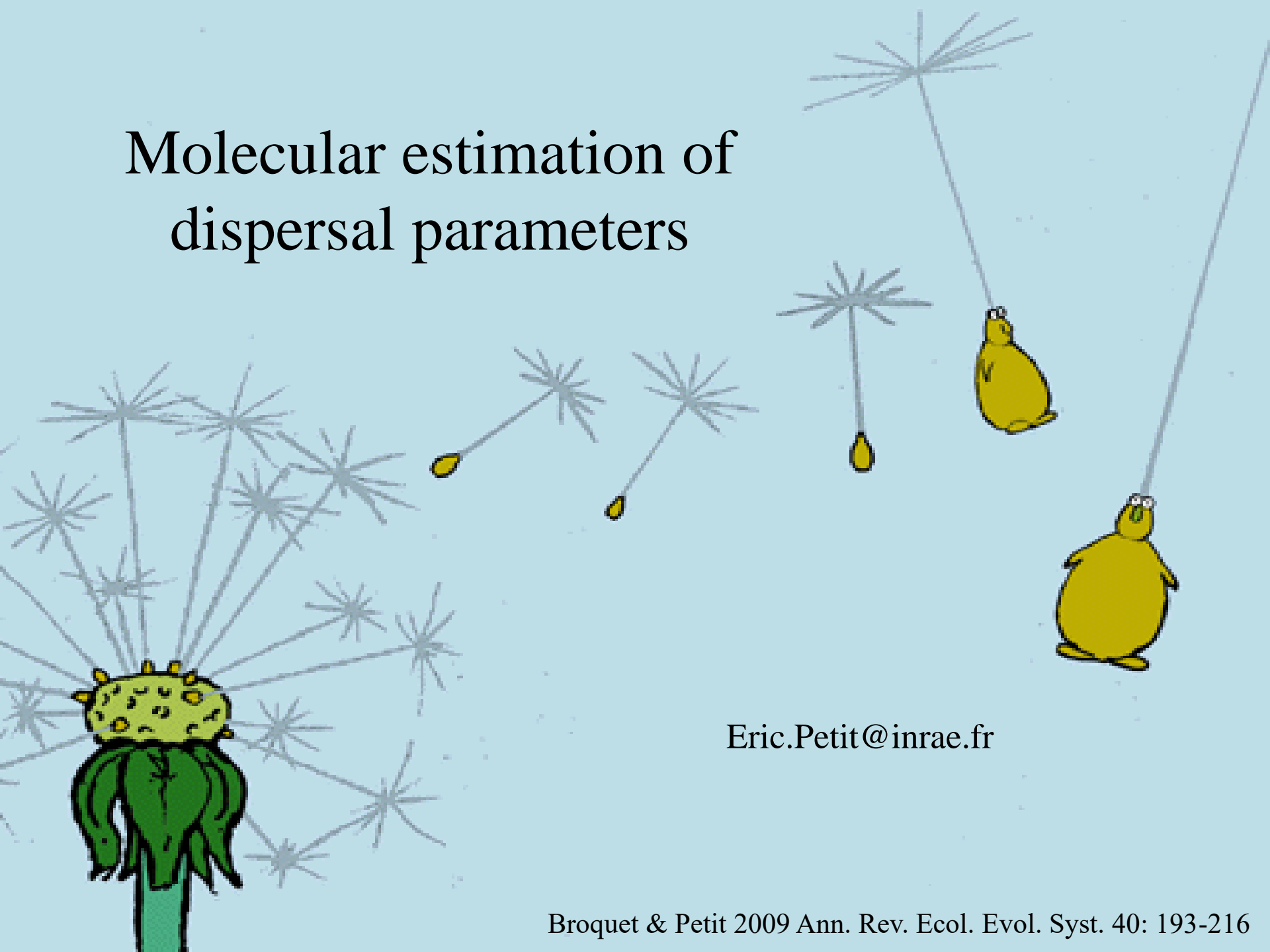


# Molecular estimation of dispersal parameters



Eric.Petit@inrae.fr

# WARNING

Today:

dispersal = migration

$m$  = migration/dispersal rate

$d$  = migration/dispersal distance



# What is dispersal?

Any movement with a  
potential effect on gene flow

Dispersal:  $m, d$

Effective dispersal:  $m_e, d_e$

# What could be estimated?

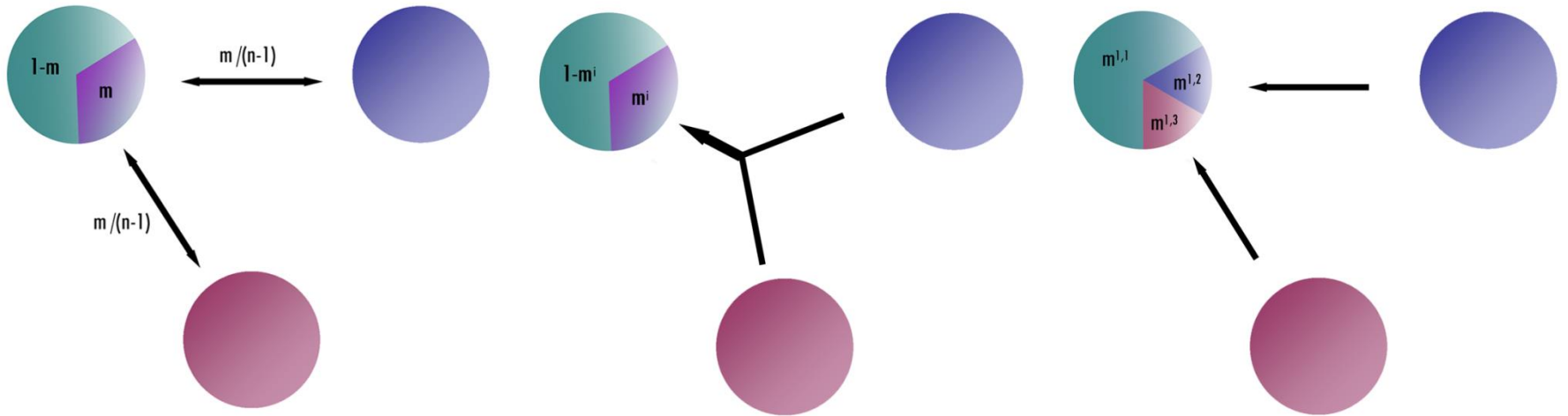


**Greater white-toothed shrew**  
*(Crocidura russula)*

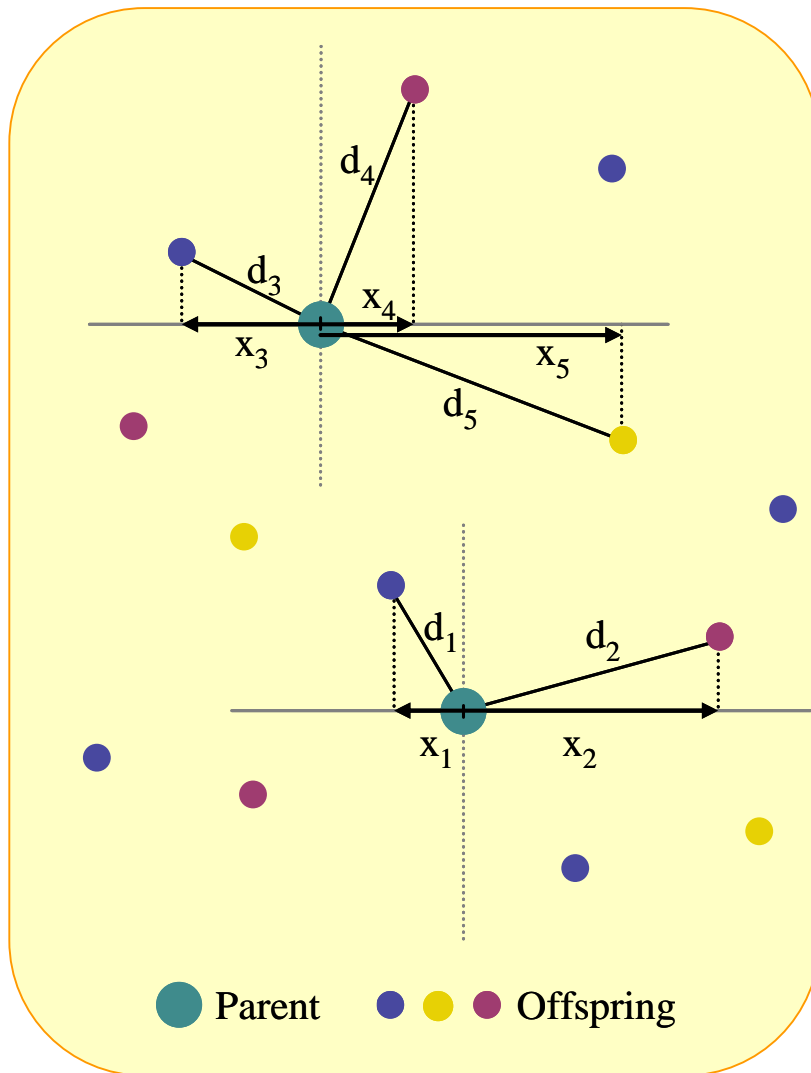


**Roe deer**  
*(Capreolus capreolus)*

# 1. Dispersal rates



## 2. Dispersal distances



Isotropy hypothesis :

$$E(x) = E(y) = 0$$

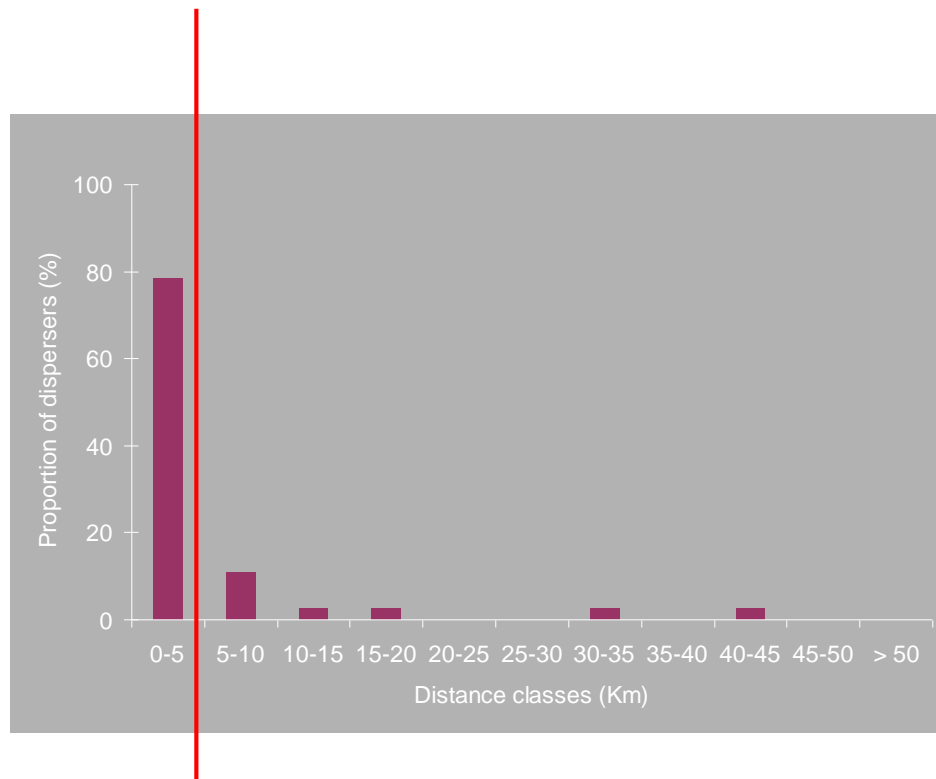
$$E(x^2) = E(y^2)$$

Link between  $x$  and  $d$  :

$$\sigma^2(x) = \text{Var}(x) = E(x^2) - [E(x)]^2 = E(x^2)$$

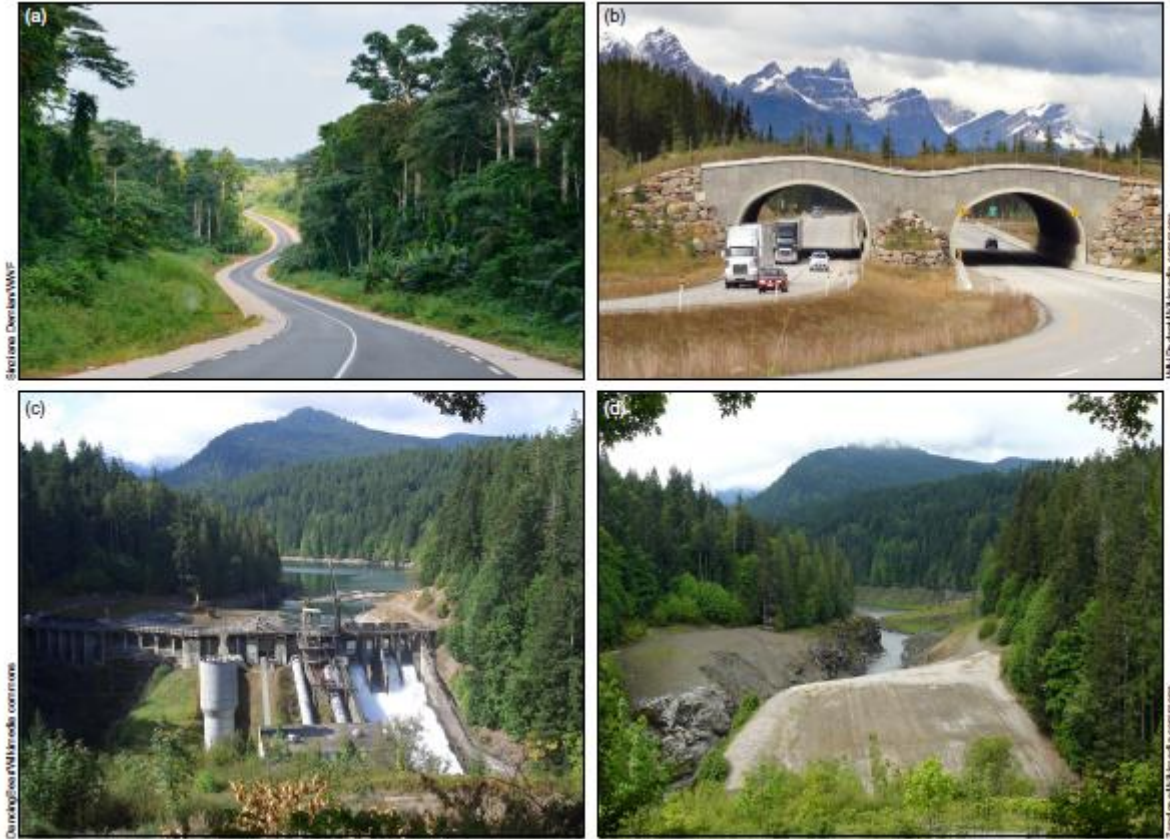
$$E(d^2) = E(x^2) + E(y^2) = 2E(x^2) = 2\sigma^2(x)$$

# Distances and rates



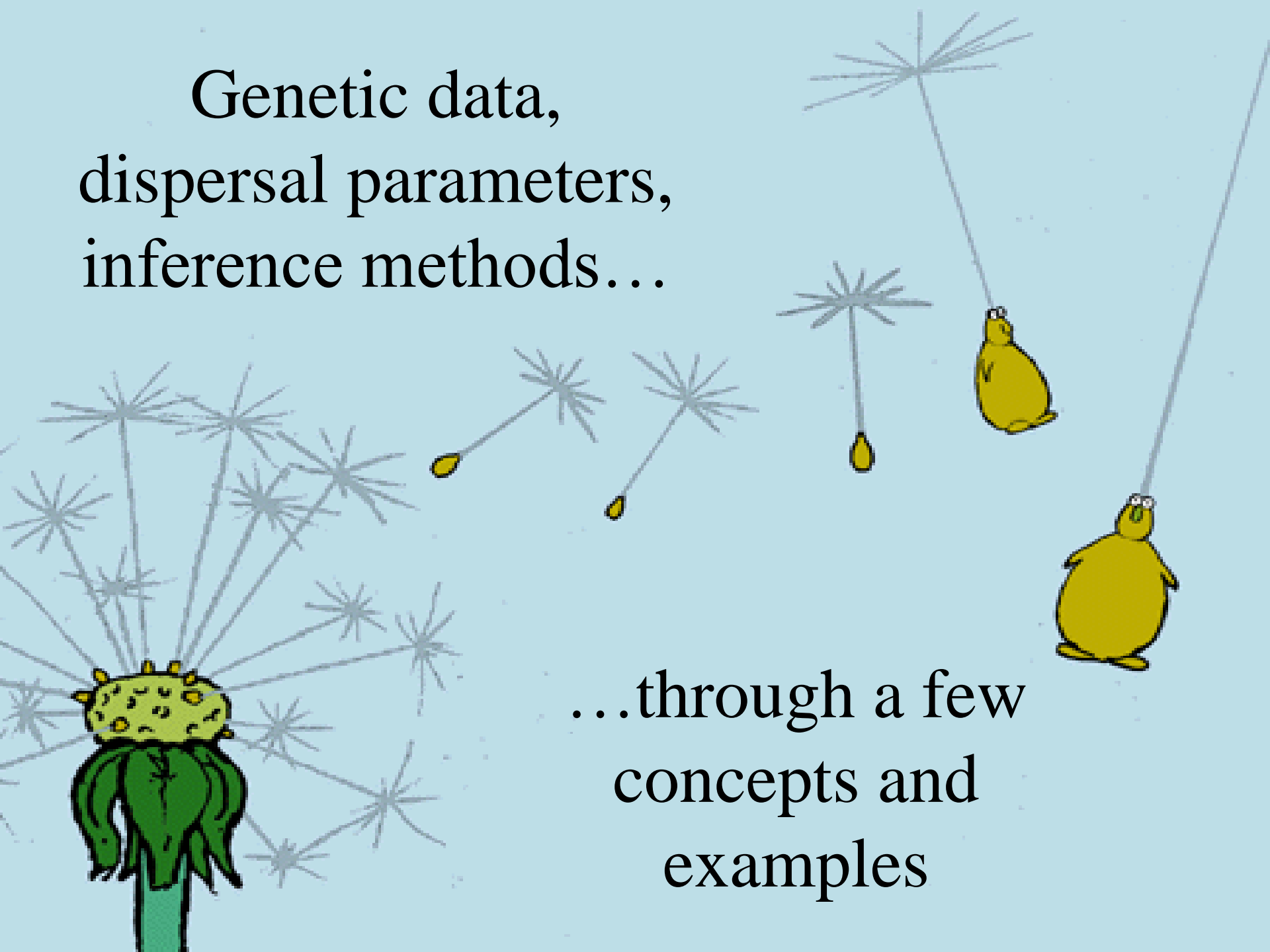
*Martes americana*

# 3. How distances and rates vary with the environment

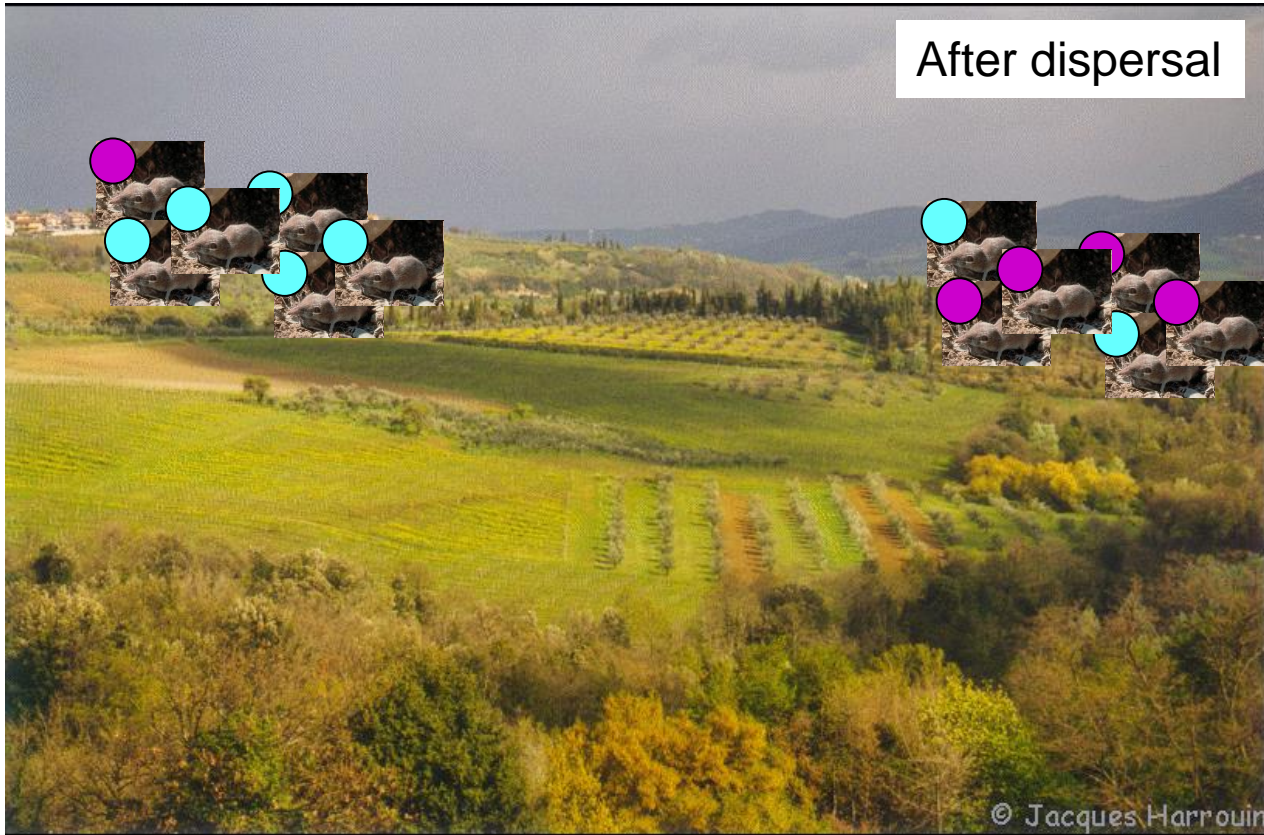




Genetic data,  
dispersal parameters,  
inference methods...

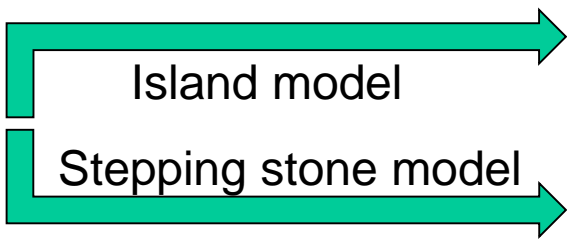


...through a few  
concepts and  
examples



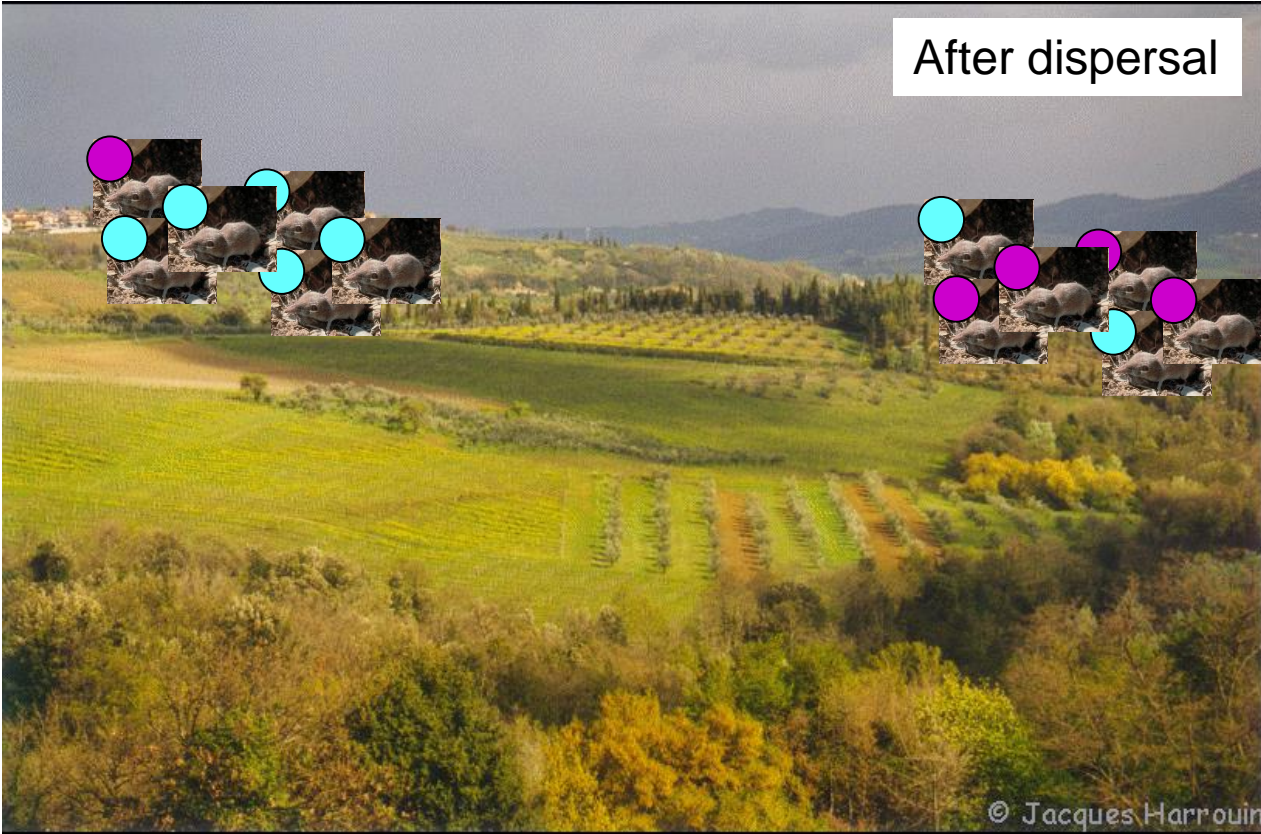
Allele frequencies

$F_{ST}$



$$N_e m_e$$

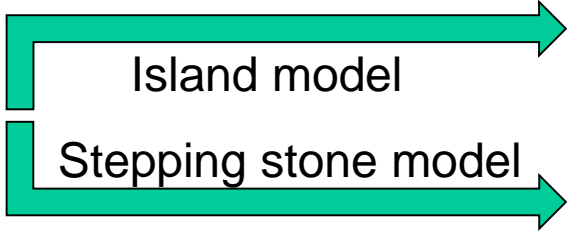
$$N_e d_e^2$$



# At equilibrium !

Allele frequencies

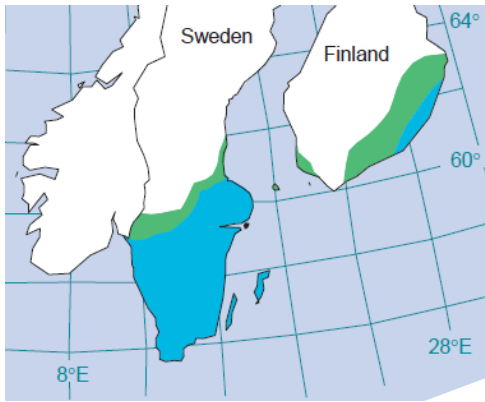
$F_{ST}$



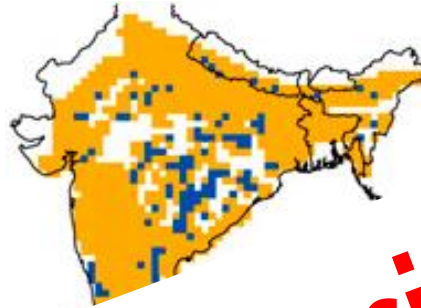
$$N_e m_e$$

$$N_e d_e^2$$

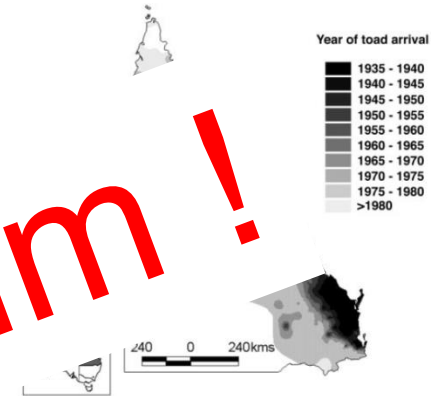
# The current context



*Argynnis*



*Argynnis*



*Bufo marinus*

**No**

**equilibrium!**

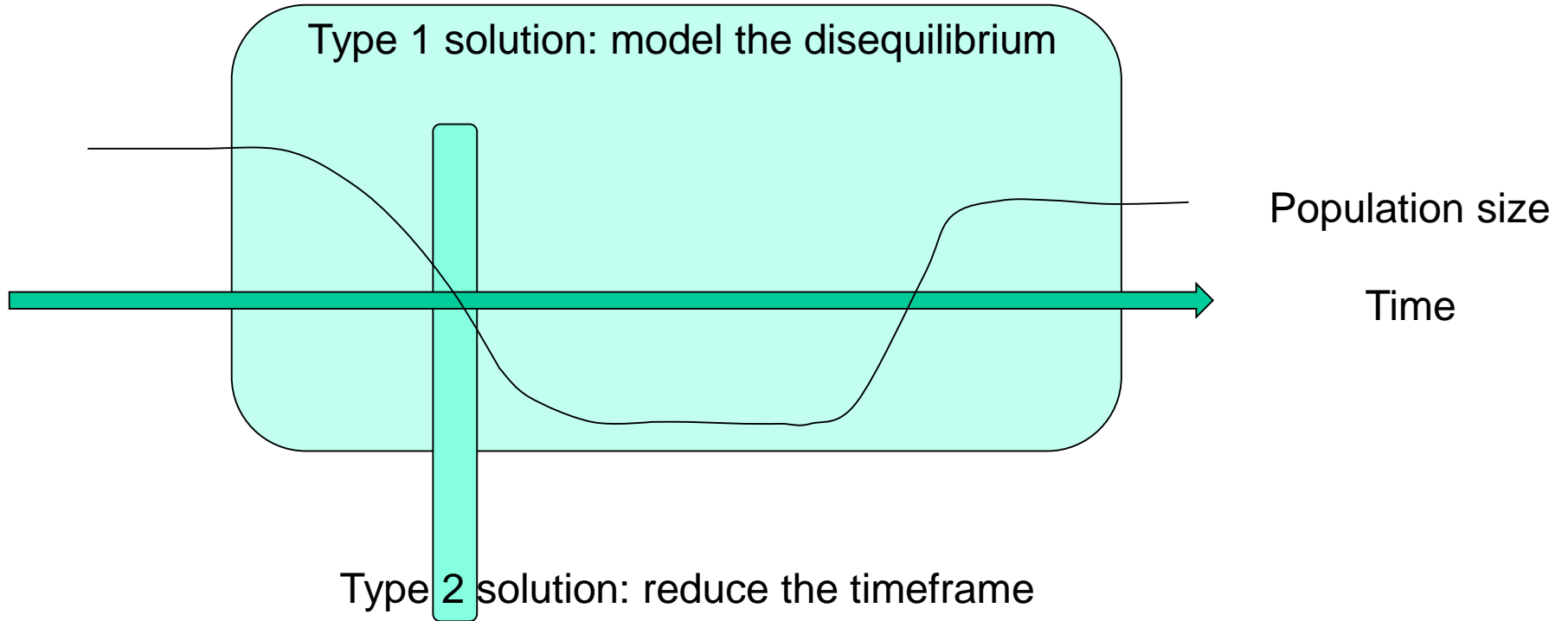


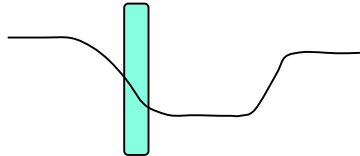
Parmesan et al 1999 Nature 399: 579-583

Phillips & Shine 2004 PNAS 101: 17150-17155

Yackulic et al 2011 PNAS 108: 4024-4029

# Potential solutions: methods not assuming equilibrium





n generations



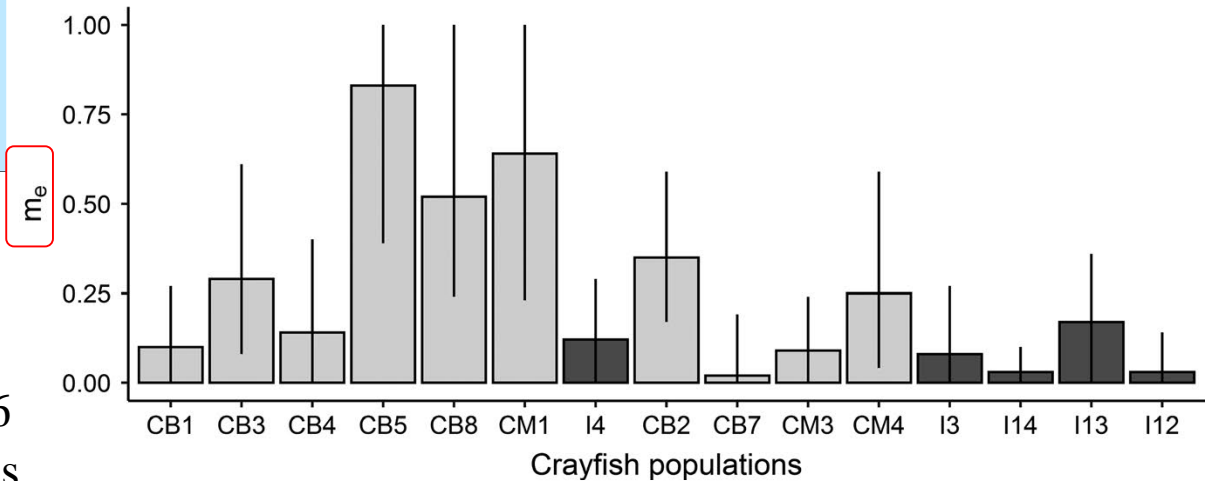
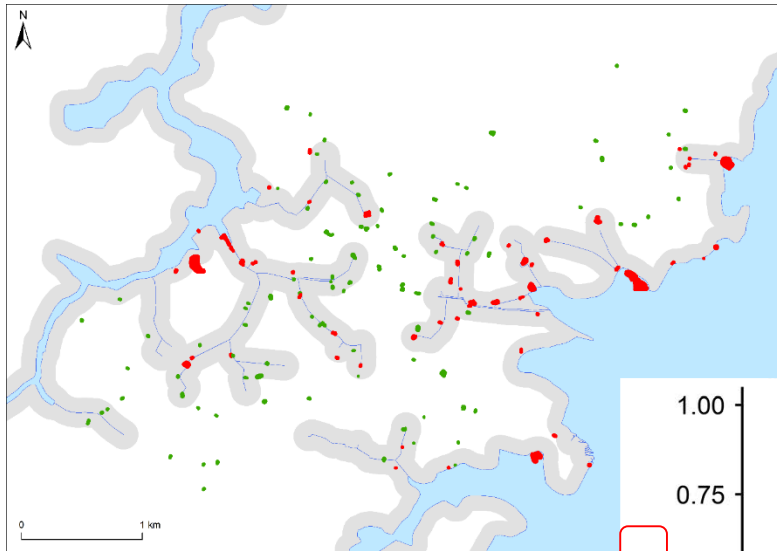
Allele frequencies

$F_{ST}$  like

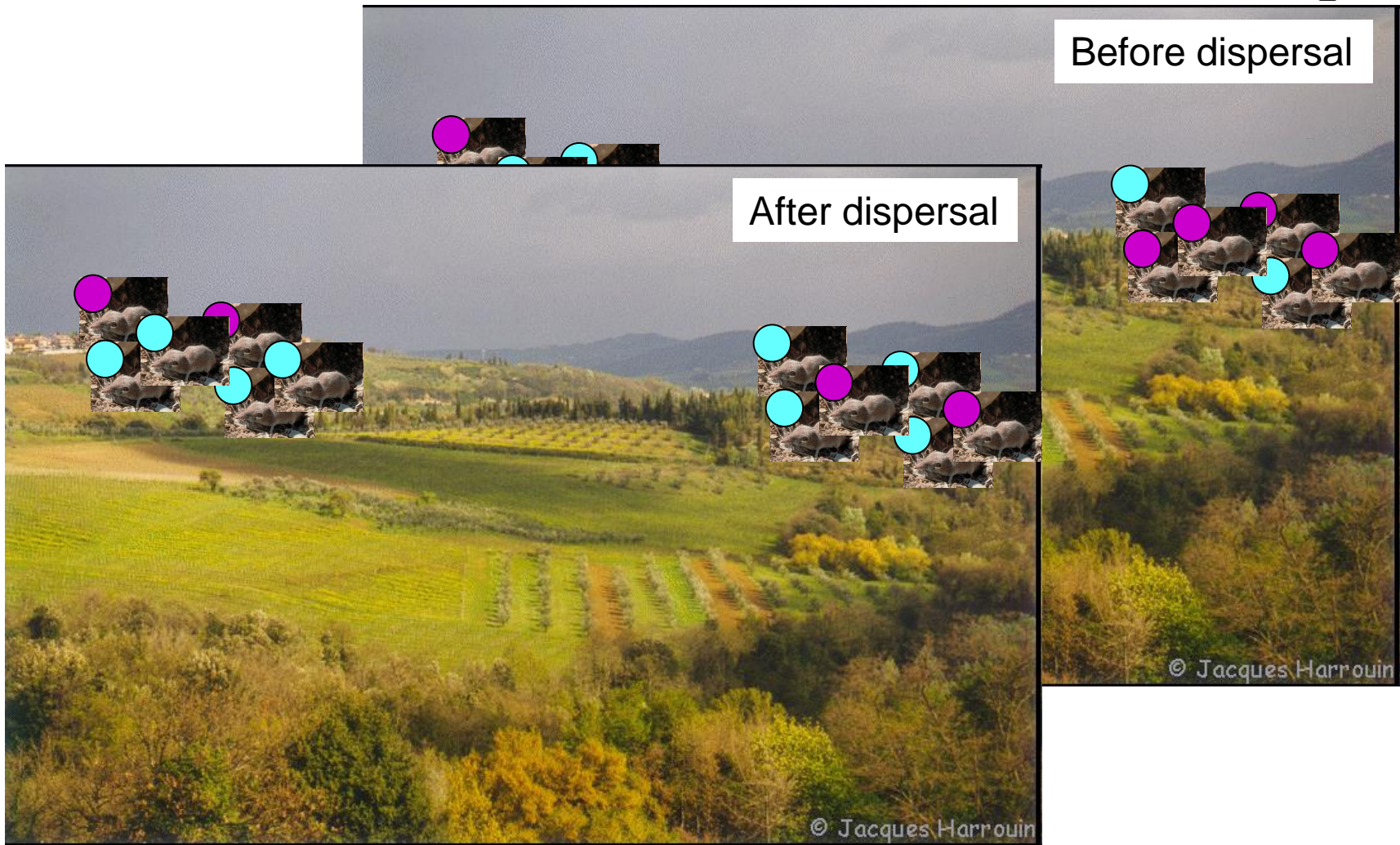
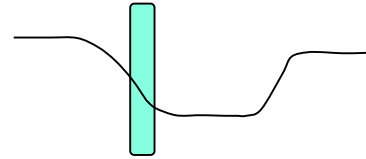


$m_e$

# Dispersal patterns in invasive populations



- 15 ponds
- sampling in 2014 and 2016
- 9 autosomal microsatellites



Allele frequencies

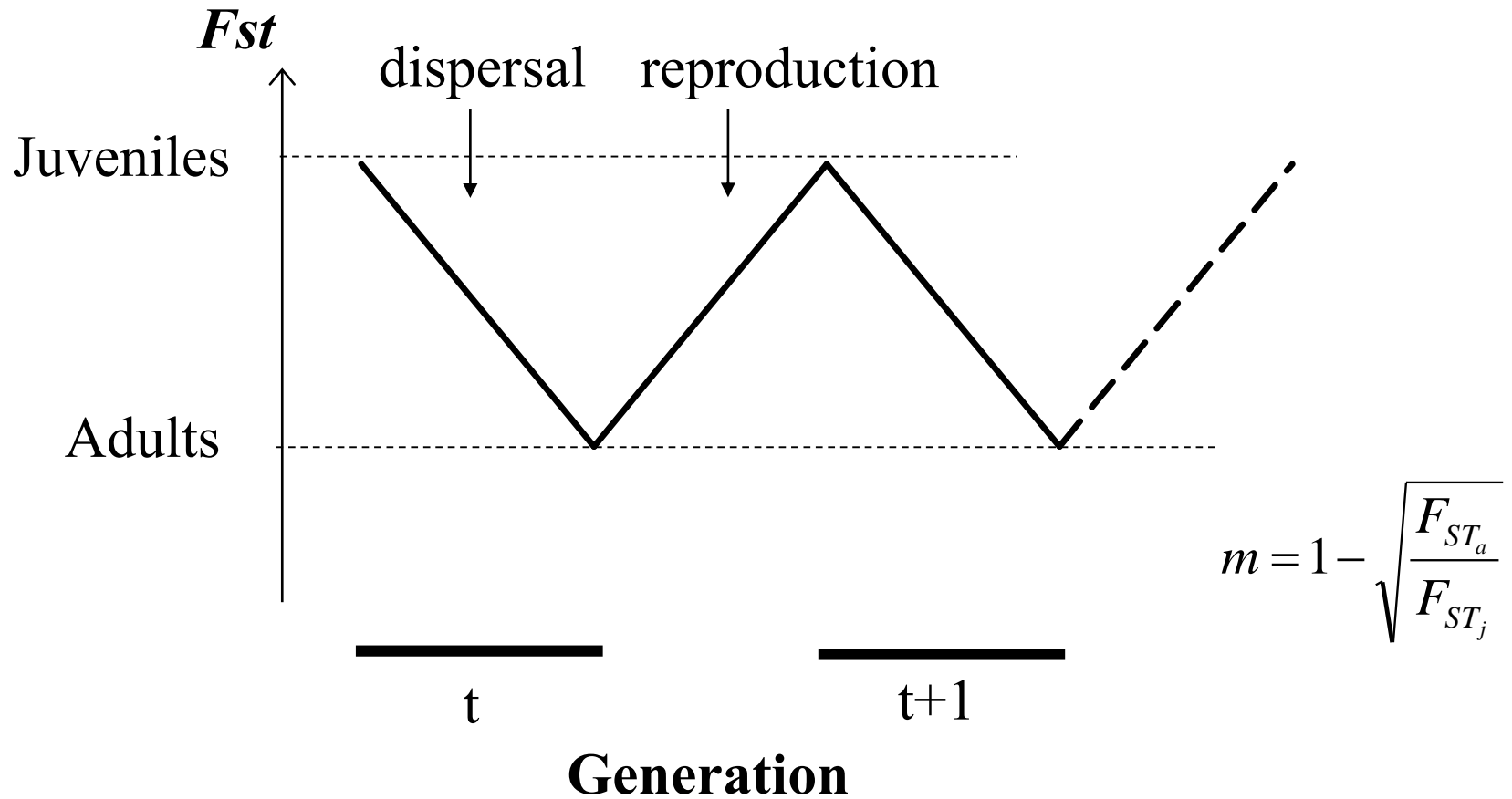
$F_{ST}$  like



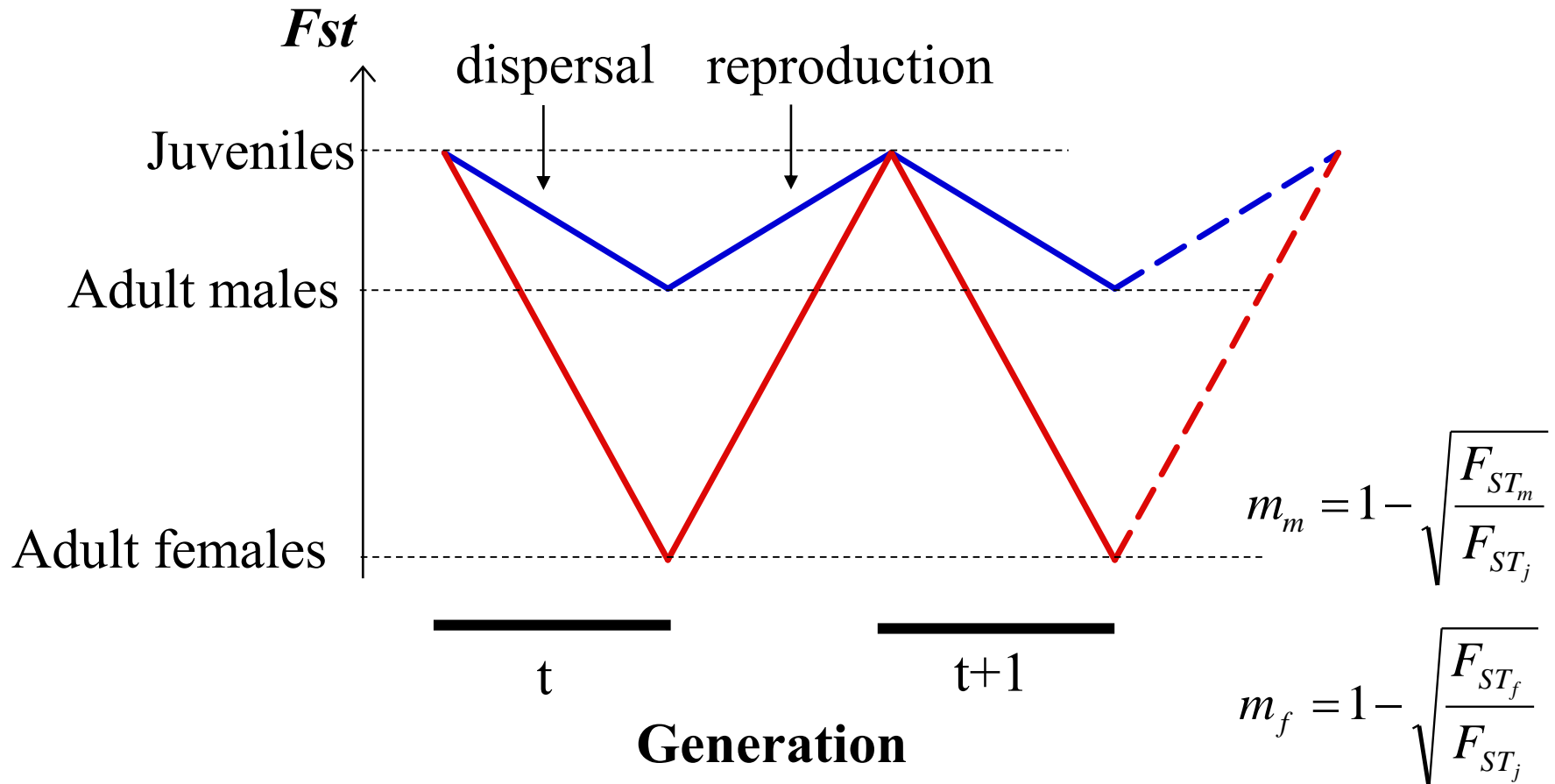
$m$



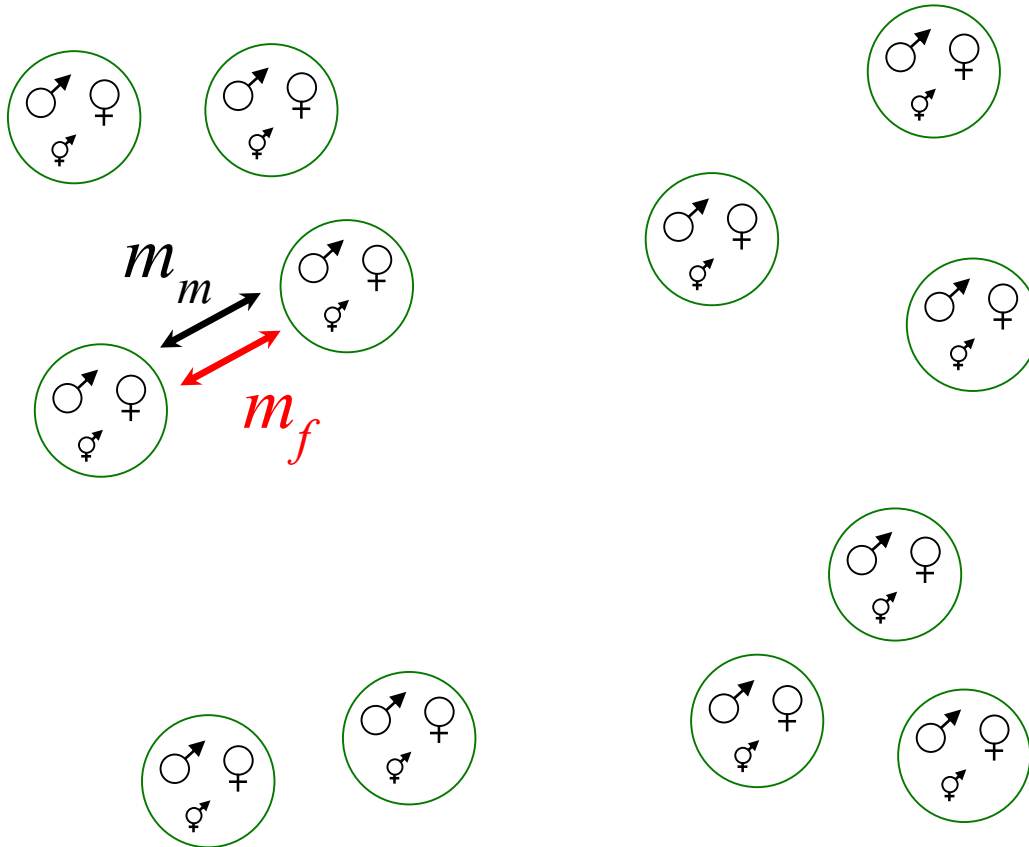
# Vitalis' method



# Vitalis' method



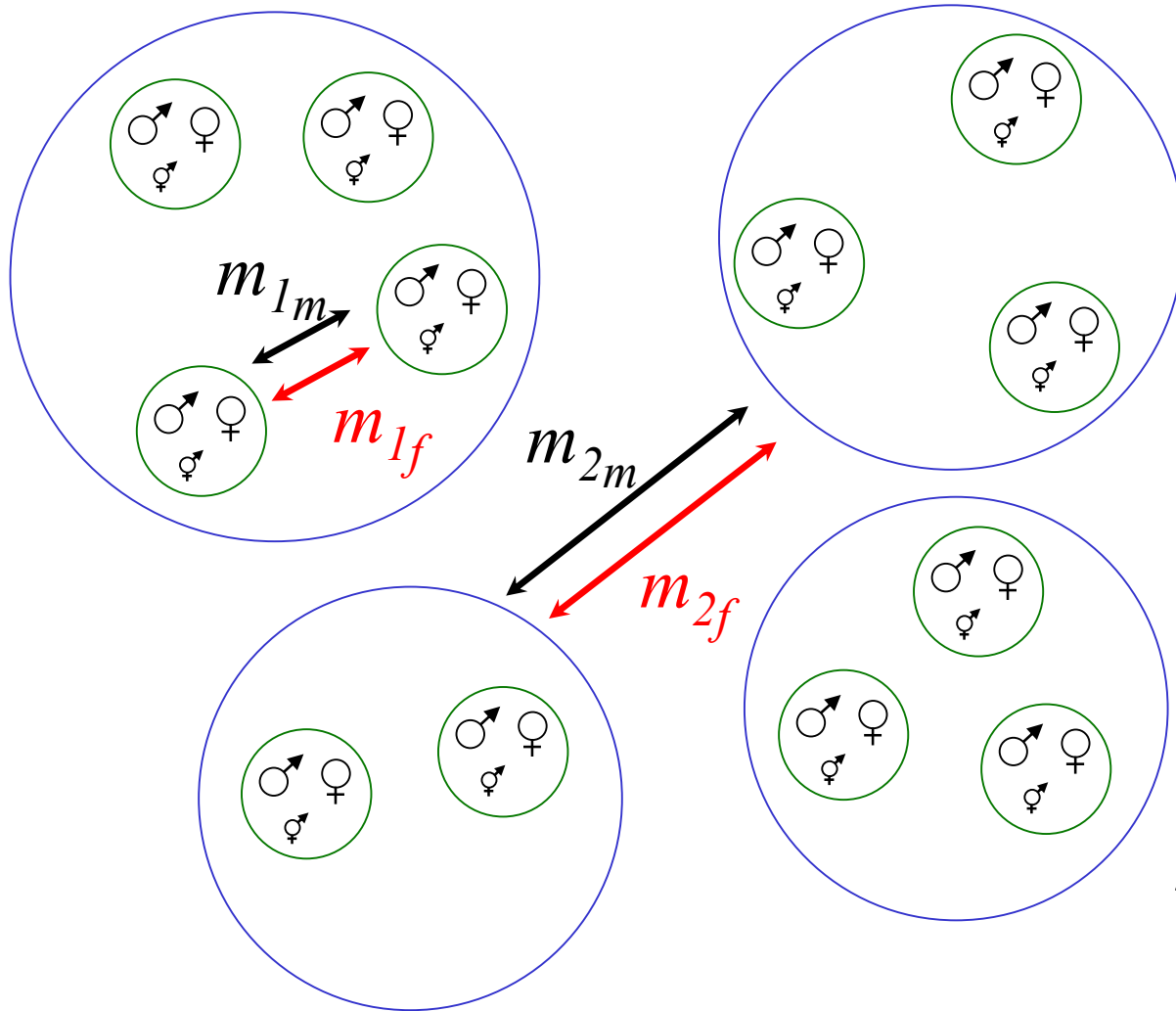
# Vitalis' method



$$m_m = 1 - \sqrt{\frac{F_{ST_m}}{F_{ST_j}}}$$

$$m_f = 1 - \sqrt{\frac{F_{ST_f}}{F_{ST_j}}}$$

# Vitalis' method



$$m_{2_m} = 1 - \sqrt{\frac{F_{ST_m}}{F_{ST_j}}}$$

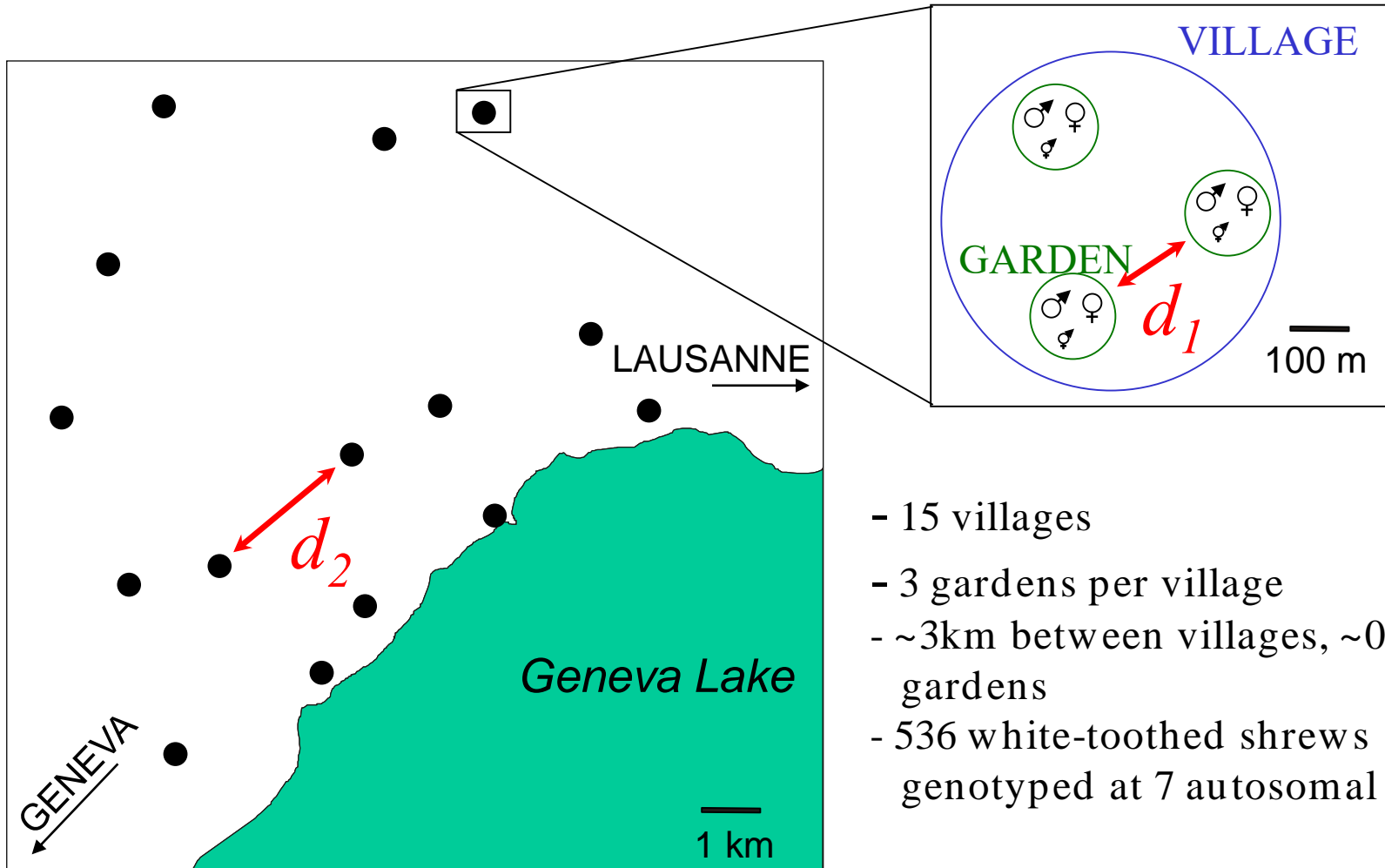
$$m_{2_f} = 1 - \sqrt{\frac{F_{ST_f}}{F_{ST_j}}}$$

$$m_{1_m} + m_{2_m} = 1 - \sqrt{\frac{F_{GT_m} - F_{ST_m}}{F_{GT_j} - F_{ST_j}}}$$

$$m_{1_f} + m_{2_f} = 1 - \sqrt{\frac{F_{GT_f} - F_{ST_f}}{F_{GT_j} - F_{ST_j}}}$$

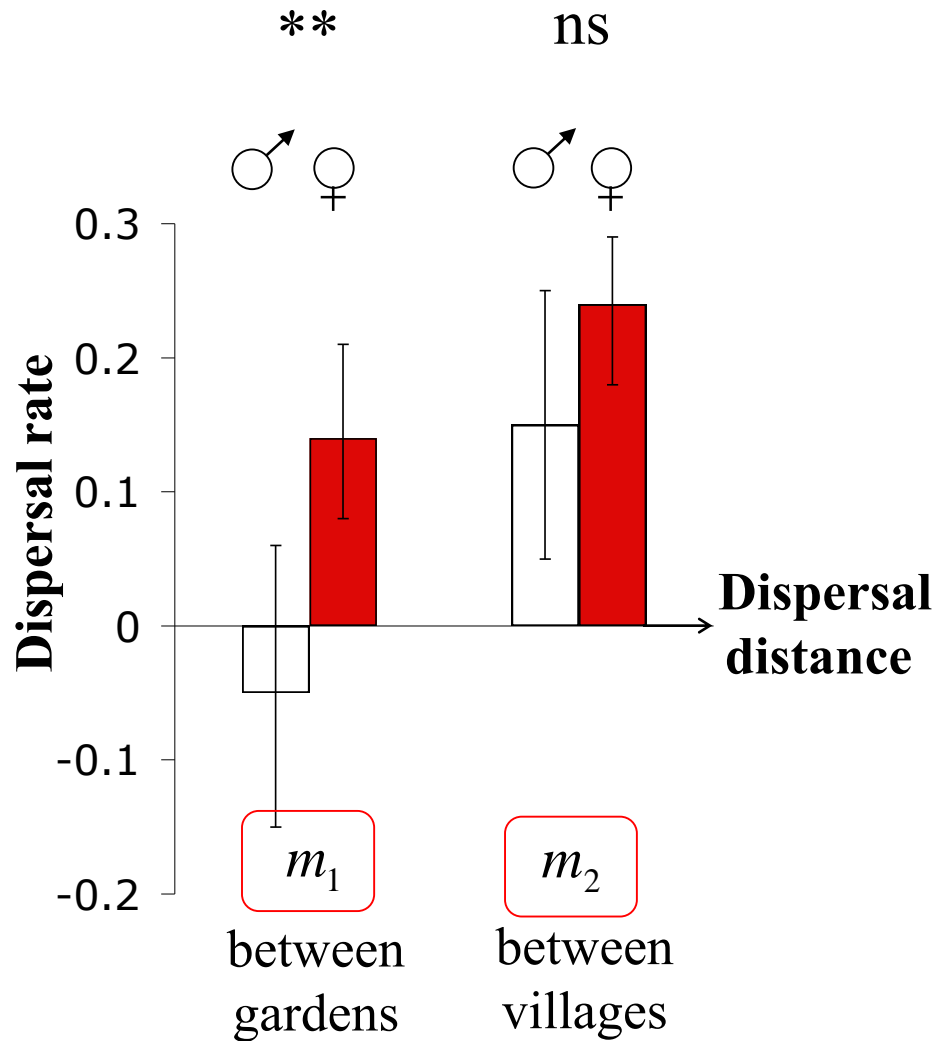


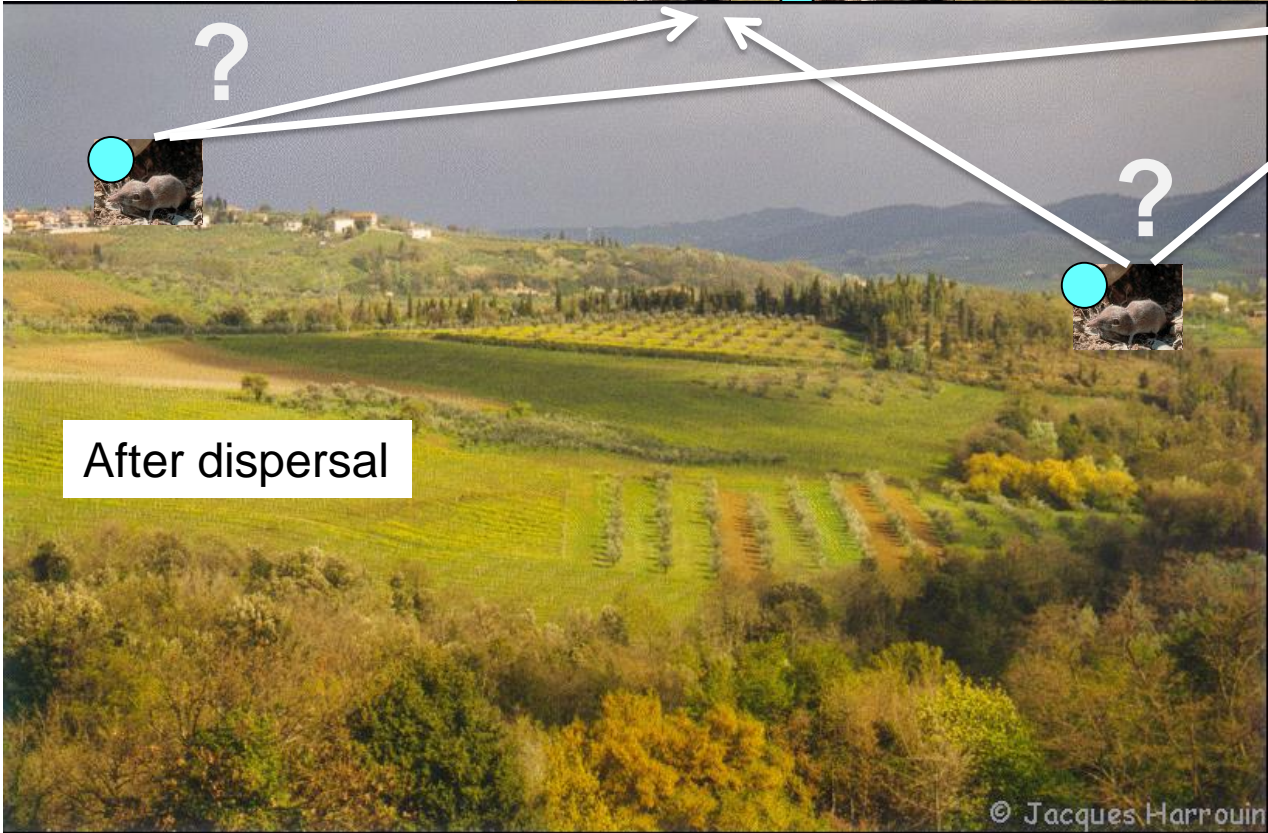
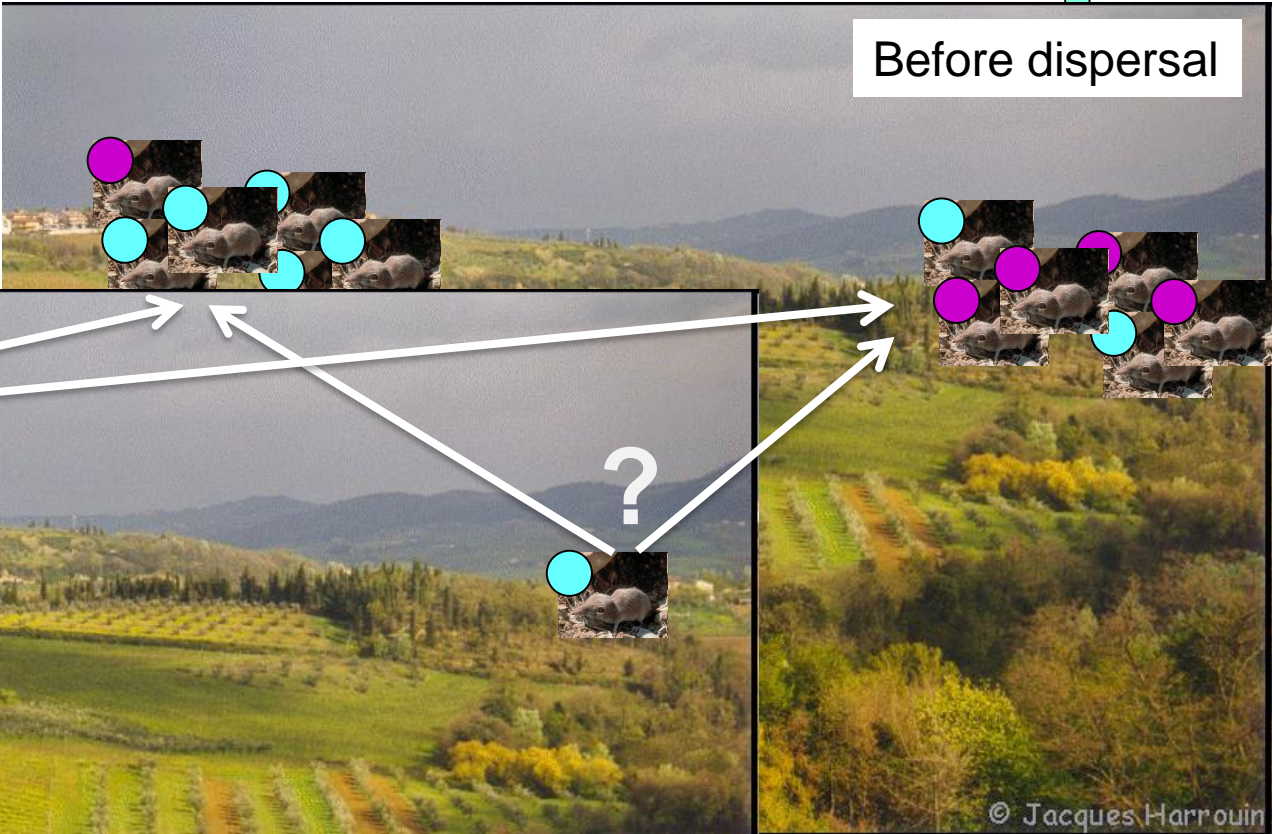
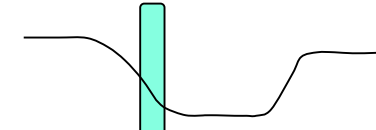
# The sampling scheme



- 15 villages
- 3 gardens per village
- ~3km between villages, ~0.3km between gardens
- 536 white-toothed shrews genotyped at 7 autosomal microsatellites

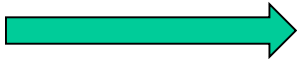
# Dispersal rates and distances in *Crocidura russula*





Multilocus genotypes and allele frequencies

Assignment



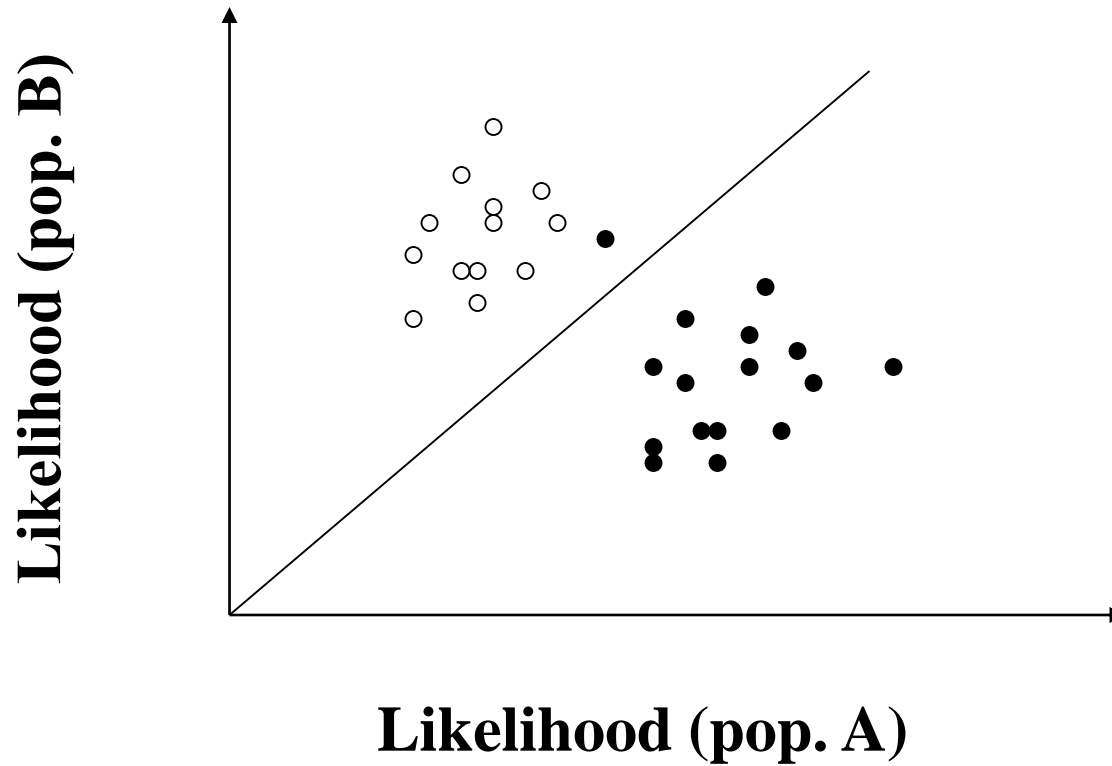
$m, d$

m : dispersal rates in *Oligosoma grande*

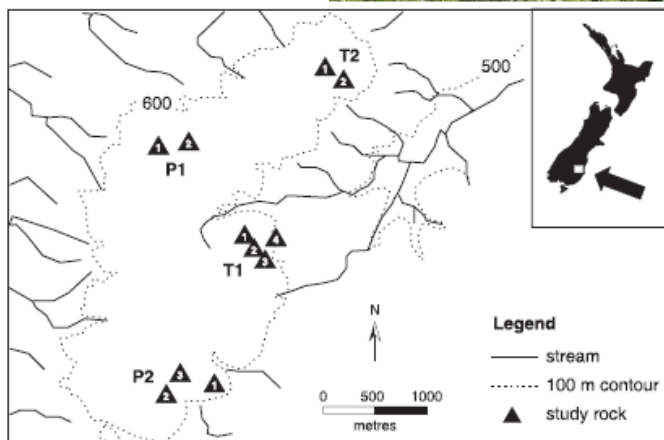




# Estimating the dispersal rate

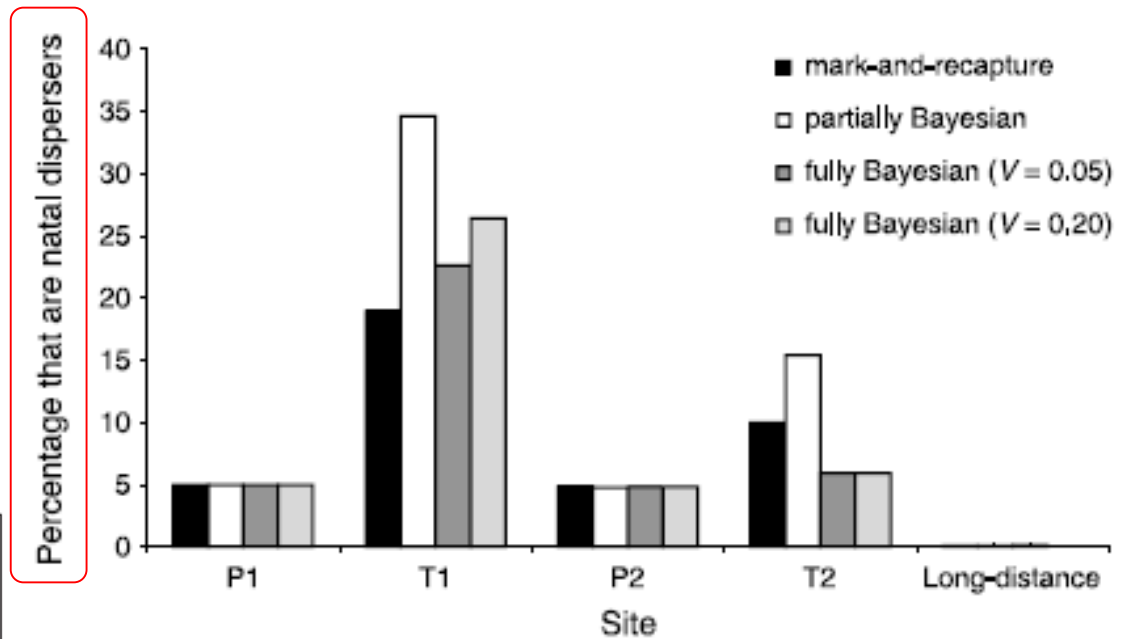
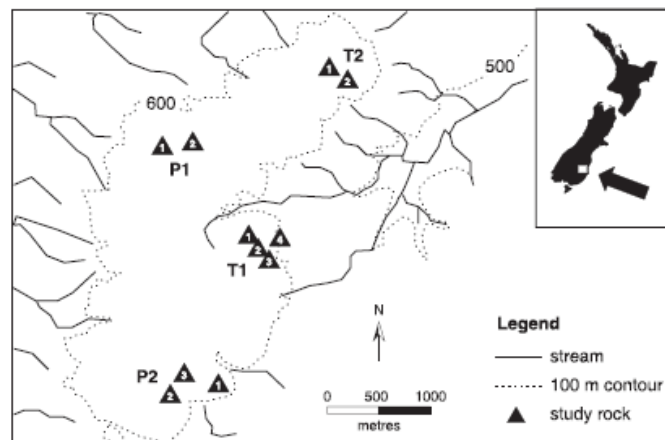


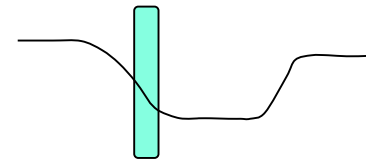
# Dispersal rates in *Oligosoma grande*



250 individuals  
13 microsatellites

# Dispersal rates in *Oligosoma grande*





Multilocus genotypes and  
allele frequencies

Parentage

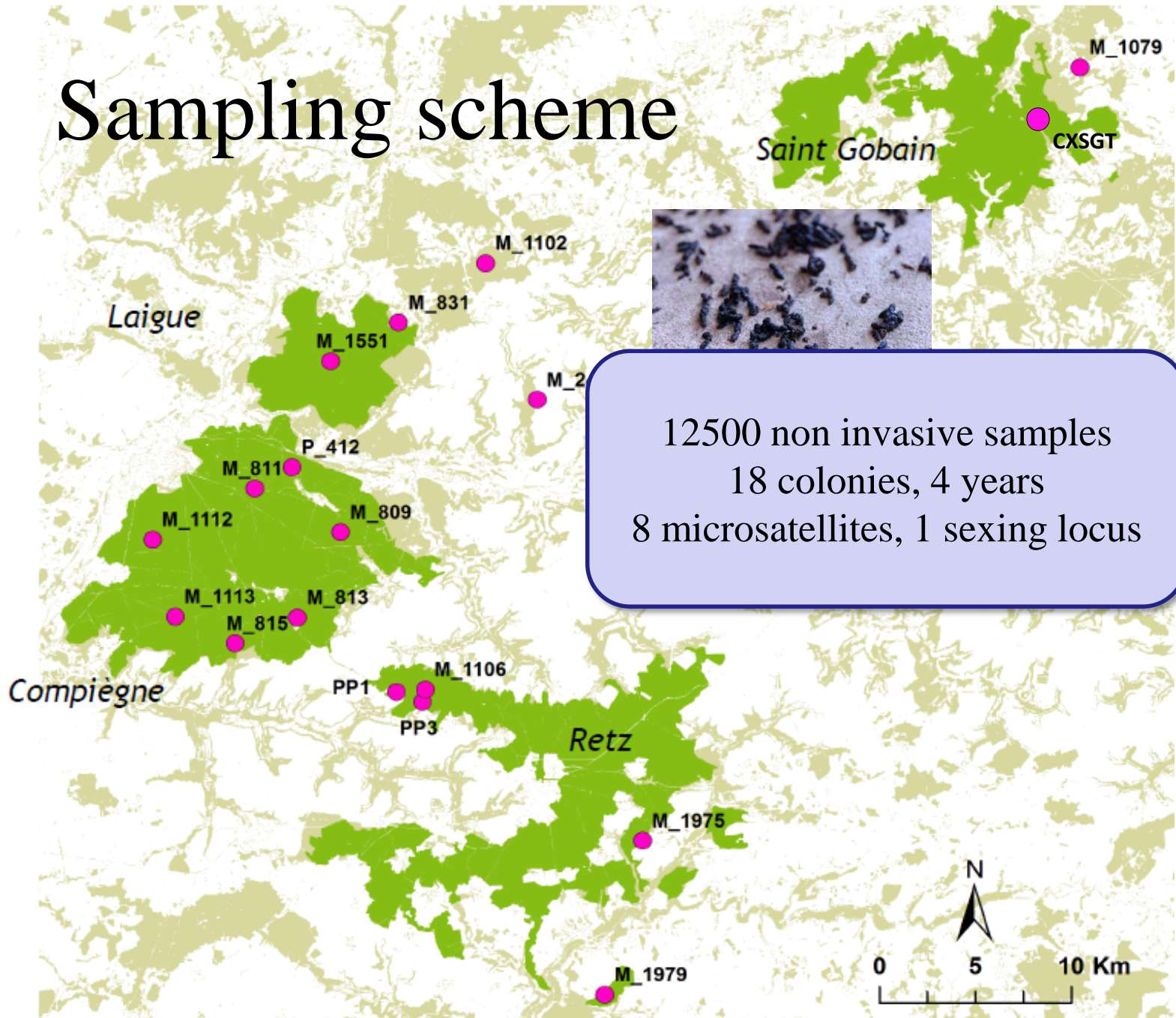


$m, d$

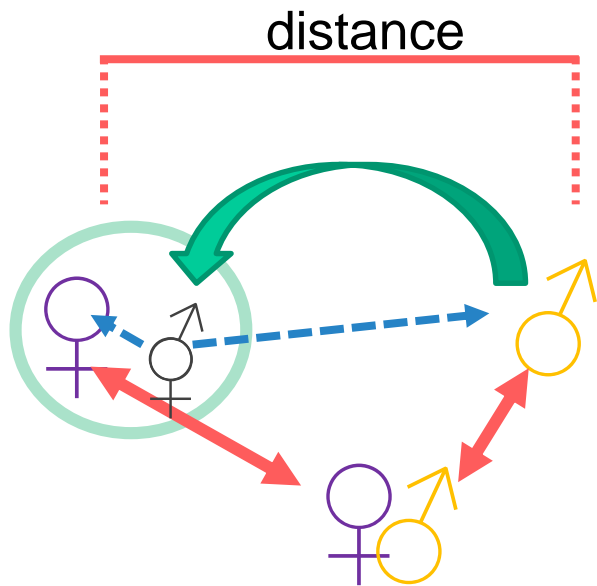
d : dispersal distance  
in the lesser horseshoe bat



# Sampling scheme



# Paternity assignment



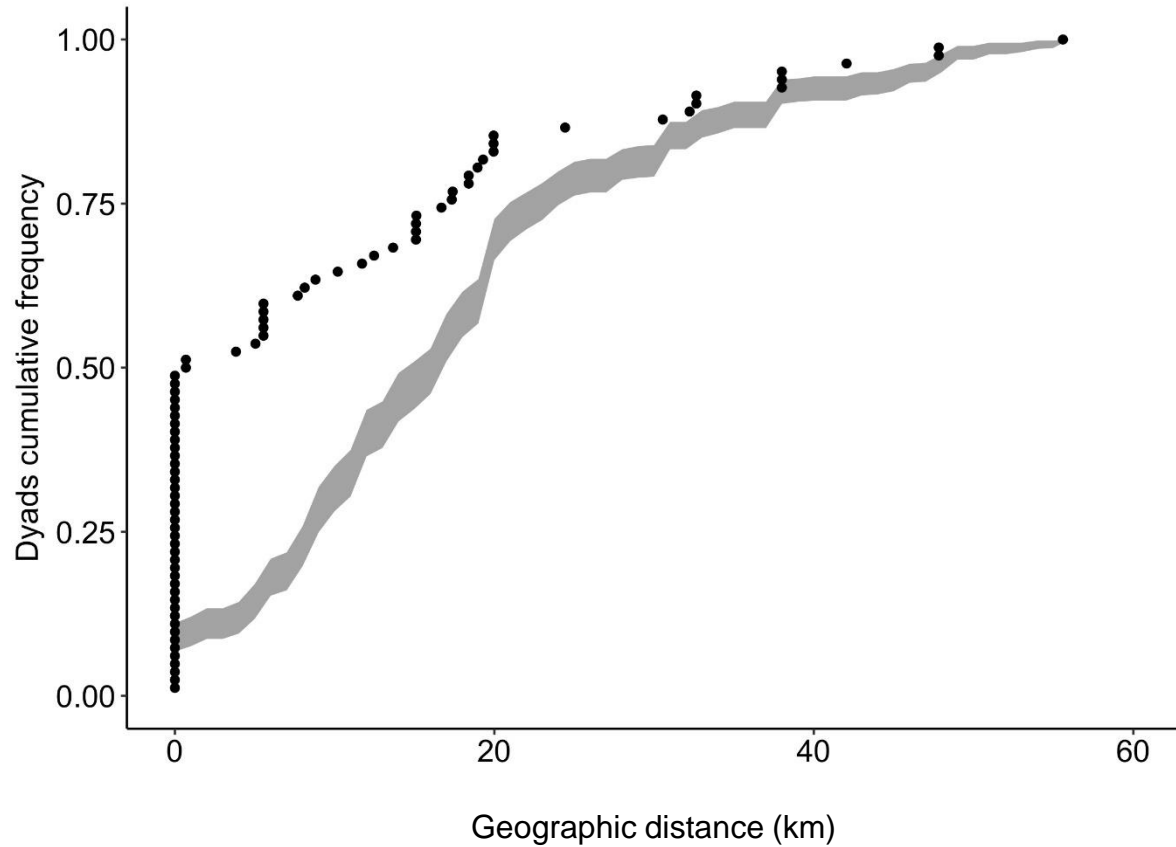
Flight



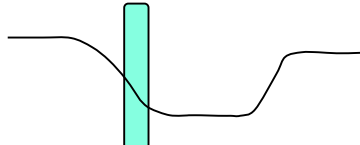
Gene flow



Parental assignment



Mating dispersal distance => **11,3 km**  
(CI<sub>95</sub> = [7,4 ; 15,7], 10 000 bootstraps)



Before dispersal



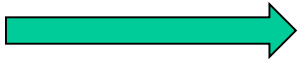
After dispersal



© Jacques Harrouin

Multilocus genotypes

CMR

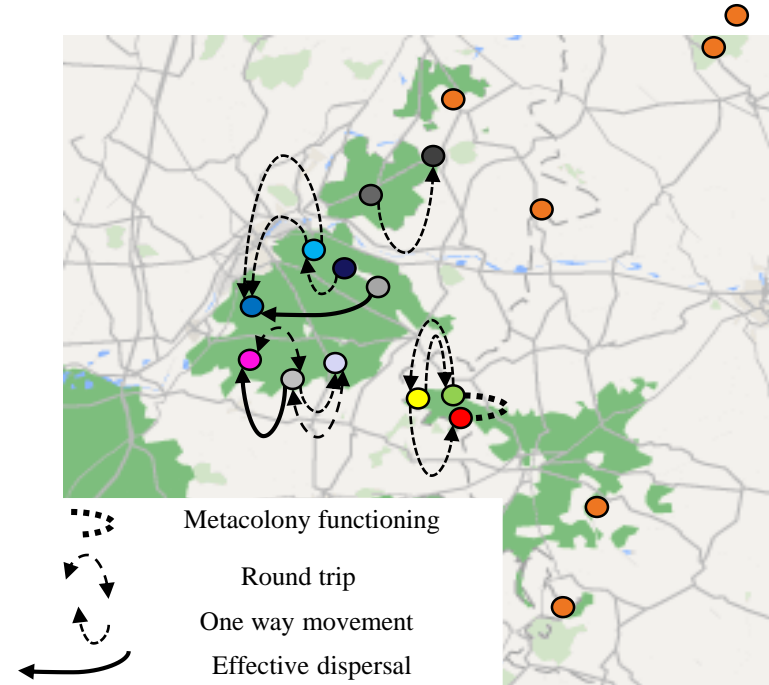


*m, d*

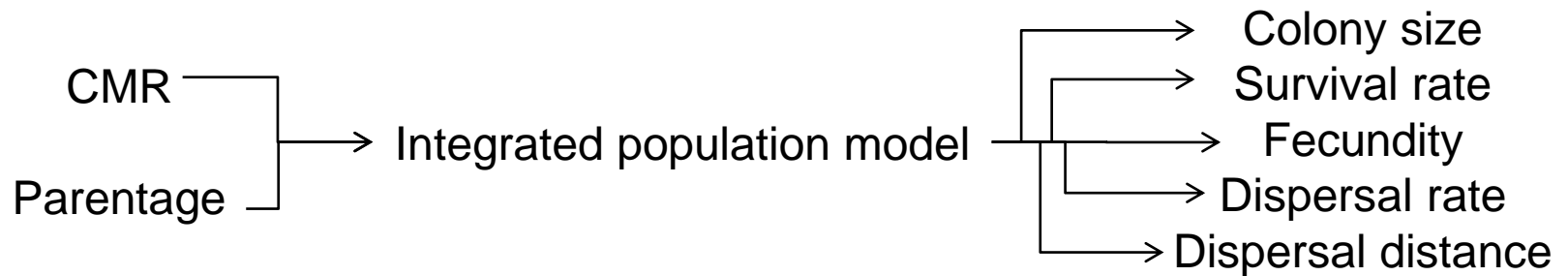


# CMR data

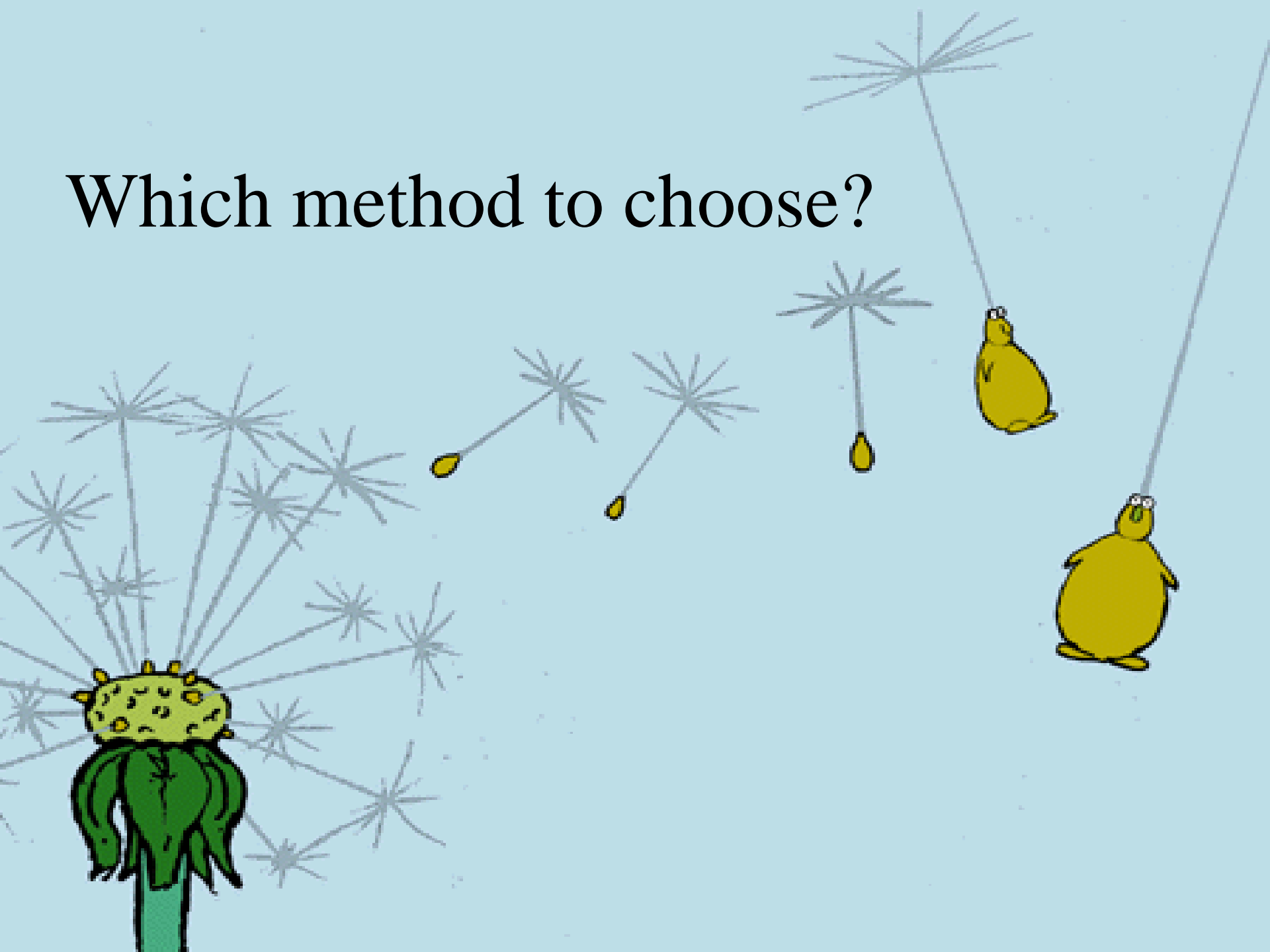
2013_av	2013_ap	2014_av	2014_ap	2015_av	2015_ap	2016_av	2016_ap	sexe	d (km)
PP1	PP1	PP1		PP3				F	1,5
M1106					PP1	PP1		F	2,3
						PP1	M1106	F	2,3
P412				M811				F	2,3
	M815	M815	M815	M1113	M815			F	3,4
				M815		M1113	M1113	F	3,4
M815			M813					M	3,5
M813		M815	M815	M813				F	3,5
M1551			M831					F	5,8
	M811	M1112						F	6
		M811		M811	M811		M1112	F	6
		M809		M1112				F	15



Effective female dispersal:  $2/2883 = 0.00069$



Which method to choose?



Island/isolation  
by distance  
model

Coalescent-  
based ABC

Wang temporal  
model

Pre/post  
dispersal model

Population  
assignment

Parentage  
assignment

CMR

Effective dispersal

Dispersal

Equilibrium

Non equilibrium

Long time

Short time

Island/isolation  
by distance  
model

Coalescent-  
based ABC

Wang temporal  
model

Pre/post  
dispersal model

Population  
assignment

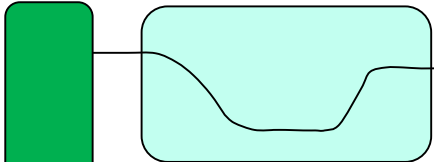
Parentage  
assignment

CMR

Effective dispersal

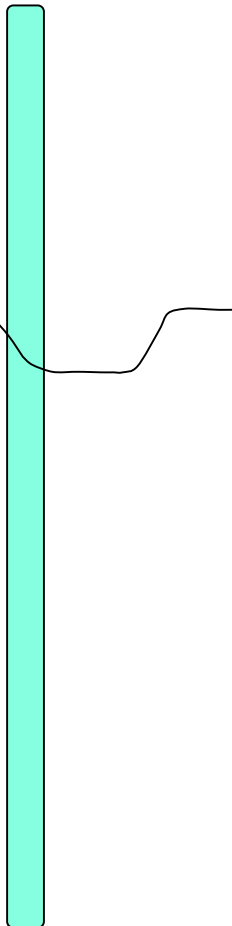
Dispersal

Equilibrium



Long time

Non equilibrium



Short time

Inter-  
generational

Intra-generational

# Sample size and life-cycle

Parentage  
assignment

CMR

Population  
assignment

Pre/post  
dispersal  
model

