

Escuela AEET

>> This course is designed to teach to usage of R for functional trait and phylogenetic analyses in ecology

Over the past decade, a large number of tools and methods have been generated to incorporate phylogenetic and functional information into traditional ecological analyses.

Increasingly these tools are implemented in R, thus greatly expanding their impact. The course is designed to be accessible to R users that have basic experience (i.e. loading files, making simple graphs, performing basic statistics) and these users will be brought up to speed quickly.

More advance R users will find the course useful particularly if they are less familiar with functional and phylogenetic analyses and/or R packages for these analyses. It is expected that those attending the course have basic knowledge of ecology and evolutionary biology, but in depth knowledge of phylogenetics is not required for attendance <<

Escuela AEET

• **Date:**
25th - 28th September 2017

• **Venue:**
University Rey Juan Carlos,
Móstoles Campus. Madrid

• **Schedule:**
9:00 - 13:00 h & 15:00 - 18:00 h
Monday to Thursday

• **Pre-registration:**
From 01/05/2017 - 15/07/2017

• **Fee:**
AEET/AIL members: 325 €
Non members: 450 €

• **Course length:** 28 h

• **Number of places:** 22

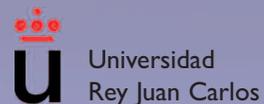
• **Registration at:**
http://www.aeet.org/Escuela_AEET_252_p.htm
e-mail: info@aeet.org
tel.: 91 4887329 (de 9:00 a 14:00)

• **Organizers:**

Asociación Española de Ecología Terrestre



With the collaboration of URJC:



Functional and Phylogenetic Ecology in R (2nd ed.)

25th - 28th September 2017,
University Rey Juan Carlos, Móstoles, Madrid

• **Teacher:**

Dr. Nathan Swenson, Associate professor of the University of Maryland, MD, USA.

► Presentation, aims and target students:

This course is designed to teach to usage of R for functional trait and phylogenetic analyses in ecology. Over the past decade, a large number of tools and methods have been generated to incorporate phylogenetic and functional information into traditional ecological analyses. Increasingly these tools are implemented in R, thus greatly expanding their impact. The course is designed to be accessible to R users that have basic experience (i.e. loading files, making simple graphs, performing basic statistics) and these users will be brought up to speed quickly. More advance R users will find the course useful particularly if they are less familiar with functional and phylogenetic analyses and/or R packages for these analyses. It is expected that those attending the course have basic knowledge of ecology and evolutionary biology, but in depth knowledge of phylogenetics is not required for attendance. The course will cover topics such as: basic handling of functional trait and phylogenetic data in R; the quantification of functional and phylogenetic diversity and the classification and interpretation of different functional and phylogenetic diversity metrics; null modeling and randomization procedures and concepts for trait and phylogenetic data in ecology; classical phylogenetic comparative methods, the quantification and interpretation of phylogenetic signal in trait data and how to interface the R environment with programs written in other languages (e.g. C). The course will use example datasets, but students will also have the opportunity to bring their own data and/or research goals to the course for consultation with the instructor. The course will have the same format for each day. The instructor will begin each day with a lecture on the conceptual development of the analyses to be performed in R that day and how they have been used in the ecological literature.

This will be followed by practical examples in R where each student will conduct analyses along with the instructor while he describes what is being done and what the results produced by R mean.

► Biosketch:

Nathan Swenson is an Associate Professor of Biology at the University of Maryland in the United States. He received his Ph.D. in Ecology and Evolutionary Biology in 2008 from the University of Arizona and was a National Science Foundation Postdoctoral Fellow in Bioinformatics at the Center for Tropical Forest Science then located at the Arnold Arboretum, Harvard University.

Swenson is a tropical plant biologist by training interested in the evolution of plant functional diversity and its consequences for the present day ecology of species. Much of his research has been conducted using large tropical forest inventory plots where he and colleagues have generated trait and phylogenetic datasets. The use of the R statistical programming language and the R environment has been essential for his research using these large datasets that often require custom R code for analysis.

In recognition of his work, Swenson has received the 2011 Jasper Loftus-Hills Young Investigator's Award from the American Society of Naturalists, the 2012 Ebbe Nielsen Prize from the Global Biodiversity Information Facility and was named a Fellow of the John Simon Guggenheim Memorial Foundation in 2014. To date, Swenson has published over 80 peer-reviewed journal articles and book chapters and has been cited over 4,000 times. Lastly, Swenson has taught short R courses in China, Taiwan, Costa Rica and the United States, which lead him to publish a R programming book in 2014 entitled "Functional and Phylogenetic Ecology in R". The topics and code in this book and additional new material will be covered in the present course.

**► Certification:**

The students will receive a certificate of attendance and completion. Attendance of a minimum of 90% of the whole teaching hours will be required.

For any enquiry or question please contact info@aet.org