



cordially invites you to an

## Interdisciplinary Seminar

with

NIMBioS Postdoctoral Fellows Invited Distinguished Visitor

### Dr. Michael Whitlock

on

### *“Selection in complex settings”*

Tuesday, April 12, 2016

3:30-5 p.m.

*Reception & refreshments at 3 p.m.*

Hallam Auditorium, Room 206

1122 Volunteer Boulevard



[Michael Whitlock](#) is a theoretical population geneticist who studies the effects of spatial subdivision on the evolutionary process. Whitlock has described the effects of space on, for example, the effective population size, fixation of new alleles, mutation load, and inbreeding depression. He has also developed new statistical approaches to use genetic data to infer demographic and evolutionary parameters, including measuring effective population size and inferring genes responsible for local adaptation. Whitlock is the former Editor-in-Chief of *The American Naturalist*, where he helped usher in the joint data archiving policy among evolution and ecology journals. He is a professor of Zoology at the University of British Columbia, where he has been for 21 years. He received his PhD from Vanderbilt University and did post-docs at the University of Chicago, the University of Edinburgh, and WWF-Indonesia.

**Abstract:** The fact that the individuals in each species are spread over space with limited dispersal means that evolutionary processes are all to some extent local. In this talk I will discuss some ways in which the basic processes of evolution—especially selection and drift—are substantially changed by their spatial context. In spatially structured populations (compared to the panmictic populations that are better studied), deleterious alleles are likely to be more effectively removed by selection at equilibrium. In contrast, in non-equilibrium populations expanding over space, deleterious alleles can reach locally high frequencies through allelic surfing. The “expansion load” that results can be a substantial burden on the mean fitness of a population. I will explore the interaction between deleterious mutations and spatially heterogeneous selection in determining the rate of population range expansion and the amount of genetic load that results.