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A DYNAMIC SYSTEM TO MANAGE SUBDIVIDED POPULATIONS USING MOLECULAR MARKERS

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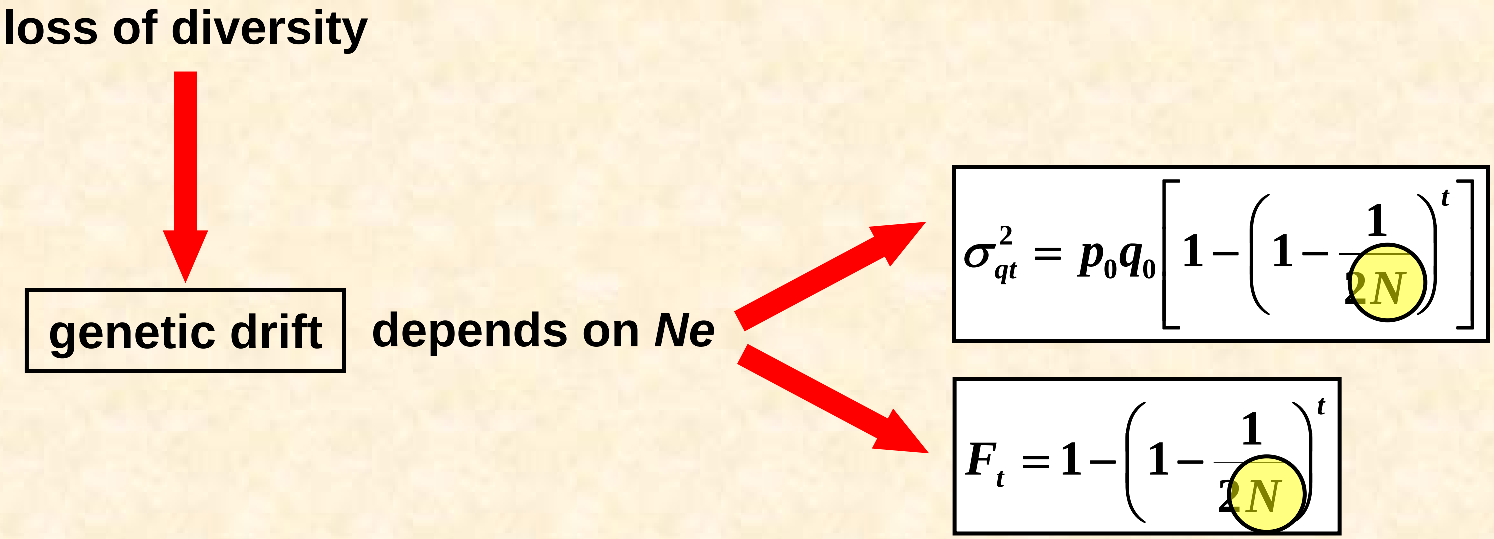
Conservation Genetics

⇒ maintenance of genetic diversity



loss of diversity

genetic drift depends on *Ne*

$$\sigma_{qt}^{2} = p_0 q_0 \left[1 - \left(1 - \frac{1}{2N} \right)^{t} \right]$$

$$F_t = 1 - \left(1 - \frac{1}{2N} \right)^{t}$$

Sensible strategy ⇒ largest populations (single)

logistic reasons

↓

several nucleus (subpopulations) kept

☺ **reduction in the risk of environmental extinctions**

(fires, infectious diseases, predators, …)

theoretically → **maximum long-term diversity by subdivision**

☹

low census size per subpopulation

↓

inbreeding depression

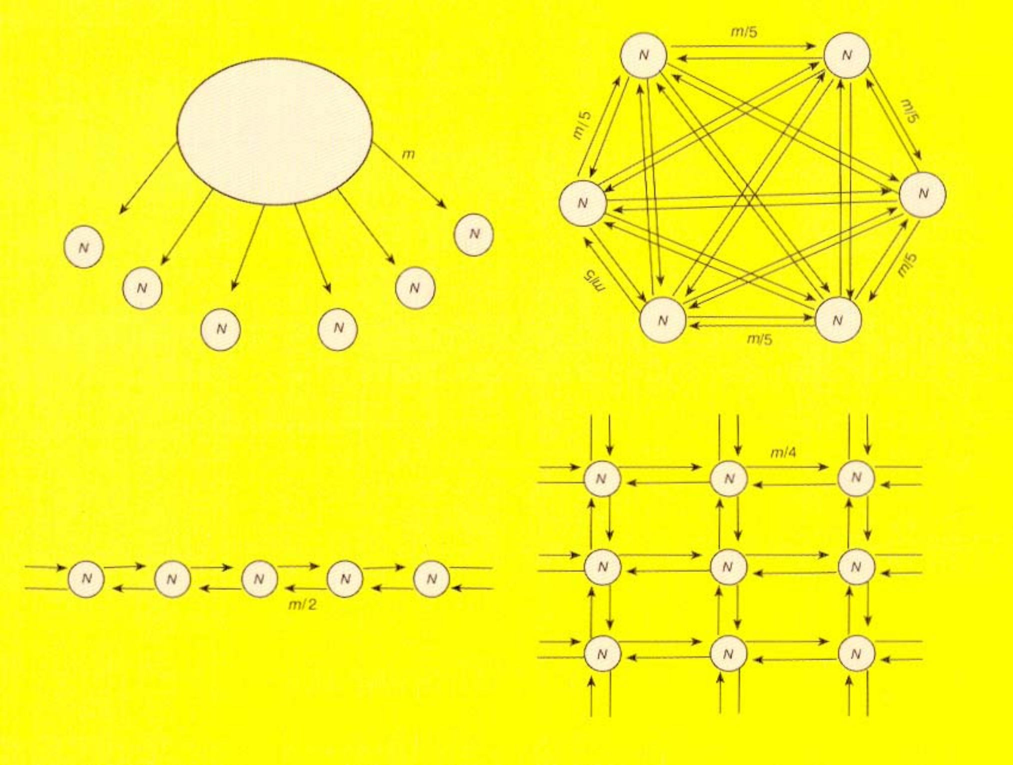
solution

↓

gene flow

↓

MIGRATION



✓ **compromise between inbreeding, global diversity and (differentiation)**

PREVIOUS WORK

Fernández et al. (2008)

Dynamic method of management of metapopulations

⇒ **based on pedigree**

global diversity

- ✓ **method efficient in balancing**

inbreeding levels

- ✓ **accounts for population structure**

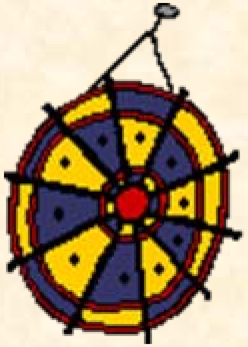
  ⇒ ***non regular rate/scheme of flow***

METAPOP

- ✓ **able to control number of migrants**

OBJECTIVE

- to test the efficiency of dynamic method when based on molecular information



MATERIAL AND METHODS

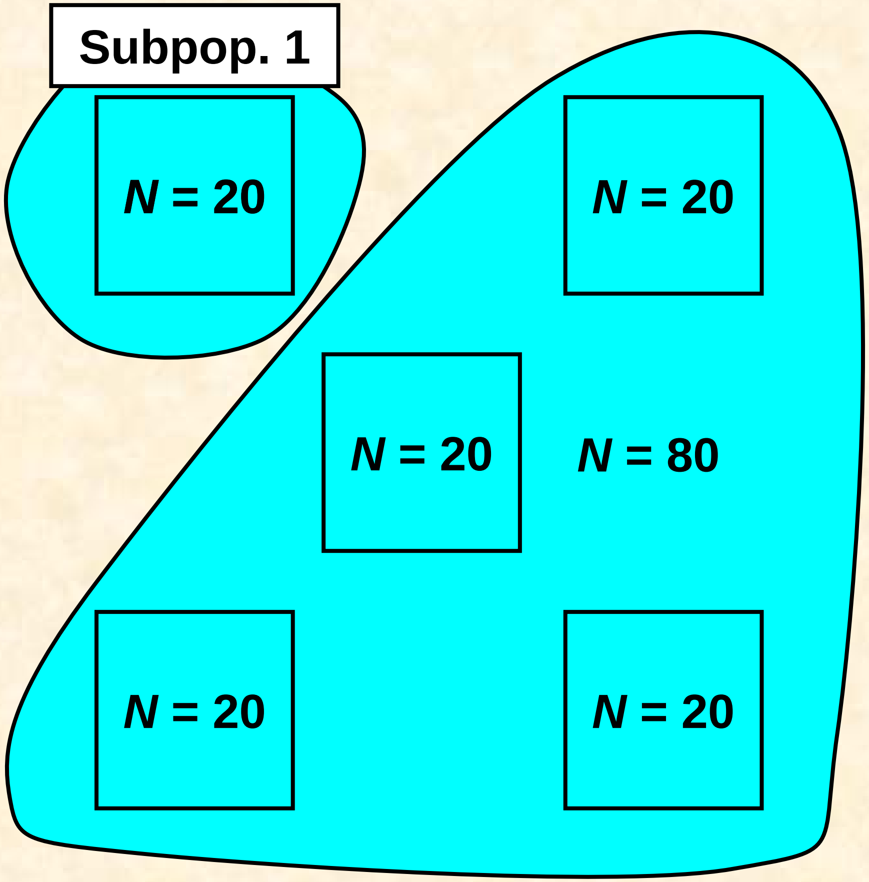
Computer simulations

- 20 chromosomes of 1 M length
- 100 genomic loci (evenly spaced) per chromosome
- pedigree recorded every generation
- 1, 2, 5 or 10 markers per chromosome
- 2, 5 or 10 alleles per locus

Base population

- **5 subpopulations**
  - ✓ **Structure**
    - **E** ***same size / 1:1 sex ratio***
    - **D** ***different sizes and sex ratios***
  - ✓ **Relation**
    - **U** ***non inbred/unrelated individuals***
    - **R** ***differential relationships***

- ✓ *more inbred*
- ✓ *less related*



Subpop. 1

N **= 20**

N **= 20**

N **= 20**

N **= 80**

N **= 20**

N **= 20**

- ✓ **same number of males and females**
- ✓ **5 discrete generations**
- ✓ **random { contributions**
  mating

✓ **ten discrete generations**

- **Management system**

✓ **Dynamic method** $\begin{cases} \lambda = 1, 10 \\ M = 1 \end{cases}$

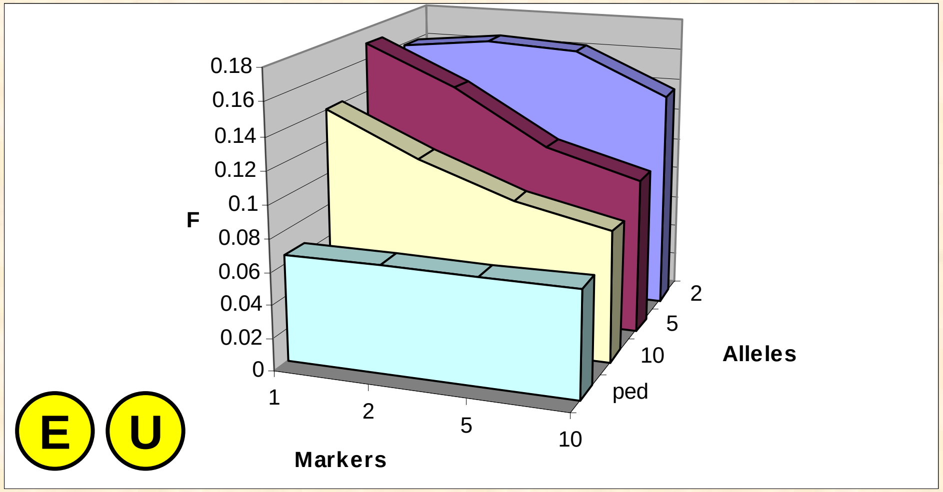
λ = within population diversity weighting factor

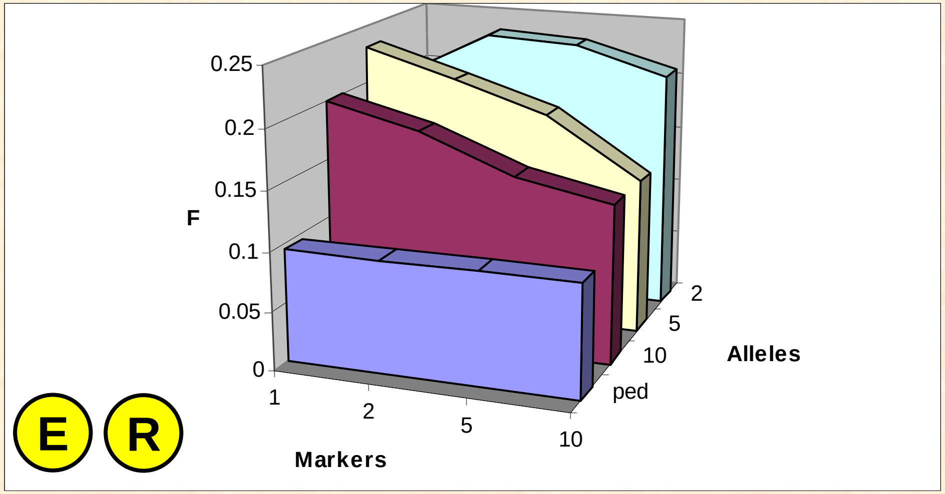
coancestry
- ✓ **from pedigree**
- ✓ **from markers**

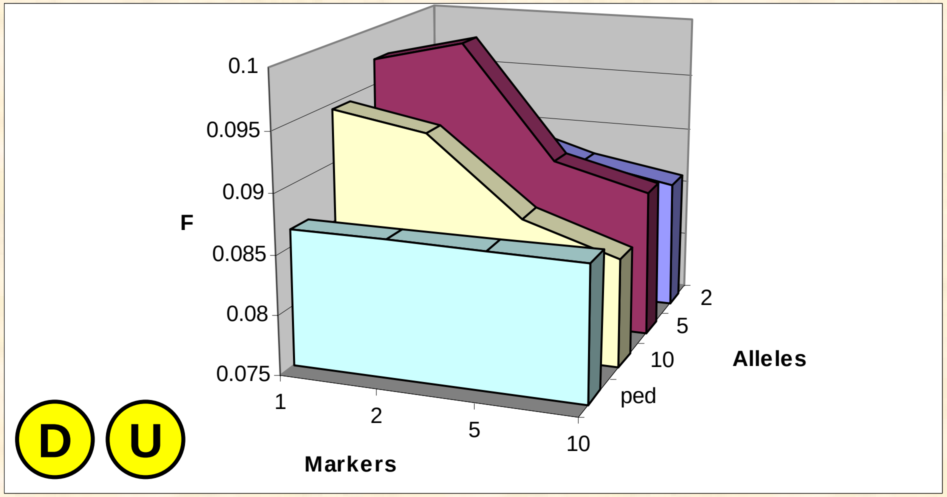
random mating within subpopulations

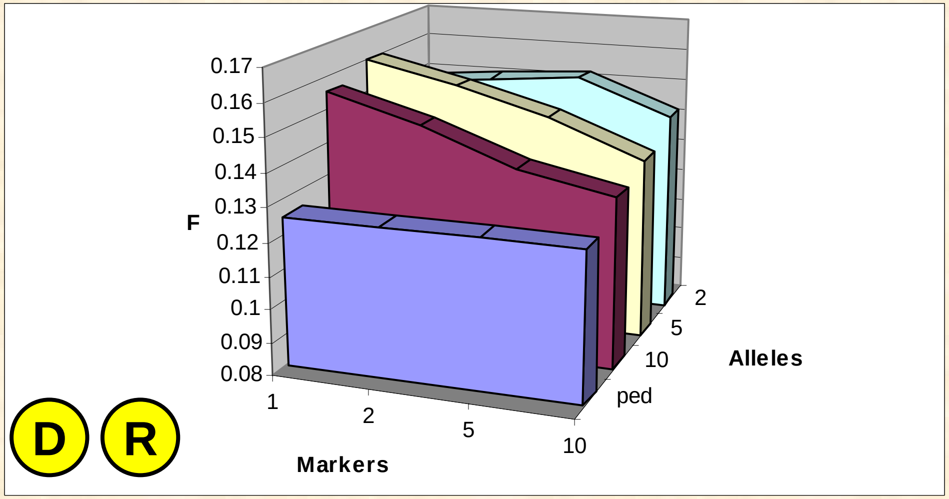
RESULTS

$\lambda = 1$

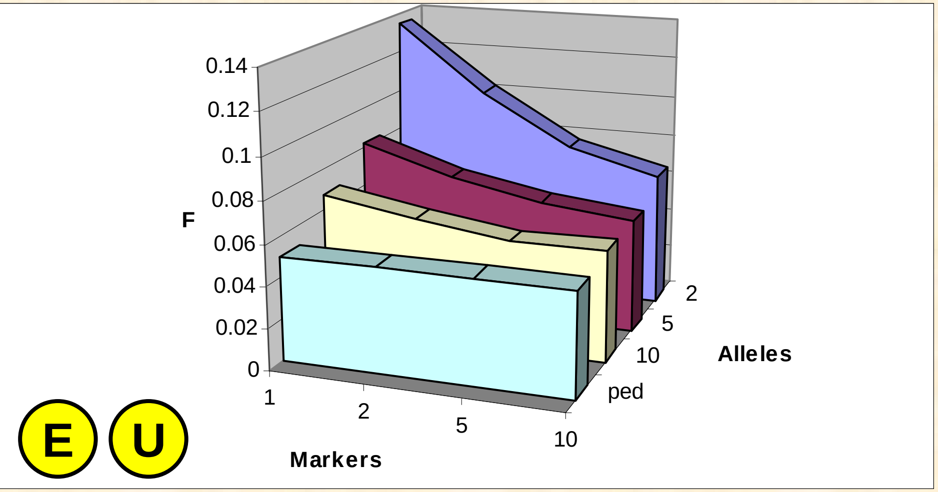








$\lambda = 10$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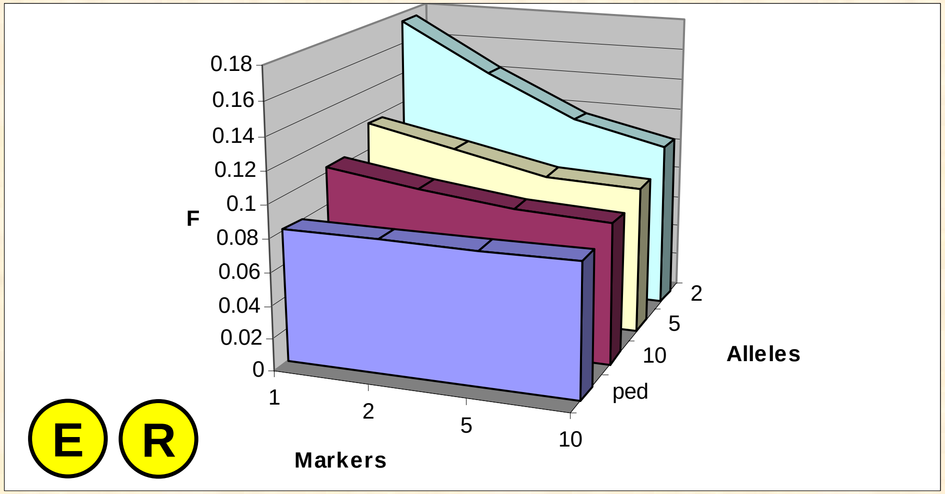
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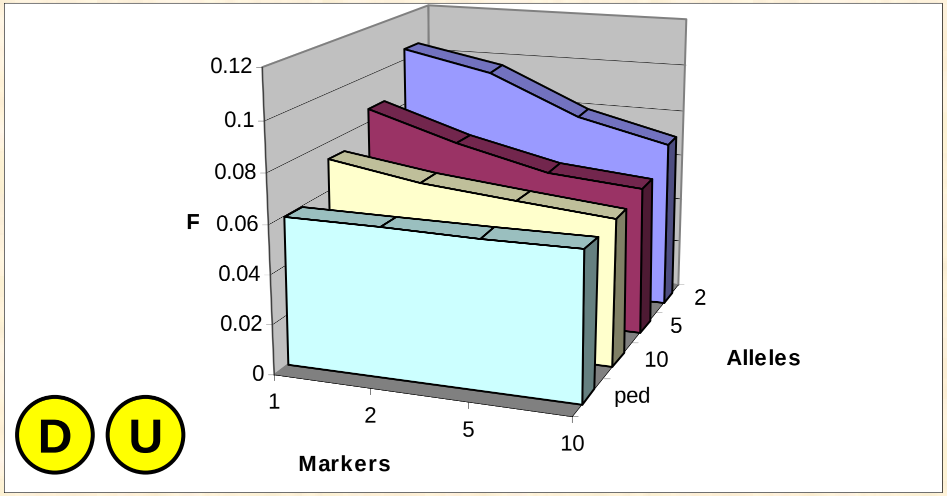
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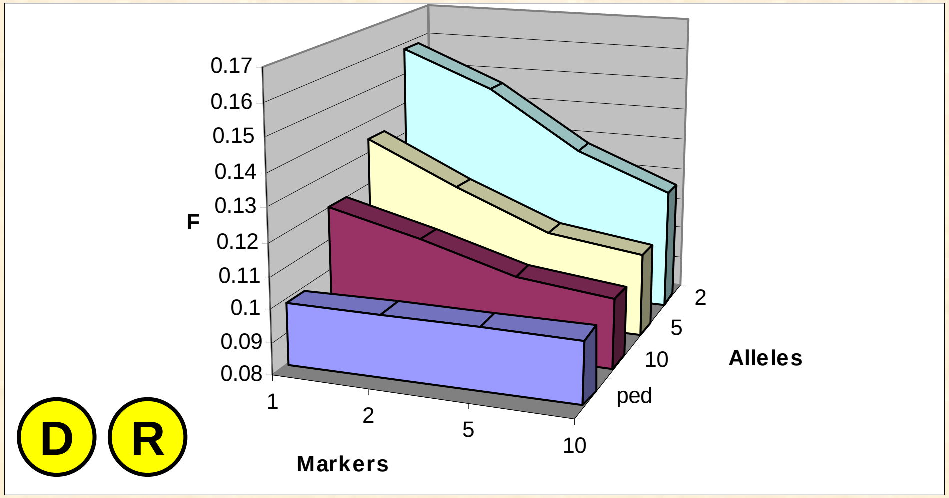
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SUMMARISING

- ✓ **pedigree outperforms markers**
  - ⇒ ***more than 10 markers per chromosome with 10 alleles***
- ✓ **similar results as with single populations**
  - ⇒ ***Fernández et al. 2005***
- ✓ **more realistic with some linkage disequilibrium**
  - ⇒ ***future work***

THANK YOU!!