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## 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  $N_e$ , generations, ect...
  3. Recombination
  4. All populations sampled
- Modifications
  1. Selection
  2. Mutation
  3. Migration
- Connecting coalescent and migration
  1. Back to migration: connection between  $F_{ST}$  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

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Neigel, J. E. 2002. Is  $F_{st}$  obsolete? *Conservation Genetics* **3**:167-173.

Slatkin, M. 1991. Inbreeding coefficients and coalescence times. *Genetics Research Cambridge*. **58**:167-175.