



Seminar

LAURENT GUÉGUEN

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Université Claude Bernard - Lyon 1

From Populations to Species: Genome Evolution and Its Modelling

Tuesday, 19 November, 2019, 2:15 p.m.

In the Thunberg Lecture Hall
SCAS, Linneanum, Thunbergsvägen 2, Uppsala
www.swedishcollegium.se

S W E D I S H
C O L L E G I U M
for ADVANCED STUDY

ABOUT LAURENT GUÉGUEN

Laurent Guéguen is a computer scientist and since 2000 Associate Professor at the Laboratoire de Biométrie et Biologie Évolutive at Université Claude Bernard - Lyon 1.

Since 2008, he has been working on phylogeny and molecular evolution, mostly in the development of models and methods. He is one of the main developers of the Bio++ libraries. His recent modeling research has focused on several levels of molecular evolution, such as codon usage (Pouyet et al., 2016, "SENCA: A Multilayered Codon Model to Study the Origins and Dynamics of Codon Usage", *GBE/Genome Biology and Evolution*), genomic convergence (Rey et al., 2018, "Accurate Detection of Convergent Amino-acid Evolution with PCOC", *MBE/Molecular Biology and Evolution*), and genome architecture (Semeria et al., 2015, "Probabilistic Modeling of the Evolution of Gene Synteny within Reconciled Phylogenies", *BMC/Bioinformatics*).

Guéguen is also interested in developing methods to dig out clues about the evolutionary process from the comparison of genomes at the level of genome organization (Biller et al., 2016, "Breaking Good: Accounting for Fragility of Genomic Regions in Rearrangement Distance Estimation", *GBE/Genome Biology and Evolution*), and at the level of genes (Guéguen & Duret, 2018, "Unbiased Estimate of Synonymous and Non-synonymous Substitution Rates with Non-stationary Base Composition", *MBE/Molecular Biology and Evolution*).

At SCAS, Guéguen, in collaboration with Carina Mugal and Hans Ellegren from the Department of Ecology and Genetics/Evolutionary Biology at Uppsala University, will model polymorphism and selection in phylogeny, and develop this theoretical work in software easily usable by biologists. This project addresses the largest problem in building a bridge between phylogeny and population genetics, a goal that is of increasing interest among biologists.

ABSTRACT

Research in genome evolution focuses on two different scales, either inter-species or intra-species. Each scale has its own discipline, phylogeny and population genetics, each with its own specific models and methods. However, both disciplines have a similar aim, understanding how life has evolved until the present time. Until now, data was distinctly built for each discipline, and researches were mostly separate. But this distinction disappears as more and more genomes are sequenced.

I will try to expose how each discipline has to make its own specific simplifications from the same biological process to answer its own questions, and how methods emerge to fill the gap between inter-species and intra-species research.