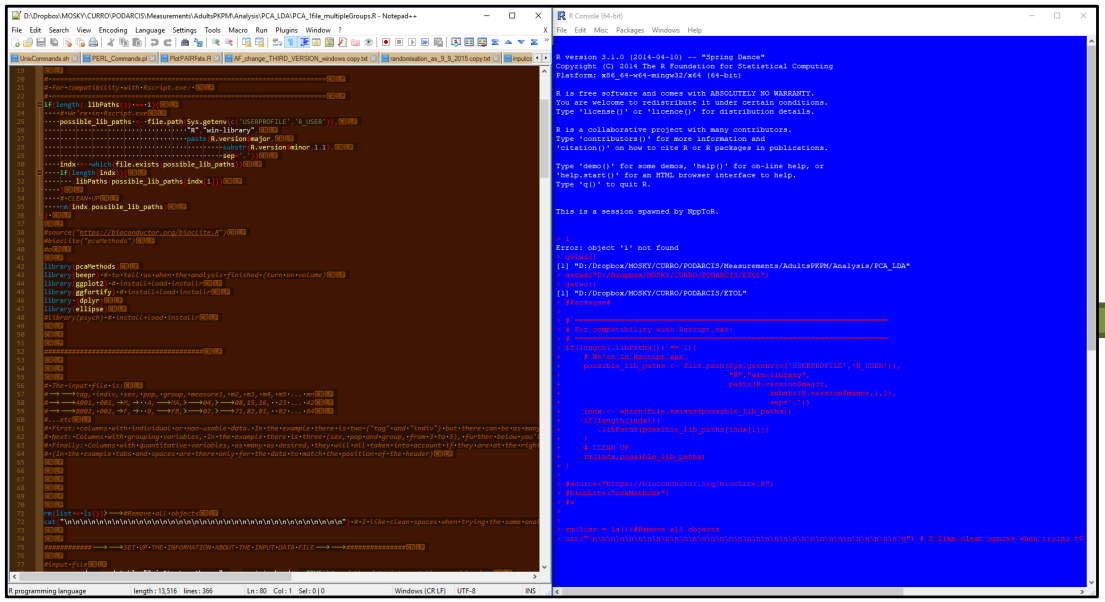
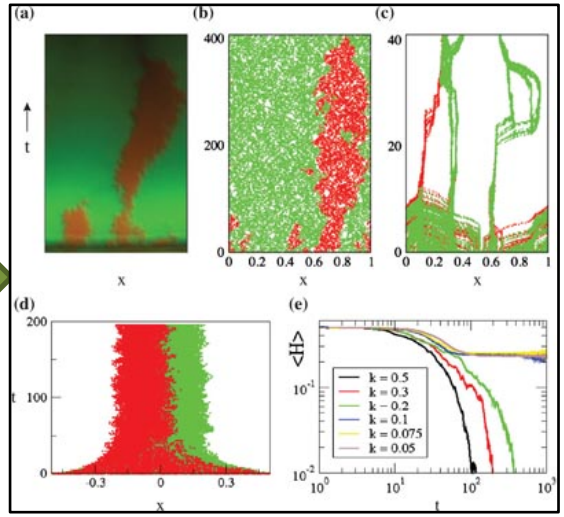
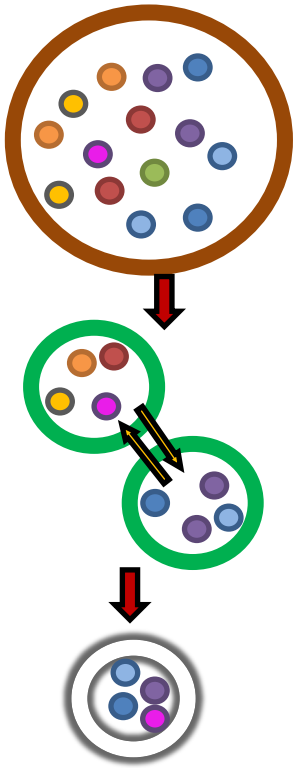
Use of R environment in **Evolutionary Ecology**





DIVERSITY

Evolutionary and adaptive potential



Population Size (N)
Isolation

Gene flow
Inbreeding
Mutation
Drift
Selection

Fitness: Fertility & Survival

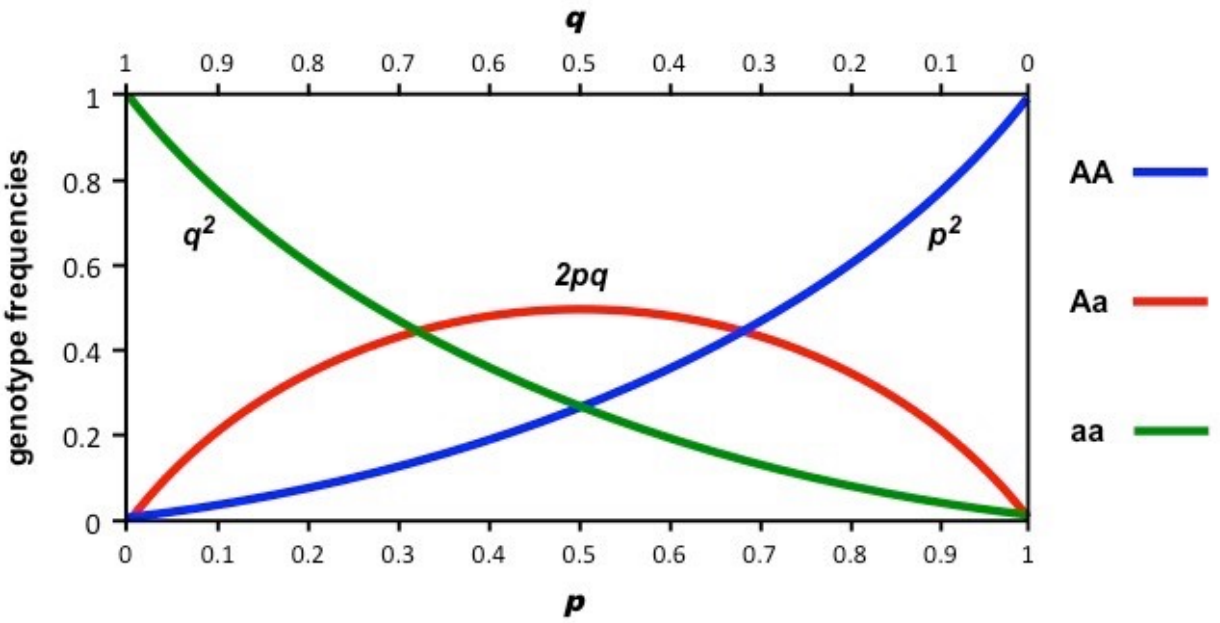
GENETIC DIVERSITY

HARDY-WEINBERG EQUILIBRIUM

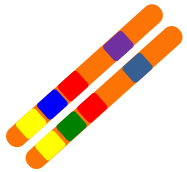
1. No mutation
2. Random mating
3. No gene flow
4. Infinite population size
5. No selection

* Random segregation (LD)!!

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



GENETIC DIVERSITY



Indexes we will calculate

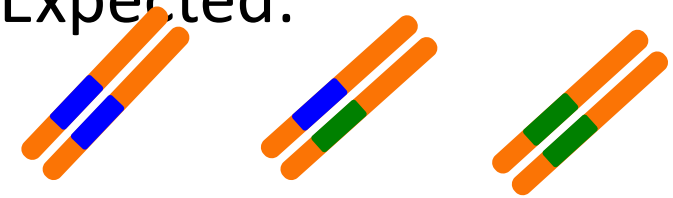
Allelic Richness: A_R

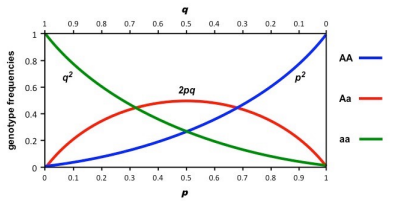
Private Allelic Richness: P_A

Heterozygosity

Observed: H_O

Expected: H_E





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

POPULATION STRUCTURE

F - STATISTICS (Wright 1969)

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

F_{IS} = Inbreeding coefficient

ANALYSIS

- Differences between populations
- AMOVA (% of variance within and among groups)
- Relationship with geography*
  - Isolation by Distance (Regression + Mantel test)
- Multivariant (allelic frequencies, alleles)
  - DACP, PCA, PCoA
- Clustering software (min HWd and LD) *
  - Structure, Geneland

R dataset

Podarcis siculus (Rafinesque-schmaltz, 1810)

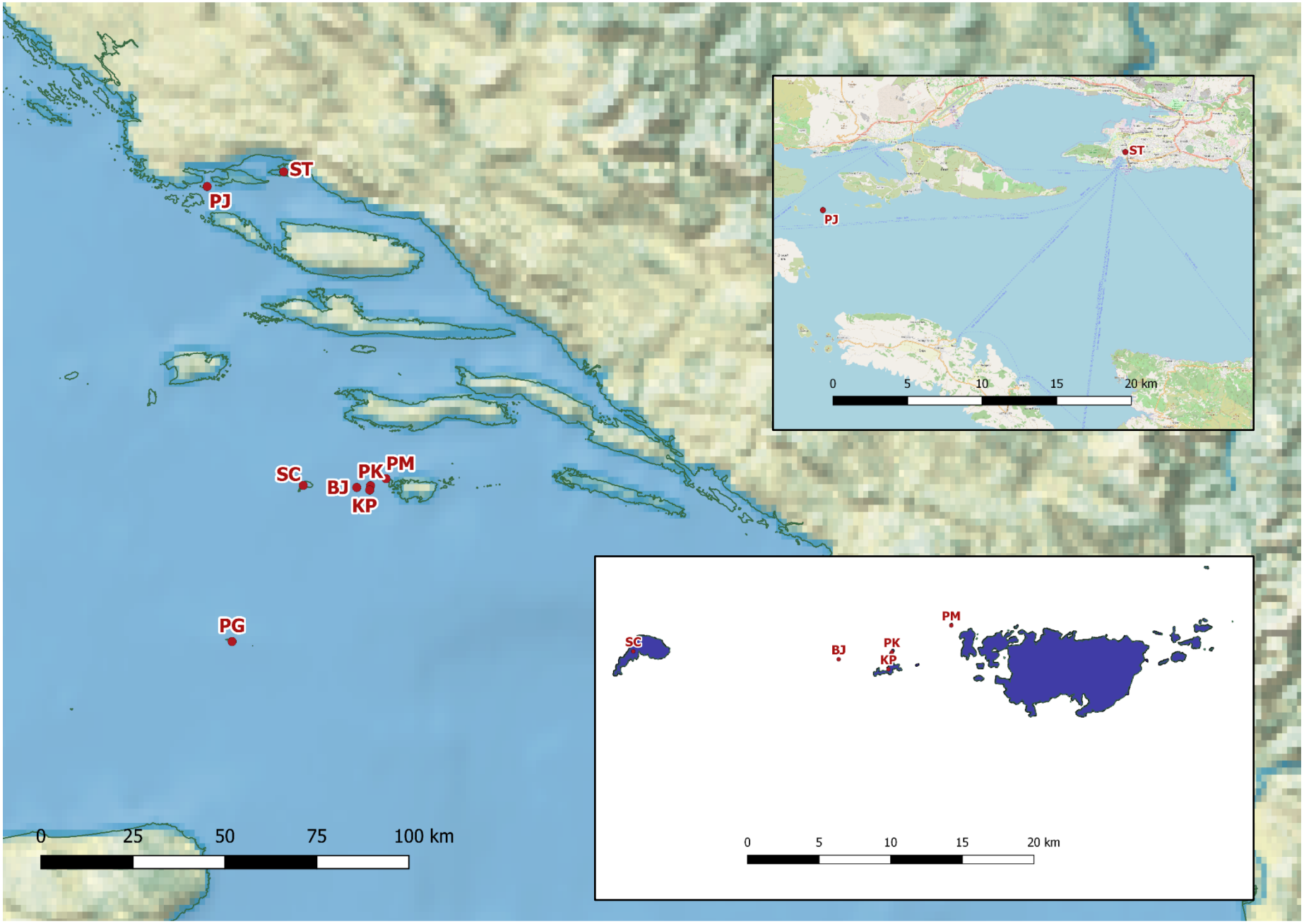
Dataset

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
SC
BJ
PK
KP
PM
0
5
10
15
20 km