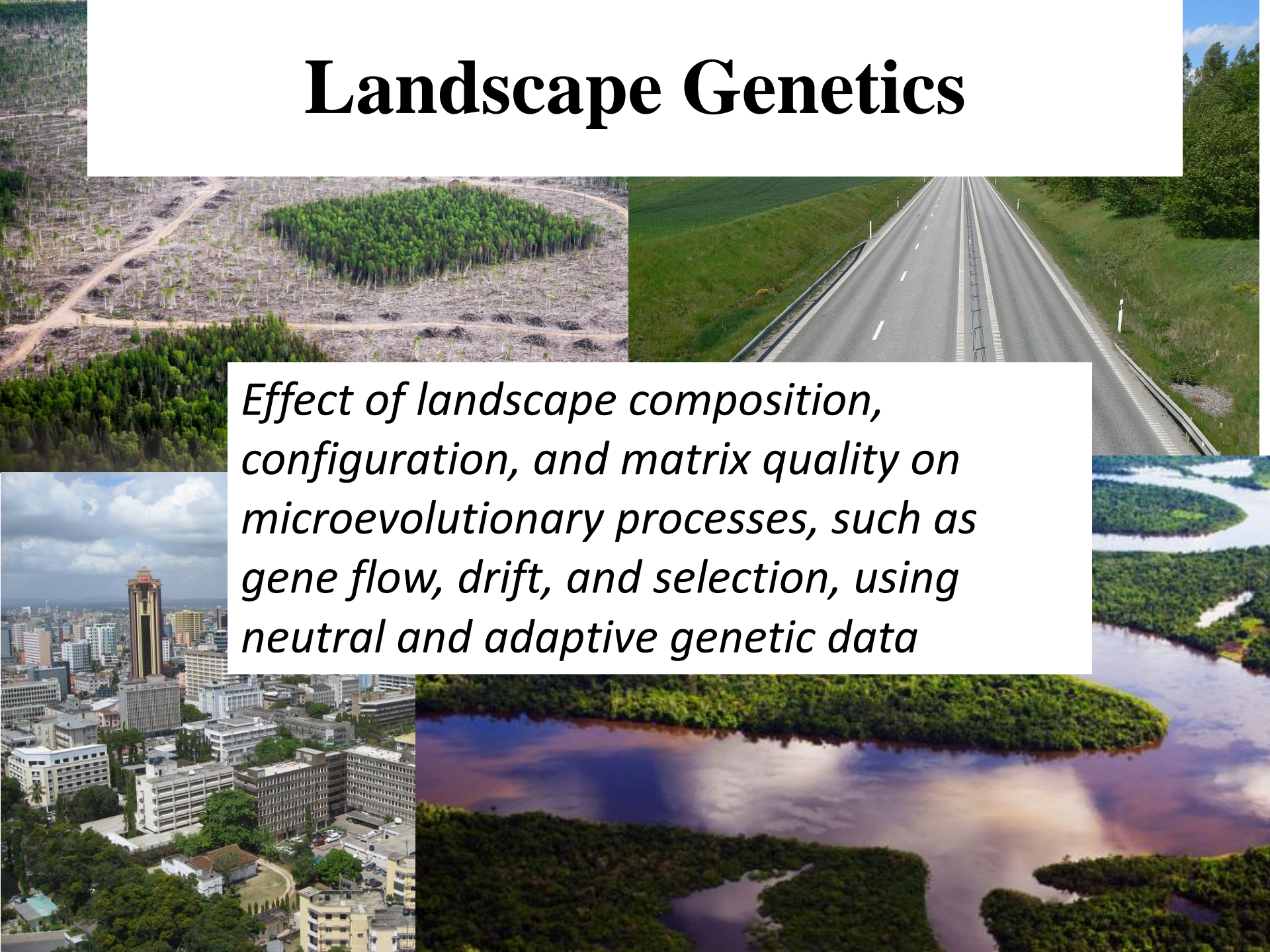


# Habitat Fragmentation



# Landscape Genetics

*Effect of landscape composition, configuration, and matrix quality on microevolutionary processes, such as gene flow, drift, and selection, using neutral and adaptive genetic data*



# Connectivity/ Landscape Genetics

- Genetic connectivity
- Demographic connectivity

Key themes:

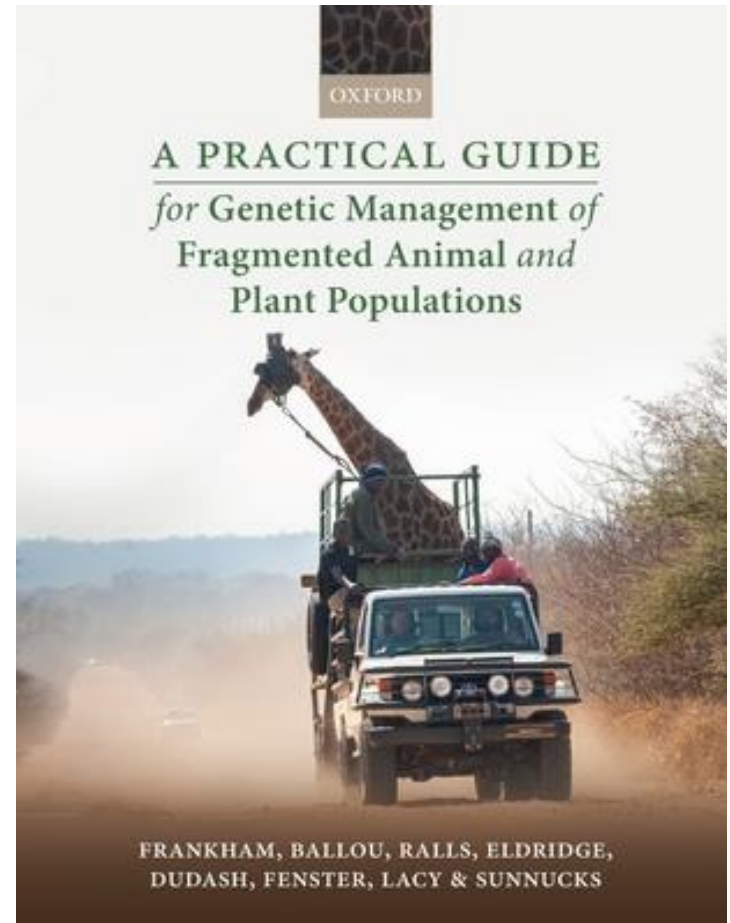
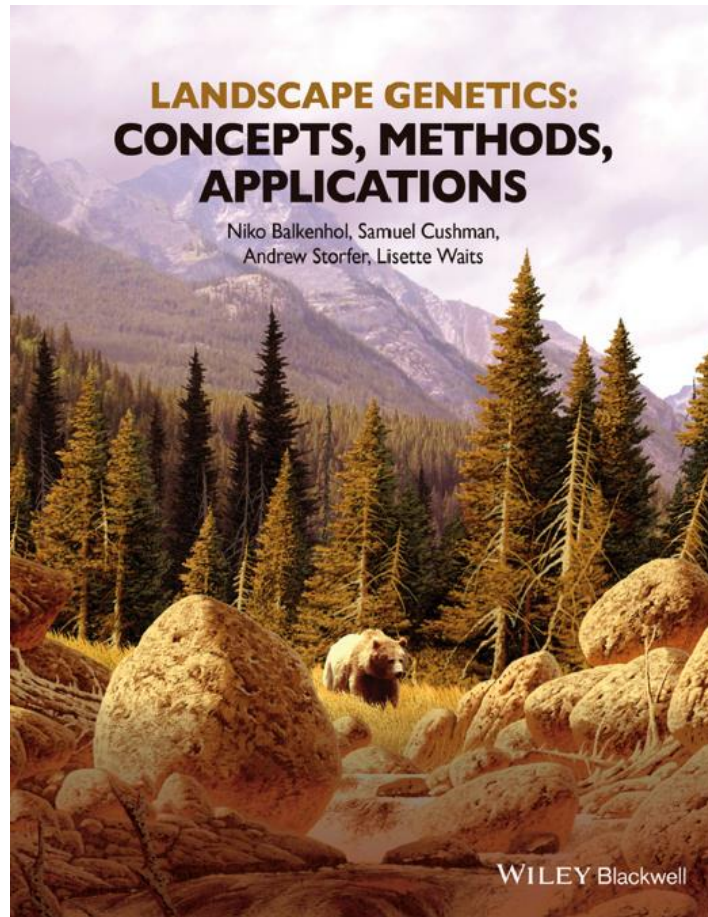
1. Infer underlying ecological processes, such as dispersal or disease transmission.
2. Understanding how landscape characteristics affect evolutionary processes

# Connectivity - definitions

1. Genetic connectivity – Degree to which gene flow affects evolutionary processes
2. Demographic connectivity – Degree to which individual movements influence demography.

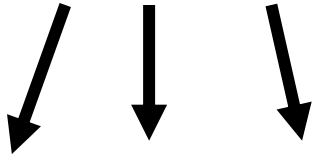


# Useful References

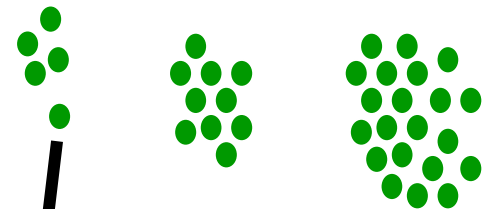


# Genetic variation and a hierarchy of biodiversity

Species:



‘Populations’  
(habitat fragments)



Individuals:



Genes:

## Research themes

Biogeography / speciation  
(species and above)



genetic structure  
/phylogeography



Paternity / relatedness  
(individual / social groups)

# Different analyses address different time scales

1/ *Genotypic analyses* are based on DNA ‘signatures’ of individual organisms that are reshuffled in every generation of a sexual species

2/ *Genic analyses*, where the focus is on frequencies of genetic variants in grouped samples, not individuals. Gene frequencies change more slowly than the generational shuffling of genotypes – measures ongoing restriction of mobility and gene flow

3/ *Genealogical analyses*, A new variant arises at a point in time and space, and will come to be distributed over landscapes according to gene flow, drift and extinction – slow process and therefore can detect processes far back in time

# Analyzing groups of individuals

- Within Patches
  - Levels of genetic variation
  - Level of inbreeding
  - Effective population size ( $N_e$ )
- Between Patches
  - Degree of genetic differentiation
  - Measures of gene flow and/or dispersal



# F-statistics

Inbreeding and drift both decrease heterozygosity and increase homozygosity. But:

- inbreeding impacts at the individual level
- drift impacts at the group level (population)

Total population variation can be partitioned into differentiation among individuals within populations and differences among populations

*F-statistics measure level of heterozygosity relative to HWE expectations at different hierarchical levels:*


$F_{IS}$ : within patches

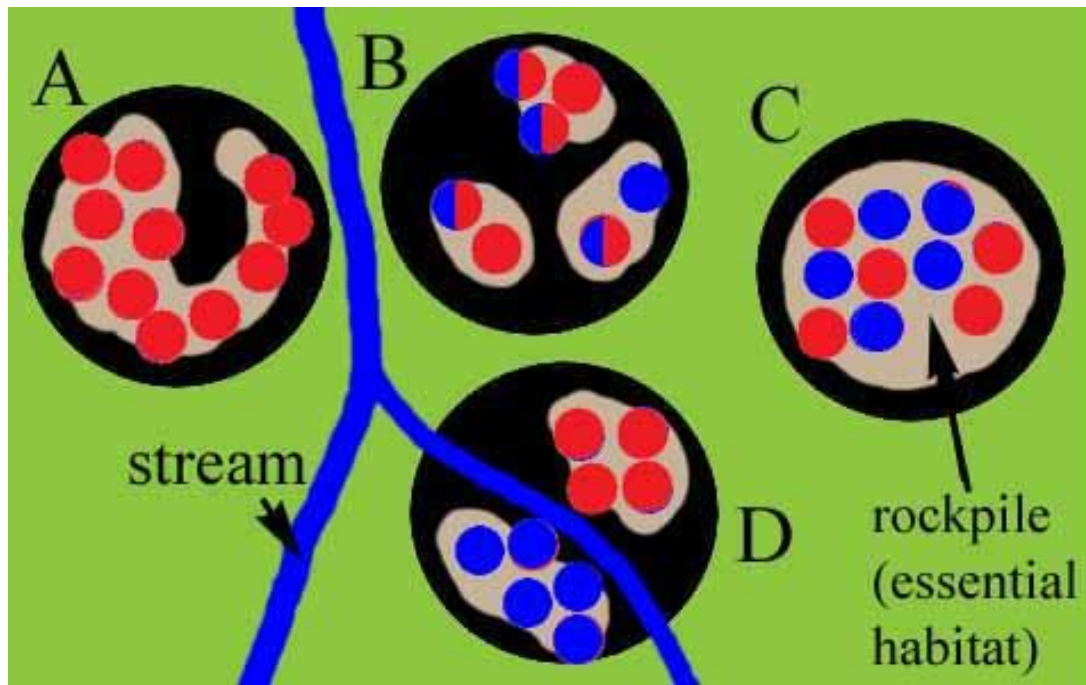
$F_{ST}$ : among patches

$F_{IS}$  is a measure of inbreeding ‘within a patch’

- $1 - H_o \text{ (within pop)}/H_e \text{ (all samples)}$
- ranges from -1 to +1
- positive: excess of homozygotes
- negative: excess of heterozygotes
- At HWE  $F_{IS}$  is 0

# $F_{ST}$ is a measure of genetic subdivision

- $1 - H_e$  (of fragment)/ $H_e$  (Total)
- ranges from -1 to +1 
- measures the proportional reduction in heterozygosity of the entire network of subpopulations relative to HWE (due to differentiation among subpopulations)
- large: at least some subpopulations have different allele frequencies
- small or 0: subpopulations have similar allele frequencies



$F_{ST}$  contributions of the subpops A, B, C, D to this would be...

A. Large - subpop A has very different allele freqs. compared to the others

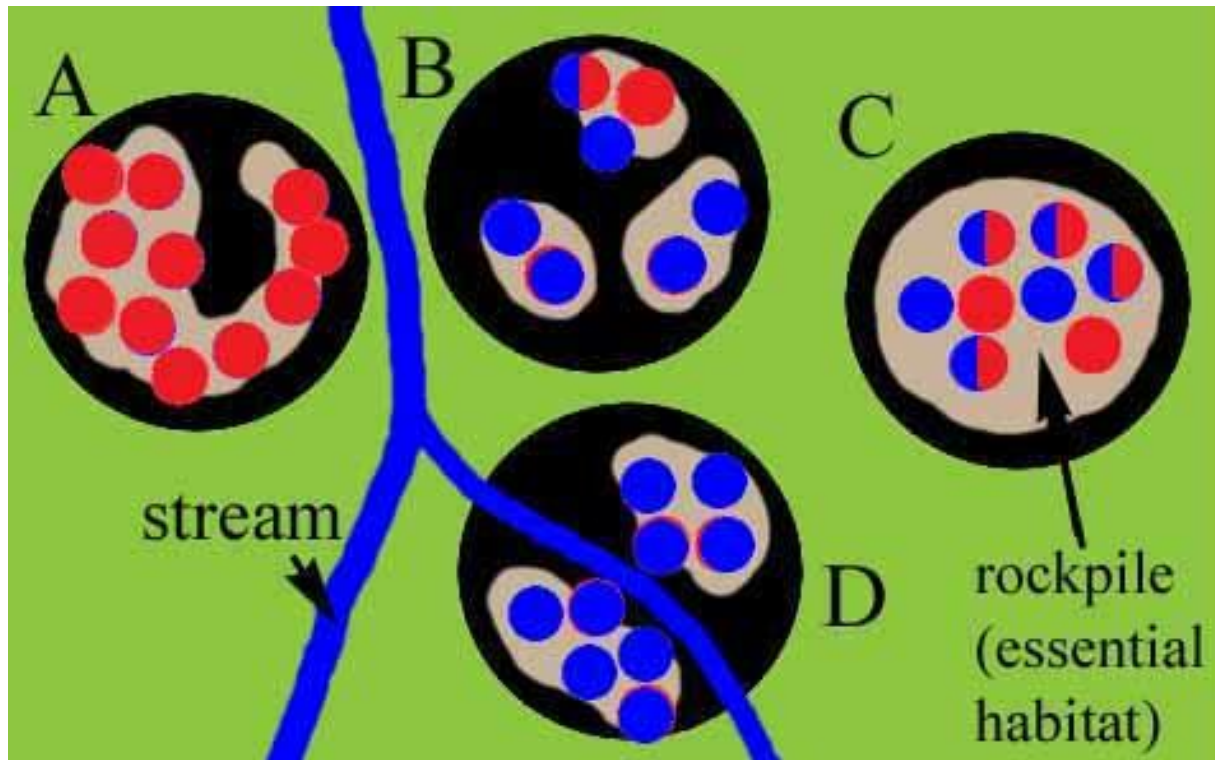
B. Little - subpop B has similar allele freqs. to C & D

C. Little - same reasons as B despite inbreeding in C

D. Little - same reasons as B despite two inbred groups in D

$F_{ST}$  and  $F_{IS}$  can operate separately...

*Scenario 1*

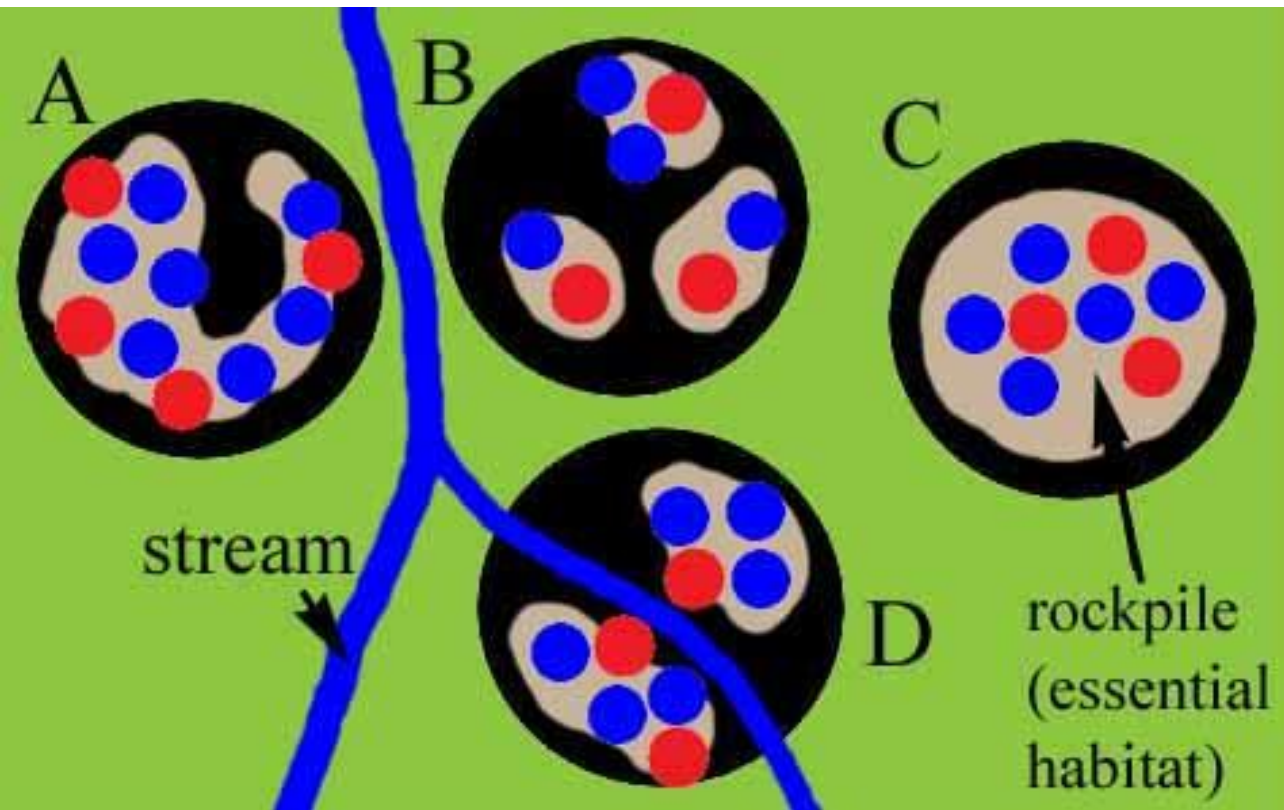


$F_{IS}$   
low, because each subpop  
is not far from HWE.

$F_{ST}$   
is high, because the  
allele freqs. in each  
subpop are very different:  
- A is fixed for red  
- B has high freq blue  
- C has equal freqs  
- D is fixed for blue

$F_{ST}$  and  $F_{IS}$  can operate separately...

*Scenario 2*



$F_{IS}$   
very high, because the reds  
and blues appear not to  
interbreed - there are no  
heterozygotes even though  
reds and blues live together

$F_{ST}$   
very low, because there are  
few differences among the  
subpops A, B, C, D. All  
have reds and blues



# The importance of the spatial scale of sampling ...

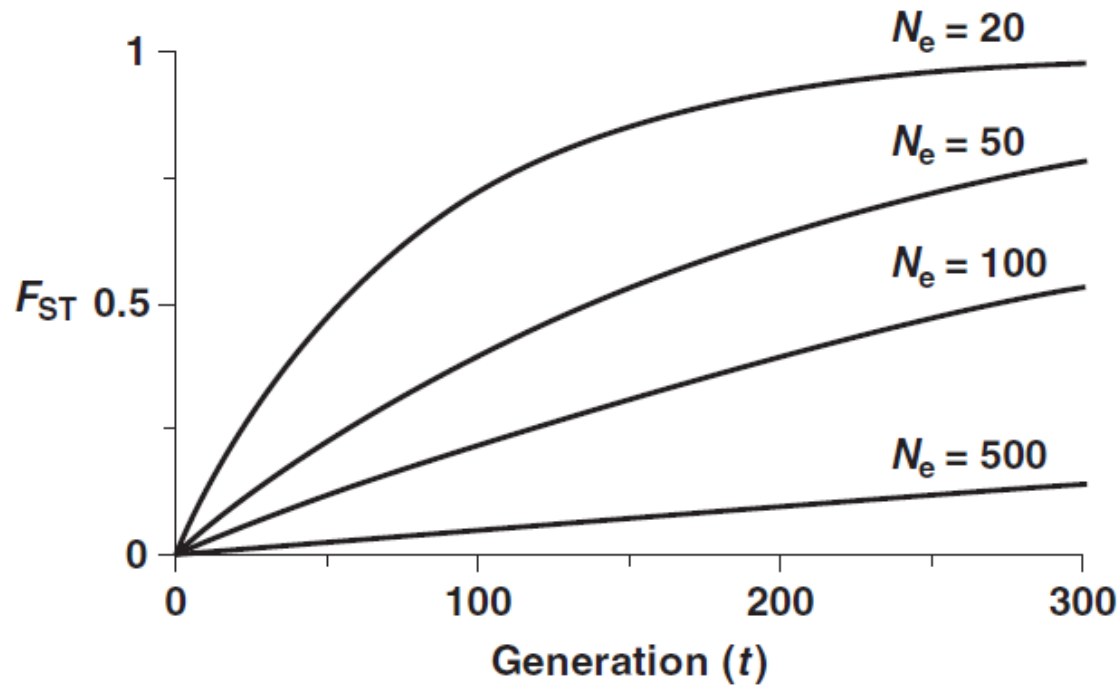


## *“Wahlund Effect”*

reduction of heterozygosity in a population caused by genetic structure

Sampling scale	$F_{IS}$	Contribution to $F_{ST}$
D as one unit	large +(ve)	very little
D split into 2	$\sim 0$	very large

# Relationship between $F_{ST}$ and $N_e$



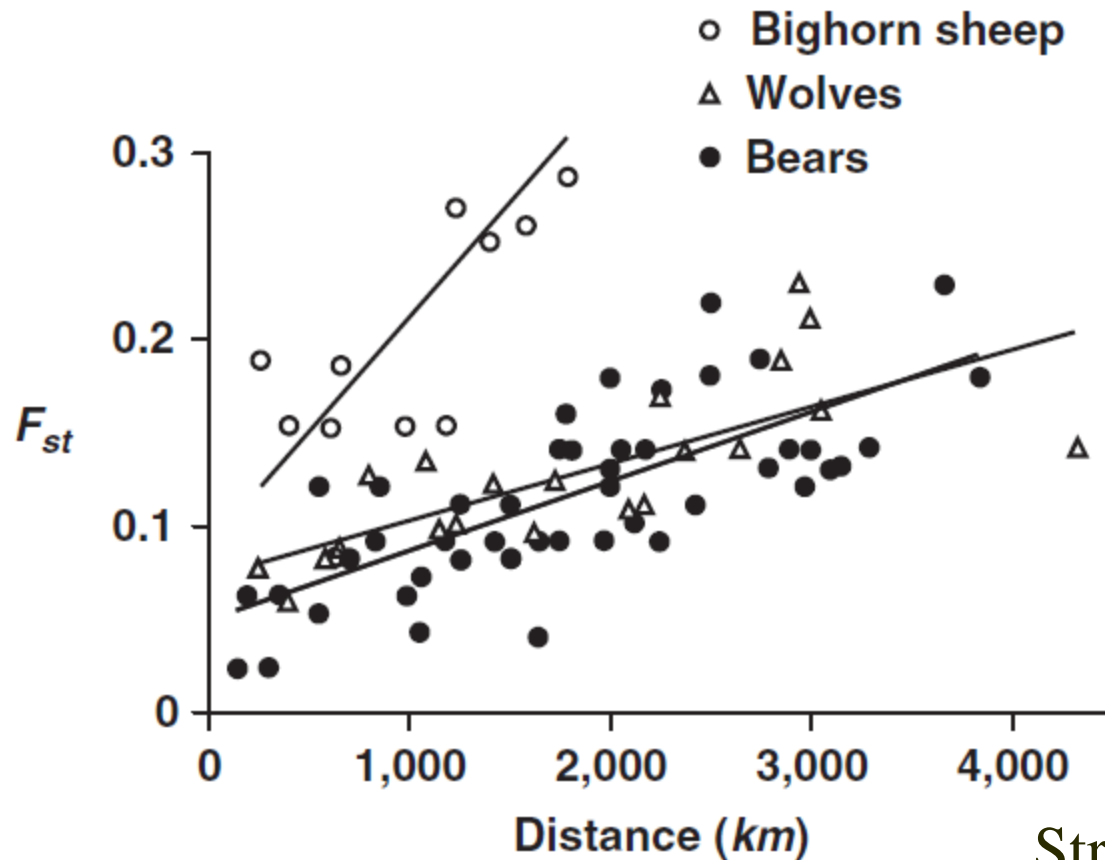
# Interpreting F-statistics

## Generalizations about the biological meaning of $F_{ST}$

**Table 2** Definitions for three types of genetic connectivity. The values for  $m$ ,  $Nm$ , and  $F_{ST}$  are the approximate values associated with each type of connectivity with the island model of migration. The actual values for each parameter will differ with other models of population structure

	Adaptive connectivity	Inbreeding connectivity	Drift connectivity
Criterion	Sufficient gene flow to spread advantageous alleles	Sufficient gene flow to avoid harmful effects of local inbreeding	Sufficient gene flow to maintain similar allele frequencies
$m$	?	?	?
$Nm$	>0.1	>1.0	>10
$F_{ST}$	<0.35	<0.20	<0.02

Lowe and Allendorf 2010



Straight line distances

**Fig. 14.12** Isolation by distance. Relationship between degree of genetic differentiation ( $F_{ST}$ ) at microsatellite loci and geographic distance among bighorn sheep, brown bear and gray wolf populations in North America (after Forbes & Hogg 1999).  $F_{ST}$  increases with distance in all three species.

# Measuring landscape effects on gene flow

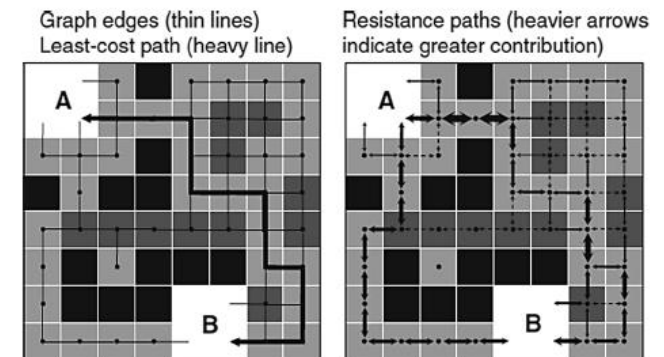
Can be characterised as:

**Least Cost Path:** A distance measure of the path of ‘least resistance’ i.e. the easiest

**Resistance:** degrees to which the environment impedes movement – accumulates with geographic distance

Balkenhol et al. landscape Genetics 2016

Continued week 10





# Demographic Connectivity

$$N_{t+1} = N_t + \underbrace{\text{Births} - \text{Deaths}}_{\text{Local recruitment}} + \underbrace{\text{Immigrants} - \text{Emigrants}}_{\text{Net immigration}}$$

Total recruitment

Measuring dispersal at the scales required can be problematic



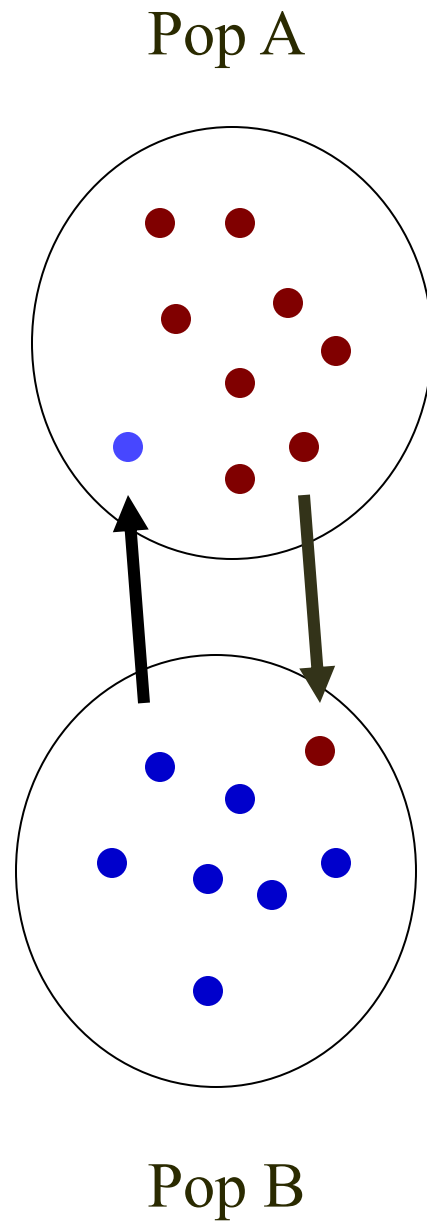
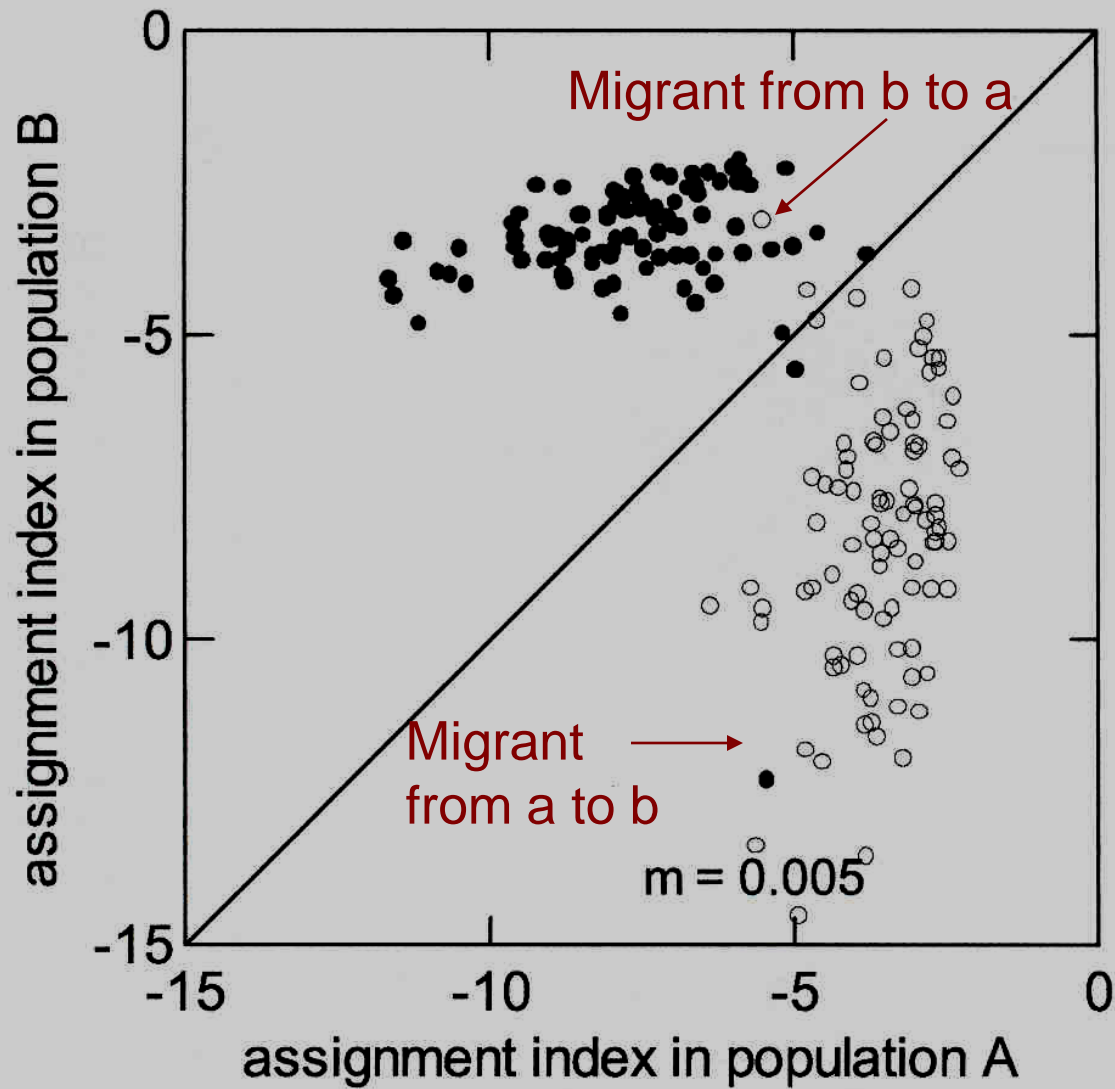
# Genotypic Approaches

## Direct Measures of Migration Rate Between Fragments

### Assignment Tests

likelihood-based technique

1. assume HWE
2. calculate population allele frequencies
3. compute the likelihood of an individual multi-locus genotype belonging to each population in a candidate set of populations
4. assigns that individual to the population where the likelihood of its genotype is the highest



		Same Location	Movement > 11m	Median distance (Range)
Parentage*	Sib	184	1	48m
	Father	17	3	70m (22-170)
	Mother	33	0	-
Recapture	Imm	85	2	20m (18-22)
	♂	16	7	43m (15-200)
	♀	17	1	40m

If sampling is sufficient then dispersal can be characterized by the distribution of parent-offspring pairs



# Next – maintaining genetic variation

