Dimarco RDD and Fordyce JA, 2017, Not all toxic butterflies are toxic: High intra and interspecific variation in sequestration in subtropical swallowtail. Ecosphere.

Appendix 2

Stan code to implement Bayesian model for aristolochic acid content.

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Data availability: This data cannot be used in other scientific publications without authors' permission.

```
data {
 int<lower=0> nObs; # number of observation
 int<lower=0> nCens; # number of censored observations
 int<lower=0> nSpp; # number of species and species with censored data
 matrix<lower=0>[nObs,nSpp] xMat; # design matrix for non-censored data
 matrix<lower=0>[nCens,nSpp] cMat; #design matrix for censored data
 vector[nObs] obs; #observed values
 real<upper=min(obs)> L; #threshold for lowest quantifiable amount
}

parameters {
 real<lower=0,upper=L> obsCens[nCens];
  vector<lower=0>[nSpp] beta;
 real sigma;
}

model {
 sigma ~ cauchy(0,5);
 beta ~ normal(0,5);

 obs ~ normal(xMat * beta, sigma);
 obsCens ~ normal(cMat * beta, sigma);
}

generated quantities {
 vector[nObs] log_lik;

 for(n in 1:nObs) {
       log_lik[n] <- normal_log(obs[n], xMat[n] * beta, sigma);
 }
}
```

All original data, R code and STAN code to reproduce the results presented here.

```
library(multcomp);library(car)

### Toughness
triangularis<-c(33.33, 18.33, 16.67, 16.67, 15, 24.33, 23, 23.67, 23.67, 24, 23, 21.67, 21, 20.33,
23, 23, 23, 23, 23, 23, 23, 23.67, 23, 23, 23, 23, 5, 15, 5, 25)
macroura<-c(231.67, 190, 230, 221.67, 201.67, 230, 253.33, 198.33, 236.67, 245, 196.67,
169.33, 183.33, 213.33, 248.33, 245, 225, 241.67, 178.33, 185, 235, 235, 218.33, 225, 241.66,
193.33, 141.67, 123.33, 193.33, 233.33)
t.test(triangularis,macroura)

### Larval preference
# P. anchisis
triangularis<-c(0, 9.602, 19.292, 23.78, 26.063, 0.384, 1.337, 0.415, 3.909, 4.376, 48.501, 4.017,
1.487, 1.795, 1.193, 0.562, 59.708, 30.013, 29.48, 0, 23.705, 1.608, 4.459, 36.001, 0)
macroura<-c(1.681, 2.045, 0, 3.743, 3.754, 0, 0, 0, 0, 0, 1.401, 0, 1.117, 0, 0, 0, 0, 0, 14.454,
3.335, 0.859, 0, 13.469, 0, 0.648)
t.test(triangularis,macroura,paired=TRUE)

# B. polydamas
triangularis<-c(1.59, 15.51, 20.53, 8.85, 3.29, 2.63, 2.8, 0, 4.34, 5.35, 2, 8.53, 3.29, 2.39, 0, 3.12,
8.05, 17.05, 17.25, 5.03, 2.5, 4.63, 16.04, 2.77, 0, 26.12, 7.18, 3.8, 2.65, 2.83, 5.19, 6.72, 1.38, 0,
14.91, 2.74)
macroura<-c(0, 0, 0, 0, 0, 0, 0, 1.14, 0, 5.7, 1.39, 0, 0, 7.04, 3.41, 4.86, 0, 0, 0, 0, 0, 4.8, 0, 0,
1.45, 0, 1.6, 8.57, 0, 0, 0, 0, 0, 5.46, 0, 0)
t.test(triangularis,macroura,paired=TRUE)

# AA augmented triangularis
# P. anchisis
control<-c(13.436, 8.518, 16.773, 23.937, 51.865, 28.275, 48.338, 0, 23.881, 2.404, 46.807,
13.782, 2.143, 40.629, 25.246, 64.255, 37.801, 41.816, 14.927, 48.434, 24.902)
AA<-c(18.709, 9.129, 71.758, 18.661, 55.206, 43.257, 30.612, 6.09, 14.398, 3.729, 26.836,
31.22, 26.261, 2.098, 35.367, 62.522, 40.966, 82.683, 26.921, 54.629, 39.484)
t.test(control,AA,paired=TRUE)

# B. polydamas
control<-c(10.646, 11.497, 72.055, 17.986, 13.507, 72.366, 65.053, 32.835, 3.096, 6.066,
23.434, 2.524, 25.25, 6.496, 33.542, 61.553, 25.338, 30.758, 49.009)
AA<-c(53.648, 7.009, 75.006, 6.945, 17.496, 100.757, 67.021, 19.686, 0, 21.195, 1.392, 60.818,
71.377, 53.106, 68.742, 48.649, 40.304, 16.001, 24.479)
t.test(control,AA,paired=TRUE)


### Larval performance and aristolochic acid presence
## survivorship
```

```
survive <-
c(1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1
,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,0,0,0,0,1,1,0,0,0,0,0,0,1,1,1,1,1,1,1,0,0)
diet<-
c("AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","AA","
AA","AA","AA","AA","AA","AA","AA","AA","Amac","Amac","Amac","Amac","Amac","Am
ac","Amac","Amac","Amac","Amac","Amac","Amac","Amac","Amac","Amac","Amac","Amac
","Amac","Amac","Amac","Amac","Amac","Amac","Atri","Atri","Atri","Atri","Atri","Atri","At
ri","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri",
"Atri","Atri","Atri","AA","AA","AA","AA","AA","AA","AA","AA","Amac","Amac","Amac","
Amac","Amac","Amac","Amac","Amac","Atri","Atri","Atri","Atri","Atri","Atri","Atri","Atri")
# Amac=A.macroura, Atri=A.triangularis, AA=A.triangularis with AA addition
species<-
c("Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan
","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan"
,"Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan",
"Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","
Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","Pan","poly","poly","poly","poly","poly
","poly","poly","poly","poly","poly","poly","poly","poly","poly","poly","poly","poly","poly","p
oly","poly","poly","poly","poly","poly")


modfull<-glm(survive~diet*species,family="binomial")
summary(modfull)
Anova(modfull,test="LR")

###fat content and dry weight of surviving individuals
## P. anchisis
total.fat<-
c(7490.14,6199.24,8736,9692.96,5405.21,7293.02,7420.83,8946.25,6666.27,4823.21,11840.43,
5295.8,7308.45,9940.22,8450.6,8990.62,12921.35,4214.71,7909.76,20310.34,8057.61,13869.84,
5304.08,8920.29,6709.24,4122.14,5970.65,4883.46)
dry.weight<-
c(0.071,0.131,0.075,0.071,0.096,0.086,0.072,0.08,0.083,0.112,0.094,0.119,0.071,0.092,0.083,0.
096,0.089,0.102,0.082,0.058,0.092,0.063,0.098,0.069,0.119,0.14,0.092,0.127)
diet<-
c("A.triang.+AA","A.triang.+AA","A.triang.+AA","A.triang.+AA","A.triang.+AA","A.triang.+
AA","A.triang.+AA","A.m.+EtOH","A.m.+EtOH","A.m.+EtOH","A.m.+EtOH","A.m.+EtOH","
A.m.+EtOH","A.m.+EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+
EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+Et
OH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtO
H")

modfat<-lm(log(total.fat)~diet)
anova(modfat)
moddw<-lm(dry.weight~diet)
```

```
anova(moddw)


## B. polydamas
total.fat<-c(8182.67,6354.29,5960.16,7601.11,9644,7902.06,11956.99,5133.88,3088.89)
dry.weight<-c(0.075,0.07,0.128,0.09,0.075,0.097,0.093,0.121,0.144)
diet<-
c("A.triang.+AA","A.triang.+AA","A.m.+EtOH","A.m.+EtOH","A.triang.+EtOH","A.triang.+Et
OH","A.triang.+EtOH","A.triang.+EtOH","A.triang.+EtOH")

modfat<-lm(log(total.fat)~diet)
anova(modfat)
moddw<-lm(dry.weight~diet)
anova(moddw)

# stan code

library(shinystan)
library(rstan)
rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores())
library(loo)


#########
# Bayesian model for AA content of wild plants

Plant<-
c("M","M","M","M","M","M","M","M","M","M","M","M","M","M","M","M","M","M","M","M","
M","M","M","M","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T
","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T"
,"T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T",
"T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","T","
T","T","T")

#design matrix
xMat<-
matrix(c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1),ncol=2)
cMat<-
matrix(c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1),ncol=2)

#data
```

```
obs<-
c(0.442735219,0.402890977,0.477154152,0.61702484,0.499270429,0.532060173,0.121319187,
0.542867653,0.713078842,0.842585594,0.752605184,1.317107111,0.265762168,1.278089953,1
.266864341,0.821089893,0.631312418,0.82601403,0.440187044,0.192385619,0.650965316,0.0
78802831,1.051640427,0.079532279,0.063112973,0.000487816,0.065220494,0.011218016,0.01
2830627,0.005742019,0.032299772,0.0566556,0.047619177,0.135146749,0.012706295,0.02879
1879,0.01845819,0.024471636)


cens <- list(nObs=38, nCens = 76, xMat = xMat, cMat = cMat, obs=obs, L = min(obs),nSpp = 2)


mod<-"
data {
        int<lower=0> nObs;
        int<lower=0> nCens;
        int<lower=0> nSpp;
        matrix<lower=0>[nObs,nSpp] xMat;
        matrix<lower=0>[nCens,nSpp] cMat;
        vector<lower=0>[nObs] obs;
        real<upper=min(obs)> L;
}

parameters {
        real<lower=0,upper=L> obsCens[nCens];
  vector<lower=0>[nSpp] beta;
        real sigma;
}

model {
        sigma ~ cauchy(0,5);
        beta ~ normal(0,5);

        obs ~ normal(xMat * beta, sigma);
        obsCens ~ normal(cMat * beta, sigma);

}
"

modCensP <- stan(model_code=mod, data=cens, iter=10000, chains=4, seed=3,control =
list(adapt_delta = 0.95),)
launch_shinystan(modCensP)
#outs<-extract(modCensP,pars=c("beta"))
#save(outs,file="PlantBetas.R")
##### Bayesian model for AA in wild butterflies
```

```
#design matrix
xMat<-
matrix(c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1),ncol=4)

cMat<-
matrix(c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,
1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1),ncol=4)

sexObs<-
c(2,1,2,2,1,2,2,2,2,2,2,2,2,2,2,2,1,2,2,1,1,1,2,1,2,2,2,2,2,2,2,2,2,2,2,2,2,1,1,2,2,2,2,2,2,2,2,2,1,1,1
,1,1,2,2,1,1,2,1,1,1,1,2,1,1,1,1,2,1,1,2,2,1,2,1,2,1,2,2,2,2,2,1,2,2,2,2,1,2,2,2,2,1,2,2,1,1,2,2,1,2,2,2
,2,2,2,2,2,2,2,2,2,2,2,2,2,1,1,2,2,2)

sexCens<-
c(2,2,2,2,2,1,2,2,2,1,2,2,2,2,2,2,2,2,2,2,2,2,1,1,2,2,2,2,2,2,2,2,2,2,1,2,2,2,2,2,2,2,2,2,2,2,1,1,2,2,2
,2,2,2,1,2,2,2,2,2,2,2,2,2,2,2,2,1,2,2,2,2,1,2,1,2,1,2,2,1,1,1,2,2,1,1,2,2,1,2,2,2,2,2,2,1,2,2,2,2,2,2,2
,1,1,2,1,2,2,2,2,2,2,2,2,2,2,1,1,1,1,2,2,2,1,1,2,2,1,2,1,1,1,1,1,1,2,2,1,2,2,1,2,2,2,2,2,1,2,2,2,2,2,2,1
,2,1,2,1,1,1,2,2,2,2,2,1,2,2,2,2,2,2,2,1,2,2,2,2,2,1,2,2,2,2,2,2,2,2,1,2,1)

xsexMat<-
matrix(c(0,1,0,0,1,0,0,0,0,0,0,0,0,0,0,1,0,0,1,1,1,0,1,0,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,0,0,0,0,0,
0,1,1,1,1,1,0,0,1,1,0,1,1,1,1,0,1,1,1,1,0,1,1,0,0,1,0,1,0,1,0,0,0,0,1,0,0,0,0,1,0,0,0,0,1,0,0,1,1,0,0,
1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,1,0,1,1,0,1,1,1,1,1,1,1,1,1,1,0,1,1,0,0,0,1,0,1,1,1,1,1,1,
1,1,1,1,1,1,1,0,0,1,1,1,1,1,1,1,1,1,0,0,0,0,1,1,0,0,1,0,0,0,0,1,0,0,0,0,1,0,0,1,1,0,1,0,1,0,1,1,1,1,1,
```

```
0,1,1,1,1,0,1,1,1,1,0,1,1,0,0,1,1,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,1,1,1),ncol=2)

csexMat<-
matrix(c(0,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,1,
1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,1,0,1,0,1,0,0,1,1,1,0,0,1,1,0,0,1,0,0,0,0,0,0,1,0,0,0,
0,0,0,0,1,1,0,1,0,0,0,0,0,0,0,0,0,0,1,1,1,1,0,0,0,1,1,0,0,1,0,1,1,1,1,1,1,0,0,1,0,0,1,0,0,0,0,0,0,1,0,0,0,
0,0,0,1,0,1,0,1,1,1,0,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,1,0,1,1,1,1,1,1,0,1,1,1,0,1,
1,1,1,1,1,1,1,1,1,1,1,0,0,1,1,1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,1,0,0,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,
1,1,1,1,0,1,1,1,1,0,1,0,1,0,1,1,0,0,0,1,1,0,0,1,1,0,1,1,1,1,1,1,1,0,1,1,1,1,1,1,1,0,0,1,0,1,1,1,1,1,1,1,1,
1,1,0,0,0,0,1,1,1,0,0,1,1,0,1,0,0,0,0,0,0,0,1,1,0,1,1,0,1,1,1,1,1,1,0,1,1,1,1,1,1,0,1,0,1,0,0,0,1,1,1,1,1,0,
1,1,1,1,1,1,1,1,0,1,1,1,1,1,1,0,1,1,1,1,1,1,1,1,1,0,1,0),ncol=2)

#AA data
obs<-
c(0.017350042,0.084032438,0.03641471,0.006920056,0.137115651,0.027327077,0.005993777,
0.044010708,0.069378846,0.010514861,0.014310915,0.03444247,0.01435424,0.033273261,0.0
11147111,0.00670304,0.023194937,0.111358709,0.032346837,0.112310053,0.007453209,0.059
143763,0.01960592,0.047680298,0.028099882,0.061890752,0.008497196,0.035403528,0.02333
7659,0.039197505,0.000613376,0.002442576,0.001152932,0.119083791,0.048393888,0.009762
529,0.184720241,0.001734263,0.007122594,0.059395677,0.218546635,0.248370012,0.0161764
79,0.085190125,0.040132681,0.009859094,0.016645073,0.03530487,0.01592091,0.024527415,
0.26626204,0.012736538,0.063586307,0.00717582,0.076497928,0.019502184,0.020986633,0.0
28614011,0.024973471,0.00119878,0.012589362,0.026679883,0.068123261,0.04589269,0.0104
35116,0.087902283,0.020572389,0.129291463,0.007176405,0.057250223,0.019863102,0.01561
1183,0.014494003,0.039229738,0.076910807,0.060384193,0.610143967,0.01223433,0.1160224
84,0.010911814,0.109203817,0.049073961,0.673655346,0.103306365,0.034933284,0.18276076
1,0.049565241,0.044059274,0.011055779,0.053891879,0.000393386,0.000711352,0.000656003
,0.000629383,0.000372505,0.023466792,0.524718386,0.016259758,0.091096528,0.104956343,
0.113427869,0.15712521,0.198383951,0.063101159,0.191890519,0.057944813,0.078956948,0.
121378273,0.000905155,0.002018225,0.111269391,0.156888955,0.197875892,0.061945904,0.1
90338663,0.05832816,0.158075899,0.060702934,0.157630345,0.018069077,0.015121769)

modcensB <- list(nObs=121, nCens = 192, xMat = xMat, cMat = cMat, obs=obs, L =
min(obs),nSpp = 4, nSex = 2, sexObs = sexObs, sexCens = sexCens,xsexMat=xsexMat,
csexMat= csexMat)

modB<-"data {
        int<lower=0> nObs;
        int<lower=0> nSex;
        int<lower=0> nCens;
        int<lower=0> nSpp;
        int<lower=0> sexObs[nObs];
        int<lower=0> sexCens[nCens];
        matrix<lower=0>[nObs,nSpp] xMat;
        matrix<lower=0>[nCens,nSpp] cMat;
        matrix<lower=0>[nObs,nSex] xsexMat;
```

```
        matrix<lower=0>[nCens,nSex] csexMat;
        vector[nObs] obs;
        real<upper=min(obs)> L;
}

parameters {
        real<lower=0,upper=L> obsCens[nCens];
  vector<lower=0>[nSpp] beta;
  vector<lower=0>[nSex] betasex;
        vector<lower=0>[nSex] sigmaRaw;
        real<lower=0> tau;
}

transformed parameters {
        vector<lower=0>[nSex] sigma;
        sigma <- sigmaRaw * tau;
}
model {
        sigmaRaw ~ cauchy(0,5);
        tau ~ cauchy(0,5);
        beta ~ normal(0,5);
        for(n in 1:nObs)
        obs[n] ~ normal(xMat[n] * beta + xsexMat[n] * betasex, sigma[sexObs[n]]);

        for(c in 1:nCens)
        obsCens[c] ~ normal(cMat[c] * beta + csexMat[c] * betasex, sigma[sexCens[c]]);
}

generated quantities {
        vector[nObs] log_lik;

        for(n in 1:nObs) {
                log_lik[n] <- normal_log(obs[n], xMat[n] * beta + xsexMat[n] * betasex,
sigma[sexObs[n]]);
        }
}"


ButterflyMod <- stan(model_code=modB, data=modcensB, iter=10000,chains=4, seed=3,control
= list(adapt_delta = 0.95))
launch_shinystan(ButterflyMod)
# buttouts<-extract(ButterflyMod,pars="beta")$beta
# save(buttouts,file="butterbetas.R")
####Butterfly sequestration experiment
modB<-"data {
        int<lower=0> nObs;
```

```
        int<lower=0> nCens;
        int<lower=0> nTreat;
        matrix<lower=0>[nObs,nTreat] xMat;
        matrix<lower=0>[nCens,nTreat] cMat;
        vector[nObs] obs;
        real<upper=min(obs)> L;
}

parameters {
        real<lower=0,upper=L> obsCens[nCens];
  vector<lower=0>[nTreat] beta;
        real sigma;
}

model {
        sigma ~ cauchy(0,5);
        beta ~ normal(0,5);
        obs ~ normal(xMat * beta, sigma);
        obsCens ~ normal(cMat * beta, sigma);
}

generated quantities {
        vector[nObs] log_lik;

        for(n in 1:nObs) {
                log_lik[n] <- normal_log(obs[n], xMat[n] * beta, sigma);
        }
}"

## P. anchises

xMat<-
matrix(c(1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,
1),ncol=3)
cMat<-matrix(c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1),ncol=3)
obs<-
c(0.076497928,0.068123261,0.024973471,0.026679883,0.040132681,0.048393888,0.03530487,
0.020986633,0.020572389,0.060384193,0.063586307,0.091096528,0.057250223,0.074173376,0
.00119878,0.008590943)
Pan<-list(nObs=16,nCens=12,nTreat=3, xMat=xMat,cMat=cMat,obs=obs,L=min(obs))
modPan<-stan(model_code=modB,data=Pan,iter=1000,chains=4, seed=3,control =
list(adapt_delta = 0.95))
#launch_shinystan(modPan)

## B. polydamas
xMat<-matrix(c(1,1,0,0,0,0,0,1,1,0,0,0,0,0,1),ncol=3)
```

```
cMat<-matrix(c(0,0,0,0,0,0,0,0,1,1,1,1),ncol=3)
obs<-c(0.008403244,0.006937885,0.008907156,0.006703048,0.003922981)
Bpo<-list(nObs=5,nCens=4,nTreat=3, xMat=xMat,cMat=cMat,obs=obs,L=min(obs))
modBpo<-stan(model_code=modB,data=Bpo,iter=1000,chains=4, seed=3,control =
list(adapt_delta = 0.95))
#launch_shinystan(modBpo)

# betaan<-extract(modPan,pars="beta")$beta
# betapo<-extract(modBpo,pars="beta")$beta
# save(betapo,file="censoredBpo.R")
# save(betaan,file="censoredPan.R")
```