



Workshop: Comparative methods in evolutionary biology

Stazione Zoologica Anton Dohrn, December 5th-7th, 2016

Day 1

- ✓ Introduction to the use of phylogeny in comparative methods
- ✓ Likelihood and bayesian inference methods
- ✓ Theoretical aspects of molecular clock analyses
- ✓ Tutorials on relaxed clocks using Beast 1.8
- ✓ Introduction to R

Day 2

- ✓ Tutorial on total-evidence dating using Beast 2.3
- ✓ Introduction to the use of remote servers (Cipres) for phylogenetic analyses
- ✓ Tutorial on comparative methods for exploring the evolution of discrete and continuous characters

Day 3

- ✓ Theory and approaches to the study of adaptive radiations
- ✓ Tutorials on comparative methods for detecting and quantifying heterogeneity in evolutionary rates (BAMM)

Registration fees: 100€ (fees include lunches); special price at 50€ for students enrolled at the Universities of Naples (Federico II and Parthenope) with no lunch included

Participants: this workshop is preferentially addressed to PhD students, postdocs and researchers with basic knowledge of phylogeny (sequence alignments, nucleotide substitution models and basic tree building). Max number 25

Tutors:

Francesco Santini
Associazione Italiana per lo
Studio della Biodiversità
(Italy)

Bruno Frédéric
University of Liège (Belgium)

Organizers:

Sergio Stefanni
Salvatore D'Aniello
Giuseppe D'Onofrio
Andrea Tarallo
Maria Vittoria Modica

Registration at:

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Please include a few lines on your background, level of confidence with R and Beast/Beauty, expectations from this workshop.

People will be admitted to the course following application review by the admissions committee.