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The concept of effective population size loses its meaning in the context of optimal management of diversity using molecular markers

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Traditional definition

The effective population size is a measure of the rate of increase in inbreeding or the rate of increase in coancestry

$$F_t = 1 - (1 - \Delta F)^t \qquad f_t = 1 - (1 - \Delta f)^t$$

$$N_{e(F)} = \frac{1}{2\Delta F}$$

Effective population size of inbreeding

$$N_{e(f)} = \frac{1}{2\Delta f}$$

Effective population size of coancestry

Traditional definition

- **Although it does not have good statistical properties it is intuitively appealing because….**

… it is the size of an idealised population, which would give rise to the rate of change in inbreeding and coancestry actually observed in the population under consideration

Molecular coancestry and inbreeding

- **Molecular coancestry f_M** is the probability that two alleles taken at random, one from each individual, are identical *by state*

- **Molecular inbreeding F_M** of an individual is the probability that the two alleles are identical *by state*

Pair	f_M
A_1A_1 , A_1A_1	1.0
A_1A_1 , A_1A_2	0.5
A_1A_2 , A_1A_2	0.5
A_1A_1 , A_2A_2	0.0

Individual	F_M
A_1A_1	1
A_1A_2	0

(Molecular similarity, Malécot similarity)

Relationship between the pedigree and the molecular coancestry?

$$f_M = f_P + (1 - f_P)Hom_{base}$$

Molecular coancestry

Pedigree coancestry

Homozygosity of the base population

In principle we can estimate the pedigree coancestry from the molecular coancestry

$$\hat{f}_P = \frac{f_M - Hom_{base}}{Het_{base}}$$

The problem is that we do not usually know the homozygosity of the base population

Relationship between the pedigree and the molecular coancestry?

But even if we *do not know* the allelic gene frequencies of the base population the following relationship holds:

$$E(\Delta f_M) = \Delta f_P \qquad E(\Delta F_M) = \Delta F_P$$

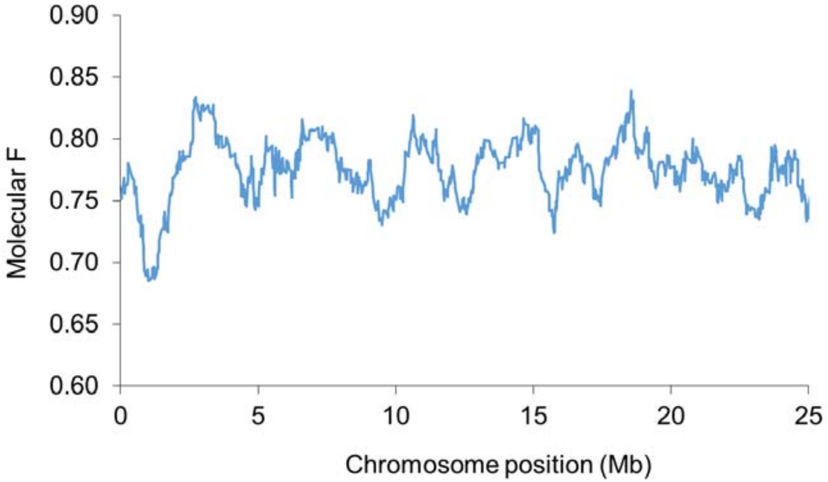
$$N_e(f_M) = N_e(f_P) \qquad N_e(F_M) = N_e(F_P)$$

Molecular measures of inbreeding and coancestry are expected to be more informative

- **They reflect realized values instead of expected ones**

- **They can detect relationships due to very distant common ancestors**

They can be calculated for particular regions of the genome



Effective population size and optimal management of genetic resources using pedigree information

We should minimize de rate of inbreeding (maximize Ne)

The optimal management criterion is to:

→ select the group of parents that
→ minimize the the average pedigree coancestry of selected animals
→ weighted by their contributions to the next generation

Optimising genetic management

Minimise $\mathbf{c}' \boldsymbol{f} \mathbf{c}$

subject to restrictions

$\sum c_i = ½$ (for each sex)

$c_i \geq 0$

c = vector of contributions to next generation (vector of solutions)

$\boldsymbol{f}$ = coancestry matrix

$f_P \rightarrow$ pedigree

$f_M \rightarrow$ molecular

It is more efficient to use molecular coancestry instead of pedigree coancestry?

Computer simulation

t = -4000 Ne = 100

random mating

Base population

t = 0 N = 100

mutation-drift equilibrium

t = 30 N = 100

Genome size

20 chromosomes (1 M)

Simulated loci/chromosome

- 5000 markers

  used in management to compute molecular coancestry (f_M)
- 5000 non-marker loci

  used to measure genomic heterozygosity ($1-f_G$)

300 replicates

Optimal management → Generate 4 offspring from each potential parents and keep offspring that minimise observed coancestry computed

genealogy → ***pedigree coancestry (f_P)***

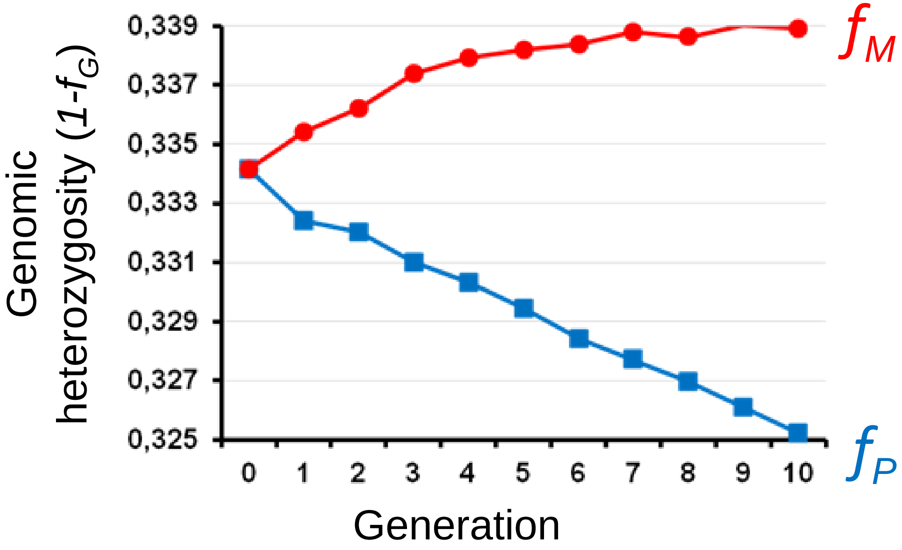
SNP markers → ***molecular coancestry (f_M)***

Expected genomic heterozygosity with management based on f_P or f_M

When management is based on f_M:

- More genomic heterozygosity is maintained
- Initial increase in genomic heterozigosiy

No meaning of Ne based on Δf_G (negative Ne_G)



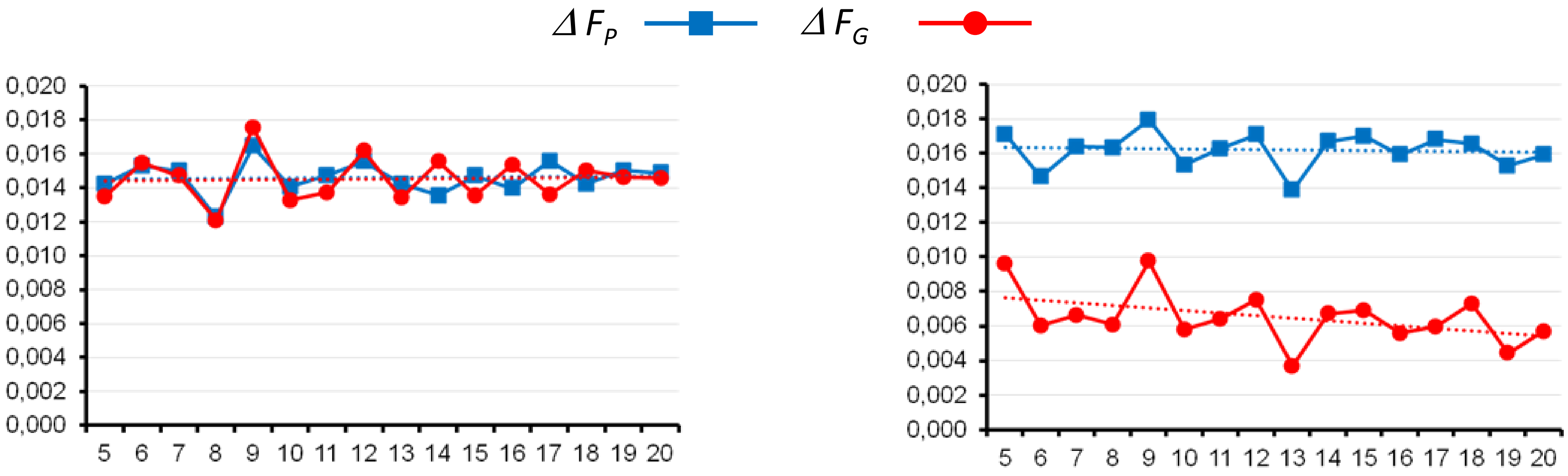
N=100

(de Cara et al. 2011)

Rate of genealogical (ΔF_P) or genomic (ΔF_G) inbreeding in the long term

Genealogical management

Molecular management



When managing with f_G

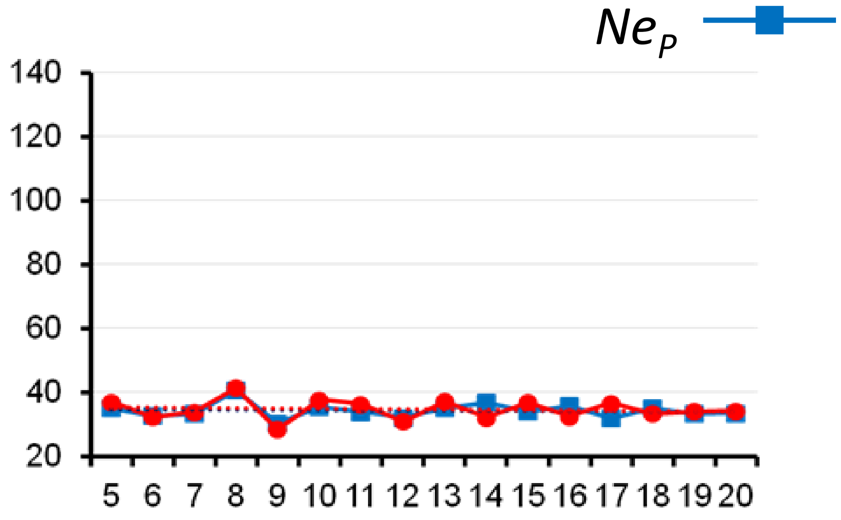
the rates for pedigree and genomic inbreeding are **equal**

When managing with f_M

more diversity is maintained and the rates for pedigree and genomic inbreeding **differ**

Effective population size calculated from genealogical or genomic inbreeding

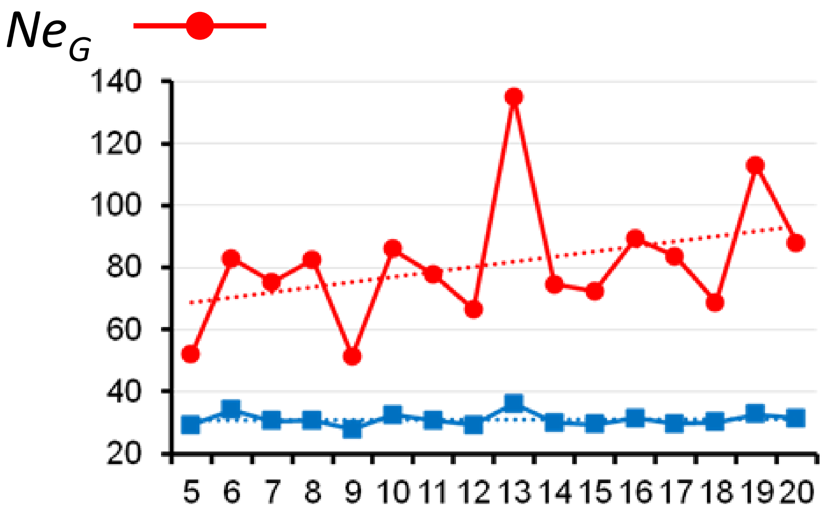
Genealogical management



When managing with f_G

the two effective sizes (Ne_G and Ne_M) are **equal**

Molecular management



When managing with f_M

Ne_G is not constant but increases and **the asymptotic nature of Ne disappears**

Concluding remarks

The use of molecular coancestry in optimal genetic management of conservation programs should be recommended

- Mantains more diversity (even it can increase)
- The concept of effective population size loses its meaning
- But it moves allelic frequencies of markers towards intermediate values

Should be called conservation or selection for genetic diversity?

Thank you for your attention