



Minisymposium 2
**Multilocus models in structured populations: migration, selection,
and recombination**

Thursday, 19 June, 09:00 – 11:30

Abstracts (in chronological order)

A multi-locus, haploid-selection, symmetric-viability model

Jeffrey Chasnov

Department of Mathematics, The Hong Kong University of Science & Technology

A multi-locus, haploid-selection, Levene model is studied. By assuming symmetric selection coefficients, the model always admits a fully polymorphic symmetric equilibrium consisting equally of two types of purebreds, which may or may not be stable. We will show how increasing recombination can act to either increase or decrease the genetic diversity of a population. By generating more hybrid offspring from the mating of the two types of purebreds, recombination can act to increase genetic diversity provided the symmetric equilibrium remains stable. But by destabilizing the symmetric equilibrium, recombination can ultimately act to favor one specific purebred over the other and decrease genetic diversity.

Multidimensional models of rapid adaptation to shifting environmental gradients

Frédéric Guillaume

Institute of Evolutionary Biology and Environmental Studies, University of Zurich

Rapidly changing environmental conditions are posing a threat to many natural species. How can we evaluate the capacity of a species to resist habitat degradation and persist over time in a given landscape? I will present a multilocus and multivariate quantitative genetics simulation model of the evolution of a species' range under shifting selection gradients. I will focus on the role of gene flow and genetic correlations among multiple phenotypic traits in limiting the capacity of a species to adapt to temporally and spatially varying local ecological conditions.



A two-locus model of spatially varying stabilizing or directional selection on a quantitative trait

Ludwig Geroldinger

Department of Mathematics, University of Vienna

The consequences of spatially varying, stabilizing or directional selection on a quantitative trait in a subdivided population are studied. A deterministic two-locus two-deme model is employed to explore the effects of migration, the degree of divergent selection, and the genetic architecture, i.e., the recombination rate and ratio of locus effects, on the maintenance of genetic variation. The possible equilibrium configurations are determined as functions of the migration rate. They depend crucially on the strength of divergent selection and the genetic architecture. The maximum migration rates are investigated below which a stable fully polymorphic equilibrium or a stable single-locus polymorphism can exist. Under stabilizing selection, but with different optima in the demes, strong recombination may facilitate the maintenance of polymorphism. However usually, and in particular with directional selection in opposite direction, the critical migration rates are maximized by a concentrated genetic architecture, i.e., by a major locus and a tightly linked minor one. Thus, complementing previous work on the evolution of genetic architectures in subdivided populations subject to diversifying selection, it is shown that concentrated architectures may aid the maintenance of polymorphism. Conditions are obtained when this is the case.

How can genetic interactions evolve in response to migration load?

Stephen Proulx

Dept. of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara

Gene flow between populations that experience different selective regimes can reduce fitness in both populations. This is particularly true for populations that experience immigration from a large, distinct source population, such as populations on the edge of a species range. How can this deleterious effect of gene flow be mitigated? We focus on the evolution of modifier loci that can affect the dominance, epistasis, or recombination rates. We first model the set of immigrant haplotypes using a branching process approach and then model the invasion of a modifier allele that may become linked to these immigrant haplotypes. We find that modifiers of the dominance coefficient and modifiers of epistasis among immigrant alleles have similar rates of spread. In principle, a modifier that reduces recombination can spread, but we find that this form of selection is much weaker than selection on epistasis or dominance. By comparing the strength of selection of this set of modifiers in a single model we are able to draw general conclusions about the evolution of genetic architecture in response to migration/selection balance.



Effective Parameters in Population Genetic Models with Class Structure

Arndt Telschow

Westfälische Wilhelms-Universität Münster, Institut für Evolution und Biodiversität

Many parameters of a population such as the total number of individuals or migration rates between subpopulations cannot be measured directly by experiments. Therefore, population geneticists estimate them by fitting a mathematical model to available data. A general problem in this approach is that the estimates often deviate from the real values. This is not only due to statistical errors but also due to idealizations of the underlying models. The value of a parameter that accounts for the pattern of data under the idealized assumptions is usually called the 'effective' value of the parameter. By definition, the effective value is not the real value as the ideal model scenario is hardly ever met in reality. Among a variety of effective parameter values, the effective population size (N_e), which measures the intensity of genetic drift, has been playing a central role since Wright's (1931) seminal work. Less acknowledged but possibly equally important is the concept of the effective migration rate (m_e), which quantifies gene flow (Bengtsson 1985). Effective parameter values are key characteristics of a population, and it is of primary importance to predict how they deviate from real values under various non-ideal situations.

The presentation gives an overview over the effective migration rate and how it relates to other effective parameters. First, I discuss scenarios where genetic influx into a population does not correspond to the real migration rate (m) of individuals, due to class structure within the population (e.g., different age, sex, allelic composition, infection status). The ratio m_e/m is called the gene flow factor, and represents the degree of gene flow modification in such situations. Second, I discuss the example where both gene flow and genetic drift is modified by cytoplasmic sex ratio distorters, and demonstrate that the allele frequency distributions are beautifully described by both m_e and N_e . Finally, it is shown how the effective migration rate relates to the effective recombination rate (r_e). Examples are presented that show how r_e can be used to analyze and compare different sym- and parapatric models of speciation.



The effect of linked selection on invasion and survival of locally beneficial mutations

Simon Aeschbacher

Department of Evolution and Ecology, University of California, Davis

We study a two-locus continent-island model with selection against migrants. Combining branching and diffusion processes, we find numerical and analytical approximations to the invasion probability, sojourn-time density, and mean extinction time of a weakly beneficial mutation arising in linkage to an established migration-selection polymorphism.

Interestingly, the invasion probability is maximised at a non-zero recombination rate if the focal mutation is sufficiently beneficial. Moreover, linked selection may increase the survival time by several orders of magnitude, which is relevant especially for island populations of small to moderate size. We also derive explicit expressions for the effective migration rate of partially linked neutral and weakly beneficial mutations. These results have implications for inference from population-genomic data and for our understanding of the genetic architecture of local adaptation.