Title: Fine-scale recombination map from a handful of unphased genomes

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Meiotic recombination determines the extent to which loci in the same chromosome share their evolutionary histories. Therefore, fine-scale recombination maps are needed to understand the impact of linked selection, demography and introgression on sequence data. Traditionally, the genomic landscape of historical recombination has been inferred by estimating Linkage Disequilibrium between single nucleotide polymorphisms. The drawbacks of this approach are that it requires phased genomes, large sample sizes and the estimates have high variance. Here we propose a new method (iSMC) based on the Sequentially Markov Coalescent, which describes the spatial distribution of coalescent trees along homologous genomes. Since this distribution concerns both homozygous and heterozygous sites, the recombination map inferred by iSMC has single-nucleotide resolution. Also, because iSMC treats input sequences in independent pairs, it does not require phase information. We first assess the performance of iSMC under different simulated scenarios. We then infer the recombination landscape of the fungal pathogen Zymoseptoria tritici, and compare our results to estimates from state-of-the-art methods, as well as from a crossover map obtained experimentally.