Supplementary Material

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2018-11-01

Evaluating assumption of multivariate normality

We used graphical checks to evaluate whether our transformations of trait values resulted in a multivariate normal distribution. Figure S1 shows that our transformations resulted in approximately normal distributions for each phenotypic trait. Note also that in the multivariate quantile-quantile (Q-Q) plot, most points fall along the expected line (fig. S2), suggesting that our transformations provide a reasonable approximation of a multivariate normal distribution.
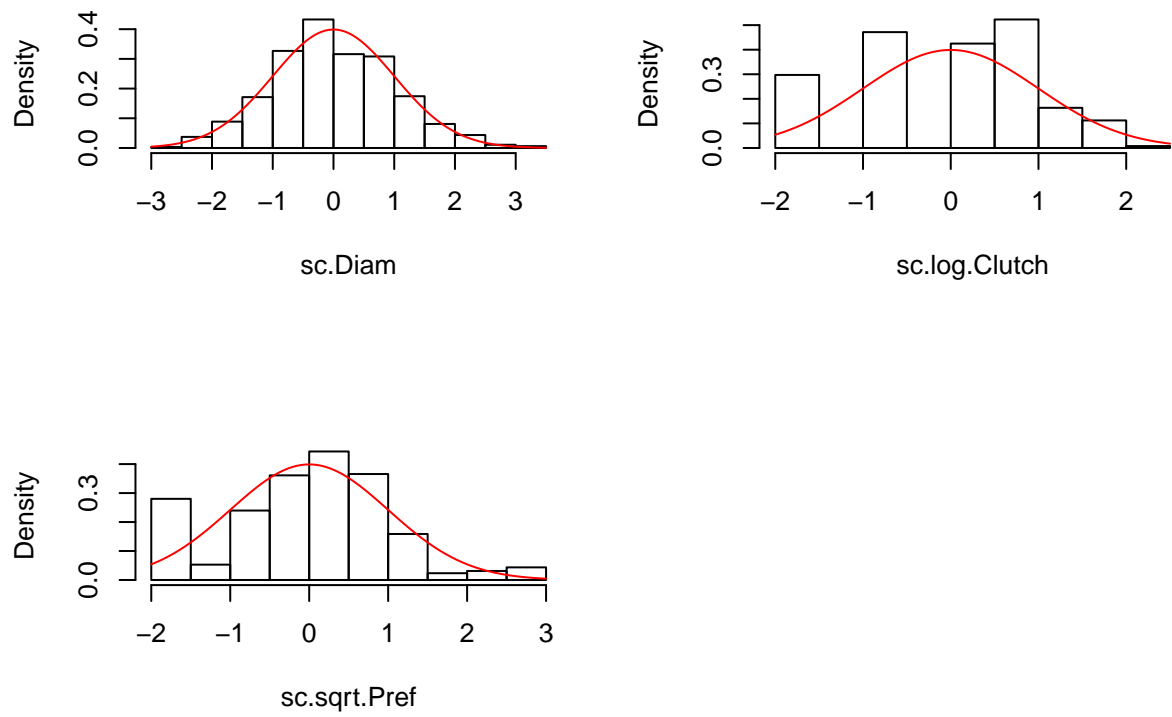
Figure 1: Histograms of each phenotypic trait after transformation. The red line illustrates a normal distribution.
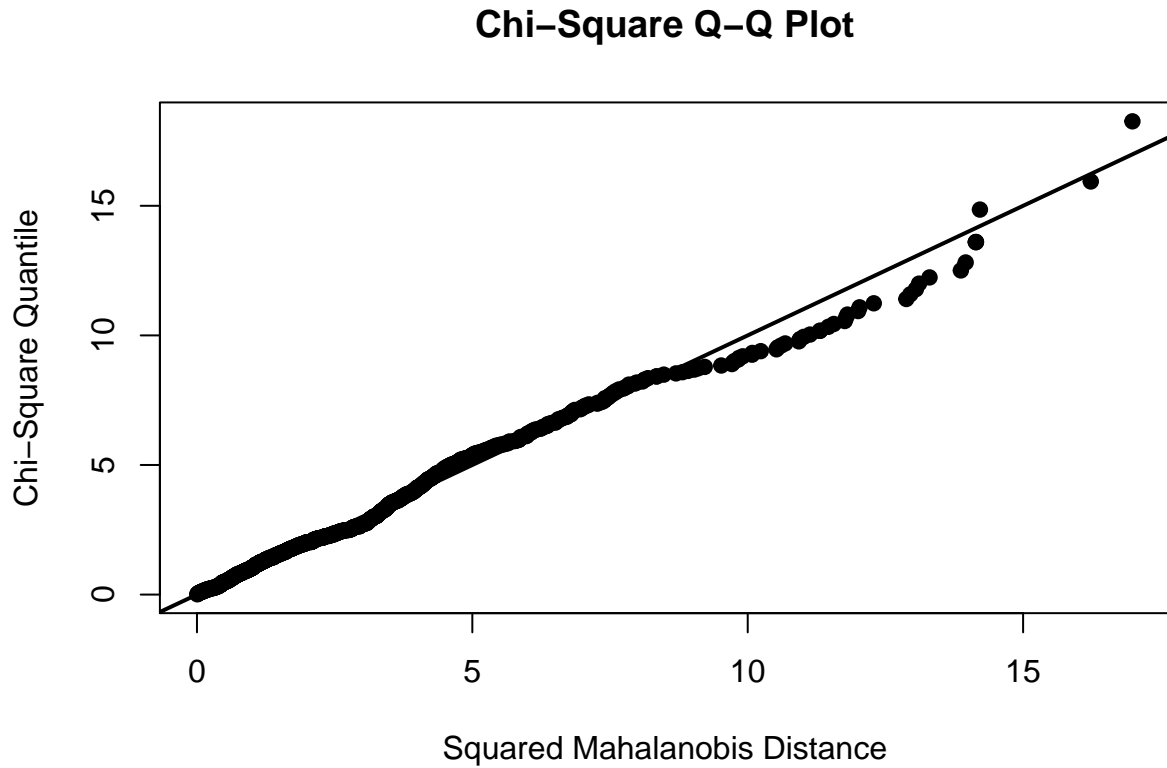
Chi–Square Q–Q Plot

Figure 2: Multivariate quantile-quantile (Q-Q) plot to assess deviations from multivariate normality (black line).

Effect of food-web treatment on trait-fitness relationships and selection gradients

We write the model in a way the independently estimates the effect of food-web treatment, each trait, and all two-way and three-way statistical interactions, on larva survival.

```
foodweb_model <- glmer(
  gall_survival ~
    -1 + Foodweb +
    Foodweb:(sc.Diam + sc.log.Clutch + sc.sqrt.Pref) +
    Foodweb:(I(sc.Diam^2) + I(sc.log.Clutch^2) + I(sc.sqrt.Pref^2)) +
```

```
    Foodweb:(sc.Diam:sc.log.Clutch + sc.Diam:sc.sqrt.Pref + sc.log.Clutch:sc.sqrt.Pref)

    (1|Genotype/Plant_Position/Gall_Number),

  data = gall_selection.df,

  family = binomial(link = logit), control=glmerControl(optimizer = "bobyqa"))
```

Note that the resulting estimates and confidence intervals are useful for determining whether trait-fitness relationships differ from zero, but not whether they differ between food-web treatments. For the later, we calculate the differences between each food-web treatment from the bootstrapped samples.

To estimate biased selection on chamber diameter, we subset our data to only include multi-chambered galls where there was variability in larva survival. We then fit a reduced model to estimate the bias in the logistic regression coefficient of chamber diameter in each food web.

```
biased_foodweb_df <- gall_selection.df %>%

  group_by(Foodweb, Gall_Number) %>%

  mutate(mean_survival = mean(gall_survival)) %>%

  filter(mean_survival > 0, mean_survival < 1) %>%

  ungroup()


biased_foodweb_model <- glmer(

  gall_survival ~ -1 + Foodweb +

    Foodweb:sc.Diam +

    (1|Genotype/Plant_Position/Gall_Number),

  data = biased_foodweb_df,

  family = binomial(link = logit), control=glmerControl(optimizer = "bobyqa"))
```

Partitioning the contribution of egg and larval parasitoids to selection gradients

Our simple food-web treatment allows us to estimate the unique contribution of egg parasitoids to selection on *Iteomyia* traits. To estimate the unique contribution of larval parasitoids, we subset our data so that our complex food-web treatment only contained attack by larval parasitoids (and gall survival). We then fit the same models as previously, including one to estimate bias.

```r
# excludes cases of egg-parasitism from Complex food web
egglarval_df <- filter(gall_selection.df, Foodweb == "Simple" | Foodweb == "Complex" & p

egglarval_model <- update(foodweb_model, data=egglarval_df)

biased_egglarval_df <- egglarval_df %>%
  group_by(Foodweb, Gall_Number) %>%
  mutate(mean_survival = mean(gall_survival)) %>%
  filter(mean_survival > 0, mean_survival < 1) %>%
  ungroup()

biased_egglarval_model <- update(biased_foodweb_model, data=biased_egglarval_df)
```

Reproduce Figure 2 of main manuscript

We combine our estimates of selection gradients for each food-web treatment as well as the contribution of larval parasitoids to selection in the complex food web.
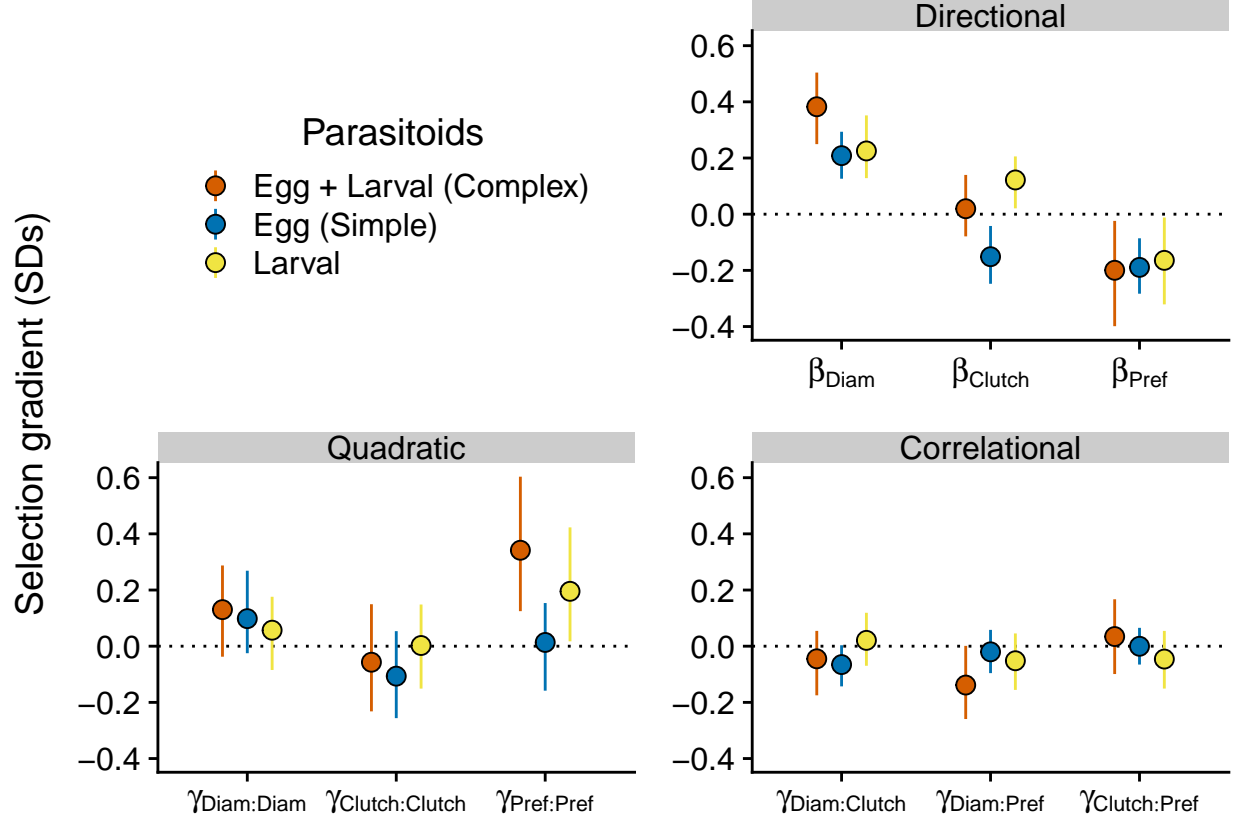
Figure 3: **Selection gradients**. Estimates of standardized selection gradients in complex (orange) and simple (blue) food webs. The contribution of larval parasitoids (yellow) was estimated with a subset of the complex food-web data that only contained attacks from larval parasitoids (and gall survival). Points and lines correspond to estimates of the mean and 95% confidence intervals, respectively. Overlapping confidence intervals with zero (dotted line) indicate no strong evidence of selection.

Partitioning the components of selection gradients

Selection gradients are influenced by both trait-fitness relationships and population mean fitness. Here, we partition selection gradients into these underlying components.
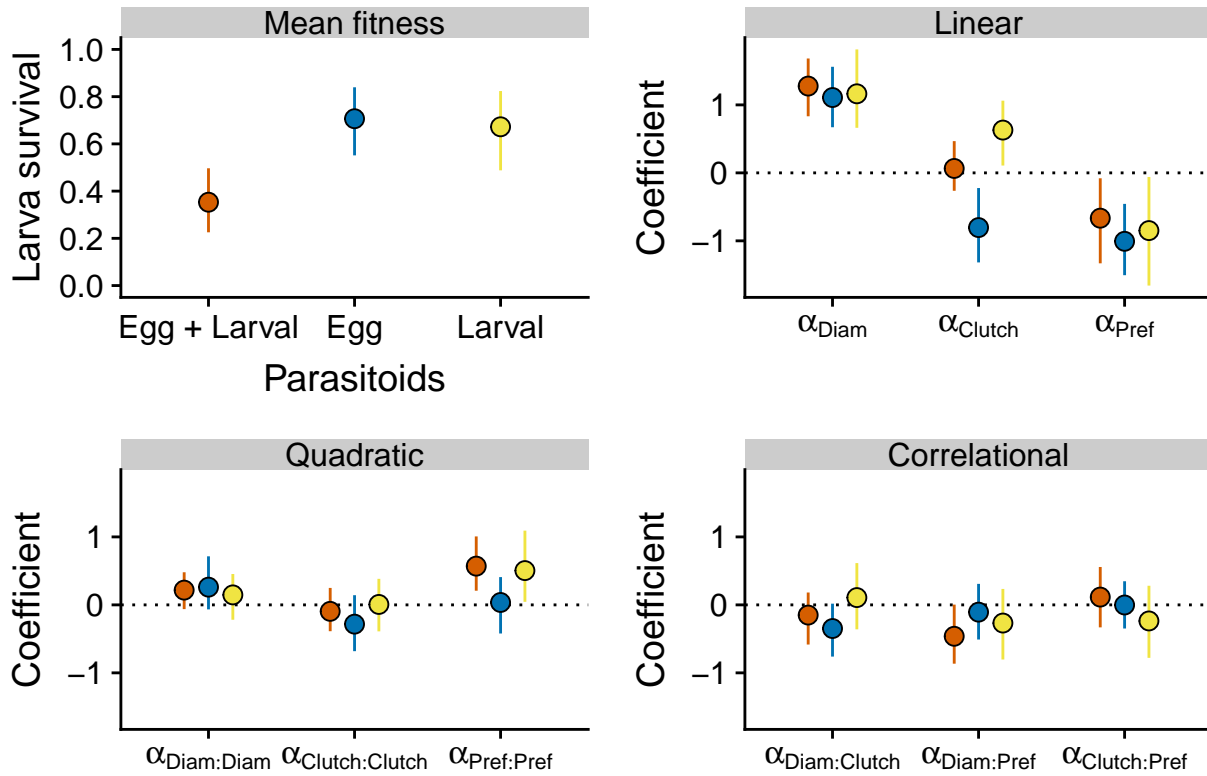
Figure 4: **Partitioning Selection Gradients.**

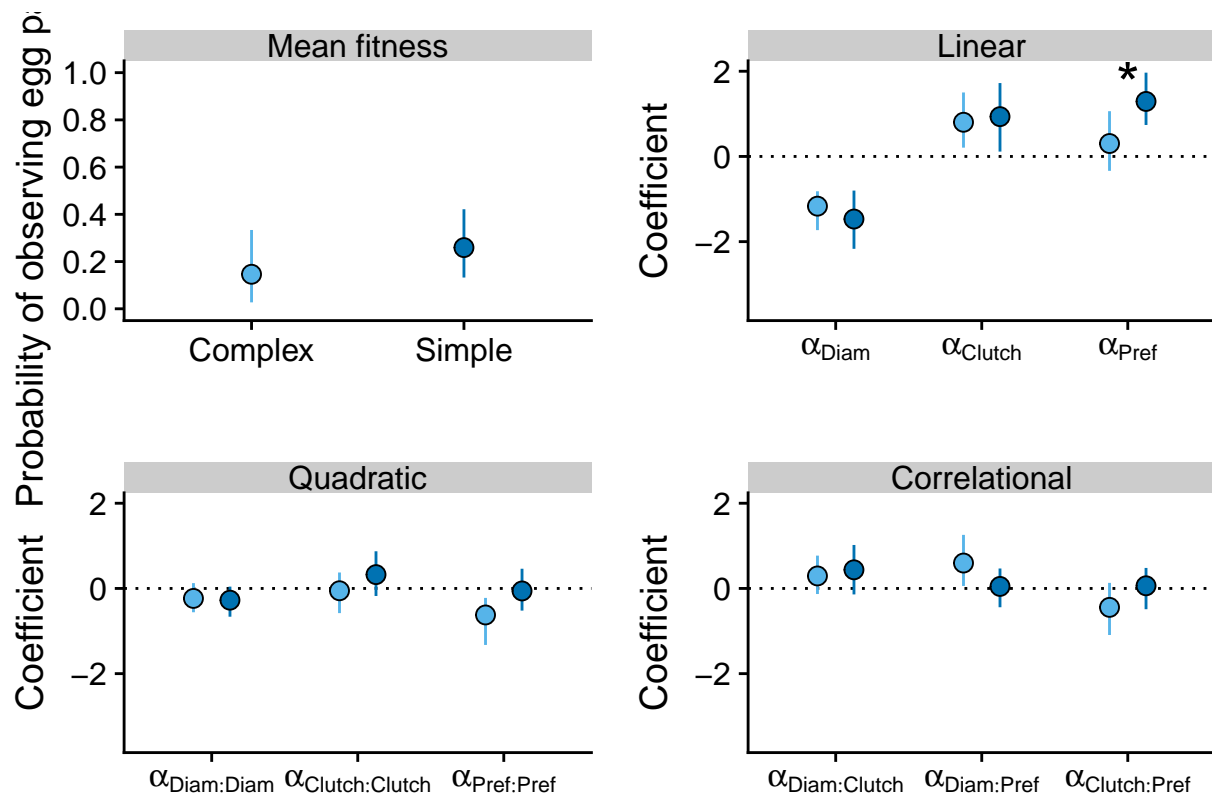# Estimating selection on the egg parasitoid *Platygaster*

```
# excludes cases of larval-parasitism from Complex food web
#eggegg_df <- #filter(gall_selection.df, Foodweb == "Simple" | Foodweb == "Complex" &
  #mutate(gall_survival = ifelse(gall_survival==1,0,1)) # attempt to look at survival


# convert "gall_survival" to egg parasitoid survival. Note that both Iteomyia pupa and
eggegg_df <- mutate(gall_selection.df, gall_survival = ifelse(egg_parasitoid==1,1,0))


eggegg_model <- update(foodweb_model, data=eggegg_df)
```
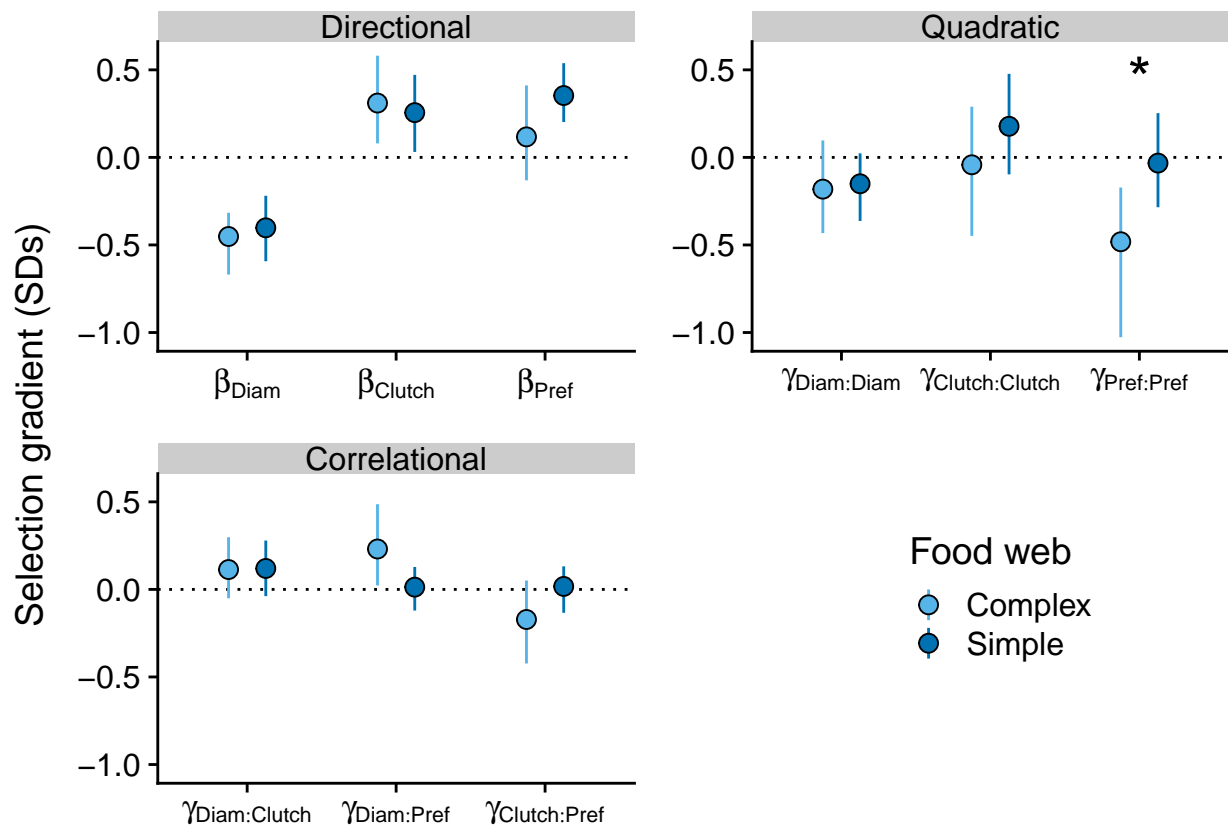
```r
biased_eggegg_df <- eggegg_df %>%

  group_by(Foodweb, Gall_Number) %>%

  mutate(mean_survival = mean(gall_survival)) %>%

  filter(mean_survival > 0, mean_survival < 1) %>%

  ungroup()


biased_eggegg_model <- update(biased_foodweb_model, data=biased_eggegg_df)
```
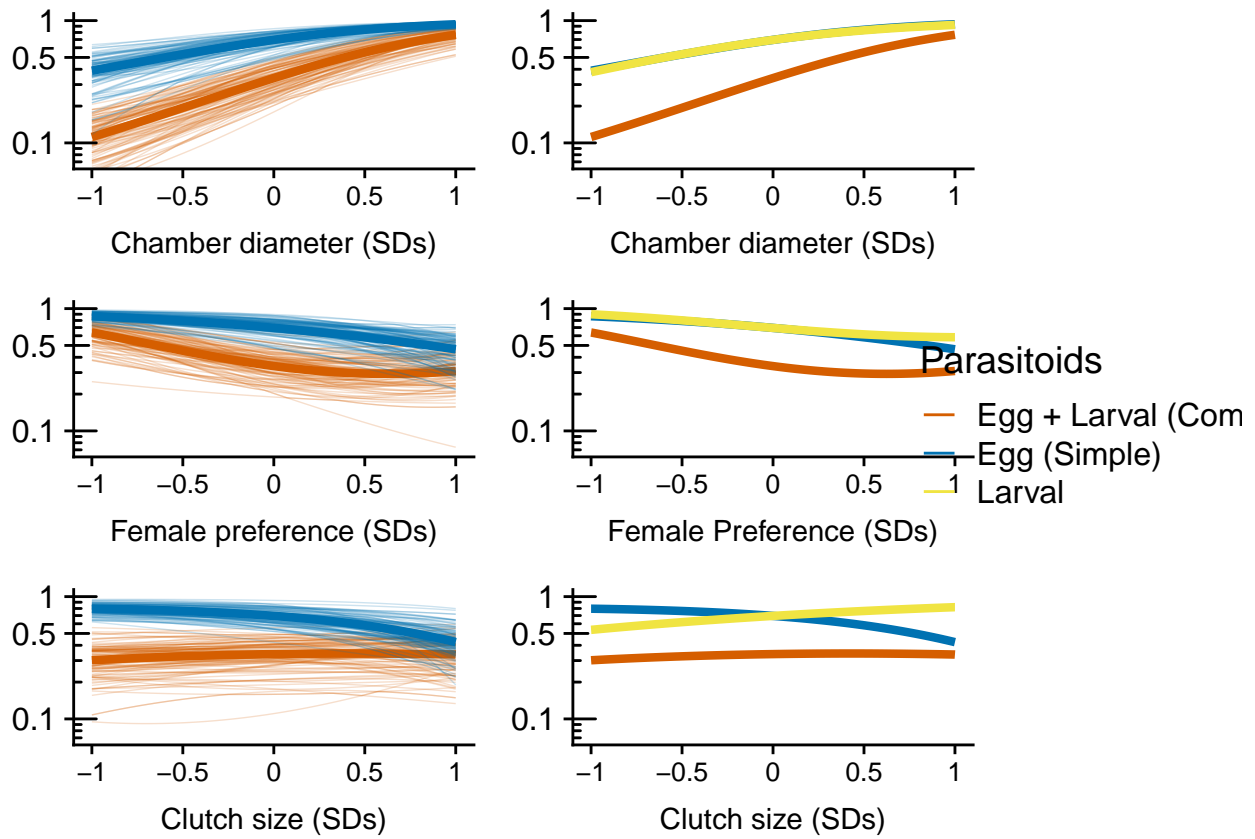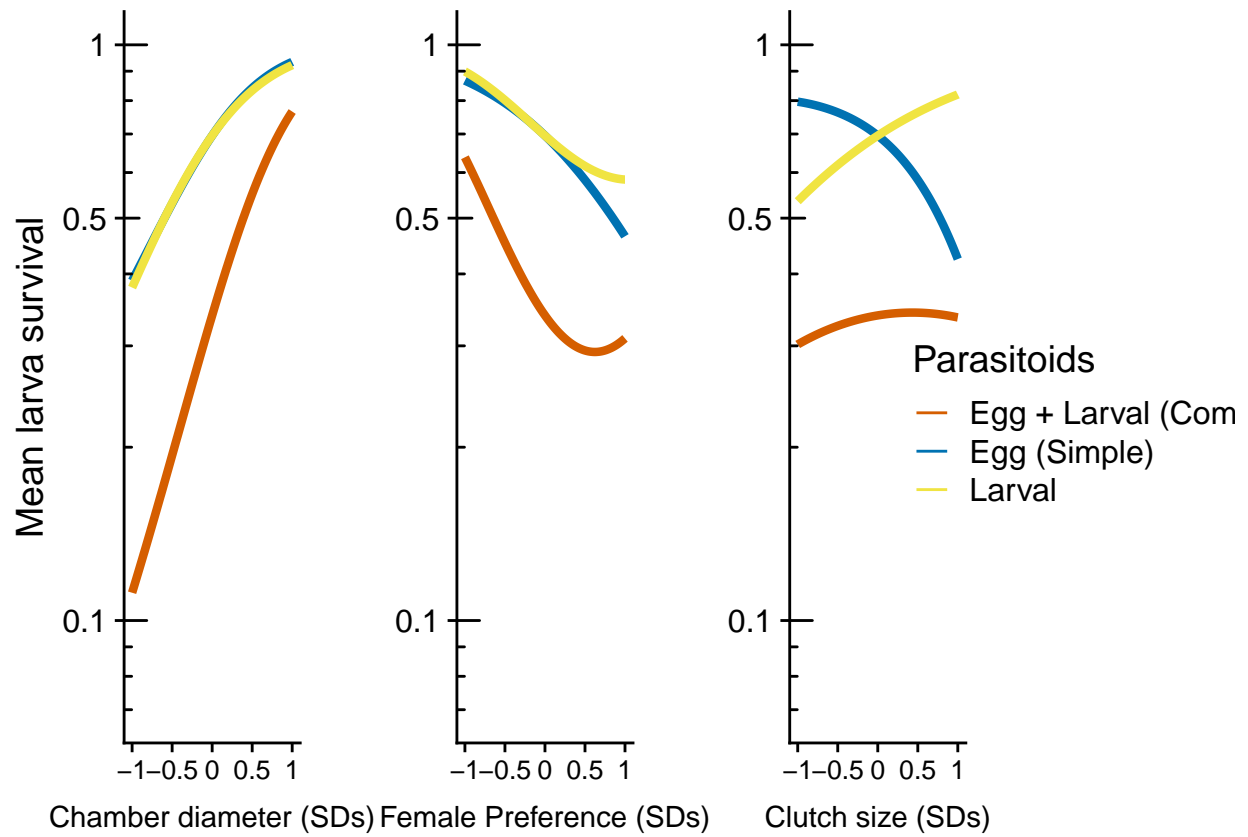
Directional

Quadratic

β_{Diam} β_{Clutch} β_{Pref}

$\gamma_{Diam:Diam}$ $\gamma_{Clutch:Clutch}$ $\gamma_{Pref:Pref}$

Correlational

$\gamma_{Diam:Clutch}$ $\gamma_{Diam:Pref}$ $\gamma_{Clutch:Pref}$

Food web
○ Complex
● Simple

Selection gradient (SDs)

Reproduce Figure 4 - Univariate adaptive landscape

Parasitoids
- Egg + Larval (Com
- Egg (Simple)
- Larval

Multivariate fitness landscapes
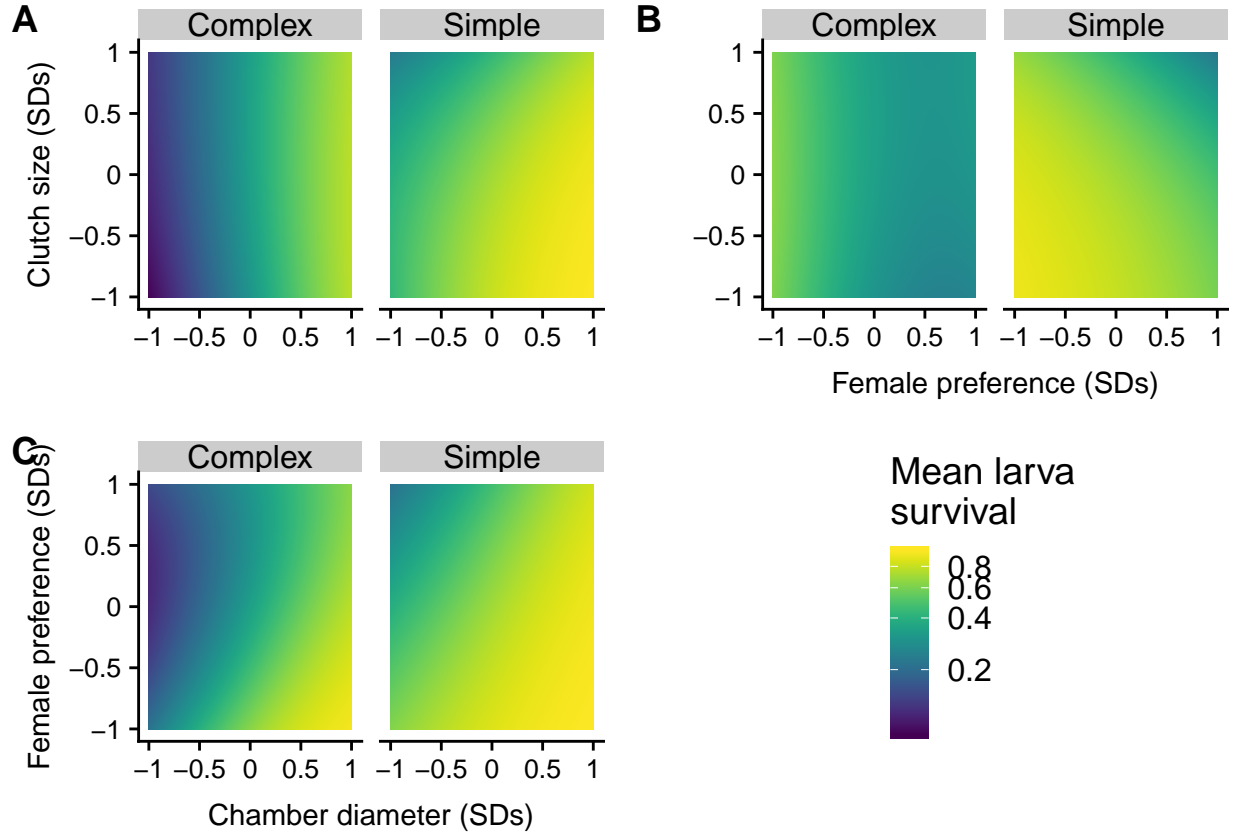
Reproduce Figure 5 in main manuscript.

Figure 5: Fitness landscapes of gall traits in complex vs. simple food webs. Each panel corresponds to a different combination of traits: clutch size and gall diameter (A); clutch size and female preference (B); female preference and gall diameter (C). Note that traits for all plots range 1 SD below and above the mean (=0).