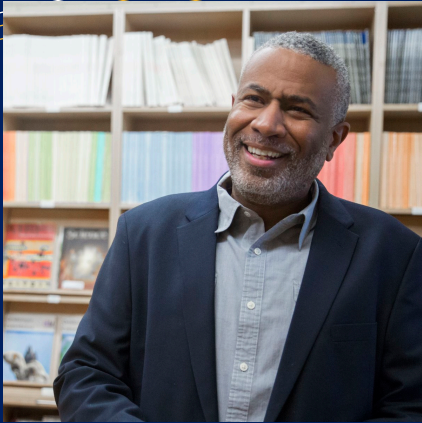




QUANTITATIVE AND SYSTEMS BIOLOGY COLLOQUIUM: Using phylogenies to connect genomic and phenotypic variation under convergent evolution



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About the Speaker:

Scott Edwards is Alexander Agassiz Professor of Zoology and Curator of Ornithology in the Museum of Comparative Zoology at Harvard University. Scott is an evolutionary biologist, with diverse interests in molecular evolution, phylogenetics, comparative genomics and population genetics. His research uses birds as model systems, focusing on their evolutionary history, phylogeography and genome evolution. His current work focuses on using phylogenetic trees and statistical models to link genomic and phenotypic variation. Scott has served as President of the Society for the Study of Evolution, and the Society of Systematic Biologists, and has served on the Advisory Boards of the National Museum of Natural History (Smithsonian) and the Cornell Lab of Ornithology. From 2013-2015 Scott served as Division Director of the Division of Biological Infrastructure at the US National Science Foundation, where he facilitated funding in areas such as undergraduate research experiences, supporting biological collections and major infrastructure and bioinformatics.

Abstract:

Connecting genotype and phenotype is of ongoing interest in evolutionary biology. Comparative genomics is now allowing us to map genes for traits using phylogenetic approaches ('PhyloG2P'), which leverage phenotypically unique lineages or convergent evolution to provide surprisingly precise mapping of loci underlying evolutionarily labile traits. The growing family of statistical models known as PhyloAcc can help identify genomic regions associated with evolution or loss of a phenotypic traits using phylogenetic trees. Three statistical models in the PhyloAcc family include associating rates of genome change and change in a binary or continuous trait, with and without the assumption of incomplete lineage sorting. New software implementations (see <https://phyloacc.github.io/> and <https://github.com/phyloacc/PhyloAcc-C>) greatly ease data analysis and allow rapid screening of thousands of loci. Such models will improve our power to detect associations between genome and phenotype evolution, particularly in situations of convergent evolution. An example focusing on loss of flight in birds reveals a strong role for non-coding regulatory evolution in the origin of key adaptations of birds. Functional tests, including measuring chromatin states using ATAC-seq and high-throughput enhancer screens help sift through hundreds of potential candidate enhancers whose evolution could influence traits associated with loss of flight.



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