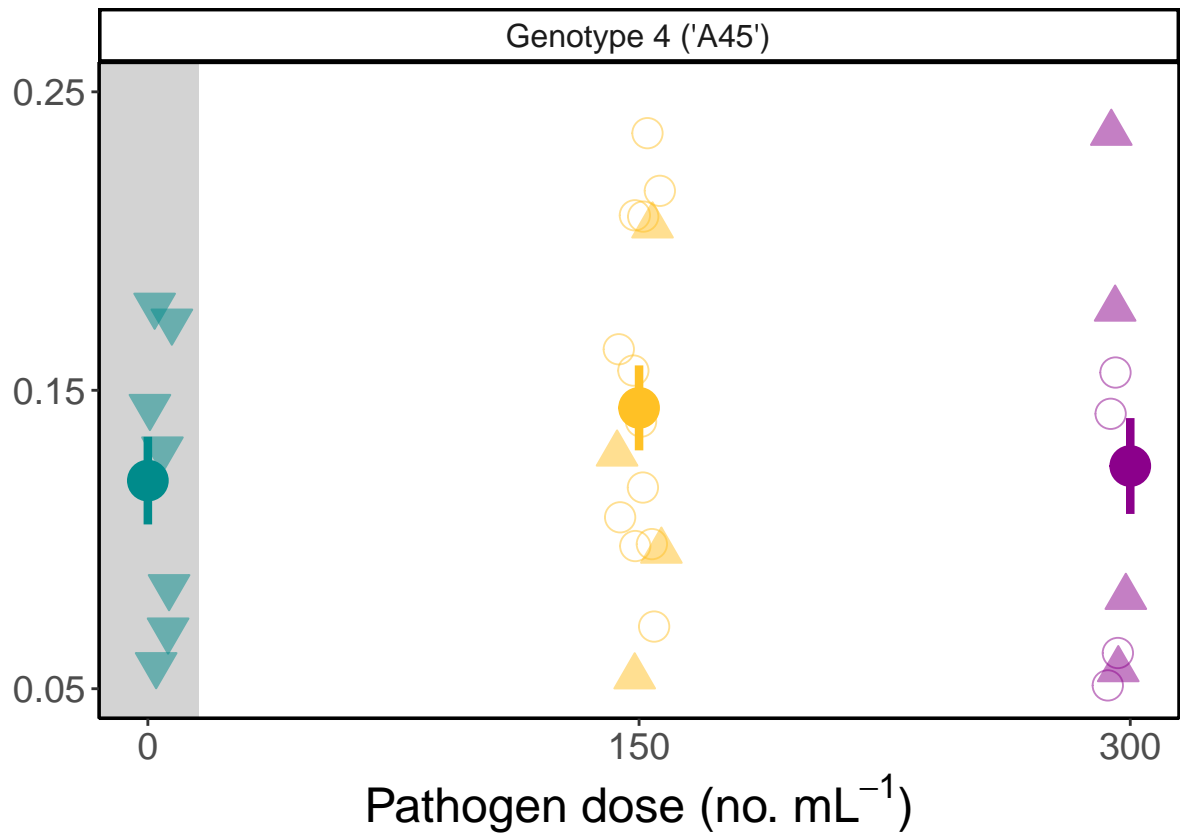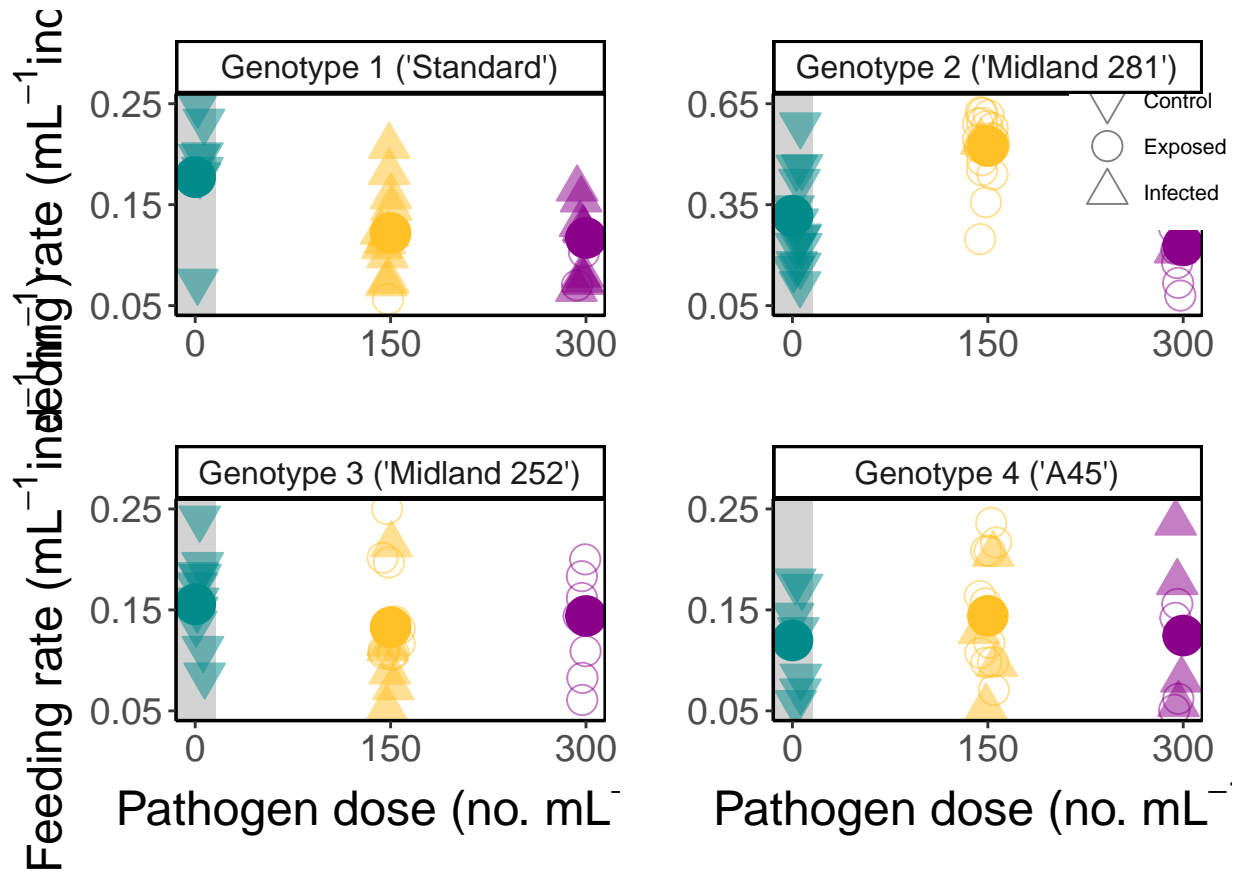
More susceptible genotypes showed stronger illness mediated anorexia relative to less genotypes

The magnitude of the anorexic response was unaffected by pathogen dose, except in the least susceptible genotype #### More susceptible genotypes, which showed stronger illness mediated anorexia relative to less genotypes #### #### Also tended to produce more pathogen spores. despite eating fewer resources, which should #### reduce the resources available to support pathogen growth. These results #### suggest that for this genotype (Midland 281), anorexia appears to function as an anti-growth resistance mechanism #### #### For the other genotype exhibiting anorexia (Standard), anorexia appears to function as a tolerance mechanism
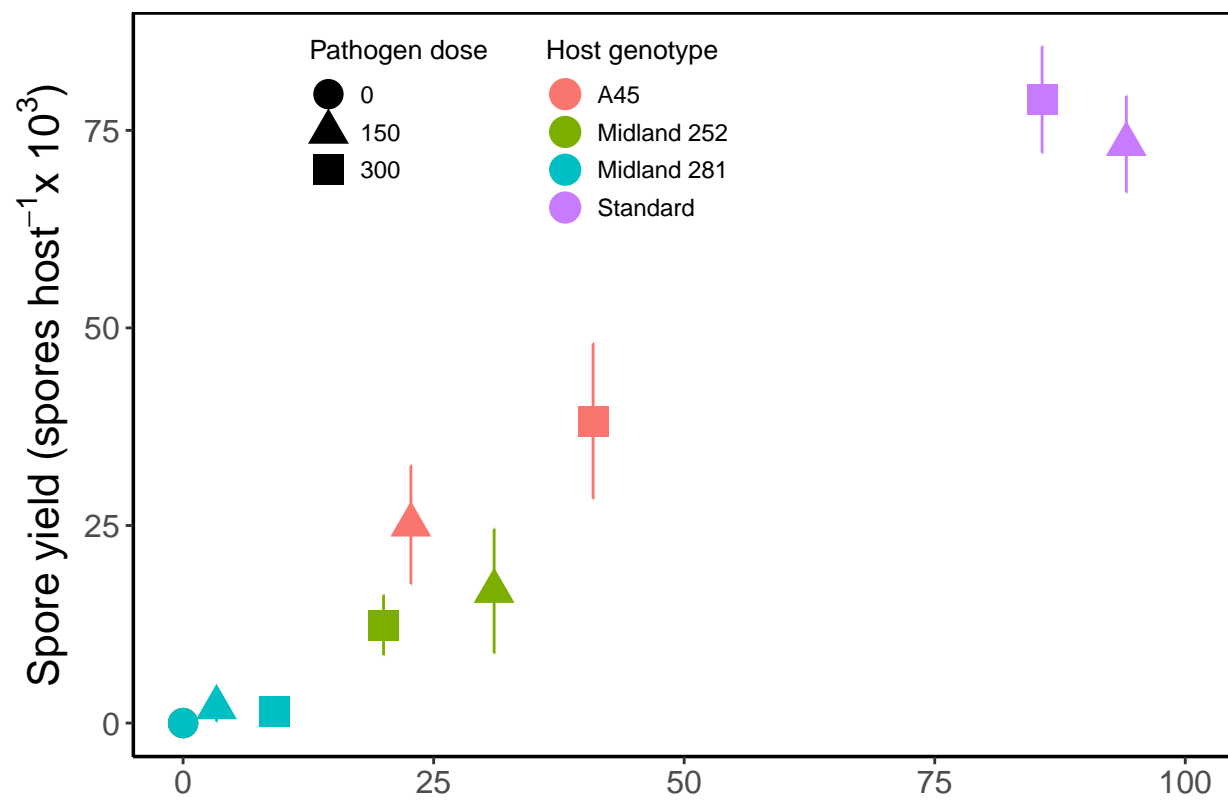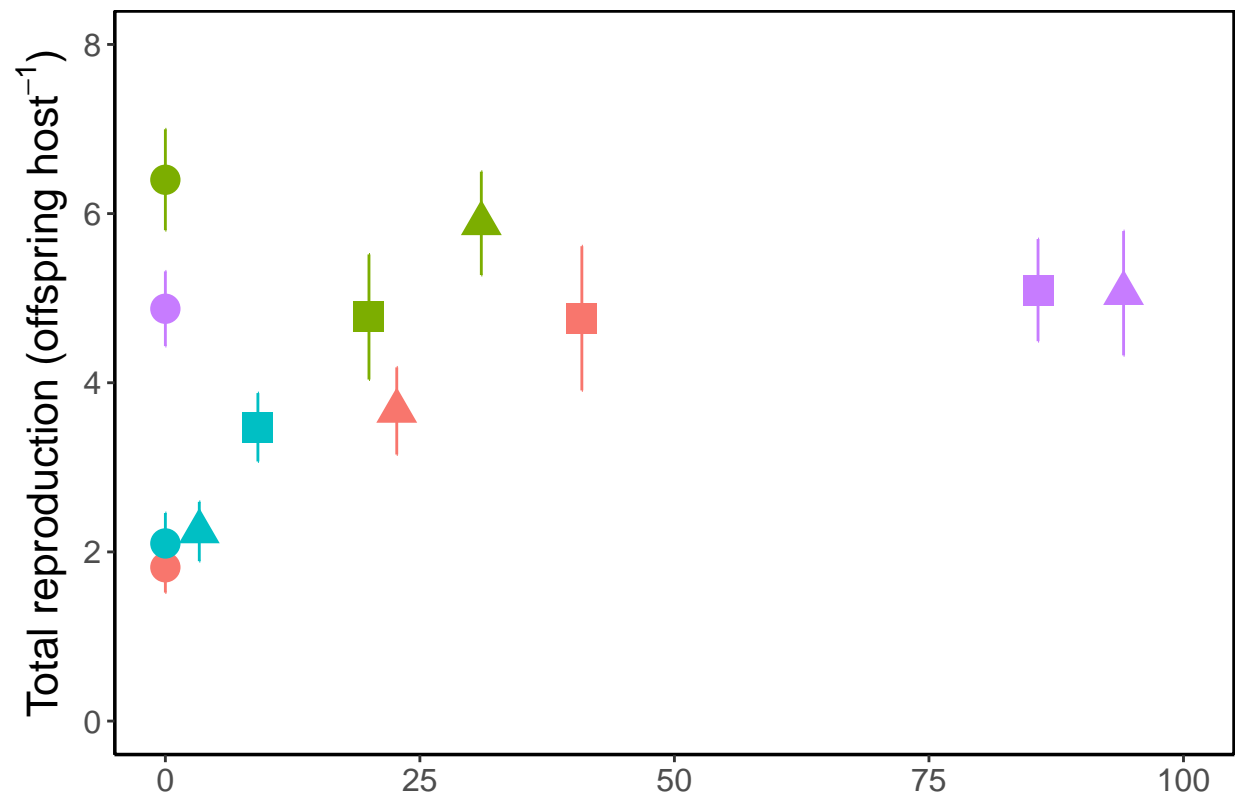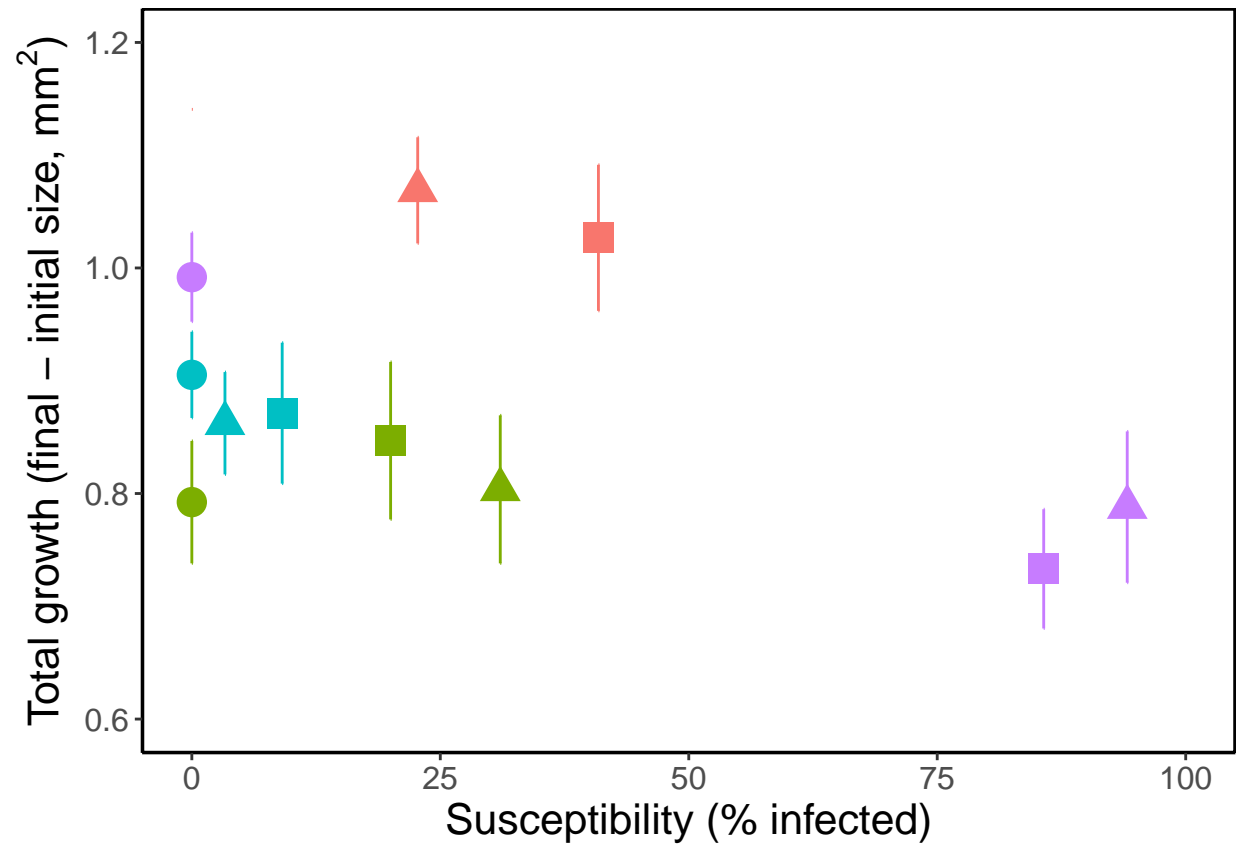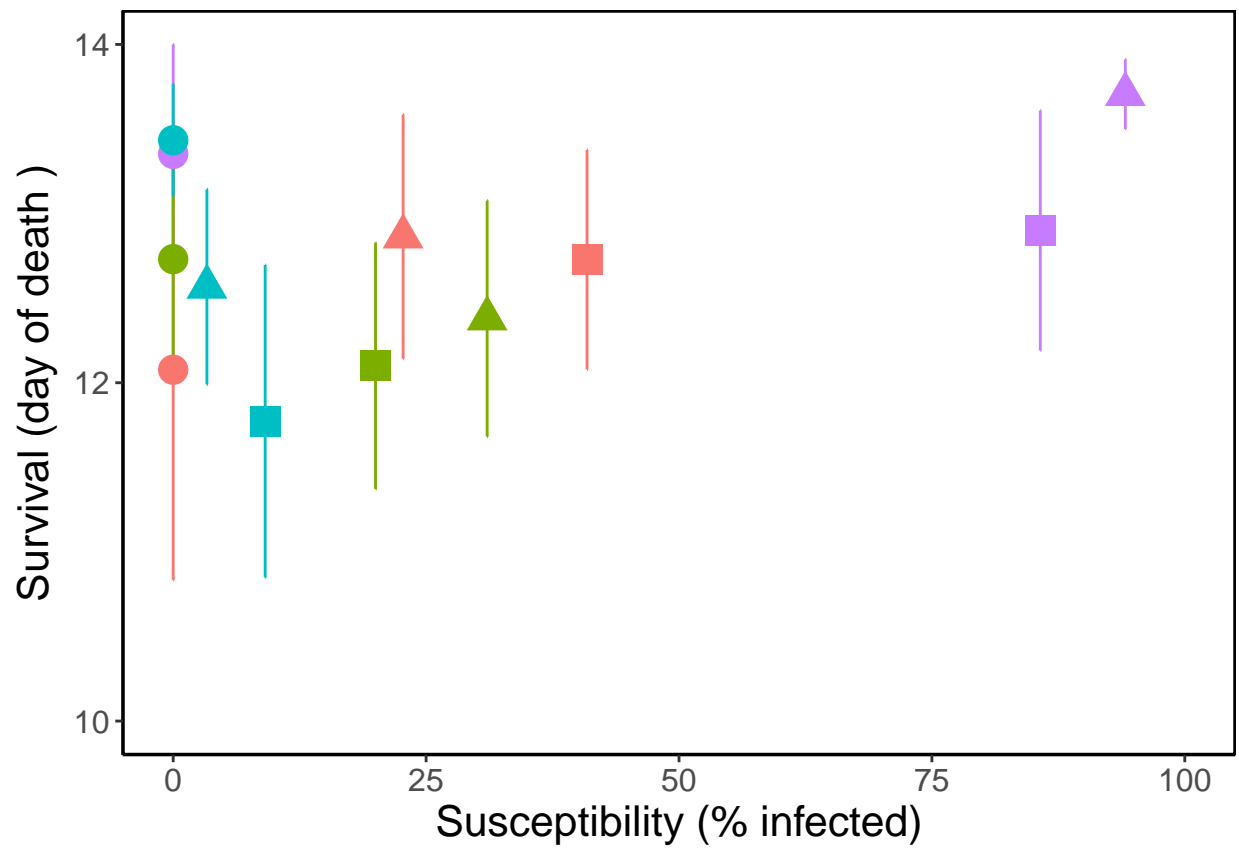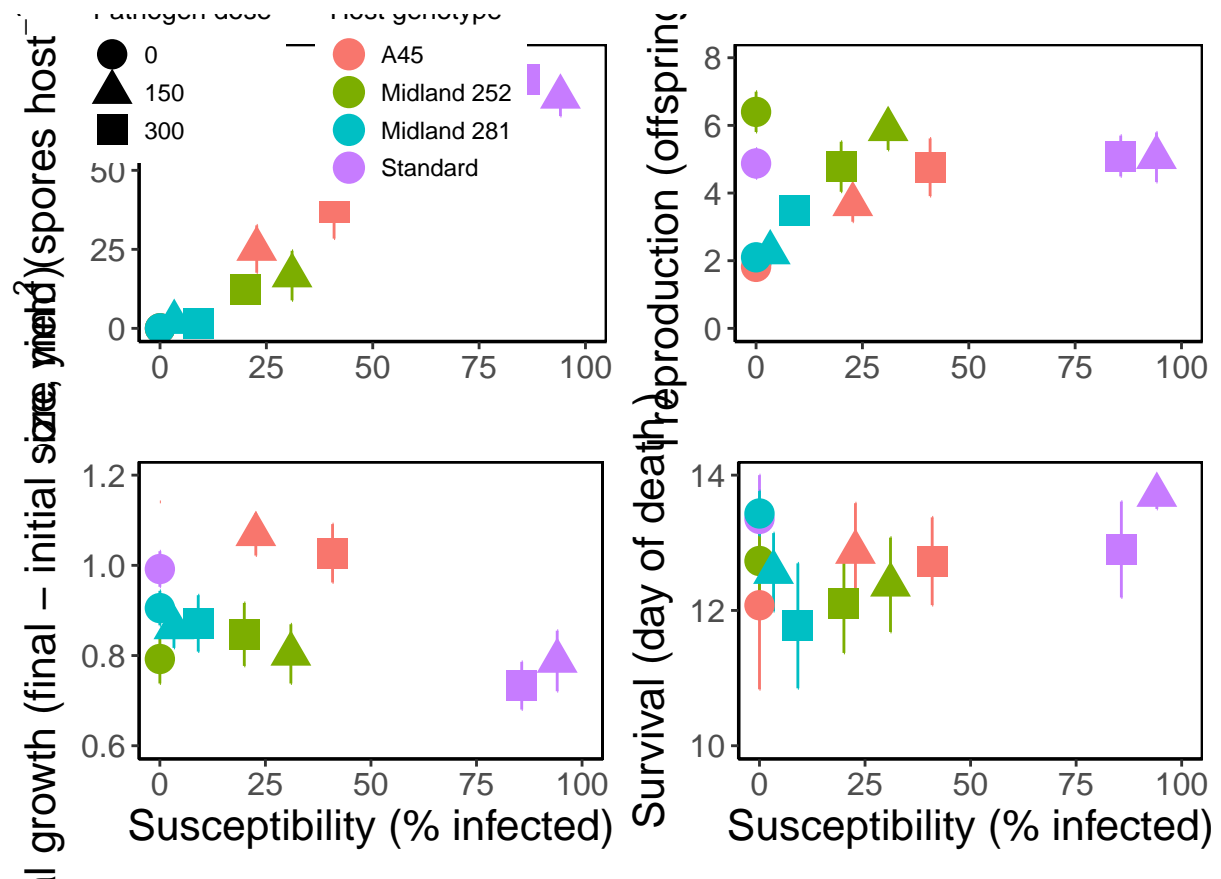
For the genotype with the strongest anorexia (Standard), anorexia helped hosts tolerate infection but

came at the cost of reduced growth. Thus, this genotype consumed fewer resources and grew less, but still produdced more spores.

The most resistant/least susceptible genotype experienced no

reduction in growth rate. A45 did not exhibit anorexia, but still suffered a reduction in growth
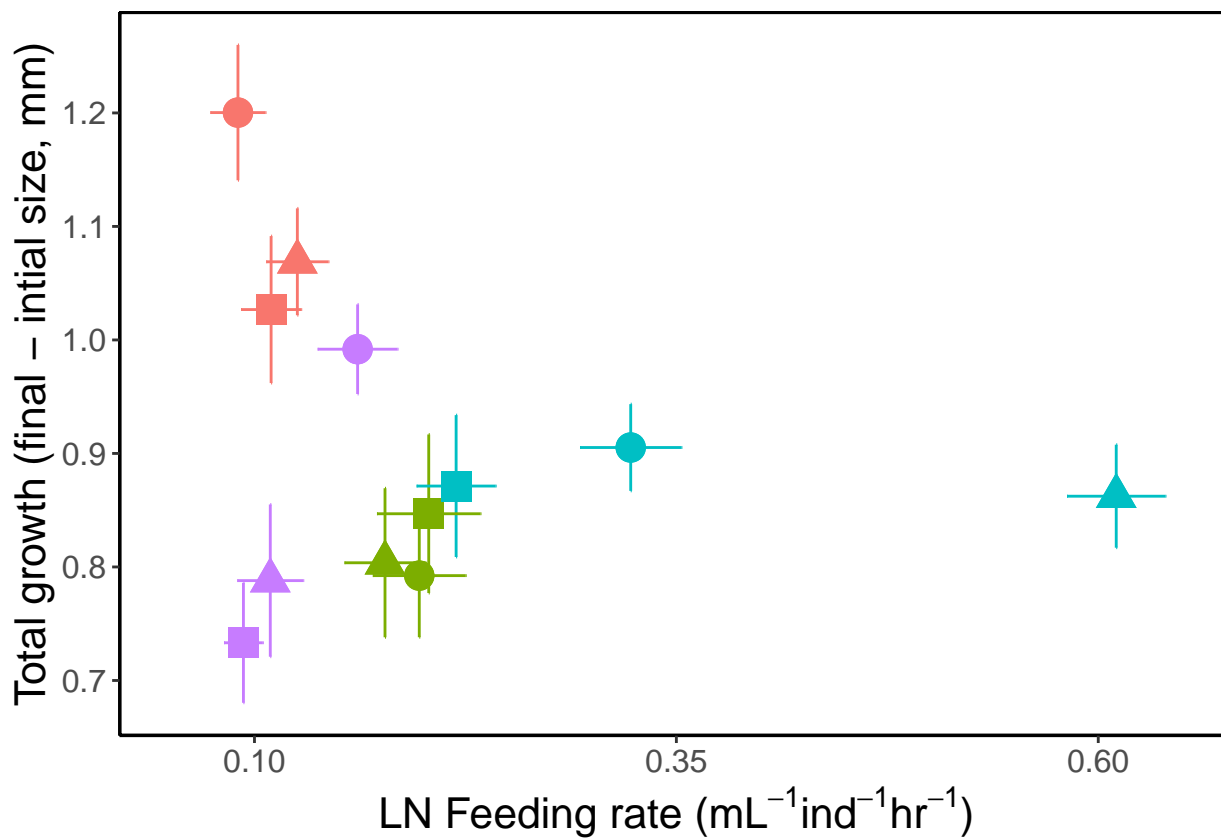
rate

Some genotypes exhibit higher total reproduction or fecundity overcompoensation, bbut only at certain spore levels

```
## <ScaleContinuousPosition>
##  Range:
##  Limits: 0.05 -- 0.65
```
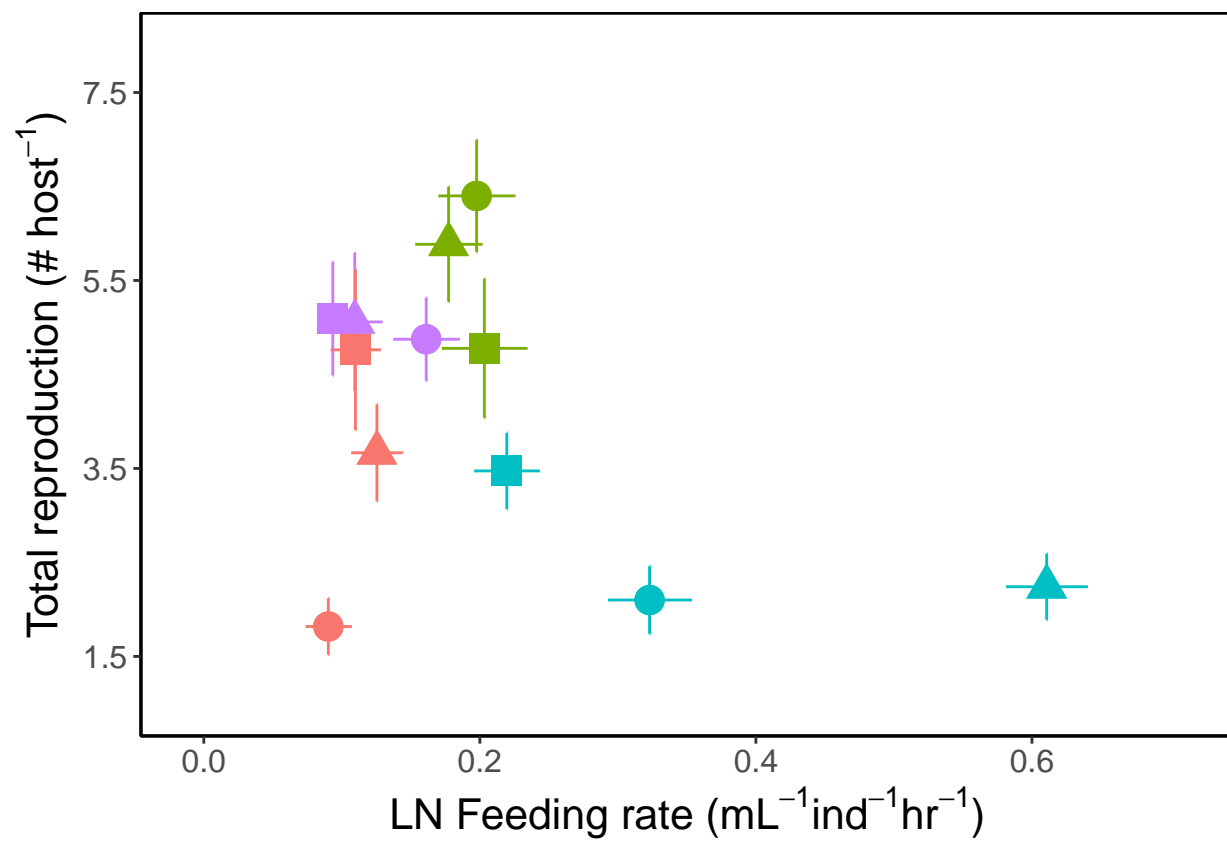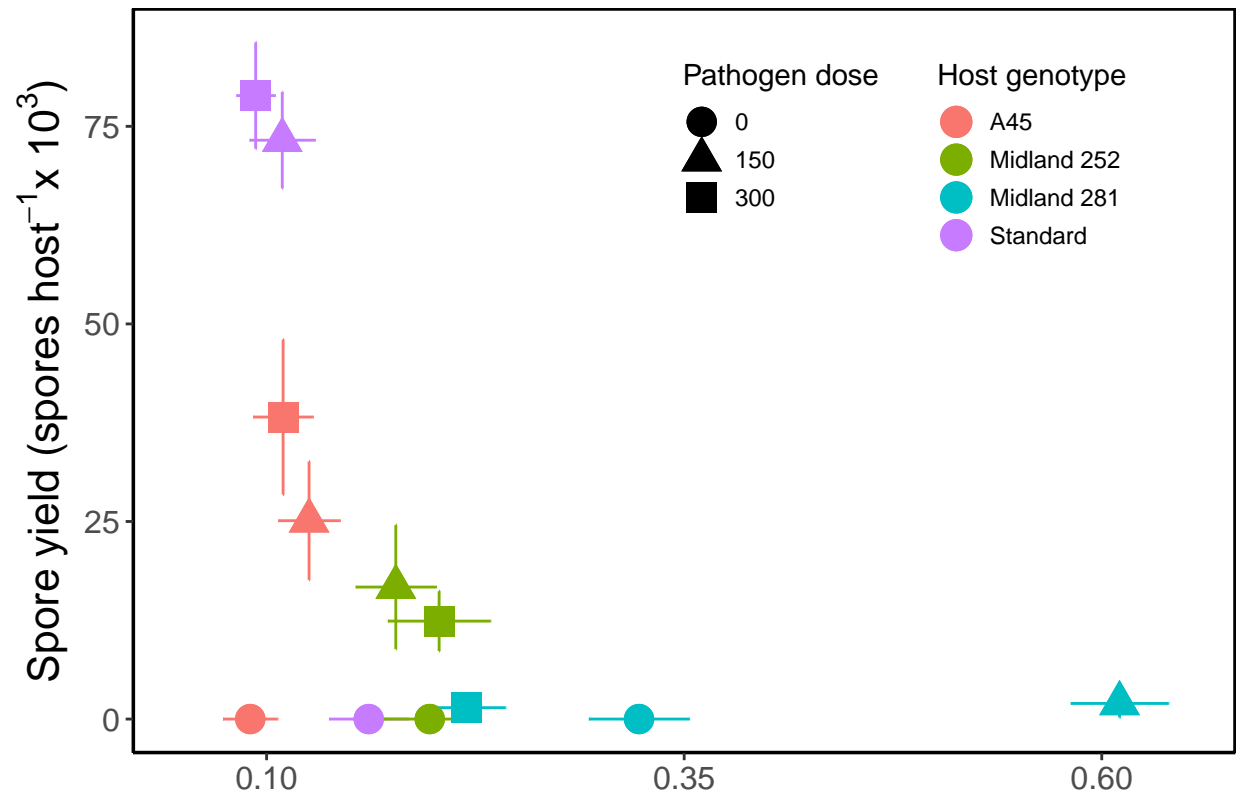
hosts ate significantly less when exposed to more pathogen spores.

Feeding and Susceptibility

Feeding and Spore Yield

Feeding and Fitness

Feeding and Growth
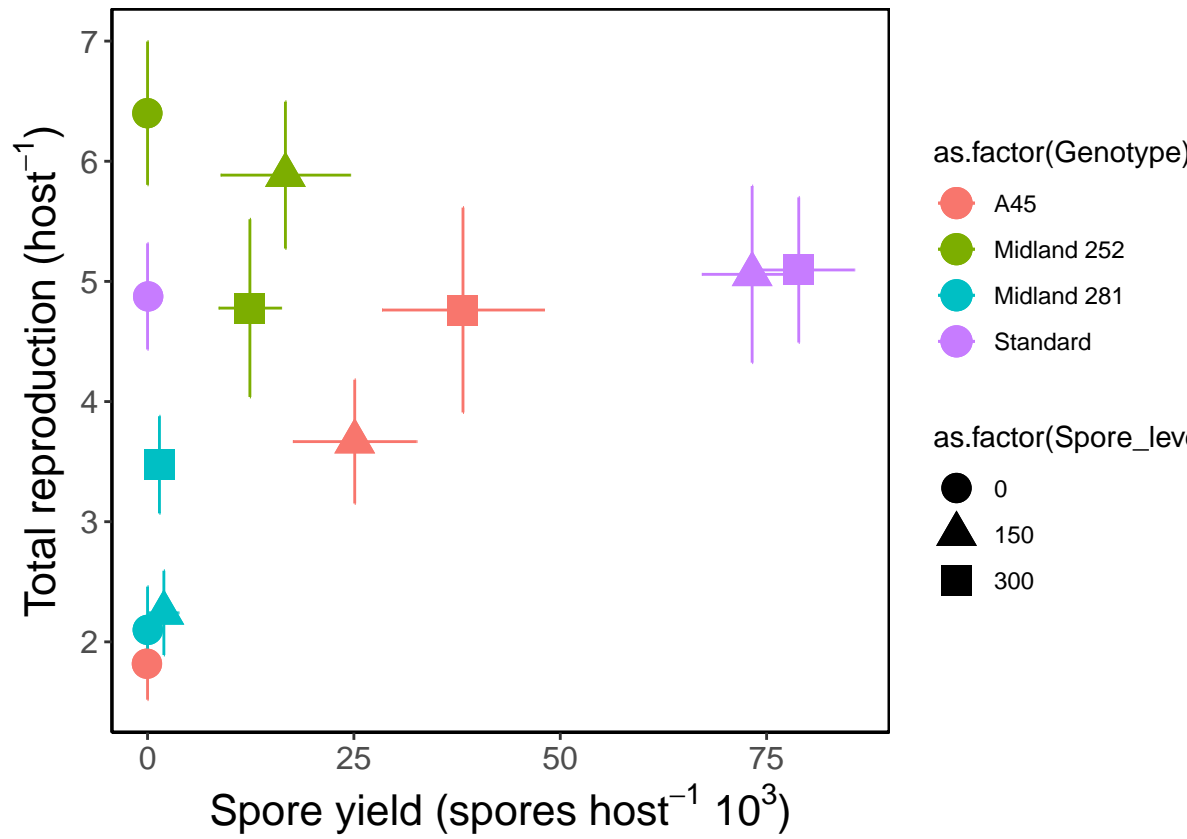
Appendix figures

Anti-growth resistance came at the cost of reduced lifespan, but otherwise, infection had little effect on lifespan (at least over the limited time frame captured in this assay - a great avenue for future exploration)
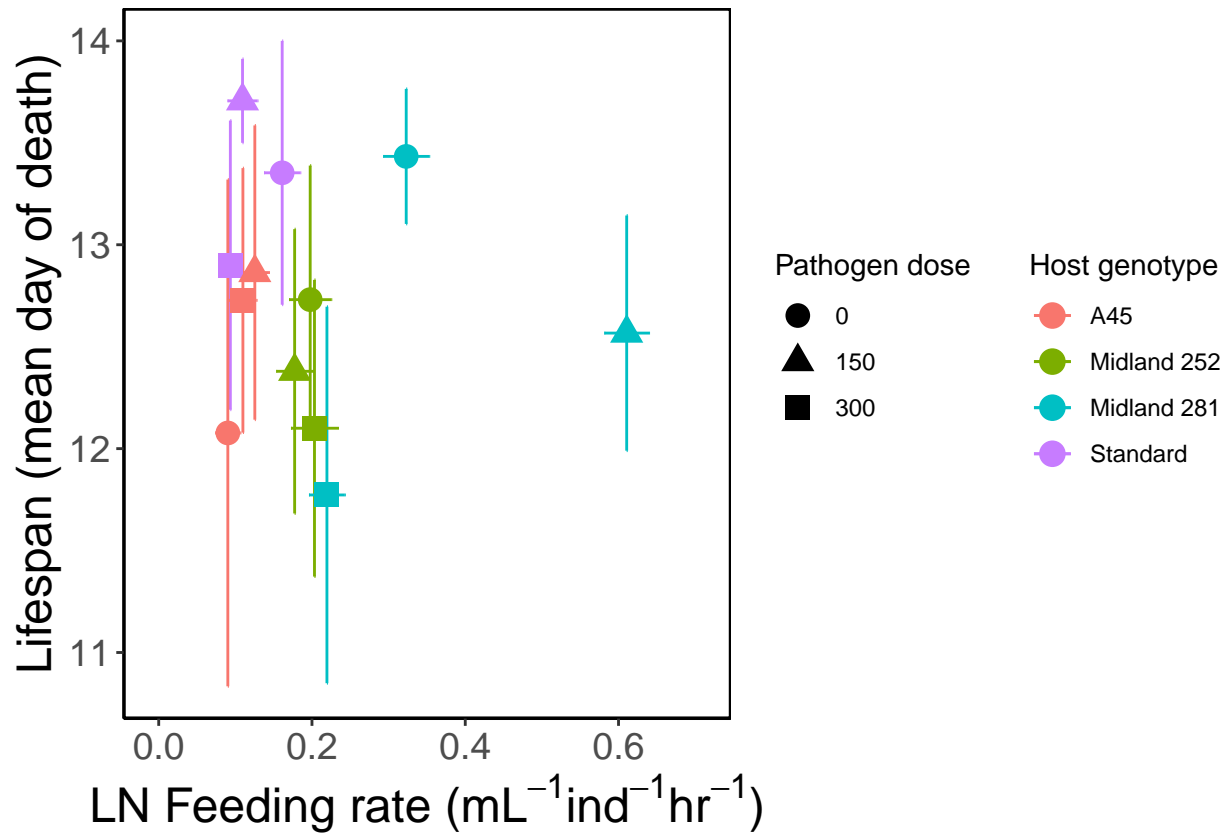
Infection (and immune responses) and little effect on first day of reproduction
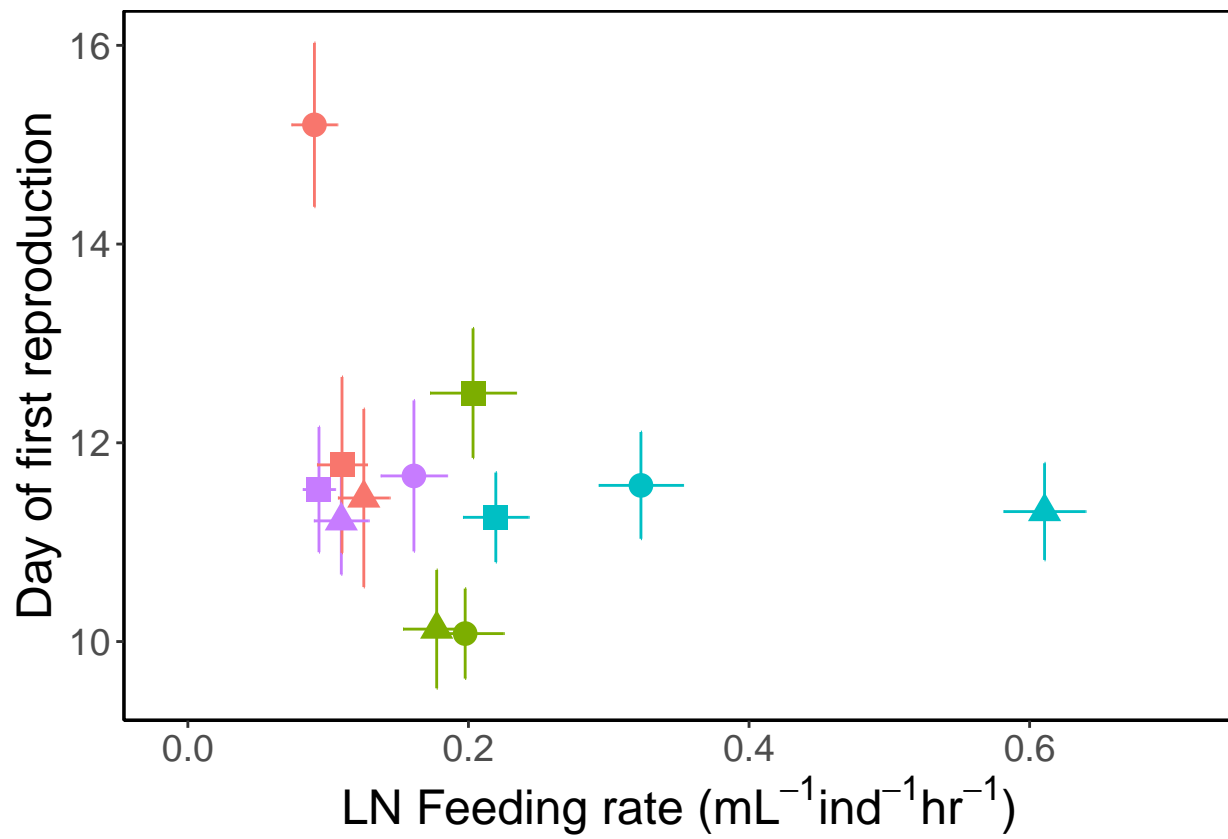
STATS SECTION

Table 1

```
##         dAICc df
## modinf2 0.0   5
## modinf1 4.3   8


##
## Call:
## glm(formula = y ~ Genotype + as.factor(Spore_level), family = binomial,
##     data = infected)
##
## Deviance Residuals:
##      Min       1Q    Median       3Q       Max
## -1.13934  -0.68016  -0.33913   0.06379   1.78693
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)               -1.16976    0.34821  -3.359 0.000781 ***
## GenotypeMidland 252       -0.22218    0.42189  -0.527 0.598459
## GenotypeMidland 281       -1.70310    0.66897  -2.546 0.010901 *
## GenotypeStandard           1.03370    0.38717   2.670 0.007588 **
## as.factor(Spore_level)300  0.04583    0.30456   0.150 0.880377
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 111.013  on 192  degrees of freedom
## Residual deviance:  78.583  on 188  degrees of freedom
##   (2 observations deleted due to missingness)
## AIC: 180.08
##
## Number of Fisher Scoring iterations: 5


## Analysis of Deviance Table (Type III tests)
##
## Response: y
##                     LR Chisq Df Pr(>Chisq)
## Genotype              32.145  3  4.878e-07 ***
## as.factor(Spore_level)  0.023  1     0.8804
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

Term	LR Chisq	Df	Pr(>Chisq)
Genotype	32.14510792	3	0.0000004877597
as.factor(Spore_level)	0.02264951	1	0.8803720828535

```
##         dAICc df
## mod3m 0      3
## mod2m 1      5


##
## Call:
## glm(formula = y ~ mean_feeding_rate + Size_mm2, family = binomial,
##     data = infected)
##
## Deviance Residuals:
##     Min      1Q   Median       3Q      Max
## -1.0168  -0.7848  -0.5477   0.4820   1.8138
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -1.4615     0.8171  -1.789  0.07368 .
## mean_feeding_rate   -3.2139     1.0594  -3.034  0.00242 **
## Size_mm2             0.6494     0.5396   1.204  0.22877
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 108.639  on 188  degrees of freedom
## Residual deviance:  95.683  on 186  degrees of freedom
##   (6 observations deleted due to missingness)
## AIC: 193.18
##
## Number of Fisher Scoring iterations: 5


## Analysis of Deviance Table (Type III tests)
##
## Response: y
##                   LR Chisq Df Pr(>Chisq)
## mean_feeding_rate   12.272  1  0.0004597 ***
## Size_mm2             1.494  1  0.2215954
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Term	LR Chisq	Df	Pr(>Chisq)
mean_feeding_rate	12.27225	1	0.000459744
Size_mm2	1.49401	1	0.221595370

Now, account for genotypic variation

```
## Analysis of Deviance Table (Type II tests)
##
## Response: y
##                              Df   Chisq Pr(>Chisq)
## mean_feeding_rate            1  0.0219  0.8823744
## Size_mm2                     1  0.3861  0.5343357
## as.factor(Genotype)          3 16.7564  0.0007931 ***
## as.factor(Spore_level)       1  0.1030  0.7482329
## mean_feeding_rate:Size_mm2   1  3.6375  0.0564906 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type II tests)
##
## Response: y
##                         Df   Chisq Pr(>Chisq)
## mean_feeding_rate        1  0.1860  0.6662878
## Size_mm2                 1  0.5353  0.4643890
## as.factor(Genotype)      3 16.6723  0.0008253 ***
## as.factor(Spore_level)   1  0.0310  0.8602011
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##        dAICc df
## mod2h 0.0    8
## mod2i 1.4    7


## Analysis of Deviance Table (Type III tests)
##
## Response: y
##                            LR Chisq Df Pr(>Chisq)
## mean_feeding_rate            3.1284  1  0.0769370 .
## Size_mm2                     3.6215  1  0.0570377 .
## as.factor(Genotype)         19.3611  3  0.0002302 ***
## as.factor(Spore_level)       0.1031  1  0.7481421
## mean_feeding_rate:Size_mm2   3.5805  1  0.0584600 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: y
##                            LR Chisq Df Pr(>Chisq)
## mean_feeding_rate            3.1284  1  0.0769370 .
## Size_mm2                     3.6215  1  0.0570377 .
## as.factor(Genotype)         19.3611  3  0.0002302 ***
## as.factor(Spore_level)       0.1031  1  0.7481421
## mean_feeding_rate:Size_mm2   3.5805  1  0.0584600 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Term	LR Chisq	Df	Pr(>Chisq)
mean_feeding_rate	3.1284463	1	0.0769370344
Size_mm2	3.6214925	1	0.0570376833
as.factor(Genotype)	19.3610810	3	0.0002302002
as.factor(Spore_level)	0.1030989	1	0.7481420645
mean_feeding_rate:Size_mm2	3.5805454	1	0.0584599561

Table 2

```
##
## Call:
## glm(formula = mean_feeding_rate ~ Genotype * Size_mm2 + Infected_Uninfected +
##     Spore_level, family = gaussian(link = "log"), data = total)
##
## Deviance Residuals:
##      Min       1Q    Median       3Q      Max
## -0.28232  -0.07199  -0.00455   0.07947   0.63002
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  -3.6790349  1.3734430  -2.679  0.00786 **
## GenotypeMidland 252           0.4129904  1.4218075   0.290  0.77169
## GenotypeMidland 281           1.7544277  1.3921475   1.260  0.20870
## GenotypeStandard              0.8783600  1.8305967   0.480  0.63175
## Size_mm2                      0.8337302  0.8508144   0.980  0.32803
## Infected_UninfectedExposed    1.1843364  0.1265402   9.359  < 2e-16 ***
## Infected_UninfectedInfected   0.9761503  0.1852444   5.270 2.85e-07 ***
## Spore_level                  -0.0046333  0.0006209  -7.462 1.25e-12 ***
## GenotypeMidland 252:Size_mm2  0.1153302  0.8790541   0.131  0.89572
## GenotypeMidland 281:Size_mm2 -0.2638278  0.8628215  -0.306  0.76002
## GenotypeStandard:Size_mm2    -0.4227152  1.1498522  -0.368  0.71345
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.01640027)
##
##     Null deviance: 10.296  on 273  degrees of freedom
## Residual deviance:  4.313  on 263  degrees of freedom
##   (7 observations deleted due to missingness)
## AIC: -335.93
##
## Number of Fisher Scoring iterations: 9


## Analysis of Deviance Table (Type III tests)
##
## Response: mean_feeding_rate
##               LR Chisq Df Pr(>Chisq)
## Genotype         9.269  3    0.02592 *
## Size_mm2         0.789  1    0.37434
```

```
## Infected_Uninfected    91.087  2    < 2e-16 ***
## Spore_level            77.146  1    < 2e-16 ***
## Genotype:Size_mm2       1.833  3     0.60772
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type II tests)
##
## Response: mean_feeding_rate
##                     LR Chisq Df Pr(>Chisq)
## Genotype             218.487  3  < 2.2e-16 ***
## Size_mm2              29.557  1  5.429e-08 ***
## Infected_Uninfected  91.087  2  < 2.2e-16 ***
## Spore_level          77.146  1  < 2.2e-16 ***
## Genotype:Size_mm2     1.833  3     0.6077
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##        dAICc df
## mod1c  0.0   9
## mod1b  4.6  12


##
## Call:
## glm(formula = mean_feeding_rate ~ Genotype + Size_mm2 + Infected_Uninfected +
##     Spore_level, family = gaussian(link = "log"), data = total)
##
## Deviance Residuals:
##      Min       1Q    Median       3Q       Max
## -0.28940  -0.07688  -0.00773   0.07413   0.62273
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  -3.3847228  0.2514575 -13.460  < 2e-16 ***
## GenotypeMidland 252           0.5905779  0.1726311   3.421 0.000722 ***
## GenotypeMidland 281           1.3315642  0.1602593   8.309 4.99e-15 ***
## GenotypeStandard              0.2143465  0.2240725   0.957 0.339640
## Size_mm2                      0.6532189  0.1179270   5.539 7.30e-08 ***
## Infected_UninfectedExposed    1.1776463  0.1260141   9.345  < 2e-16 ***
## Infected_UninfectedInfected   0.9654600  0.1846276   5.229 3.45e-07 ***
## Spore_level                  -0.0046315  0.0006148  -7.534 7.73e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.01632856)
##
##     Null deviance: 10.2961  on 273  degrees of freedom
## Residual deviance:  4.3431  on 266  degrees of freedom
##   (7 observations deleted due to missingness)
## AIC: -340.03
##
## Number of Fisher Scoring iterations: 8
```

Term	LR Chisq	Df	P
Genotype	219.44633	3	0.000000000000000000000000000000000000000000000
Size_mm2	29.68707	1	0.00000005077239218380875567536151984730785624
Infected_Uninfected	90.68973	2	0.000000000000000000020275692473066484838647916
Spore_level	78.06434	1	0.000000000000000000099738420801168999133819181

```
## Genotype = A45:
##  contrast            estimate    SE  df t.ratio p.value
##  Control - Exposed     -1.178 0.126 266  -9.345  <.0001
##  Control - Infected    -0.965 0.185 266  -5.229  <.0001
##  Exposed - Infected     0.212 0.140 266   1.512  0.2867
##
## Genotype = Midland 252:
##  contrast            estimate    SE  df t.ratio p.value
##  Control - Exposed     -1.178 0.126 266  -9.345  <.0001
##  Control - Infected    -0.965 0.185 266  -5.229  <.0001
##  Exposed - Infected     0.212 0.140 266   1.512  0.2867
##
## Genotype = Midland 281:
##  contrast            estimate    SE  df t.ratio p.value
##  Control - Exposed     -1.178 0.126 266  -9.345  <.0001
##  Control - Infected    -0.965 0.185 266  -5.229  <.0001
##  Exposed - Infected     0.212 0.140 266   1.512  0.2867
##
## Genotype = Standard:
##  contrast            estimate    SE  df t.ratio p.value
##  Control - Exposed     -1.178 0.126 266  -9.345  <.0001
##  Control - Infected    -0.965 0.185 266  -5.229  <.0001
##  Exposed - Infected     0.212 0.140 266   1.512  0.2867
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Table4a

```
##
## Call:
## glm(formula = Spores_ul ~ mean_feeding_rate + as.factor(Spore_level),
##     data = total)
##
## Deviance Residuals:
##     Min      1Q   Median      3Q      Max
## -39.925  -24.637   -3.703   11.404  138.041
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                10.216      4.128   2.475    0.014 *
## mean_feeding_rate         -46.881     10.760  -4.357 1.95e-05 ***
## as.factor(Spore_level)150  27.941      4.932   5.665 4.20e-08 ***
```

```
## as.factor(Spore_level)300    30.621       4.991    6.135 3.49e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 992.8513)
##
##     Null deviance: 307338  on 243  degrees of freedom
## Residual deviance: 238284  on 240  degrees of freedom
##   (37 observations deleted due to missingness)
## AIC: 2382.2
##
## Number of Fisher Scoring iterations: 2


## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                      LR Chisq Df Pr(>Chisq)
## mean_feeding_rate      18.984  1  1.318e-05 ***
## as.factor(Spore_level) 48.256  2  3.321e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Call:
##    aov(formula = mod2k)
##
## Terms:
##                 mean_feeding_rate as.factor(Spore_level) Residuals
## Sum of Squares          21142.83               47911.20 238284.30
## Deg. of Freedom                1                      2       240
##
## Residual standard error: 31.50954
## Estimated effects may be unbalanced
## 37 observations deleted due to missingness


## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                            LR Chisq Df Pr(>Chisq)
## mean_feeding_rate           0.22312  1     0.6367
## Size_mm2                    2.19853  1     0.1381
## Spore_level_fct             0.06526  1     0.7984
## mean_feeding_rate:Size_mm2  0.65240  1     0.4193


## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                             LR Chisq Df Pr(>Chisq)
## mean_feeding_rate            0.79702  1     0.3720
## Size_mm2                     0.08375  1     0.7723
## Spore_level_fct             1.05072  1     0.3053
## Final_Size_mm2              0.55722  1     0.4554
## Spore_level_fct:Final_Size_mm2 1.28394 1     0.2572
```

```
## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                 LR Chisq Df Pr(>Chisq)
## Spore_level_fct   0.4621  1     0.4967
## Final_Size_mm2    5.2617  1     0.0218 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##                 df      AIC
## modfeedspores1   6 644.8335
## modfeedspores2   7 610.9386
## modfeedspores3   6 610.3441
## modfeedspores4   4 607.3463
```

Table 4b Spore yield

```
## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                          LR Chisq Df Pr(>Chisq)
## mean_feeding_rate          1.4557  1    0.22762
## Size_mm2                   0.0266  1    0.87046
## Spore_level_fct            1.0240  1    0.31158
## Final_Size_mm2             6.6193  1    0.01009 *
## Genotype                   6.7155  3    0.08154 .
## mean_feeding_rate:Size_mm2 1.4536  1    0.22796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                 LR Chisq Df Pr(>Chisq)
## mean_feeding_rate 0.0253  1    0.87353
## Size_mm2          0.8198  1    0.36524
## Spore_level_fct   0.7896  1    0.37421
## Final_Size_mm2    6.2452  1    0.01245 *
## Genotype          5.6513  3    0.12986
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Deviance Table (Type III tests)
##
## Response: Spores_ul
##                 LR Chisq Df Pr(>Chisq)
## mean_feeding_rate 0.2142  1     0.6435
## Size_mm2          0.6809  1     0.4093
## Spore_level_fct   0.0722  1     0.7881
## Genotype          3.2987  3     0.3478


## Analysis of Deviance Table (Type III tests)
```

```
## 
## Response: Spores_ul
##                   LR Chisq Df Pr(>Chisq)
## mean_feeding_rate    1.214  1     0.2705
## Spore_level_fct     52.335  2  4.320e-12 ***
## Genotype            74.429  3  4.804e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
## 
## Response: Spores_ul
##                 LR Chisq Df Pr(>Chisq)
## Spore_level_fct   51.567  2  6.343e-12 ***
## Genotype          97.760  3  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## 
## Call:
## glm(formula = Spores_ul ~ mean_feeding_rate + Size_mm2 + Spore_level_fct +
##     Final_Size_mm2 + Genotype, family = gaussian(link = "identity"),
##     data = totalpos)
## 
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -52.833  -23.933   -0.319   20.326   95.758
## 
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)           -12.719     37.399  -0.340   0.7351
## mean_feeding_rate       5.891     37.012   0.159   0.8741
## Size_mm2              -16.291     17.993  -0.905   0.3693
## Spore_level_fct300      7.395      8.322   0.889   0.3782
## Final_Size_mm2         40.740     16.302   2.499   0.0155 *
## GenotypeMidland 252     5.831     14.571   0.400   0.6906
## GenotypeMidland 281   -27.677     26.048  -1.063   0.2927
## GenotypeStandard       18.712     10.329   1.811   0.0756 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for gaussian family taken to be 945.2518)
## 
##     Null deviance: 62483  on 61  degrees of freedom
## Residual deviance: 51044  on 54  degrees of freedom
##   (3 observations deleted due to missingness)
## AIC: 610.17
## 
## Number of Fisher Scoring iterations: 2


## Analysis of Deviance Table (Type III tests)
## 
## Response: Spores_ul
```

```
##                    LR Chisq Df Pr(>Chisq)
## mean_feeding_rate   0.0253  1    0.87353
## Size_mm2            0.8198  1    0.36524
## Spore_level_fct     0.7896  1    0.37421
## Final_Size_mm2      6.2452  1    0.01245 *
## Genotype            5.6513  3    0.12986
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Term	LR Chisq	Df	Pr(>Chisq)
mean_feeding_rate	0.02533612	1	0.87353240
Size_mm2	0.81979692	1	0.36523955
Spore_level_fct	0.78963588	1	0.37421025
Final_Size_mm2	6.24521611	1	0.01245292
Genotype	5.65134086	3	0.12986181

```
## Spore_level_fct = 150:
##  contrast                 estimate   SE df t.ratio p.value
##  A45 - Midland 252           -5.83 14.6 54  -0.400  0.9781
##  A45 - Midland 281           27.68 26.0 54   1.063  0.7135
##  A45 - Standard             -18.71 10.3 54  -1.811  0.2792
##  Midland 252 - Midland 281   33.51 25.2 54   1.327  0.5500
##  Midland 252 - Standard     -12.88 12.6 54  -1.024  0.7363
##  Midland 281 - Standard     -46.39 25.8 54  -1.801  0.2840
##
## Spore_level_fct = 300:
##  contrast                 estimate   SE df t.ratio p.value
##  A45 - Midland 252           -5.83 14.6 54  -0.400  0.9781
##  A45 - Midland 281           27.68 26.0 54   1.063  0.7135
##  A45 - Standard             -18.71 10.3 54  -1.811  0.2792
##  Midland 252 - Midland 281   33.51 25.2 54   1.327  0.5500
##  Midland 252 - Standard     -12.88 12.6 54  -1.024  0.7363
##  Midland 281 - Standard     -46.39 25.8 54  -1.801  0.2840
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

#Susceptibility and Spore yield

```
##
##   Pearson's product-moment correlation
##
## data:  probinf and meanspores * finalsize + Spore_level
## t = 11.422, df = 218, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5218357 0.6884279
## sample estimates:
##       cor
## 0.6118732
```

Cullen and Frey graph
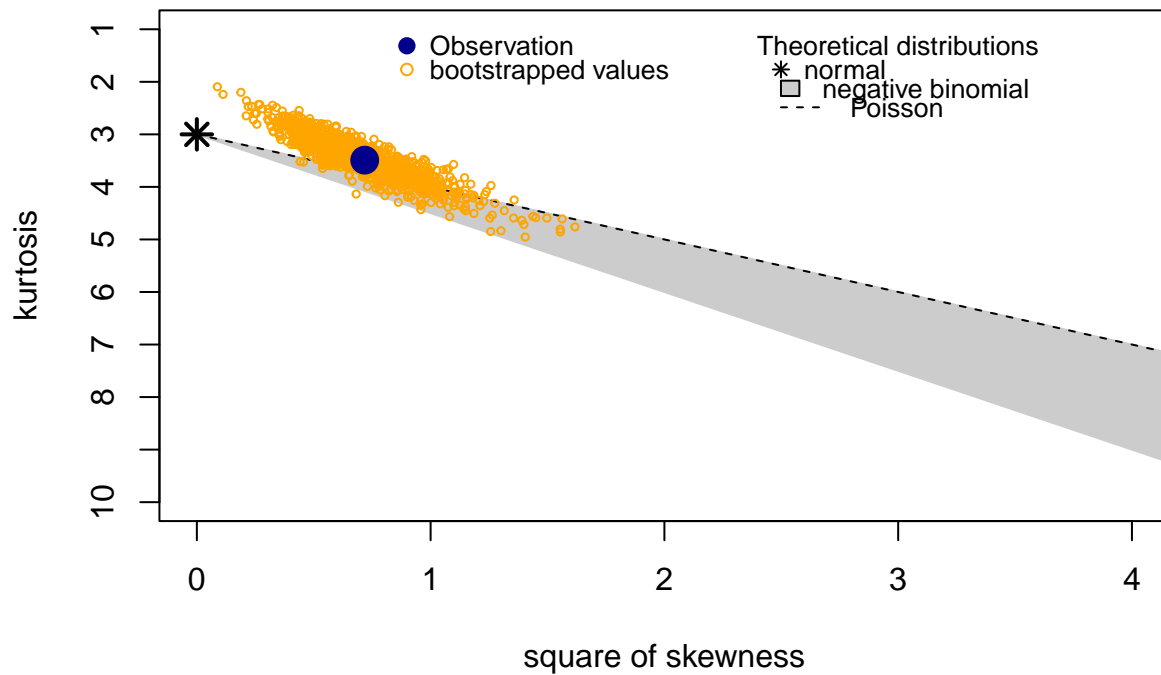

```
## summary statistics
## ------
## min:  0    max:  15
## median:  3
## mean:  3.733591
## estimated sd:  3.124433
## estimated skewness:  0.8473916
## estimated kurtosis:  3.491364
```

Histogram of Total_Fecundity
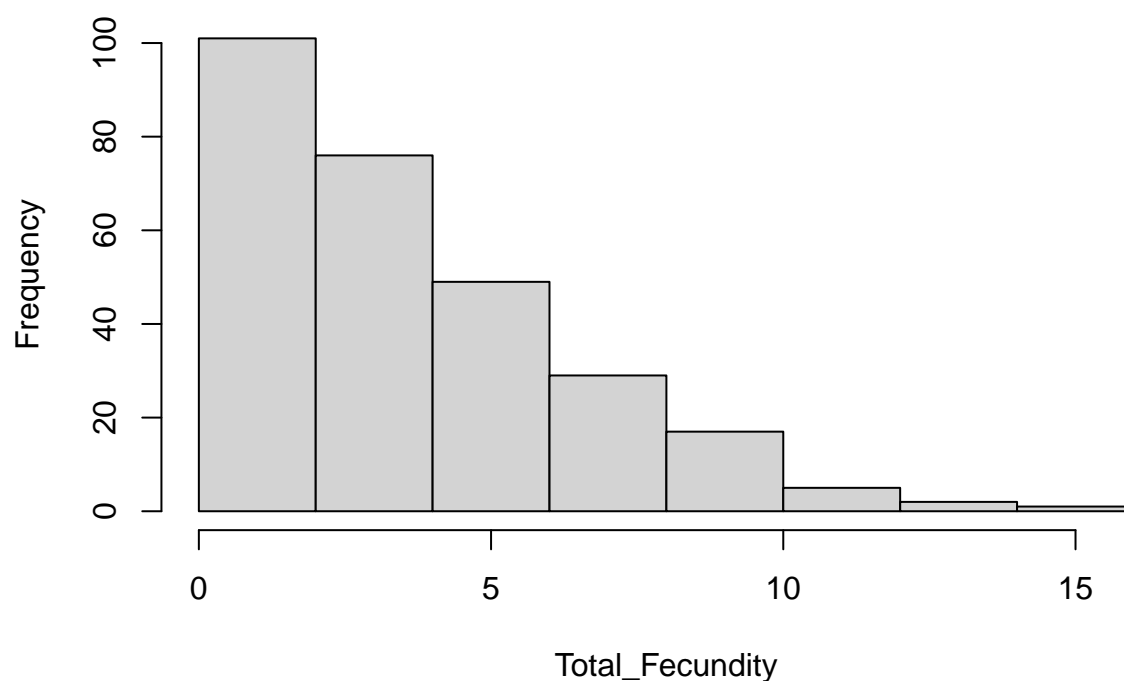

```
##           dAICc df
## nb.fit    0     9
## pois.fit  24    8


##           dAICc df
## nb.fit1   0.0   8
## nb.fit    1.7   9
## pois.fit  25.7  8


## Analysis of Deviance Table
##
## Model: Negative Binomial(7.1924), link: log
##
## Response: Total_Fecundity
##
## Terms added sequentially (first to last)
##
##
##                     Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                                224      361.17
## Total_Growth        1   15.832      223      345.34 6.924e-05 ***
## Genotype            3   71.028      220      274.31 2.571e-15 ***
## Infected_Uninfected 2    3.272      218      271.04    0.1948
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
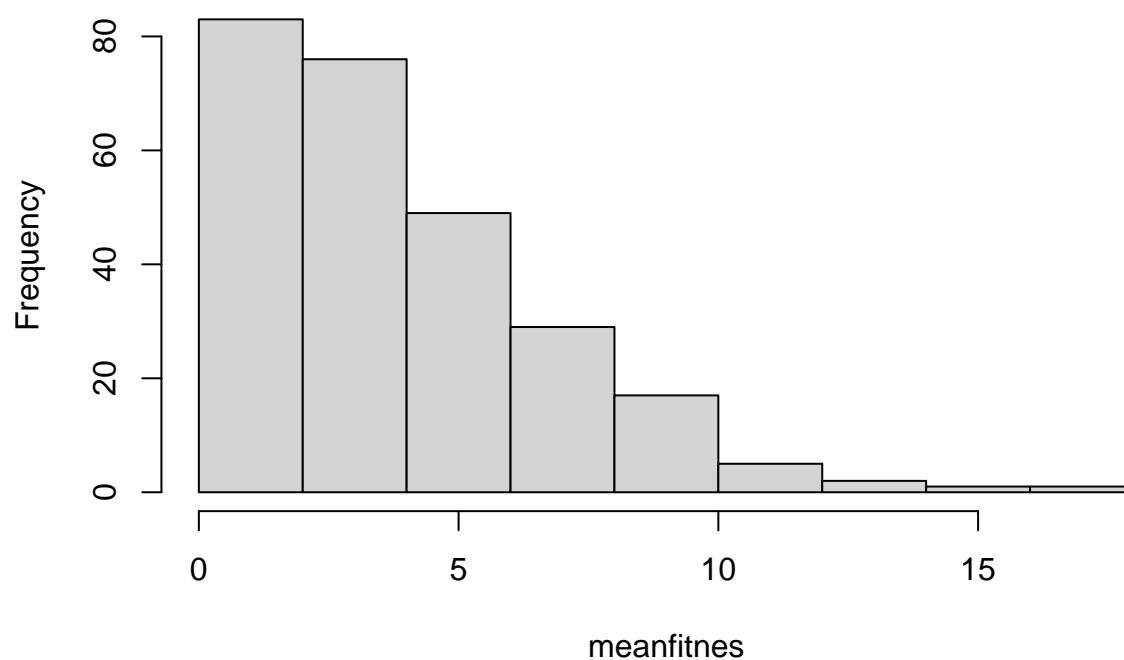
Term	LR Chisq	Df	Pr(>Chisq)
Total_Growth	6.300600	1	0.0120697115775295112389
Genotype	72.543393	3	0.000000000000001217612
Infected_Uninfected	3.271743	2	0.194782510593732333115

Cullen and Frey graph
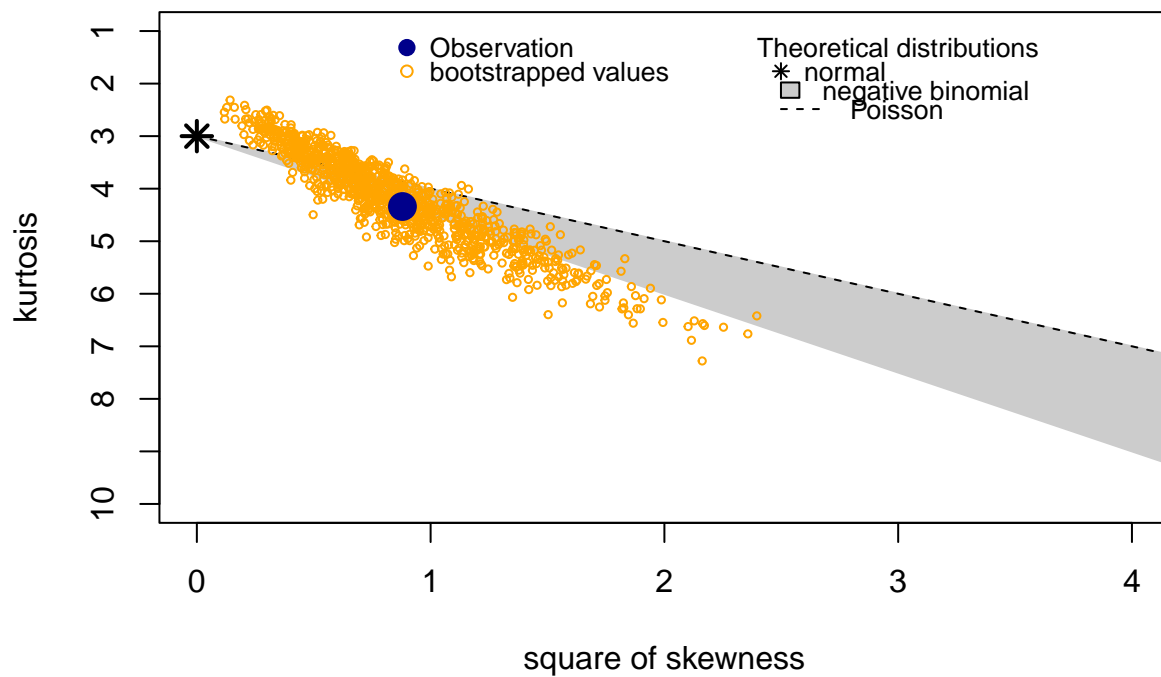

```
## summary statistics
## ------
## min:  0    max:  18
## median:  4
## mean:  4.197719
## estimated sd:  3.13909
## estimated skewness:  0.9378296
## estimated kurtosis:  4.339088
```
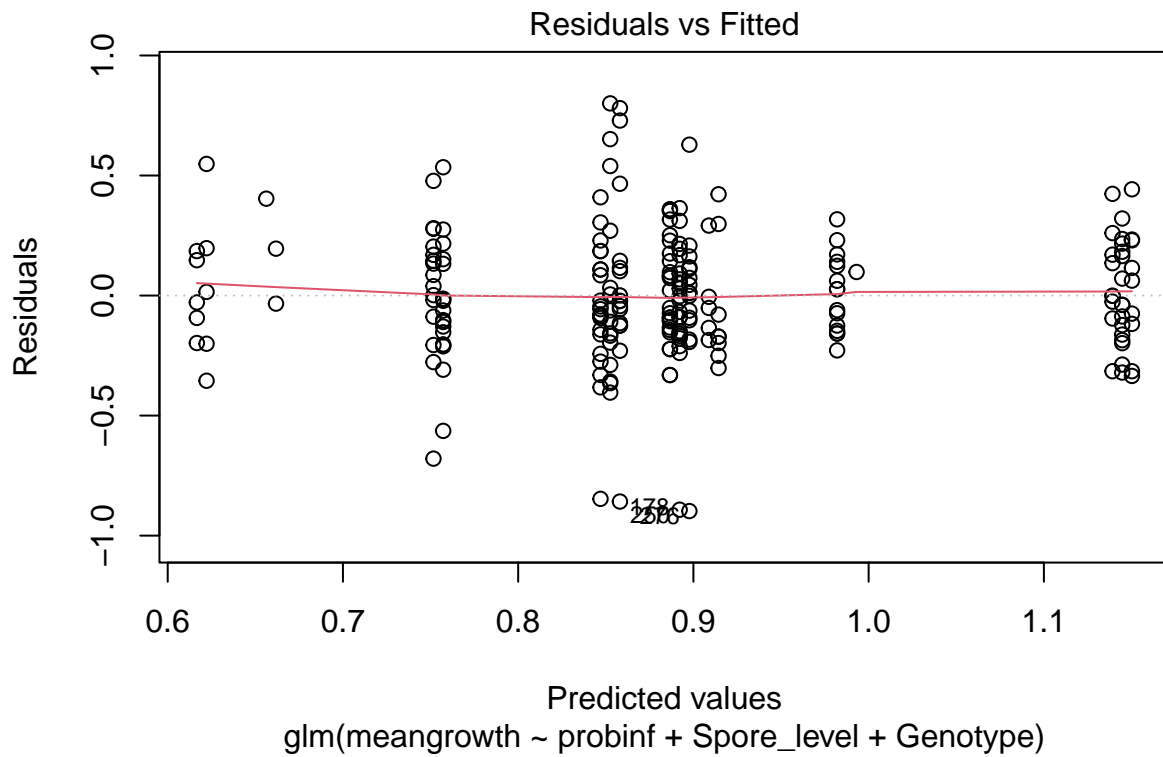
Histogram of meanfitnes


```
##          dAICc df
## nb.fit1   0.0  11
## nb.fit    5.7  8
## pois.fit 15.4  7
```

Term	LR Chisq	Df	Pr(>Chisq)
meangrowth	21.309003	1	0.0000039089143045511835
Genotype	69.010824	3	0.0000000000000006951048
Spore_level	10.288162	1	0.0013388637220072796119
probinf	5.312153	1	0.0211771720218794440283
Genotype:Spore_level	12.556357	3	0.0057011829885516527265

Cullen and Frey graph
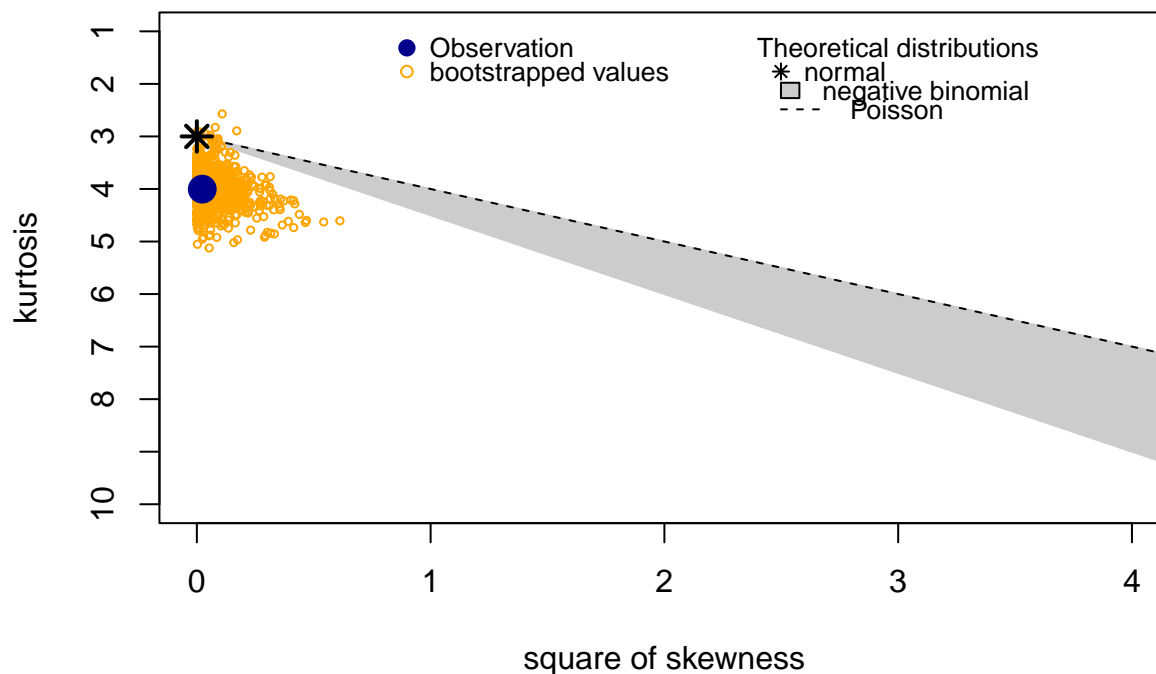

```
## summary statistics
## ------
## min:  0    max:  1.653
## median:  0.8571
## mean:  0.8918884
## estimated sd:  0.2927738
## estimated skewness:  -0.1523719
## estimated kurtosis:  4.003321


## Analysis of Deviance Table (Type III tests)
##
## Response: meangrowth
##            LR Chisq Df Pr(>Chisq)
## probinf       20.439  1  6.158e-06 ***
## Spore_level    0.052  1     0.8201
## Genotype      35.573  3  9.218e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: meangrowth
##               LR Chisq Df Pr(>Chisq)
## probinf        15.4920  1  8.286e-05 ***
## Spore_level     0.2772  1  0.5985306
```
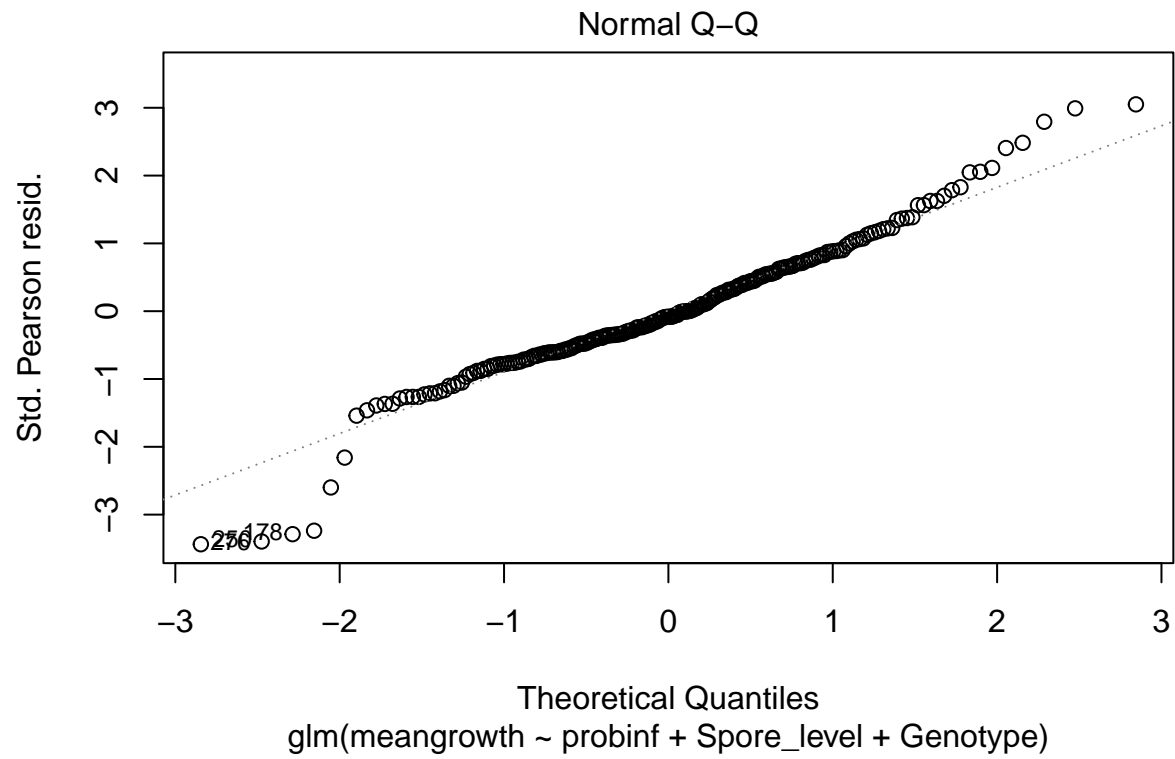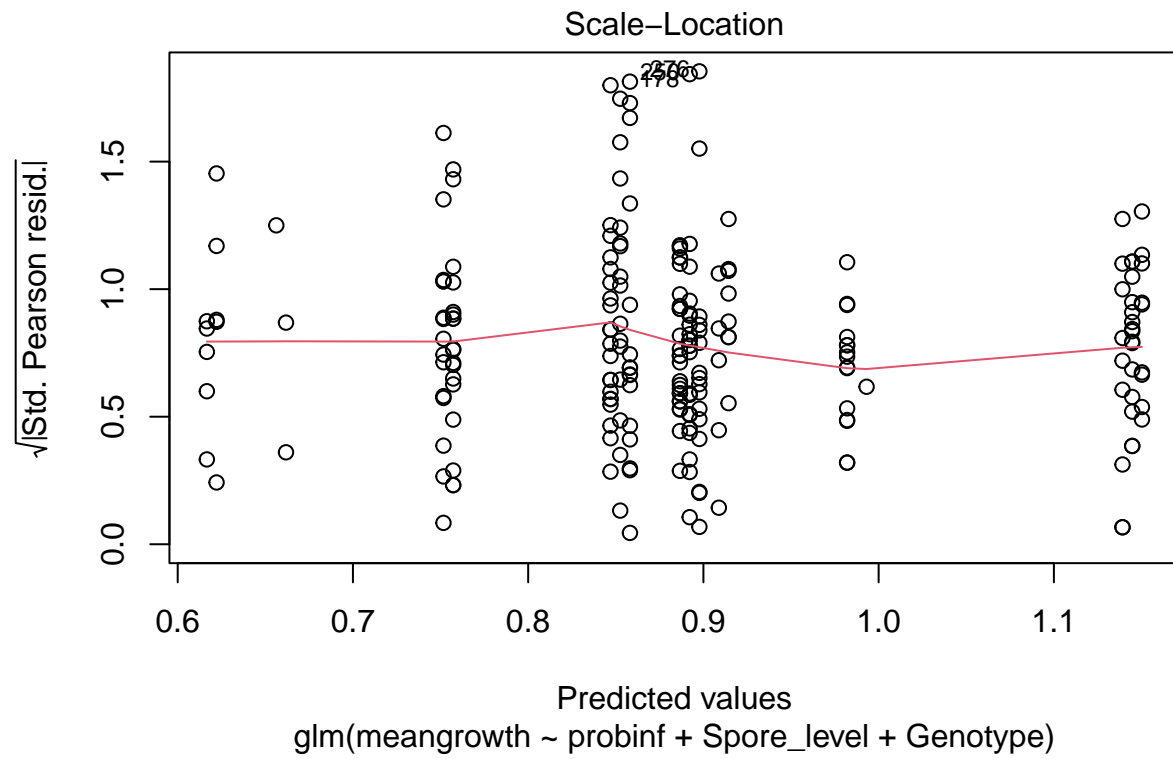
```
## Genotype                  19.3286  3  0.0002338 ***
## Spore_level:Genotype        2.2663  3  0.5190147
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##             dAICc df
## modgrowth1  0.0   7
## modgrowth2  4.2  10
```
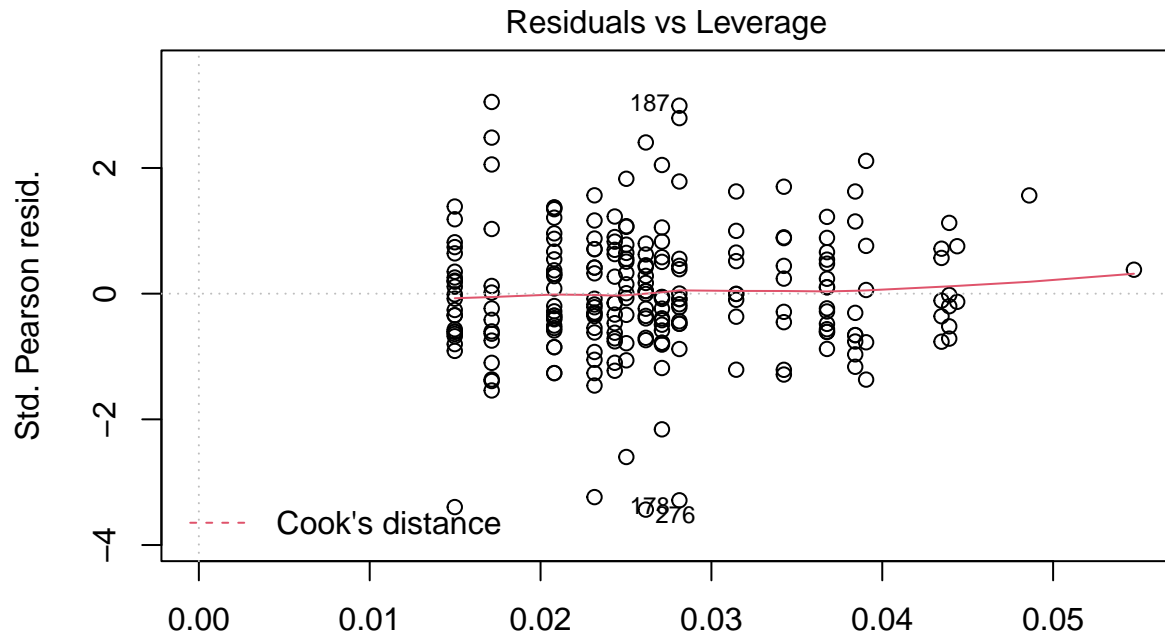

Residuals vs Fitted

Predicted values
glm(meangrowth ~ probinf + Spore_level + Genotype)

Normal Q–Q

Std. Pearson resid.

Theoretical Quantiles
glm(meangrowth ~ probinf + Spore_level + Genotype)

Scale–Location

√|Std. Pearson resid.|

Predicted values
glm(meangrowth ~ probinf + Spore_level + Genotype)

33

Residuals vs Leverage

Leverage
glm(meangrowth ~ probinf + Spore_level + Genotype)

Term	LR Chisq	Df	Pr(>Chisq)
probinf	20.43854921	1	0.00000615768743
Spore_level	0.05174202	1	0.82005928669708
Genotype	35.57316185	3	0.00000009217609

```
## contrast                estimate     SE  df t.ratio p.value
## A45 - Midland 252          0.2922 0.0518 219   5.635  <.0001
## A45 - Midland 281          0.2525 0.0518 219   4.875  <.0001
## A45 - Standard             0.1571 0.0584 219   2.690  0.0383
## Midland 252 - Midland 281 -0.0396 0.0468 219  -0.847  0.8321
## Midland 252 - Standard    -0.1350 0.0569 219  -2.375  0.0850
## Midland 281 - Standard    -0.0954 0.0585 219  -1.630  0.3640
##
## Results are averaged over the levels of: probinf
## P value adjustment: tukey method for comparing a family of 4 estimates
```
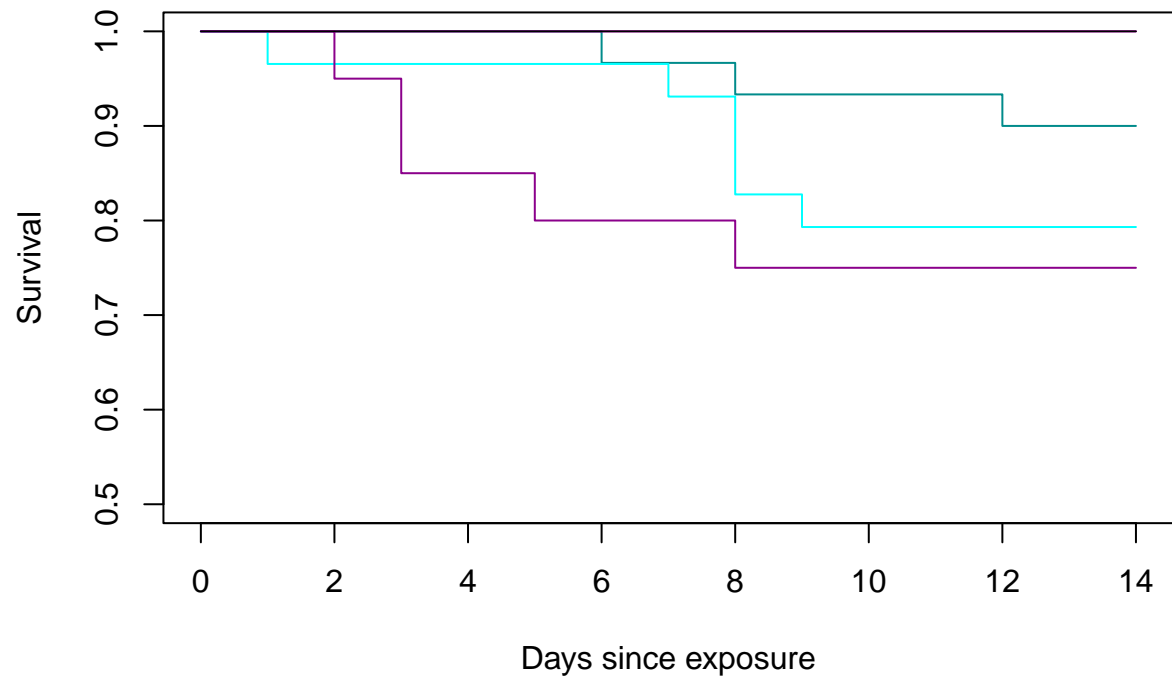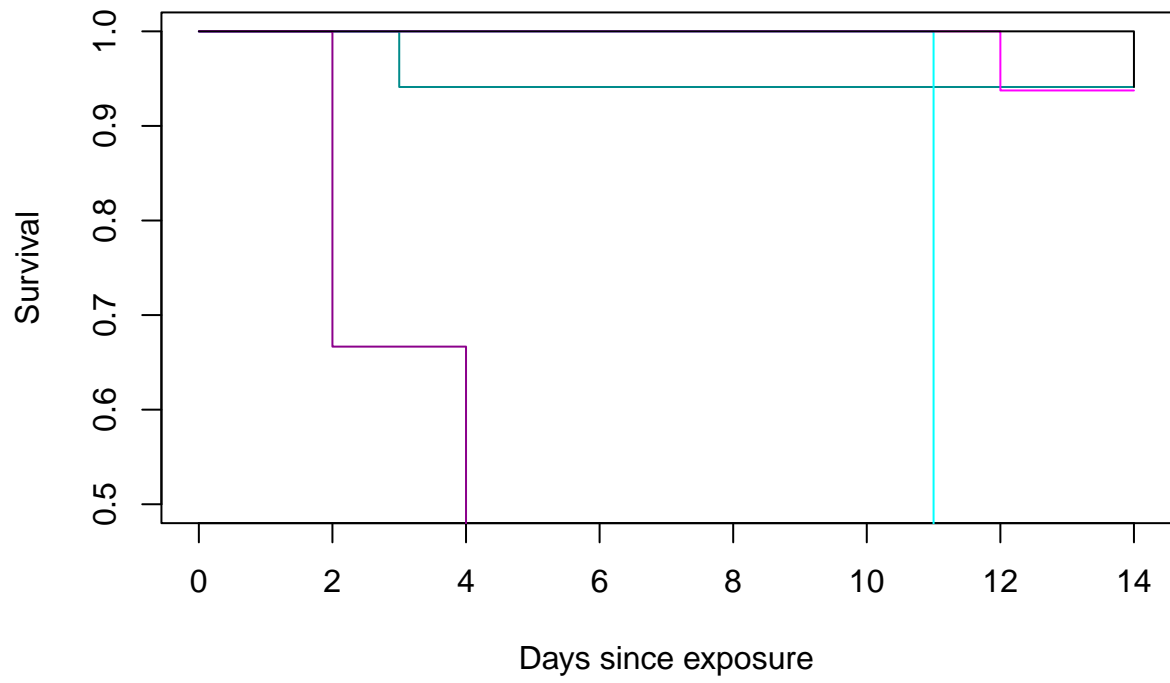
A45
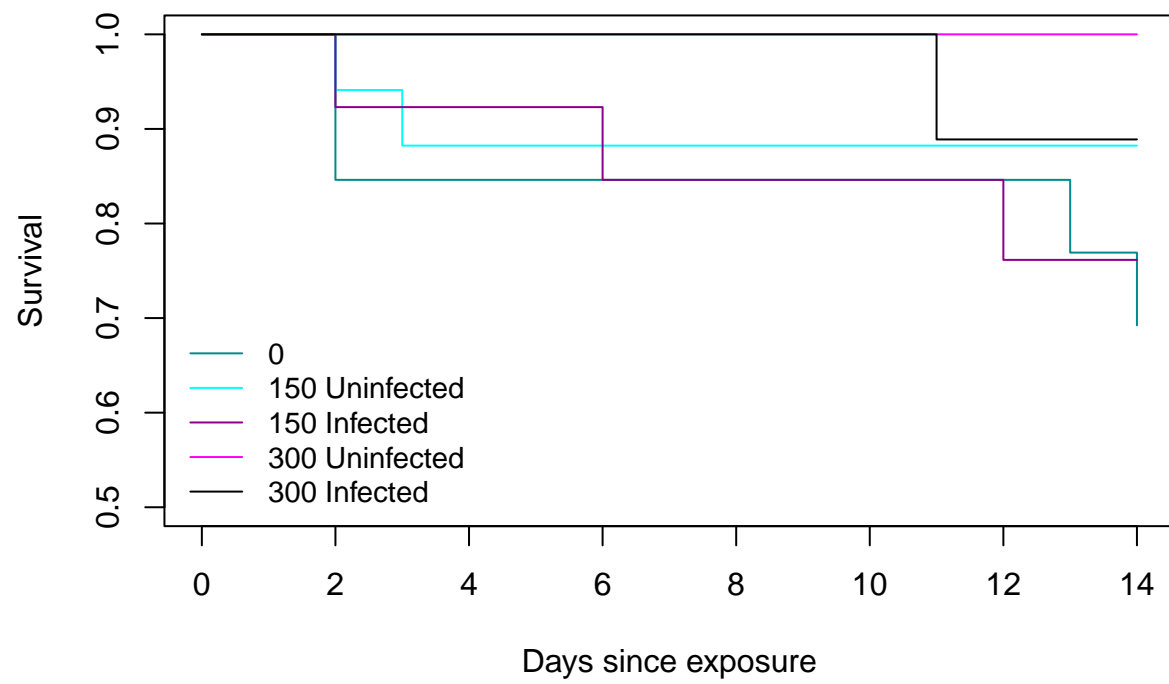
M252
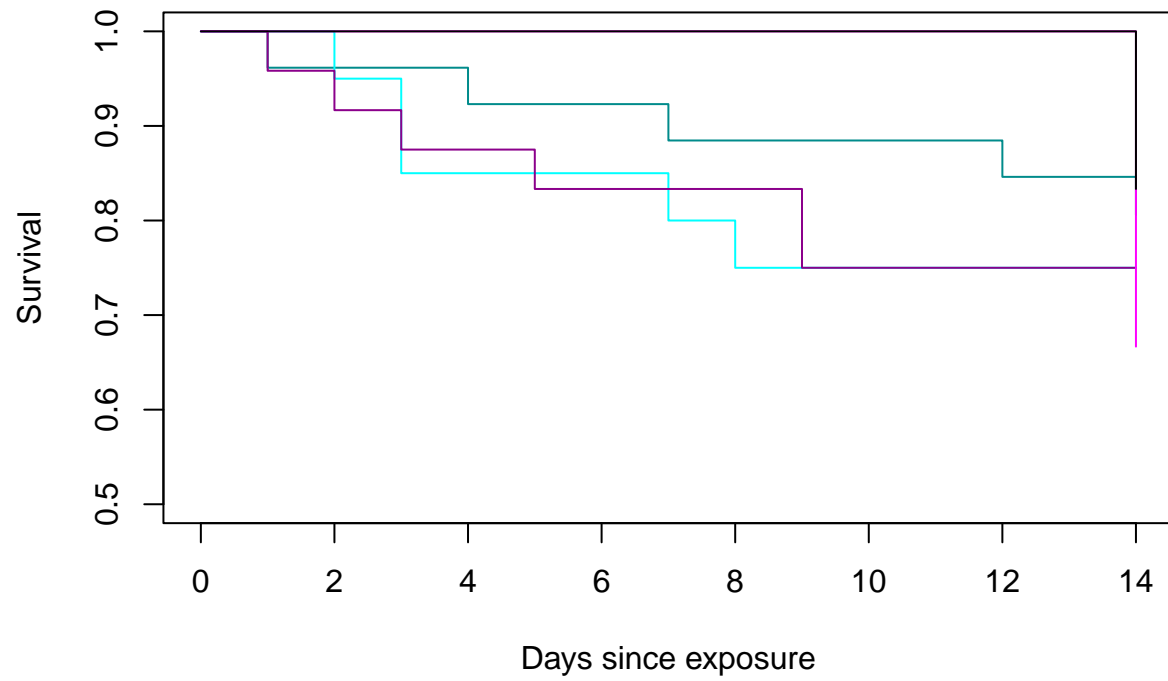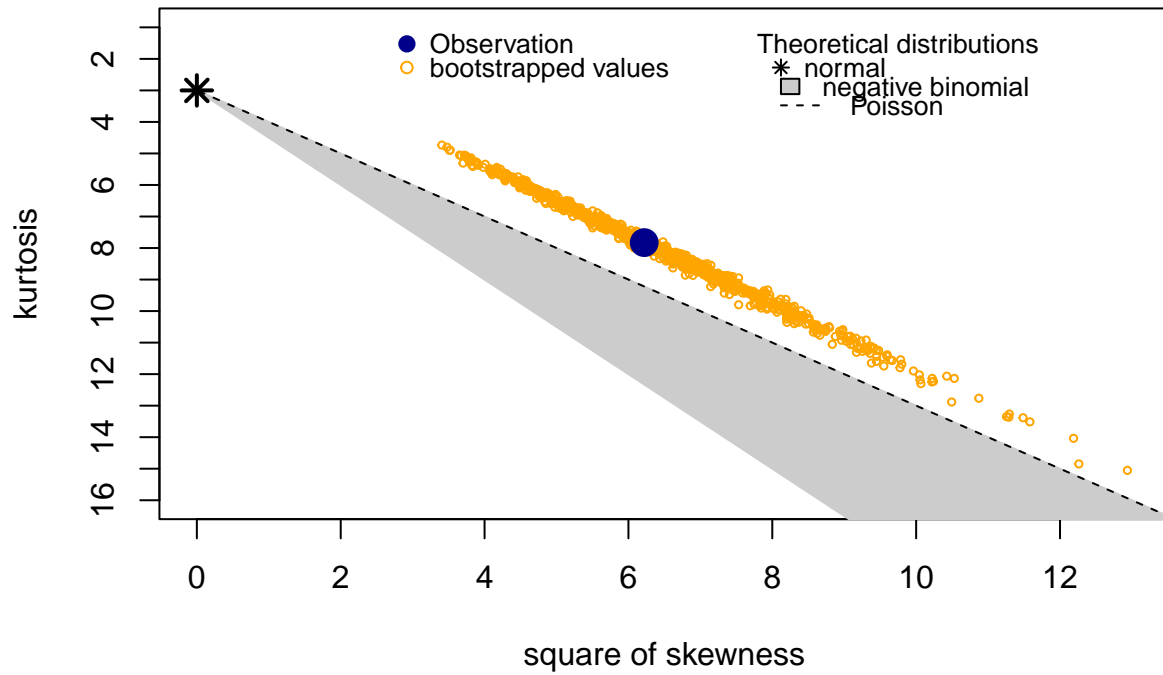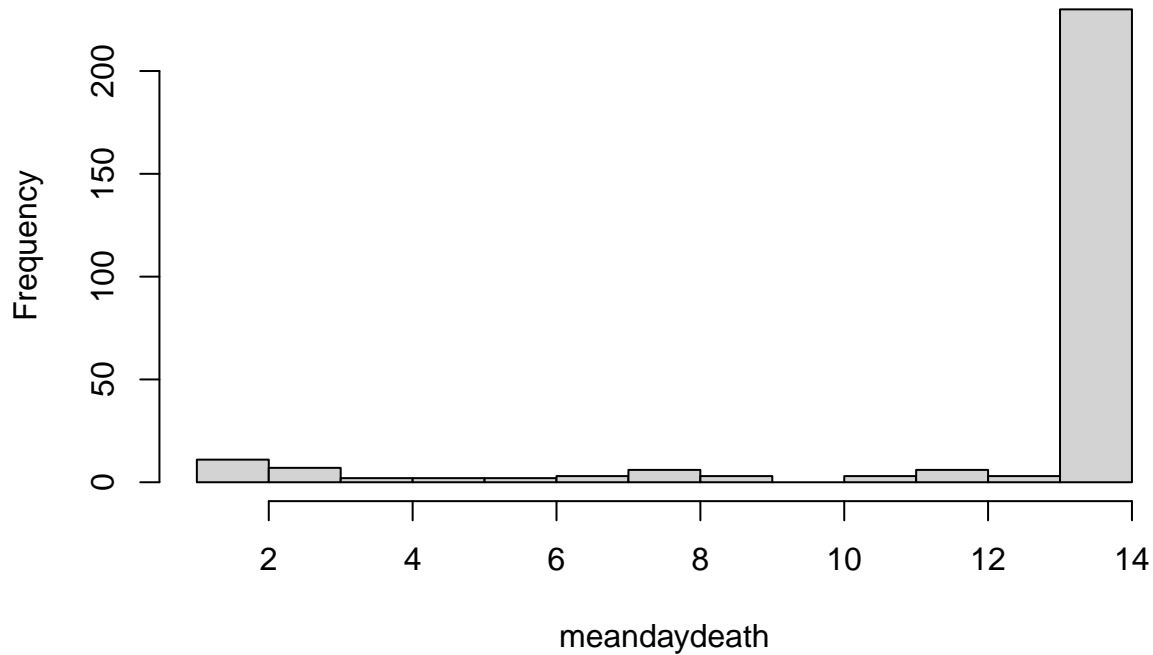
M281

STD

Cullen and Frey graph


```
## summary statistics
## ------
## min:  1    max:  14
## median:  14
## mean:  12.69784
## estimated sd:  3.300049
## estimated skewness:  -2.49387
## estimated kurtosis:  7.827662
```

Histogram of meandaydeath


```
## Analysis of Deviance Table (Type III tests)
##
## Response: meandaydeath
##            LR Chisq Df Pr(>Chisq)
## probinf     15.5138  1   8.19e-05 ***
## Spore_level  7.3418  1   0.006737 **
## Genotype     1.1084  3   0.775053
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: meandaydeath
##                   LR Chisq Df Pr(>Chisq)
## probinf            15.0621  1   0.000104 ***
## Spore_level         0.1011  1   0.750506
## Genotype            2.1170  3   0.548486
## Spore_level:Genotype 2.0732 3   0.557358
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##          dAICc df
## modsurv1  0.0  7
## modsurv2  4.3  10
```

Term	LR Chisq	Df	Pr(>Chisq)
probinf	15.513826	1	0.000081904
Spore_level	7.341782	1	0.006737001
Genotype	1.108374	3	0.775053010

```
## Genotype = A45:
##  contrast estimate   SE  df t.ratio p.value
##  0 - 1      -2.18 0.553 272  -3.939  0.0001
##
## Genotype = Midland 252:
##  contrast estimate   SE  df t.ratio p.value
##  0 - 1      -2.18 0.553 272  -3.939  0.0001
##
## Genotype = Midland 281:
##  contrast estimate   SE  df t.ratio p.value
##  0 - 1      -2.18 0.553 272  -3.939  0.0001
##
## Genotype = Standard:
##  contrast estimate   SE  df t.ratio p.value
##  0 - 1      -2.18 0.553 272  -3.939  0.0001


## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##           LR Chisq Df Pr(>Chisq)
## probinf    12.0179  1  0.0005269 ***
## finalsize   1.4061  1  0.2357066
## Spore_level 0.4192  1  0.5173307
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##               LR Chisq Df Pr(>Chisq)
## probinf          3.527  1    0.06038 .
## finalsize        2.749  1    0.09729 .
## Spore_level      0.964  1    0.32623
## Genotype       105.966  3    < 2e-16 ***
## probinf:finalsize 3.566 1    0.05898 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##               LR Chisq Df Pr(>Chisq)
## probinf          3.230  1    0.07232 .
## finalsize        2.748  1    0.09737 .
## Genotype       105.663  3    < 2e-16 ***
```

```
## probinf:finalsize    3.466  1    0.06263 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##                 LR Chisq Df Pr(>Chisq)
## probinf             3.527  1    0.06038 .
## finalsize           2.749  1    0.09729 .
## Spore_level         0.964  1    0.32623
## Genotype          105.966  3    < 2e-16 ***
## probinf:finalsize   3.566  1    0.05898 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Deviance Table (Type III tests)
##
## Response: meanfeedrate
##                 LR Chisq Df Pr(>Chisq)
## probinf             3.081  1    0.07920 .
## finalsize           1.369  1    0.24192
## Genotype          105.706  3    < 2e-16 ***
## probinf:finalsize   3.384  1    0.06583 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


##            dAICc df
## modfeedinfb 0.0    8
## modfeedinfd 0.4    8
## modfeedinf  1.2    9
## modfeedinfc 1.2    9


##
## Call:
## glm(formula = meanfeedrate ~ probinf * finalsize + Genotype,
##     family = gaussian(link = "identity"), data = inf1)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.39125  -0.08163  -0.01700   0.07431   0.53012
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -0.17391    0.17409  -0.999  0.31894
## probinf            0.37294    0.20752   1.797  0.07373 .
## finalsize          0.10804    0.06518   1.658  0.09884 .
## GenotypeMidland 252 0.11927    0.03774   3.160  0.00181 **
## GenotypeMidland 281 0.30358    0.03335   9.102  < 2e-16 ***
## GenotypeStandard   0.03748    0.03485   1.075  0.28337
## probinf:finalsize  -0.15923    0.08552  -1.862  0.06401 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## (Dispersion parameter for gaussian family taken to be 0.02436518)
## 
##     Null deviance: 8.3950  on 220  degrees of freedom
## Residual deviance: 5.2141  on 214  degrees of freedom
##   (60 observations deleted due to missingness)
## AIC: -184.87
## 
## Number of Fisher Scoring iterations: 2


## Analysis of Deviance Table (Type III tests)
## 
## Response: meanfeedrate
##                 LR Chisq Df Pr(>Chisq)
## probinf            3.230  1    0.07232 .
## finalsize          2.748  1    0.09737 .
## Genotype         105.663  3    < 2e-16 ***
## probinf:finalsize  3.466  1    0.06263 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Term	LR Chisq	Df	Pr(>Chisq)
probinf	3.229664	1	0.0723155236503466420218035730
finalsize	2.748078	1	0.0973714312825156441677521020
Genotype	105.662556	3	0.0000000000000000000009410693
probinf:finalsize	3.466209	1	0.0626346862125734538118138061