

Appendix 1: Detailed description of the data collection process

Concept inventory project

Participants

We recruited students from three public institutions: a mid-sized, doctoral-granting, public university in the Rocky Mountain west; a large, doctoral-granting, public institution in the western US; and a branch campus of the western institution that primarily serves undergraduates. Within these institutions, we recruited students from sophomore through senior level biology courses. Student responses were collected under exempt status from the IRBs at participating institutions (TA092111-EX & HSD#41485). Students had previously taken an introductory biology course, and in some cases upper-division courses, that covered genetic drift, **but we assumed a high degree of variability among students in term of their background on genetic drift**. We recruited students by speaking briefly during class time and following up with interested students. Most students completed a written questionnaire, but some responded to questions online. We did not compensate students for their participation, nor did they receive any class credit. As a result, our response rates were generally low, ranging from 5-20% of students in each course we targeted, and our sample may disproportionately include highly motivated students. Therefore our results may overestimate the quality of student conceptions about genetic drift. The present study included 37 student responses collected as part of the concept inventory project.

Data collection

Students responded to 11 questions designed as pilot questions for a forthcoming concept inventory on genetic drift:

1. What do biologists mean when they use the phrase “random processes”?
2. What is genetic drift?
3. Why does genetic drift occur?
4. The default explanation considered by scientists when they discover that a version of a gene (an allele) has become more or less common in a population is genetic drift. Why?
5. Louise has been studying a population of wild daisies with different colors. Over 15 years of research, the purple daisies have become much more common than the white ones. List four possible explanations for this result along with the kind of information you would need to determine whether your explanations are right.
6. Which of the explanations that you provided above invoke natural selection? If all of them involve selection, provide another explanation that uses a different evolutionary mechanism. Once again, list the kind of data you would need to determine if this explanation can account for the fact that purple daisies have become more common.

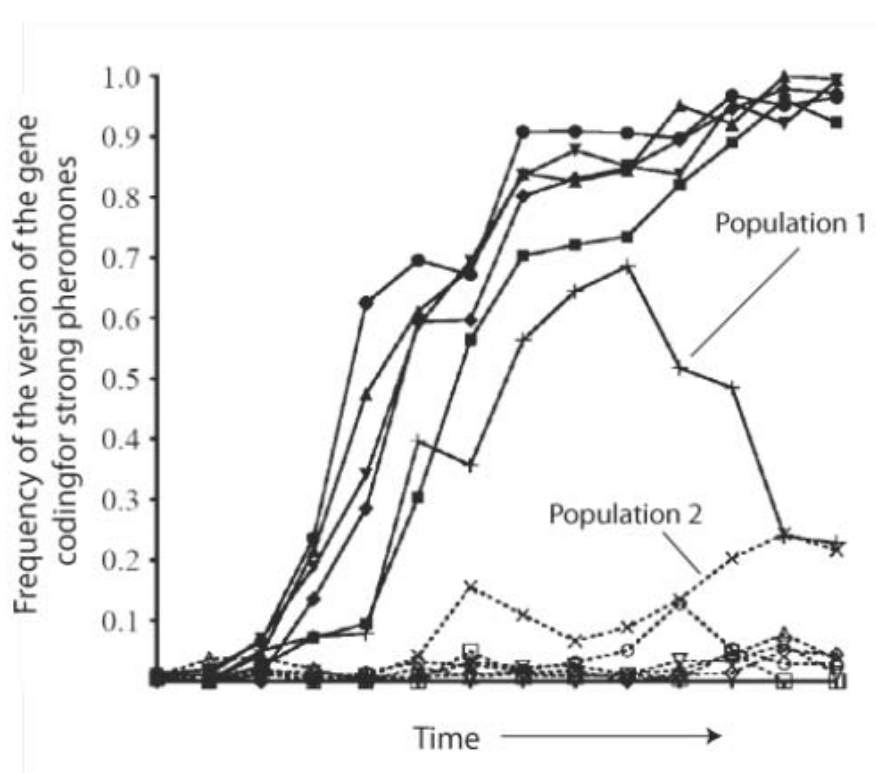


Figure 1. Changes in the frequency of a trait that attracts mates in yeast. The solid lines are yeast that live in an environment that favors the trait, and the dotted lines are from an environment in which that trait does not affect survival or reproduction. from Rogers and Grieg 2009.

Using Figure 1:

7. Describe which evolutionary processes are apparent from this graph.

8. What evolutionary processes could have caused the version of the gene in Population 1 to decrease?
9. Assume that Population 1 is much smaller than the other populations. Does your previous answer still apply? Explain.
10. Now assume that Population 1 is much larger than the other populations. Does your previous answer still apply? Explain.
11. Why does the frequency of the version of the gene that codes for a strong pheromone increase in Population 2?

Case study project

Participants

We collected data from students who were enrolled in classes participating in an NSF-funded project to assess the effectiveness of using case studies for instruction. This study included three instructors, each teaching two sections of introductory biology during one semester. Two of these courses took place at a large, doctoral-granting, public institution in the southeastern US and one course took place at a large, masters-granting, public institution in the midwestern US. One course was for biology majors and was primarily taken by sophomores. The other two courses were composed primarily of non-majors who were freshmen and sophomores. We collected student responses under exempt status from the IRB at the corresponding author's institution (Project 2010-10431-0).

Instructors ran their courses as usual except for the inclusion of eight pre-designed case studies covering cells, metabolism, DNA replication, genetic code, Mendelian genetics, the genetics of sex linkage and crossing over, evolutionary mechanisms (including genetic drift), and human evolution. The cases were incorporated into lecture-based courses that included the use of clickers and varying use of active learning techniques among instructors. All instructors used clickers throughout the semester; two used group testing and one solicited feedback from

students about their rationale for responses to clicker questions. Instructors taught **a modified version of** a case study by Horvath (2009) on the evolution of canids **and Isle Royale wolves**. **Compared to the published version of the case, which focused entirely on the evolutionary mechanisms of artificial and natural selection, the modified version also focused on the mechanism of genetic drift. Specifically,** as part of the story line, instructors introduced students to genetic drift by defining it as evolution purely due to chance and then used the evolution of Isle Royale wolves to illustrate and explain genetic drift. **Instructors prompted students to think about genetic drift with a question that asked them to consider how genetic drift could account for the relatively high proportion of congenital malformations in the bones of Isle Royale wolves as well as for decreased genetic diversity among Isle Royale wolves compared to Eastern Timber Wolf populations.**

Instructors tested students at the beginning and end of the term. The course instructor administered the first questionnaire during a regular class session. Students did not receive credit for test completion, but they were verbally encouraged to do their best. Instructors administered the second questionnaire as part of the final exam and students earned course credit for responding to the questions. The estimated student response rate for this dataset was 86%; response rates of individual sections ranged from 81% - 100%. Across all six sections, a total of 1233 students turned in both questionnaires. For the present study, we sampled from these matched exams to ensure students included in our sample were enrolled through the entire term. **We used a systematic sampling design with a random start to select 18 – 33 questionnaires completed before instruction and 24 – 32 completed after instruction from each of the six sections surveyed.** The number of questionnaires varied by section because we excluded blank questionnaires and the number of blank questionnaires varied by section. We assumed two

different students' conceptions of genetic drift would be more divergent than one student's conception assessed before and after instruction. Therefore, in order to maximize the breadth of student conceptions we were able to detect in our analyses, we chose not to match questionnaires by student. The present study included 319 student responses collected as part of the case study project.

Data collection

The results presented here are based on a single item from a questionnaire that was designed to measure students' content knowledge of natural selection and genetic drift and their ability to apply this knowledge to a novel scenario:

- Imagine you are doing a summer internship as a research assistant at Mountain Lake Biological Station in Virginia. During your internship you observe two distinct species of butterflies in the area. They have similar body shapes and they both drink nectar. But their color patterns are different; one is bright green and one is dark green. You further observe that their habitat ranges overlap, but are distinct in that the dark green butterfly prefers shady, cool forest interiors while the bright green butterfly prefers sunny meadows. Both species are camouflaged well in their respective habitats. You have seen both species preyed upon by birds. Finally, the population size of the two species is about equal. Based on the information given, was the evolution of these two species of butterflies more likely due to natural selection or genetic drift? Write an answer in which you concisely *define* both mechanisms, *state which evolutionary mechanism is more likely* and *logically explain why*.

This question was part of a 42-question assessment that included 40 multiple-choice and 2 short essay questions covering topics taught during the eight case studies mentioned above.

Horvath, T. (2009). Not necessarily on purpose: domestication and speciation in the Canidae Family. National Center for Case Study Teaching in Science (http://sciencecases.lib.buffalo.edu/cs/collection/detail.asp?case_id=477&id=477).