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EINLADUNG ZU VORTRÄGEN

im Rahmen der Fast Tenure Track-Professur
„*Mathematische Evolutionsgenetik*“

von

Himani Sachdeva, MSc PhD
(Universität Wien)

Montag, 26. Mai 2025, 10:00 Uhr, HS 2 (EG), OMP

Didaktischer Vortrag:

„Evolutionary change due to natural selection“

Abstract:
Natural selection is a fundamental evolutionary process that allows organisms to adapt to their environments and may eventually lead to the evolution of new species. In this talk, I will start with examples of how natural selection can produce striking patterns of evolutionary change over time and across space. I will then introduce simple models to quantify the rate of evolutionary change due to selection. I will conclude by briefly examining to what extent evolution may be stochastic (random) and how we can model such stochasticity.

Montag, 26. Mai 2025, 10:50 Uhr, HS 2 (EG), OMP

Wissenschaftlicher Vortrag:

„Understanding polygenic adaptation in the era of genomics“

Abstract:
Many traits in diverse organisms – related to morphology, size, or the risk of common diseases – are highly polygenic, i.e., influenced by a large number of genetic variants across the genome. However, the consequences of natural selection acting on polygenic traits remain poorly understood. A major complication is that polygenic selection causes different genetic variants to evolve in a correlated manner, with the scale of correlation depending on myriad factors – whether variants are tightly linked, how stochastic evolution is (due to finite population sizes), and how structured populations are (e.g., due to subdivision into smaller groups that rarely mix). In this talk, I will explore some of these complexities – focusing in particular on how linkage between selected variants and population structure shape polygenic adaptation and its signatures in genomic data. I will illustrate the utility of coarse-grained descriptions of polygenic evolution – in terms of continuous blocks of genome (as opposed to discrete variants) and effective parameters (that average over ‘fast’ evolutionary processes). These descriptions provide a principled way of understanding which genetic details matter for the distribution of genetic variation across different spatial, temporal and genomic scales and to what extent we can hope to make inferences about the individual genes involved in adaptation or speciation from genomic data.

Radu Ioan Bot

Karl-Heinz Wagner