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Session 1 – Presentation number 5 – Abstract number 3853

Deterministic and stochastic prediction of the evolution of QTL genotype frequencies with overlapping generations and finite population size

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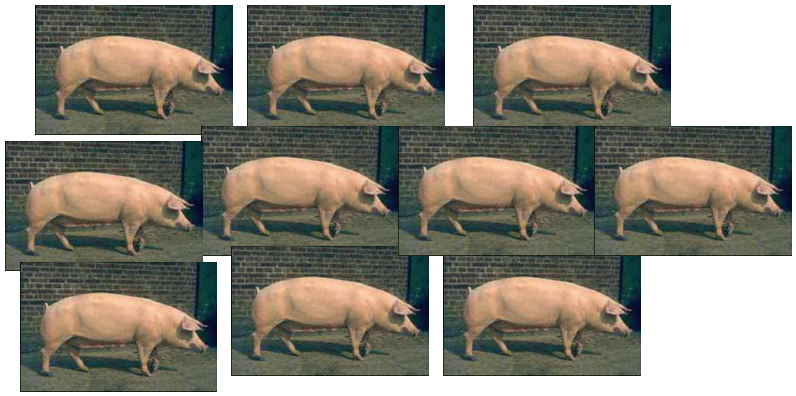
Introduction

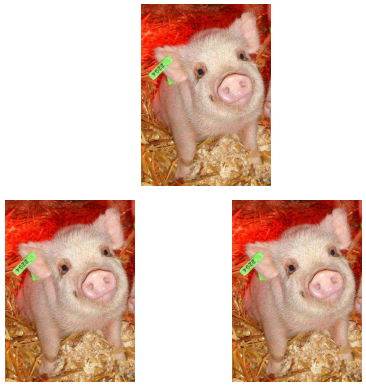
- More and more Quantitative Trait Loci (QTL) precisely localized
- Even some genes known
- QTL mapping not done in every breed
- Genes underlying a quantitative variation in 2 breeds may be used for Marker (or Gene) Assisted Selection

German Landrace (Herdbook sows(2006) : ~ 24000)

KIT-Gene, growth genes, feed conversion,…



Göttingen minipig (<1200 sows)



Introduction

- Further step: prediction of the evolution of the frequency of the favorable mutation in the population

- Main streams:
  - Optimum contribution selection
  - Optimal control approach

Introduction

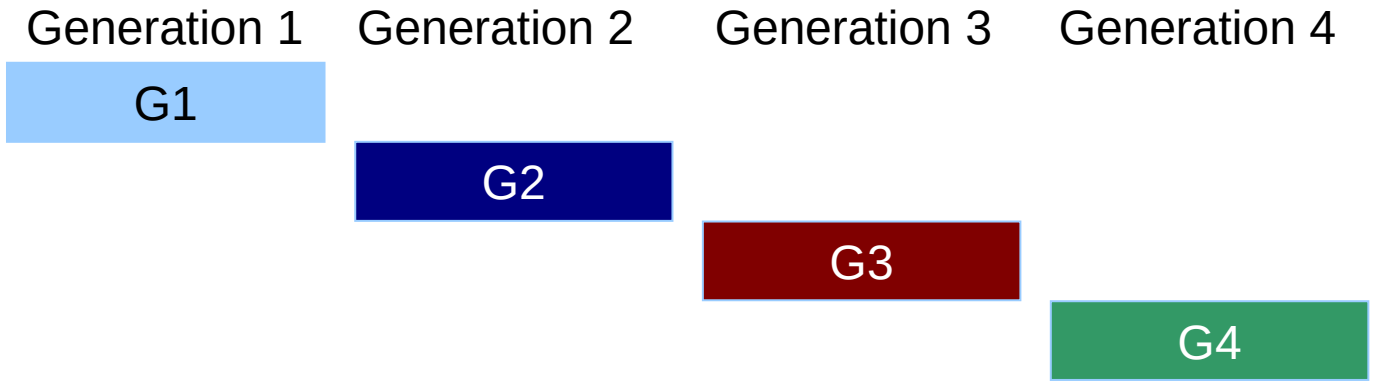
- Further step: prediction of the evolution of the frequency of the favourable mutation in the population

- 2 main streams:
  - Optimum contribution selection
  - Optimal control approach

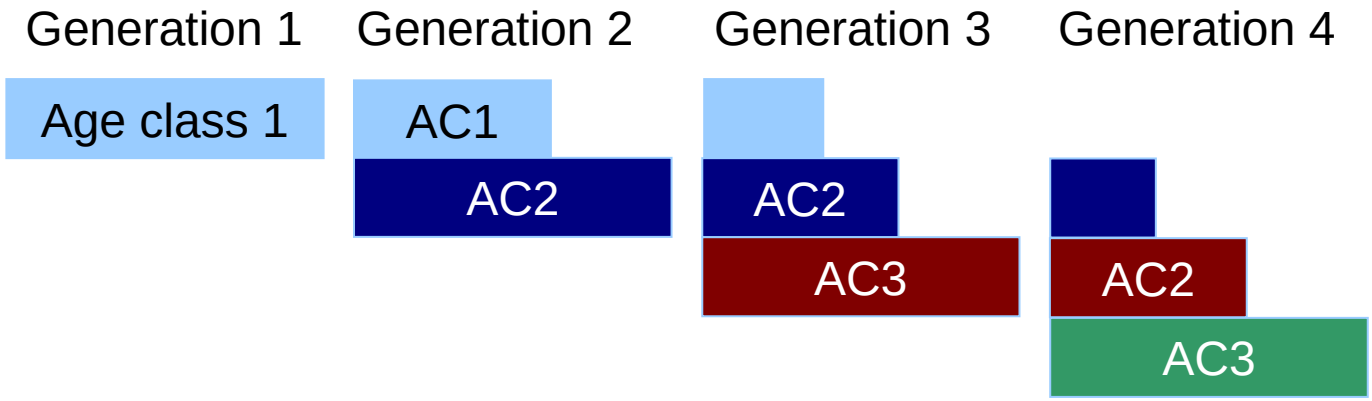
⇒ Method of Chakraborty et al. (2002)

Introduction

- Method initially for discrete generations



- Here enlarged to overlapping generations, i.e. several generations in the population



Aim of the study

	Deterministic	Simulation
Variability	-	+
Speed	+ +	±
Population size	-	+
Variable polygenic variance	-	+
Generality	+ +	-

Material and methods

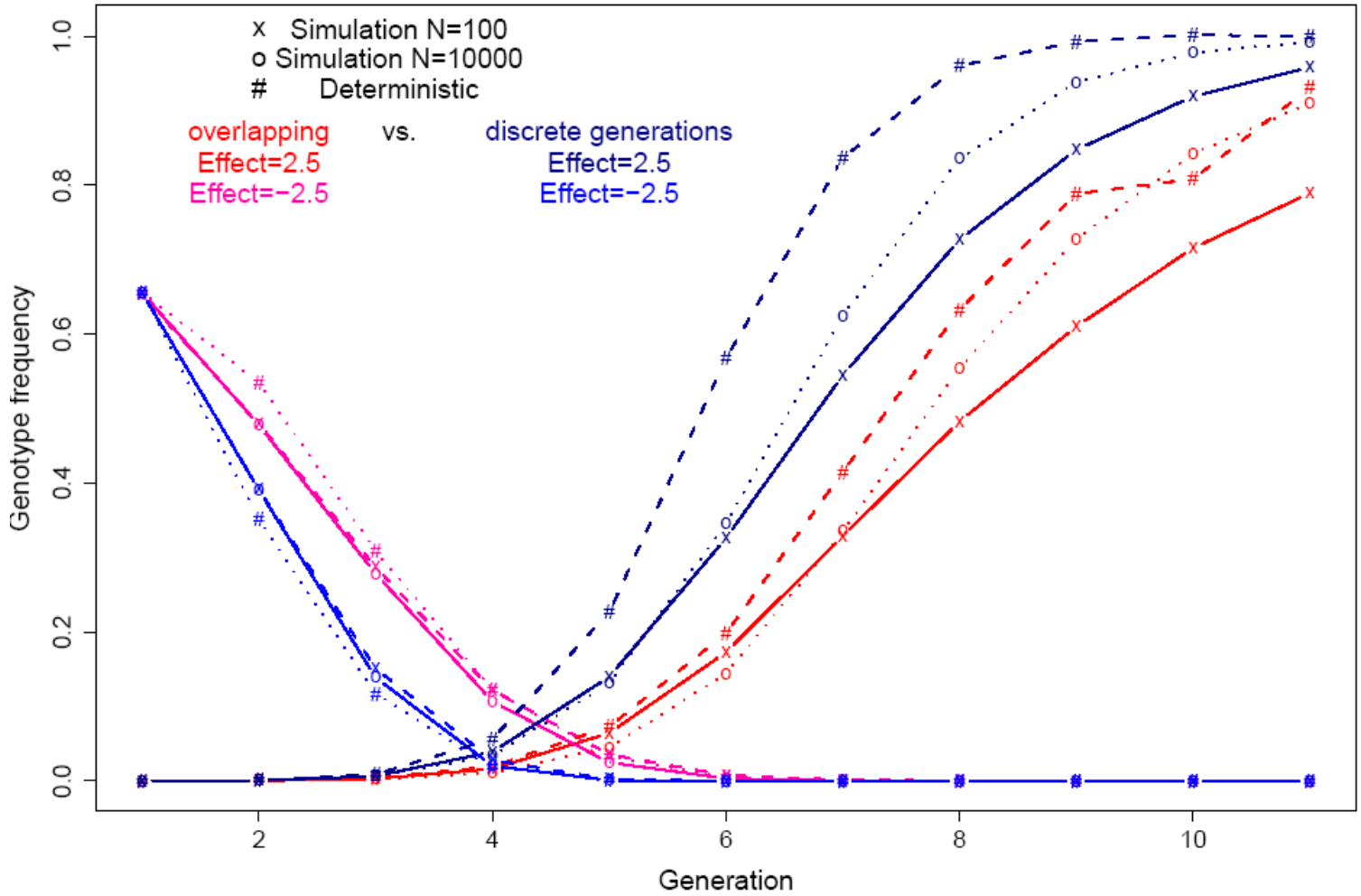
- Selection on the sum of the QTL and the polygenic values
- Discrete and overlapping generations (3 generations in the population)
- Method of Chakraborty et al. adapted to overlapping generations
- Simulations :
  - Populations of 100 or 10‘000 individuals

Material and methods

- Overlapping generations: repartition of the age classes: 0.7 / 0.2 / 0.1
- 2 QTL linked (d = 5cM)
- Additive effects, $a_1=1.0\ \sigma_P$, $a_2=1.5\ \sigma_P$
- Initial HW equilibrium,
  Initial frequency (+ +) = 1%

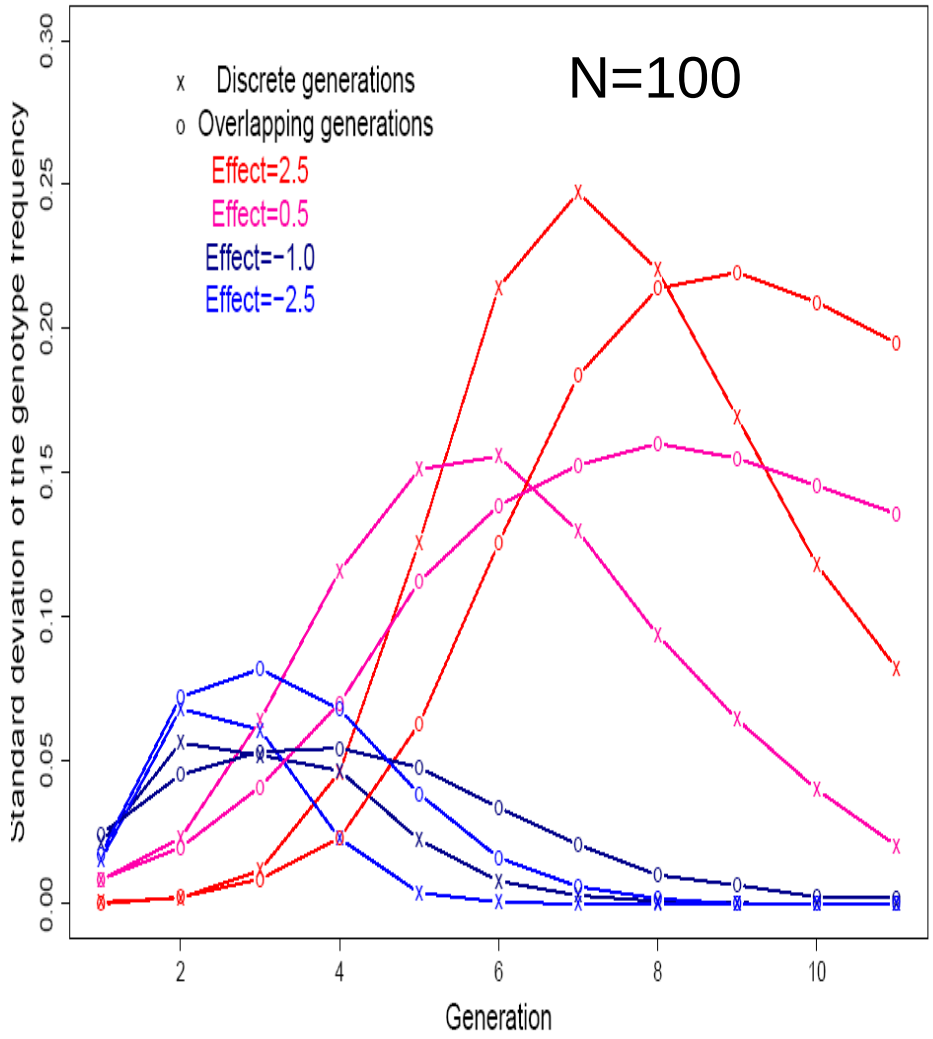
Results

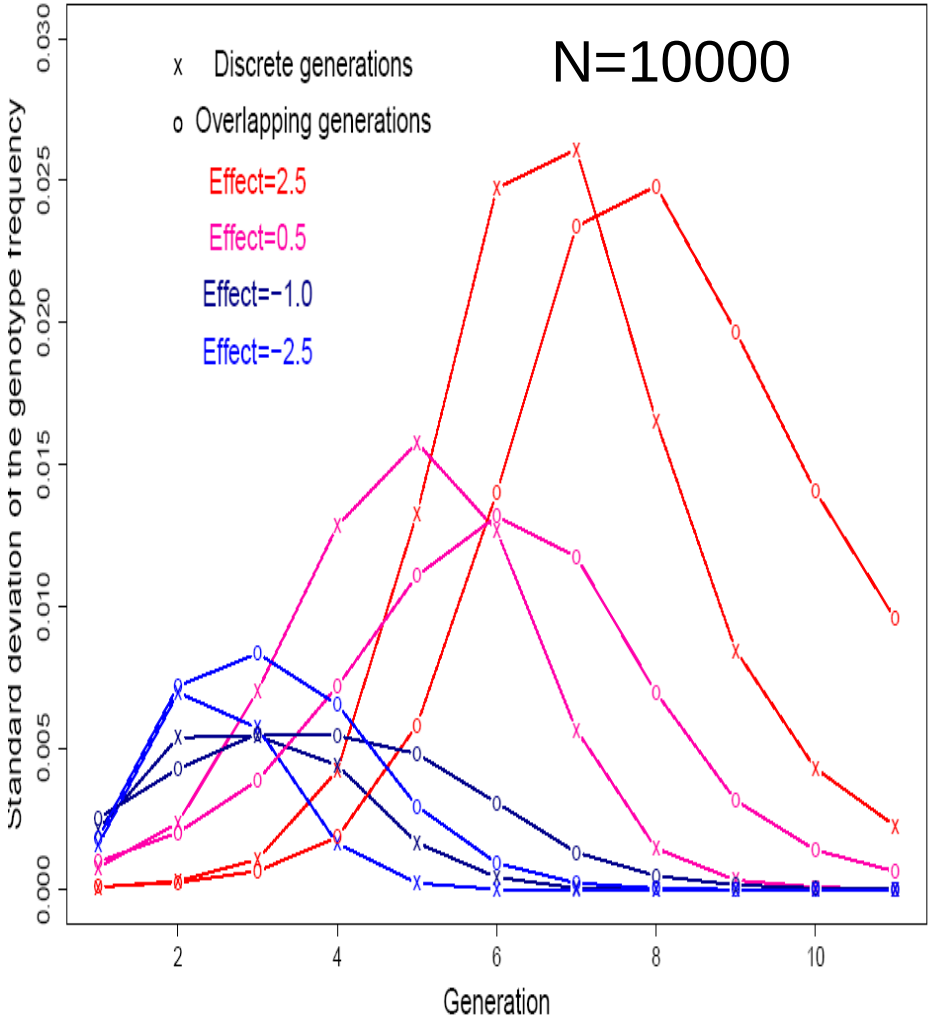
Genotype frequencies



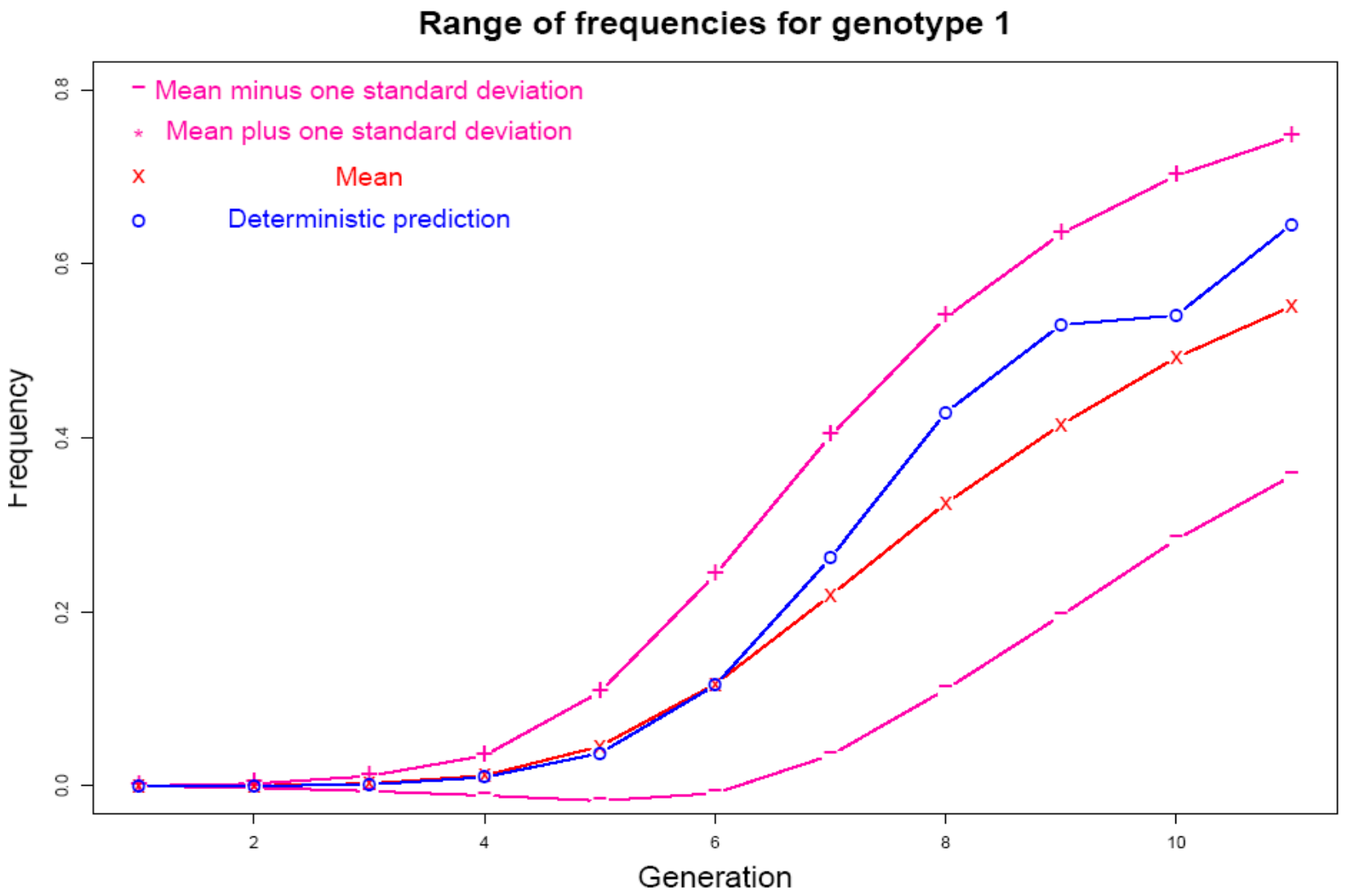
Results

Variability of the genotype frequencies





Results


Range of frequencies for genotype 1
Mean minus one standard deviation
Mean plus one standard deviation
Mean
Deterministic prediction
Frequency
0.0
0.2
0.4
0.6
0.8
2
4
6
8
10
Generation

Conclusions

- Slight overestimation for both discrete and overlapping generations
- Still suitable as an approximation even for small population sizes
- Standard deviation higher with small population sizes → may be good to account for it
- Limit: no constraint on the inbreeding
- Further steps
  - Description of the variability
  - Inclusion in whole breeding programs

Acknowledgments

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HANNOVERANER VERBAND

Verband hannoverscher Warmblutzüchter

HOLSTEINER

Verband der Züchter des Holsteiner Pferdes e.V.

Trakehner Verband

Westfälisches Pferdestammbuch e.V.

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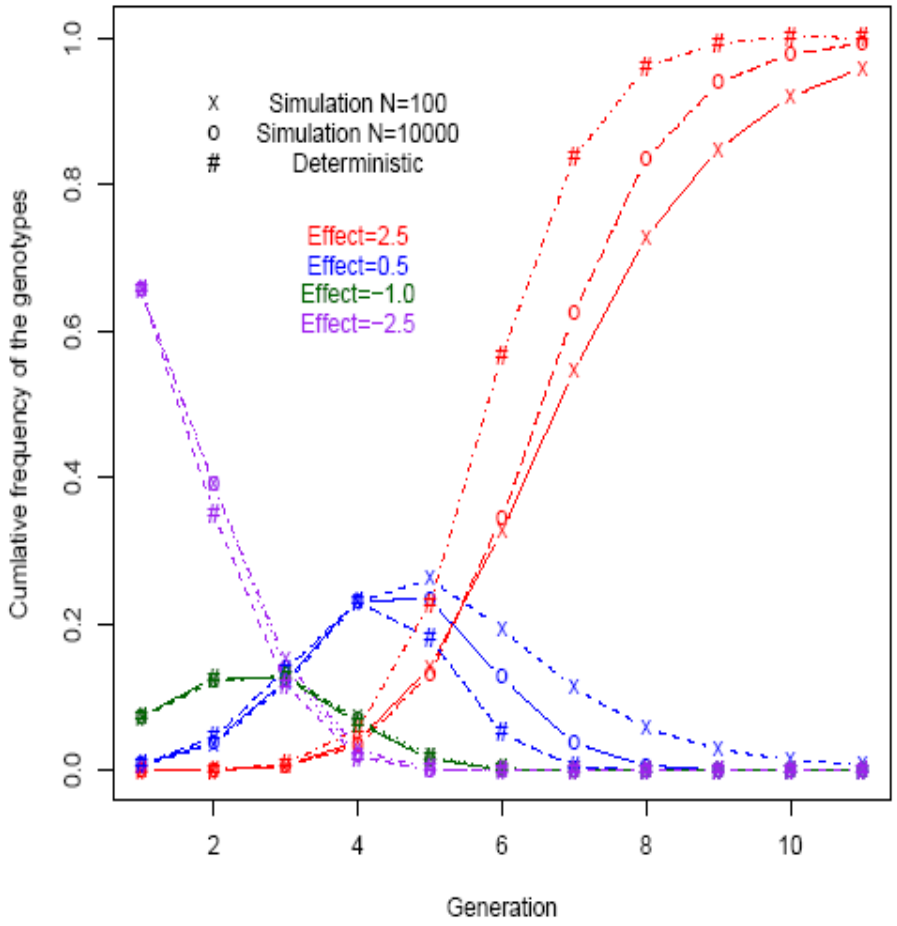
Thank you for your attention !

Results

Discrete generations



Results

Overlapping generations