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Evaluation of Ancestral Inbreeding Coefficients: *Ballou's formula versus Gene Dropping*

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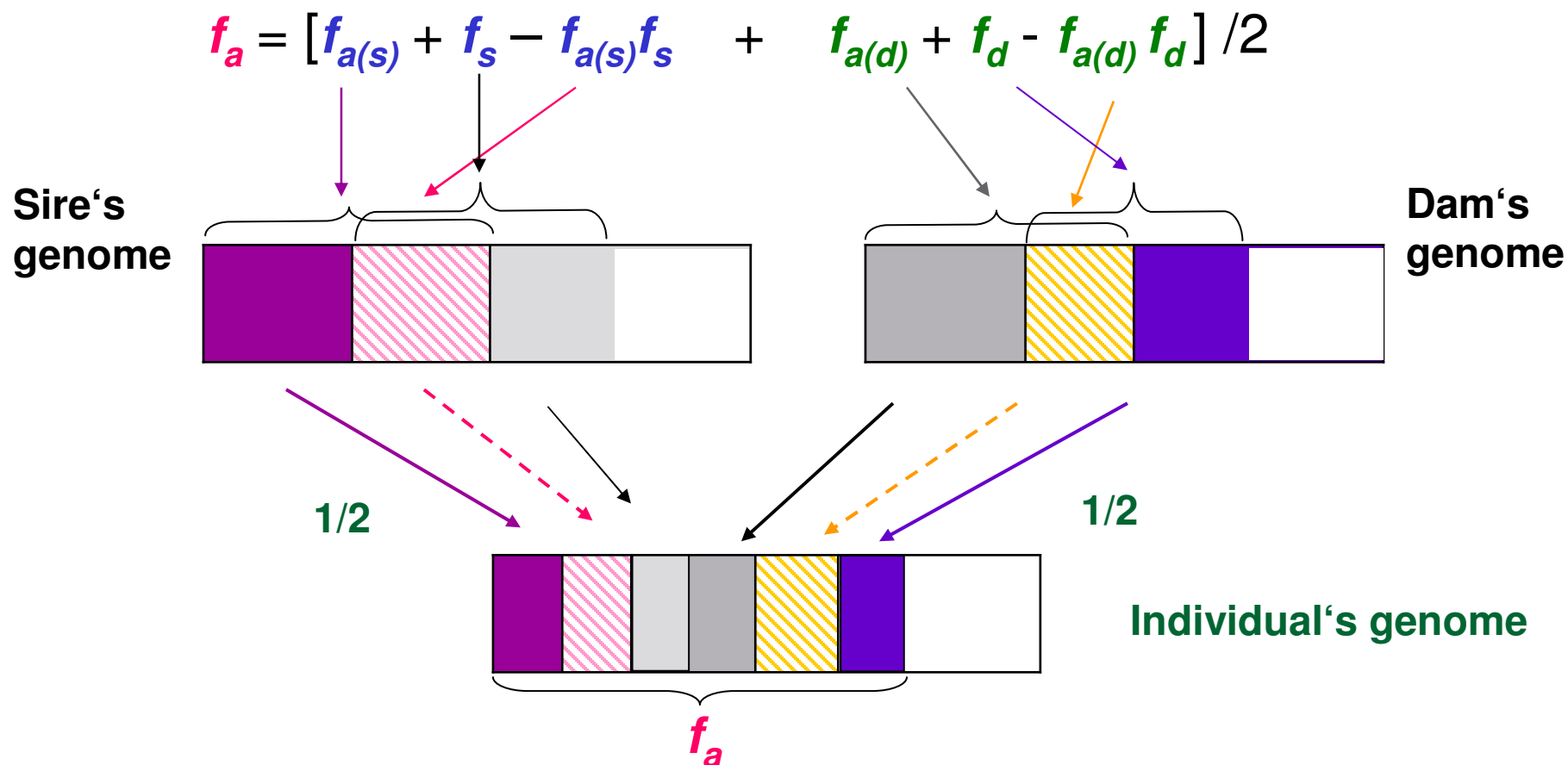
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Ancestral inbreeding coefficient (f_a)

$$f_a = [f_{a(s)} + (1 - f_{a(s)}) f_s + f_{a(d)} + (1 - f_{a(d)}) f_d] / 2 \quad \text{Ballou's formula}$$



Objectives

To determine the validity of Ballou's formula and **propose a new method for an unbiased estimation of ancestral Inbreeding**

Simulation model

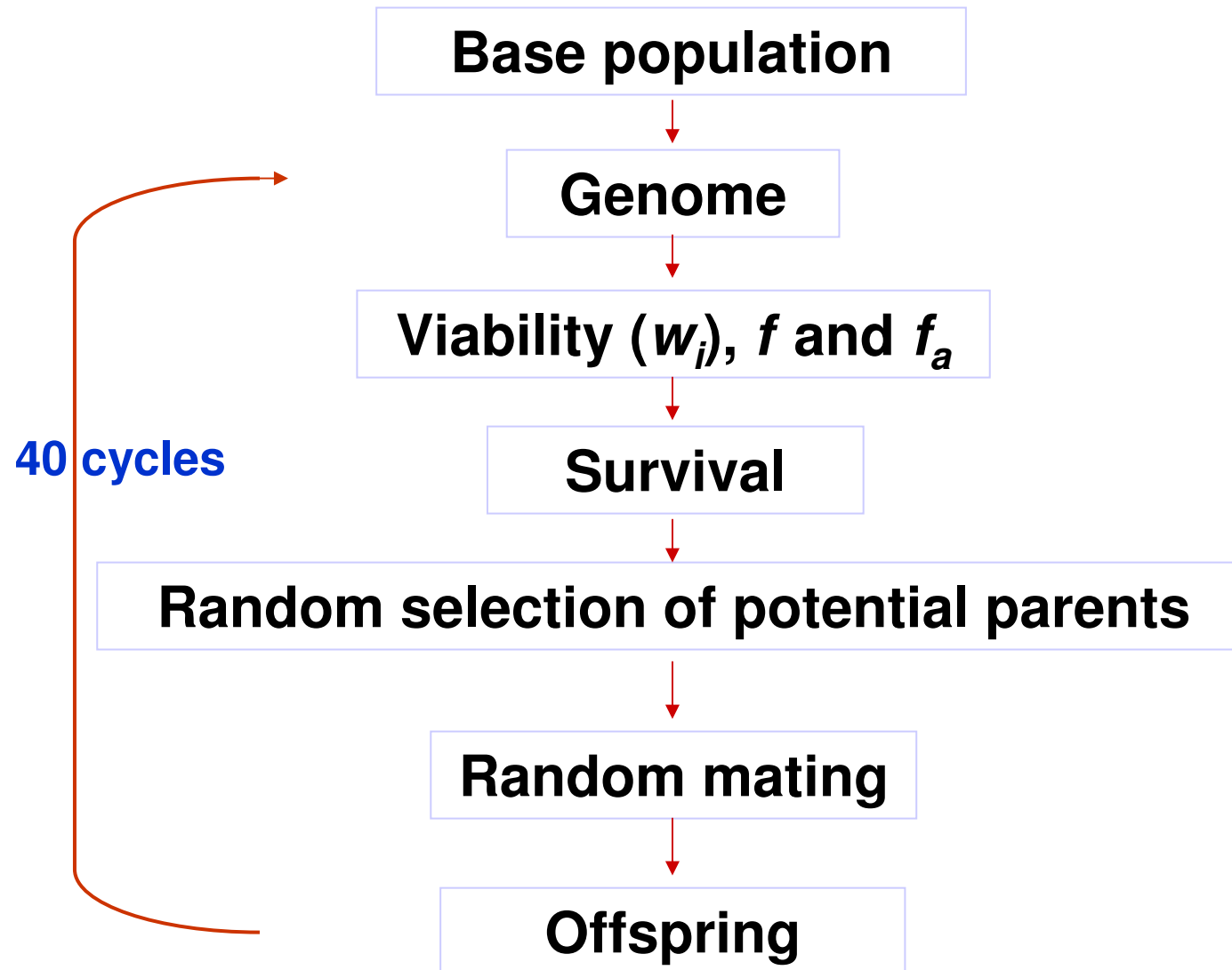
- Population size: 50, 100, 200 with sex ratio 1:2
- Genome: 500 unlinked loci

genotype	relative viability (w)
AA	1
Aa	$1 - hs$
aa	$1 - s$

h is the dominance coefficient of a

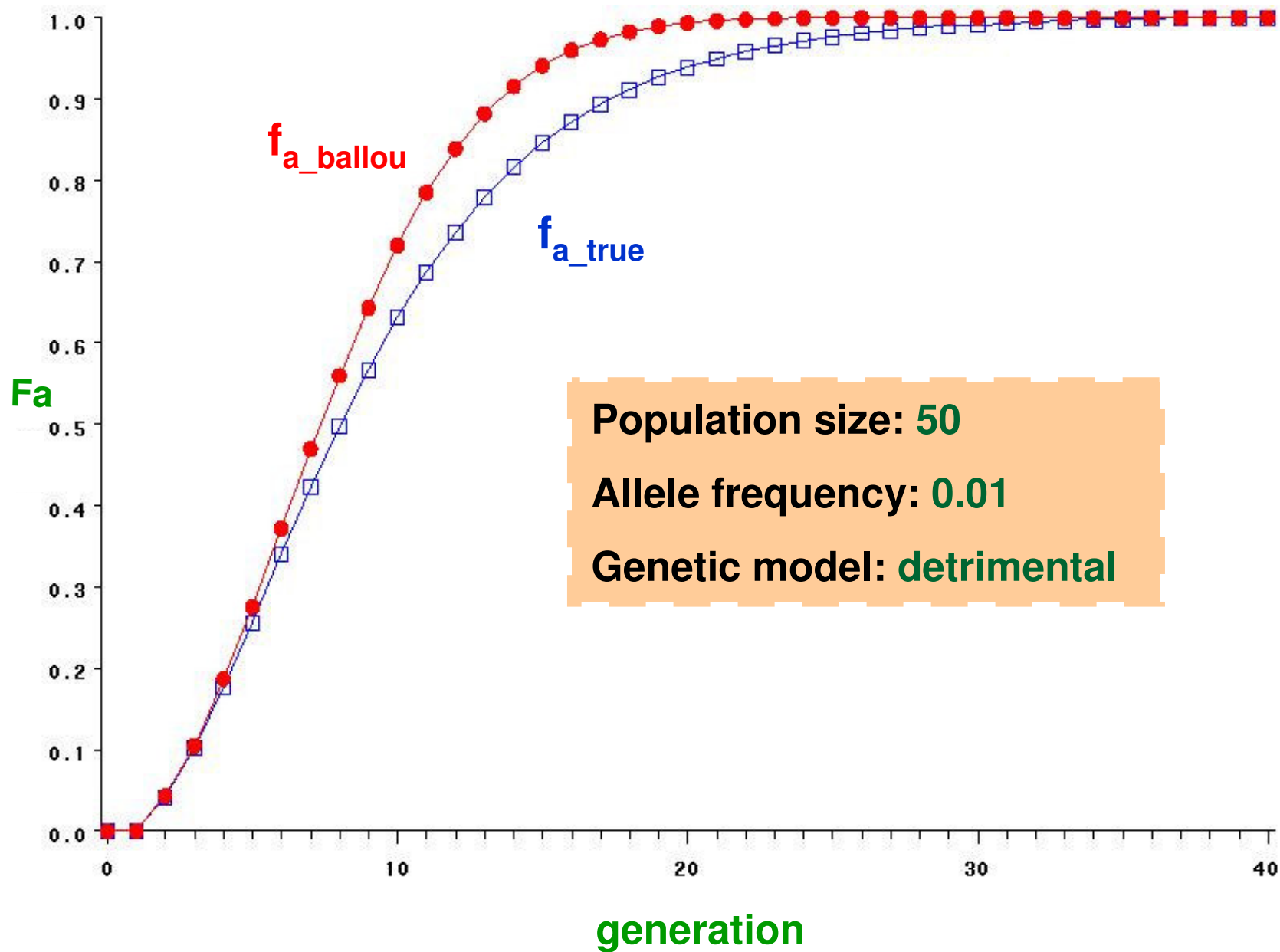
s is the coefficient of selective against aa

Simulation procedure



Ancestral inbreeding coefficients (f_a)

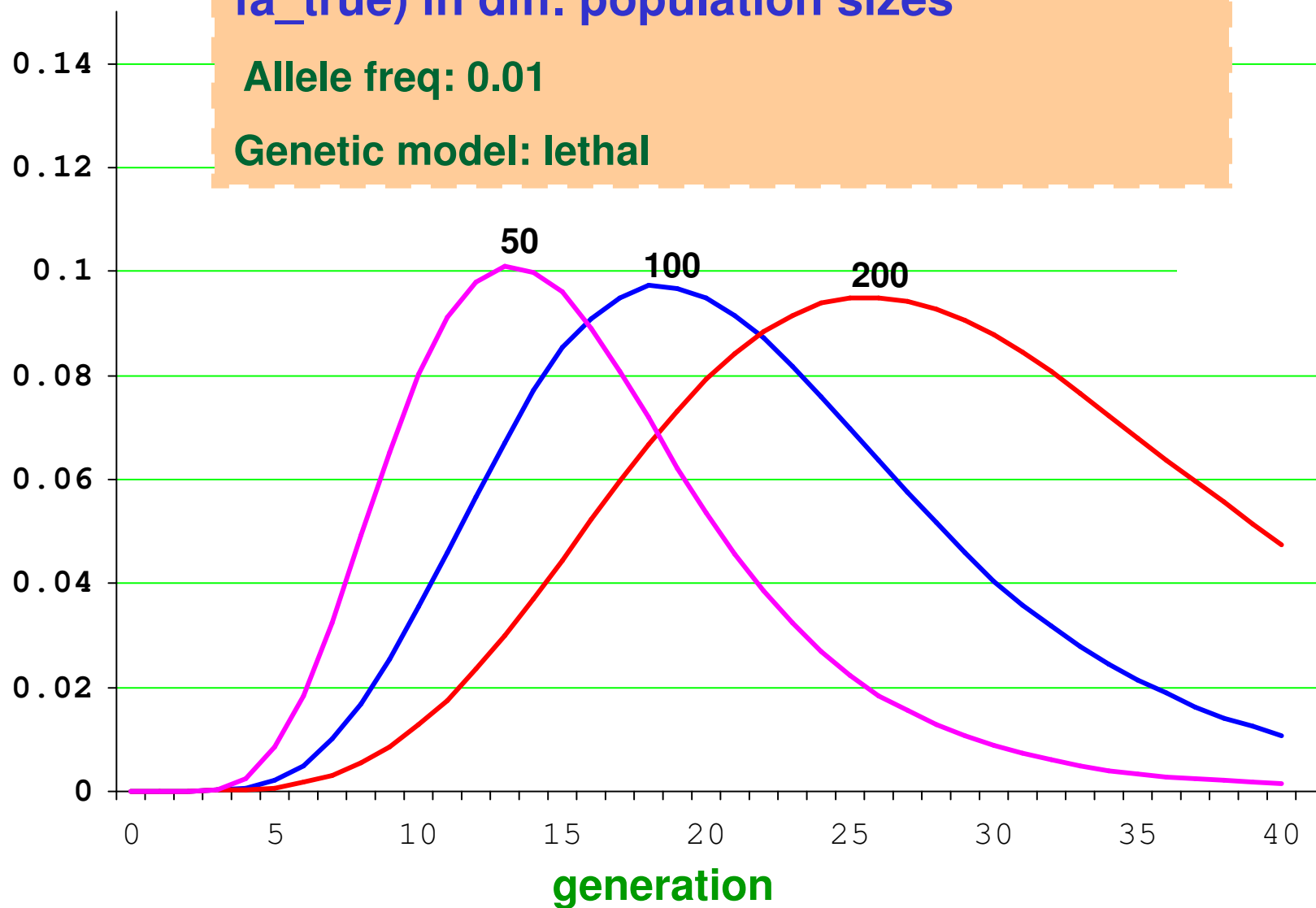
- f_{a-true} : true proportion of alleles of an individual that has undergone inbreeding in the past
- $f_{a-Ballou}$: f_a calculated by Ballou's formula
- $f_{a-genedrop}$: f_a estimated by gene dropping method



Degree of overestimation (Ballou's coeff. – fa_true) in diff. population sizes

Allele freq: 0.01

Genetic model: lethal



According to Ballou, f_a is the part of individual's genome that has undergone IBD in the past

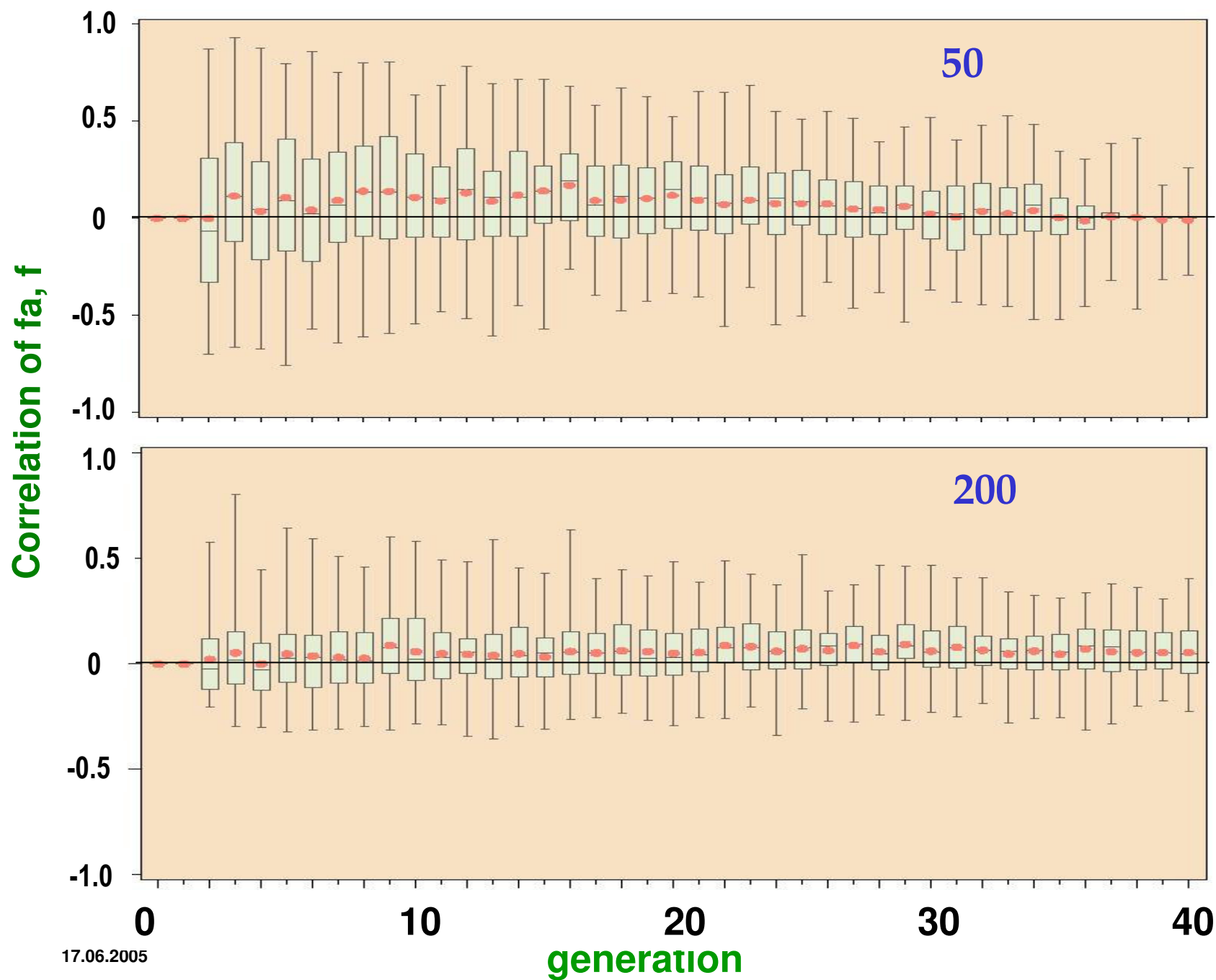


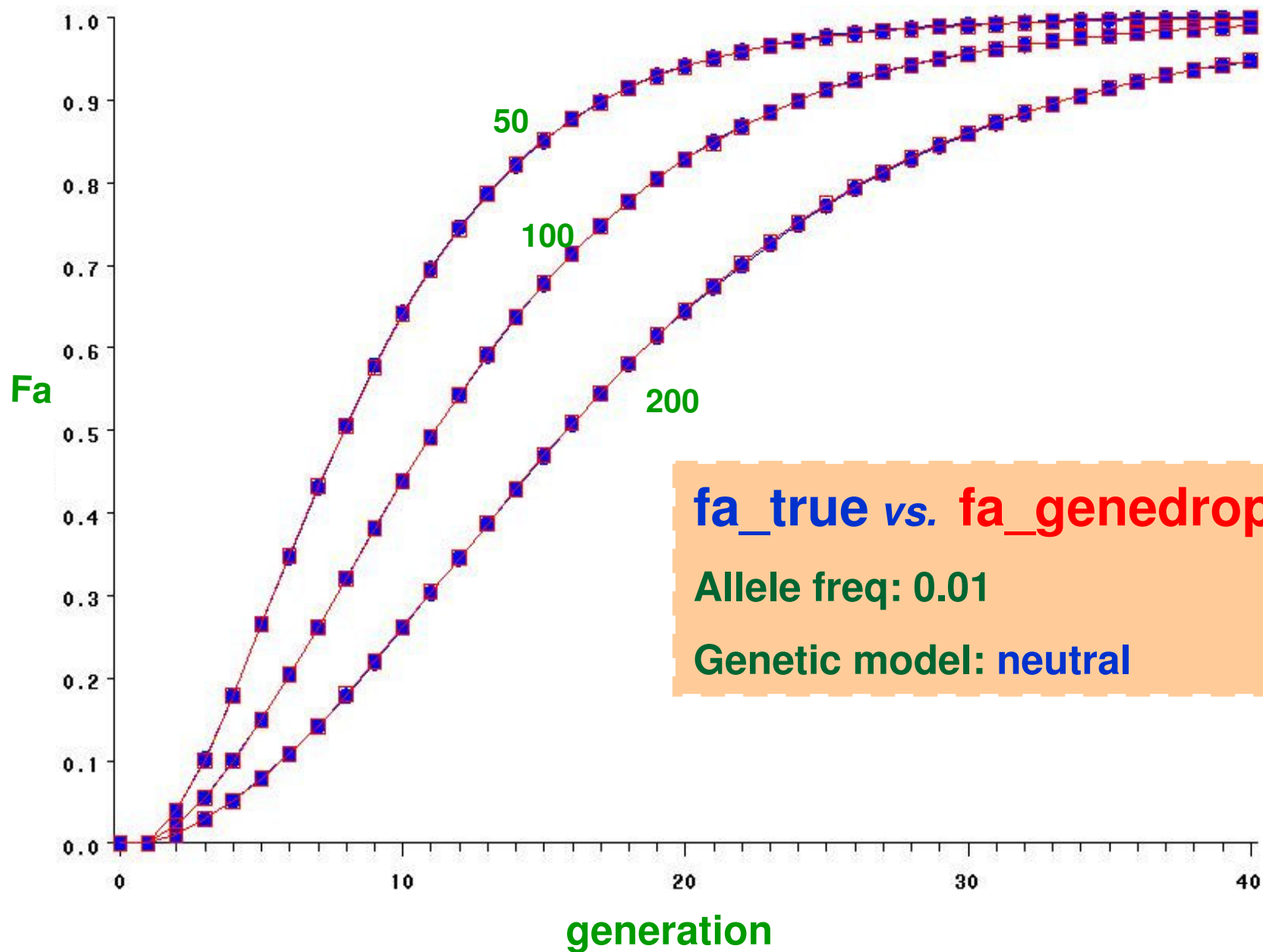
$$f_a = [(f_{a(s)} \cup f_s) + (f_{a(d)} \cup f_d)] / 2$$

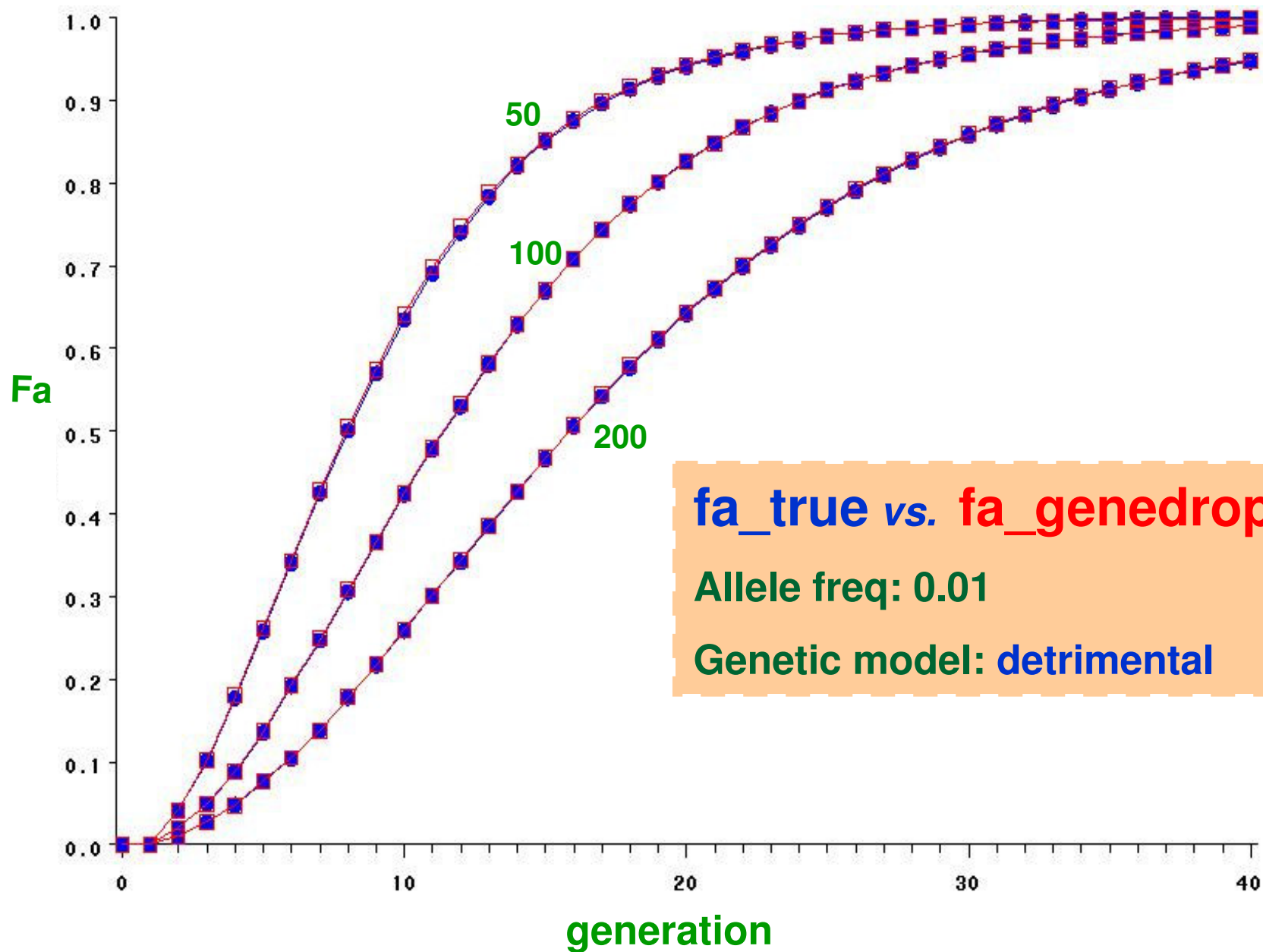
$$f_a = [f_{a(s)} + f_s - f_{a(s)} \cap f_s + f_{a(d)} + f_d - f_{a(d)} \cap f_d] / 2$$

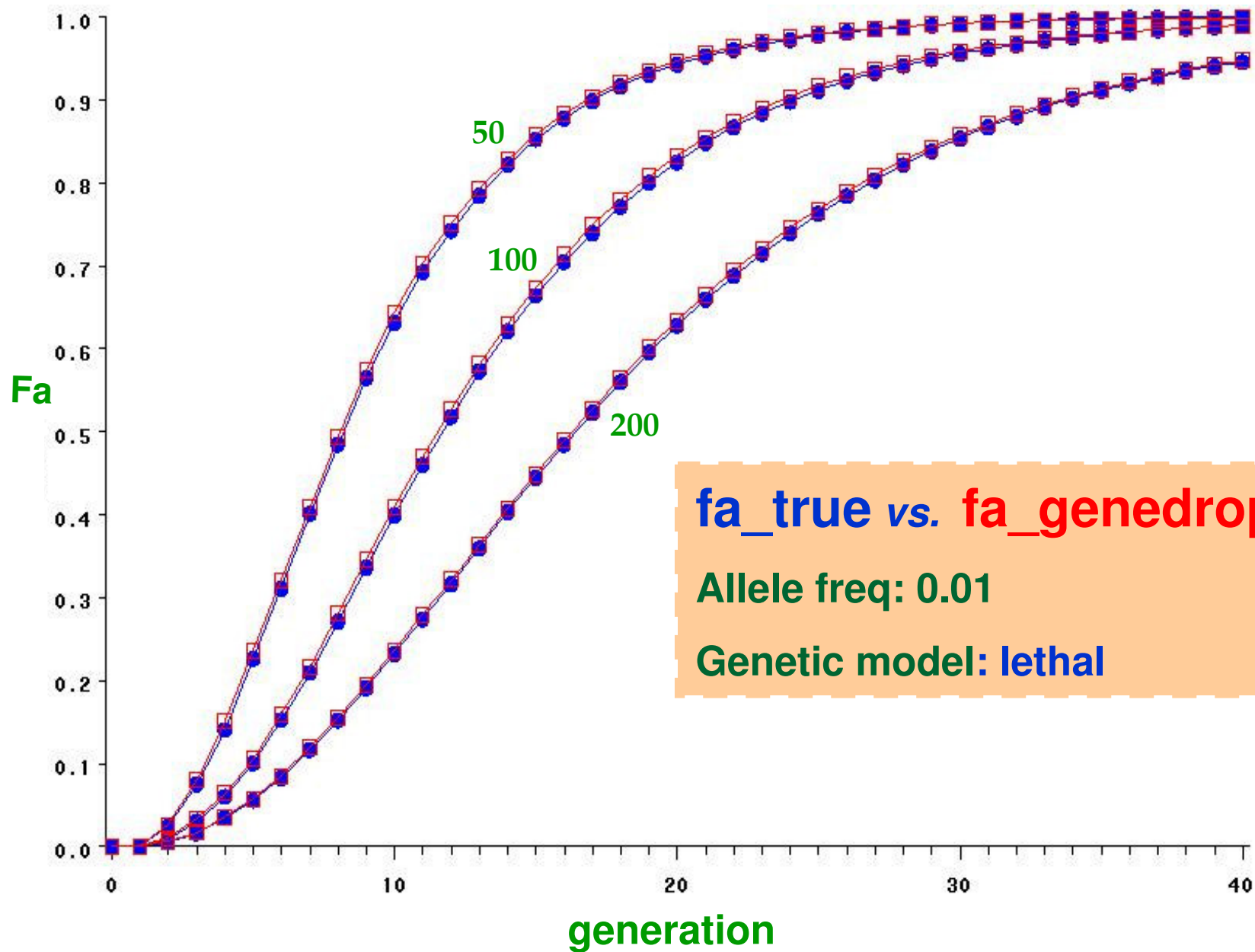
$$\begin{aligned} \Pr(f_{a(s)} \cap f_s) &= \Pr(f_{a(s)} | f_s) * \Pr(f_s) \\ &= \Pr(f_s | f_{a(s)}) * \Pr(f_{a(s)}) \quad \left. \vphantom{\Pr(f_{a(s)} \cap f_s)} \right\} \dots \text{dependent} \\ &= \Pr(f_{a(s)}) * \Pr(f_s) \quad \dots \text{independent} \end{aligned}$$

$$f_a = [f_{a(s)} + f_s - f_{a(s)} f_s + f_{a(d)} + f_d - f_{a(d)} f_d] / 2 \quad \text{Ballou's formula}$$









Conclusions

- Ballou's formula overestimated true ancestral inbreeding in all scenarios, because f_a and f are not independent.
- Overestimation was not influenced by initial allele frequency and the genetic model.
- Overestimation occurred earlier in smaller populations and reached higher values.

Conclusions

- **The gene dropping method provided unbiased estimates for ancestral inbreeding in a neutral or a detrimental allele model but marginally biased estimates in a lethal allele model.**

Thank you for your attention !!



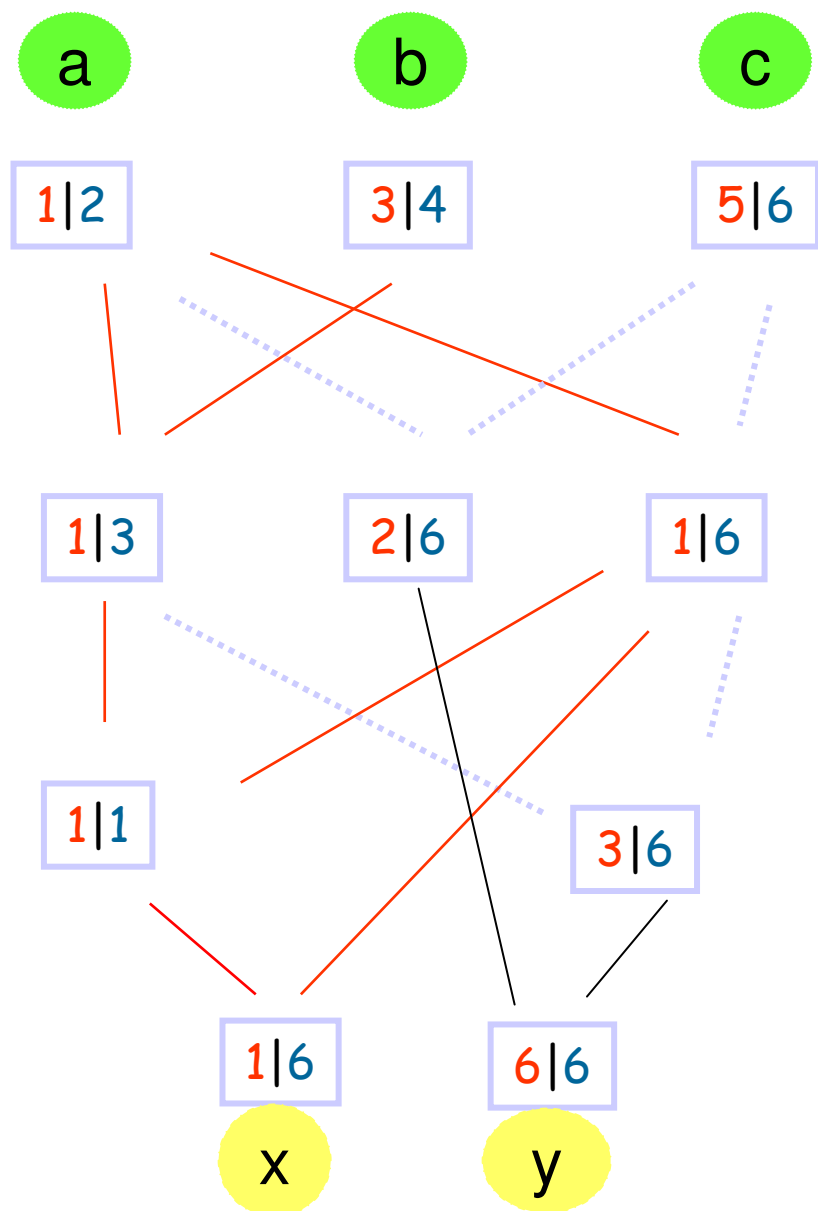
Background

Ancestral inbreeding coefficient (f_a)

$$f_a = [f_{a(s)} + (1 - f_{a(s)}) f_s + f_{a(d)} + (1 - f_{a(d)}) f_d] / 2 \quad \text{Ballou's formula}$$

$$f_a = [f_{a(s)} + f_s - f_{a(s)} f_s + f_{a(d)} + f_d - f_{a(d)} f_d] / 2$$

- f_a : the cumulative proportion of an individual's genome that has been previously exposed to inbreeding in its ancestors
- f : inbreeding coefficient



$f_{a\text{-genedrop}}$:
fa estimated by
gene dropping
method

$$= \frac{\text{\# alleles undergone IBD in the past at least once}}{\text{\# run} * 2}$$

run 1; $f_{a(x)} = 1/(1 * 2) = 0.5$

$f_{a(y)} = 0/(1 * 2) = 0$