

Zufällige Genealogien und Selektive Sweeps

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Random genealogies - with Kingman's coalescent as their prototype - are strong mathematical tools for modelling the genetic diversity in a sample from a population. In the lecture we will illustrate this by explaining some features of the so called genetic hitchhiking effect: Assume a mutant allele occurs in a large population which is so beneficial that it fixates in the population in a relatively short time. Then also the alleles carried by the founder of the sweep at neutral loci neighbouring to the selective locus are lucky: they are dragged along by the beneficial allele, and genetic diversity is reduced near the selective locus in a sort of selective sweep. The ancestry of a sample at the selective locus, viewed back from the completion of the selective sweep, is simple: everybody traces back to the founder of the sweep. But what about a neutral locus in the neighbourhood of the selective one? Here, recombination counteracts the hitchhiking of that neutral allele which was carried by the founder of the sweep. Using random genealogies, we describe and interpret an approximation to the sample partition with respect to identity by descent from the beginning of the sweep. The lecture is based on joint work with Alison Etheridge (Oxford) and Peter Pfaffelhuber (Munich), see <http://arxiv.org/abs/math.PR/0503485>

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