Estimating Migration: Comparing $F_{st}$ and Coalescent.

Introduction

- Gene flow is an important consideration for conservation biologists who try to maintain historical levels in the face of anthropogenic habitat fragmentation.
- Since Wright showed that at equilibrium, $F_{st} = \frac{1}{Nm+1}$, many papers have used $F_{st}$ to estimate the number of migrants per generation.
- Due to several problems with assumptions, this estimation of migration and even use of $F_{st}$ to estimate gene flow has been called into question.

$F_{st}$ as a method of estimating gene flow and migration

- History of $F_{st}$
- Assumptions of $F_{st}$
- When does $F_{st}$ work and when doesn’t it

Using the coalescent approach as a method of estimating gene flow and migration

- The basics/history of coalescent theory
  1. Kingman
  2. Visuals
  3. Forward vs backwards looking
  4. MMC

- Assumptions
  1. Wright Fisher model (and Moran)
  2. Neutrality, constant Ne, generations, etc...
  3. Recombination
  4. All populations sampled

- Modifications
  1. Selection
  2. Mutation
  3. Migration

- Connecting coalescent and migration
  1. Back to migration: connection between FST and coalescent (Slatkin 1997)
  2. Ghost populations

Real world comparison of $F_{st}$ and Coalescent estimates

- Bittner and King (2003) compared different types of genetic markers as well as $F_{st}$ and Coalescent approaches for estimating the number of migrants.
- $F_{st}$ resulted in much higher migration rate estimates compared to Coalescent for both types of genetic markers.
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- Based on biology and geographical barriers, coalescent estimate makes more biological sense.

Literature Cited


