

# Test of Biomass as Covariate in Aster Models for Lifetime Fitness

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## Introduction

The following code tests, on the advice of Dr. Daniel Bolnick and Dr. Lynda Delph, the effect of biomass on female and male fitness, as determined with aster models.

## Preliminaries

Set working directory and load data.

Examine data

```
fin<- read.csv("data/aster.dat.csv")
```

```
names(fin)
```

```
## [1] "Treat"      "plotID"     "Den"        "Gen"        "plantID"
## [6] "familyID"   "surv"       "flw"        "frt"        "frt.2"
## [11] "seeds"      "aborted"    "rel.seeds"  "seed.wt"    "mass.a"
## [16] "mass.b"
```

```
head(fin)
```

```
##   Treat plotID Den Gen plantID familyID surv flw frt frt.2 seeds aborted
## 1 HDHG      5  H  HG      1         4    1  1  3    2    33      14
## 2 HDHG      5  H  HG      2         6    1  1 21    6    69      22
## 3 HDHG      5  H  HG      3        11    1  1 16    7    73      19
## 4 HDHG      5  H  HG      4        14    1  1 18    8   107      23
## 5 HDHG      5  H  HG      5         6    1  1  1    1    16       4
## 6 HDHG      5  H  HG      6        14    1  1  0    0     0       0
##   rel.seeds seed.wt mass.a mass.b
## 1 0.5714286  6.792   5.8   0.8
## 2 1.1948052  6.995   1.9   0.2
## 3 1.2640693  7.413  20.8   1.3
## 4 1.8528139  8.554  18.2   1.1
## 5 0.2770563  7.771  65.8   6.1
## 6 0.0000000  0.000   6.6   1.2
```

Make sure Den (density treatment), Gen ( $N_e$  treatment), plotID, plantID, and familyID are all classified as factors. Otherwise

```
fin$Den<- as.factor(fin$Den)
fin$Gen<- as.factor(fin$Gen)
fin$plotID<- as.factor(fin$plotID)
fin$plantID<- as.factor(fin$plantID)
fin$familyID<- as.factor(fin$familyID)
```

## Setting up for aster analyses

Load aster package (make sure you have most current version)

```
library(aster)
```

Begin by naming variables that will be used in the graphical model of the aster analyses:

**flw** - total number of flowers produced **frr** - total number of fruits produced **frr.2** - subsetting number of fruits collected **seeds** - total number of seeds collected from subsetting fruits

```
vars<- c( "flw", "frr", "frr.2","seeds")
```

Reshape the data so that all response variables are located in a single vector, in a new data set called “redata”

```
redata <- reshape(fin, varying = list(vars), direction = "long",timevar = "varb", times = as.factor(varb))
```

Designate the terminal fitness variable “seeds” (make it numeric), and then add it to the reshaped data

```
fit <- grepl("seeds", as.character(redata$varb))
fit<- as.numeric(fit)
redata$fit <- fit
```

Check

```
with(redata, sort(unique(as.character(varb)[fit == 0])))
```

```
## [1] "flw" "frr" "frr.2"
```

```
with(redata, sort(unique(as.character(varb)[fit == 1])))
```

```
## [1] "seeds"
```

Add a variable “root” to redata, where value is 1. This is the “starting point” of the aster graphical model (i.e. a seed planted)

```
redata<- data.frame(redata, root=1)
```

Set up the graphical model and designate the statistical distribution for each node. This graphical model has four nodes (in object **pred**) described earlier. Statistical family for each node is described by object **fam**.

```
pred<- c(0,1,2,3)
fam<- c(1,2,2,2)
```

Show distribution family for each node

```
sapply(fam.default(), as.character)[fam]
```

```
## [1] "bernoulli" "poisson" "poisson" "poisson"
```

## Main Aster Analyses for Female Fitness (Seeds set)

First aster analysis with only fitness data. Note, **aster** reads the **redata** version of the data.

```
aout<- aster(resp~varb, pred, fam, varb, id, root, data=redata)
```

```
aout1<- aster(resp~varb + fit:(mass.a), pred, fam, varb, id, root, data=redata)
```

```
aout2<- aster(resp~varb + fit:(mass.a + familyID), pred, fam, varb, id, root, data=redata)
```

```
aout3<- aster(resp~varb + fit:(mass.a + familyID + Gen), pred, fam, varb, id, root, data=redata)
```

```

aout4<- aster(resp~varb + fit:(mass.a + familyID + Gen + Den), pred, fam, varb, id, root, data=redata)

aout5<- aster(resp~varb + fit:(mass.a + familyID + Gen + Den + Gen*Den) , pred, fam, varb, id, root, da

anova(aout, aout1, aout2, aout3, aout4, aout5)

## Analysis of Deviance Table
##
## Model 1: resp ~ varb
## Model 2: resp ~ varb + fit:(mass.a)
## Model 3: resp ~ varb + fit:(mass.a + familyID)
## Model 4: resp ~ varb + fit:(mass.a + familyID + Gen)
## Model 5: resp ~ varb + fit:(mass.a + familyID + Gen + Den)
## Model 6: resp ~ varb + fit:(mass.a + familyID + Gen + Den + Gen * Den)
##   Model Df Model Dev Df Deviance P(>|Chi|)
## 1      4    132606
## 2      5    132608 1      1.44    0.2295
## 3     16    132998 11    390.06 <2e-16 ***
## 4     17    133296 1    298.06 <2e-16 ***
## 5     19    133915 2    619.32 <2e-16 ***
## 6     21    134028 2    112.83 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## Interpretation

Sequential addition of `familyID`, `Gen` ( $N_e$ ), `Den` (density), `Gen * Den` (Gen by Den interaction), and finally `mass.a` (above ground biomass) consistently explained more variation in total lifetime fitness. Next, move on to specific models to estimate fitness across treatments.

## Test of effectos of biomass on male fitness (relative number of seeds sired)

Load data with relative number of seeds set (`rel.seeds`) and sired (`sires`).

```
fin<- read.csv("C:/Users/Mason Kulbaba/Dropbox/git/density-gen-Ne/data/aster.sire.dat.csv")
```

Perform preliminary tasks of factor class setting, and organizing of data for density-treatment specific analyses, as the number of seeds sired was only estimated for the high  $N_e$  treatment.

```

fin$Den<- as.factor(fin$Den)
fin$Gen<- as.factor(fin$Gen)
fin$plotID<- as.factor(fin$plotID)
fin$plantID<- as.factor(fin$plantID)
fin$familyID<- as.factor(fin$familyID)

#subset data to density-specific treatments and 'drop' unused levels
datH<- subset(fin, Den=="H")
datH$familyID<- droplevels(datH$familyID)
datM<- subset(fin, Den=="M")
datM$familyID<- droplevels(datM$familyID)
datL<- subset(fin, Den=="L")
datL$familyID<- droplevels(datL$familyID)

```

```
#set vars
vars<- c( "flw", "frt", "sires")

redata<- reshape(fin, varying = list(vars), direction = "long",timevar = "varb", times = as.factor(vars))
```

Designate fitness var

```
#Designation of fitness variable
fit <- grepl("sires", as.character(redata$varb))
fit<- as.numeric(fit)

#add fit to each of three redata files (one for each ensity treat)
redata$fit <- fit
```

Add a variable “root” to redata, where value is 2

```
redata<- data.frame(redata, root=2)
```

Set graphical model and statistical family for each node

```
pred<- c(0,1,2)
fam<- c(1,2,2)

sapply(fam.default(), as.character)[fam]
```

```
## [1] "bernoulli" "poisson" "poisson"
```

Build aster models

```
aout.sire<- aster(resp~varb, pred, fam, varb, id, root, data=redata)

aout.sire2<- aster(resp~varb + fit:(mass.a), pred, fam, varb, id, root, data=redata)

aout.sire3<- aster(resp~varb + fit:(mass.a + familyID), pred, fam, varb, id, root, data=redata)

aout.sire4<- aster(resp~varb + fit:(mass.a + familyID + Den), pred, fam, varb, id, root, data=redata)

anova(aout.sire, aout.sire2, aout.sire3, aout.sire4)
```

## Analysis of Deviance Table

##

## Model 1: resp ~ varb

## Model 2: resp ~ varb + fit:(mass.a)

## Model 3: resp ~ varb + fit:(mass.a + familyID)

## Model 4: resp ~ varb + fit:(mass.a + familyID + Den)

##   Model Df Model Dev Df Deviance P(>|Chi|)

## 1       3       25316

## 2       4       25323   1    6.4129   0.01133 \*

## 3       14       25341  10  18.4162   0.04834 \*

## 4       16       25341   2    0.3874   0.82389

## ---

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