Appendix S1 - Full model results

```
knitr::opts_chunk$set(echo = T)

library(soar)
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##      filter, lag

## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union
```

```
library(multipanelfigure)
library(nlme)
```

```
##
## Attaching package: 'nlme'

## The following object is masked from 'package:dplyr':
##
##      collapse
```

```
library(emmeans)

theme_set(theme_bw())

treatl <- get_treatment_means()
```

```
## Loading in data version 2.95.0

## Joining, by = "plot"
```

Compensation & total energy use

Compensation

Model:

```
compensation <- get_compensation(treatl)
```

```
## Joining, by = "period"
```

```
comp_mean_gls <- gls(smgran_comp ~ era,  correlation = corCAR1(form = ~ period), data = compensation)

comp_mean_gls_emmeans <- emmeans(comp_mean_gls, specs = ~ era)

comp_mean_pred <-  as.data.frame(comp_mean_gls_emmeans) %>%
  right_join(compensation)
```

```
## Joining, by = "era"
```

Results of generalized least squares:

```
(summary(comp_mean_gls))
```

```
## Generalized least squares fit by REML
##   Model: smgran_comp ~ era
##   Data: compensation
##        AIC      BIC    logLik
##   62.62169 81.75169 -26.31084
##
## Correlation Structure: Continuous AR(1)
##  Formula: ~period
##  Parameter estimate(s):
##       Phi
## 0.5141927
##
## Coefficients:
##                     Value  Std.Error  t-value p-value
## (Intercept)     0.1887873 0.04849229 3.893142  0.0001
## erab_pre_reorg  0.3596238 0.06442326 5.582204  0.0000
## erac_post_reorg 0.0296368 0.06914950 0.428590  0.6685
##
##  Correlation:
##                 (Intr) erb_p_
## erab_pre_reorg  -0.742
## erac_post_reorg -0.701  0.528
##
## Standardized residuals:
##         Min         Q1        Med         Q3        Max
## -2.2604463 -0.4462201 -0.1654825  0.4070499  7.5010175
##
## Residual standard error: 0.2973631
## Degrees of freedom: 342 total; 339 residual
```

Estimates:
```

```
compensation_estimates <- as.data.frame(comp_mean_gls_emmeans)
compensation_estimates
```

```
##            era    emmean         SE       df   lower.CL  upper.CL
## 1     a_pre_pb 0.1887873 0.04849229 56.08128 0.09164873 0.2859260
## 2  b_pre_reorg 0.5484112 0.04322376 60.40971 0.46196281 0.6348595
## 3 c_post_reorg 0.2184241 0.04931009 59.73403 0.11978024 0.3170680
```

Contrasts:

```
compensation_contrasts <- as.data.frame(pairs(comp_mean_gls_emmeans))
compensation_contrasts
```

```
##                   contrast     estimate         SE       df    t.ratio
## 1     a_pre_pb - b_pre_reorg -0.35962380 0.06442326 60.44042 -5.5822045
## 2    a_pre_pb - c_post_reorg -0.02963679 0.06914950 57.97849 -0.4285901
## 3 b_pre_reorg - c_post_reorg  0.32998701 0.06502290 62.66119  5.0749352
##        p.value
## 1 1.767478e-06
## 2 9.038819e-01
## 3 1.099306e-05
```

Total energy use

Model:

```
energy_ratio <- get_e_ratio(treatl)
```

```
## Joining, by = "period"
```

```
totale_mean_gls <- gls(total_e_rat ~  era,  correlation = corCAR1(form = ~ period), data = energy_ratio
```

Model summary:

```
summary(totale_mean_gls)
```

```
## Generalized least squares fit by REML
##   Model: total_e_rat ~ era
##   Data: energy_ratio
##        AIC       BIC  logLik
##   -148.4102 -129.2802 79.2051
##
## Correlation Structure: Continuous AR(1)
##  Formula: ~period
##  Parameter estimate(s):
##       Phi
## 0.6318768
##
## Coefficients:
```

```
##                  Value   Std.Error  t-value  p-value
## (Intercept)     0.2955610 0.04616723 6.401964  0.0000
## erab_pre_reorg  0.3881293 0.06052106 6.413128  0.0000
## erac_post_reorg 0.1666183 0.06555100 2.541812  0.0115
##
##  Correlation:
##                 (Intr) erb_p_
## erab_pre_reorg  -0.740
## erac_post_reorg -0.703  0.537
##
## Standardized residuals:
##        Min         Q1        Med        Q3        Max
## -1.9222140 -0.6293278 -0.1030659  0.5885477  5.4080459
##
## Residual standard error: 0.2404411
## Degrees of freedom: 342 total; 339 residual
```

Estimates:

```
totale_mean_gls_emmeans <- emmeans(totale_mean_gls, specs = ~ era)

totale_estimates <- as.data.frame(totale_mean_gls_emmeans)
totale_estimates
```

```
##           era     emmean         SE       df  lower.CL  upper.CL
## 1    a_pre_pb 0.2955610 0.04616723 36.54729 0.2019781 0.3891438
## 2  b_pre_reorg 0.6836903 0.04074287 38.89409 0.6012729 0.7661077
## 3 c_post_reorg 0.4621793 0.04658963 38.01610 0.3678648 0.5564937
```

Contrasts:

```
totale_contrasts <- as.data.frame(pairs(totale_mean_gls_emmeans))
totale_contrasts
```

```
##                    contrast   estimate         SE       df   t.ratio
## 1      a_pre_pb - b_pre_reorg -0.3881293 0.06052106 40.83178 -6.413128
## 2     a_pre_pb - c_post_reorg -0.1666183 0.06555100 37.48394 -2.541812
## 3 b_pre_reorg - c_post_reorg  0.2215110 0.06082448 41.78673  3.641807
##        p.value
## 1 3.379158e-07
## 2 3.965179e-02
## 3 2.096605e-03
```

Community composition

Kangaroo rats

Model:
```

```
dipo_dat <- treatl %>%
  mutate(dipo_prop = dipo_e / total_e,
         smgran_prop= smgran_e / total_e) %>%
  group_by(oplottype) %>%
  mutate(smgran_prop_ma = maopts(smgran_prop),
         dipo_prop_ma = maopts(dipo_prop)) %>%
  ungroup()

dipo_c_dat <- dipo_dat %>%
  filter(oplottype == "CC")

dipo_glm <- glm(dipo_prop ~ oera, family = quasibinomial(), data= dipo_c_dat)
```

Model summary:

```
summary(dipo_glm)
```

```
##
## Call:
## glm(formula = dipo_prop ~ oera, family = quasibinomial(), data = dipo_c_dat)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.04138  -0.27463   0.06426   0.34579   0.83853
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.40325    0.05941  23.620  < 2e-16 ***
## oera.L      -1.10008    0.11350  -9.693  < 2e-16 ***
## oera.Q       0.58555    0.09108   6.429 4.36e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.1561938)
##
##     Null deviance: 81.582  on 341  degrees of freedom
## Residual deviance: 59.814  on 339  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

Estimates:

Estimates from `emmeans` differ numerically (very slightly) from estimates obtained via `predict()` and back transformation. Below are estimates from `emmeans`, because those are what are used for contrasts.

```
dipoemmeans <- regrid(emmeans(dipo_glm, specs = ~ oera))

dipoestimates <- as.data.frame(dipoemmeans)

dipoestimates
```

```
##           oera      prob        SE  df asymp.LCL asymp.UCL
```

```
## 1      a_pre_pb 0.9183528 0.01013571 Inf 0.8984872 0.9382184
## 2  b_pre_reorg 0.7160901 0.01575074 Inf 0.6852192 0.7469610
## 3 c_post_reorg 0.7035835 0.01804849 Inf 0.6682091 0.7389579
```

Estimates from `predict`:

```
dipo_glm_se <- est_glm_ilink(dipo_glm, dipo_c_dat) %>%
  left_join(select(dipo_c_dat, period, dipo_prop_ma)) %>%
  mutate(Treatment = ifelse(oplottype == "CC", "Control", "Exclosure"),
         Rodents = "All small granivores\n(non-Dipodomys)") %>%
  rename(rod_prop_ma = dipo_prop_ma)
```

```
## Joining, by = c("period", "oplottype")
```

```
## Joining, by = "period"
```

```
select(dipo_glm_se, oera, est, lower, upper) %>% distinct()
```

```
##           oera       est      lower      upper
## 1      a_pre_pb 0.9183528 0.8956519 0.9364654
## 2  b_pre_reorg 0.7160901 0.6835646 0.7465121
## 3 c_post_reorg 0.7035835 0.6662647 0.7383680
```

Contrasts:

```
dipocontrasts <- as.data.frame(pairs(dipoemmeans))
dipocontrasts
```

```
##                    contrast   estimate         SE  df   z.ratio      p.value
## 1    a_pre_pb - b_pre_reorg 0.20226269 0.01873015 Inf 10.7987757 2.764455e-14
## 2   a_pre_pb - c_post_reorg 0.21476925 0.02069978 Inf 10.3754389 2.653433e-14
## 3 b_pre_reorg - c_post_reorg 0.01250656 0.02395483 Inf  0.5220892 8.605416e-01
```

C. baileyi

Model:

```
pb <- get_pb(treatl)

pb_nozero <- pb %>%
  filter(as.numeric(oera) > 1)

pb_glm_treat <- glm(pb_prop ~ oera * oplottype, family = quasibinomial(), data= pb_nozero)
```

Model summary:

```
summary(pb_glm_treat)
```

```
##
## Call:
## glm(formula = pb_prop ~ oera * oplottype, family = quasibinomial(),
##     data = pb_nozero)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.77785  -0.23751  -0.07486   0.18362   1.66203
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         -2.0044     0.1601 -12.523  < 2e-16 ***
## oera.L              -2.0922     0.2263  -9.243  < 2e-16 ***
## oplottype.L          2.7474     0.2263  12.138  < 2e-16 ***
## oera.L:oplottype.L   0.8987     0.3201   2.807  0.00521 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.1092629)
##
##     Null deviance: 242.507  on 454  degrees of freedom
## Residual deviance:  51.407  on 451  degrees of freedom
##   (1 observation deleted due to missingness)
## AIC: NA
##
## Number of Fisher Scoring iterations: 8
```

Estimates:

```
pb_emmeans <- regrid(emmeans(pb_glm_treat, specs = ~ oera | oplottype))

pb_estimates <- as.data.frame(pb_emmeans)

pb_estimates
```

```
##         oera oplottype        prob          SE  df      asymp.LCL    asymp.UCL
## 1  b_pre_reorg        CC 0.117288823 0.009400892 Inf  0.0988634136 0.135714232
## 2 c_post_reorg        CC 0.002798409 0.001746027 Inf -0.0006237412 0.006220559
## 3  b_pre_reorg        EE 0.724806906 0.013048523 Inf  0.6992322718 0.750381541
## 4 c_post_reorg        EE 0.251282850 0.014409839 Inf  0.2230400854 0.279525616
```

Estimates from `predict`:

```
pb_glm_treat_se <- est_glm_ilink(pb_glm_treat, pb_nozero) %>%
  full_join(select(pb, period, oplottype, pb_prop_ma, censusdate)) %>%
  mutate(Treatment = ifelse(oplottype == "CC", "Control", "Exclosure"),
         Rodents = "C. baileyi") %>%
  rename(rod_prop_ma = pb_prop_ma)
```

```
## Joining, by = c("period", "oplottype")
```

```
## Joining, by = c("period", "oplottype", "censusdate")
```

```r
select(pb_glm_treat_se, oplottype, oera, est, lower, upper) %>% distinct()
```

```
##   oplottype        oera         est        lower       upper
## 1        CC  b_pre_reorg 0.117288823 0.0997539092 0.137435493
## 2        EE  b_pre_reorg 0.724806906 0.6979584533 0.750123216
## 3        CC c_post_reorg 0.002798409 0.0008022601 0.009713007
## 4        EE c_post_reorg 0.251282850 0.2235730526 0.281183261
## 5        CC        <NA>          NA           NA          NA
## 6        EE        <NA>          NA           NA          NA
```

Contrasts:

```r
pb_contrasts <- as.data.frame(pairs(pb_emmeans))
pb_contrasts
```

```
##                      contrast oplottype  estimate          SE  df  z.ratio
## 1 b_pre_reorg - c_post_reorg        CC 0.1144904 0.009561662 Inf 11.97390
## 2 b_pre_reorg - c_post_reorg        EE 0.4735241 0.019439841 Inf 24.35843
##        p.value
## 1  4.868315e-33
## 2 4.719332e-131
```

```r
select(pb_glm_treat_se, oplottype, oera, est, lower, upper) %>% distinct()
```

```
##   oplottype        oera         est        lower       upper
## 1        CC  b_pre_reorg 0.117288823 0.0997539092 0.137435493
## 2        EE  b_pre_reorg 0.724806906 0.6979584533 0.750123216
## 3        CC c_post_reorg 0.002798409 0.0008022601 0.009713007
## 4        EE c_post_reorg 0.251282850 0.2235730526 0.281183261
## 5        CC        <NA>          NA           NA          NA
## 6        EE        <NA>          NA           NA          NA
```

Contrasts:

```r
pb_contrasts <- as.data.frame(pairs(pb_emmeans))
pb_contrasts
```

```
##                      contrast oplottype  estimate          SE  df  z.ratio
## 1 b_pre_reorg - c_post_reorg        CC 0.1144904 0.009561662 Inf 11.97390
## 2 b_pre_reorg - c_post_reorg        EE 0.4735241 0.019439841 Inf 24.35843
##        p.value
## 1  4.868315e-33
## 2 4.719332e-131
```