Optimal management of gene and allelic diversity in subdivided populations

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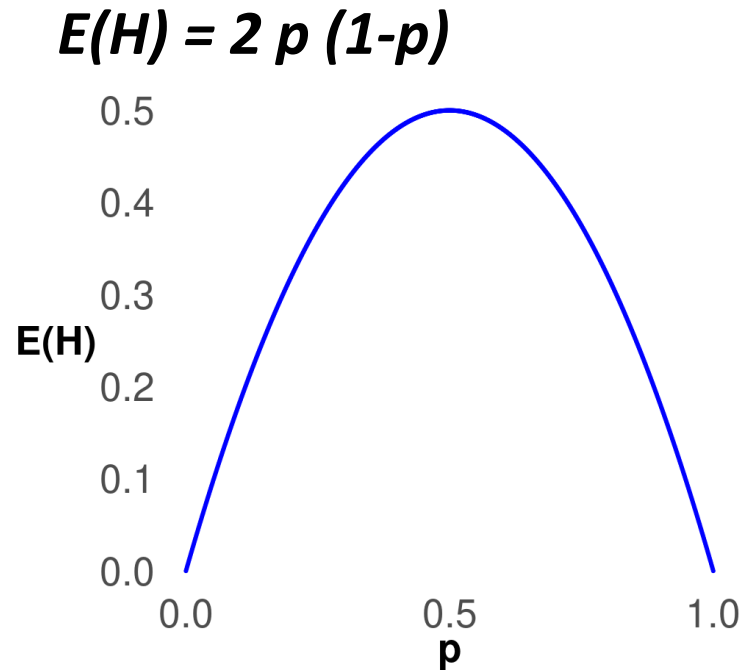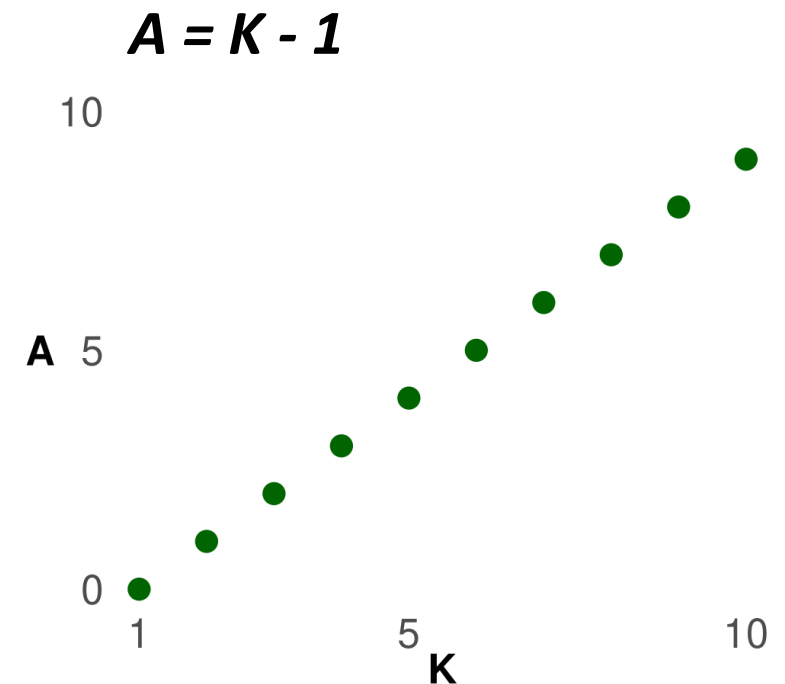
Managing genetic diversity

Heterozygosity

Depends on:

- allelic frequencies:

$$E(H) = 2\,p\,(1-p)$$

Allelic diversity

- the absence / presence of alleles

$$A = K - 1$$

Managing genetic diversity

Heterozygosity
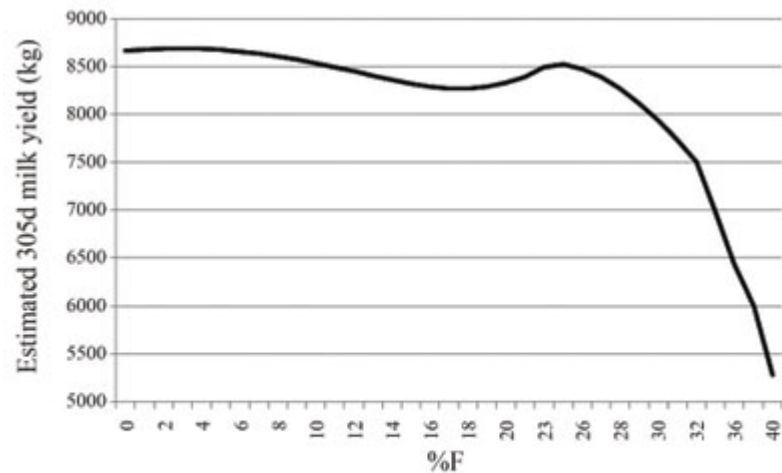
Relates to:

- Inbreeding: $F = 1 - H$

Figure 2 - Estimated 305 d milk yields (kg) by inbreeding level (%F) from the cubic-spline model adjusted for herd-year-season effects.
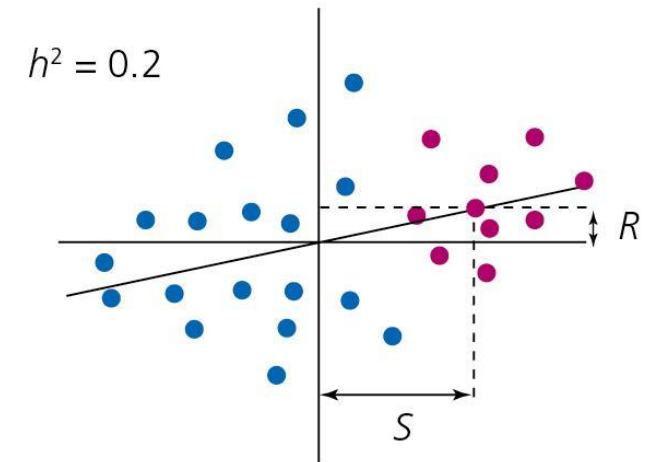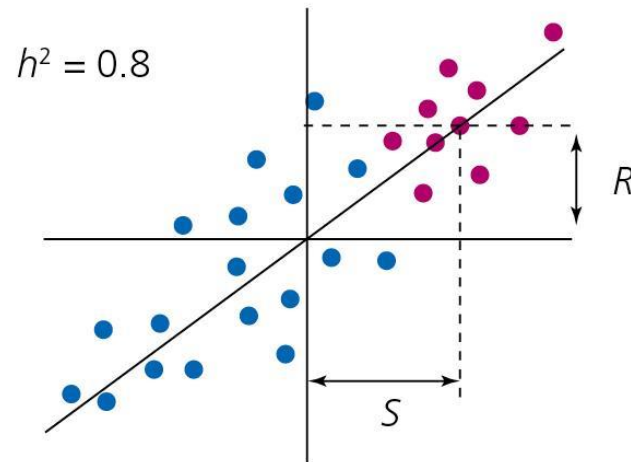
(from Geha MJ *et al.* 2011)

Managing genetic diversity

Heterozygosity

Relates to:

- Inbreeding: **$F = 1 - H$**

- Additive variance: **$V_A = 2\,p\,(1-p)\,\alpha^2$**
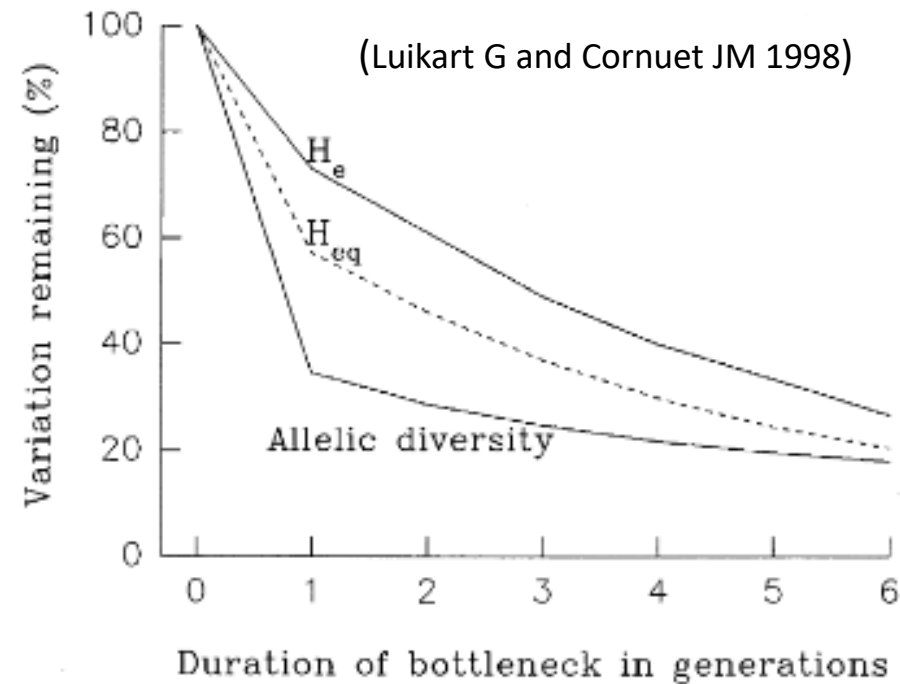 (and the response to selection)

$h^2 = 0.8$

R

S

$h^2 = 0.2$

R

S

Managing genetic diversity

Allelic diversity

Is more sensitive to:

- Bottlenecks

(Luikart G and Cornuet JM 1998)
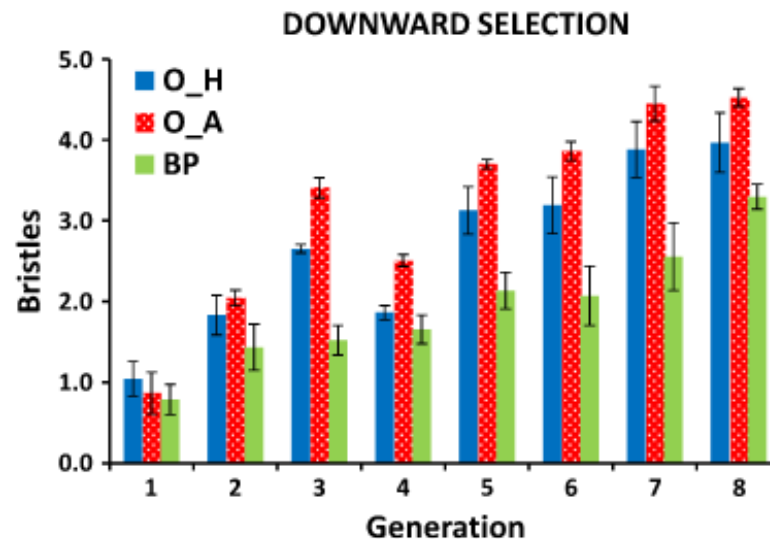
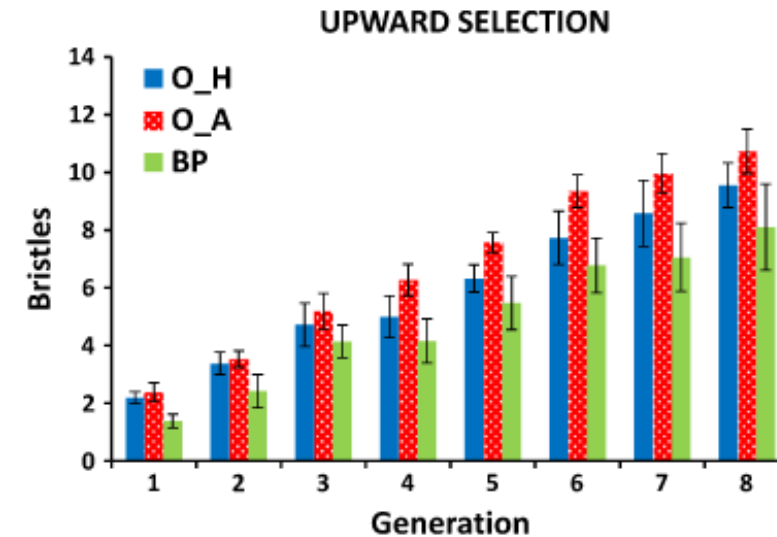# Managing genetic diversity

Allelic diversity

Is more sensitive to:

- Bottlenecks

Relates to:

- Long-term response to selection
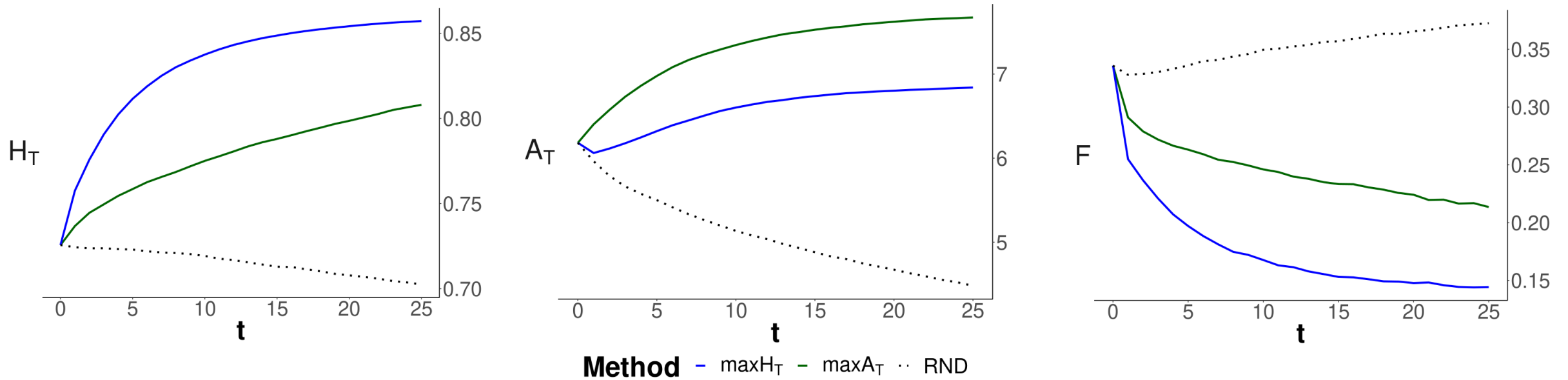 (*i.e.* adaptive potential)

(from Vilas A *et al.* 2015)

Heterozygosity / Allelic diversity
Within populations

Maximization of heterozygosity should be the strategy of choice
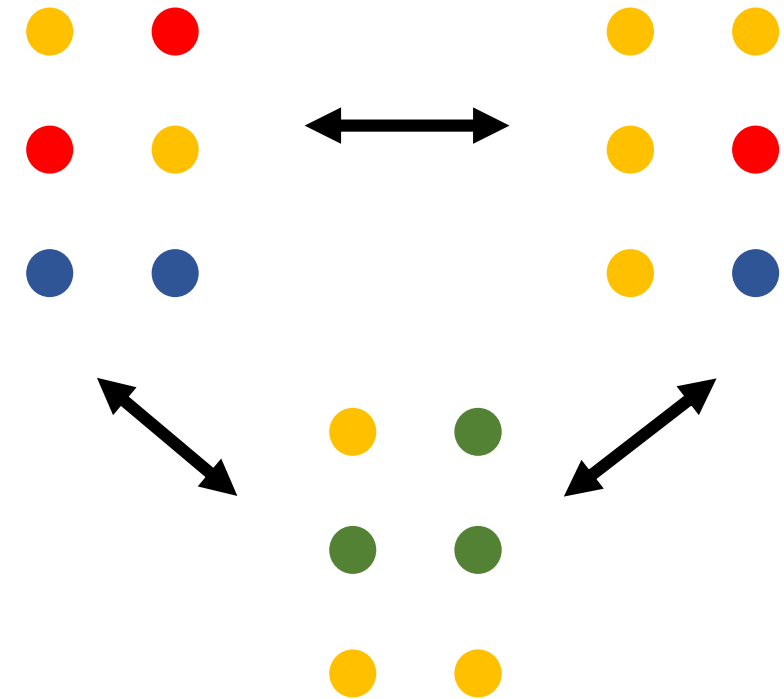**(Fernández et al 2004)**

Allelic diversity
in subdivided populations

Total allelic diversity: $\boldsymbol{A}_{\boldsymbol{T}} = AS + DA$

$$A_S = \left(\frac{1}{n}\sum a_i\right) - 1$$

$$D_A = \frac{1}{n^2}\sum\sum d_{A,ij}$$
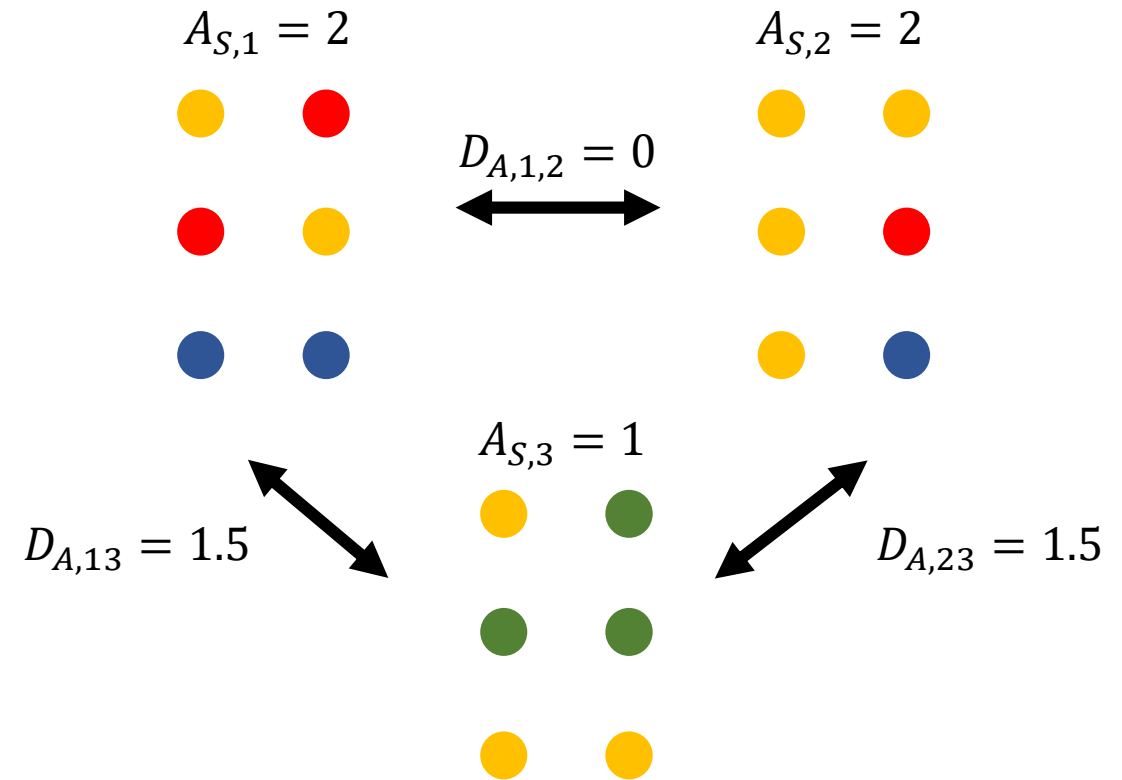
Allelic diversity
in subdivided populations

Total allelic diversity: $A_T = AS + DA$

$$A_S = \left(\frac{1}{n}\sum a_i\right) - 1 = \mathbf{1.67}$$

$$D_A = \frac{1}{n^2}\sum\sum d_{A,ij} = \mathbf{0.67}$$

$$A_T = \mathbf{2.33}$$

$$K = \mathbf{4}$$

$A_{S,1} = 2$

$A_{S,2} = 2$

$D_{A,1,2} = 0$

$A_{S,3} = 1$

$D_{A,13} = 1.5$

$D_{A,23} = 1.5$

Metapop2 software

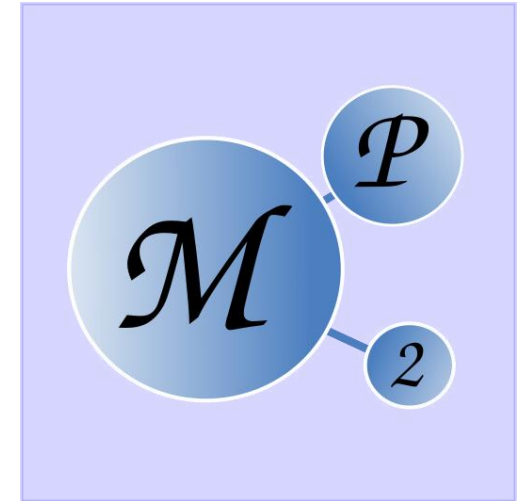**RESOURCE ARTICLE**

MOLECULAR ECOLOGY RESOURCES WILEY

METAPOP2: Re-implementation of software for the analysis and management of subdivided populations using gene and allelic diversity

Eugenio López-Cortegano[1,2] | Andrés Pérez-Figueroa[1,3] | Armando Caballero[1,2]
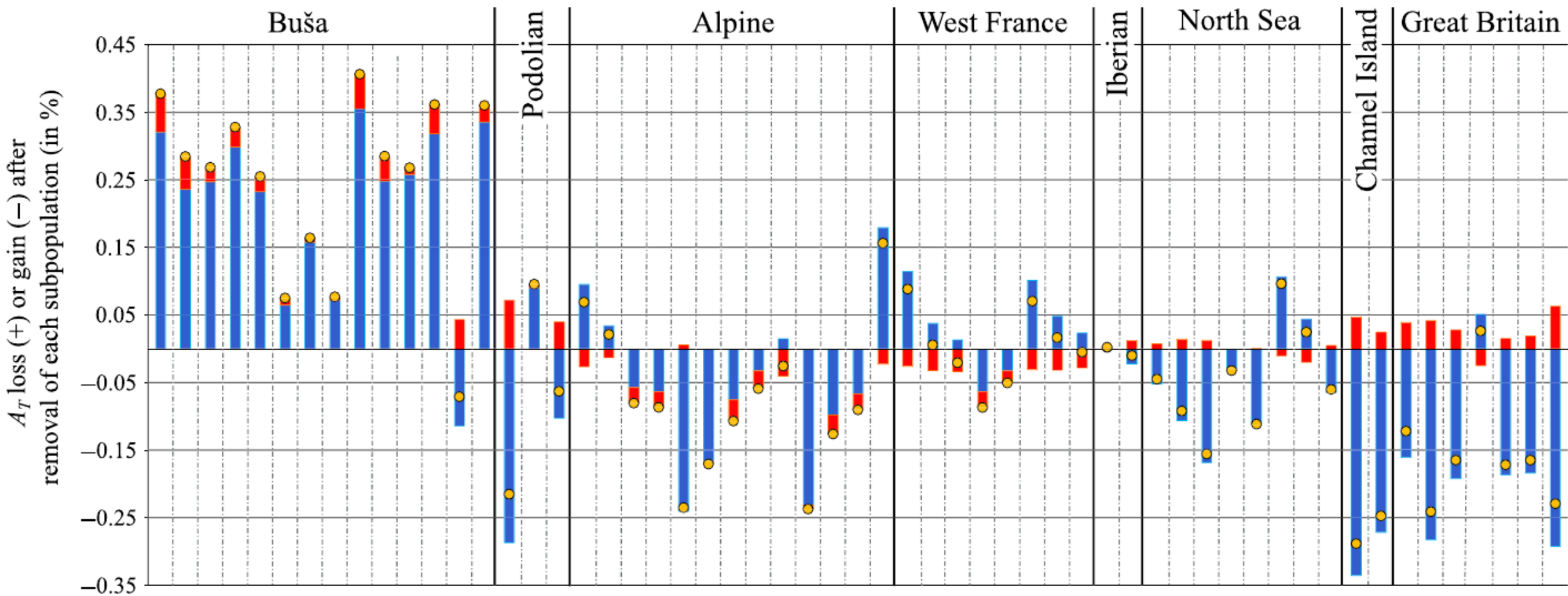
- Available at GitLab: https://gitlab.com/elcortegano/metapop2

Example data from Cattle

Subpopulations contribution to diversity:

- Most breeds contribute to total diversity

- JER breed breed harbors little H_S and A_S

- PIED contributes differently to D_G and D_A

(López-Cortegano et al 2019; Cattle data from Decker et al 2014)

Example data from Cattle

(Ramljak et al 2018)
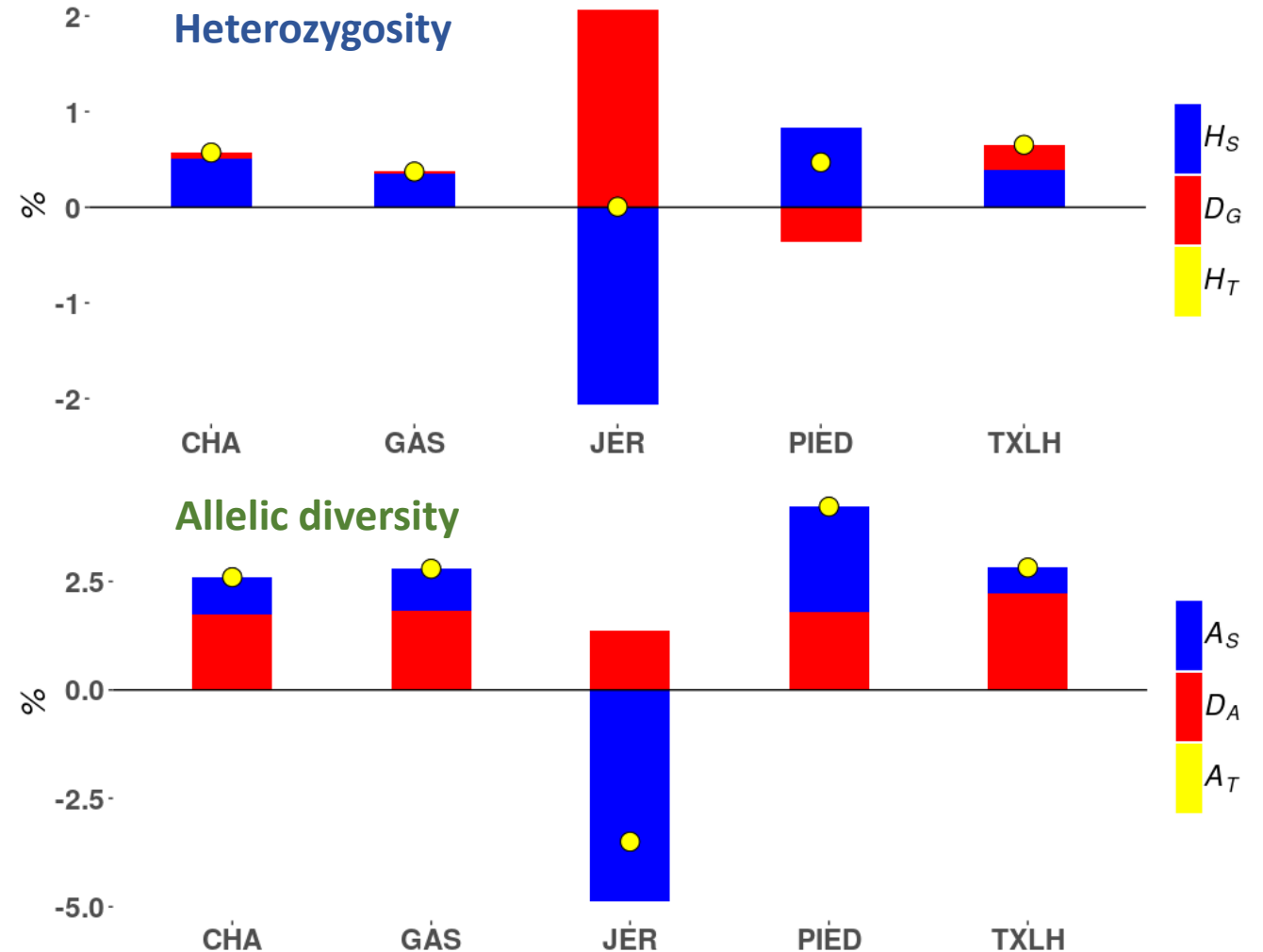
1ˢᵗ Take-home message

Allelic diversity matters

Management simulations

Genomic markers:

- High density of haplotypes
  (about 1,000 per Morgan)

Population composition:

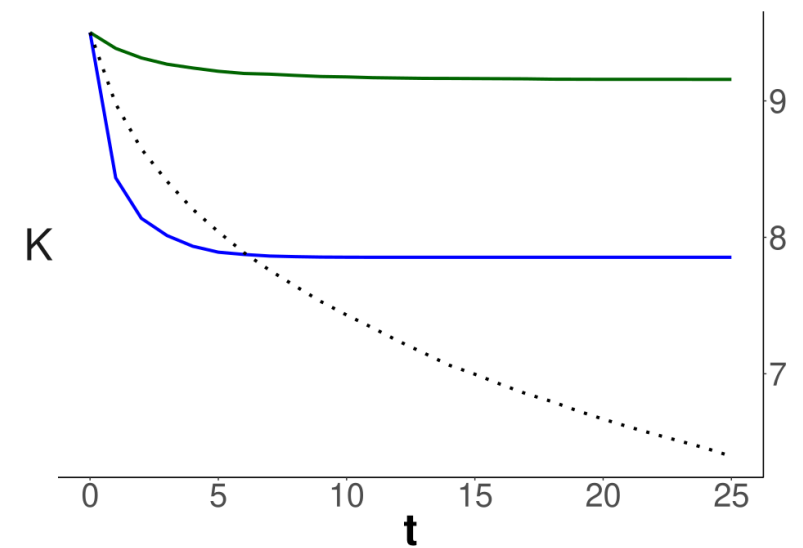- 5 subpopulations ($N = 40$)
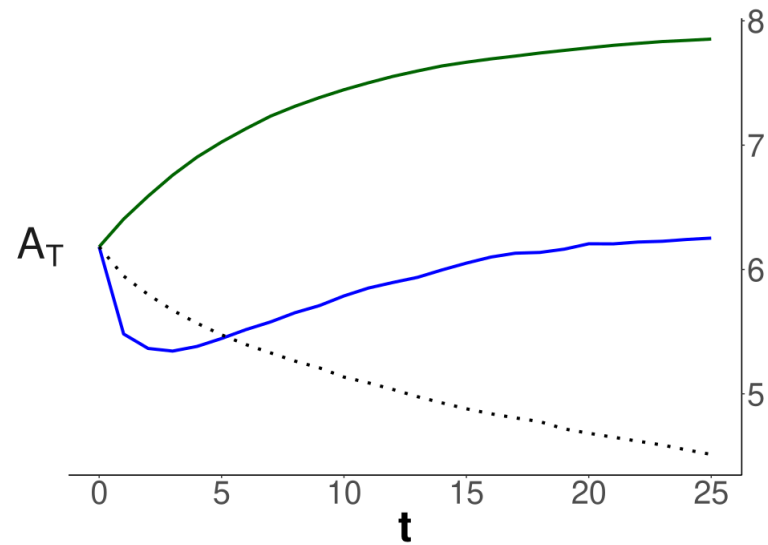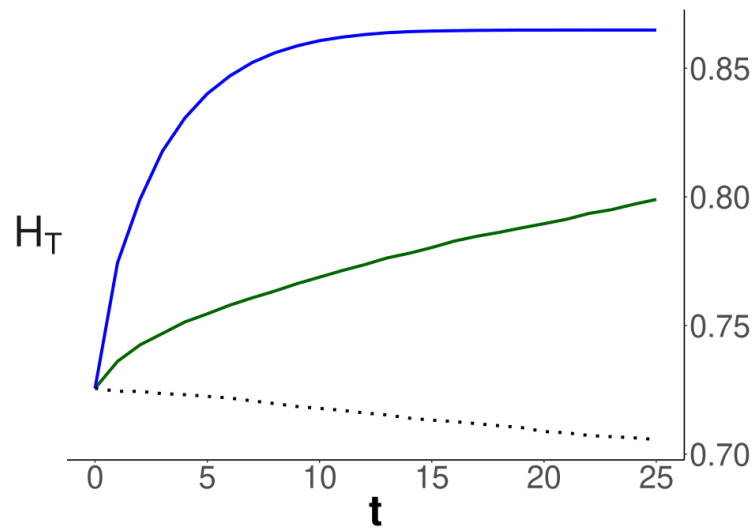- Balanced sex ratio

Computing individuals contributions:

- Using Simulated Annealing
- No limit to number of offspring
- Migration (5 migrants per generation)

5000 generations

25 generations

25 generations

$N = 4000$

2000 100 100 100 100

Conservation Management
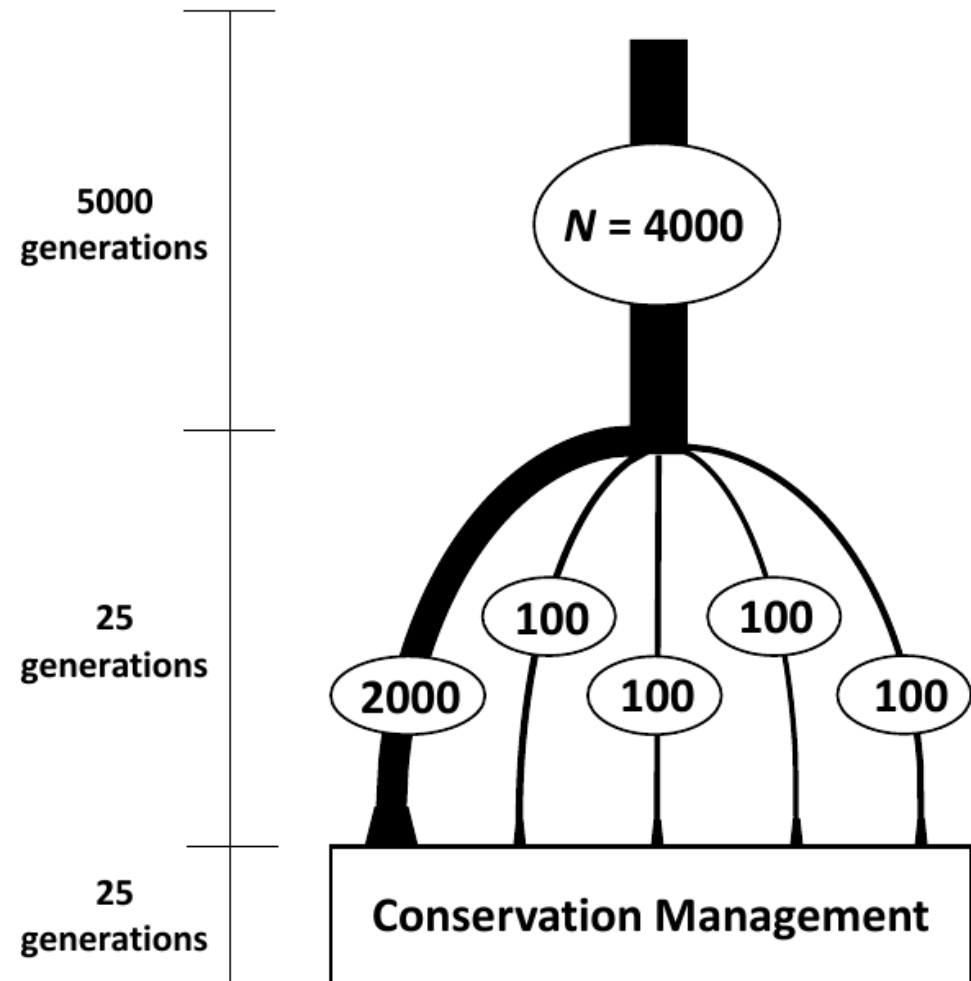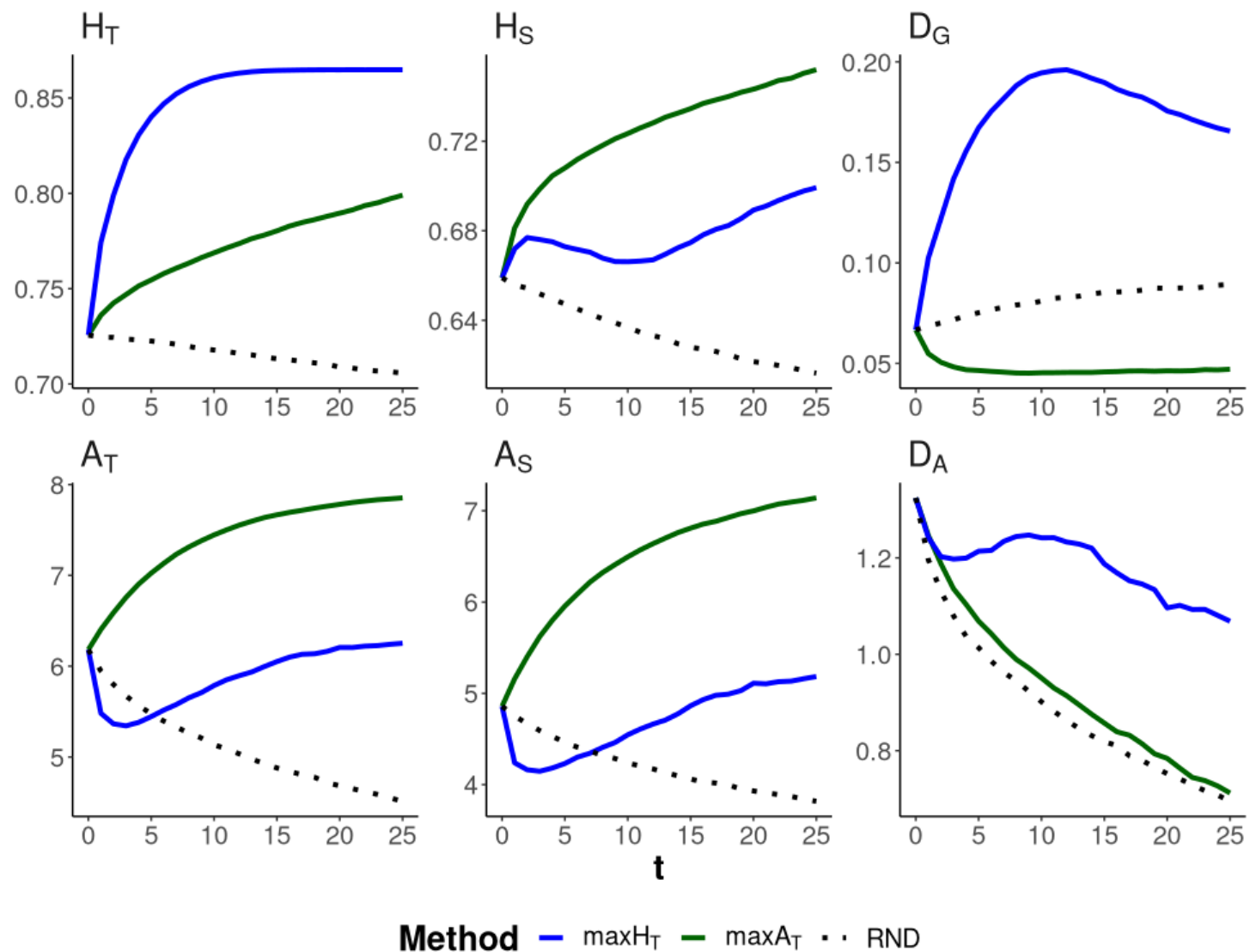
Management simulations

The different optimization methods achieved their objectives

Method — maxH$_T$ — maxA$_T$ ·· RND
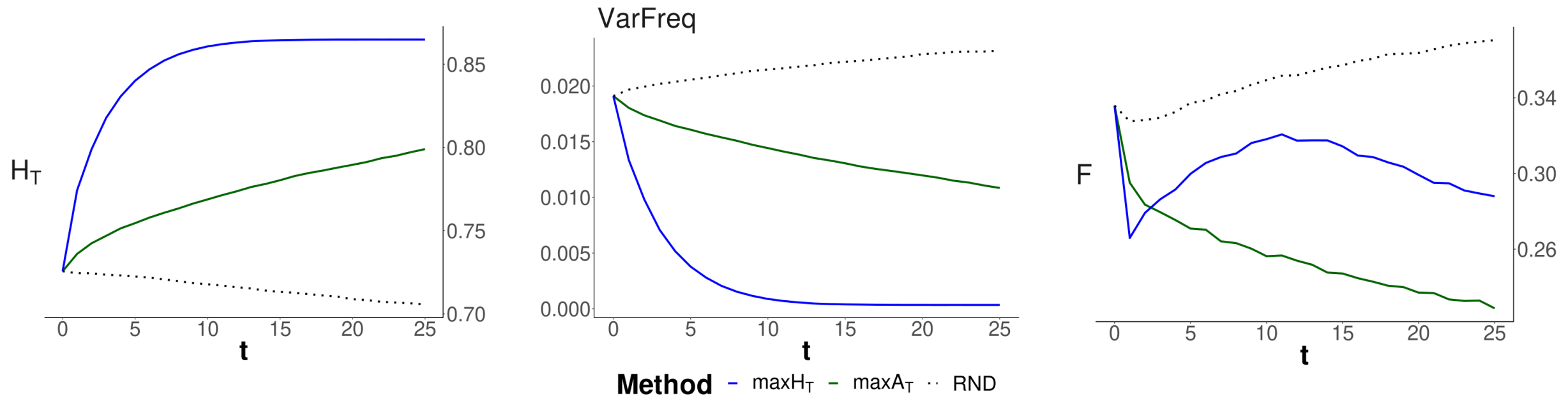
Management simulations

Optimizing allelic diversity

maximizes genetic diversity

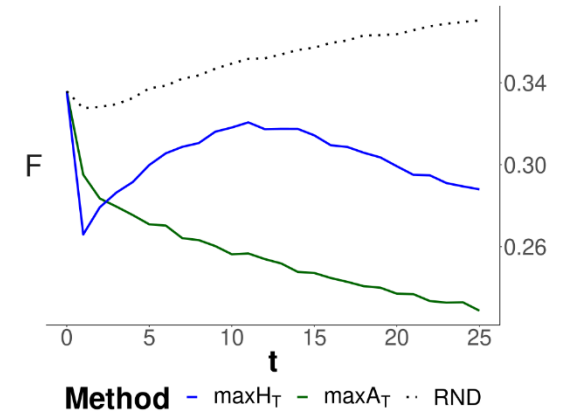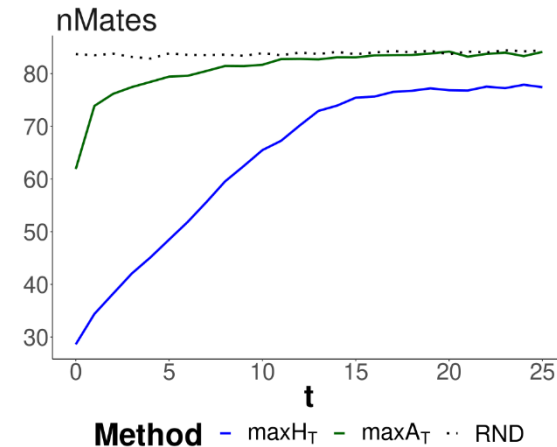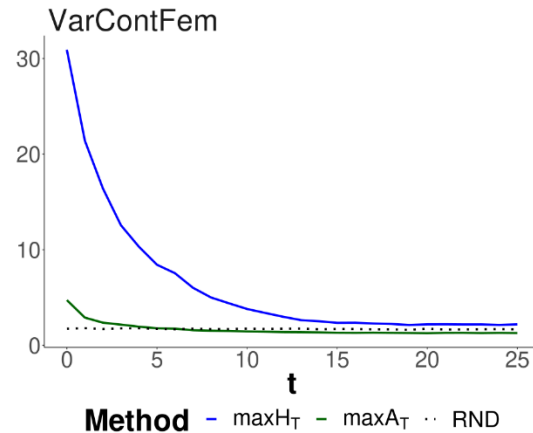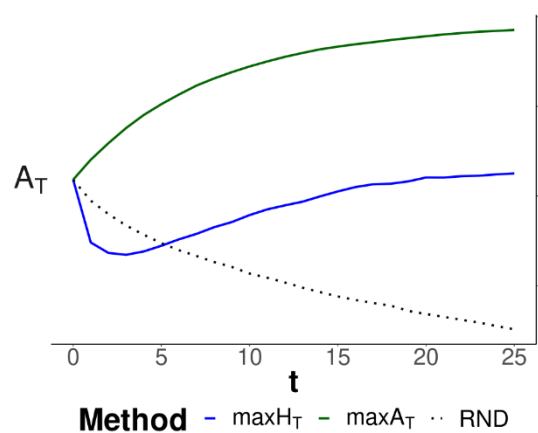within subpopulations

Management simulations

**Maximizing total heterozygosity does not minimize inbreeding
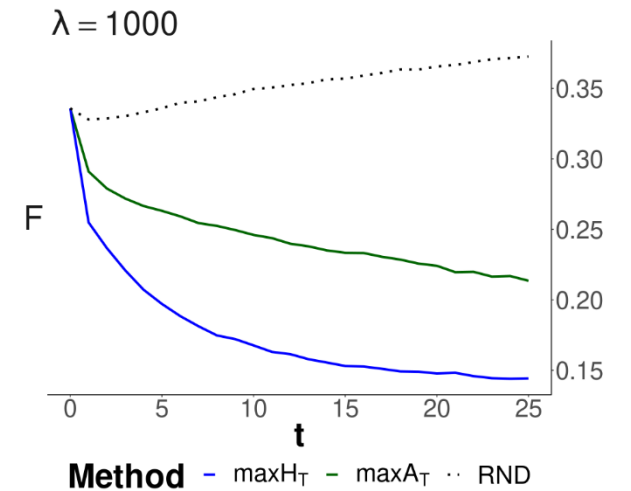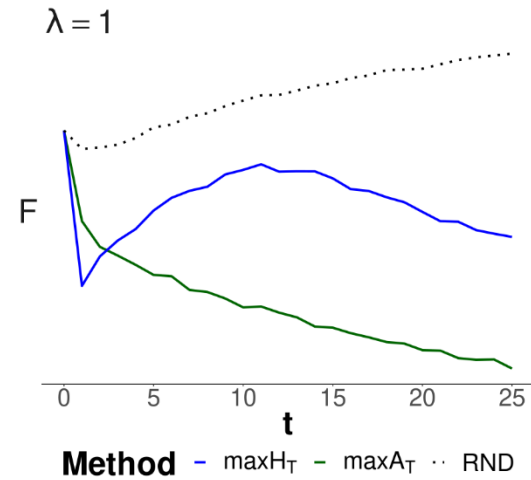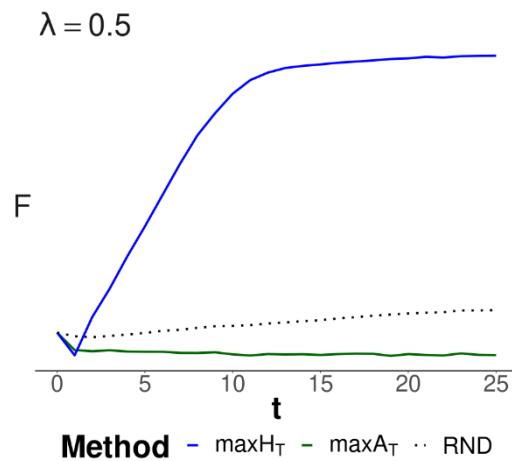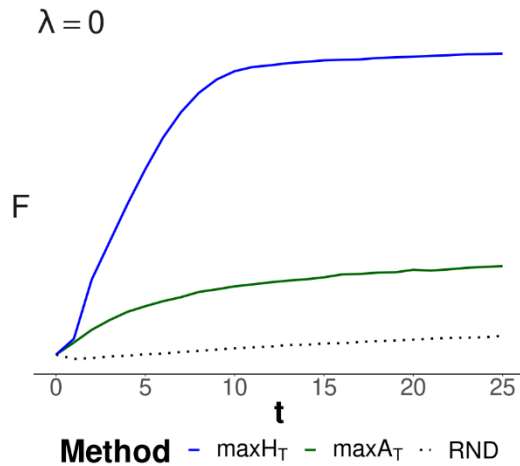In subdivided populations**

Management simulations

Maximizing allelic diversity can be reached by equalling individuals contributions, and minimizes inbreeding

Management simulations

Maximizing heterozygosity is the best choice to minimize inbreeding
Only when managing single, undivided populations

$$A_T = \lambda A_S + DA$$

2nd Take-home message

Allelic diversity minimizes inbreeding in subdivided populations

Optimal management of genetic diversity in subdivided populations

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Thank you!

Thanks to:

People at:

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