Plant defense resistance in natural enemies of a specialist insect herbivore

Zhang et al.

09/09/2019

Contents

```
library(lme4)
library(car)
library(emmeans)
library(multcomp)
library(RVAideMemoire)
library(MuMIn)
library(stats)
```

Figure 1

Figure 1B

```
tab.1B <- read.table("Fig1B.txt",header=TRUE)
with(tab.1B, t.test(MBOA.Glc[larvae=="BCB"],MBOA.Glc[larvae=="WCR"],var.equal=TRUE))
```

```
	Two Sample t-test

data:  MBOA.Glc[larvae == "BCB"] and MBOA.Glc[larvae == "WCR"]
t = -4.3402, df = 8, p-value = 0.002478
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -45.36581 -13.88507
sample estimates:
mean of x mean of y 
  2.85099  32.47643 
```

```
with(tab.1B, t.test(HDMBOA.Glc[larvae=="BCB"],MBOA.Glc[larvae=="WCR"],var.equal=TRUE))
```

```
	Two Sample t-test

data:  HDMBOA.Glc[larvae == "BCB"] and MBOA.Glc[larvae == "WCR"]
t = -4.5213, df = 8, p-value = 0.001947
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -46.41587 -15.06090
sample estimates:
mean of x mean of y 
 1.738045 32.476431 
```

Figure 1C

```
tab.1C <- read.table("Fig1C.txt",header=TRUE)
mod.1C <- glmer(cbind(dead,alive)~origin*larvae+(1|origin:strain),family=binomial,
                data=tab.1C)
Anova(mod.1C)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(dead, alive)
               Chisq Df Pr(>Chisq)    
origin        11.125  1  0.0008516 ***
larvae        41.825  1  9.982e-11 ***
origin:larvae 18.972  1  1.327e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.1C,~origin:larvae,type="response"),adjust="fdr")
```

```
 origin larvae      prob         SE  df asymp.LCL asymp.UCL .group
 WCR-   WCR    0.2402075 0.03378813 Inf 0.1660411 0.3342254  1    
 WCR-   BCB    0.4744115 0.05180587 Inf 0.3494663 0.6026452   2   
 WCR+   WCR    0.5311696 0.06567572 Inf 0.3696138 0.6864457   2   
 WCR+   BCB    0.5448768 0.07451161 Inf 0.3611247 0.7171706   2   

Confidence level used: 0.95 
Conf-level adjustment: bonferroni method for 4 estimates 
Intervals are back-transformed from the logit scale 
P value adjustment: fdr method for 6 tests 
```

```
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 2

Figure 2A

```
tab.2A <- read.table("Fig2A.txt",header=TRUE)
with(tab.2A, t.test(MBOA.Glc[larvae=="B73"],MBOA.Glc[larvae=="BX1"],var.equal=TRUE))
```

```

    Two Sample t-test

data:  MBOA.Glc[larvae == "B73"] and MBOA.Glc[larvae == "BX1"]
t = 6.9441, df = 8, p-value = 0.0001191
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 14.06841 28.05768
sample estimates:
mean of x mean of y 
27.134014  6.070968 
```

```
with(tab.2A, t.test(HDMBOA.Glc[larvae=="B73"],MBOA.Glc[larvae=="BX1"],var.equal=TRUE))
```

```

    Two Sample t-test

data:  HDMBOA.Glc[larvae == "B73"] and MBOA.Glc[larvae == "BX1"]
t = 15.532, df = 8, p-value = 2.94e-07
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 304.0213 410.0354
sample estimates:
 mean of x  mean of y 
363.099332   6.070968 
```

Figure 2B

```
tab.2B <- read.table("Fig2B.txt",header=TRUE)
mod.2B <- glmer(cbind(dead,alive)~origin*larvae+(1|origin:strain),family=binomial,data=tab.2B)
Anova(mod.2B)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(dead, alive)
                Chisq Df Pr(>Chisq)    
origin        24.7915  1  6.388e-07 ***
larvae        30.3407  1  3.624e-08 ***
origin:larvae  7.5457  1   0.006015 ** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.2B,~origin:larvae,type="response"),adjust="fdr")
```

```
 origin larvae      prob         SE  df asymp.LCL asymp.UCL .group
```

```
 WCR-   BX+    0.3208637 0.02885345 Inf 0.2534064 0.3967358  1
 WCR-   BX-    0.5522952 0.03850239 Inf 0.4553749 0.6453986   2
 WCR+   BX+    0.6359723 0.04372018 Inf 0.5215471 0.7368399   2
 WCR+   BX-    0.6777277 0.05155519 Inf 0.5383691 0.7913230   2

Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
Intervals are back-transformed from the logit scale
P value adjustment: fdr method for 6 tests
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 2D

```
tab.2D <- read.table("Fig2D.txt",header=TRUE)
tab.2D$ind <- factor(1:nrow(tab.2D))
mod.2D <- glmer(cbind(dead,alive)~origin*treatment+(1|origin:strain)+(1|ind),
                family=binomial,data=tab.2D)
Anova(mod.2D)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(dead, alive)
                  Chisq Df Pr(>Chisq)
origin           2.3181  1    0.12788
treatment        5.9105  1    0.01505 *
origin:treatment 1.4040  1    0.23606
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.2D,~origin:treatment,type="response"),adjust="fdr")
```

```
 origin treatment       prob         SE  df  asymp.LCL asymp.UCL .group
 WCR+   CON       0.04587901 0.01716471 Inf 0.01773741 0.1135096  12
 WCR+   HDG       0.05358120 0.01991302 Inf 0.02078964 0.1311667  12
 WCR-   CON       0.06475794 0.01736137 Inf 0.03273142 0.1241008  1
 WCR-   HDG       0.12433673 0.03080158 Inf 0.06546125 0.2235006   2

Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
Intervals are back-transformed from the logit scale
P value adjustment: fdr method for 6 tests
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 2E

```
tab.2E <- read.table("Fig2E.txt",header=TRUE)
tab.2E$ind <- factor(1:nrow(tab.2E))
mod.2E <- glmer(cbind(dead,alive)~origin*treatment+(1|origin:strain)+(1|ind),
                family=binomial,data=tab.2E)
Anova(mod.2E)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
Response: cbind(dead, alive)
                 Chisq Df Pr(>Chisq)
origin          2.3212  1    0.12763
treatment       5.0581  1    0.02451 *
origin:treatment 0.9744  1    0.32357
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.2E,~origin:treatment,type="response"),adjust="fdr")
```

```
 origin treatment       prob         SE  df  asymp.LCL asymp.UCL .group
 WCR+   CON       0.04736612 0.01615564 Inf 0.01992607 0.1084137  1
 WCR+   M         0.05598840 0.01874183 Inf 0.02387693 0.1257235  1
 WCR-   CON       0.06619384 0.01611620 Inf 0.03564315 0.1196806  1
 WCR-   M         0.11573834 0.02620727 Inf 0.06458453 0.1987976  1

Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
Intervals are back-transformed from the logit scale
P value adjustment: fdr method for 6 tests
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 2F

```
tab.2F <- read.table("Fig2F.txt",header=TRUE)
with(tab.2F[tab.2F$origin=="WCR-",],wald.ptheo.test(cbind(MG,CON),blocks=strain))
```

```

    Wald test

data:  cbind(MG, CON) and strain
z = -9.4497, p-value < 2.2e-16
alternative hypothesis: true probability of success is not equal to 0.5
sample estimates:
probability of success
             0.4081634
```

```
with(tab.2F[tab.2F$origin=="WCR+",],wald.ptheo.test(cbind(MG,CON),blocks=strain))
```

```

    Wald test

data:  cbind(MG, CON) and strain
z = 0.70107, p-value = 0.4833
alternative hypothesis: true probability of success is not equal to 0.5
sample estimates:
probability of success
             0.5130041
```

```
mod.2F <- glmer(cbind(MG,CON)~origin+(1|origin:strain),family=binomial,data=tab.2F)
Anova(mod.2F)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(MG, CON)
```

```
       Chisq Df Pr(>Chisq)
origin 56.33  1  6.128e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Deltas

```
mod.2B <- glm(cbind(dead,alive)~larvae*strain,family=binomial,data=tab.2B)
means.2B <- as.data.frame(summary(emmeans(mod.2B,~larvae:strain),type="response"))
delta.2B <- apply(with(means.2B,tapply(prob,list(larvae,strain),identity)),2,
                  function(x) x[1]-x[2])

mod.2D <- glm(cbind(dead,alive)~treatment*strain,family=binomial,data=tab.2D)
means.2D <- as.data.frame(summary(emmeans(mod.2D,~treatment:strain),type="response"))
delta.2D <- apply(with(means.2D,tapply(prob,list(treatment,strain),identity)),2,
                  function(x) x[2]-x[1])

mod.2E <- glm(cbind(dead,alive)~treatment*strain,family=binomial,data=tab.2E)
means.2E <- as.data.frame(summary(emmeans(mod.2E,~treatment:strain),type="response"))
delta.2E <- apply(with(means.2E,tapply(prob,list(treatment,strain),identity)),2,
                  function(x) x[2]-x[1])

mod.2F <- glm(cbind(MG,CON)~strain,family=binomial,data=tab.2F)
means.2F <- as.data.frame(summary(emmeans(mod.2F,~strain),type="response"))
delta.2F <- means.2F$prob
names(delta.2F) <- means.2F$strain
```

Figure 2G

```
tab.2G <- read.table("Fig2G-I.txt",header=TRUE)
mod.2G <- lm(Infectivity~HDGmotality,data=tab.2G)
summary(mod.2G)
```

```

Call:
lm(formula = Infectivity ~ HDGmotality, data = tab.2G)

Residuals:
    Min      1Q  Median      3Q     Max 
-24.953  -9.795  -4.570  15.379  33.568 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 15.58304    3.80685   4.093 0.000446 ***
HDGmotality  0.02005    0.02986   0.671 0.508777    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 16.16 on 23 degrees of freedom
Multiple R-squared:  0.01921,   Adjusted R-squared:  -0.02343 
F-statistic: 0.4505 on 1 and 23 DF,  p-value: 0.5088
```

Figure 2H

```
tab.2H <- read.table("Fig2G-I.txt",header=TRUE)
mod.2H <- lm(Infectivity~Mmotality,data=tab.2H)
summary(mod.2H)
```

```
Call:
lm(formula = Infectivity ~ Mmotality, data = tab.2H)

Residuals:
    Min      1Q  Median      3Q     Max 
-24.930  -9.546  -3.876  11.206  34.833 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 15.37908    3.81556   4.031 0.000521 ***
Mmotality    0.02644    0.03474   0.761 0.454349    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 16.12 on 23 degrees of freedom
Multiple R-squared:  0.02457,   Adjusted R-squared:  -0.01785 
F-statistic: 0.5792 on 1 and 23 DF,  p-value: 0.4543
```

Figure 2I

```
tab.2I <- read.table("Fig2G-I.txt",header=TRUE)
mod.2I <- lm(Infectivity~EPNbehavior,data=tab.2I)
summary(mod.2I)
```

```
Call:
lm(formula = Infectivity ~ EPNbehavior, data = tab.2I)

Residuals:
    Min      1Q  Median      3Q     Max 
-22.682 -11.337   0.313  10.535  33.139 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)   
(Intercept)   7.5604     3.8549   1.961  0.06207 . 
EPNbehavior   0.8228     0.2441   3.371  0.00264 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 13.35 on 23 degrees of freedom
Multiple R-squared:  0.3307,    Adjusted R-squared:  0.3016 
F-statistic: 11.36 on 1 and 23 DF,  p-value: 0.002639
```

Model selection

```
fig2.mod.global <- lm(delta.2B~(delta.2D+delta.2E+delta.2F)^2,na.action="na.pass")
dredge(fig2.mod.global,rank="AICc",extra="R^2")
```

```
Global model call: lm(formula = delta.2B ~ (delta.2D + delta.2E + delta.2F)^2, na.action = "na.pass")
---
Model selection table
    (Int) dlt.2D   dlt.2E dlt.2F dlt.2D:dlt.2E dlt.2D:dlt.2F dlt.2E:dlt.2F
5  0.9104                 -1.665
6  0.8516 0.2576          -1.565
7  0.8838         0.15610 -1.619
22 0.7287 2.2500          -1.304                      -4.424
8  0.8596 0.4841 -0.35070 -1.579
39 0.8472         1.09100 -1.539                                    -2.163
24 0.7292 2.6540 -0.40450 -1.302                      -4.741
40 0.7166 0.7099  2.77600 -1.271                                    -7.783
16 0.8740 0.3817 -0.50610 -1.606        1.8090
1  0.1666
2  0.1292 0.6787
3  0.1390         0.69250
4  0.1297 0.7605 -0.12450
32 0.7401 2.5070 -0.43950 -1.324        0.4429        -4.474
56 0.7354 3.0180 -1.09200 -1.315                      -5.644         1.686
48 0.7271 0.6781  2.57600 -1.293        0.3451                      -7.359
12 0.1285 0.8138 -0.04191              -0.9862
64 0.7538 3.0940 -1.63800 -1.354        0.5698        -5.958         2.915
       R^2 df logLik  AICc delta weight
5  0.37380  3 17.524 -27.9  0.00  0.547
6  0.38530  4 17.757 -25.5  2.39  0.165
7  0.37640  4 17.576 -25.2  2.75  0.138
22 0.39520  5 17.959 -22.8  5.14  0.042
8  0.38960  5 17.844 -22.5  5.37  0.037
39 0.37740  5 17.596 -22.0  5.87  0.029
24 0.40090  6 18.077 -19.5  8.42  0.008
40 0.39930  6 18.044 -19.4  8.48  0.008
16 0.39280  6 17.911 -19.2  8.75  0.007
1  0.00000  2 11.674 -18.8  9.10  0.006
2  0.08964  3 12.848 -18.6  9.35  0.005
3  0.05706  3 12.408 -17.7 10.23  0.003
4  0.09019  4 12.855 -15.7 12.20  0.001
32 0.40100  7 18.080 -15.6 12.33  0.001
56 0.40090  7 18.078 -15.6 12.34  0.001
48 0.39940  7 18.046 -15.5 12.40  0.001
12 0.09117  5 12.868 -12.6 15.33  0.000
64 0.40110  8 18.082 -11.2 16.74  0.000
Models ranked by AICc(x)
```

Figure 3

Figure 3A

```r
tab.3A <- read.table("Fig3A.txt",header=TRUE)
mod.3A <- glmer(cbind(dead,alive)~host*larvae+(1|host:line),family=binomial,data=tab.3A)
Anova(mod.3A)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
Response: cbind(dead, alive)
              Chisq Df Pr(>Chisq)
host         0.7190  1     0.3965
larvae      74.6992  1     <2e-16 ***
host:larvae  0.0325  1     0.8569
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.3A,~host:larvae,type="response"),adjust="fdr")
```

```
 host larvae      prob         SE  df asymp.LCL asymp.UCL .group
 WCR  B73    0.2515723 0.02433272 Inf 0.1957560 0.3170300  1
 BCB  B73    0.2660550 0.02443652 Inf 0.2096064 0.3313331  1
 WCR  bx1    0.4789644 0.02841875 Inf 0.4088740 0.5498929   2
 BCB  bx1    0.5085714 0.02672209 Inf 0.4420701 0.5747708   2

Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
Intervals are back-transformed from the logit scale
P value adjustment: fdr method for 6 tests
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 3B

```
tab.3B <- read.table("Fig3B.txt",header=TRUE)
mod.3B <- glmer(cbind(dead,alive)~host*larvae+(1|host:line),family=binomial,data=tab.3B)
Anova(mod.3B)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(dead, alive)
              Chisq Df Pr(>Chisq)
host        23.5352  1  1.227e-06 ***
larvae       0.0607  1     0.8054
host:larvae 29.5126  1  5.555e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.3B,~host:larvae,type="response"),adjust="fdr")
```

```
 host larvae      prob         SE  df asymp.LCL asymp.UCL .group
 BCB  BX+    0.3352399 0.03645427 Inf 0.2510252 0.4314329  1
 BCB  BX-    0.4903373 0.04352552 Inf 0.3837470 0.5978134   2
 WCR  BX-    0.5656125 0.04317916 Inf 0.4563658 0.6688363   2
 WCR  BX+    0.7067292 0.03426852 Inf 0.6145751 0.7845730    3

Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
Intervals are back-transformed from the logit scale
P value adjustment: fdr method for 6 tests
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 3C

```
tab.3C <- read.table("Fig3C.txt",header=TRUE)
mod.3C <- glmer(cbind(dead,alive)~host*treatment+(1|host:line),family=binomial,
                data=tab.3C)
Anova(mod.3C)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(dead, alive)
                 Chisq Df Pr(>Chisq)    
host            0.0719  1     0.7887    
treatment      25.8523  1  3.686e-07 ***
host:treatment 25.8504  1  3.689e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.3C,~host:treatment,type="response"),adjust="fdr")
```

```
 host treatment      prob         SE  df   asymp.LCL asymp.UCL .group
 BCB  CON       0.0620952 0.01327357 Inf 0.03611577 0.1047321  1    
 WCR  CON       0.0974913 0.01882142 Inf 0.05954092 0.1556278  12   
 WCR  HDG       0.1037234 0.01985898 Inf 0.06356147 0.1647962  12   
 BCB  HDG       0.1539801 0.02763673 Inf 0.09677303 0.2361628   2   

Confidence level used: 0.95 
Conf-level adjustment: bonferroni method for 4 estimates 
Intervals are back-transformed from the logit scale 
P value adjustment: fdr method for 6 tests 
Tests are performed on the log odds ratio scale 
significance level used: alpha = 0.05 
```

Figure 3D

```
tab.3D <- read.table("Fig3D.txt",header=TRUE)
mod.3D <- glmer(cbind(dead,alive)~host*treatment+(1|host:line),family=binomial,
                data=tab.3D)
Anova(mod.3D)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(dead, alive)
                 Chisq Df Pr(>Chisq)    
host            0.1156  1    0.73384    
treatment       6.0029  1    0.01428 *  
host:treatment 17.5740  1  2.763e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
cld(emmeans(mod.3D,~host:treatment,type="response"),adjust="fdr")
```

```
 host treatment       prob         SE  df   asymp.LCL  asymp.UCL .group
 BCB  CON       0.05956500 0.01253571 Inf 0.03495136 0.09972107  1    
 WCR  M         0.08964486 0.01721077 Inf 0.05495438 0.14292222  12   
 WCR  CON       0.09879677 0.01853701 Inf 0.06118707 0.15569019  12   
 BCB  M         0.11339495 0.02124362 Inf 0.07015608 0.17817645   2   
```

```
Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
Intervals are back-transformed from the logit scale
P value adjustment: fdr method for 6 tests
Tests are performed on the log odds ratio scale
significance level used: alpha = 0.05
```

Figure 3E

```
tab.3E <- read.table("Fig3E.txt",header=TRUE)
with(tab.3E[tab.3E$host=="BCB",],wald.ptheo.test(cbind(MG,CON),blocks=line))
```

```

    Wald test

data:  cbind(MG, CON) and line
z = -13.15, p-value < 2.2e-16
alternative hypothesis: true probability of success is not equal to 0.5
sample estimates:
probability of success
             0.3591139
```

```
with(tab.3E[tab.3E$host=="WCR",],wald.ptheo.test(cbind(MG,CON),blocks=line))
```

```

    Wald test

data:  cbind(MG, CON) and line
z = 11.003, p-value < 2.2e-16
alternative hypothesis: true probability of success is not equal to 0.5
sample estimates:
probability of success
             0.6437042
```

```
mod.3E <- glmer(cbind(MG,CON)~host+(1|host:line),family=binomial,data=tab.3E)
Anova(mod.3E)
```

```
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: cbind(MG, CON)
      Chisq Df Pr(>Chisq)
host 306.03  1  < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 3F

```
tab.3F <- read.table("Fig3F-H.txt",header=TRUE)
mod.3F <- lm(Infectivity~HDGmotality,data=tab.3F)
summary(mod.3F)
```

```

Call:
lm(formula = Infectivity ~ HDGmotality, data = tab.3F)
```

```
Residuals:
     Min       1Q   Median       3Q      Max 
-19.2249  -9.0747  -0.6894   8.3050  20.9011 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -8.19412    3.19966  -2.561   0.0196 *  
HDGmotality  0.09858    0.01945   5.069    8e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 11.62 on 18 degrees of freedom
Multiple R-squared:  0.588, Adjusted R-squared:  0.5651 
F-statistic: 25.69 on 1 and 18 DF,  p-value: 8.001e-05
```

Figure 3G

```r
tab.3G <- read.table("Fig3F-H.txt",header=TRUE)
mod.3G <- lm(Infectivity~Mmotality,data=tab.3G)
summary(mod.3G)
```

```
Call:
lm(formula = Infectivity ~ Mmotality, data = tab.3G)

Residuals:
    Min      1Q  Median      3Q     Max 
-25.943  -7.945   1.055   7.679  20.932 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -5.18014    3.25726  -1.590 0.129169    
Mmotality    0.14697    0.03492   4.209 0.000528 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 12.86 on 18 degrees of freedom
Multiple R-squared:  0.496, Adjusted R-squared:  0.468 
F-statistic: 17.71 on 1 and 18 DF,  p-value: 0.0005279
```

Figure 3H

```r
tab.3H <- read.table("Fig3F-H.txt",header=TRUE)
mod.3H <- lm(Infectivity~EPNbehavior,data=tab.3G)
summary(mod.3H)
```

```
Call:
lm(formula = Infectivity ~ EPNbehavior, data = tab.3G)

Residuals:
    Min      1Q  Median      3Q     Max 
-26.837  -5.246   1.426   9.226  13.704 
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.6517     2.4355   0.678    0.506
EPNbehavior   0.4601     0.0816   5.639 2.38e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.89 on 18 degrees of freedom
Multiple R-squared:  0.6385,    Adjusted R-squared:  0.6184
F-statistic: 31.79 on 1 and 18 DF,  p-value: 2.382e-05
```

Deltas

```r
mod.3B <- glm(cbind(dead,alive)~larvae*line,family=binomial,data=tab.3B)
means.3B <- as.data.frame(summary(emmeans(mod.3B,~larvae:line),type="response"))
delta.3B <- apply(with(means.3B,tapply(prob,list(larvae,line),identity)),2,
                  function(x) x[1]-x[2])

mod.3C <- glm(cbind(dead,alive)~treatment*line,family=binomial,data=tab.3C)
means.3C <- as.data.frame(summary(emmeans(mod.3C,~treatment:line),type="response"))
delta.3C <- apply(with(means.3C,tapply(prob,list(treatment,line),identity)),2,
                  function(x) x[2]-x[1])

mod.3D <- glm(cbind(dead,alive)~treatment*line,family=binomial,data=tab.3D)
means.3D <- as.data.frame(summary(emmeans(mod.3D,~treatment:line),type="response"))
delta.3D <- apply(with(means.3D,tapply(prob,list(treatment,line),identity)),2,
                  function(x) x[2]-x[1])

mod.3E <- glm(cbind(MG,CON)~line,family=binomial,data=tab.3E)
means.3E <- as.data.frame(summary(emmeans(mod.3E,~line),type="response"))
delta.3E <- means.3E$prob
names(delta.3E) <- means.3E$line
```

Model selection

```r
fig3.mod.global <- lm(delta.3B~(delta.3C+delta.3D+delta.3E)^2,na.action="na.pass")
fig3.mod.selection <- dredge(fig3.mod.global,rank="AICc",extra="R^2")
fig3.mod.selection
```

```
Global model call: lm(formula = delta.3B ~ (delta.3C + delta.3D + delta.3E)^2, na.action = "na.pass")
---
Model selection table
      (Int)  dlt.3C   dlt.3D  dlt.3E dlt.3C:dlt.3D dlt.3C:dlt.3E
5   0.50470                 -0.9829
6   0.37790  0.5779         -0.7916
7   0.51610        -0.08335 -1.0020
22  0.43420 -0.9180         -0.8919                       3.667
8   0.43950  0.7312 -0.69660 -0.8986
39  0.47920         3.05800 -0.9691
24  0.51540 -0.9218 -0.83820 -1.0330                       4.129
56  0.53100 -2.5480  4.75600 -1.1140                       7.893
40  0.41430  0.6749  1.99500 -0.8790
```

```
48  0.21880  2.1750  9.35900 -0.6022       -29.360
16  0.41440  1.0180 -0.40470 -0.8569        -5.205
2  -0.07151  1.5620
32  0.78070 -5.4180 -2.53600 -1.4890        25.560        11.840
4  -0.07278  1.1440  1.01700
64  0.40830 -0.7744  6.81700 -0.9156       -12.150         5.070
3  -0.04307          2.37200
12 -0.07709  1.9690  1.67000               -16.010
1   0.01202
   dlt.3D:dlt.3E    R^2 df logLik  AICc delta weight
5                0.6498  3 17.258 -27.0  0.00  0.423
6                0.6850  4 18.317 -26.0  1.05  0.251
7                0.6500  4 17.263 -23.9  3.16  0.087
22               0.7039  5 18.935 -23.6  3.43  0.076
8                0.6959  5 18.670 -23.1  3.96  0.058
39        -7.371 0.6745  5 17.989 -21.7  5.32  0.030
24               0.7194  6 19.474 -20.5  6.53  0.016
56       -13.190 0.7771  7 21.778 -20.2  6.79  0.014
40        -6.204 0.7130  6 19.249 -20.0  6.98  0.013
48       -19.380 0.7737  7 21.626 -19.9  7.10  0.012
16               0.7003  6 18.814 -19.2  7.85  0.008
2                0.4369  3 12.508 -17.5  9.50  0.004
32               0.7420  7 20.313 -17.3  9.72  0.003
4                0.4698  4 13.111 -15.6 11.46  0.001
64       -16.150 0.7793  8 21.877 -14.7 12.35  0.001
3                0.3496  3 11.067 -14.6 12.38  0.001
12               0.5155  5 14.011 -13.7 13.28  0.001
1                0.0000  2  6.766  -8.8 18.19  0.000
Models ranked by AICc(x)
```

```r
fig3.mod.averaging <- model.avg(fig3.mod.selection,subset=(delta<=2),fit=TRUE)
summary(fig3.mod.averaging)
```

```

Call:
model.avg(object = get.models(object = fig3.mod.selection, subset = (delta <=
    2)))

Component model call:
lm(formula = delta.3B ~ <2 unique rhs>, na.action = na.pass)

Component models:
   df logLik   AICc delta weight
2   3  17.26 -27.02  0.00   0.63
12  4  18.32 -25.97  1.05   0.37

Term codes:
delta.3C delta.3E
       1        2

Model-averaged coefficients:
(full average)
            Estimate Std. Error Adjusted SE z value Pr(>|z|)
(Intercept)   0.4576     0.1209      0.1276   3.586 0.000336 ***
delta.3E     -0.9118     0.2100      0.2227   4.094 4.23e-05 ***
```

```
delta.3C      0.2149     0.3787      0.3921   0.548 0.583719

(conditional average)
            Estimate Std. Error Adjusted SE z value Pr(>|z|)
(Intercept)   0.4576     0.1209      0.1276   3.586 0.000336 ***
delta.3E     -0.9118     0.2100      0.2227   4.094 4.23e-05 ***
delta.3C      0.5779     0.4193      0.4514   1.280 0.200486
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Relative variable importance:
                     delta.3E delta.3C
Importance:          1.00     0.37
N containing models:    2        1
```