

From: Soledad De Esteban-Trivigno
Subject: Course: Mapping Trait Evolution, June 4-8, Barcelona (Spain)

Dear colleagues,

Registration is open for the second edition of the course “Mapping Trait Evolution”, June 4th-8th, 2018.

Instructor: Dr. Jeroen Smaers (Stony Brook University, USA).

PROGRAM:

Monday. (R packages: ape, Geiger).

Morning: Phylogenetic data.

- * What is the basic structure of phylogenetic data?
- * How to visualize and manipulate phylogenetic data?

Afternoon: Models of evolution.

- * What are models of evolution?
- * What are the assumptions of the different models of evolution?
- * How are models of evolution utilized?

Tuesday. (R packages: ape, nlme, caper, evomap).

Morning: Phylogenetic regression.

- * Assumptions, properties, and applications of the phylogenetic regression.

Afternoon: Phylogenetic ancova.

- * Testing for grade shifts using the phylogenetic regression.

Wednesday. (R packages: phytools, motmot, geiger, ape, evomap, BayesTraits).

Morning: Ancestral estimation.

- * Using models of evolution to estimate values of ancestral nodes.

Afternoon: Analysis of rates of evolution.

- * Estimation of rates of evolution.
- * Testing hypothesis about rates of evolution.

Thursday. (R packages: bayou, phylolm, surface, OUwie, mvMORPH).

Morning: Inferring the structure of a macroevolutionary landscape.

- * Using Ornstein-Uhlenbeck models to map macroevolutionary patterns.

Afternoon: Testing the structure of a macroevolutionary landscape.

- * Applications and assumptions of OU models.
- * Using OU models to test macroevolutionary hypotheses.

Friday. (R packages: geomorph).

Morning: Modularity and integration.

- * What is ‘phylogenetic’ modularity and integration?
- * Applications and assumptions.

Afternoon: Case study.

MORE INFO: <http://bit.ly/transmittingscience-mapping-trait-evolution>

With best regards

Sole

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