Computational Biology Seminar Series for Undergraduates

From Shotguns to Shotgun Sequencing: Natural History Collections Provide "Big Data" for Comparative Genomics

Mike Harvey, Louisiana State University

Life Sciences Building Annex A101
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Abstract:

Natural history museums provide a wealth of resources for biological investigation, and new DNA sequencing technologies allow us to use genomic methods to unlock even more of their secrets. Museum collections are useful because they contain many individuals from thousands of species, which allows researchers to address questions using a comparative framework. The application of genomic methods to comparative studies, however, produces huge datasets that present bioinformatics and computational challenges. I will discuss how I, as a graduate student studying birds at the LSU Museum of Natural Science, combine 19th Century methods for obtaining museum samples with 21st Century laboratory and bioinformatics techniques. I will explain some of the computational challenges we have encountered and methods we are developing to overcome them. I will discuss how genomic datasets from museum collections are providing insights never before possible, and review the diverse opportunities that exist for the application of computational approaches to the treasure trove of data in natural history museums.

Speaker's Bio:

Mike Harvey's research focuses on combining the priceless reservoir of information in natural history museums with cutting-edge techniques in order to answer both old and new questions in evolutionary biology. He studies birds in the Neotropics (Central and South America), home to more bird species than any other region on Earth. His research focuses on understanding where this avian diversity came from by studying populations in the very early stages of speciation. He is currently a PhD student at Louisiana State University studying the avian populations through the Louisiana State Univerity Museum of Natural Science in the lab of Dr. Robb Brumfield.

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