

Homework on Aster Models

your name

Due on: May 1st at 11:59 PM

Problem 1 [80 points]: We are going to analyze fitness for a population of yellow monkey flowers, *Mimulus guttatus*. The dataset comes from [Lowry and Willis \(2010\)](#) and the study in which the data is obtained investigates the role of chromosomal inversions in adaptation and speciation. Phenotypic traits and covariates are recorded for 2313 *M. guttatus*. Complete the following:

part a [10 points]: These plants either survive or die. Conditional on survival these plants then reproduce. Reproduction is taken to be Darwinian fitness. All surviving plants have non-zero reproduction. Write out the graphical structure corresponding to a life history of *M. guttatus*. Include the distributions specifying the relationships between nodes in the graph.

part b [10 points]: Load in the `Mguttatus` data set (the `Mguttatus.rda` file located in the same directory as this assignment is the relevant data set) and copy the code:

```
data = Mguttatus
redata = Mguttatus.redata
vars = quantities$vars
pred = quantities$pred
group = quantities$group
code = quantities$code
fam = quantities$fam
nnode = length(vars)
n = nrow(redata) / nnode
families = quantities$families
root = redata$root
fit = redata$fit
varvar = quantities$varvar
idvar = quantities$idvar
```

part c [20 points]: Fit the main effects only aster model including terms for genetic background (`gen_bac`), site (`site`), inversion (`inversion`), and type (`type`). Note that your call to `aster` will require you to specify the following arguments: `varvar = varvar`, `idvar = idvar`, `data = redata`, `root = root`, i.e. the hard work has already been done for you.

part d [20 points]: Obtain estimates of expected Darwinian fitness for all unique factor-level combinations of the variables used to fit the main effects only aster model. The code below will come in handy for creating the unique factor-level combinations:

```
test = data$redata
a = levels(test$gen_bac)
b = levels(test$site)
c = levels(test$inversion)
d = levels(test$type)
fred = expand.grid(a = a, b = b, c = c, d = d)
colnames(fred) = c("gen_bac", "site", "inversion", "type")
fred$sur_flw = 1
```

`fred$flws = 1`

part e [10 points]: Report which 5 combinations of phenotypic traits are estimated to have the highest expected Darwinian fitness, and report which 5 combinations of phenotypic traits are estimated to have the lowest expected Darwinian fitness.

part f [10 points]: Read through [Lowry and Willis \(2010\)](#) and briefly explain in your own words reasons for why these researchers chose to study *M. guttatus* in their analysis.

Problem 2 [20 points]: In the Aster model notes it was stated that the system of equations

$$\phi_j = \theta_j - \sum_{G \in p^{-1}(\{j\})} c_G(\theta_G), \quad j \in J,$$

determine an invertible change of parameters. Show this. There are linked references in the Aster model notes that may be helpful.