



Conférence Inférence de réseaux phylogénétiques pour la détection d'hybridations et d'introgessions

*Charles-Elie Rabier,
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Lundi 9 novembre 2020

14h00 – 15h30

Salle 109 – Bâtiment 9

Université de Montpellier – Campus Triolet



Charles-Elie is postdoc at ISE-M (Université de Montpellier) working on the inference of phylogenetic networks with Celine Scornavacca.

He is part of the team “Phylogeny and Molecular Evolution” and is funded by the Key Initiative Muse Data & Life Sciences. His interdisciplinary research is done in collaboration with different institutes from Montpellier: LIRMM (computational aspects), IMAG (mathematical aspects), CIRAD (biological aspects).

In genomics, he is interested in gene mapping, reconciliation between gene trees and species trees, whole genome duplications and also in genomic selection.

In applied mathematics, he is interested in gaussian and chi square processes, mixture models and high-dimensional data analysis.

On the inference of complex phylogenetic networks for detecting hybridizations and introgressions

In this talk, I will present my recent work on phylogenetic networks, in collaboration with V. Berry and F. Pardi (LIRMM), JC Glaszmann (CIRAD) and C. Scornavacca (ISE-M).

Nowadays, to make the best use of the vast amount of genomic data at our disposal, there is a real need for methods able to model complex biological mechanisms such as hybridization and introgression. Understanding such mechanisms can help geneticists to elaborate strategies in crop improvement that may help reducing poverty and dealing with climate change. However, reconstructing such evolution scenarios is challenging. Indeed, the inference of phylogenetic networks, which explicitly model reticulation events such as hybridization and introgression, requires high computational resources. Then, on large data sets, biologists generally deduce reticulation events indirectly using species tree inference tools.

In this context, we present a new Bayesian method, called SnappNet, dedicated to phylogenetic network inference. Our method is competitive in terms of execution speed with respect to its competitors. This speed gain enables us to consider more complex evolution scenarios during Bayesian analyses. When applied to rice genomic data, SnappNet suggested a new evolution scenario, compatible with the existing ones: it posits cAus as the result of an early combination between the Indica and Japonica lineages, followed by a later combination between the cAus and Japonica lineages to derive cBasmati. This accounts for the well-documented wide hybrid compatibility of cAus.

INSCRIPTION OBLIGATOIRE pour participation sur place (nombre de places limité) :

<https://framaforms.org/seminaire-kim-du-0911-1603191566>

WEBINAIRE ouvert à toutes et tous : <https://umontpellier-fr.zoom.us/j/85813807839>

Pour toute question, s'adresser à paul.bastide@umontpellier.fr
