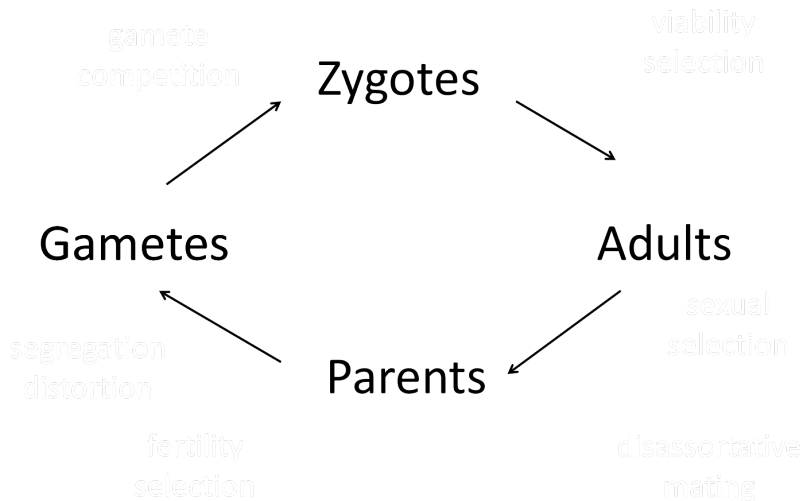


Nora Mitchell
February 14, 2017

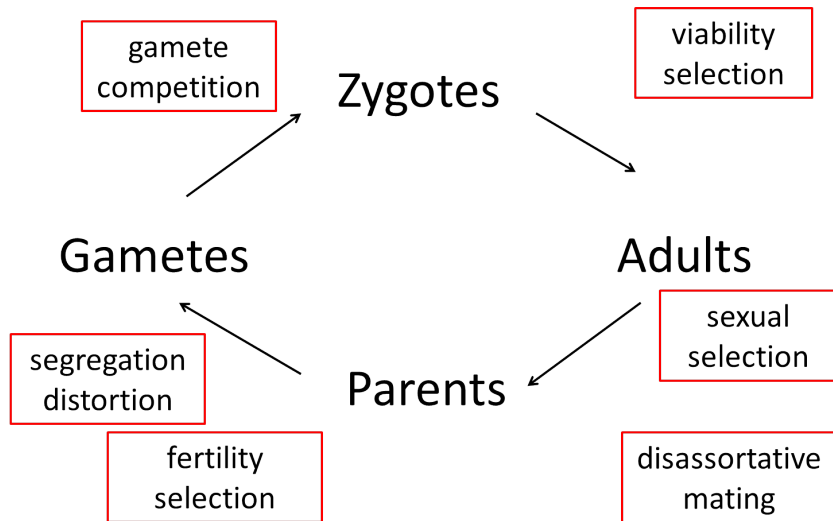
Goals for Today's Lab

- ▶ Brief diagram learning
- ▶ Install command-line STRUCTURE
- ▶ Learn how to use R package *strataG*
- ▶ Check default prior assumption

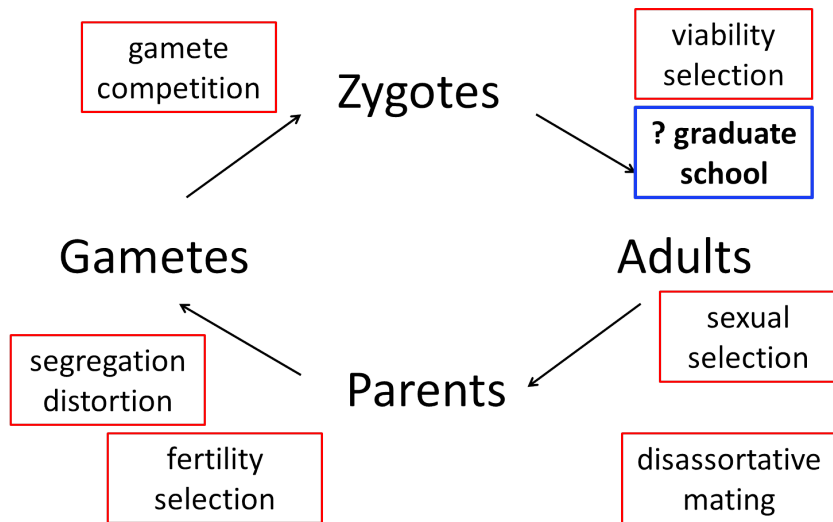
Life



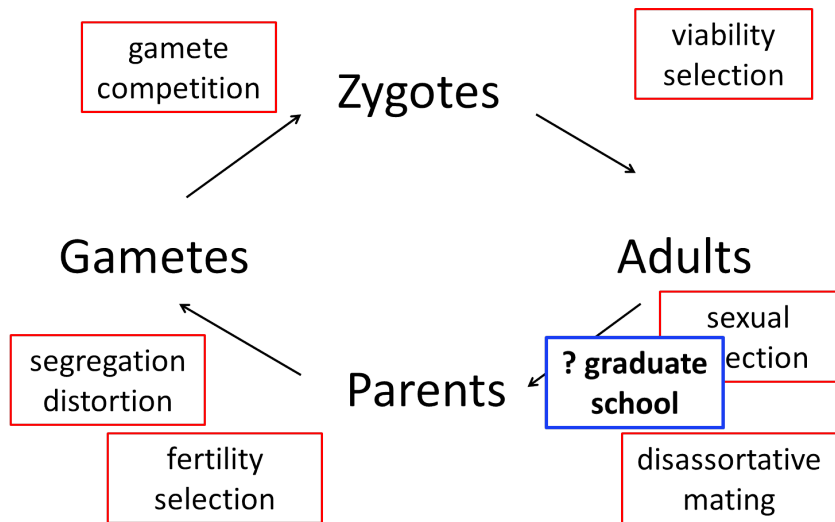
Components of Selection



Grad School Selection



Grad School Selection



STRUCTURE

Last week we learned how to use the Bayesian program STRUCTURE to perform individual assignment analysis.

This program takes genetic data from individuals and is iteratively run over different values of K groups, then evaluated for which value(s) of K are most supported

STRUCTURE

STRUCTURE has a graphical user interface, which can be nice, but can also be inconvenient.

What if you want to run it on a cluster? Or for a long time?

Why is it so buggy?

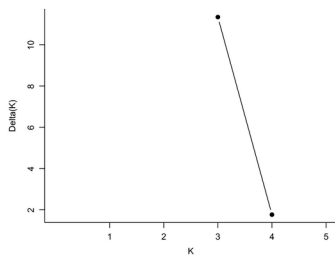
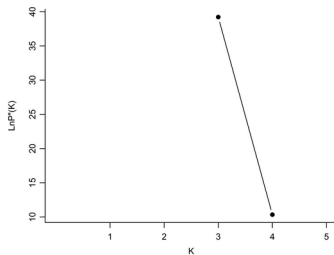
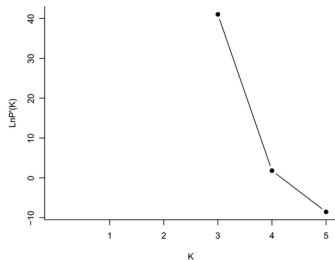
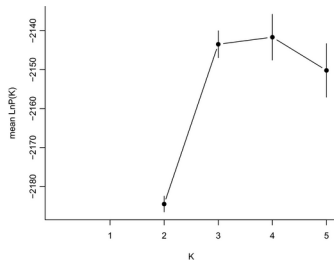
There is a command-line version of STRUCTURE that you can download.

Archer et al. (2016) came out an R wrapper package for a number of programs, including STRUCTURE

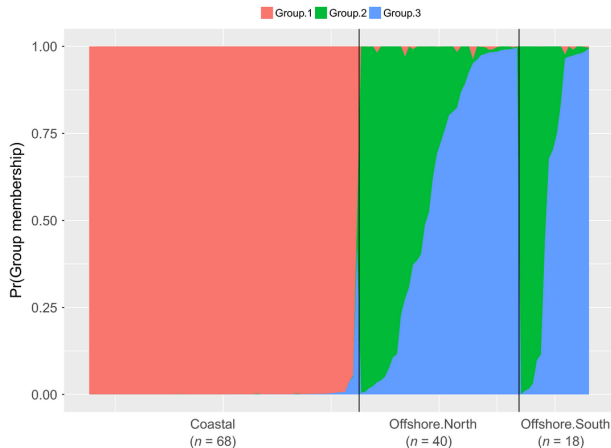
strataG, similar to *R2jags*, can run executables in R.

Today, we'll install the command-line version and learn how to use it in R!

strataG runs STRUCTURE and can make plots!



strataG runs STRUCTURE and can make plots!



Settings

Additionally, the parameter settings that we use include more than just the burnin and number of iterations/ reps to run

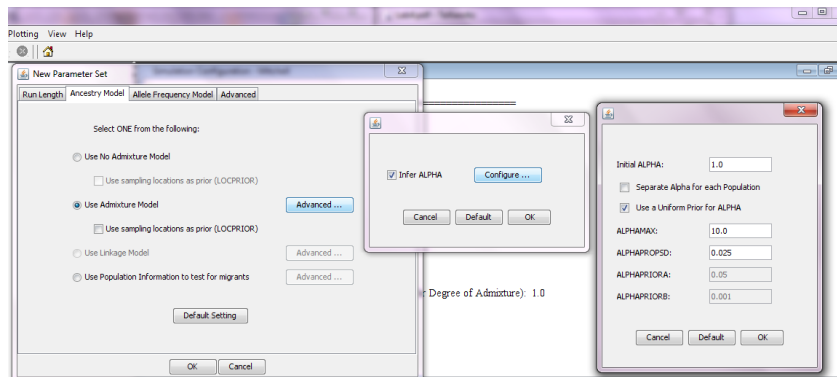
Wang (2016) investigated the use of the ALPHA ancestry prior, which assumes that all populations contribute equally to the pool of individuals sampled

“The computer program structure for assigning individuals to populations: easy to use but easier to misuse”

Why might this be a problem?

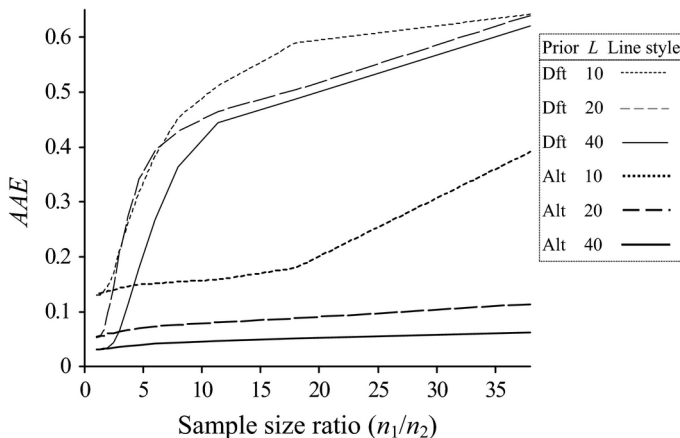
Wang (2016)

The non-default version (alternative ancestry prior) of ALPHA allows for populations to contribute differentially to the pool, but it's kind of hidden



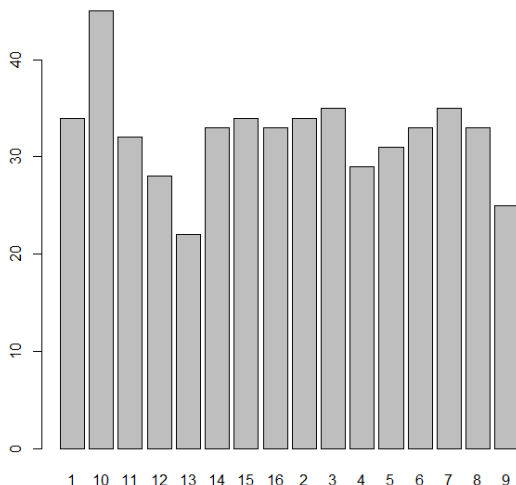
Wang (2016)

When sample sizes from populations are unequal, how does choice of prior affect results?



Prunier (Accepted)

When sample sizes from populations are unequal, how does choice of prior affect results?



Today's Activity

1. Use strataG tutorial
2. Download STRUCTURE executable
3. Make sure it's location is added to PATH (see OS-specific instructions)
4. Install strataG package in R
5. Use strataG to run STRUCTURE on repens data and make plots
6. Use Nora-edited function to run STRUCTURE using alternative ancestry prior
7. Compare interpretation using default and alternative priors

Works Cited

- ▶ Archer, F. I., Adams, P. E. and Schneiders, B. B. (2016), strataG: An R package for manipulating, summarizing and analysing population genetic data. Mol Ecol Resour. doi:10.1111/1755-0998.12559
- ▶ Evanno, G., S. Regnaut, and J. Goudet. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Molecular Ecology 14:2611-2620.
- ▶ Pritchard, J. K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155:945-959.
- ▶ Rosenberg, N.A., J.K. Pritcharad, J.L. Weber, H.M. Cann, K.K. Kidd, L.A. Zhivotovsky, and M.W. Feldman. 2002. Genetic Structure of Human Populations. Science 298(5602): 2381-2385.
- ▶ Wang, J. (2016). The computer program Structure for assigning individuals to populations: easy to use but easier to misuse. Molecular Ecology Resources.