

COURSE: Analysis and manipulation of phylogenomic data using the ETE python toolkit and TreeKo



Organized by the CRG [Bioinformatics Core Facility at CRG](#) and [Toni Gabaldon's lab](#).

Location: [Centre for Genomic Regulation](#), Barcelona (Spain).



Duration: 3 days, **April 6th- 8th (2011)**

free registration (limited places) **deadline: 15th of March**

Details of the course and application: http://ete.cgenomics.org/course_2011

The Environment for Tree Exploration (ETE, <http://ete.cgenomics.org>) is a Python programming toolkit to deal with hierarchical trees. It allows, for instance, to perform a number of operations on phylogenetic trees, as well as designing automatic pipelines. It also provides a highly customizable drawing engine, which can be used to create complex annotated tree images in an automatic way or to interactively explore single trees. Moreover, the ETE toolkit is not only limited to large scale analyses, as it can be used to easily develop specific tree analysis methods for single trees. For instance, [TreeKo](http://treeko.cgenomics.com) (<http://treeko.cgenomics.com>) is a novel software based on ETE which is designed to perform large scale comparisons of tree topologies taking into account speciation a duplication events.

This course will provide an introduction to the analysis of phylogenetic trees with ETE and treeKO. It will cover a broad range of tasks, including tree rooting, prediction of orthology and paralogy relationships, tree annotation, calculating distances among sequences or species, tree pruning, trees comparison, and tree visualization. The use of large scale phylogenomic resources, such as [PhylomeDB](#) or [Ensembl Compara](#).

