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Grande salle de réunion

KIMTREE: DEALING WITH ASCERTAINMENT BIAS AND SELECTION USING SNP DATA

par

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- 📌 The revolution in sequence data generation for model and non-model species has led to various approaches trying to make this ever-increasing amount of information accessible. Whereas early methods were forced to rely on mathematically convenient approximations to the underlying evolutionary processes, advances in computing power now enable complex likelihood-based inference.
- 📌 Here, we present an extension of KimTree, a previously developed method for estimating divergence times among populations based on the Kimura diffusion approximation for the evolution of neutral alleles. We explore different ways to correct for ascertainment bias created due to analysing SNP data and apply the model to simulated data of autosomes and sex chromosomes to jointly infer divergence times, which are informative about the effective sex-ratio in the studied populations. Moreover, we extend the method to identify loci under positive selection, using information about the expected allele frequency distribution after a selective sweep.
- 📌 The performance of the model is evaluated under various demographic scenarios. We find considerable improvement in the accuracy and robustness of parameter estimation compared to the original version of KimTree.