

RESEARCH STATEMENT

CATHERINE NEWMAN

My general interests are in biogeography and conservation of amphibians in the United States – particularly in the southeastern U.S. I am interested in exploring questions in phylogeography, phylogenetics, population genetics, conservation genetics, landscape genetics, and ecological niche modeling (species distribution modeling) to better understand the patterns and processes of the evolution of biodiversity in the southeastern U.S. **I view my research as a teaching tool for student training** in DNA lab work and genetic data analysis, computer-based geographic information system (GIS) methods, coding, field work, and the process of becoming a scientist. My research is very amenable to undergraduate participation and master's students. Students will be fully involved in project design, data collection, data analysis, and manuscript writing for publication, as well as presentation of research at regional, national, and international conferences. I am particularly excited to use the zoology collection at the ULM Museum of Natural History in my research, and to contribute to the collection. My research program can be maintained on a limited budget, and I have a history of successfully obtaining external funding for research. ULM's location in the Coastal Plain and relatively near the southern Appalachians is ideal for a research program with salamanders, as the region is home to a number of salamander species.

CURRENT PROJECTS

My research examines how geography and climate have influenced current amphibian distributions in the Southeast and how we can use this knowledge to make predictions given future climate projections. Specifically, I aim to understand (1) the evolutionary processes underlying amphibian geographic distributions in the southeastern U.S., and (2) the effects of climate, landscape, and geography on phylogeny and patterns of genetic variation in southeastern amphibians.

My research uses the southern red-back salamander *Plethodon serratus* as a model for investigating the processes driving disjunct, patchy amphibian species ranges in the Southeast – ranges that consist of multiple isolated regions. The Southeast is home to at least 30 vertebrate species with these disjunct distributions, including 18 amphibians. For the first project of my dissertation, I use genetic data and spatially explicit natural history collection and environmental data (through ecological niche modeling and palaeodistribution modeling) to describe the patterns of genetic variation within *P. serratus* and test hypotheses about demographic and biogeographic history. I discovered that the evolutionary history of *P. serratus* is complex – for example, one population in Louisiana is more closely related to populations in the Ouachita Mountains in Oklahoma than to the other population in Louisiana. I also found evidence suggesting the range of *P. serratus* was much broader across the Southeast and more contiguous during periods of cooler climate, opposite of the pattern typically seen in the literature for terrestrial amphibians in this region. This project is published in *PLOS One* (Newman & Austin, 2015).

Next, I used next-generation sequencing methods to generate a genetic data set of thousands of loci to further address questions of *P. serratus* phylogeography and population genetics. The large genomes of amphibians, and particularly salamanders, pose unique challenges for novel methods of generating these massive genetic data sets. Salamander genome

sizes can be up to 40 times the size of the human genome. This part of the project involves testing the utility and effectiveness of new protocols for next-generation sequencing of ultraconserved elements (UCEs) for generating a large multilocus phylogeographic data set for *P. serratus* to further elucidate the evolutionary history of this species. This project was funded by a Doctoral Dissertation Improvement Grant from the National Science Foundation. I successfully generated a genetic data set of more than 1,500 loci. Species delimitation analyses suggested that *P. serratus* as currently recognized actually consists of seven cryptic species, and I was able to reconstruct a fully resolved species tree showing the relationships among the seven species. A manuscript of this project is in press at *Molecular Ecology*.

The genome size of *Plethodon serratus* was previously unknown. I led fieldwork at Sicily Island Hills Wildlife Management Area in Louisiana to collect blood smears from *P. serratus* salamanders to be analyzed by a collaborator to determine the species' genome size. The genome size of *P. serratus* was estimated to be 21 Gb, or seven times the size of the human genome. Because only 14 of the 55 species of *Plethodon* have genome size data available (Gregory, 2016), I performed an ancestral character reconstruction analysis to reconstruct the genome sizes of ancestral nodes on the *Plethodon* phylogeny as well as infer genome sizes for the 41 species without empirical genome size data. My results show a complex pattern of genome size expansion and reduction throughout the evolutionary history of *Plethodon*. A manuscript of this project is currently in press at *Genome*.

Scaling up my research to more broadly examine patterns of salamander distributions in the Southeast, I am currently working on a project comparing ecological niche models (ENMs) of salamander species in the region with disjunct current distributions to test the hypothesis that climate is the major driver of distribution patchiness. Traditionally, ENMs have been built using climate layers (temperature, precipitation) only; however, climate-based ENMs that poorly predict a species known distribution would suggest that factors other than climate are the primary drivers of the species' distribution. Salamander geographic ranges in the Southeast span a wide continuum from fully contiguous to extremely fragmented. I am quantifying the extent of range fragmentation and selecting species with highly fragmented ranges for further study.

FUTURE DIRECTIONS FOR UNDERGRADUATE-CENTERED RESEARCH

1. **Phylogeography of *Plethodon websteri* and *Plethodon ventralis***, two other salamander species with extremely disjunct and restricted geographic ranges in the Southeast: Students will collect multilocus genetic sequence data from tissue samples requested on loan from museums and supplemented by additional field collecting. Specimens collected in the field will be deposited to the ULM Museum of Natural History. Field work will be sustainable on a minimal budget, as all sites are in the southeastern U.S., and collecting salamanders does not require expensive specialized equipment. In addition, *Plethodon* salamanders in the Southeast are most active on the ground surface during the winter months, so major collecting trips can coincide with winter break and not interfere with semester classes. Students will analyze data using bioinformatics methods. Students will also use GIS-based tools to explore how the geographic distributions of *P. websteri* and *P. ventralis* have changed through time by generating species distribution models using climate layers from various time periods (current, paleo, predicted future).

2. **Generate a well-resolved phylogeny of species in the genus *Plethodon* using next-generation sequencing of UCEs.** The genus *Plethodon* is the most species-rich genus of salamanders in North America, and recent phylogenetic studies of the genus using one to tens of loci have left many relationships among species unresolved. I am currently collecting thousands of UCE loci for a number of *Plethodon* species and will have this raw dataset in hand by August 2017. The data will be ready for students to begin analyzing immediately.
3. **Use GIS-based tools to study how climate and landscape features affect the geographic distributions of amphibians in the Southeast.** Students will use collection locality data downloaded from online databases such as VertNet (<http://vertnet.org>), combined with climate layers (Hijmans et al., 2005) and other environmental layers to build models of ecological niche, connectivity, and movement. This project will be extremely inexpensive; the only substantial cost would be software licensing fees, but even this cost could be minimized by utilizing the several powerful but free and open-source GIS programs currently available.
4. **Systematics, population genetics, comparative phylogeography of amphibians in the Coastal Plain.** The Coastal Plain has a rich geologic history and is the location of several well-known phylogeographic breaks within species. Students will use genetics and morphological approaches to study the evolutionary history of species in the Louisiana Coastal Plain. In particular, students will learn about the ULM Museum of Natural History, use the collection in their projects, and contribute to the collection.

OTHER PAST PROJECTS

I used phylogenetics, GIS-based ecological niche modeling, and morphology to resolve taxonomic controversy and reconstruct the evolutionary history of the widespread leopard frog *Rana sphenocephala*. This study is published in *Molecular Ecology* (Newman & Rissler, 2011). I was also one of two lead researchers on a collaboration among several institutions investigating multiple leopard frog populations of interest in the northeastern U.S. Our genetic analyses showed that the region is host to a previously undescribed cryptic species, which we named *Rana kauffeldi*, the Atlantic Coast leopard frog. The phylogenetics paper is published in *Molecular Phylogenetics & Evolution* (Newman et al., 2012) and the species description in *PLOS ONE* (Feinberg et al., 2014). Leopard frogs of the genus *Rana* comprise an enormously complex system with potential opportunities to develop collaborative projects with high-profile researchers.

REFERENCES

All cited publications are listed in CV except the following:

Gregory TR (2016) Animal Genome Size Database. Available from <http://genomesize.com>.
Hijmans RJ, Cameron SE, Parra JL, Jones PG, Jarvis A (2015) Very high resolution interpolated climate surfaces for global land areas. *International Journal of Climatology*, 25(15): 1965-1978.