COEVOL COÉVOLUTION MULTI-ECHELLES

EQUIPE GÉNOMIQUE EVOLUTIVE ET FONCTIONNELLE

GUEGUEN Laurent

MAÎTRE DE CONFÉRENCES

UCBL

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Teaching :

I teach mathematics, modelling in biology and computer science in Licence and Masters
BEE@Lyon
and
Bioinfo@Lyon
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Mostly, I write programming courses for biologists, in R and Python, in the form of a tutorials, to give students practical experience, where they develop simulation programs of simple biological models (genetics and population dynamics) in individual-centered mode. This allows them to discover this type of modelling and awakens their in/erest in the role of computational tools in biology. On the modelling part, I design Markov modelling tutorials in R (HMM, phylogeny) in which the students start from the mathematical model and work their way up to data analysis. In math&meth, beyond usual linear algebra, I am interested into teaching data analysis techniques, such as clustering methods & Singular Value Decomposition.

Research:

I work on molecular modeling in evolution, mostly in phylogeny. I currently work on methods and models that focus on branch specific estimates of selection and of other evolutive features (such as GC bias), and also on the inclusion of polymorphism information in phylogenetic scale analysis.

An essential part of my research activity consists of developing the Bio++ suite of libraries (see on
Github
), in collaboration with Julien Dutheil (Max Planck Institute for Evolutionary Biology , Plön). **Bio++** is a set of C++ libraries for Bioinformatics, including sequence analysis, phylogenetics, molecular evolution and population genetics. Bio++ is Object Oriented and is designed to be both easy to use and computer efficient. Bio++ intends to help programmers to write computer expensive programs, by providing them a set of re-usable tools.

Using these libraries, many softwares are available for maximum likelihood inference, ancestral reconstruction, sequence simulation, in BppSuite, and substitution mapping,branch clustering in TestNH.

I maintain the **DGINN** pipeline, developed by Léa Picard, a PhD student under my supervision and that of Lucie ÉTIENNE (CIRI, ENS Lyon). DGINN is dedicated to find signs of innovation in a gene family, performing automatically all the process from a sequence to positive selection detection, through homologous sequence retrieval, curation, alignment, reconciliation, recombination detection and finally phylogenetic analysis.