Centre de Biologie pour
la Gestion des Populations

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Salle de réunion

JOINT INFERENCE OF DEMOGRAPHY AND SELECTION FROM GENOMIC TEMPORAL DATA USING APPROXIMATE BAYESIAN COMPUTATION

par

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Traditional population genetic studies use genotypic or allelic frequency data obtained from several populations sampled at the same time point. However, temporal population genetics data offers a more powerful way of studying complex dynamics, since we can follow allele frequency changes over time in the population.

Disentangling the effects of selection and demography is a longstanding difficulty in population genetics. Recent theoretical works based on simulations have shown that the interaction between the signal of selection bias the demographic inference when selection is pervasive. One potential solution is the co-estimation of neutral and selective parameters using simulation-based methods as Approximation Bayesian Computation (ABC). However, traditional ABC approaches are computationally expensive, and their implementation in complex settings was unrealistic until recently.

The introduction of random forests in ABC reduced the computational burden, making it possible to study complex dynamics with few simulations. We propose the use of ABC Random-Forests to implement the joint inference and co-estimate neutral and selective parameters in temporal population genomics datasets. Our results show that the proposed framework can jointly infer demography and selection, allowing to distinguish true demography (census size) from genetic drift (effective population size), as well as estimate the population genetic load (selection parameter).