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AVR.
2008

🕒 de 11h à 12h

SÉMINAIRE

Genome rearrangement: what is possible to analyze and what is not yet?

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In the first part of this talk we present a recent analysis of Yersinia genomes. The Yersinia family accumulated many rearrangement mutations in the last few tenthousands years, which offers an unprecedented opportunity to study evolution of genome structure and arrangement. During the analysis, we realized that the current MCMC methods that provide samples from the posterior distribution of genome rearrangement scenarios converge slowly. The second part of the talk is about the theoretical convergence of MCMC methods for inferring genome rearrangements.