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Single–crossover recombination and ancestral recombination trees

Modeling the dynamics of populations under recombination leads to a large coupled non-linear dynamical system that is notoriously difficult to treat. In my talk, I will present a model that describes recombination in an 'infinite' population with single crossovers only.

The common way to solve these systems relies on a certain nonlinear transformation from (gamete or haplotype) frequencies to suitable correlation functions. This provides an elegant solution in principle, but the price to be paid is that the coefficients of the transformation must be constructed via recursions that involve the parameters of the recombination model [1], i.e. an explicit solution of the dynamics cannot be stated.

I will describe a new approach to infer an explicit solution to the dynamics. To this end, I use the underlying stochastic process to trace recombination backwards in time, i.e. by backtracking the ancestry of the various independent segments each type is composed of. This results in binary tree structures, which can be used as a tool to formulate an explicit solution of the dynamics.

REFERENCES

[1] von Wangenheim, U., Baake, E., Baake, M. *Single–crossover recombination in discrete time* J. Math. Biol **60** 727–760 (2010).