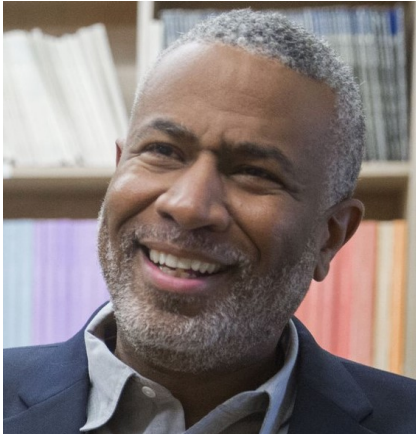


# iFAST: The International Forum on Advanced Environmental Sciences and Technology

*A series of distinguished seminars by eminent scientists*

**8 a.m. CST, 9 a.m. EST, 2 p.m. GMT, 10 p.m. China**  
**Wednesday, Feb. 28, 2024**



**SCOTT EDWARDS**

HARVARD UNIVERSITY

<https://edwards.oeb.harvard.edu/people/scott-v-edwards>

Scott Edwards is the Alexander Agassiz Professor of Zoology and curator of ornithology at Harvard University's Museum of Comparative Zoology. Edwards joined Harvard in 2003 following nine years as faculty in the Zoology Department and Burke Museum at the University of Washington, Seattle. Edwards' research delves into avian biology, spanning evolutionary history, disease ecology, population genetics and comparative genomics. With extensive fieldwork in Australia since 1987, he pioneered phylogeographic analyses using DNA sequencing. His postdoctoral fellowship in immunogenetics at the University of Florida honed his focus on the major histocompatibility complex of birds, crucial for disease interactions and mate choice. Edwards' recent work employs comparative genomics to explore the genetic underpinnings of phenotypic innovation in birds and develop novel methods for phylogenetic tree estimation. As the division director of the Biological Infrastructure at the U.S. National Science Foundation from 2013-2015, he oversaw diverse funding programs and has held leadership roles in international scientific societies. Edwards is a member of the American Academy of Arts and Sciences, a Fellow of the American Association for the Advancement of Science, and a member of the National Academy of Sciences, among other prestigious honors.

## **Using phylogenies to connect genomic and phenotypic variation under convergent evolution**

**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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**INSTITUTE FOR ENVIRONMENTAL GENOMICS**  
The UNIVERSITY of OKLAHOMA



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**Zoom webinar ID: 934 8142 2012 ([zoom.us/j/93481422012](https://zoom.us/j/93481422012))**

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