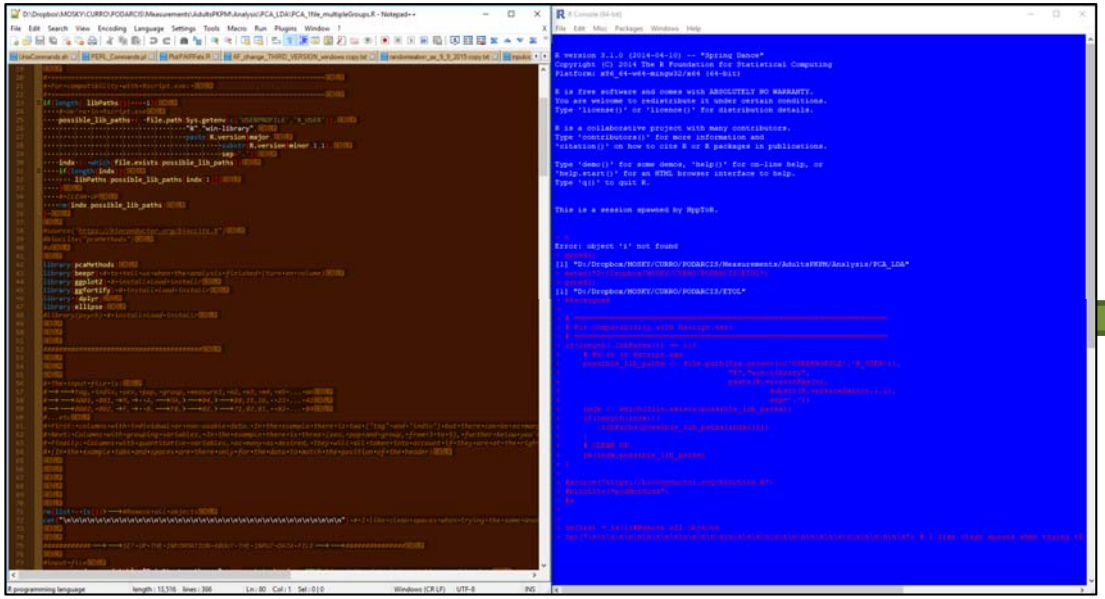
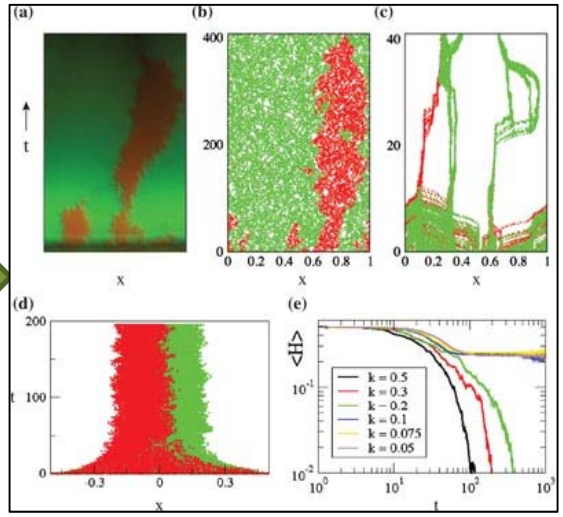
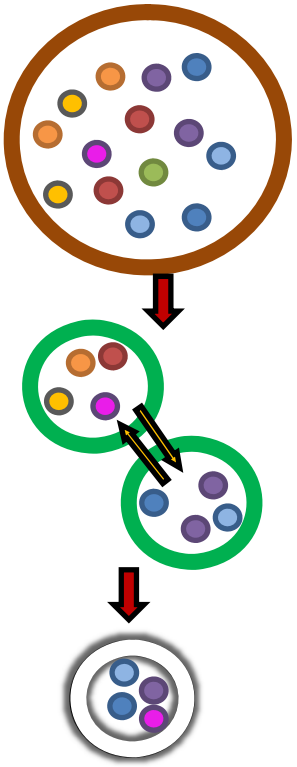
Use of R environment in **Evolutionary Ecology**





DIVERSITY

Evolutionary and adaptative potential



Population Size (N)
Isolation

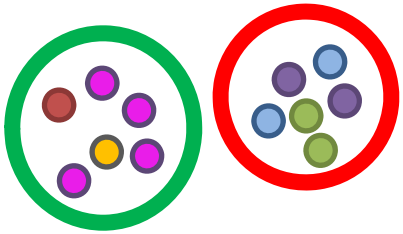
Gene flow
Inbreeding
Mutation
Drift

Fitness: Fertility & Survival

DIVERSITY INDEXES

Richness: Number of species

number of pink



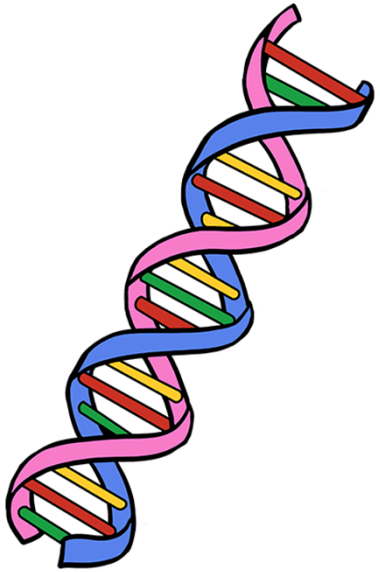
Evenness: Relative abundance of species

number of pink vs number of yellow

Variance:

Probability that two samples are the same species

GENETIC DIVERSITY

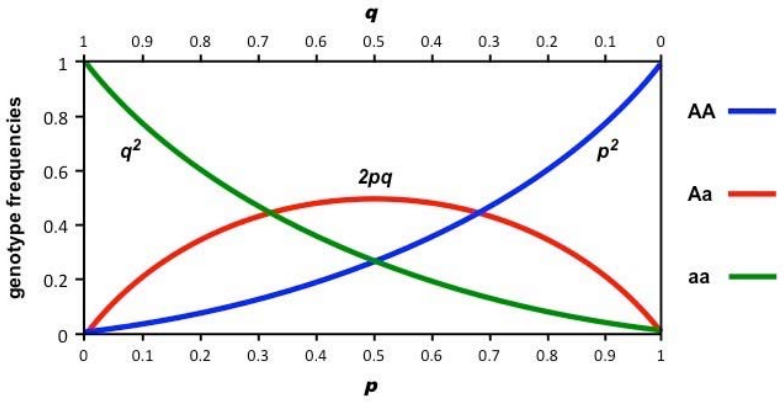


HARDY-WEINBERG EQUILIBRIUM

1. No mutation
2. Random mating
3. No gene flow
4. Infinite population size
5. No selection

* Random segregation (LD)!!

$$p^2 + 2pq + q^2 = 1$$



GENETIC DIVERSITY

Indexes we will calculate

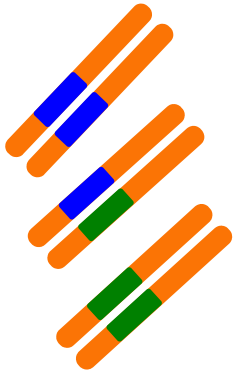
Allelic Richness: A_R

Private Allelic Richness: P_A

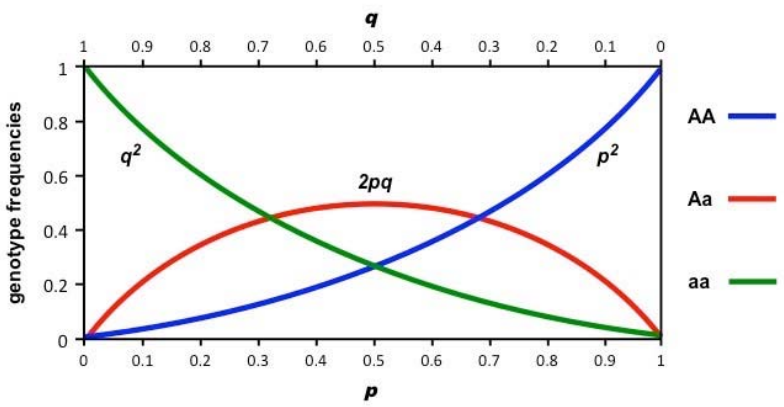
Heterozygosity

Observed:

Expected:



$p^2 + 2pq + q^2 = 1$



POPULATION STRUCTURE

F - STATISTICS (Wright 1969)

F_{ST} = Wright's Genetic Distance (biallelic)

F_{IS} = Inbreeding coefficient

ANALYSIS

- Differences between populations
- AMOVA (% of variance)
- Relationship with geography*
  - Isolation by Distance (Regression + Mantel test)
- Multivariant (Allelic Freq, allele)
  - DACP, PCA, PCoA
- Clustering software (min HWd and LD) *
  - Structure, Geneland

R dataset

Podarcis siculus (Rafinesque-schmaltz, 1810)

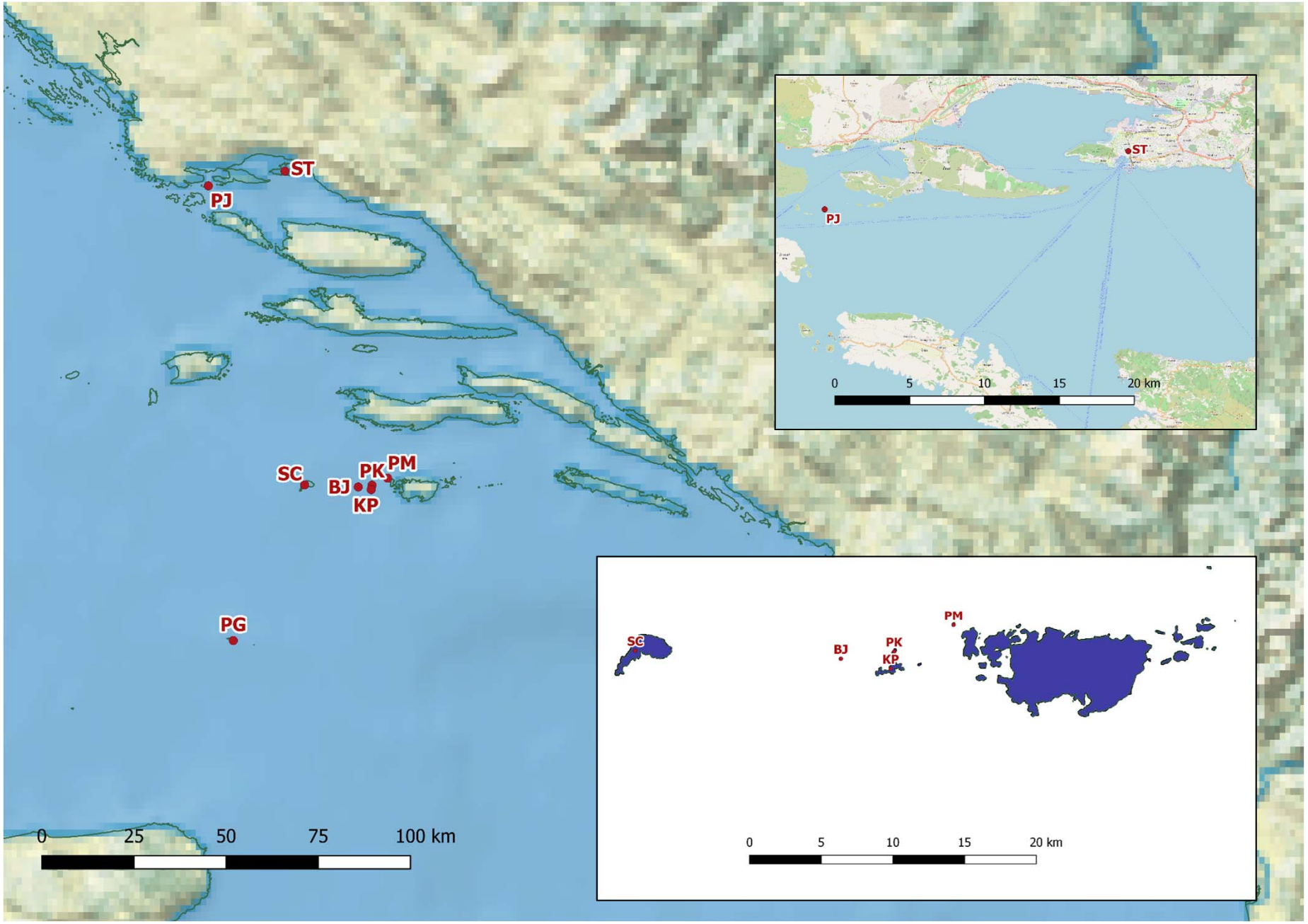
Dataset

Single Nucleotide Polymorphism data (SNP)

Structure format (clustering)

Eight Adriatic populations

Split	ST
Pijavica	PJ
Sušac	SC
Bijelac	BJ
Otok Kopište	KP
Pod Kopište	PK
Pod Mrčaru	PM
Mala Palagruža	PG


ST
PJ
SC
BJ
PK
PM
KP
PG
0 25 50 75 100 km
ST
PJ
0 5 10 15 20 km
PM
SC
BJ
PK
KP
0 5 10 15 20 km