Population Genetics Project #5

Janis Antonovics and his colleagues have been studying a plant venereal disease (anther-smut, *Microbotryum*) in members of the genus *Silene* and *Dianthus*. Emily Bruns and colleagues ([1] recently investigated the role of anther-smut in maintaining a sexual polymoprhism in *Dianthus pavonius*. Specifically, *D. pavonius* is gynodioecious, meaning that individuals may be either female or hermaphrodite. Bruns et al. show that females are more common in populations where anther-smut is more common.

As part of their analysis, Bruns et al. provide data on (a) the number of inflorescences (flower-bearing stalks) and (b) the size of flowers for individuals grouped by maternal family. You'll find these data on the course website in `flower-size.csv`.[1] The columns in the file are

- **ID**: a unique numeric identifier for each individual
- **Site**: the site from which the individual is derived (L or U)
- **Fam**: a unique numeric identifier for each maternal family
- **Female**: a number indicating if the individual is female (1) or hermaphrodite (0)
- **inflos**: the number of inflorescences on this individual
- **flower1**: the size of the first flower on this individual

Using these data, answer the following questions:

1. Is there evidence that the number of inflorescences or the size of flowers differs between sites?
2. Is there evidence that the number of inflorescences or the size of flowers differs between hermaphrodites and females?
3. What is the narrow-sense heritability of inflorescence number?

[1] This file is a slightly simplified version of the original data, which is available in [2].

4. What is the narrow-sense heritability of flower size?

5. You are likely to find that the credible interval for the narrow-sense heritability of flower size is very broad. Suppose you had the opportunity to gather a new sample of individuals from maternal families where the total number of individuals is twice as great as in the current sample. Use your estimates of mean flower size and of the variance within and among families, determine whether you'd be better off (a) increasing the number of families, (b) increasing the number of offspring per familty, or (c) some combination of (a) and (b). There are 20 families and 164 individuals in the original data. Assume that there were 20 families with exactly 8 individuals per family for purposes of answering this question.

Hints

- Kristen will show you how to fit a linear model with mixed effects to data like those presented here using `stan_glmer()` from `rstanarm`.

- You will want to specify `family = "neg_binomial_2"` in your analysis of the number of inflorescences. Kristen will help you with the syntax and provide a general explanation. If you want a deeper explanation, ask me in class on Thursday.

- Use `nb_within()` to extract the posterior distribution of the within family variance for the inflorescence analysis, `within()` to extract the within family variance for the flower size analysis, and `among()` to extract the among family variance for either analysis. You can report the posterior mean and 80% credible intervals for these components of variance and for the heritability with `report()`.[2].

- Use `simulate_analysis()` to explore different sample configurations. Note: It defaults to simulating 10 sets of experiments with the same configuration (`n_reps = 10`). You can increase that by including a number bigger than 10 as the last argument when you call it.[3] I recommend running it once with the default for `n_reps` so that you get a sense of how long the simulation will take on your computer. Then increase the `n_reps` to 25, 50, 100, or more depending on how long you can run the simulation. The longer you run the simulation, the more reliable the results will be.

[2] If you want to use 95% credible intervals, change the `quantile()` statement to read `int <- quantile(x, c(0.025, 0.975))`

[3] You could also decrease the number, but 10 simnulations doesn't take too long, and fewer than 10 won't give you a very good idea of what's going on.

References

[1] EL Bruns, I Miller, ME Hood, V Carasso, and J Antonovics. The role of infectious disease in the evolution of females: Evidence from anther-smut disease on a gynodioecious alpine carnation. *Evolution*, 73:497–510, 2019.

[2] EL Bruns, I Miller, ME Hood, V Carasso, and J Antonovics. The role of infectious disease in the evolution of females: Evidence from anther-smut disease on a gynodioecious alpine carnation. *Dryad Digital Repository*, 2019. `https://doi.org/10.5061/dryad.7dv1tg7`.