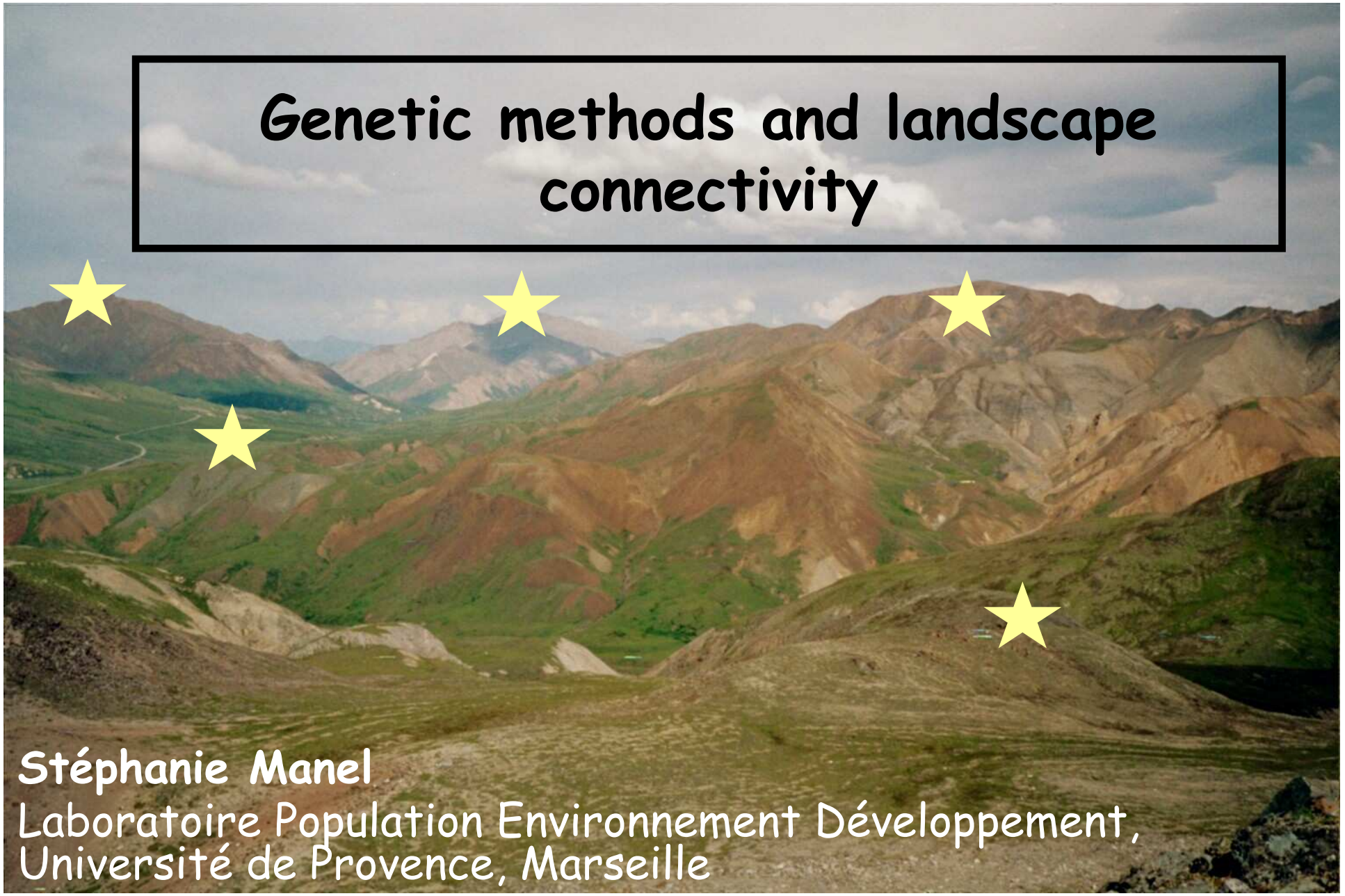
Workshop ECONNET; 4 au 7 novembre 2009; Grenoble

# Genetic methods and landscape connectivity



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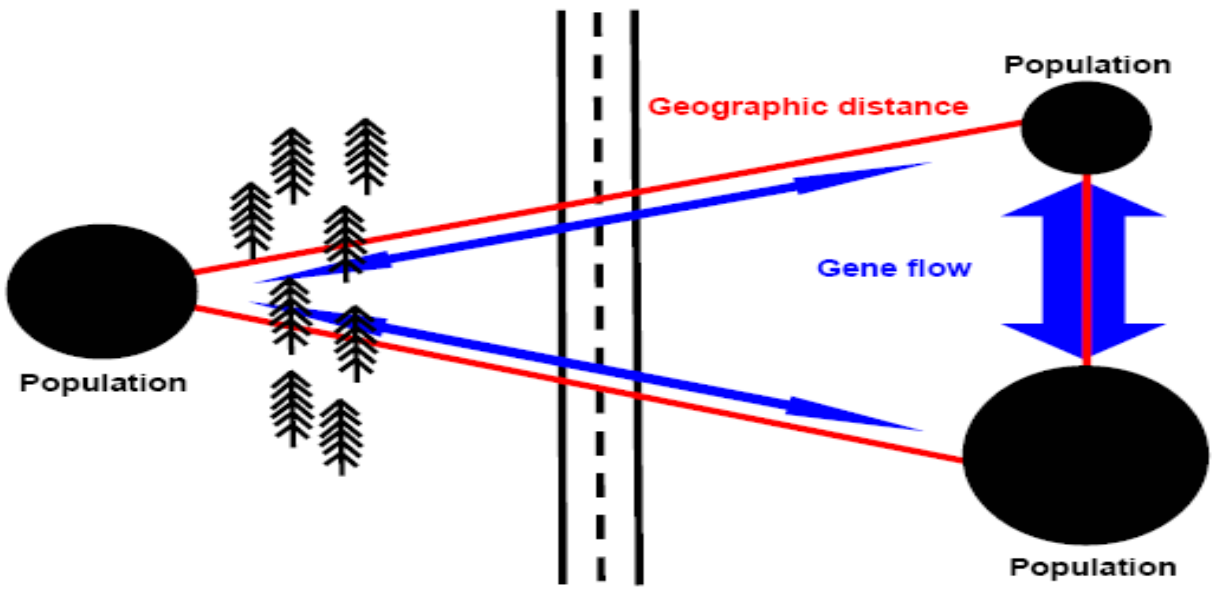
Université de Provence, Marseille

# Landscape fragmentation: the question to solve

How gene flow  is affected by landscape?

**Road is a barrier to gene flow?**




**Effect of geographic distance?**

**Effect of another landscape element?**

# Plan

1- Definition: connectivity , landscape genetics

2-Genetic methods: genetic distances / boundary to gene flow

3-Influence of landscape on genetic component : understanding functional connectivity from a genetic perspective

# Landscape connectivity

**Landscape connectivity** is the degree to which the landscape facilitates or impedes movement among resources patches

It has two components:

- Structural connectivity: the spatial structure of a landscape and can be described from map elements

-Biological component: the response of individuals to landscape features (functional connectivity)

**→Plays a key role in conservation biology**

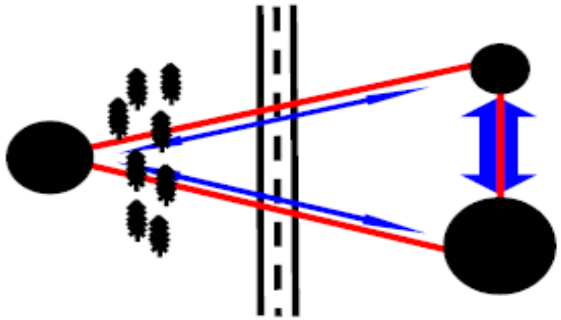
Taylor, P.D., Fahrig, L., Henein, K. and Merriam, G., 1993. Connectivity is a vital element of landscape structure. Oikos, 68: 571-573.

Brooks, C. P. 2003. A scalar analysis of landscape connectivity. Oikos 102:433-439.

1-Definition

# Landscape genetics: A framework to study connectivity

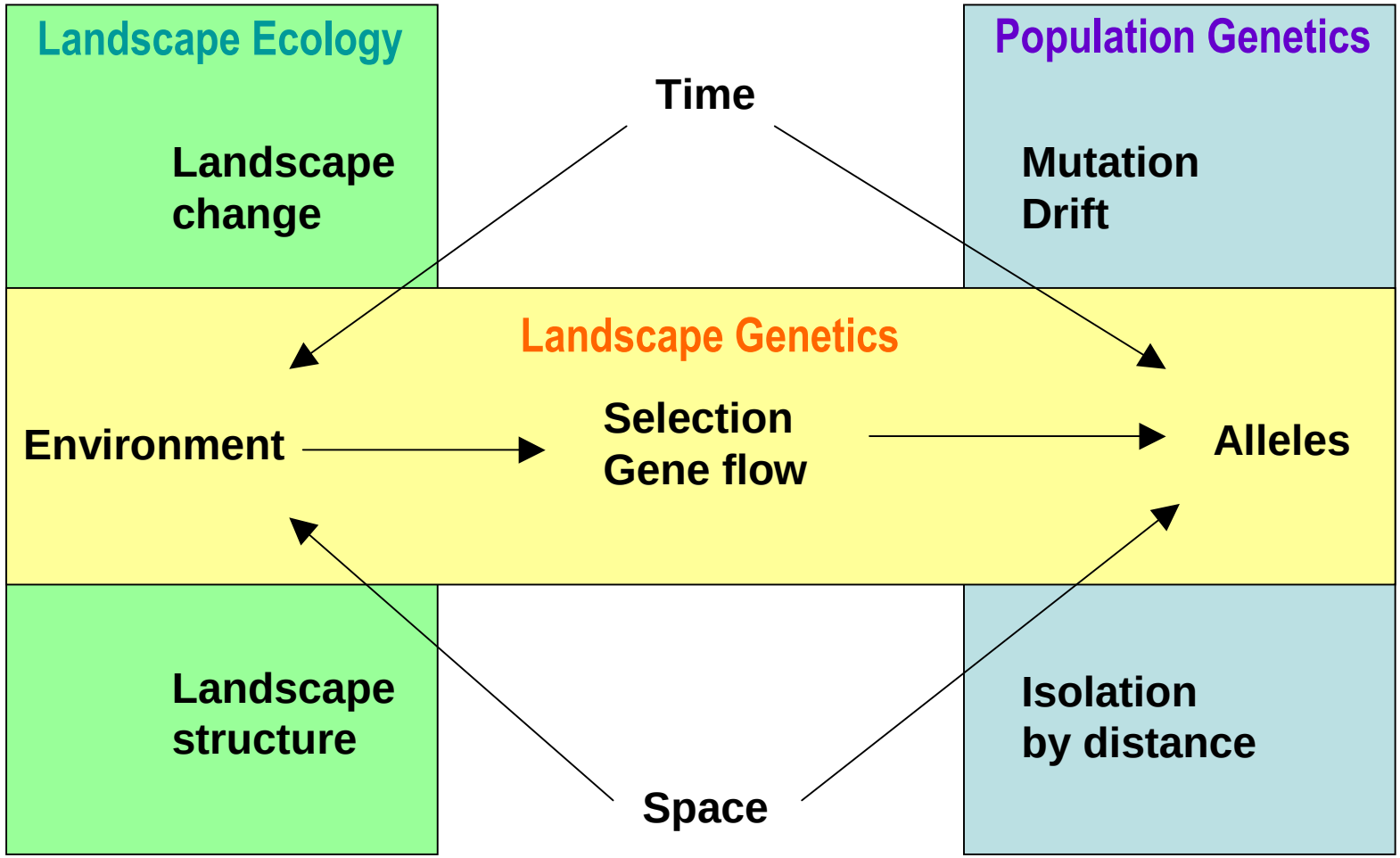
**Landscape genetics studies the effects of landscape or environment on genetic diversity, differentiation or contemporary gene flow**



**Discriminate between the effects of geographic distance, road and forest**

Manel S et al. (2003), Tree, 18, 189-197

# Integration of population genetics and landscape ecology



**Steps**:

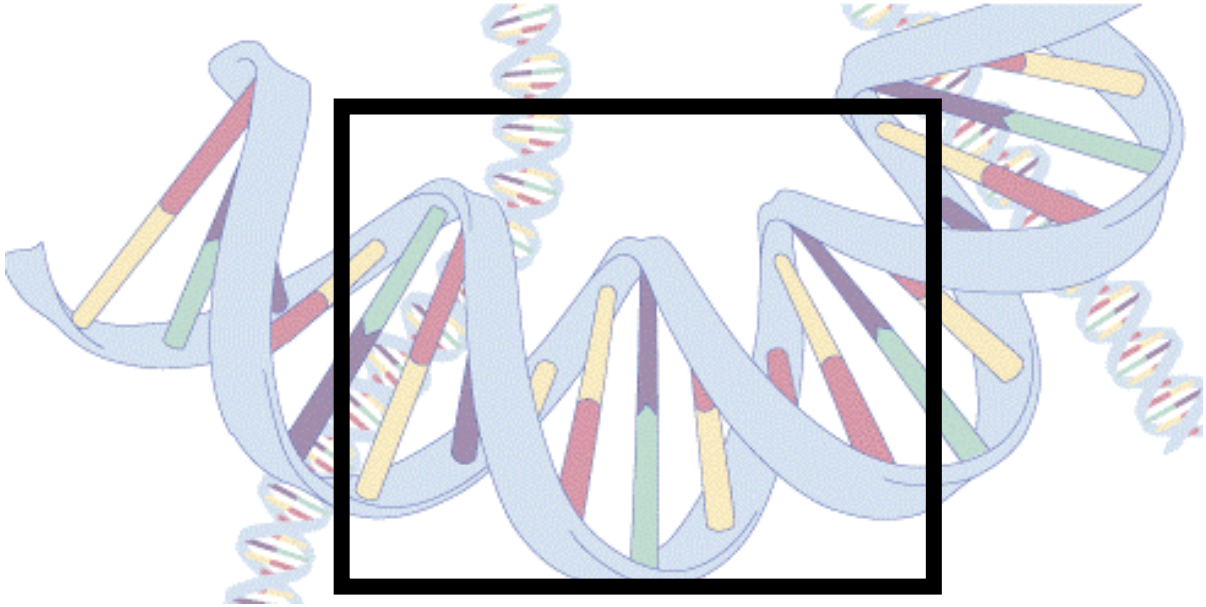
- Sampling individuals/ populations - Development of molecular markers

- Quantification of the movement:

→Estimating gene flow from the measurement of genetic distances (individual or population levels)

→Identification of genetic boundaries, i.e. populations

# Locus



**A physical location in the genome**

## Neutral Loci vs Loci under selection

Genes = loci influenced by natural selection

Other sections of DNA with no known function are neutral

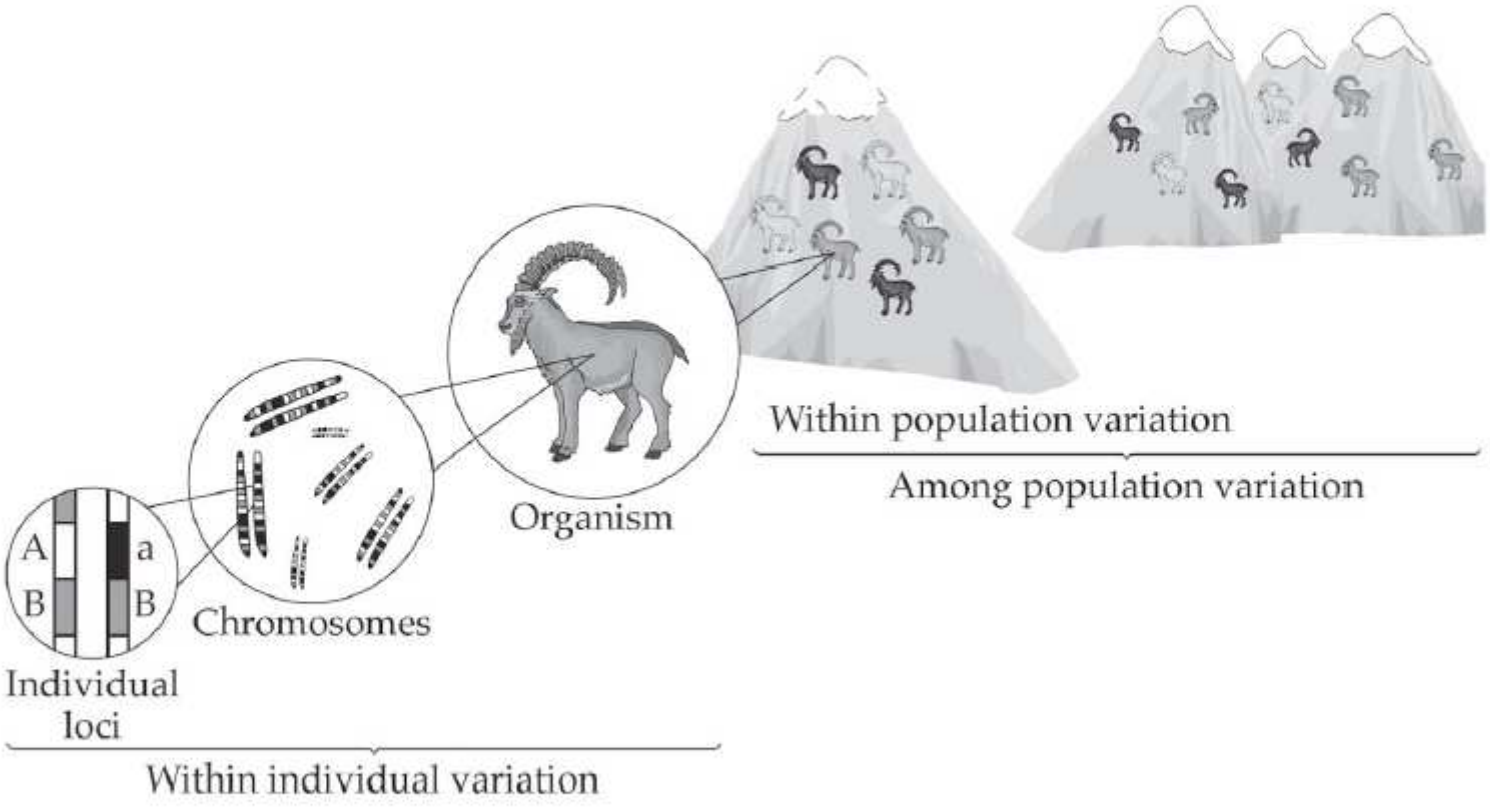
Molecular markers=fragment of DNA sequence associated to a part of the genome (i.e. a loci)

# Techniques for Detecting Genetic Variation

- Allozyme analysis - proteins
- Restriction Fragment Length Polymorphism Analysis (RFLP)
- Amplified Fragment Length Polymorphism Analysis (AFLP)
- DNA sequencing
- Microsatellite analysis
- Single Nucleotide Polymorphism Analysis (SNPs) or SCN - single copy nuclear analysis

## 2-Genetic method

Genetic diversity and level of measure




*PRINCIPLES OF CONSERVATION BIOLOGY, Third Edition*, Figure 11.1 

# Quantification of the movement

Species dispersal = movement away from an existing population or away from the parent organism.

Gene flow=In population genetics, **gene flow** is the transfer of allele of gene from one population to another.

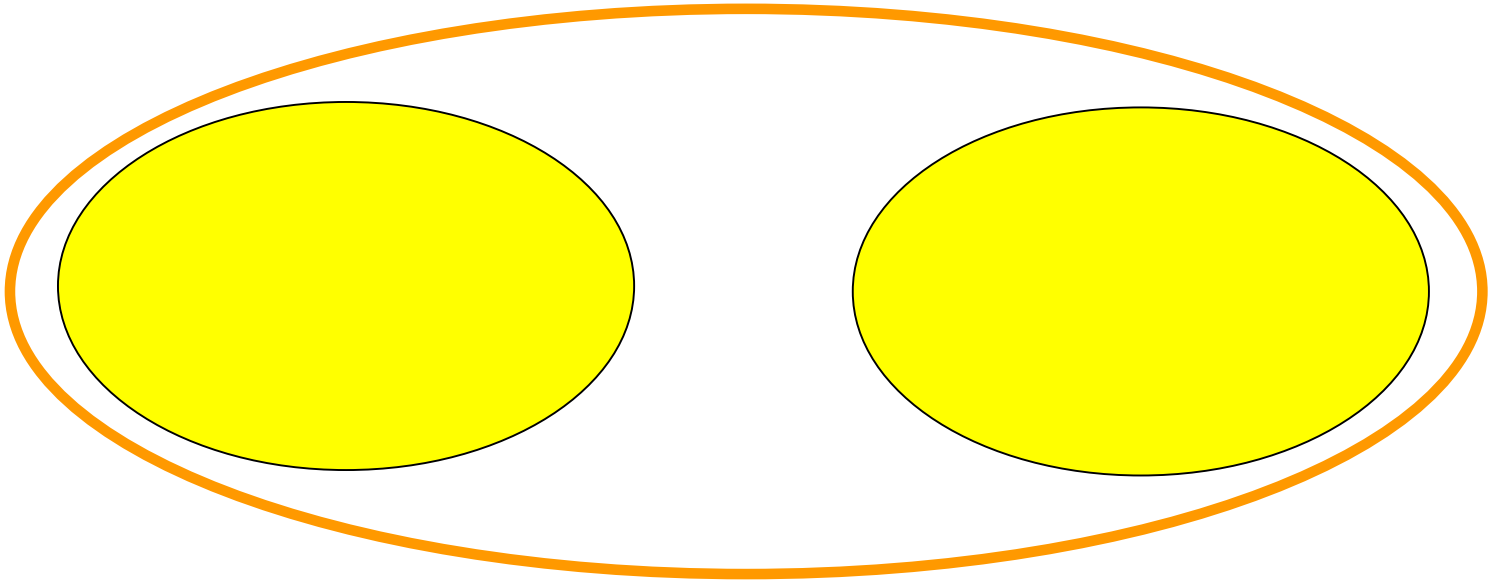
Current gene flow vs historical gene flow

→**Conventional approach to quantify gene flow has been to transform measures of population structure into direct estimates of the average number of migrants exchanged per generation among a set of populations most commonly using an island model.**

(Sork et al. 1999 tree)

# F-Statistics

Originally developed by Sewall Wright (1931, 1951)



If a large total population becomes subdivided, comparing genetic variability in the subpopulations can be used to measure strength of subdivision

# Estimating Gene Flow
## Assumptions

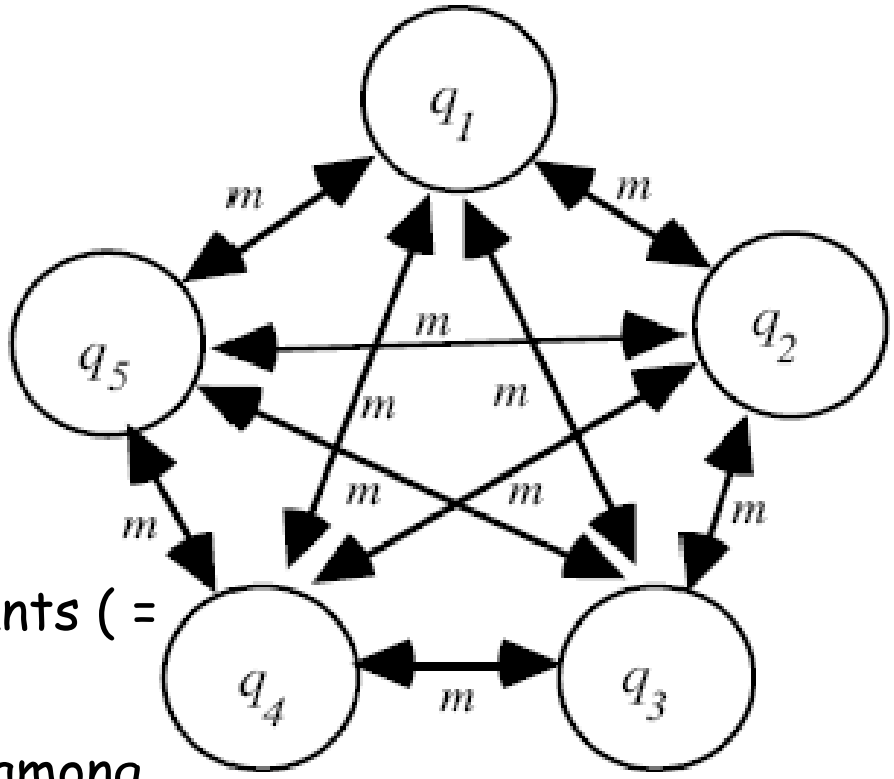
- Infinite island model of migration

Large (infinite) number of populations

They all have the same size

They all share equal numbers of migrants ( = gene flow)

Gene flow not influenced by distance among populations




- Total population (before subdivision) was in HWE
- No selection
- Weak mutation, following an infinite allele model
- Equilibrium between gene flow and drift

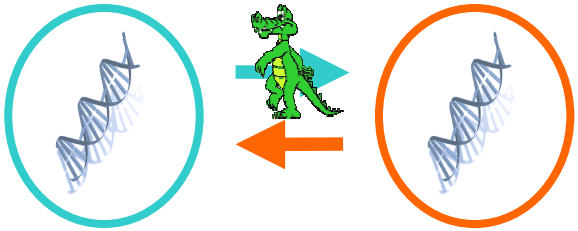
# Estimating Gene Flow

- $F_{ST}$ is a function of:
  - migration rate
  - Level of sub-populations and movement patterns between them
  - Ne

- If island model assumptions hold:

$$F_{ST} = 1 / (4Nm+1)$$

(where Nm = absolute number of migrants per generation)



# Genetic Distance

## Example:

AA/BB **1**

aa/Bb **2**

aa/bb **3**

**1** vs. **2** 1 of 4 alleles in common → Rather dissimilar

**1** vs. **3** 0 of 4 alleles in common → Very dissimilar

**2** vs. **3** 3 of 4 alleles in common → Very similar

# Genetic Distance Measures

**Population based**

Fst based distance (differentiation based measure)

Nei's Standard genetic distance $D_s$ (or D) (Nei 1972)

Distance measures that use SMM model and developed for usats ($D_{SW}$ - Shriver et al 1995 )

Cavalli-Sforza Chord Distance Dc (Cavalli-Sforza and Edward 1967)

$D_{LR}$ (Paetkau et al 1997) - likelihood distance

**Individual based**

Rousset's A (Rousset 2000)

Kinship (Loiselle et al 1995)

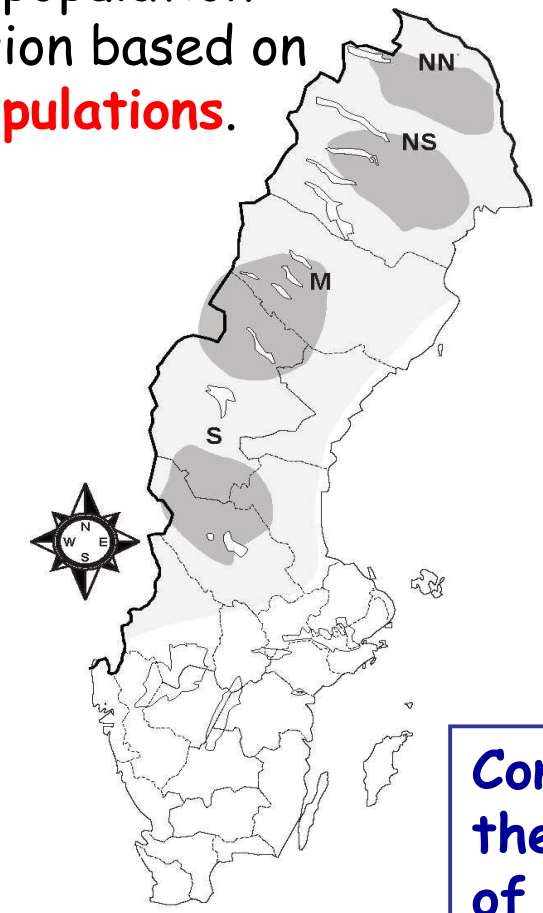
Relatedness (Queller and Goodnight1989)

Shared allele distance

**<u>A case study</u>: Spatial genetic structure of the Scandinavian brown bears revisited**

**366 individuals, 18 microsatellites**

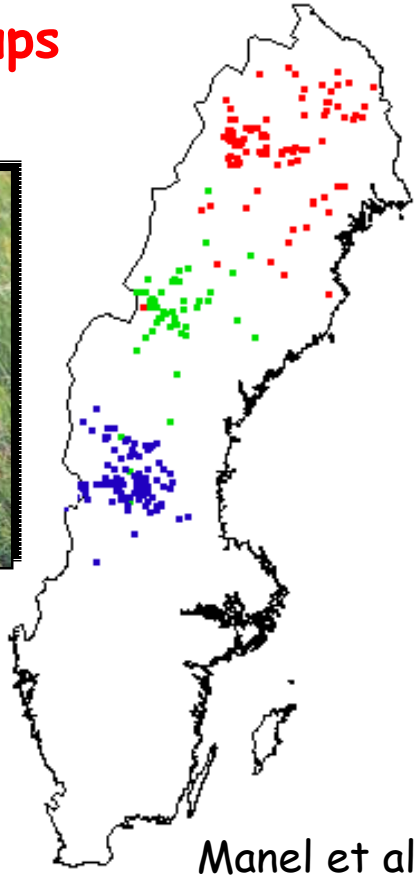
*a priori* population subdivision based on **4 subpopulations**.




Waits et al. (2000)

**Consequences for the conservation of the species**

Individual clustering with STRUCTURE: **3 groups**

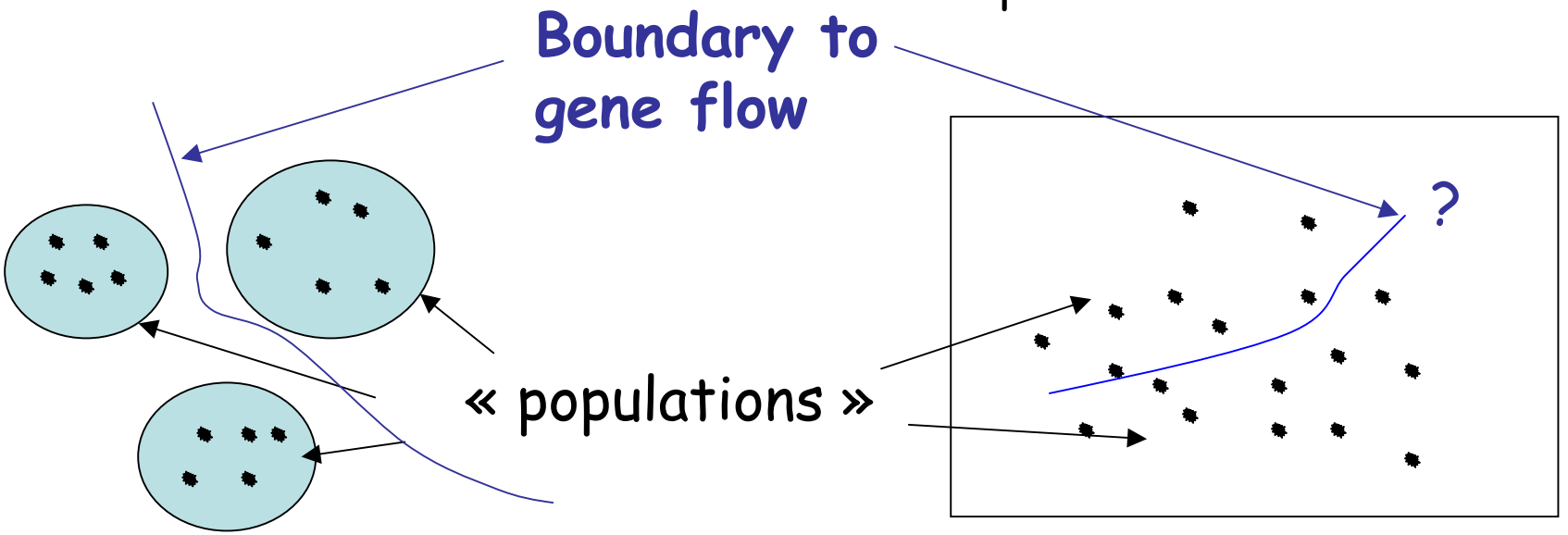


Manel et al. (2004)

# When will we look for populations?

(1) Individuals are grouped in units well defined

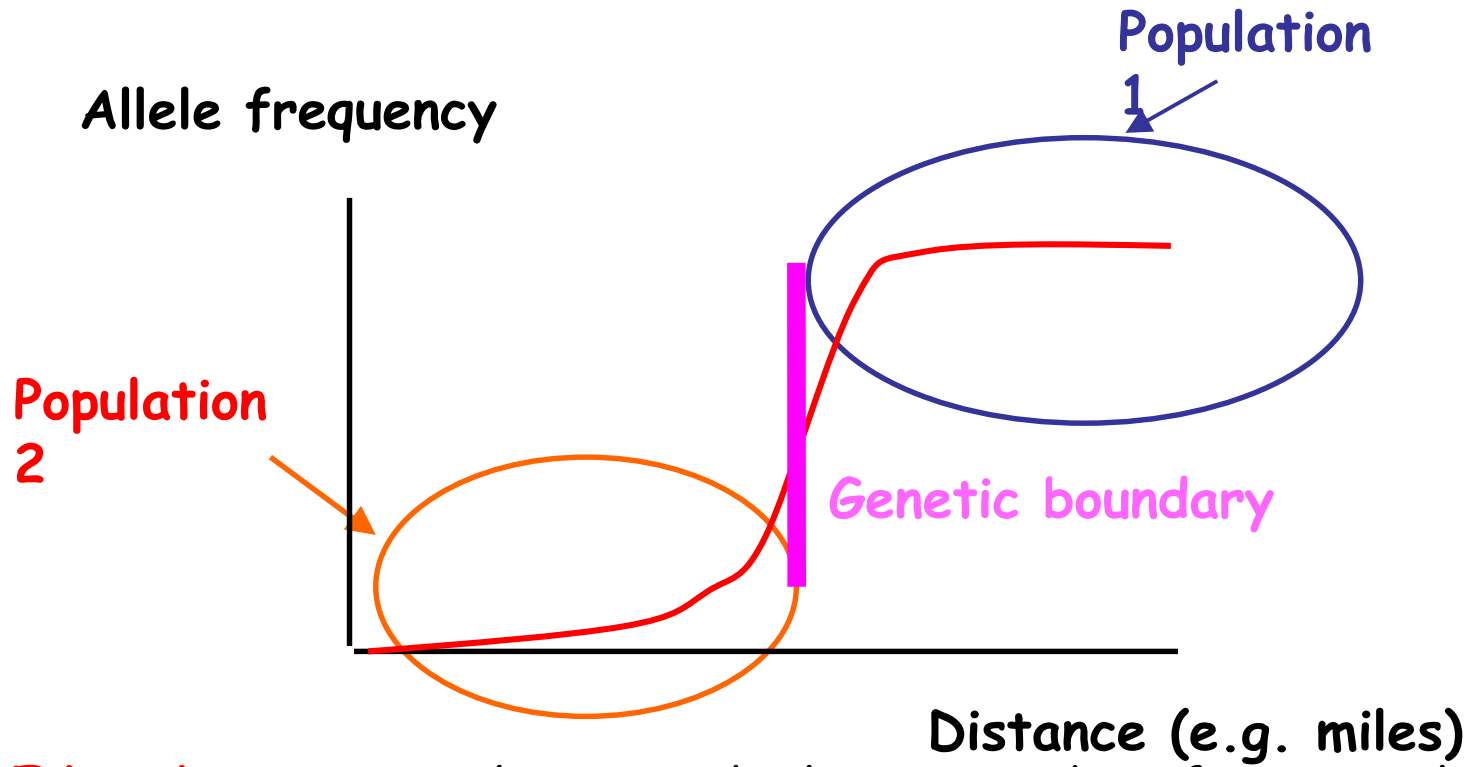
(2) Individuals are distributed continuously in space




**We might be interested to look for populations 1) to check for populations or group of populations 2) to make populations when individuals are continuously distributed**

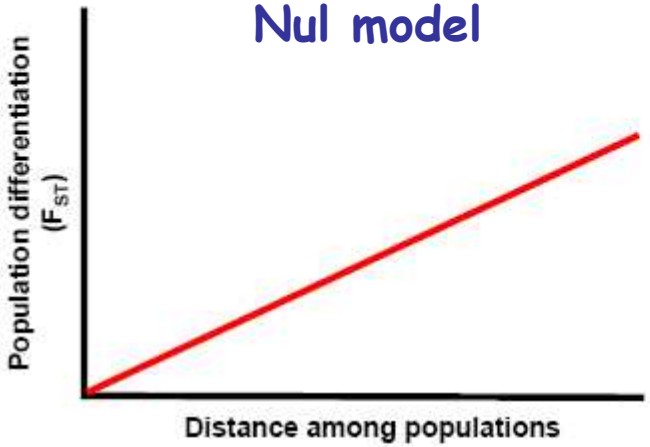
Manel et al. (2007) – Crida & Manel (2007)

**Boundary to gene flow: Area of sharp variation in allele frequency**



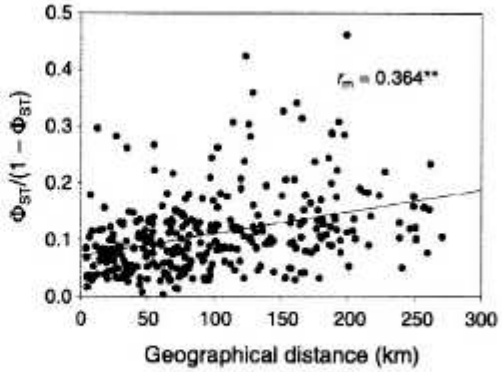

- **Edge detection** techniques which aim to identify areas where changes in variables occur (Fortin & Drapeau 1995)
- **Bayesian clustering algorithms** which strive to identify discrete sets of individuals based on genetic data without a priori assumptions on the number of populations that may exist (Pritchard et al. 2000)

# 3-functional connectivity from a genetic perspective

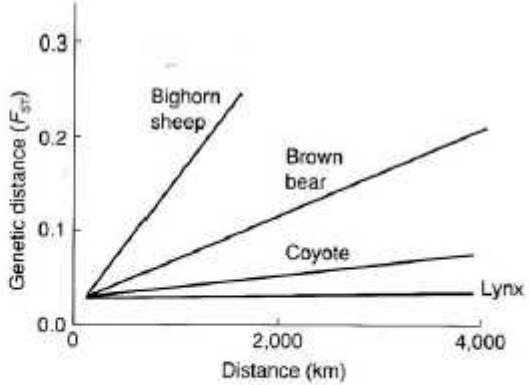



**Isolation by distance**

(Wright 1943 Genetics 28:114-138)




(Angelone et al 2007 Mol Ecol 16:1291-1301)




(Allendorf & Luikart 2007 Conservation and the genetics of populations, Blackwell)

→Mantel test

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# Gene Flow in Complex Landscapes: Testing Multiple Hypotheses with Causal Modeling

Samuel A. Cushman,[1,*] Kevin S. McKelvey,[1,†] Jim Hayden,[2,‡] and Michael K. Schwartz[1,§]

Functional connectivity in black bears (Ursus americanus) sampled in northern Idaho, Genetic similarities=genetic distance based on 9 microsatellites - Landscape resistance models : movement cost and land cover, slope elevation, roads, euclidienne distance

Table 1: Description of factors and levels combined to create 108 landscape-resistance hypotheses

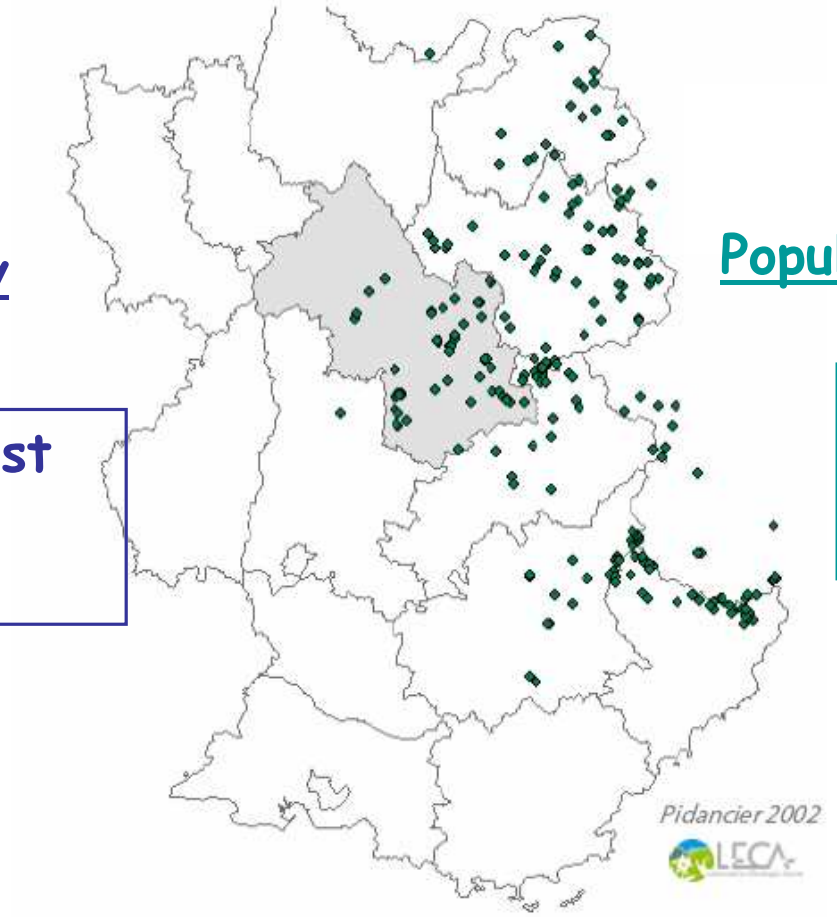
| Factor and level | Code | Description |
|---|---|---|
| Land cover: | | |
| High selectivity | FH | Low-resistance forest; high-resistance nonforest[a] |
| Low selectivity | FL | Low-resistance forest; moderate-resistance nonforest[a] |
| Null | FN | No relationship with land cover classes |
| Slope: | | |
| High resistance | SH | High resistance due to slope[b] |
| Low resistance | SL | Low resistance due to slope[b] |
| Null | SN | No relationship with slope |
| Roads: | | |
| High resistance | RH | High resistance due to roads[c] |
| Low resistance | RL | Low resistance due to roads[c] |
| Null | RN | No relationship with roads |
| Elevation: | | |
| High elevation | EH | Minimum resistance at high elevation[d] |
| Middle elevation | EM | Minimum resistance at middle elevation[d] |
| Low elevation | EL | Minimum resistance at low elevation[d] |
| Null | EN | No relationship with elevation |

→ ¨Partial Mantel tests = effect of land cover and elevation

# *Landscape genetics of the common frogs, Rana temporaria*

*S. Descout, S. Manel, C. Miaud, P. Delcros, S. Lucque*

228 individuals sampled across French and Italian ALps, 13 microsatellites




**Landscape ecology**

**Population genetics**

**SIG- Least cost modelling**

**Pairewise genetic distances**

**Effect of habitat on the genetic connectivity of the common frogs**