

Fine-scale recombination maps: From simulation to empirical data

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Abstract:

Meiotic recombination is one of the central evolutionary parameters. While until recently technological challenges limited empirical estimation of fine-scale recombination rates, sequencing technology and method development now allow us to infer its variations on a genome-wide scale.

Genetic polymorphism within population provides information on linkage disequilibrium among loci and permits the inference of recombination history, including in non-model species. However, this information is sensitive to other evolutionary processes: e.g., changes in demography, selection, or migration. Disentangling the relative contribution of each of these phenomena on the linkage and diversity patterns is of prime importance when looking at the effect of recombination in evolutionary studies, for example while studying speciation or adaptation. Simulations are a strong tool to obtain a neutral expectation against which to compare empirical results and gain a better understanding of the processes shaping them.

In this talk, I propose to evaluate how good is inference of fine-scale recombination maps based on population genetic data. I am going to use and compare: (i) fine-scale recombination maps obtained from two ecotypes of the cichlid fish species *Astatotilapia calliptera*, that are on the path to speciation, and (ii) simulation-based maps obtained under matching evolutionary parameters (divergence time, gene flow, demographic history). I will then use this comparison to interpret the difference in fine-scale recombination maps between the two ecotypes. In addition, I am going to focus on the effect of selection on recombination inference, as reflected in the pattern of genetic differentiation between the ecotypes (e.g., F_{st} and D_{xy}).