Phylogenetic or evolutionary inference has become an essential tool in many disciplines across the life sciences, from molecular epidemiology to paleontology. Long dominated by simple optimization or parsimony methods, the field is now broadly moving towards parametric statistical approaches. Bayesian MCMC techniques in particular have become popular in tackling the challenging inferential problems associated with phylogenetics and evolution. In this course, the participants will learn the theoretical and technical basis of model-based methods for estimating trees, mainly maximum likelihood and Bayesian inference, as well as build up new models from existing functions. At the end of the course, the student will have an understanding of the assumptions of a modern phylogenetic analysis.

The course will be taught by Professor John Huelsenbeck (University of California, Berkeley), a visiting professor at the Real Jardín Botánico, CSIC, and considered one of the most eminent scientists in this field. He has developed many of the methodological and computing tools routinely used in modern phylogenetic inference and evolutionary biology. The course will consist on one master lecture per day, given in English and with a duration of 1.30 hours (10.30-12.00 am); except the last two days (26-27 Enero), with two lectures, one in the morning (10.30-12.00 am) and one in the afternoon (13.30-15.00 pm). No computers are needed but students are encouraged to bring their own laptops.
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The titles of the presentations are:

L1. An introduction to probability, statistics, and phylogenetics
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L3. The phylogenetic model, II: stochastic processes of character change
L4. Finding the best tree using maximum likelihood
L5. Confidence intervals on phylogenies: the bootstrap (and other methods)
L6. Let's be Bayesian about phylogenies
L7. Markov chain Monte Carlo (MCMC) is your friend
L8. Our buddies, MrBayes and RevBayes
L9. Comparing models using Bayes factors
L10. Stochastic mapping of characters and comparative analysis
L11. Biogeography and likelihood
L12. Chinese restaurants and phylogenetics