New VertLife project will sprout a forest of family trees

September 18 2014, by Jim Shelton

Credit: Michael S. Helfenbein

A Yale-led effort to bring "big data" to the study of biodiversity has received a $2.5 million boost, courtesy of the National Science Foundation. The grant is part of a new, Genealogy of Life program at the NSF, and will be used to create annotated family trees, computational tools, and a digital database addressing all terrestrial vertebrates.

This comes on the heels of a $1.6 million NSF grant, together with funding from Google, for the second phase of a related Yale-led project,

an online biodiversity platform called Map of Life.

Walter Jetz, associate professor of ecology and [evolutionary biology](#), and director of the Yale Program in Spatial Biodiversity Science & Conservation, is the lead principal investigator for both efforts. He and his collaborators will use the new, four-year NSF grant to launch VertLife Terrestrial—which will tell the stories of all 33,000 [species](#) of mammals, birds, amphibians, and reptiles alive today.

"Our goal, essentially, is a distribution of thousands of trees that cover all species together with any remaining uncertainty about their exact placement," Jetz said. "But it is not just thinking about the trees. It is about all the other data that makes the trees important."

Got a nagging question about the distribution or traits of snakes? Want to know the phylogenetic placement of parakeets? VertLife will have information for students and scientists alike.

The project aims to provide comprehensive data and visualizations for each species. There will be full life histories, as well as descriptions of key evolutionary and ecological attributes. The project also will use parallel sequencing methods to collect new genetic information for about 4,000 species currently lacking such data.

In addition, analysis and visualization tools built into VertLife will allow users to conduct a broad range of inquiry, from trait and geographical comparisons to conservation monitoring.

The project will extend recent research by Jetz on a comprehensive family tree devoted to all living bird species and the calculation of evolutionarily distinct species, as well as a study providing trait information for all mammals and birds.

"Even to understand only our own U.S. species, we need the global context," Jetz said. "Our project will provide people with information that can enrich their own analysis." All VertLife information will be integrated with the Map of Life and accessible to anyone. Users will be able to learn more about the relationships, traits, and threat status of species anywhere on the planet by traversing a family tree or browsing a map.

Other institutions contributing to VertLife will include Louisiana State University, the University of California at Berkeley, George Washington University, and the University of Florida. VertLife will be a flagship project within the NSF's Genealogy of Life program to build an open access, universal database, and biodiversity analysis tools for the next generation of comparative biologists and other scientists.

Likewise, VertLife is aimed at students. There will be online tutorials embedded in the project, along with a museum display developed around the family trees.

"This effort is linking big data with the latest tools in biodiversity informatics," Jetz said. "It will bring ecological and evolutionary information for a large and charismatic group of animals together in one place and link it with relevant tools for rapid access and synthesis."

Provided by Yale University