Analysis for *The biological basis of Taylor's Power Law revisited: using host-parasite interactions to reveal the drivers of aggregation*

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Load in the data and transform all of the necessary variables

```r
fs_data = read.csv("../data/fs_data_w_density.csv")
fs_data$year = as.factor(fs_data$year)

# Feasible set residuals
fs_data$diff = fs_data$logvar - log10(fs_data$fs_var)
```

These are all of the standardizations and transformations on the predictor variables

```r
# Host specific variables
scale_host_vars = c("resid_svlbyspp", "resid_densitybyspp",
                    "logmean_density", "logmean_svl", "pondarea_ha")


for(var in scale_host_vars){

  if(var == "pondarea_ha"){ # log-transforming pond areas
    fs_data[[paste(var, "_sd", sep="")]] = scale(log10(fs_data[[var]]))
    # hist(fs_data[[paste(var, "_sd", sep="")]], main=var)
  } else{
    fs_data[[paste(var, "_sd", sep="")]] = scale(fs_data[[var]])
    # hist(fs_data[[paste(var, "_sd", sep="")]], main=var)

  }
}

scale_life_history_vars = c("hostsizemeta", "hostrange",
                "hostlarvalperiod", "hosteggsize",
                "hostclutch", "hostagemax")


for(var in scale_life_history_vars){
    # Scale and log-transform each of these variables

    fs_data[[paste(var, "_sd", sep="")]] = scale(log10(fs_data[[var]]))

    # Uncomment to plot
    # hist(fs_data[[paste(var, "_sd", sep="")]], main=var)
}
```

```r
# Parasite-specific variables

# Load in the specific parasite variables
snail_dat = as.data.table(read.csv("../data/parasite_snail_values.csv"))
```

```
## Warning in read.table(file = file, header = header, sep = sep, quote
## = quote, : incomplete final line found by readTableHeader on '../data/
## parasite_snail_values.csv'
cerc_dat = as.data.table(read.csv("../data/TrematodeSheddingAvg.csv"))

## Warning in read.table(file = file, header = header, sep = sep, quote
## = quote, : incomplete final line found by readTableHeader on '../data/
## TrematodeSheddingAvg.csv'
comb_dat = list(parasite=snail_dat$parasite,
                infect_snail_prev=snail_dat$infect_snail_prev,
                infect_snail_dens=snail_dat$infect_snail_density,
                cerc_shedding=cerc_dat$shedavg)
comb_dat = as.data.table(comb_dat)

# Merge these values with the full data
fs_dt = as.data.table(fs_data)
setkey(fs_dt, parasite)
setkey(comb_dat, parasite)
fs_data = as.data.frame(merge(fs_dt, comb_dat, all.x=T))

# Scale all parasite variables
scale_para_vars = c("parasitemass", "infect_snail_prev",
                    "infect_snail_dens", "cerc_shedding")

for(name in scale_para_vars){

    if(name == "cerc_shedding"){ # Log transform ceriae shedding
      fs_data[[paste(name, "_sd", sep="")]] = scale(log10(fs_data[[name]]))
    } else{
      fs_data[[paste(name, "_sd", sep="")]] = scale(fs_data[[name]])
    }

}

# Host-by-parasite variables
fs_data$infectionsuccess_sd = scale(fs_data$infectionsuccess)
fs_data$oddsratio_sd = scale(log10(fs_data$oddsratio)) # dealing with the non-linearity in oddsratio
fs_data$parasitemass_sd = scale(fs_data$parasitemass)

# Extract lab data
labdata = as.data.table(fs_data)[, list(competence=unique(infectionsuccess), virulence=unique(oddsratio
write.csv(labdata, "../data/laboratory_comp_vir_data.csv", row.names = FALSE)

# Include updated virulence measures, conditional on infection.
cond_val = as.data.table(read.csv("../data/conditional_virulence_ests.csv"))

# Merge data.frames
setkey(cond_val, species, parasite)
fs_data = as.data.table(fs_data)
setkey(fs_data, species, parasite)
fs_data = merge(fs_data, cond_val)[, c(colnames(fs_data), "oddsratio_conditional"), with=F]
fs_data = as.data.frame(fs_data)
```

```
# Log and scale
fs_data$oddsratio_conditional_sd = scale(log10(fs_data$oddsratio_conditional))

# Oddsratio not described by infection success
fs_data$oddsratio_resid = scale(residuals(lm(oddsratio_sd ~ infectionsuccess_sd, data=fs_data)))
```

All predictor variables are transformed and scaled

Host, parasite and host by parasite models

```
fs_mod1 = lmer(diff ~ logmean + species +
                      parasite +
                      logmean:species +
                      logmean:parasite +
                      species:parasite +
                      logmean:species:parasite +
                      (1 | year) + (1 | site), data=fs_data, REML=F)
```

```
## fixed-effect model matrix is rank deficient so dropping 6 columns / coefficients
# Is the interaction with logmean imporant...no evidence for an interaction
fs_no_int = update(fs_mod1, .~. - logmean:species:parasite)
```

```
## fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients

anova(fs_mod1, fs_no_int)
```

```
## Data: fs_data
## Models:
## fs_no_int: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_no_int:     logmean:species + logmean:parasite + species:parasite
## fs_mod1: diff ~ logmean + species + parasite + logmean:species + logmean:parasite +
## fs_mod1:     species:parasite + logmean:species:parasite + (1 | year) +
## fs_mod1:     (1 | site)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_no_int 28 632.96 769.55 -288.48   576.96
## fs_mod1   37 637.03 817.53 -281.51   563.03 13.929      9     0.1249
```

```
# No evidence for an interaction between species and parasite
fs_no_int2 = update(fs_no_int, .~. - species:parasite)
anova(fs_mod1, fs_no_int2)
```

```
## Data: fs_data
## Models:
## fs_no_int2: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_no_int2:     logmean:species + logmean:parasite
## fs_mod1: diff ~ logmean + species + parasite + logmean:species + logmean:parasite +
## fs_mod1:     species:parasite + logmean:species:parasite + (1 | year) +
## fs_mod1:     (1 | site)
##            Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_no_int2 19 623.27 715.96 -292.63   585.27
## fs_mod1    37 637.03 817.53 -281.51   563.03 22.241     18     0.2214
```

```
# Host effect on logmean.  Not much of an effect
fs_host = update(fs_no_int2, .~. - logmean:species)
anova(fs_host, fs_no_int2)
```

```
## Data: fs_data
## Models:
## fs_host: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_host:     logmean:parasite
## fs_no_int2: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_no_int2:     logmean:species + logmean:parasite
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_host    15 623.78 696.96 -296.89   593.78
## fs_no_int2 19 623.27 715.96 -292.63   585.27 8.5128      4     0.0745 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Large effect of host on intercept
fs_host2 = update(fs_host, .~. - species)
anova(fs_host, fs_host2)
```

```
## Data: fs_data
## Models:
## fs_host2: diff ~ logmean + parasite + (1 | year) + (1 | site) + logmean:parasite
## fs_host: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_host:     logmean:parasite
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_host2 11 636.38 690.04 -307.19   614.38
## fs_host   15 623.78 696.96 -296.89   593.78 20.594      4  0.0003811 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Effect of parasite on logmean? Large effect
fs_para = update(fs_no_int2, .~. - logmean:parasite)
anova(fs_para, fs_no_int2)
```

```
## Data: fs_data
## Models:
## fs_para: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_para:     logmean:species
## fs_no_int2: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_no_int2:     logmean:species + logmean:parasite
##          Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_para    16 646.49 724.55 -307.25   614.49
## fs_no_int2 19 623.27 715.96 -292.63   585.27 29.223      3  2.011e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Effect of parasite on intercept? Large effect
fs_para2 = update(fs_para, .~. - parasite)
anova(fs_para, fs_para2)
```

```
## Data: fs_data
## Models:
## fs_para2: diff ~ logmean + species + (1 | year) + (1 | site) + logmean:species
## fs_para: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_para:     logmean:species
```

```
##          Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## fs_para2 13 769.10 832.51 -371.55   743.10
## fs_para  16 646.49 724.55 -307.25   614.49 128.6      3  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Best model with host and parasite identity
summary(fs_host)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
##     logmean:parasite
##    Data: fs_data
##
##       AIC      BIC   logLik deviance df.resid
##     623.8    697.0   -296.9    593.8      956
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1683 -0.6799 -0.0450  0.6157  2.9110
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.007715 0.08783
##  year     (Intercept) 0.005735 0.07573
##  Residual             0.100561 0.31711
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                          Estimate Std. Error t value
## (Intercept)               0.25019    0.06069   4.123
## logmean                  -0.07159    0.05017  -1.427
## speciesPSRE               0.07708    0.03471   2.221
## speciesRACA               0.19469    0.06285   3.098
## speciesTAGR               0.21241    0.11130   1.908
## speciesTATO               0.17956    0.04509   3.982
## parasiteEchino           -0.14079    0.05103  -2.759
## parasiteGlobbie          -0.12589    0.05834  -2.158
## parasiteRib              -0.25126    0.05124  -4.904
## logmean:parasiteEchino   -0.04272    0.05496  -0.777
## logmean:parasiteGlobbie  -0.04486    0.07397  -0.607
## logmean:parasiteRib      -0.21760    0.05942  -3.662
##
## Correlation of Fixed Effects:
##            (Intr) logmen spPSRE spRACA spTAGR spTATO prstEc prstGl prstRb
## logmean    -0.462
## speciesPSRE -0.515  0.000
## speciesRACA -0.249 -0.001  0.475
## speciesTAGR -0.157  0.003  0.281  0.158
## speciesTATO -0.359  0.010  0.662  0.389  0.258
## parasitEchn -0.624  0.543  0.097  0.061  0.004 -0.033
## parasitGlbb -0.492  0.474 -0.017 -0.029 -0.002 -0.040  0.596
## parasiteRib -0.586  0.542  0.028 -0.022 -0.043 -0.090  0.698  0.598
## lgmn:prstEc  0.448 -0.912 -0.050 -0.072 -0.005  0.015 -0.694 -0.435 -0.506
## lgmn:prstGl  0.312 -0.681  0.012 -0.007  0.006  0.027 -0.380 -0.615 -0.380
```

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```
## lgmn:prstRb  0.403 -0.848 -0.014 -0.043 -0.005 -0.024 -0.465 -0.404 -0.672
##            lgmn:E lgmn:G
## logmean
## speciesPSRE
## speciesRACA
## speciesTAGR
## speciesTATO
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl  0.625
## lgmn:prstRb  0.779  0.581
```

```
rsquared.glmm(list(fs_host))
```

```
##      Class   Family    Link  Marginal Conditional      AIC
## 1 lmerMod gaussian identity 0.2012654   0.2954914 623.7835
```

```
summary(update(fs_host, .~. - logmean))
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ species + parasite + (1 | year) + (1 | site) + logmean:parasite
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    623.8    697.0   -296.9    593.8      956
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1683 -0.6799 -0.0450  0.6157  2.9110
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.007715 0.08783
##  year     (Intercept) 0.005735 0.07573
##  Residual             0.100561 0.31711
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             0.25019    0.06069   4.123
## speciesPSRE             0.07708    0.03471   2.221
## speciesRACA             0.19469    0.06285   3.098
## speciesTAGR             0.21241    0.11130   1.908
## speciesTATO             0.17956    0.04509   3.982
## parasiteEchino         -0.14079    0.05103  -2.759
## parasiteGlobbie        -0.12589    0.05834  -2.158
## parasiteRib            -0.25126    0.05124  -4.904
## parasiteAlaria:logmean -0.07159    0.05017  -1.427
## parasiteEchino:logmean -0.11431    0.02249  -5.083
## parasiteGlobbie:logmean -0.11645   0.05416  -2.150
## parasiteRib:logmean    -0.28919    0.03146  -9.192
##
```

```
## Correlation of Fixed Effects:
##            (Intr) spPSRE spRACA spTAGR spTATO prstEc prstGl prstRb prstA:
## speciesPSRE -0.515
## speciesRACA -0.249  0.475
## speciesTAGR -0.157  0.281  0.158
## speciesTATO -0.359  0.662  0.389  0.258
## parasitEchn -0.624  0.097  0.061  0.004 -0.033
## parasitGlbb -0.492 -0.017 -0.029 -0.002 -0.040  0.596
## parasiteRib -0.586  0.028 -0.022 -0.043 -0.090  0.698  0.598
## prstAlr:lgm -0.462  0.000 -0.001  0.003  0.010  0.543  0.474  0.542
## prstEchn:lg  0.064 -0.122 -0.178 -0.003  0.060 -0.483 -0.004 -0.028  0.001
## prstGlbb:lg -0.002  0.016 -0.010  0.011  0.045 -0.015 -0.401 -0.017 -0.004
## prstRb:lgmn  0.024 -0.027 -0.084 -0.004 -0.029 -0.011 -0.006 -0.406 -0.008
##            prstE: prstG:
## speciesPSRE
## speciesRACA
## speciesTAGR
## speciesTATO
## parasitEchn
## parasitGlbb
## parasiteRib
## prstAlr:lgm
## prstEchn:lg
## prstGlbb:lg  0.013
## prstRb:lgmn  0.022  0.007
```

Some of the main results are

1. No effect of host-parasite interaction when host and parasite are included (maybe a marginal main effect of the interaction)
2. Sig. density-independent effect of host (no density-dependent effect)
3. Sig. density dependent and density independent effect of parasite

Moreover, this result actually shows us that the effect of logmean is not statistically different than 0, though it is trending that way. This means that the feasible set approach is likely an adequate null model. However, note that we do tend to see that the feasible set underestimates variance for low means and overestimates variance for high means (slightly).

Effects of year and site

Do year and site have a significant interaction with logmean?

```
# Testing year int effect
fs_no_year = fs_year_mod = lmer(diff ~ logmean +
                   parasite +
                   species +
                   logmean:parasite +
                    (1 | site), data=fs_data, REML=F)


anova(fs_host, fs_no_year)

## Data: fs_data
## Models:
## fs_no_year: diff ~ logmean + parasite + species + logmean:parasite + (1 |
```

```
## fs_no_year:      site)
## fs_host: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_host:     logmean:parasite
##            Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_no_year 14 649.33 717.63 -310.67    621.33
## fs_host    15 623.78 696.96 -296.89    593.78 27.548      1  1.532e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Testing for site int effect
fs_no_site = fs_year_mod = lmer(diff ~ logmean +
                    parasite +
                    species +
                    logmean:parasite +
                     (1 | year), data=fs_data, REML=F)


anova(fs_host, fs_no_site)
```

```
## Data: fs_data
## Models:
## fs_no_site: diff ~ logmean + parasite + species + logmean:parasite + (1 |
## fs_no_site:     year)
## fs_host: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_host:     logmean:parasite
##            Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_no_site 14 631.56 699.86 -301.78    603.56
## fs_host    15 623.78 696.96 -296.89    593.78 9.7757      1   0.001768 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Testing for year slope effect
fs_year_mod = lmer(diff ~ logmean +
                    parasite +
                    species +
                    logmean:parasite +
                    (logmean | year) + (1 | site), data=fs_data, REML=F)


anova(fs_year_mod, fs_host)
```

```
## Data: fs_data
## Models:
## fs_host: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_host:     logmean:parasite
## fs_year_mod: diff ~ logmean + parasite + species + logmean:parasite + (logmean |
## fs_year_mod:     year) + (1 | site)
##             Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## fs_host     15 623.78 696.96 -296.89    593.78
## fs_year_mod 17 621.57 704.50 -293.79    587.57 6.211      2     0.0448 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
fs_site_mod = lmer(diff ~ logmean +
                    parasite +
                    species +
                    logmean:parasite +
                    (1 | year) + (logmean | site), data=fs_data, REML=F)
```

```
anova(fs_host, fs_site_mod)
```

```
## Data: fs_data
## Models:
## fs_host: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_host:     logmean:parasite
## fs_site_mod: diff ~ logmean + parasite + species + logmean:parasite + (1 |
## fs_site_mod:     year) + (logmean | site)
##              Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_host     15 623.78 696.96 -296.89   593.78
## fs_site_mod 17 625.03 707.96 -295.51   591.03 2.7555      2     0.2521
```

A marginally significant effect of year on the slope (remember that this p-value is conservative), which we can see in the slopes of the year effect. There is no real effect of site on the slope.

Let's try removing 2009 to see how this drives the effect of year.

```
fs_mod_no2009 = lmer(diff ~ logmean +
                    parasite +
                    species +
                    logmean:parasite +
                    (1 | year) + (1 | site),
                data=fs_data[fs_data$year != 2009, ], REML=F)

fs_year_no2009 = lmer(diff ~ logmean +
                    parasite +
                    species +
                    logmean:parasite +
                    (logmean | year) + (1 | site),
                data=fs_data[fs_data$year != 2009, ], REML=F)

anova(fs_year_no2009, fs_mod_no2009)
```

```
## Data: fs_data[fs_data$year != 2009, ]
## Models:
## fs_mod_no2009: diff ~ logmean + parasite + species + logmean:parasite + (1 |
## fs_mod_no2009:     year) + (1 | site)
## fs_year_no2009: diff ~ logmean + parasite + species + logmean:parasite + (logmean |
## fs_year_no2009:     year) + (1 | site)
##                Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_mod_no2009  15 525.26 595.38 -247.63   495.26
## fs_year_no2009 17 525.72 605.19 -245.86   491.72 3.5413      2     0.1702
```

Once 2009 is dropped there is no real significant effect of year on the slope.

Host population-level effects

Let's look at some correlations in our host variables

```
# Correlations between these population-level variables?
cor(fs_data[, sapply(scale_host_vars, function(x) paste(x, "_sd", sep=""))])
```

```
##                   resid_svlbyspp_sd resid_densitybyspp_sd
## resid_svlbyspp_sd        1.00000000            0.06239779
```

```
## resid_densitybyspp_sd          0.06239779              1.00000000
## logmean_density_sd            -0.02987678              0.01208332
## logmean_svl_sd                 0.01339937              0.04423478
## pondarea_ha_sd                 0.03206465              0.10411661
##                      logmean_density_sd logmean_svl_sd pondarea_ha_sd
## resid_svlbyspp_sd           -0.02987678     0.01339937     0.03206465
## resid_densitybyspp_sd        0.01208332     0.04423478     0.10411661
## logmean_density_sd           1.00000000    -0.30056782    -0.24826508
## logmean_svl_sd              -0.30056782     1.00000000     0.18984028
## pondarea_ha_sd              -0.24826508     0.18984028     1.00000000
```

Now we want to explore if we can replace host-identity with these variables

```
fs_pop_mod = lmer(diff ~ logmean + resid_svlbyspp_sd +
                        resid_densitybyspp_sd +
                        logmean_density_sd +
                        logmean_svl_sd +
                        pondarea_ha_sd +
                        logmean:resid_svlbyspp_sd +
                        logmean:resid_densitybyspp_sd +
                        logmean:logmean_density_sd +
                        logmean:logmean_svl_sd +
                        logmean:pondarea_ha_sd +
                        parasite +
                        logmean:parasite +
                        (1 | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_pop_mod)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_density_sd + logmean_svl_sd + pondarea_ha_sd + logmean:resid_svlbyspp_sd +
##     logmean:resid_densitybyspp_sd + logmean:logmean_density_sd +
##     logmean:logmean_svl_sd + logmean:pondarea_ha_sd + parasite +
##     logmean:parasite + (1 | year) + (1 | site)
##                                Df    AIC
## <none>                            629.22
## logmean:resid_svlbyspp_sd       1 628.50
## logmean:resid_densitybyspp_sd   1 627.43
## logmean:logmean_density_sd      1 628.50
## logmean:logmean_svl_sd          1 628.16
## logmean:pondarea_ha_sd          1 627.36
## logmean:parasite                3 646.72
```

Again, none of the interactions with logmean seem very important. Let's go ahead and drop them.

```
fs_pop_mod2 = lmer(diff ~ logmean + resid_svlbyspp_sd +
                        resid_densitybyspp_sd +
                        logmean_density_sd +
                        logmean_svl_sd +
                        pondarea_ha_sd +
                        parasite +
                        logmean:parasite +
                        (1 | year) + (1 | site), data=fs_data, REML=F)
```

```
drop1(fs_pop_mod2)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_density_sd + logmean_svl_sd + pondarea_ha_sd + parasite +
##     logmean:parasite + (1 | year) + (1 | site)
##                        Df    AIC
## <none>                    623.05
## resid_svlbyspp_sd       1 628.69
## resid_densitybyspp_sd   1 625.09
## logmean_density_sd      1 621.17
## logmean_svl_sd          1 631.78
## pondarea_ha_sd          1 621.51
## logmean:parasite        3 640.58
```

Dropping density and pond area look like they improve the model.

```
fs_pop_mod3 = lmer(diff ~ logmean + resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          logmean_svl_sd +
                          parasite +
                          logmean:parasite +
                          (1 | year) + (1 | site), data=fs_data, REML=F)
```

```
drop1(fs_pop_mod3)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + logmean:parasite + (1 | year) +
##     (1 | site)
##                        Df    AIC
## <none>                    619.78
## resid_svlbyspp_sd       1 625.25
## resid_densitybyspp_sd   1 621.77
## logmean_svl_sd          1 627.97
## logmean:parasite        3 637.30
```

```
summary(fs_pop_mod3)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + logmean:parasite + (1 | year) +
##     (1 | site)
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    619.8    688.1   -295.9    591.8      957
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1398 -0.6565 -0.0510  0.5924  3.0142
```

```
##
## Random effects:
##  Groups     Name         Variance Std.Dev.
##  site     (Intercept) 0.004894 0.06996
##  year     (Intercept) 0.006634 0.08145
##  Residual              0.102036 0.31943
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                         Estimate Std. Error t value
## (Intercept)              0.32323    0.05304   6.094
## logmean                 -0.06149    0.05014  -1.226
## resid_svlbyspp_sd        0.02915    0.01064   2.739
## resid_densitybyspp_sd    0.02198    0.01095   2.008
## logmean_svl_sd           0.03640    0.01122   3.245
## parasiteEchino          -0.12644    0.05040  -2.509
## parasiteGlobbie         -0.10093    0.05842  -1.727
## parasiteRib             -0.22864    0.05077  -4.504
## logmean:parasiteEchino  -0.05617    0.05465  -1.028
## logmean:parasiteGlobbie -0.07276    0.07387  -0.985
## logmean:parasiteRib     -0.22361    0.05933  -3.769
##
## Correlation of Fixed Effects:
##            (Intr) logmen rsd_s_ rsd_d_ lgmn__ prstEc prstGl prstRb lgmn:E
## logmean     -0.528
## rsd_svlbys_ -0.004  0.028
## rsd_dnstyb_ -0.035  0.018 -0.066
## lgmn_svl_sd  0.034  0.031 -0.017 -0.022
## parasitEchn -0.670  0.553  0.007  0.022 -0.004
## parasitGlbb -0.576  0.476  0.026  0.049 -0.004  0.603
## parasiteRib -0.667  0.548  0.021  0.015 -0.066  0.694  0.599
## lgmn:prstEc  0.485 -0.918 -0.026 -0.002 -0.053 -0.690 -0.437 -0.502
## lgmn:prstGl  0.364 -0.682 -0.038 -0.018 -0.016 -0.382 -0.615 -0.380  0.626
## lgmn:prstRb  0.449 -0.849 -0.040  0.012 -0.046 -0.469 -0.405 -0.679  0.782
##            lgmn:G
## logmean
## rsd_svlbys_
## rsd_dnstyb_
## lgmn_svl_sd
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl
## lgmn:prstRb  0.580
```

```
rsquared.glmm(list(fs_pop_mod3))
```
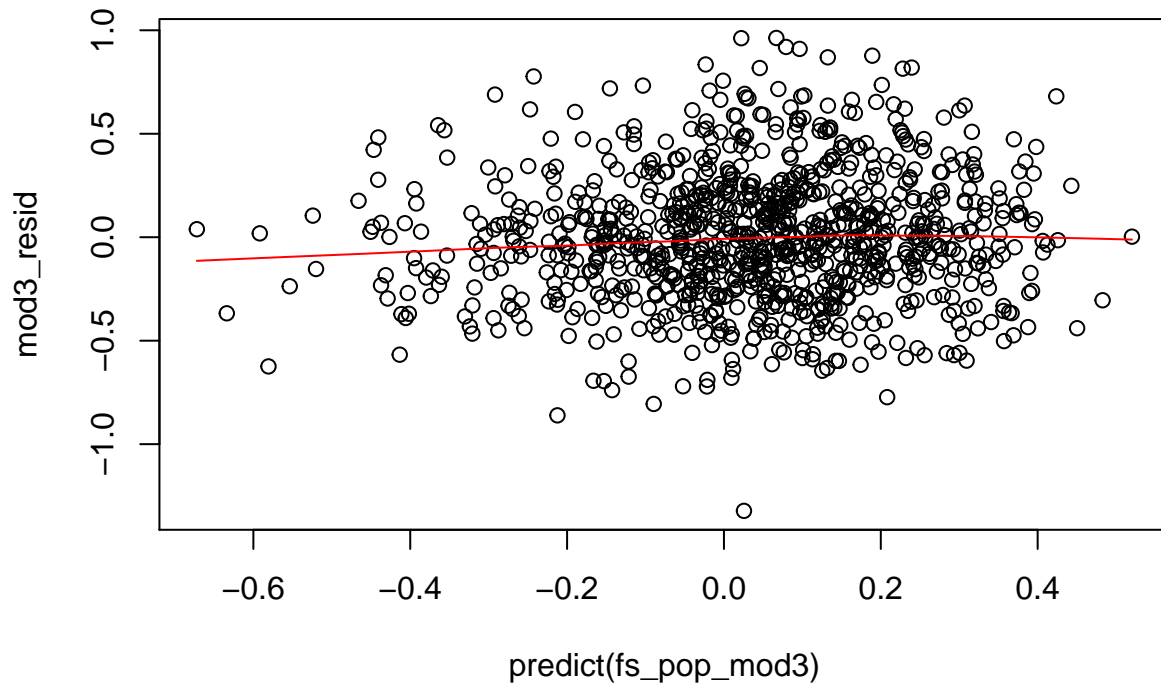
```
##      Class    Family     Link Marginal Conditional      AIC
## 1 lmerMod gaussian identity 0.204182   0.2849656 619.7783
```
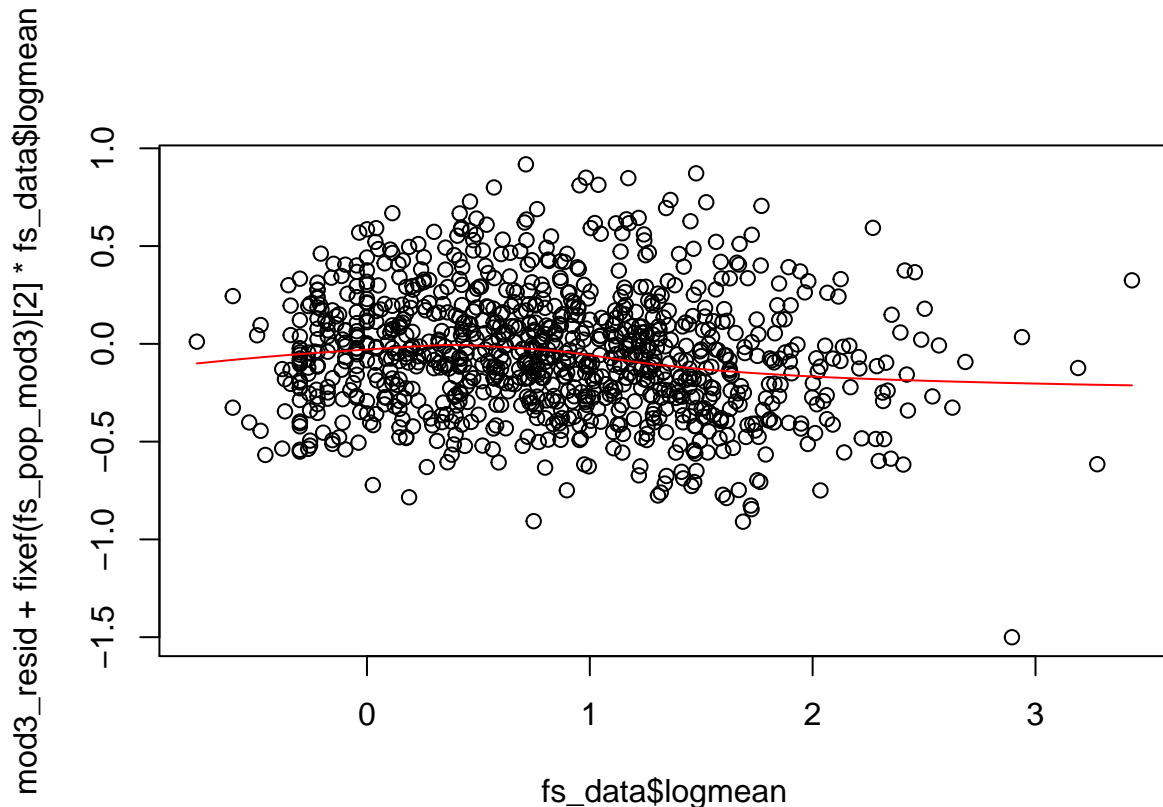
We see that after we account for host and parasite identity, the effect of logmean is 0 indicating that the feasible set is doing a pretty reasonable job. Also, count isn't necessary in this model. We see that the effects of host are primarily density-independent.

Let's make some diagnostic plots for this model

```r
# Residual plot
mod3_resid = resid(fs_pop_mod3, type="pearson")
plot(predict(fs_pop_mod3), mod3_resid)
lines(lowess(predict(fs_pop_mod3), mod3_resid), col="red")
```



```r
# Partial residual plot
plot(fs_data$logmean, mod3_resid + fixef(fs_pop_mod3)[2]*fs_data$logmean)
lines(lowess(fs_data$logmean, mod3_resid + fixef(fs_pop_mod3)[2]*fs_data$logmean),col="red")
```

There is not compelling evidence for a quadratic effect.

Let's take the best model and add a year and slope effect

```
fs_pop_mod3_year = lmer(diff ~ logmean + resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          logmean_svl_sd +
                          parasite +
                          logmean:parasite +
                          (logmean | year) + (1 | site),
                        data=fs_data, REML=F)
anova(fs_pop_mod3_year, fs_pop_mod3)
```

```
## Data: fs_data
## Models:
## fs_pop_mod3: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_pop_mod3:     logmean_svl_sd + parasite + logmean:parasite + (1 | year) +
## fs_pop_mod3:     (1 | site)
## fs_pop_mod3_year: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_pop_mod3_year:     logmean_svl_sd + parasite + logmean:parasite + (logmean |
## fs_pop_mod3_year:     year) + (1 | site)
##                  Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_pop_mod3      14 619.78 688.07 -295.89   591.78
## fs_pop_mod3_year 16 617.36 695.42 -292.68   585.36 6.4152      2
##                  Pr(>Chisq)
## fs_pop_mod3
## fs_pop_mod3_year    0.04045 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(fs_pop_mod3_year)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + logmean:parasite + (logmean |
##     year) + (1 | site)
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    617.4    695.4   -292.7    585.4      955
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.3013 -0.6550 -0.0368  0.6053  3.0052
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  site     (Intercept) 0.004468 0.06684
##  year     (Intercept) 0.002236 0.04729
##           logmean     0.001937 0.04401  1.00
##  Residual             0.101497 0.31859
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             0.32198    0.04622   6.966
## logmean                -0.07383    0.05282  -1.398
## resid_svlbyspp_sd       0.02977    0.01060   2.809
## resid_densitybyspp_sd   0.02092    0.01089   1.922
## logmean_svl_sd          0.03784    0.01114   3.398
## parasiteEchino         -0.12366    0.05010  -2.468
## parasiteGlobbie        -0.11255    0.05807  -1.938
## parasiteRib            -0.23033    0.05050  -4.561
## logmean:parasiteEchino -0.04794    0.05449  -0.880
## logmean:parasiteGlobbie -0.05253   0.07371  -0.713
## logmean:parasiteRib    -0.20989    0.05928  -3.541
##
## Correlation of Fixed Effects:
##             (Intr) logmen rsd_s_ rsd_d_ lgmn__ prstEc prstGl prstRb lgmn:E
## logmean     -0.445
## rsd_svlbys_ -0.004  0.025
## rsd_dnstyb_ -0.038  0.017 -0.064
## lgmn_svl_sd  0.043  0.028 -0.017 -0.027
## parasitEchn -0.759  0.521  0.007  0.020 -0.006
## parasitGlbb -0.655  0.452  0.024  0.048 -0.003  0.601
## parasiteRib -0.758  0.518  0.020  0.015 -0.068  0.693  0.599
## lgmn:prstEc  0.551 -0.871 -0.026 -0.002 -0.051 -0.689 -0.438 -0.501
## lgmn:prstGl  0.413 -0.647 -0.036 -0.017 -0.016 -0.379 -0.615 -0.378  0.626
## lgmn:prstRb  0.511 -0.807 -0.040  0.010 -0.044 -0.468 -0.406 -0.678  0.783
##             lgmn:G
## logmean
## rsd_svlbys_
```

```
## rsd_dnstyb_
## lgmn_svl_sd
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl
## lgmn:prstRb   0.581
```

Again, a significant effect of year on the slope that is right on the edge (and driven by 2009).

Include the host-life history variables instead of the population-level variables

Above we included host population-level variables in place of host identity. Here we use host life history variables as described in Johnson et al. 2012 (Eco. Let.)

```
# Checking on correlation between predictors
cor(fs_data[, paste(scale_life_history_vars, "_sd", sep="")])
```

```
##                     hostsizemeta_sd hostrange_sd hostlarvalperiod_sd
## hostsizemeta_sd          1.00000000  -0.08861226          0.960071111
## hostrange_sd            -0.08861226   1.00000000         -0.105782652
## hostlarvalperiod_sd      0.96007111  -0.10578265          1.000000000
## hosteggsize_sd           0.42472296  -0.81447399          0.297592751
## hostclutch_sd            0.14060013   0.86757523         -0.007257884
## hostagemax_sd            0.54599408  -0.54563153          0.349340652
##                     hosteggsize_sd hostclutch_sd hostagemax_sd
## hostsizemeta_sd          0.4247230    0.140600129    0.54599408
## hostrange_sd            -0.8144740    0.867575234   -0.54563153
## hostlarvalperiod_sd      0.2975928   -0.007257884    0.34934065
## hosteggsize_sd           1.0000000   -0.432083501    0.93054010
## hostclutch_sd           -0.4320835    1.000000000   -0.07490318
## hostagemax_sd            0.9305401   -0.074903185    1.00000000
```

Because of the correlations between the life history variables, let's choose hostlarvalperiod, hostrange, hosteggsize, hostclutch, hostagemax.

```
fs_hl_mod = lmer(diff ~ logmean +
                        hostlarvalperiod_sd +
                        hostrange_sd +
                        hosteggsize_sd +
                        hostclutch_sd +
                        logmean:hostlarvalperiod_sd +
                        logmean:hostrange_sd +
                        logmean:hosteggsize_sd +
                        logmean:hostclutch_sd +
                        parasite +
                        logmean:parasite +
                        (1 | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_hl_mod)
```

```
## Single term deletions
##
```

```
## Model:
## diff ~ logmean + hostlarvalperiod_sd + hostrange_sd + hosteggsize_sd +
##     hostclutch_sd + logmean:hostlarvalperiod_sd + logmean:hostrange_sd +
##     logmean:hosteggsize_sd + logmean:hostclutch_sd + parasite +
##     logmean:parasite + (1 | year) + (1 | site)
##                              Df    AIC
## <none>                          623.27
## logmean:hostlarvalperiod_sd  1 622.62
## logmean:hostrange_sd         1 622.21
## logmean:hosteggsize_sd       1 622.43
## logmean:hostclutch_sd        1 622.56
## logmean:parasite             3 646.49
```

Drop the interactions

```
fs_hl_mod1 = lmer(diff ~ logmean +
                         hostlarvalperiod_sd +
                         hostrange_sd +
                         hosteggsize_sd +
                         hostclutch_sd +
                         parasite +
                         logmean:parasite +
                         (1 | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_hl_mod1)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + hostlarvalperiod_sd + hostrange_sd + hosteggsize_sd +
##     hostclutch_sd + parasite + logmean:parasite + (1 | year) +
##     (1 | site)
##                        Df    AIC
## <none>                    623.78
## hostlarvalperiod_sd     1 628.34
## hostrange_sd            1 621.82
## hosteggsize_sd          1 621.85
## hostclutch_sd           1 622.03
## logmean:parasite        3 642.40
```

```
fs_hl_mod2 = update(fs_hl_mod1, .~. - hostrange_sd)
fs_hl_mod2a = update(fs_hl_mod1, .~. - hosteggsize_sd)
fs_hl_mod3 = update(fs_hl_mod2, .~. - hosteggsize_sd)
```

Include parasite-specific variables

We have three parasite specific variables that might be important: parasite body mass, cercariae released per snail, and snail infection prevelance and density.

Step 1: We need to load these files and merge them with the dataset. We already did that above.

```
# Any obvious problematic correlations?
cor(fs_data[, paste(scale_para_vars, "_sd", sep="")])
```

```
##                    parasitemass_sd infect_snail_prev_sd
## parasitemass_sd          1.00000000          -0.887670546
## infect_snail_prev_sd    -0.88767055           1.000000000
## infect_snail_dens_sd     0.41139879          -0.008059876
## cerc_shedding_sd         0.07445068          -0.157204346
##                    infect_snail_dens_sd cerc_shedding_sd
## parasitemass_sd             0.411398794       0.07445068
## infect_snail_prev_sd       -0.008059876      -0.15720435
## infect_snail_dens_sd        1.000000000      -0.59082704
## cerc_shedding_sd           -0.590827044       1.00000000
```

Seems to be some correlations between parasitemass and infection prevlance. Let's include parasite mass. Similarly a correlation between density and shedding. Just use mass, shedding and density to try to avoid multi-collinearity. Not including prevelance because of the high correlation coefficient.

```
fs_para_mod = lmer(diff ~ logmean +
                       species +
                       parasitemass_sd +
                       cerc_shedding_sd +
                       infect_snail_dens_sd +
                       infect_snail_dens_sd:logmean +
                       parasitemass_sd:logmean +
                       cerc_shedding_sd:logmean +
                       (1 | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_para_mod)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + infect_snail_dens_sd:logmean + parasitemass_sd:logmean +
##     cerc_shedding_sd:logmean + (1 | year) + (1 | site)
##                               Df    AIC
## <none>                           623.78
## species                        4 636.38
## logmean:infect_snail_dens_sd   1 623.78
## logmean:parasitemass_sd        1 628.03
## logmean:cerc_shedding_sd       1 623.39
```

```
fs_para_mod1 = lmer(diff ~ logmean +
                       species +
                       parasitemass_sd +
                       cerc_shedding_sd +
                       infect_snail_dens_sd +
                       infect_snail_dens_sd:logmean +
                       parasitemass_sd:logmean +
                       (1 | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_para_mod1)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + infect_snail_dens_sd:logmean + parasitemass_sd:logmean +
```

```
##     (1 | year) + (1 | site)
##                                Df     AIC
## <none>                            623.39
## species                        4 636.08
## cerc_shedding_sd               1 638.02
## logmean:infect_snail_dens_sd   1 631.22
## logmean:parasitemass_sd        1 626.05
```

It looks like including these parasite specific variables we can almost get back to parasite identity. And we see that cercaria shedding could be driving the increased variation in Alaria, independent of log mean.

What if I include the effect of year on logmean?

```
fs_para_mod1_year = lmer(diff ~ logmean +
                         species +
                         parasitemass_sd +
                         cerc_shedding_sd +
                         infect_snail_dens_sd +
                         infect_snail_dens_sd:logmean +
                         parasitemass_sd:logmean +
                         (logmean | year) + (1 | site),
                       data=fs_data, REML=F)
anova(fs_para_mod1_year, fs_para_mod1)
```

```
## Data: fs_data
## Models:
## fs_para_mod1: diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
## fs_para_mod1:     infect_snail_dens_sd + infect_snail_dens_sd:logmean + parasitemass_sd:logmean +
## fs_para_mod1:     (1 | year) + (1 | site)
## fs_para_mod1_year: diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
## fs_para_mod1_year:     infect_snail_dens_sd + infect_snail_dens_sd:logmean + parasitemass_sd:logmean
## fs_para_mod1_year:     (logmean | year) + (1 | site)
##                   Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_para_mod1      14 623.39 691.68 -297.69   595.39
## fs_para_mod1_year 16 620.45 698.50 -294.22   588.45 6.9372      2
##                   Pr(>Chisq)
## fs_para_mod1
## fs_para_mod1_year    0.03116 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model is better and the effects don't change when we include the effect of year on the slope.

Include species-specific variables

Now we are specifically focusing on the host by parasite interaction. Going to look at both the virulence, competence, and host:parasite

```
# Starting with interaction model
fs_hp_mod = lmer(diff ~ logmean + species:parasite +
                        logmean:species:parasite +
                        (1 | year) + (1 | site),
                      data=fs_data, REML=F)
```

```
## fixed-effect model matrix is rank deficient so dropping 8 columns / coefficients
```

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```
AIC(fs_hp_mod)
```

[1] 637.0293

Now working on quantitative model with virulence and competence.

```
fs_hp_mod_vir = lmer(diff ~ logmean + oddsratio_sd +
                            logmean:oddsratio_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)

fs_hp_mod_comp = lmer(diff ~ logmean + infectionsuccess_sd +
                            logmean:infectionsuccess_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)
```

Now let's try adding back host and parasite-specific variables

Starting with host specific variables

```
fs_hp_mod_vir1 = lmer(diff ~ logmean + oddsratio_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            logmean:oddsratio_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)

fs_hp_mod_comp1 = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            logmean:infectionsuccess_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)

anova(fs_hp_mod_vir1, fs_hp_mod_comp1)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir1: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir1:     logmean:oddsratio_sd + (1 | year) + (1 | site)
## fs_hp_mod_comp1: diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_comp1:     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
##                 Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## fs_hp_mod_vir1   9 655.59 699.49 -318.79   637.59
## fs_hp_mod_comp1  9 699.04 742.95 -340.52   681.04     0      0          1
```

Try adding in parasite specific variables.

```
fs_hp_mod_vir2 = lmer(diff ~ logmean + oddsratio_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            logmean:oddsratio_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)

anova(fs_hp_mod_vir2, fs_hp_mod_vir1)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir1: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir1:     logmean:oddsratio_sd + (1 | year) + (1 | site)
```

```
## fs_hp_mod_vir2: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir2:     cerc_shedding_sd + logmean:oddsratio_sd + (1 | year) + (1 |
## fs_hp_mod_vir2:     site)
##                Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
## fs_hp_mod_vir1  9 655.59 699.49 -318.79   637.59
## fs_hp_mod_vir2 10 641.75 690.53 -310.87   621.75 15.84      1  6.894e-05
##
## fs_hp_mod_vir1
## fs_hp_mod_vir2 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
fs_hp_mod_vir3 = lmer(diff ~ logmean + oddsratio_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          cerc_shedding_sd +
                          parasitemass_sd +
                          logmean:parasitemass_sd +
                          logmean:oddsratio_sd +
                          (1 | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_hp_mod_vir3)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + logmean:parasitemass_sd +
##     logmean:oddsratio_sd + (1 | year) + (1 | site)
##                         Df    AIC
## <none>                     634.76
## resid_svlbyspp_sd        1 639.74
## resid_densitybyspp_sd    1 636.65
## cerc_shedding_sd         1 655.57
## logmean:parasitemass_sd  1 634.67
## logmean:oddsratio_sd     1 636.44
```

```r
# Drop the interaction with parasitemass_sd

fs_hp_mod_vir4 = lmer(diff ~ logmean + oddsratio_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          cerc_shedding_sd +
                          parasitemass_sd +
                          infect_snail_dens_sd +
                          logmean:oddsratio_sd +
                          (1 | year) + (1 | site), data=fs_data, REML=F)

# Host does RIB affect these predictions?
fs_hp_mod_vir4_norib = lmer(diff ~ logmean + oddsratio_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          cerc_shedding_sd +
                          logmean:oddsratio_sd +
                          (1 | year) + (1 | site),
```

```
                                        data=fs_data[fs_data$parasite != "Rib", ], REML=F)
```

infectsnaildens is correlated with oddsratio so it doesn't really make sense to include them both in the model.
Definitely should not be including interactions with both of these variables.

Look at the competence model. Same model but swapping out oddsratio for infection success.

```
fs_hp_mod_comp2 = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            logmean:infectionsuccess_sd +
                            (1 | year) + (1 | site), data=fs_data, REML=F)

fs_hp_mod_comp3 = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            parasitemass_sd +
                            logmean:infectionsuccess_sd +
                            (1 | year) + (1 | site), data=fs_data, REML=F)

fs_hp_mod_comp4 = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            parasitemass_sd +
                            infect_snail_dens_sd +
                            logmean:infectionsuccess_sd +
                            (1 | year) + (1 | site),
                            data=fs_data, REML=F)
```

Even with a host-parasite interaction, we still have effects of host and parasite that show up in the model.
Let's try adding in logmean year again.

```
fs_hp_mod_comp4_year = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            parasitemass_sd +
                            infect_snail_dens_sd +
                            logmean:infectionsuccess_sd +
                            (logmean | year) + (1 | site),
                            data=fs_data, REML=F)
anova(fs_hp_mod_comp4_year, fs_hp_mod_comp4)
```
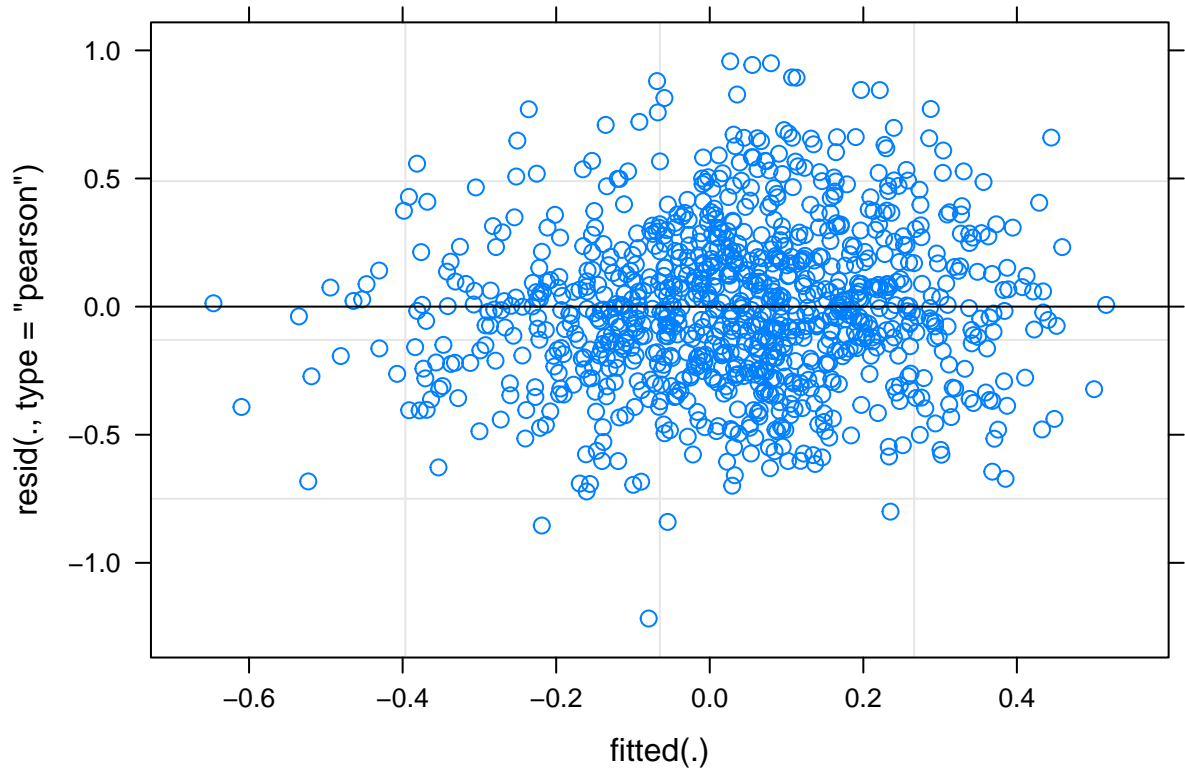
```
## Data: fs_data
## Models:
## fs_hp_mod_comp4: diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_comp4:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_comp4:     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
## fs_hp_mod_comp4_year: diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_s
## fs_hp_mod_comp4_year:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_comp4_year:     logmean:infectionsuccess_sd + (logmean | year) + (1 | site)
##                      Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_hp_mod_comp4      12 631.57 690.11 -303.79   607.57
```

```
## fs_hp_mod_comp4_year 14 629.18 697.47 -300.59   601.18 6.3968       2
##                          Pr(>Chisq)
## fs_hp_mod_comp4
## fs_hp_mod_comp4_year    0.04083 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
fs_hp_mod_vir4_year = lmer(diff ~ logmean + oddsratio_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          cerc_shedding_sd +
                          parasitemass_sd +
                          infect_snail_dens_sd +
                          logmean:oddsratio_sd +
                          (logmean | year) + (1 | site),
                          data=fs_data, REML=F)
anova(fs_hp_mod_vir4, fs_hp_mod_vir4_year)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir4: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir4:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_vir4:     logmean:oddsratio_sd + (1 | year) + (1 | site)
## fs_hp_mod_vir4_year: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir4_year:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_vir4_year:     logmean:oddsratio_sd + (logmean | year) + (1 | site)
##                      Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_hp_mod_vir4       12 630.99 689.53 -303.50   606.99
## fs_hp_mod_vir4_year  14 629.48 697.78 -300.74   601.48 5.5097       2
##                      Pr(>Chisq)
## fs_hp_mod_vir4
## fs_hp_mod_vir4_year    0.06362 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Marginal effect of year on slope for both the virulence and the competence model. Improves the model slightly in both cases but doesn't change anything about our inference.
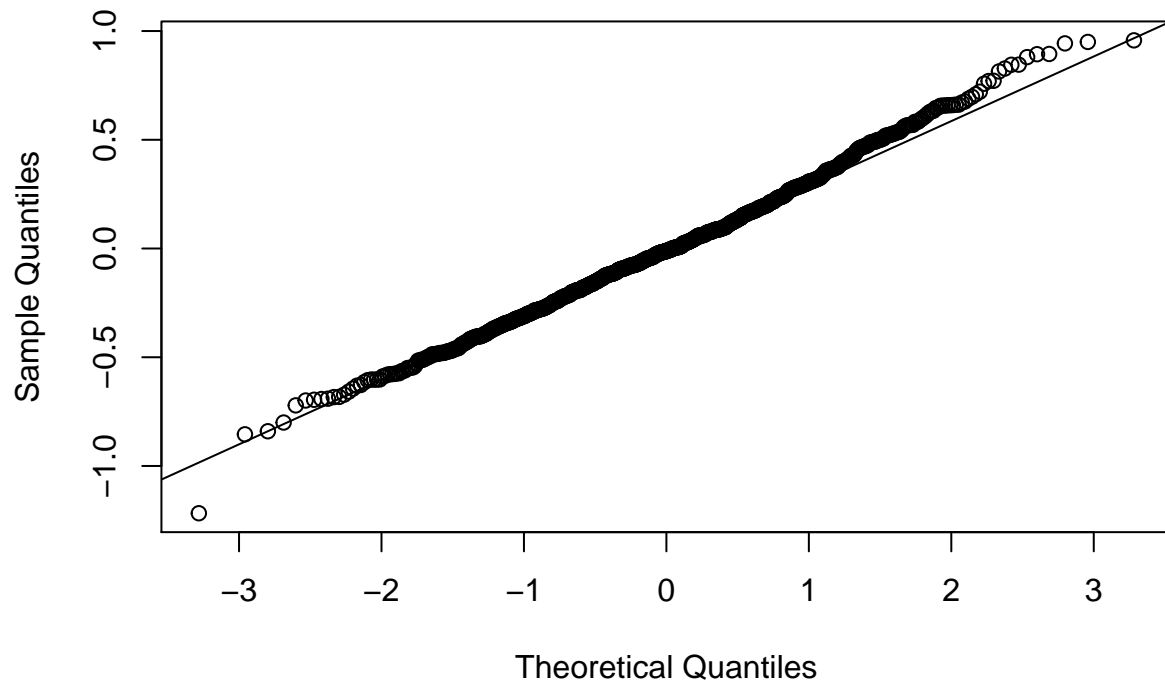
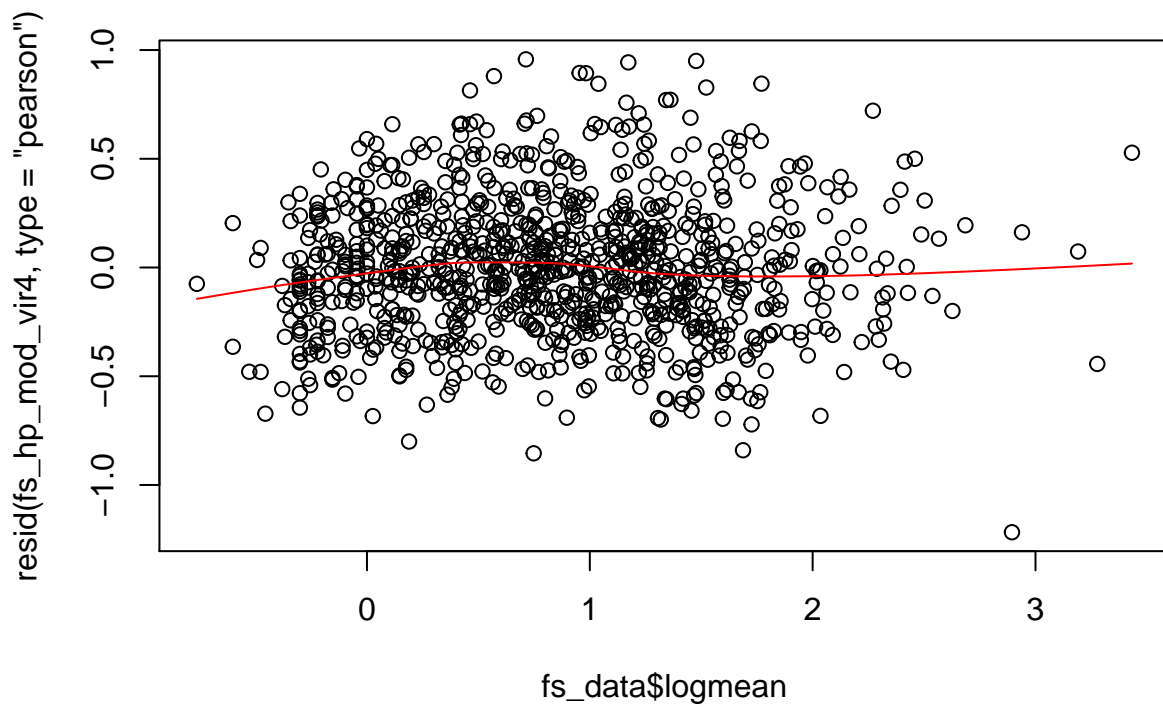Let's look at some diagnostic plots

```r
plot(fs_hp_mod_vir4)
```

```r
qqnorm(resid(fs_hp_mod_vir4, type="pearson"))
qqline(resid(fs_hp_mod_vir4, type="pearson"))
```
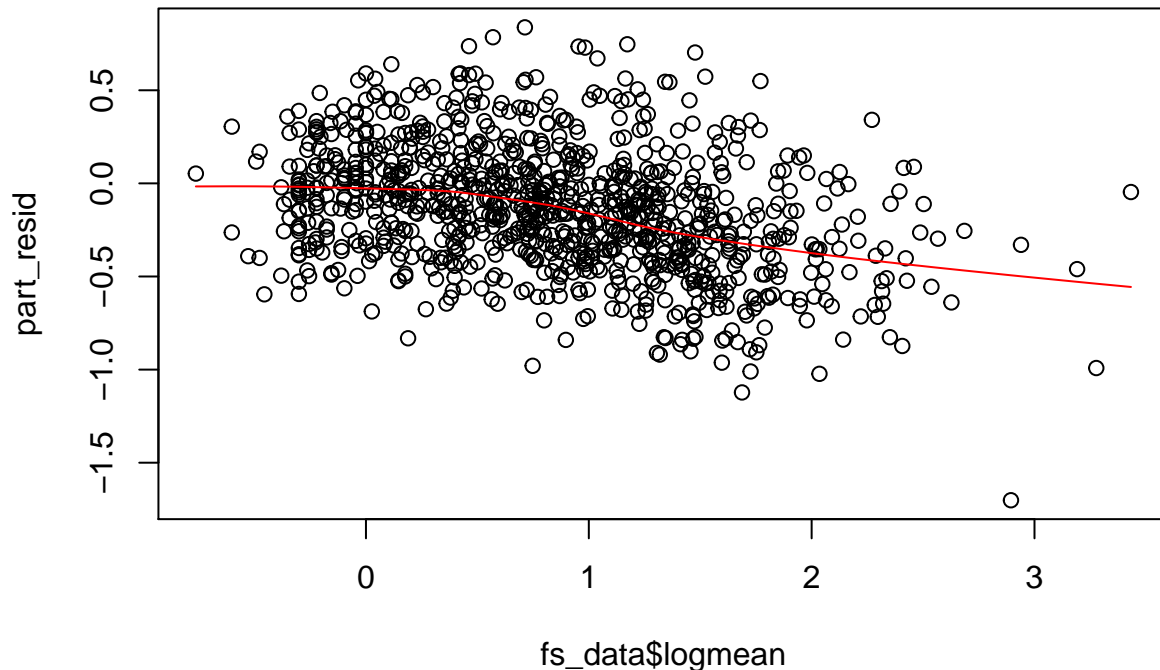
Normal Q−Q Plot


```r
plot(fs_data$logmean, resid(fs_hp_mod_vir4, type="pearson"))
lines(lowess(fs_data$logmean, resid(fs_hp_mod_vir4, type="pearson")), col="red")
```

```r
# The quadratic effect seems quite small...but it is on the same scale
part_resid = resid(fs_hp_mod_vir4) + fixef(fs_hp_mod_vir4)[2] * fs_data$logmean
plot(fs_data$logmean, part_resid)
lines(lowess(fs_data$logmean, part_resid), col="red")
```

There doesn't seem to be much evidence for a quadratic effect of logmean when you look at the partial residual plots.

However, we do see that it is statistically significant when we include it into the model.

Some basic results:

1. A strong negative main effect of oddsratio and a significant interactive effect of oddsratio with logmean. Same for competence.
2. We see a significant interactive effect between competence and logmean
3. We see positive main effects of host heterogeneity in body size and spatial aggregation.
4. We see a positive effect of cercariae shedding on the intercept (driven by Alaria) and negative effects of parasmite mass (somewhat...) and infected snail density on the intercept (after accounting for the host by parasite interaction).

Trying to decorrelate oddsratio and infectionsuccess

Above, we tried decorrelating oddsratio and infectionsuccess in two ways

1. Calculated the oddsratio coefficient by using the dose * competence and the predictor variable in the logistic regression instead of simply dose. Problems: This led to some VERY high values of oddsratio, particularly for TAGR-ECHINO

2. Took the residuals of a regression of competence on virulence which gave us the bit of virulence that was not described by competence. This should be pretty equivalent to just including them both in the model.

```
# The model without controlling for the correlation between oddsratio and infectionsuccess
fs_hp_mod_vir_comp_full = lmer(diff ~ logmean + oddsratio_sd + infectionsuccess_sd +
                            logmean:oddsratio_sd + logmean:infectionsuccess_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)


# The model with the residuals
fs_hp_mod_vir_comp_resid = lmer(diff ~ logmean + oddsratio_resid + infectionsuccess_sd +
                            logmean:oddsratio_resid + logmean:infectionsuccess_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)


anova(fs_hp_mod_vir_comp_full, fs_hp_mod_vir_comp_resid, fs_hp_mod_vir)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir: diff ~ logmean + oddsratio_sd + logmean:oddsratio_sd + (1 | year) +
## fs_hp_mod_vir:     (1 | site)
## fs_hp_mod_vir_comp_full: diff ~ logmean + oddsratio_sd + infectionsuccess_sd + logmean:oddsratio_sd
## fs_hp_mod_vir_comp_full:     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
## fs_hp_mod_vir_comp_resid: diff ~ logmean + oddsratio_resid + infectionsuccess_sd + logmean:oddsratio
## fs_hp_mod_vir_comp_resid:     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
##                          Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_hp_mod_vir             7 663.47 697.62 -324.74   649.47
## fs_hp_mod_vir_comp_full   9 663.64 707.55 -322.82   645.64 3.8291      2
## fs_hp_mod_vir_comp_resid  9 663.64 707.55 -322.82   645.64 0.0000      0
##                          Pr(>Chisq)
## fs_hp_mod_vir
## fs_hp_mod_vir_comp_full      0.1474
## fs_hp_mod_vir_comp_resid     1.0000
```

As expected, just looking at the residuals of oddsratio gives exactly the same model as including the full predictor because this is exactly what regression is doing. So no point.

There is minimal improvement when including the residuals of oddsratio. That is expected as the regression approach already does this.

Let's try using the updated virulence measures keeping in mind the major outlier of TAGR-ECHINO.

```
fs_hp_mod_vir_comp_cond = lmer(diff ~ logmean + oddsratio_conditional_sd + infectionsuccess_sd +
                            logmean:oddsratio_conditional_sd + logmean:infectionsuccess_sd +
                        (1 | year) + (1 | site), data=fs_data, REML=F)


anova(fs_hp_mod_vir_comp_cond, fs_hp_mod_vir_comp_full)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir_comp_cond: diff ~ logmean + oddsratio_conditional_sd + infectionsuccess_sd +
## fs_hp_mod_vir_comp_cond:     logmean:oddsratio_conditional_sd + logmean:infectionsuccess_sd +
## fs_hp_mod_vir_comp_cond:     (1 | year) + (1 | site)
## fs_hp_mod_vir_comp_full: diff ~ logmean + oddsratio_sd + infectionsuccess_sd + logmean:oddsratio_sd
## fs_hp_mod_vir_comp_full:     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
##                          Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_hp_mod_vir_comp_cond   9 707.55 751.45 -344.77   689.55
## fs_hp_mod_vir_comp_full   9 663.64 707.55 -322.82   645.64 43.906      0
##                          Pr(>Chisq)
## fs_hp_mod_vir_comp_cond
## fs_hp_mod_vir_comp_full  < 2.2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
# Drop the outlier to see the effect on coefficients
fs_hp_mod_vir_comp_cond_drop = lmer(diff ~ logmean + oddsratio_conditional_sd +
                                    infectionsuccess_sd +
                                    logmean:oddsratio_conditional_sd + logmean:infectionsuccess_sd +

                       (1 | year) + (1 | site),
                       data=fs_data[(fs_data$parasite != "ECHINO") & (fs_data$species != "TAGR"),], REI

summary(fs_hp_mod_vir_comp_cond)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ logmean + oddsratio_conditional_sd + infectionsuccess_sd +
##     logmean:oddsratio_conditional_sd + logmean:infectionsuccess_sd +
##     (1 | year) + (1 | site)
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    707.5    751.5   -344.8    689.5      962
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2205 -0.6700 -0.0618  0.6450  3.1271
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.006664 0.08163
##  year     (Intercept) 0.007811 0.08838
##  Residual             0.111971 0.33462
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                                   Estimate Std. Error t value
## (Intercept)                        0.18287    0.03866   4.731
## logmean                           -0.16534    0.01645 -10.050
## oddsratio_conditional_sd          -0.03187    0.02007  -1.588
## infectionsuccess_sd               -0.02986    0.01665  -1.793
## logmean:oddsratio_conditional_sd   0.02869    0.02602   1.103
## logmean:infectionsuccess_sd       -0.06556    0.01715  -3.823
##
## Correlation of Fixed Effects:
##             (Intr) logmen odds__ infct_ lgm:__
## logmean     -0.334
## oddsrt_cnd_  0.000 -0.079
## infctnsccs_ -0.048  0.009  0.158
## lgmn:ddsr__ -0.025  0.162 -0.830 -0.100
## lgmn:nfctn_  0.011  0.146 -0.085 -0.739  0.055

summary(fs_hp_mod_vir_comp_cond_drop)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
```

```
## diff ~ logmean + oddsratio_conditional_sd + infectionsuccess_sd +
##     logmean:oddsratio_conditional_sd + logmean:infectionsuccess_sd +
##     (1 | year) + (1 | site)
##    Data: fs_data[(fs_data$parasite != "ECHINO") & (fs_data$species !=
##     "TAGR"), ]
##
##       AIC      BIC   logLik deviance df.resid
##     697.8    741.6   -339.9    679.8      952
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2494 -0.6636 -0.0557  0.6363  3.1048
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.006692 0.08181
##  year     (Intercept) 0.007307 0.08548
##  Residual             0.111653 0.33415
## Number of obs: 961, groups:  site, 173; year, 7
##
## Fixed effects:
##                                   Estimate Std. Error t value
## (Intercept)                        0.18480    0.03774   4.897
## logmean                           -0.17306    0.01666 -10.390
## oddsratio_conditional_sd          -0.04071    0.02331  -1.747
## infectionsuccess_sd               -0.02967    0.01664  -1.784
## logmean:oddsratio_conditional_sd  -0.01329    0.03181  -0.418
## logmean:infectionsuccess_sd       -0.06154    0.01717  -3.584
##
## Correlation of Fixed Effects:
##             (Intr) logmen odds__ infct_ lgm:__
## logmean     -0.339
## oddsrt_cnd_  0.006 -0.088
## infctnsccs_ -0.050  0.008  0.139
## lgmn:ddsr__ -0.028  0.217 -0.733 -0.090
## lgmn:nfctn_  0.012  0.133 -0.076 -0.736  0.013
# Not a huge effect of these outliers on the coefficients
```

There doesn't seem to be much evidence that this is decoupling virulence and competence in a meaningful way.

Assessing the impact of outliers

We identified two potential outliers

The outliers are

1. BNPND002 2014 TAGR Echino: 1 animal with 102. Without it, n = 9, mean = 3.222, var = 16.694

- After double checking it seems like there is nothing wrong with this data at there was a TAGR with 102 which is leading to a huge variance given the mean.

2. PRPND009 2015 TATO Echino: N = 10, mean = 0.5, var = 2.5 [7/22]. This excludes 5 animals collected on a later date

```
# Identify the outliers

outid1 = which(with(fs_data, (site == "BNPND002") & (year == 2014) & (species == "TAGR") & (parasite ==
outid2 = which(with(fs_data, (site == "PRPND009") & (year == 2015) & (species == "TATO") & (parasite ==
```

Let's see if these outliers are affecting our inference. Let's try removing them to see if they effect our models.

```
fs_hp_mod_vir4_drop = lmer(diff ~ logmean + oddsratio_sd +
                           resid_svlbyspp_sd +
                           resid_densitybyspp_sd +
                           cerc_shedding_sd +
                           parasitemass_sd +
                           infect_snail_dens_sd +
                           logmean:oddsratio_sd +
                           (1 | year) + (1 | site),
                         data=fs_data[-c(outid1, outid2), ], REML=F)

summary(fs_hp_mod_vir4_drop)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     logmean:oddsratio_sd + (1 | year) + (1 | site)
##    Data: fs_data[-c(outid1, outid2), ]
##
##      AIC      BIC   logLik deviance df.resid
##    620.1    678.6   -298.0    596.1      957
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.8073 -0.6556 -0.0296  0.6069  2.9958
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.006589 0.08117
##  year     (Intercept) 0.006331 0.07957
##  Residual             0.101561 0.31869
## Number of obs: 969, groups:  site, 173; year, 7
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             0.18380    0.03562   5.161
## logmean                -0.16865    0.01648 -10.232
## oddsratio_sd            0.01764    0.02306   0.765
## resid_svlbyspp_sd       0.02879    0.01068   2.696
## resid_densitybyspp_sd   0.02130    0.01106   1.925
## cerc_shedding_sd        0.05167    0.01554   3.326
## parasitemass_sd        -0.03439    0.01601  -2.148
## infect_snail_dens_sd   -0.04284    0.01783  -2.402
## logmean:oddsratio_sd   -0.06676    0.01740  -3.837
##
```

```
## Correlation of Fixed Effects:
##            (Intr) logmen oddsr_ rsd_s_ rsd_d_ crc_s_ prstm_ inf___
## logmean    -0.363
## oddsrati_sd -0.044  0.025
## rsd_svlbys_  0.015 -0.017  0.012
## rsd_dnstyb_ -0.021  0.059  0.001 -0.067
## crc_shddng_  0.024 -0.060  0.277 -0.003 -0.041
## parstmss_sd -0.076  0.209 -0.367  0.009  0.006 -0.530
## infct_snl__  0.088 -0.223 -0.394 -0.016 -0.029  0.456 -0.271
## lgmn:ddsrt_  0.005  0.152 -0.586 -0.020  0.014  0.000 -0.096  0.143
```

```
fs_hp_mod_comp4_drop = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            parasitemass_sd +
                            infect_snail_dens_sd +
                            logmean:infectionsuccess_sd +
                            (1 | year) + (1 | site), data=fs_data[-c(outid1, outid2), ], REML=F)

summary(fs_hp_mod_comp4_drop)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
##    Data: fs_data[-c(outid1, outid2), ]
##
##      AIC      BIC   logLik deviance df.resid
##    624.0    682.5   -300.0    600.0      957
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5156 -0.6574 -0.0422  0.6283  3.0124
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.007240 0.08509
##  year     (Intercept) 0.006715 0.08195
##  Residual             0.101550 0.31867
## Number of obs: 969, groups:  site, 173; year, 7
##
## Fixed effects:
##                             Estimate Std. Error t value
## (Intercept)                  0.17697    0.03644   4.856
## logmean                     -0.15804    0.01626  -9.721
## infectionsuccess_sd          0.01498    0.02108   0.711
## resid_svlbyspp_sd            0.02823    0.01070   2.637
## resid_densitybyspp_sd        0.02138    0.01111   1.924
## cerc_shedding_sd             0.05710    0.01475   3.871
## parasitemass_sd             -0.02750    0.01989  -1.383
## infect_snail_dens_sd        -0.04934    0.01668  -2.958
## logmean:infectionsuccess_sd -0.05983    0.01670  -3.583
##
```

```
## Correlation of Fixed Effects:
##            (Intr) logmen infct_ rsd_s_ rsd_d_ crc_s_ prstm_ inf___
## logmean     -0.353
## infctnsccs_  0.002 -0.107
## rsd_svlbys_  0.015 -0.015  0.013
## rsd_dnstyb_ -0.019  0.056  0.016 -0.067
## crc_shddng_  0.044 -0.101 -0.125 -0.005 -0.048
## parstmss_sd -0.098  0.284 -0.546  0.000 -0.007 -0.256
## infct_snl__  0.071 -0.184 -0.213 -0.017 -0.031  0.690 -0.286
## lgmn:nfctn_  0.030  0.081 -0.468 -0.009  0.008  0.107 -0.175  0.113
```

```r
fs_pop_mod3_drop = lmer(diff ~ logmean + resid_svlbyspp_sd +
                        resid_densitybyspp_sd +
                        logmean_svl_sd +
                        parasite +
                        logmean:parasite +
                        (1 | year) + (1 | site), data=fs_data[-c(outid1, outid2), ], REML=F)

summary(fs_pop_mod3_drop)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + logmean:parasite + (1 | year) +
##     (1 | site)
##    Data: fs_data[-c(outid1, outid2), ]
##
##      AIC      BIC   logLik deviance df.resid
##    609.0    677.2   -290.5    581.0      955
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1471 -0.6642 -0.0448  0.5999  3.0350
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.004729 0.06877
##  year     (Intercept) 0.006128 0.07828
##  Residual             0.101154 0.31805
## Number of obs: 969, groups:  site, 173; year, 7
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             0.32245    0.05217   6.180
## logmean                -0.06151    0.04990  -1.233
## resid_svlbyspp_sd       0.02899    0.01059   2.738
## resid_densitybyspp_sd   0.02062    0.01091   1.890
## logmean_svl_sd          0.03752    0.01116   3.361
## parasiteEchino         -0.12686    0.05016  -2.529
## parasiteGlobbie        -0.10130    0.05815  -1.742
## parasiteRib            -0.22880    0.05053  -4.528
## logmean:parasiteEchino -0.05873    0.05440  -1.080
## logmean:parasiteGlobbie -0.07290   0.07352  -0.992
## logmean:parasiteRib    -0.22318    0.05904  -3.780
##
## Correlation of Fixed Effects:
```

```
##              (Intr) logmen rsd_s_ rsd_d_ lgmn__ prstEc prstGl prstRb lgmn:E
## logmean      -0.534
## rsd_svlbys_ -0.004  0.028
## rsd_dnstyb_ -0.035  0.018 -0.066
## lgmn_svl_sd  0.035  0.031 -0.017 -0.023
## parasitEchn -0.678  0.553  0.007  0.022 -0.004
## parasitGlbb -0.583  0.476  0.026  0.049 -0.004  0.603
## parasiteRib -0.675  0.548  0.021  0.016 -0.066  0.694  0.599
## lgmn:prstEc  0.491 -0.918 -0.026 -0.001 -0.053 -0.690 -0.437 -0.501
## lgmn:prstGl  0.369 -0.682 -0.038 -0.018 -0.016 -0.382 -0.615 -0.380  0.626
## lgmn:prstRb  0.454 -0.849 -0.040  0.012 -0.046 -0.470 -0.405 -0.679  0.782
##              lgmn:G
## logmean
## rsd_svlbys_
## rsd_dnstyb_
## lgmn_svl_sd
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl
## lgmn:prstRb  0.580
```

No effect on the model coefficients.

What if we try replacing the values in the second site with only the samples at the earlier date?

```
fs_data_up = fs_data

# Add in new values given data
fs_data_up[outid2, "logmean"] = log10(0.5)
fs_data_up[outid2, "logvar"] = log10(2.5)
fs_data_up[outid2, "H"] = 10
fs_data_up[outid2, "P"] = 5 # Huge reduction from P=884
fs_data_up[outid2, "fs_var"] = 0.85 # Median variance from 1000 samples of feasible set with P=5, H=10
fs_data_up[outid2, "diff"] = fs_data_up[outid2, "logvar"] - log10(fs_data_up[outid2, "fs_var"]) # Calc

fs_hp_mod_vir4_reval = lmer(diff ~ logmean + oddsratio_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            parasitemass_sd +
                            infect_snail_dens_sd +
                            logmean:oddsratio_sd +
                            (1 | year) + (1 | site),
                          data=fs_data_up, REML=F)

summary(fs_hp_mod_vir4_reval)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##      cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##      logmean:oddsratio_sd + (1 | year) + (1 | site)
##    Data: fs_data_up
##
```

```
##      AIC      BIC   logLik deviance df.resid
##    623.7    682.2   -299.9    599.7      959
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.8027 -0.6576 -0.0281  0.5989  2.9912
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.006586 0.08115
##  year     (Intercept) 0.006431 0.08019
##  Residual             0.101821 0.31909
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)            0.18513    0.03580   5.171
## logmean               -0.16892    0.01647 -10.257
## oddsratio_sd           0.01753    0.02309   0.759
## resid_svlbyspp_sd      0.02889    0.01069   2.703
## resid_densitybyspp_sd  0.02102    0.01106   1.901
## cerc_shedding_sd       0.05206    0.01555   3.348
## parasitemass_sd       -0.03519    0.01600  -2.199
## infect_snail_dens_sd  -0.04239    0.01785  -2.374
## logmean:oddsratio_sd  -0.06686    0.01742  -3.839
##
## Correlation of Fixed Effects:
##            (Intr) logmen oddsr_ rsd_s_ rsd_d_ crc_s_ prstm_ inf___
## logmean    -0.360
## oddsrati_sd -0.043  0.024
## rsd_svlbys_  0.015 -0.017  0.012
## rsd_dnstyb_ -0.022  0.063  0.002 -0.067
## crc_shddng_  0.023 -0.060  0.277 -0.003 -0.041
## parstmss_sd -0.074  0.206 -0.368  0.009  0.008 -0.530
## infct_snl__  0.087 -0.222 -0.394 -0.016 -0.030  0.456 -0.270
## lgmn:ddsrt_  0.004  0.153 -0.587 -0.020  0.012  0.000 -0.096  0.142
```

```r
fs_hp_mod_comp4_reval = lmer(diff ~ logmean + infectionsuccess_sd +
                       resid_svlbyspp_sd +
                       resid_densitybyspp_sd +
                       cerc_shedding_sd +
                       parasitemass_sd +
                       infect_snail_dens_sd +
                       logmean:infectionsuccess_sd +
                       (1 | year) + (1 | site), data=fs_data_up, REML=F)

summary(fs_hp_mod_comp4_reval)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     logmean:infectionsuccess_sd + (1 | year) + (1 | site)
##    Data: fs_data_up
##
```

```
##      AIC      BIC   logLik deviance df.resid
##    626.7    685.2   -301.4    602.7      959
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5070 -0.6662 -0.0398  0.6211  3.0104
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.007197 0.08483
##  year     (Intercept) 0.006839 0.08270
##  Residual             0.101731 0.31895
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                            Estimate Std. Error t value
## (Intercept)                 0.17817    0.03666   4.860
## logmean                    -0.15836    0.01624  -9.750
## infectionsuccess_sd         0.01272    0.02099   0.606
## resid_svlbyspp_sd           0.02830    0.01071   2.643
## resid_densitybyspp_sd       0.02119    0.01110   1.909
## cerc_shedding_sd            0.05762    0.01476   3.904
## parasitemass_sd            -0.02598    0.01988  -1.307
## infect_snail_dens_sd       -0.04857    0.01667  -2.913
## logmean:infectionsuccess_sd -0.06098    0.01662  -3.668
##
## Correlation of Fixed Effects:
##             (Intr) logmen infct_ rsd_s_ rsd_d_ crc_s_ prstm_ inf___
## logmean     -0.350
## infctnsccs_  0.006 -0.112
## rsd_svlbys_  0.015 -0.015  0.013
## rsd_dnstyb_ -0.021  0.059  0.020 -0.067
## crc_shddng_  0.043 -0.100 -0.123 -0.005 -0.049
## parstmss_sd -0.097  0.284 -0.548  0.000 -0.005 -0.257
## infct_snl__  0.069 -0.182 -0.209 -0.017 -0.033  0.690 -0.287
## lgmn:nfctn_  0.027  0.087 -0.467 -0.009  0.002  0.106 -0.172  0.111
```

```r
fs_pop_mod3_reval = lmer(diff ~ logmean + resid_svlbyspp_sd +
                         resid_densitybyspp_sd +
                         logmean_svl_sd +
                         parasite +
                         logmean:parasite +
                         (1 | year) + (1 | site), data=fs_data_up, REML=F)

summary(fs_pop_mod3_reval)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + logmean:parasite + (1 | year) +
##     (1 | site)
##    Data: fs_data_up
##
##      AIC      BIC   logLik deviance df.resid
##    613.0    681.3   -292.5    585.0      957
##
```

```
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.1359 -0.6635 -0.0524  0.5960  3.0271
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  site     (Intercept) 0.004787 0.06919
##  year     (Intercept) 0.006259 0.07911
##  Residual             0.101411 0.31845
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                          Estimate Std. Error t value
## (Intercept)               0.32355    0.05241   6.174
## logmean                  -0.06167    0.04998  -1.234
## resid_svlbyspp_sd         0.02912    0.01060   2.746
## resid_densitybyspp_sd     0.02038    0.01091   1.868
## logmean_svl_sd            0.03679    0.01118   3.292
## parasiteEchino           -0.12582    0.05014  -2.509
## parasiteGlobbie          -0.10200    0.05823  -1.752
## parasiteRib              -0.22909    0.05060  -4.527
## logmean:parasiteEchino   -0.05870    0.05444  -1.078
## logmean:parasiteGlobbie  -0.07272    0.07362  -0.988
## logmean:parasiteRib      -0.22348    0.05913  -3.780
##
## Correlation of Fixed Effects:
##             (Intr) logmen rsd_s_ rsd_d_ lgmn__ prstEc prstGl prstRb lgmn:E
## logmean     -0.533
## rsd_svlbys_ -0.004  0.028
## rsd_dnstyb_ -0.035  0.018 -0.066
## lgmn_svl_sd  0.035  0.031 -0.017 -0.023
## parasitEchn -0.677  0.554  0.007  0.019 -0.004
## parasitGlbb -0.581  0.476  0.026  0.049 -0.004  0.604
## parasiteRib -0.673  0.548  0.021  0.016 -0.066  0.695  0.599
## lgmn:prstEc  0.490 -0.919 -0.026  0.001 -0.053 -0.690 -0.437 -0.502
## lgmn:prstGl  0.367 -0.682 -0.038 -0.018 -0.016 -0.382 -0.615 -0.380  0.626
## lgmn:prstRb  0.453 -0.849 -0.040  0.012 -0.046 -0.470 -0.405 -0.679  0.782
##             lgmn:G
## logmean
## rsd_svlbys_
## rsd_dnstyb_
## lgmn_svl_sd
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl
## lgmn:prstRb  0.580
```
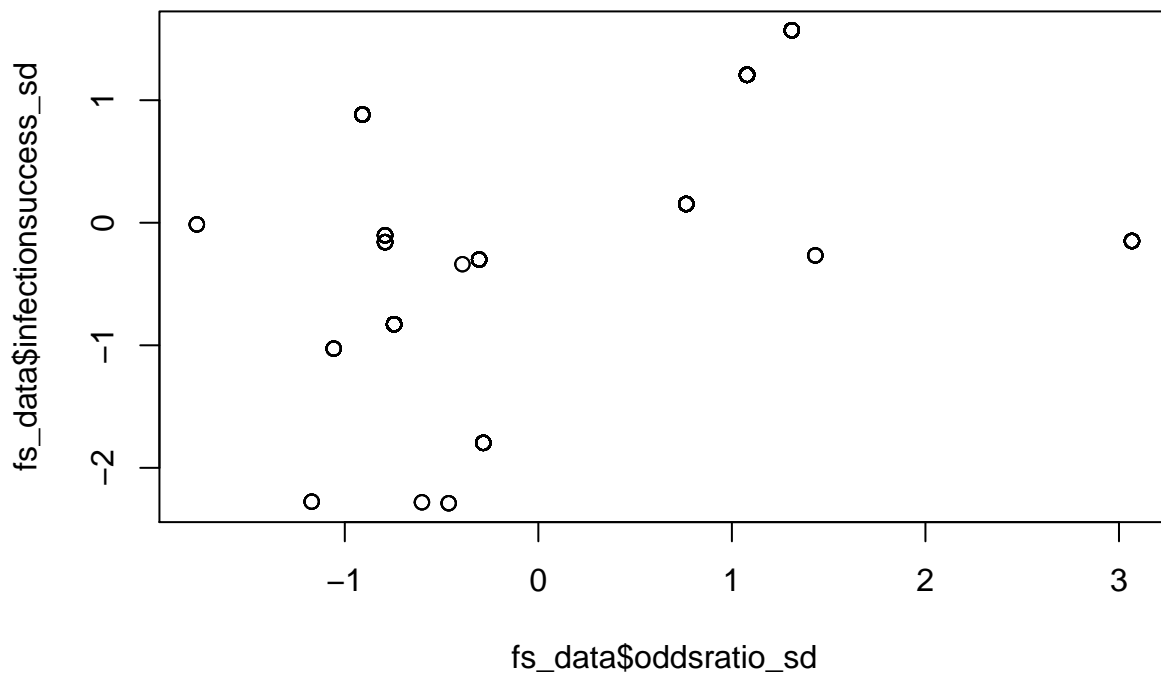
Again, no effect on the coefficients. Given that these points have no effects and splitting the second point could potentially introduce some autocorrelation (though it would have no effect) we chose to leave the second point as is. As we just showed, this has no effects on any results.

Parsing out the interactive effects of infection success and competence (if any)

First let's group these measures to see if we can detect an interaction

```r
# Group low high by factors
fs_data$infectionsuccess_group = as.factor(fs_data$infectionsuccess_sd > -0.5)
fs_data$oddsratio_group = as.factor((fs_data$oddsratio_sd > 0.1))
levels(fs_data$infectionsuccess_group) = c("low", "high")
levels(fs_data$oddsratio_group) = c("low", "high")

plot(fs_data$oddsratio_sd, fs_data$infectionsuccess_sd)
```



```r
aggregate(oddsratio_sd ~ infectionsuccess_group + oddsratio_group, length, data=fs_data)
```

```
##   infectionsuccess_group oddsratio_group oddsratio_sd
## 1                    low             low          393
## 2                   high             low          226
## 3                   high            high          352
```

There are no data points with high virulence and low infection success. Therefore, an interaction term doesn't make sense.

Analysis with logmean | year effect included

Doing additional analyses to ensure that the marginal random slope effect of logmean is not changing our results.

```
fs_mod1_year = lmer(diff ~ logmean + species +
                    parasite +
                    logmean:species +
                    logmean:parasite +
                    species:parasite +
                    logmean:species:parasite +
                    (logmean | year) + (1 | site), data=fs_data, REML=F)
```

```
## fixed-effect model matrix is rank deficient so dropping 6 columns / coefficients
# Is the interaction with logmean imporant important...no evidence for an interaction
fs_no_int_year = update(fs_mod1_year, .~. - logmean:species:parasite)
```

```
## fixed-effect model matrix is rank deficient so dropping 3 columns / coefficients
anova(fs_mod1, fs_no_int)
```

```
## Data: fs_data
## Models:
## fs_no_int: diff ~ logmean + species + parasite + (1 | year) + (1 | site) +
## fs_no_int:     logmean:species + logmean:parasite + species:parasite
## fs_mod1: diff ~ logmean + species + parasite + logmean:species + logmean:parasite +
## fs_mod1:     species:parasite + logmean:species:parasite + (1 | year) +
## fs_mod1:     (1 | site)
##           Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_no_int 28 632.96 769.55 -288.48   576.96
## fs_mod1   37 637.03 817.53 -281.51   563.03 13.929      9     0.1249
# No evidence for an interaction between species and parasite
fs_no_int2_year = update(fs_no_int_year, .~. - species:parasite)
anova(fs_mod1_year, fs_no_int2_year)
```

```
## Data: fs_data
## Models:
## fs_no_int2_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_no_int2_year:     site) + logmean:species + logmean:parasite
## fs_mod1_year: diff ~ logmean + species + parasite + logmean:species + logmean:parasite +
## fs_mod1_year:     species:parasite + logmean:species:parasite + (logmean |
## fs_mod1_year:     year) + (1 | site)
##                 Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_no_int2_year 21 622.37 724.81 -290.18   580.37
## fs_mod1_year    39 635.88 826.14 -278.94   557.88 22.483     18     0.2112
# Host effect on logmean.  Not much of an effect
fs_host_year = update(fs_no_int2_year, .~. - logmean:species)
anova(fs_host_year, fs_no_int2_year)
```

```
## Data: fs_data
## Models:
## fs_host_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_host_year:     site) + logmean:parasite
## fs_no_int2_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_no_int2_year:     site) + logmean:species + logmean:parasite
```

```
##                    Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_host_year    17 621.57 704.50 -293.79    587.57
## fs_no_int2_year 21 622.37 724.81 -290.18    580.37 7.2044      4     0.1255
```

```r
# Huge effect of host on intercept
fs_host2_year = update(fs_host_year, .~. - species)
anova(fs_host_year, fs_host2_year)
```

```
## Data: fs_data
## Models:
## fs_host2_year: diff ~ logmean + parasite + (logmean | year) + (1 | site) + logmean:parasite
## fs_host_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_host_year:     site) + logmean:parasite
##                  Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_host2_year 13 634.94 698.35 -304.47    608.94
## fs_host_year  17 621.57 704.50 -293.79    587.57 21.363      4  0.0002683
##
## fs_host2_year
## fs_host_year  ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Effect of parasite on logmean? Big effect
fs_para_year = update(fs_no_int2_year, .~. - logmean:parasite)
anova(fs_para_year, fs_no_int2_year)
```

```
## Data: fs_data
## Models:
## fs_para_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_para_year:     site) + logmean:species
## fs_no_int2_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_no_int2_year:     site) + logmean:species + logmean:parasite
##                    Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_para_year    18 642.65 730.46 -303.33    606.65
## fs_no_int2_year 21 622.37 724.81 -290.18    580.37 26.285      3  8.311e-06
##
## fs_para_year
## fs_no_int2_year ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Effect of parasite on intercept? Big effect
fs_para2_year = update(fs_para_year, .~. - parasite)
anova(fs_para_year, fs_para2_year)
```

```
## Data: fs_data
## Models:
## fs_para2_year: diff ~ logmean + species + (logmean | year) + (1 | site) + logmean:species
## fs_para_year: diff ~ logmean + species + parasite + (logmean | year) + (1 |
## fs_para_year:     site) + logmean:species
##                  Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## fs_para2_year 15 762.08 835.25 -366.04    732.08
## fs_para_year  18 642.65 730.46 -303.33    606.65 125.43      3   < 2.2e-16
##
## fs_para2_year
## fs_para_year  ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
# Best model with host and parasite identity
summary(fs_host_year)

## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + species + parasite + (logmean | year) + (1 |
##     site) + logmean:parasite
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    621.6    704.5   -293.8    587.6      954
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.2976 -0.6810 -0.0362  0.6120  2.8719
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  site     (Intercept) 0.007435 0.08623
##  year     (Intercept) 0.002112 0.04595
##           logmean     0.002361 0.04859  0.63
##  Residual             0.099724 0.31579
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             0.25174    0.05596   4.499
## logmean                -0.08931    0.05360  -1.666
## speciesPSRE             0.07892    0.03450   2.287
## speciesRACA             0.20040    0.06259   3.202
## speciesTAGR             0.21430    0.11064   1.937
## speciesTATO             0.18013    0.04455   4.043
## parasiteEchino         -0.13943    0.05077  -2.746
## parasiteGlobbie        -0.13865    0.05806  -2.388
## parasiteRib            -0.25478    0.05100  -4.996
## logmean:parasiteEchino -0.03174    0.05485  -0.579
## logmean:parasiteGlobbie -0.02204   0.07391  -0.298
## logmean:parasiteRib    -0.20035    0.05944  -3.371
##
## Correlation of Fixed Effects:
##            (Intr) logmen spPSRE spRACA spTAGR spTATO prstEc prstGl prstRb
## logmean    -0.403
## speciesPSRE -0.558  0.004
## speciesRACA -0.266 -0.001  0.474
## speciesTAGR -0.166  0.000  0.280  0.155
## speciesTATO -0.388  0.012  0.664  0.385  0.252
## parasitEchn -0.674  0.508  0.100  0.060  0.003 -0.029
## parasitGlbb -0.533  0.447 -0.014 -0.027 -0.003 -0.034  0.594
## parasiteRib -0.634  0.508  0.031 -0.022 -0.043 -0.086  0.698  0.598
## lgmn:prstEc  0.486 -0.856 -0.051 -0.070 -0.002  0.013 -0.693 -0.436 -0.506
## lgmn:prstGl  0.339 -0.641  0.010 -0.007  0.008  0.023 -0.378 -0.616 -0.379
## lgmn:prstRb  0.438 -0.798 -0.015 -0.041 -0.003 -0.025 -0.464 -0.406 -0.672
##            lgmn:E lgmn:G
```

```
## logmean
## speciesPSRE
## speciesRACA
## speciesTAGR
## speciesTATO
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl  0.626
## lgmn:prstRb  0.780  0.582
```

```r
rsquared.glmm(list(fs_host_year))
```

```
##    Class    Family    Link  Marginal Conditional      AIC
## 1 lmerMod gaussian identity 0.2006914   0.3033465 621.5725
```

```r
summary(update(fs_host_year, .~. - logmean))
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ species + parasite + (logmean | year) + (1 | site) + logmean:parasite
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    621.6    704.5   -293.8    587.6      954
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.2976 -0.6810 -0.0362  0.6120  2.8719
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  site     (Intercept) 0.007435 0.08623
##  year     (Intercept) 0.002112 0.04595
##           logmean     0.002361 0.04859  0.63
##  Residual             0.099724 0.31579
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                         Estimate Std. Error t value
## (Intercept)              0.25174    0.05596   4.499
## speciesPSRE              0.07892    0.03450   2.287
## speciesRACA              0.20040    0.06259   3.202
## speciesTAGR              0.21430    0.11064   1.937
## speciesTATO              0.18013    0.04455   4.043
## parasiteEchino          -0.13943    0.05077  -2.746
## parasiteGlobbie         -0.13865    0.05806  -2.388
## parasiteRib             -0.25478    0.05100  -4.996
## parasiteAlaria:logmean  -0.08931    0.05360  -1.666
## parasiteEchino:logmean  -0.12104    0.02910  -4.159
## parasiteGlobbie:logmean -0.11135    0.05709  -1.950
## parasiteRib:logmean     -0.28966    0.03637  -7.964
##
## Correlation of Fixed Effects:
```

```
##              (Intr) spPSRE spRACA spTAGR spTATO prstEc prstGl prstRb prstA:
## speciesPSRE -0.558
## speciesRACA -0.266  0.474
## speciesTAGR -0.166  0.280  0.155
## speciesTATO -0.388  0.664  0.385  0.252
## parasitEchn -0.674  0.100  0.060  0.003 -0.029
## parasitGlbb -0.533 -0.014 -0.027 -0.003 -0.034  0.594
## parasiteRib -0.634  0.031 -0.022 -0.043 -0.086  0.698  0.598
## prstAlr:lgm -0.403  0.004 -0.001  0.000  0.012  0.508  0.447  0.508
## prstEchn:lg  0.172 -0.090 -0.134 -0.004  0.047 -0.370  0.001 -0.019  0.228
## prstGlbb:lg  0.060  0.016 -0.010  0.009  0.041 -0.012 -0.378 -0.014  0.110
## prstRb:lgmn  0.121 -0.019 -0.069 -0.006 -0.024 -0.009 -0.005 -0.350  0.170
##           prstE: prstG:
## speciesPSRE
## speciesRACA
## speciesTAGR
## speciesTATO
## parasitEchn
## parasitGlbb
## parasiteRib
## prstAlr:lgm
## prstEchn:lg
## prstGlbb:lg  0.215
## prstRb:lgmn  0.338  0.169
```

No change when you include the random effect of year, other than a slightly better fitting model.

Populaton-level effects

```
fs_pop_mod_year = lmer(diff ~ logmean + resid_svlbyspp_sd +
                        resid_densitybyspp_sd +
                        logmean_density_sd +
                        logmean_svl_sd +
                        pondarea_ha_sd +
                        logmean:resid_svlbyspp_sd +
                        logmean:resid_densitybyspp_sd +
                        logmean:logmean_density_sd +
                        logmean:logmean_svl_sd +
                        logmean:pondarea_ha_sd +
                        parasite +
                        logmean:parasite +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_pop_mod_year)

## Single term deletions
##
## Model:
## diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_density_sd + logmean_svl_sd + pondarea_ha_sd + logmean:resid_svlbyspp_sd +
##     logmean:resid_densitybyspp_sd + logmean:logmean_density_sd +
##     logmean:logmean_svl_sd + logmean:pondarea_ha_sd + parasite +
##     logmean:parasite + (logmean | year) + (1 | site)
##                             Df    AIC
## <none>                         627.03
## logmean:resid_svlbyspp_sd    1 626.29
```

```
## logmean:resid_densitybyspp_sd  1 625.13
## logmean:logmean_density_sd      1 625.78
## logmean:logmean_svl_sd          1 625.99
## logmean:pondarea_ha_sd          1 625.45
## logmean:parasite                3 642.78
```

Again, none of the interactions with logmean seem very important. Let's go ahead and drop them.

```
fs_pop_mod2_year = lmer(diff ~ logmean + resid_svlbyspp_sd +
                        resid_densitybyspp_sd +
                        logmean_density_sd +
                        logmean_svl_sd +
                        pondarea_ha_sd +
                        parasite +
                        logmean:parasite +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)
drop1(fs_pop_mod2_year)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 1 negative
## eigenvalues

## Single term deletions
##
## Model:
## diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_density_sd + logmean_svl_sd + pondarea_ha_sd + parasite +
##     logmean:parasite + (logmean | year) + (1 | site)
##                        Df    AIC
## <none>                    620.60
## resid_svlbyspp_sd      1 626.62
## resid_densitybyspp_sd  1 622.30
## logmean_density_sd     1 618.71
## logmean_svl_sd         1 637.54
## pondarea_ha_sd         1 619.11
## logmean:parasite       3 636.40
```

Again, dropping density and pond area look like they improve the model. Some convergence issues with this model

```
fs_pop_mod3_year = lmer(diff ~ logmean + resid_svlbyspp_sd +
                        resid_densitybyspp_sd +
                        logmean_svl_sd +
                        parasite +
                        logmean:parasite +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)


drop1(fs_pop_mod3_year)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
```

```
##      logmean_svl_sd + parasite + logmean:parasite + (logmean |
##      year) + (1 | site)
##                          Df    AIC
## <none>                       617.36
## resid_svlbyspp_sd       1 623.21
## resid_densitybyspp_sd   1 619.02
## logmean_svl_sd          1 626.49
## logmean:parasite        3 633.14
```

summary(fs_pop_mod3_year)

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##      logmean_svl_sd + parasite + logmean:parasite + (logmean |
##      year) + (1 | site)
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    617.4    695.4   -292.7    585.4      955
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -4.3013 -0.6550 -0.0368  0.6053  3.0052
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  site     (Intercept) 0.004468 0.06684
##  year     (Intercept) 0.002236 0.04729
##           logmean     0.001937 0.04401  1.00
##  Residual             0.101497 0.31859
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                          Estimate Std. Error t value
## (Intercept)               0.32198    0.04622   6.966
## logmean                  -0.07383    0.05282  -1.398
## resid_svlbyspp_sd         0.02977    0.01060   2.809
## resid_densitybyspp_sd     0.02092    0.01089   1.922
## logmean_svl_sd            0.03784    0.01114   3.398
## parasiteEchino           -0.12366    0.05010  -2.468
## parasiteGlobbie          -0.11255    0.05807  -1.938
## parasiteRib              -0.23033    0.05050  -4.561
## logmean:parasiteEchino   -0.04794    0.05449  -0.880
## logmean:parasiteGlobbie  -0.05253    0.07371  -0.713
## logmean:parasiteRib      -0.20989    0.05928  -3.541
##
## Correlation of Fixed Effects:
##             (Intr) logmen rsd_s_ rsd_d_ lgmn__ prstEc prstGl prstRb lgmn:E
## logmean     -0.445
## rsd_svlbys_ -0.004  0.025
## rsd_dnstyb_ -0.038  0.017 -0.064
## lgmn_svl_sd  0.043  0.028 -0.017 -0.027
## parasitEchn -0.759  0.521  0.007  0.020 -0.006
## parasitGlbb -0.655  0.452  0.024  0.048 -0.003  0.601
## parasiteRib -0.758  0.518  0.020  0.015 -0.068  0.693  0.599
```

```
## lgmn:prstEc  0.551 -0.871 -0.026 -0.002 -0.051 -0.689 -0.438 -0.501
## lgmn:prstGl  0.413 -0.647 -0.036 -0.017 -0.016 -0.379 -0.615 -0.378  0.626
## lgmn:prstRb  0.511 -0.807 -0.040  0.010 -0.044 -0.468 -0.406 -0.678  0.783
##             lgmn:G
## logmean
## rsd_svlbys_
## rsd_dnstyb_
## lgmn_svl_sd
## parasitEchn
## parasitGlbb
## parasiteRib
## lgmn:prstEc
## lgmn:prstGl
## lgmn:prstRb  0.581
```

```r
rsquared.glmm(list(fs_pop_mod3_year))
```

```
##     Class   Family    Link  Marginal Conditional      AIC
## 1 lmerMod gaussian identity 0.2017467   0.2890429 617.3632
```

Parasite-specific variables

```r
fs_para_mod_year = lmer(diff ~ logmean +
                        species +
                        parasitemass_sd +
                        cerc_shedding_sd +
                        infect_snail_dens_sd +
                        infect_snail_dens_sd:logmean +
                        parasitemass_sd:logmean +
                        cerc_shedding_sd:logmean +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)
```

```r
drop1(fs_para_mod_year)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + infect_snail_dens_sd:logmean + parasitemass_sd:logmean +
##     cerc_shedding_sd:logmean + (logmean | year) + (1 | site)
##                                Df    AIC
## <none>                            621.57
## species                         4 634.94
## logmean:infect_snail_dens_sd    1 621.99
## logmean:parasitemass_sd         1 625.04
## logmean:cerc_shedding_sd        1 620.45
```

```r
fs_para_mod1_year = lmer(diff ~ logmean +
                         species +
                         parasitemass_sd +
                         cerc_shedding_sd +
                         infect_snail_dens_sd +
                         infect_snail_dens_sd:logmean +
                         parasitemass_sd:logmean +
                         (logmean | year) + (1 | site), data=fs_data, REML=F)
```

```
drop1(fs_para_mod1)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + infect_snail_dens_sd:logmean + parasitemass_sd:logmean +
##     (1 | year) + (1 | site)
##                            Df    AIC
## <none>                        623.39
## species                     4 636.08
## cerc_shedding_sd            1 638.02
## logmean:infect_snail_dens_sd  1 631.22
## logmean:parasitemass_sd     1 626.05
```

Same results as before when year was just an intercept effect. Overall, the model is slightly better.

```
fs_hp_mod_vir_year = lmer(diff ~ logmean + oddsratio_sd +
                          logmean:oddsratio_sd +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)


fs_hp_mod_comp_year = lmer(diff ~ logmean + infectionsuccess_sd +
                          logmean:infectionsuccess_sd +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)
```

```
anova(fs_hp_mod_vir_year, fs_hp_mod_comp_year)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir_year: diff ~ logmean + oddsratio_sd + logmean:oddsratio_sd + (logmean |
## fs_hp_mod_vir_year:     year) + (1 | site)
## fs_hp_mod_comp_year: diff ~ logmean + infectionsuccess_sd + logmean:infectionsuccess_sd +
## fs_hp_mod_comp_year:     (logmean | year) + (1 | site)
##                     Df    AIC    BIC  logLik deviance Chisq Chi Df
## fs_hp_mod_vir_year   9 659.75 703.66 -320.88   641.75
## fs_hp_mod_comp_year  9 701.24 745.15 -341.62   683.24     0      0
##                     Pr(>Chisq)
## fs_hp_mod_vir_year
## fs_hp_mod_comp_year          1
```

Similarly, virulence is a much stronger predictor than competence, even when year has a slope effect as well.

```
fs_hp_mod_vir1_year = lmer(diff ~ logmean + oddsratio_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          logmean:oddsratio_sd +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)


fs_hp_mod_comp1_year = lmer(diff ~ logmean + infectionsuccess_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          logmean:infectionsuccess_sd +
                        (logmean | year) + (1 | site), data=fs_data, REML=F)
```

```
anova(fs_hp_mod_vir1_year, fs_hp_mod_comp1_year)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir1_year: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir1_year:     logmean:oddsratio_sd + (logmean | year) + (1 | site)
## fs_hp_mod_comp1_year: diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_s
## fs_hp_mod_comp1_year:     logmean:infectionsuccess_sd + (logmean | year) + (1 | site)
##                    Df    AIC    BIC  logLik deviance Chisq Chi Df
## fs_hp_mod_vir1_year  11 651.84 705.50 -314.92    629.84
## fs_hp_mod_comp1_year 11 693.99 747.65 -336.00    671.99     0      0
##                    Pr(>Chisq)
## fs_hp_mod_vir1_year
## fs_hp_mod_comp1_year          1
```

Try adding in parasite specific variables.

```
fs_hp_mod_vir2_year = lmer(diff ~ logmean + oddsratio_sd +
                           resid_svlbyspp_sd +
                           resid_densitybyspp_sd +
                           cerc_shedding_sd +
                           logmean:oddsratio_sd +
                       (logmean | year) + (1 | site), data=fs_data, REML=F)


anova(fs_hp_mod_vir2_year, fs_hp_mod_vir1_year)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir1_year: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir1_year:     logmean:oddsratio_sd + (logmean | year) + (1 | site)
## fs_hp_mod_vir2_year: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir2_year:     cerc_shedding_sd + logmean:oddsratio_sd + (logmean | year) +
## fs_hp_mod_vir2_year:     (1 | site)
##                    Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_hp_mod_vir1_year  11 651.84 705.50 -314.92    629.84
## fs_hp_mod_vir2_year  12 639.22 697.76 -307.61    615.22 14.617      1
##                    Pr(>Chisq)
## fs_hp_mod_vir1_year
## fs_hp_mod_vir2_year  0.0001317 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
fs_hp_mod_vir3_year = lmer(diff ~ logmean + oddsratio_sd +
                           resid_svlbyspp_sd +
                           resid_densitybyspp_sd +
                           cerc_shedding_sd +
                           parasitemass_sd +
                           logmean:oddsratio_sd +
                           (logmean | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_hp_mod_vir3_year)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + logmean:oddsratio_sd +
##     (logmean | year) + (1 | site)
```

```
##                       Df    AIC
## <none>                   631.89
## resid_svlbyspp_sd      1 637.28
## resid_densitybyspp_sd  1 633.54
## cerc_shedding_sd       1 653.09
## parasitemass_sd        1 639.22
## logmean:oddsratio_sd   1 640.37
```

```r
# Drop the interaction with parasitemass_sd

fs_hp_mod_vir4_year = lmer(diff ~ logmean + oddsratio_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          cerc_shedding_sd +
                          parasitemass_sd +
                          infect_snail_dens_sd +
                          logmean:oddsratio_sd +
                          (logmean | year) + (1 | site), data=fs_data, REML=F)

anova(fs_hp_mod_vir4, fs_hp_mod_vir4_year)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_vir4: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir4:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_vir4:     logmean:oddsratio_sd + (1 | year) + (1 | site)
## fs_hp_mod_vir4_year: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir4_year:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_vir4_year:     logmean:oddsratio_sd + (logmean | year) + (1 | site)
##                     Df    AIC    BIC  logLik deviance  Chisq Chi Df
## fs_hp_mod_vir4      12 630.99 689.53 -303.50   606.99
## fs_hp_mod_vir4_year 14 629.48 697.78 -300.74   601.48 5.5097      2
##                     Pr(>Chisq)
## fs_hp_mod_vir4
## fs_hp_mod_vir4_year    0.06362 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Same thing for competence

```r
fs_hp_mod_comp2_year = lmer(diff ~ logmean + infectionsuccess_sd +
                          resid_svlbyspp_sd +
                          resid_densitybyspp_sd +
                          cerc_shedding_sd +
                          logmean:infectionsuccess_sd +
                          (logmean | year) + (1 | site), data=fs_data, REML=F)
drop1(fs_hp_mod_comp2_year)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + logmean:infectionsuccess_sd + (logmean |
##     year) + (1 | site)
##                       Df    AIC
## <none>                   637.36
```

```
## resid_svlbyspp_sd          1 642.36
## resid_densitybyspp_sd      1 638.62
## cerc_shedding_sd           1 693.99
## logmean:infectionsuccess_sd  1 650.31
```

```r
fs_hp_mod_comp3_year = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            infect_snail_dens_sd +
                            parasitemass_sd +
                            logmean:infect_snail_dens_sd +
                            logmean:infectionsuccess_sd +
                            (logmean | year) + (1 | site), data=fs_data, REML=F)

drop1(fs_hp_mod_comp3_year)
```

```
## Single term deletions
##
## Model:
## diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + infect_snail_dens_sd + parasitemass_sd +
##     logmean:infect_snail_dens_sd + logmean:infectionsuccess_sd +
##     (logmean | year) + (1 | site)
##                                Df    AIC
## <none>                            624.25
## resid_svlbyspp_sd             1 629.92
## resid_densitybyspp_sd         1 625.75
## cerc_shedding_sd              1 636.50
## parasitemass_sd               1 623.73
## logmean:infect_snail_dens_sd  1 629.18
## logmean:infectionsuccess_sd   1 627.98
```

```r
fs_hp_mod_comp4_year = lmer(diff ~ logmean + infectionsuccess_sd +
                            resid_svlbyspp_sd +
                            resid_densitybyspp_sd +
                            cerc_shedding_sd +
                            parasitemass_sd +
                            infect_snail_dens_sd +
                            logmean:infectionsuccess_sd +
                            (logmean | year) + (1 | site), data=fs_data, REML=F)

summary(fs_hp_mod_comp4_year)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     logmean:infectionsuccess_sd + (logmean | year) + (1 | site)
##    Data: fs_data
##
##      AIC      BIC   logLik deviance df.resid
##    629.2    697.5   -300.6    601.2      957
##
## Scaled residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -3.6595 -0.6537 -0.0390  0.6251  3.0108
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  site     (Intercept) 0.006634 0.08145
##  year     (Intercept) 0.002869 0.05356
##           logmean     0.002281 0.04776  0.71
##  Residual             0.101594 0.31874
## Number of obs: 971, groups:  site, 173; year, 7
##
## Fixed effects:
##                            Estimate Std. Error t value
## (Intercept)                 0.17799    0.02770   6.425
## logmean                    -0.16225    0.02443  -6.641
## infectionsuccess_sd         0.01318    0.02100   0.628
## resid_svlbyspp_sd           0.02903    0.01069   2.715
## resid_densitybyspp_sd       0.02155    0.01106   1.948
## cerc_shedding_sd            0.05833    0.01472   3.961
## parasitemass_sd            -0.02742    0.01984  -1.382
## infect_snail_dens_sd       -0.04479    0.01665  -2.690
## logmean:infectionsuccess_sd -0.06330    0.01661  -3.812
##
## Correlation of Fixed Effects:
##             (Intr) logmen infct_ rsd_s_ rsd_d_ crc_s_ prstm_ inf___
## logmean      0.075
## infctnsccs_  0.003 -0.069
## rsd_svlbys_  0.019 -0.012  0.012
## rsd_dnstyb_ -0.025  0.036  0.019 -0.065
## crc_shddng_  0.058 -0.068 -0.126 -0.004 -0.047
## parstmss_sd -0.133  0.189 -0.543  0.001 -0.008 -0.258
## infct_snl__  0.097 -0.127 -0.213 -0.016 -0.034  0.690 -0.289
## lgmn:nfctn_  0.042  0.053 -0.472 -0.010  0.009  0.108 -0.174  0.115
```

```r
anova(fs_hp_mod_comp4_year, fs_hp_mod_vir4_year)
```

```
## Data: fs_data
## Models:
## fs_hp_mod_comp4_year: diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_s
## fs_hp_mod_comp4_year:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_comp4_year:     logmean:infectionsuccess_sd + (logmean | year) + (1 | site)
## fs_hp_mod_vir4_year: diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
## fs_hp_mod_vir4_year:     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
## fs_hp_mod_vir4_year:     logmean:oddsratio_sd + (logmean | year) + (1 | site)
##                       Df    AIC    BIC  logLik deviance Chisq Chi Df
## fs_hp_mod_comp4_year  14 629.18 697.47 -300.59   601.18
## fs_hp_mod_vir4_year   14 629.48 697.78 -300.74   601.48     0      0
##                       Pr(>Chisq)
## fs_hp_mod_comp4_year
## fs_hp_mod_vir4_year            1
```

Manuscript results

Extracting some of the test statistics used in the analysis

Main text: Delta AIC for model without host and parasite

```
red_mod = update(fs_host, .~. - species - parasite - logmean:parasite)
AIC(red_mod) - AIC(fs_host)
```

```
## [1] 136.2468
```

SI Table 2: Host and parasite models

```
aic_vals_tab2 = AIC(fs_mod1, fs_no_int, fs_no_int2, fs_host, fs_host_year, fs_host2, fs_para, fs_para2)
```

```
# Get delta AIC
aic_vals_tab2$delta = round(aic_vals_tab2$AIC, digits=2) -
                          round(min(aic_vals_tab2$AIC), digits=2)
aic_vals_tab2[order(aic_vals_tab2$delta),]
```

```
##                df      AIC  delta
## fs_host_year 17 621.5725   0.00
## fs_no_int2   19 623.2707   1.70
## fs_host      15 623.7835   2.21
## fs_no_int    28 632.9582  11.39
## fs_host2     11 636.3774  14.81
## fs_mod1      37 637.0293  15.46
## fs_para      16 646.4932  24.92
## fs_para2     13 769.0953 147.53
```

SI Table 3: Quantitative host and parasite identity models

```
aic_vals_tab3 = AIC(fs_pop_mod, fs_pop_mod2, fs_pop_mod3, fs_pop_mod3_year, fs_hl_mod, fs_hl_mod1, fs_hl
```

```
aic_vals_tab3$delta = round(aic_vals_tab3$AIC, digits=2) -
                          round(min(aic_vals_tab3$AIC), digits=2)
aic_vals_tab3[order(aic_vals_tab3$delta),]
```

```
##                   df      AIC delta
## fs_pop_mod3_year 16 617.3632  0.00
## fs_pop_mod3      14 619.7783  2.42
## fs_hl_mod3       13 620.0663  2.71
## fs_pop_mod2      16 623.0481  5.69
## fs_hl_mod        19 623.2707  5.91
## fs_hl_mod1       15 623.7835  6.42
## fs_pop_mod       21 629.2237 11.86
```

SI Table 4: Quantitative parasite and host

```
aic_vals_tab4 = AIC(fs_para_mod, fs_para_mod1, fs_para_mod1_year)
```

```
aic_vals_tab4$delta = round(aic_vals_tab4$AIC, digits=2) -
                          round(min(aic_vals_tab4$AIC), digits=2)
aic_vals_tab4[order(aic_vals_tab4$delta), ]
```

```
##                    df      AIC delta
## fs_para_mod1_year 16 620.4479  0.00
## fs_para_mod1      14 623.3850  2.94
## fs_para_mod       15 623.7835  3.33
```

SI Table 5: Host by parasite interactions

```
aic_vals_tab5 = AIC(fs_hp_mod, fs_hp_mod_vir, fs_hp_mod_comp,
                    fs_hp_mod_vir1, fs_hp_mod_comp1, fs_hp_mod_vir4,
                    fs_hp_mod_comp4, fs_hp_mod_vir4_year, fs_hp_mod_comp4_year)

aic_vals_tab5$delta = round(aic_vals_tab5$AIC, digits=2) -
                        round(min(aic_vals_tab5$AIC), digits=2)
aic_vals_tab5[order(aic_vals_tab5$delta), ]
```

```
##                       df      AIC delta
## fs_hp_mod_comp4_year 14 629.1776  0.00
## fs_hp_mod_vir4_year  14 629.4833  0.30
## fs_hp_mod_vir4       12 630.9930  1.81
## fs_hp_mod_comp4      12 631.5744  2.39
## fs_hp_mod            37 637.0293  7.85
## fs_hp_mod_vir1        9 655.5877 26.41
## fs_hp_mod_vir         7 663.4712 34.29
## fs_hp_mod_comp1       9 699.0414 69.86
## fs_hp_mod_comp        7 706.2098 77.03
```

Manuscript and Table 1 results

Helpful functions and packages for performing a parameteric bootstrap on the models

```
library(pbkrtest)
```

```
parametric_bootstrap = function(best_model, data, response_name,
                                nsims=2000){
    # Calculates 95% CI for model parameters based on parametric bootstrap
    # Returns a matrix with the lower bound (2.5%) and upper bound (97.5%) of
    # a 95% CI around each parameter in the model.  Also returns the median
    # estimate (50%).  The median should be approximately the same as the
    # summary(best_model)$coefficients[, "Estimate"], though not exactly the
    # same.

    # best_model: glmer/lmer model
    # data: data that you used to fit the model
    # response_name: name of the response variable, i.e. "logze"

    bootstrap_coefs = function(x){

        data[[response_name]] = unlist(simulate(best_model))
        tfit <- lmer(formula(best_model), REML=F, data=data)
        return(summary(tfit)$coefficient[, "Estimate"])

    }

    # Takes a few minutes to run the parameteric bootstrap
    coefs = lapply(1:nsims, bootstrap_coefs)
    coefs = do.call(rbind, coefs)

    return(apply(coefs, 2, quantile, c(0.025, 0.5, 0.975)))

}
```

First analyze the host by parasite factor model

```
# Best model with host and parasite identity
hpi_mod_coefs = parametric_bootstrap(fs_host, fs_data, "diff", nsims=500)
hpi_mod_coefs_with_int = parametric_bootstrap(fs_no_int2, fs_data, "diff", nsims=500)

# Effect of host interaction with logmean
hpi_spp_int = PBmodcomp(fs_no_int2, update(fs_no_int2, .~. - logmean:species), nsim=500)

# Effect of host factor
hpi_spp = PBmodcomp(fs_host, update(fs_host, .~. - species), nsim=500)

# Effect of parasite factor
hpi_parasite = PBmodcomp(fs_host, update(fs_host, .~. - parasite), nsim=500)
hpi_parasite_int = PBmodcomp(fs_host, update(fs_host, .~. - logmean:parasite), nsim=500)
```

Analyze best model with continuous host predictors

```
hpop_mod_coefs = parametric_bootstrap(fs_pop_mod3, fs_data, "diff", nsims=500)
hpop_para = PBmodcomp(fs_pop_mod3, update(fs_pop_mod3, .~. - parasite), nsim=500)
hpop_para_int = PBmodcomp(fs_pop_mod3, update(fs_pop_mod3, .~. - logmean:parasite), nsim=500)
```

Analyze best model with contiunuous parasite predictors

```
p_mod_coefs = parametric_bootstrap(fs_para_mod1, fs_data, "diff", nsims=500)
pmod_spp = PBmodcomp(fs_para_mod1, update(fs_para_mod1, .~. - species), nsim=500)
```

Analyze best model with all continuous predictors

```
vir_mod_coefs = parametric_bootstrap(fs_hp_mod_vir4, fs_data, "diff", nsims=500)
comp_mod_coefs = parametric_bootstrap(fs_hp_mod_comp4, fs_data, "diff", nsims=500)
```

R^2 for the best fit models

```
rsquared.glmm(list(hp_mod=fs_host, host=fs_pop_mod3, para=fs_para_mod1, vir=fs_hp_mod_vir4, comp=fs_hp_m
```

```
##            Class    Family     Link  Marginal Conditional       AIC
## hp_mod lmerMod gaussian identity 0.2012654   0.2954914 623.7835
## host   lmerMod gaussian identity 0.2041820   0.2849656 619.7783
## para   lmerMod gaussian identity 0.1993003   0.2983687 623.3850
## vir    lmerMod gaussian identity 0.1900187   0.2842428 630.9930
## comp   lmerMod gaussian identity 0.1886728   0.2888301 631.5744
```

AICs for Table 1

```
aic_vals_tab1 = AIC(fs_no_int2, fs_pop_mod3, fs_para_mod1,
            fs_hp_mod_vir4, fs_hp_mod_comp4)

aic_vals_tab1$delta = round(aic_vals_tab1$AIC, digits=2) -
                   round(min(aic_vals_tab1$AIC), digits=2)
aic_vals_tab1
```

```
##                 df     AIC delta
## fs_no_int2      19 623.2707  3.49
## fs_pop_mod3     14 619.7783  0.00
## fs_para_mod1    14 623.3850  3.61
## fs_hp_mod_vir4  12 630.9930 11.21
## fs_hp_mod_comp4 12 631.5744 11.79
```

SI Table S6: Replicating Table 1 in main manuscript for models with logmean | year random

effects

While the (logmean | year) random effect leads to the best model, it is relatively unstable such that performing a parametric bootstrap leads to a number of convergence issues. Therefore, we use the Kenward-Roger approximate F-test to test the significance of the fixed effects in the models. Given the large sample sie of our data, i

Analyze the host by parasite factor model with year random effect

```
# Drop host factor
host_eff = KRmodcomp(fs_host_year, update(fs_host_year, .~. - species))
```

```
## Note: method with signature 'sparseMatrix#ANY' chosen for function 'kronecker',
##   target signature 'dgCMatrix#ngCMatrix'.
##   "ANY#sparseMatrix" would also be valid
```

```
host_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 6.60 sec.
## large : diff ~ logmean + species + parasite + (logmean | year) + (1 |
##      site) + logmean:parasite
## small : diff ~ logmean + parasite + (logmean | year) + (1 | site) + logmean:parasite
##           stat      ndf      ddf F.scaling   p.value
## Ftest   5.2232   4.0000 909.0834   0.99988 0.0003666 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Drop main effect of parasite
para_eff = KRmodcomp(fs_host_year, update(fs_host_year, .~. - parasite))
para_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.89 sec.
## large : diff ~ logmean + species + parasite + (logmean | year) + (1 |
##      site) + logmean:parasite
## small : diff ~ logmean + species + (logmean | year) + (1 | site) + logmean:parasite
##           stat      ndf      ddf F.scaling   p.value
## Ftest   8.6836   3.0000 941.6804   0.99999 1.097e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Drop interactive effect of parasite
para_int_eff = KRmodcomp(fs_host_year, update(fs_host_year, .~. - logmean:parasite))
para_int_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.69 sec.
## large : diff ~ logmean + species + parasite + (logmean | year) + (1 |
##      site) + logmean:parasite
## small : diff ~ logmean + species + parasite + (logmean | year) + (1 |
##      site)
##           stat     ndf      ddf F.scaling  p.value
## Ftest   7.491   3.000 952.503   0.99999 5.86e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Test logmean effect using normal approximation...OK because sample size is huge
pm = 1.96 * summary(fs_host_year)$coefficients["logmean", "Std. Error"]
est =  summary(fs_host_year)$coefficients["logmean", "Estimate"]
print(c(est - pm, est + pm))
```

```
## [1] -0.19436343  0.01575276
```

Analyze model with quantitative host predictor

```r
fixef(fs_pop_mod3_year)
```

```
##           (Intercept)                  logmean        resid_svlbyspp_sd
##            0.32198089               -0.07383250               0.02976998
##   resid_densitybyspp_sd              logmean_svl_sd            parasiteEchino
##            0.02092291                0.03783927              -0.12365686
##         parasiteGlobbie              parasiteRib  logmean:parasiteEchino
##           -0.11255156               -0.23032687              -0.04794351
## logmean:parasiteGlobbie     logmean:parasiteRib
##           -0.05252813               -0.20989277
```

```r
# Body size effect
body_size_eff = KRmodcomp(fs_pop_mod3_year,
                          update(fs_pop_mod3_year, .~. - resid_svlbyspp_sd))
body_size_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 6.08 sec.
## large : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + (logmean | year) + (1 | site) +
##     logmean:parasite
## small : diff ~ logmean + resid_densitybyspp_sd + logmean_svl_sd + parasite +
##     (logmean | year) + (1 | site) + logmean:parasite
##          stat       ndf       ddf F.scaling  p.value
## Ftest  7.6893    1.0000  940.1482         1 0.005665 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Spatial heterogeneity effect
spatial_eff = KRmodcomp(fs_pop_mod3_year,
                        update(fs_pop_mod3_year, .~. - resid_densitybyspp_sd))
spatial_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 6.01 sec.
## large : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + (logmean | year) + (1 | site) +
##     logmean:parasite
## small : diff ~ logmean + resid_svlbyspp_sd + logmean_svl_sd + parasite +
##     (logmean | year) + (1 | site) + logmean:parasite
##          stat       ndf       ddf F.scaling p.value
## Ftest  3.5036    1.0000  781.7021         1 0.06161 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Mean body size effect
mean_body_eff = KRmodcomp(fs_pop_mod3_year,
                          update(fs_pop_mod3_year, .~. - logmean_svl_sd))
mean_body_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 6.01 sec.
## large : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + (logmean | year) + (1 | site) +
##     logmean:parasite
## small : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     parasite + (logmean | year) + (1 | site) + logmean:parasite
```

```
##          stat    ndf     ddf F.scaling    p.value
## Ftest  11.035   1.000 760.445         1 0.0009368 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
```r
# Parasite main effect
para_eff_mod3_year = KRmodcomp(fs_pop_mod3_year,
                               update(fs_pop_mod3_year, .~. - parasite))
para_eff_mod3_year
```
```
## F-test with Kenward-Roger approximation; computing time: 6.02 sec.
## large : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + (logmean | year) + (1 | site) +
##     logmean:parasite
## small : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + (logmean | year) + (1 | site) + logmean:parasite
##          stat    ndf     ddf F.scaling  p.value
## Ftest  7.3912  3.0000 943.4278  0.99999 6.75e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
```r
# Parasite int effect
para_int_mod3_year = KRmodcomp(fs_pop_mod3_year,
                               update(fs_pop_mod3_year, .~. - logmean:parasite))
para_int_mod3_year
```
```
## F-test with Kenward-Roger approximation; computing time: 6.25 sec.
## large : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + (logmean | year) + (1 | site) +
##     logmean:parasite
## small : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     logmean_svl_sd + parasite + (logmean | year) + (1 | site)
##          stat   ndf     ddf F.scaling  p.value
## Ftest   7.157  3.000 950.868  0.99999 9.37e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
```r
# Normal approximation of logmean coefficient
pm_mod3_year = 1.96 * summary(fs_pop_mod3_year)$coefficients["logmean", "Std. Error"]
est_mod3_year =  summary(fs_pop_mod3_year)$coefficients["logmean", "Estimate"]
print(c(est_mod3_year - pm_mod3_year, est_mod3_year + pm_mod3_year))
```
```
## [1] -0.17735272  0.02968771
```
```r
est_mod3_year
```
```
## [1] -0.0738325
```

Analyze model with quantitative parasite predictors

```r
# Host effect
host_eff_para_mod = KRmodcomp(fs_para_mod1_year,
                              update(fs_para_mod1_year, .~. - species))
host_eff_para_mod
```
```
## F-test with Kenward-Roger approximation; computing time: 6.00 sec.
## large : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
```

```
##      logmean:parasitemass_sd
## small : diff ~ logmean + parasitemass_sd + cerc_shedding_sd + infect_snail_dens_sd +
##      (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
##           stat      ndf       ddf F.scaling   p.value
## Ftest    5.2676   4.0000  913.5597   0.99989 0.0003385 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Parasite mass effect
para_mass_eff = KRmodcomp(fs_para_mod1_year,
                          update(fs_para_mod1_year, .~. - parasitemass_sd))
para_mass_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 6.00 sec.
## large : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##      infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
## small : diff ~ logmean + species + cerc_shedding_sd + infect_snail_dens_sd +
##      (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
##           stat      ndf       ddf F.scaling p.value
## Ftest    1.8177   1.0000  951.6261         1  0.1779
```

```
# Cercaria effect
cerc_eff = KRmodcomp(fs_para_mod1_year,
                     update(fs_para_mod1_year, .~. - cerc_shedding_sd))
cerc_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.90 sec.
## large : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##      infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
## small : diff ~ logmean + species + parasitemass_sd + infect_snail_dens_sd +
##      (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
##           stat      ndf       ddf F.scaling   p.value
## Ftest   17.362   1.000  944.495         1 3.372e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Infected snail density
inf_eff = KRmodcomp(fs_para_mod1_year,
                    update(fs_para_mod1_year, .~. - infect_snail_dens_sd))
inf_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.82 sec.
## large : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##      infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
## small : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##      (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##      logmean:parasitemass_sd
##           stat      ndf       ddf F.scaling p.value
## Ftest    1.262   1.000  945.692         1  0.2616
```

```
# Infected snail int density
inf_int_eff = KRmodcomp(fs_para_mod1_year,
                        update(fs_para_mod1_year, .~. - logmean:infect_snail_dens_sd))
inf_int_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.82 sec.
## large : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##     logmean:parasitemass_sd
## small : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:parasitemass_sd
##          stat      ndf       ddf F.scaling  p.value
## Ftest  8.9014   1.0000 954.0201         1 0.002922 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Paraiste mass int effect
para_mass_int_eff = KRmodcomp(fs_para_mod1_year,
                              update(fs_para_mod1_year, .~. - logmean:parasitemass_sd))
para_mass_int_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.90 sec.
## large : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd +
##     logmean:parasitemass_sd
## small : diff ~ logmean + species + parasitemass_sd + cerc_shedding_sd +
##     infect_snail_dens_sd + (logmean | year) + (1 | site) + logmean:infect_snail_dens_sd
##          stat      ndf       ddf F.scaling p.value
## Ftest  4.6162   1.0000 954.0340         1 0.03192 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Normal approximation to the logmean
pm_para_mod = 1.96 * summary(fs_para_mod1_year)$coefficients["logmean", "Std. Error"]
est_para_mod =  summary(fs_para_mod1_year)$coefficients["logmean", "Estimate"]
print(c(est_para_mod - pm_para_mod, est_para_mod + pm_para_mod))
```

```
## [1] -0.2191174 -0.1185161
```

```
est_para_mod
```

```
## [1] -0.1688167
```

Quantitative host and parasite with virulence

```
# Host body size effect
host_bodysize_eff = KRmodcomp(fs_hp_mod_vir4_year,
                              update(fs_hp_mod_vir4_year, .~. - resid_svlbyspp_sd))
host_bodysize_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.82 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + oddsratio_sd + resid_densitybyspp_sd + cerc_shedding_sd +
##     parasitemass_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:oddsratio_sd
```

```
##           stat      ndf      ddf F.scaling  p.value
## Ftest   7.4621   1.0000 946.9326         1 0.006419 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Host density effect
host_dens_eff_vir = KRmodcomp(fs_hp_mod_vir4_year,
                              update(fs_hp_mod_vir4_year, .~. - resid_densitybyspp_sd))
host_dens_eff_vir
```

```
## F-test with Kenward-Roger approximation; computing time: 5.75 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + cerc_shedding_sd +
##     parasitemass_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:oddsratio_sd
##           stat      ndf      ddf F.scaling p.value
## Ftest   3.7499   1.0000 817.5182         1 0.05316 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Cercaia eff
cerc_eff_vir = KRmodcomp(fs_hp_mod_vir4_year,
                         update(fs_hp_mod_vir4_year, .~. - cerc_shedding_sd))
cerc_eff_vir
```

```
## F-test with Kenward-Roger approximation; computing time: 5.92 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     parasitemass_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:oddsratio_sd
##          stat     ndf      ddf F.scaling  p.value
## Ftest  11.297   1.000 953.043         1 0.000807 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Parasite mass effect
para_mass_eff_vir = KRmodcomp(fs_hp_mod_vir4_year,
                              update(fs_hp_mod_vir4_year, .~. - parasitemass_sd))
para_mass_eff_vir
```

```
## F-test with Kenward-Roger approximation; computing time: 5.83 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:oddsratio_sd
##          stat     ndf      ddf F.scaling p.value
## Ftest   5.562   1.000 946.918         1 0.01856 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Infected snail density effect
inf_eff_vir = KRmodcomp(fs_hp_mod_vir4_year,
                        update(fs_hp_mod_vir4_year, .~. - infect_snail_dens_sd))
inf_eff_vir
```

```
## F-test with Kenward-Roger approximation; computing time: 5.93 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + (logmean | year) + (1 |
##     site) + logmean:oddsratio_sd
##           stat      ndf      ddf F.scaling p.value
## Ftest   4.4766   1.0000 942.1261         1 0.03462 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Virulence main effect
vir_eff = KRmodcomp(fs_hp_mod_vir4_year,
                    update(fs_hp_mod_vir4_year, .~. - oddsratio_sd))
vir_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.97 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
##           stat      ndf      ddf F.scaling p.value
## Ftest   0.3285   1.0000 934.3772         1  0.5667
```

```r
# Virulence interaction effect
vir_int_eff = KRmodcomp(fs_hp_mod_vir4_year,
                        update(fs_hp_mod_vir4_year, .~. - logmean:oddsratio_sd))
vir_int_eff
```

```
## F-test with Kenward-Roger approximation; computing time: 5.82 sec.
## large : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:oddsratio_sd
## small : diff ~ logmean + oddsratio_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site)
##           stat    ndf     ddf F.scaling p.value
## Ftest   12.20   1.00  947.96         1   5e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
pm_vir = 1.96 * summary(fs_hp_mod_vir4_year)$coefficients["logmean", "Std. Error"]
est_vir =  summary(fs_hp_mod_vir4_year)$coefficients["logmean", "Estimate"]
print(c(est_vir - pm_vir, est_vir + pm_vir))
```

```
## [1] -0.2157775 -0.1241927
```

```r
est_vir
```

```
## [1] -0.1699851
```

Quantitative host and parasite with competence

```r
# Host body size effect
host_bodysize_eff_comp = KRmodcomp(fs_hp_mod_comp4_year,
                                   update(fs_hp_mod_comp4_year, .~. - resid_svlbyspp_sd))
host_bodysize_eff_comp
```

```
## F-test with Kenward-Roger approximation; computing time: 5.65 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + infectionsuccess_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
##           stat       ndf       ddf F.scaling  p.value
## Ftest   7.2534    1.0000 947.7756         1 0.007202 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Host density effect
host_dens_eff_comp = KRmodcomp(fs_hp_mod_comp4_year,
                               update(fs_hp_mod_comp4_year, .~. - resid_densitybyspp_sd))
host_dens_eff_comp
```

```
## F-test with Kenward-Roger approximation; computing time: 5.69 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + cerc_shedding_sd +
##     parasitemass_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:infectionsuccess_sd
##           stat       ndf       ddf F.scaling p.value
## Ftest   3.6418    1.0000 827.8124         1 0.05669 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Cercaia eff
cerc_eff_comp = KRmodcomp(fs_hp_mod_comp4_year,
                          update(fs_hp_mod_comp4_year, .~. - cerc_shedding_sd))
cerc_eff_comp
```

```
## F-test with Kenward-Roger approximation; computing time: 5.85 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     parasitemass_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:infectionsuccess_sd
##          stat      ndf     ddf F.scaling   p.value
## Ftest   15.488    1.000 949.546         1 8.909e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Parasite mass effect
para_mass_eff_comp = KRmodcomp(fs_hp_mod_comp4_year,
```

```
                                    update(fs_hp_mod_comp4_year, .~. - parasitemass_sd))
para_mass_eff_comp

## F-test with Kenward-Roger approximation; computing time: 5.59 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + infect_snail_dens_sd + (logmean | year) +
##     (1 | site) + logmean:infectionsuccess_sd
##          stat      ndf        ddf F.scaling p.value
## Ftest  1.8433   1.0000 940.5469          1  0.1749
```
Infected snail density effect
```
inf_eff_comp = KRmodcomp(fs_hp_mod_comp4_year,
                         update(fs_hp_mod_comp4_year, .~. - infect_snail_dens_sd))
inf_eff_comp

## F-test with Kenward-Roger approximation; computing time: 5.73 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + (logmean | year) + (1 |
##     site) + logmean:infectionsuccess_sd
##          stat      ndf        ddf F.scaling  p.value
## Ftest  7.1471   1.0000 948.6078          1 0.007638 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
Competence main effect
```
comp_eff = KRmodcomp(fs_hp_mod_comp4_year,
                     update(fs_hp_mod_comp4_year, .~. - infectionsuccess_sd))
comp_eff

## F-test with Kenward-Roger approximation; computing time: 5.87 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
##          stat      ndf        ddf F.scaling p.value
## Ftest  0.3727   1.0000 941.7308          1  0.5417
```
Virulence interaction effect
```
comp_int_eff = KRmodcomp(fs_hp_mod_comp4_year,
                         update(fs_hp_mod_comp4_year, .~. - logmean:infectionsuccess_sd))
comp_int_eff

## F-test with Kenward-Roger approximation; computing time: 6.16 sec.
## large : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
##     (logmean | year) + (1 | site) + logmean:infectionsuccess_sd
## small : diff ~ logmean + infectionsuccess_sd + resid_svlbyspp_sd + resid_densitybyspp_sd +
##     cerc_shedding_sd + parasitemass_sd + infect_snail_dens_sd +
```

```
##     (logmean | year) + (1 | site)
##          stat     ndf     ddf F.scaling    p.value
## Ftest  14.251   1.000 957.063           1 0.0001699 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
pm_comp = 1.96 * summary(fs_hp_mod_comp4_year)$coefficients["logmean", "Std. Error"]
est_comp =  summary(fs_hp_mod_comp4_year)$coefficients["logmean", "Estimate"]
print(c(est_comp - pm_comp, est_comp + pm_comp))
```

```
## [1] -0.2101345 -0.1143598
```

```
est_comp
```

```
## [1] -0.1622472
```

AIC comparison of the five models (logmean | year) + (1 | site) models for Table 6

```
aic_vals_year = AIC(fs_host_year, fs_pop_mod3_year, fs_para_mod1_year,
            fs_hp_mod_vir4_year, fs_hp_mod_comp4_year)

aic_vals_year$delta = round(aic_vals_year$AIC, digits=2) -
                    round(min(aic_vals_year$AIC), digits=2)
aic_vals_year
```

```
##                      df      AIC delta
## fs_host_year         17 621.5725  4.21
## fs_pop_mod3_year     16 617.3632  0.00
## fs_para_mod1_year    16 620.4479  3.09
## fs_hp_mod_vir4_year  14 629.4833 12.12
## fs_hp_mod_comp4_year 14 629.1776 11.82
```