

# Through the Years: A Quantitative Biology Curriculum

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## INTRODUCTION

QUANTITATIVE REASONING is a skill that must be mastered by biology students before they graduate (NRC, 2003; AAAS, 2011; Hurney et al., 2011). Yet, experience suggests that biology students do not always see the need for this skill (“I just want to work with plants.”) or fear analytical problems (“I am not good at math.”). Student aversion to quantitative analysis poses pedagogical problems for teaching the process of science.

To address these problems, some biology faculty at Southeast have coordinated to teach skills that are built upon across the curriculum. For example, the first biology course for majors uses Microsoft Excel extensively to teach fundamental graphing and math functions for data analysis. Later courses require students to employ those early skills and to learn more advanced skills and new software such as R for simulations and analyses. **Here, I feature exercises from three courses that span the curriculum of a typical organismal biology student at Southeast.**

## LITERATURE CITED

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## YEAR 1: EVOLUTION AND ECOLOGY

EVOLUTION AND ECOLOGY is a new lecture and laboratory course for freshmen majors. The lab emphasizes course concepts via quantitative exercises. Specifically, students learn how to use Excel for basic calculations and graphical analyses of real and simulated data.

### HARDY-WEINBERG EQUILIBRIUM

Students use two equations to model allele and genotype frequencies in a population. The equation for the frequencies of two alleles ( $p$  and  $q$ ) is

$$p + q = 1,$$

and the equation for the three possible genotypes is

$$p^2 + 2pq + q^2 = 1.$$

Students build formulas in Excel to generate values for the five variables from  $p = 0.01$  to 1.0 and plot the three genotype frequencies (Fig. 1).

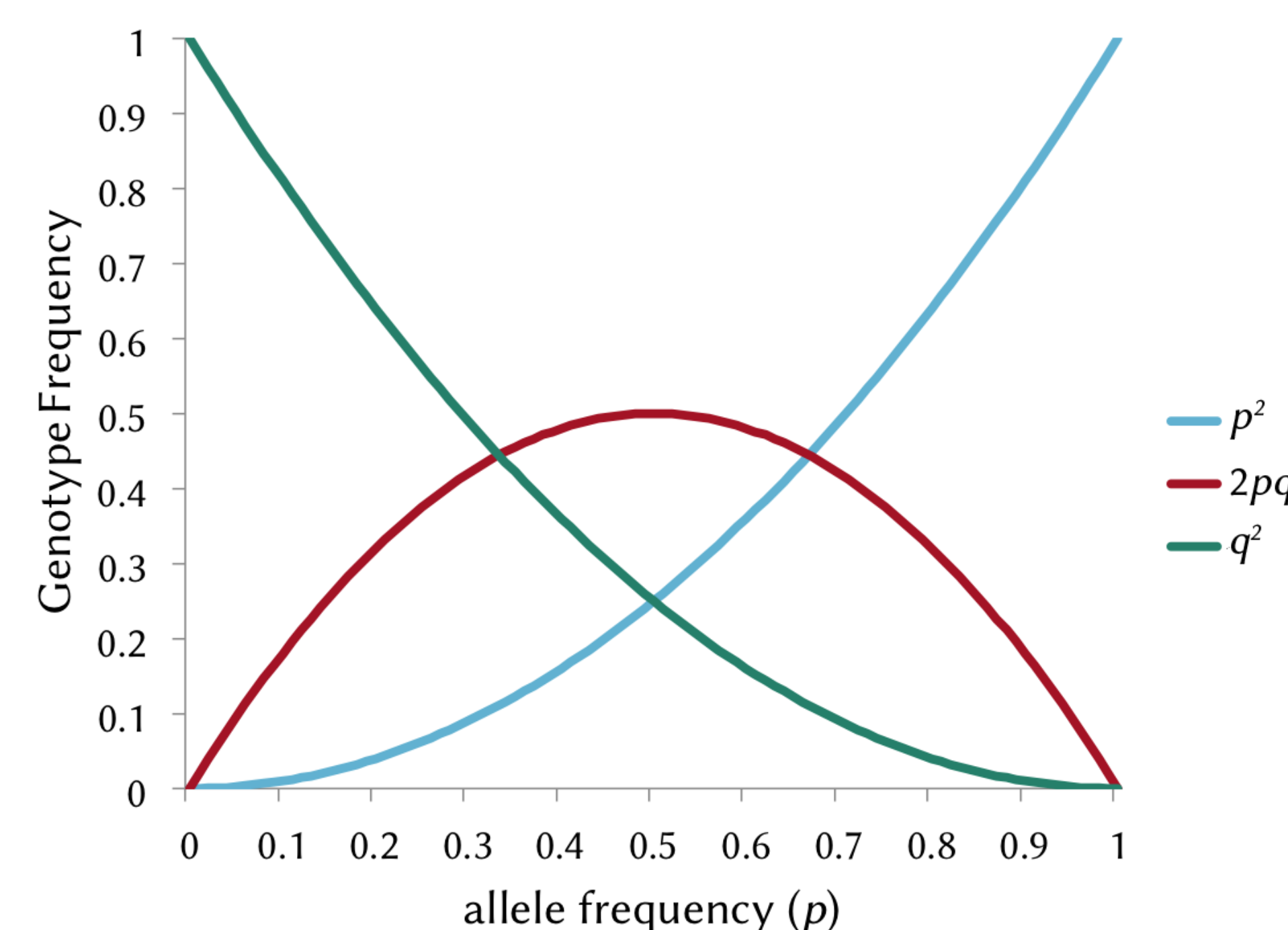


Figure 1. Expected genotype frequencies for the  $p$  allele frequency for a population in Hardy-Weinberg equilibrium.

Students next apply “beanbag” biology (Jungck et al., 2010) by sampling “alleles” from a “population” with known allele frequencies, and then apply a  $\chi^2$  test to compare observed to expected genotype frequencies. Students also explore how migration and natural selection affect allele frequencies in a population.

Representative questions from the migration component are

- Predict how the frequency of each allele will change for each population due to gene flow.
- Use the results of your migration simulation to explain why gene flow between populations should prevent them from becoming genetically different.

## YEARS 2–3: EVOLUTIONARY BIOLOGY

INTRODUCTION TO EVOLUTIONARY BIOLOGY is taken by sophomores and juniors. The course now is lecture-only but is being redesigned to include a once-per-week lab that reinforces lecture concepts through analyses of real-world data.

### POPULATION GENETICS

Students use PopG software (Felsenstein, 2016) to simulate allele frequencies in a population subject to different evolutionary scenarios such as natural selection and genetic drift. With PopG, students change population size, strength of selection, and migration and mutation rates to learn how these affect allele frequencies over time.

In one exercise, students explore the interaction between the strength of selection ( $s$ ) and the effective population size ( $N_e$ ). If  $2N_e s \gg 1$  then selection has a better chance of overcoming drift to cause a beneficial mutation to become fixed in the population. In simulations where  $2N_e s = 0$  and  $2N_e s = 2$ , students see that drift has the greatest effect in the first scenario but a beneficial mutation in the second scenario has about a  $4\times$  greater chance of becoming fixed in the population (Fig. 2).

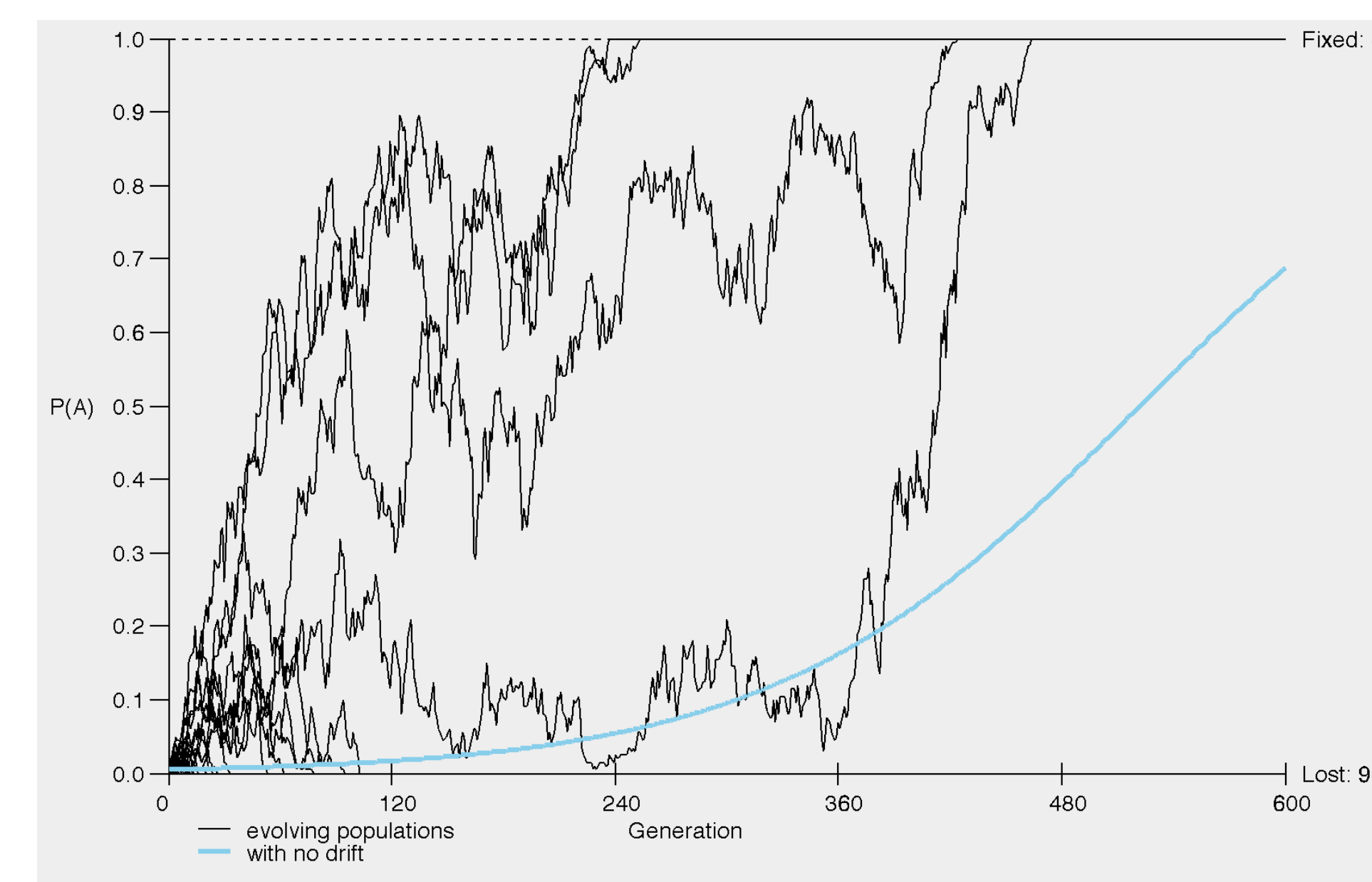


Figure 2. Simulation results for 100 populations with 100 individuals in each population and  $s = 0.01$ . The blue line represents a population without genetic drift.

Representative questions from this exercise are

- Predict how  $N_e$  affects the probability of fixation for an allele under weak positive selection ( $s = 0.01$ ). Justify your predictions for populations of  $N = 1000$  and  $N = 10,000$ .
- What should be the strength of selection in a population of  $N_e = 1000$  to overcome the effects of genetic drift? If  $N_e = 10,000$  or  $50,000$ ? Show your work.

## YEAR 4: BIOGEOGRAPHY

BIOGEOGRAPHY is a senior and graduate level course. Students use the R Statistical Package (R Core Team, 2016) to analyze real-world data to discover and report biogeographic patterns.

### BIOGEOGRAPHIC PROVINCES

Students compare distribution patterns of freshwater fishes and crayfishes by performing a principal coordinates ordination (PCO) for each taxonomic group. Watersheds with shared species occur together in ordinated space (Fig. 3).

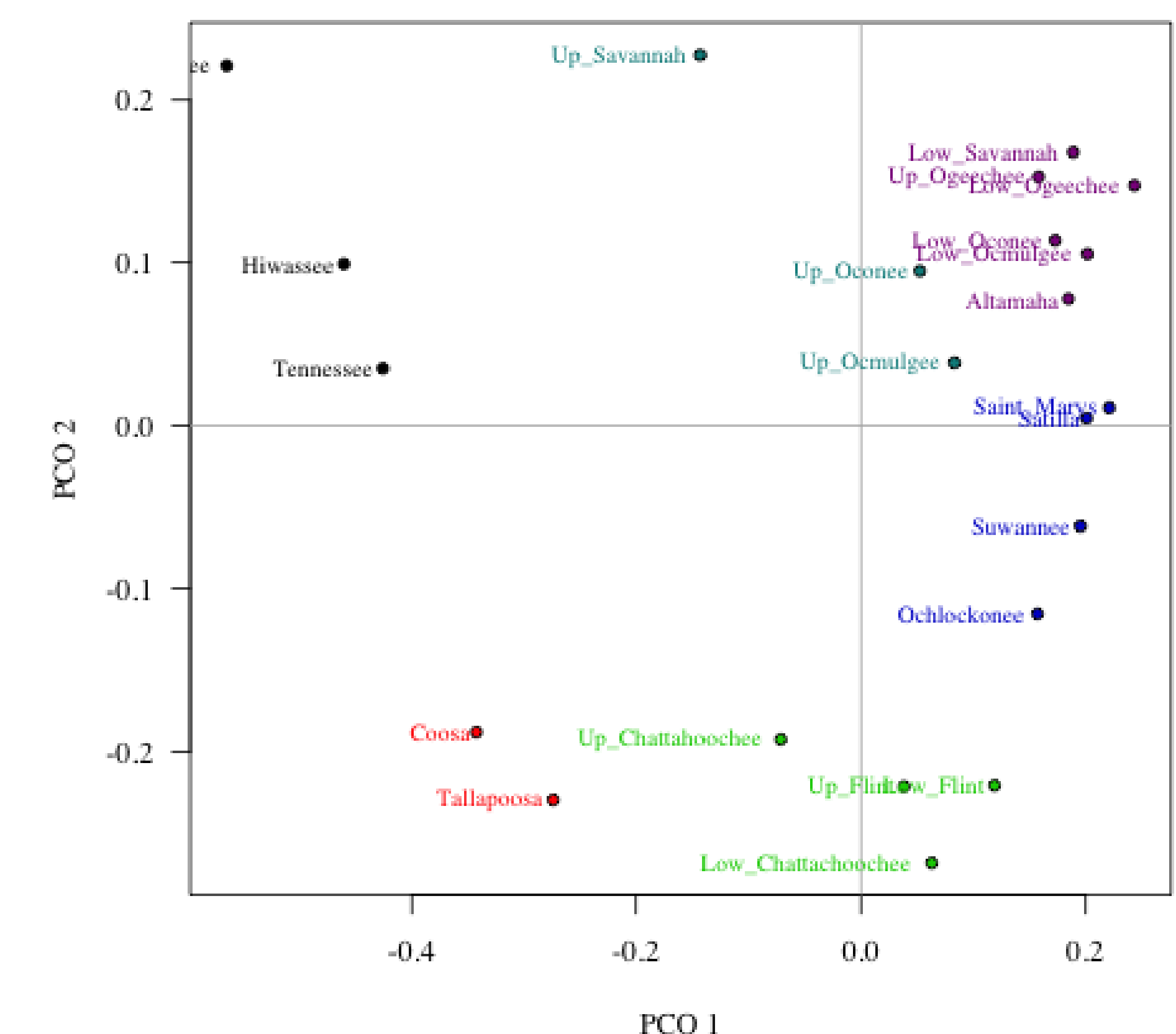


Figure 3. First two axes from a PCO of Georgia fishes. Colors indicate watersheds with a similar fauna.

Students compare fish and crayfish ordinations with a Procrustes analysis. A significant result suggests that fishes and crayfishes share a common biogeographic history (Fig. 4).

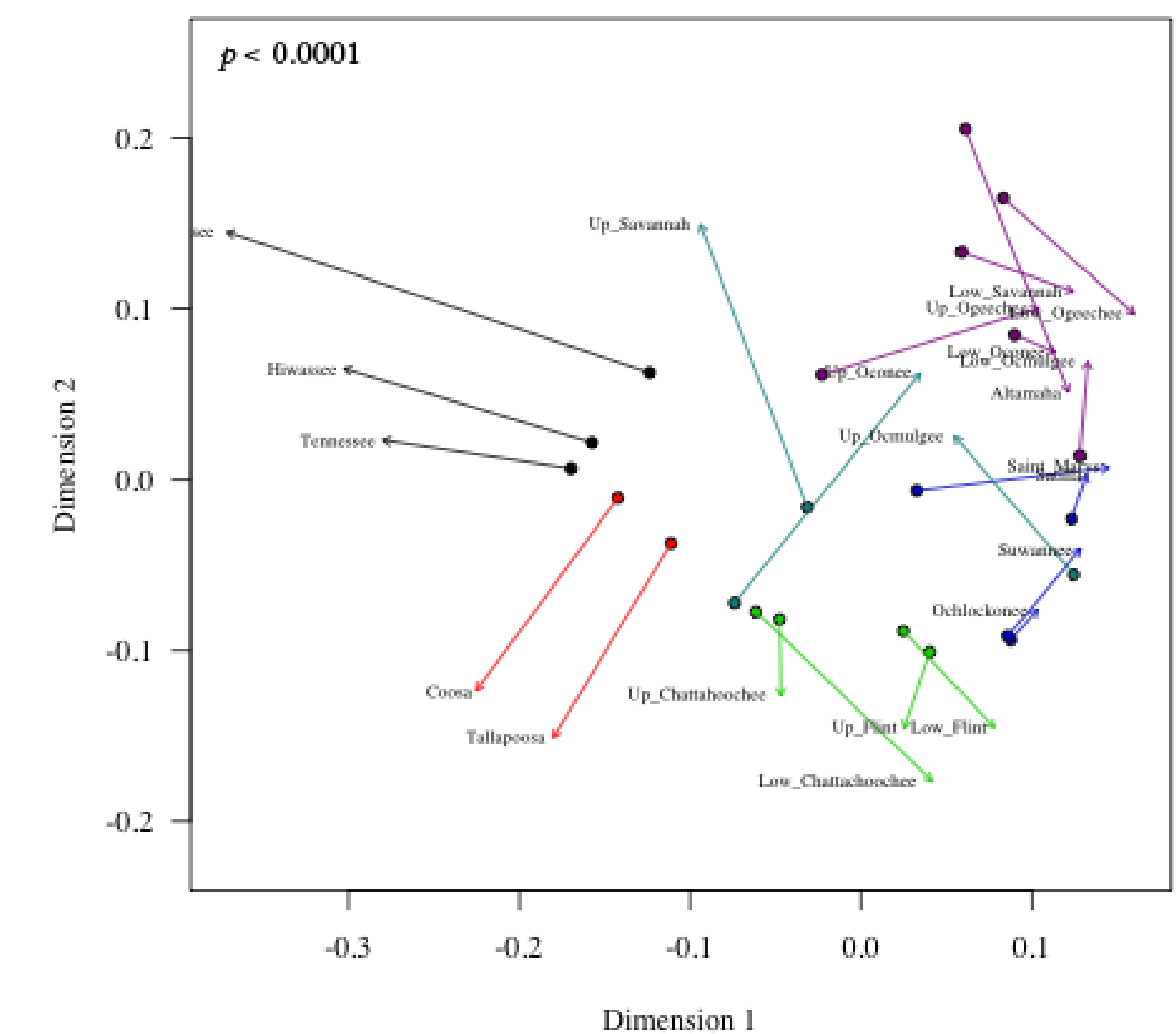


Figure 4. Procrustes analysis of fish and crayfish PCOs. The watersheds have a similar spatial relationships.