Appendix S1 - Full model results

```r
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
```

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

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

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

```r
library(emmeans)

theme_set(theme_bw())


# Get data using 'portalr':
#treatl <- get_treatment_means()
# Alternatively, read data from 'data/':
 treatl <- read.csv(here::here("data", "treatl.csv"), stringsAsFactors = T)

 treatl <- treatl %>%
   mutate(censusdate = as.Date(censusdate),
          oera = ordered(oera),
          oplottype = ordered(oplottype))

pb <- get_pb(treatl)
```

```
pb_nozero <- pb %>%
  filter(as.numeric(oera) > 1)
energy_ratio <- get_e_ratio(treatl)
```

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

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

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

Compensation & total energy use

Compensation

Model:

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

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

comp_mean_pred <-  as.data.frame(comp_mean_gls_emmeans) %>%
  mutate(oera = ordered(oera)) %>%
  right_join(compensation)
```

```
## Joining, by = "oera"
```

Results of generalized least squares:

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

```
## Generalized least squares fit by REML
##   Model: smgran_comp ~ oera
##   Data: compensation
##        AIC      BIC     logLik
##    63.7203 82.8503 -26.86015
##
## Correlation Structure: Continuous AR(1)
##  Formula: ~period
##  Parameter estimate(s):
##        Phi
## 0.5141927
##
## Coefficients:
##                  Value  Std.Error  t-value p-value
## (Intercept)  0.3185409 0.02747495 11.59387  0.0000
## oera.L       0.0209564 0.04889608  0.42859  0.6685
## oera.Q      -0.2815324 0.04467478 -6.30182  0.0000
##
```

```
##  Correlation:
##        (Intr) oera.L
## oera.L 0.014
## oera.Q 0.108  0.010
##
## 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
```

```
##          oera    emmean         SE       df    lower.CL  upper.CL
## 1     a_pre_pb 0.1887873 0.04849229 65.54814 0.09195691 0.2856178
## 2  b_pre_reorg 0.5484112 0.04322376 70.42672 0.46221325 0.6346090
## 3 c_post_reorg 0.2184241 0.04931009 69.66681 0.12007000 0.3167783
```

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 70.46124 -5.5822045
## 2     a_pre_pb - c_post_reorg -0.02963679 0.06914950 67.68957 -0.4285901
## 3 b_pre_reorg - c_post_reorg  0.32998701 0.06502290 72.95450  5.0749352
##         p.value
## 1 1.234443e-06
## 2 9.038589e-01
## 3 8.477698e-06
```

Total energy use

Model:

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

Model summary:

```
summary(totale_mean_gls)
```

```
## Generalized least squares fit by REML
##   Model: total_e_rat ~ oera
##   Data: energy_ratio
##         AIC       BIC   logLik
```

```
##    -147.3116 -128.1816 78.65579
##
## Correlation Structure: Continuous AR(1)
##  Formula: ~period
##  Parameter estimate(s):
##       Phi
## 0.6318768
##
## Coefficients:
##                  Value  Std.Error    t-value p-value
## (Intercept)  0.4804768 0.02630297 18.267021  0.0000
## oera.L       0.1178169 0.04635156  2.541812  0.0115
## oera.Q      -0.2488846 0.04168913 -5.970013  0.0000
##
##  Correlation:
##        (Intr) oera.L
## oera.L 0.008
## oera.Q 0.106  0.006
##
## 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 = ~ oera)

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

```
##          oera    emmean         SE       df  lower.CL  upper.CL
## 1     a_pre_pb 0.2955610 0.04616723 36.61089 0.2019837 0.3891382
## 2  b_pre_reorg 0.6836903 0.04074287 38.96128 0.6012774 0.7661031
## 3 c_post_reorg 0.4621793 0.04658963 38.08195 0.3678702 0.5564884
```

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 40.90187 -6.413128
## 2    a_pre_pb - c_post_reorg -0.1666183 0.06555100 37.54898 -2.541812
## 3 b_pre_reorg - c_post_reorg  0.2215110 0.06082448 41.85824  3.641807
##       p.value
## 1 3.354875e-07
## 2 3.963399e-02
## 3 2.093712e-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.

```r
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`:

```r
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"
```

```r
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:

```r
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:

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

Model summary:

```r
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:

```r
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`:

```r
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
```