

Homework on Aster Models

your name

Due on: May 3rd at 11:59 PM

Problem 1: 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:

1. 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.
2. 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
```

3. 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.
4. 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
```

5. 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.
6. Read through [Lowry and Willis \(2010\)](#) and briefly explain in your own words why *M. guttatus* were particularly relevant for their analysis.

Problem 2: In the **Conditional and unconditional distributions** section of 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.