universität wien

FAKULTÄT FÜR MATHEMATIK
Dekan Univ.-Prof. Dr. Radu Ioan Boţ

Einladung zur öffentlichen Defensio

Hannah GÖTSCH

Thema der Dissertation

A multilocus model for the adaptation of complex ecological traits, and beyond

Abstract:
In my thesis, I present the outcomes of my research within the area of mathematical population genetics.
The first chapter contains an introduction to the used mathematical concepts, the most important results and the biological motivation.
The main part of my thesis consists of the manuscript "Polygenic dynamics underlying the response of quantitative traits to directional selection". Here, we study the response of a quantitative trait to exponential directional selection in a finite haploid population, both at the genetic and the phenotypic level. We assume an infinite sites model, adaptation due to de novo mutations, beneficial mutation effects drawn from a distribution and unlinked sites that contribute additively to the trait. Assuming that selection is stronger than random genetic drift, we model the initial phase of the dynamics by a supercritical Galton-Watson process. This enables us to obtain time-dependent results. A suitable transformation yields the approximate dynamics of the mutant frequency distribution in a Wright-Fisher population of size N. On this basis, we derive explicitly the (approximate) time dependence of the expected mean and variance of the trait and of the expected number of segregating sites. Unexpectedly, we obtain highly accurate approximations for all times, even for the quasi-stationary phase when the expected per-generation response has equilibrated. The latter refine classical results. In addition, we find that the mutation rate is the main determinant of the pattern of adaptation at the genetic level, i.e., whether the initial allele-frequency dynamics are best described by sweep-like patterns at few loci or by small allele-frequency shifts at many.
The next two chapters provide additional results and ideas, which are not part of the manuscript, and an extension of the one locus model to recurrent mutations for a low mutation rate.

In the last chapter, we present a statistical tool named PhyloThin that can detect and correct oversampling in prokaryotic population-samples which are often generated by biased sampling schemes. Strong sampling bias of bacteria does not only reduce the effective information on NCBI but can also result in misleading conclusions in various analyses. PhyloThin is based on phylogenetic relationships between genomic samples and results from coalescent theory.

Prüfungssenat

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Zeit und Ort

Dienstag, 23. Juli 2024, 17:00 Uhr

Online:

https://univienna.zoom.us/j/67973960172?pwd=mcBSBt9CfTsgQ5Vqga9sq1A4e6rHVi.1

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