Unlocking the Potential of Phylogenetic Comparative Methods in Ecology, Agriculture, and Nature Conservation

3-7 November 2025

Hula Research Center Hula Valley, Israel

Instructors



Prof. Liam Revell,Department of Biology,
University of Massachusetts,
USA
(liam.revell@umb.edu)



Prof. Luke Harmon,
Department of Biological
Sciences, University of Idaho,
USA
(lukeh@uidaho.edu)

About

Phylogenetics plays a key role in the study of genetic relationships among organisms, including evolutionary processes, adaptation to different environments and disease transmission. It is essential to comparative biology, epidemiology, and agriculture. The R packages Phytools and geiger, developed by Prof. Liam Revell (UMass) and Prof. Luke Harmon (Uldaho), respectively, provide essential tools for visualizing, analyzing, and manipulating phylogenetic trees.

Organizers

Dr. Tali Berman | Hula Research Center, Tel-Hai & Migal (taliber@telhai.ac.il) **Avi Eliyahu** | Newe Ya'ar Research Center (avi.eliyahu9@gmail.com)

This workshop is aimed at ecologists looking to enhance their phylogenetic research skills and those interested in incorporating phylogenetic tools into their work.

Designated audience: Master students, Ph.D. students, post-doctoral researchers and young PIs with basic knowledge of bioinformatics and R coding.

Prior knowledge required: Basic nucleotide and amino acid alignments and R coding.

Accreditation: 3 credit points. **Language of instruction:** English.

To register, click here ■ For more information ■ phylogeny2025@m.telhai.ac.il







