Models in population genetics with continuous geography Richard Liang University of British Columbia

The simplest models of population genetics, useful as they are in analyzing data, often have obvious shortcomings. Such models might ignore the effects of natural selection, mutation, or, as we will be concerned with in this talk, geography and migration. We will briefly look at the Wright-Fisher model of evolution of a single population; then, we will look at a so-called stepping stone model, where instead of a single population living all in one place, we model several populations living on discrete islands, with migration between the islands. It is often useful to consider these models' associated dual processes, which correspond to tracing the lineages of a current-day sample backwards through history. We will discuss these dual processes as well.

We will then discuss two models of evolution with *continuous* geography. Unlike the previous models, which describe directly the dynamics of a population evolving as time moves forward, the continuous geography models are instead defined in terms of prescribed dual processes. Time permitting, we will also discuss some properties of these models, such as continuity.

This is joint work with Steve Evans.