Facultad de Veterinaria
Universidad Zaragoza

QUANTITATIVE GENETICS LAB
Universidad Zaragoza

HLab

ROSLIN

Probabilistic breeder's equation for retrospective and prospective analyses

D. López-Carbonell, *I. Pocrnic, G. Gorjanc, L. Varona*

EAAP • WAAP • INTERBULL • 2023 • LYON • FRANCE
74th

Breeder's equation

- $\Delta G = i\ \sigma_{EBV} = i\ r\ \sigma_{TBV} = S_{TBV}$
- r = cor(TBV,EBV)

- This ΔG is salt of selecting the best animals (including their new Mendelian Samplings) in each generation

- A Mendelian Sampling Term (ϕ) is generated in each individual at each generation,

  but $\phi \sim N(0, \frac{1}{2}\ \sigma^2_{TBV})$

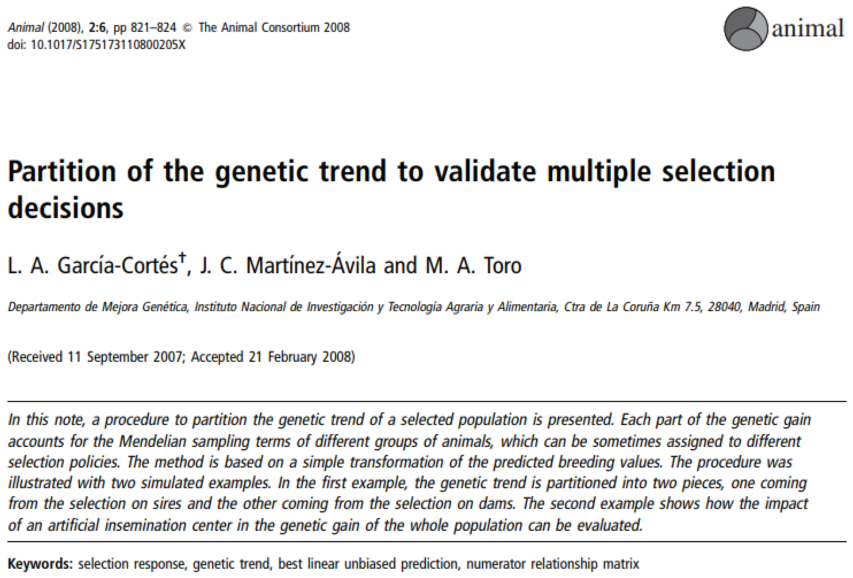
Genetic trends

- They are the **representation of the genetic gain** (ΔG) over time
- It is a **retrospective analysis** of the breeding program
- It can be partitioned to different paths of selection

Partitioning genetic trends

García-Cortés et al. (2008)

- **To establish the relevance of different paths of selection**
- $\hat{a} = \hat{a}_1 + \hat{a}_2 + \ldots + \hat{a}_n$
- $\hat{a}_i$ is the part of the breeding value that can be assigned to the group ‘i’



Animal (2008), **2:6**, pp 821–824 © The Animal Consortium 2008
doi: 10.1017/S175173110800205X

animal

Partition of the genetic trend to validate multiple selection decisions

L. A. García-Cortés†, J. C. Martínez-Ávila and M. A. Toro

Departamento de Mejora Genética, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Ctra de La Coruña Km 7.5, 28040, Madrid, Spain

(Received 11 September 2007; Accepted 21 February 2008)

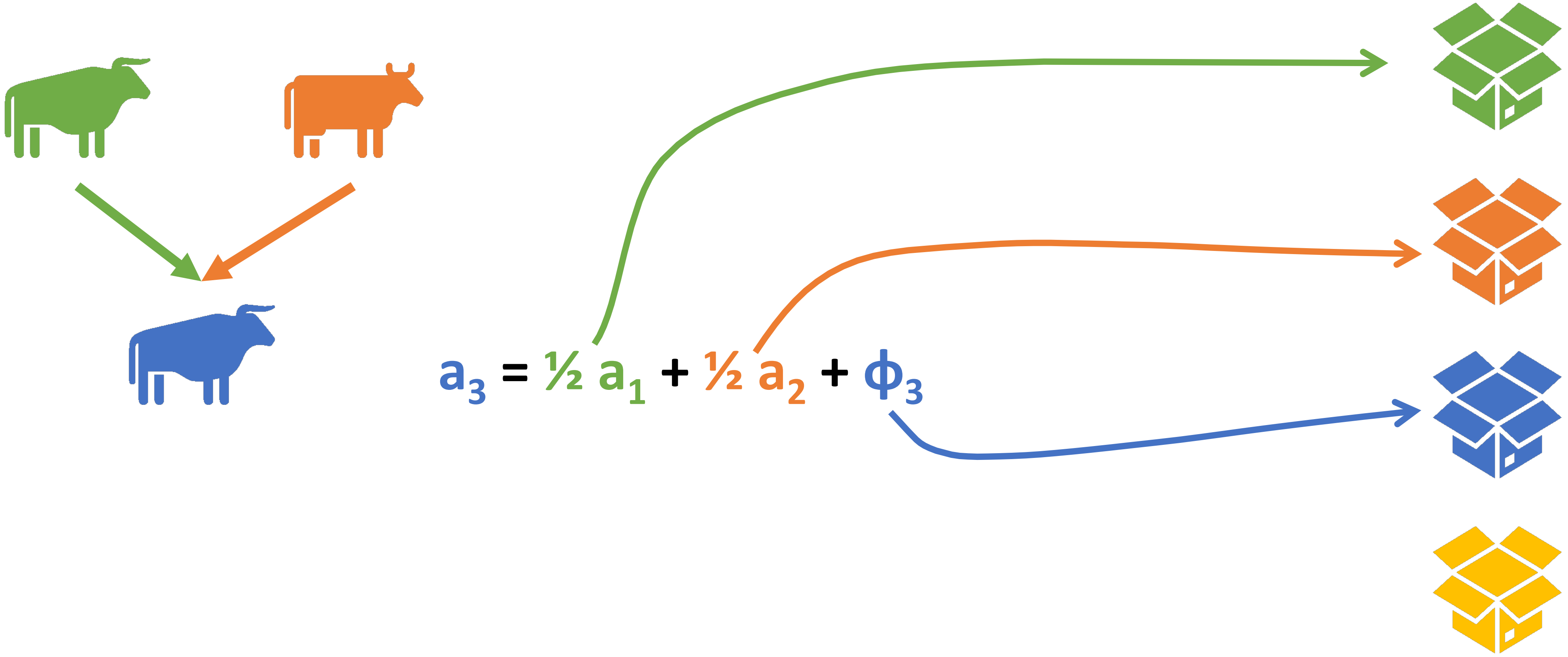
In this note, a procedure to partition the genetic trend of a selected population is presented. Each part of the genetic gain accounts for the Mendelian sampling terms of different groups of animals, which can be sometimes assigned to different selection policies. The method is based on a simple transformation of the predicted breeding values. The procedure was illustrated with two simulated examples. In the first example, the genetic trend is partitioned into two pieces, one coming from the selection on sires and the other coming from the selection on dams. The second example shows how the impact of an artificial insemination center in the genetic gain of the whole population can be evaluated.

Keywords: selection response, genetic trend, best linear unbiased prediction, numerator relationship matrix

Our objective: Probabilistic breeder’s equation analysis

- Applied to EBV
- Partition genetic trend
- Partitioning of the Breeder’s equation

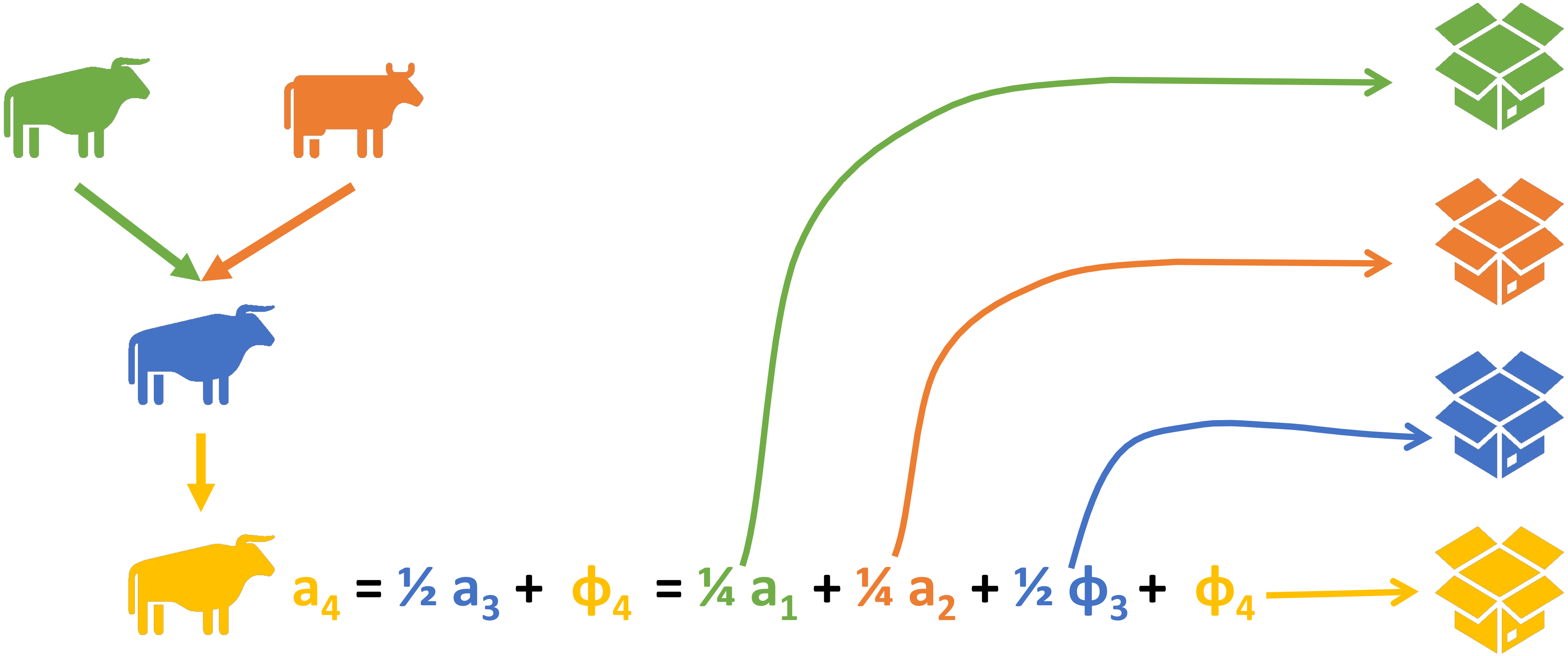
How?



$$a_3 = \tfrac{1}{2}\, a_1 + \tfrac{1}{2}\, a_2 + \phi_3$$

García-Cortés et al., 2008

How?



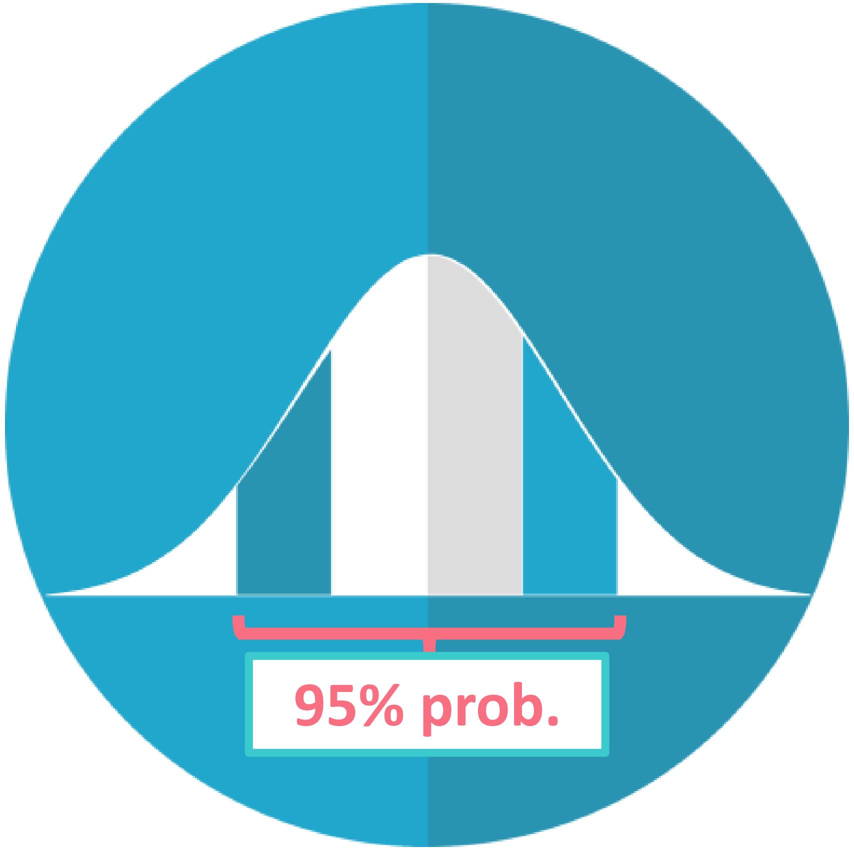
$$a_4 = \tfrac{1}{2} a_3 + \phi_4 = \tfrac{1}{4} a_1 + \tfrac{1}{4} a_2 + \tfrac{1}{2} \phi_3 + \phi_4$$

García-Cortés et al., 2008

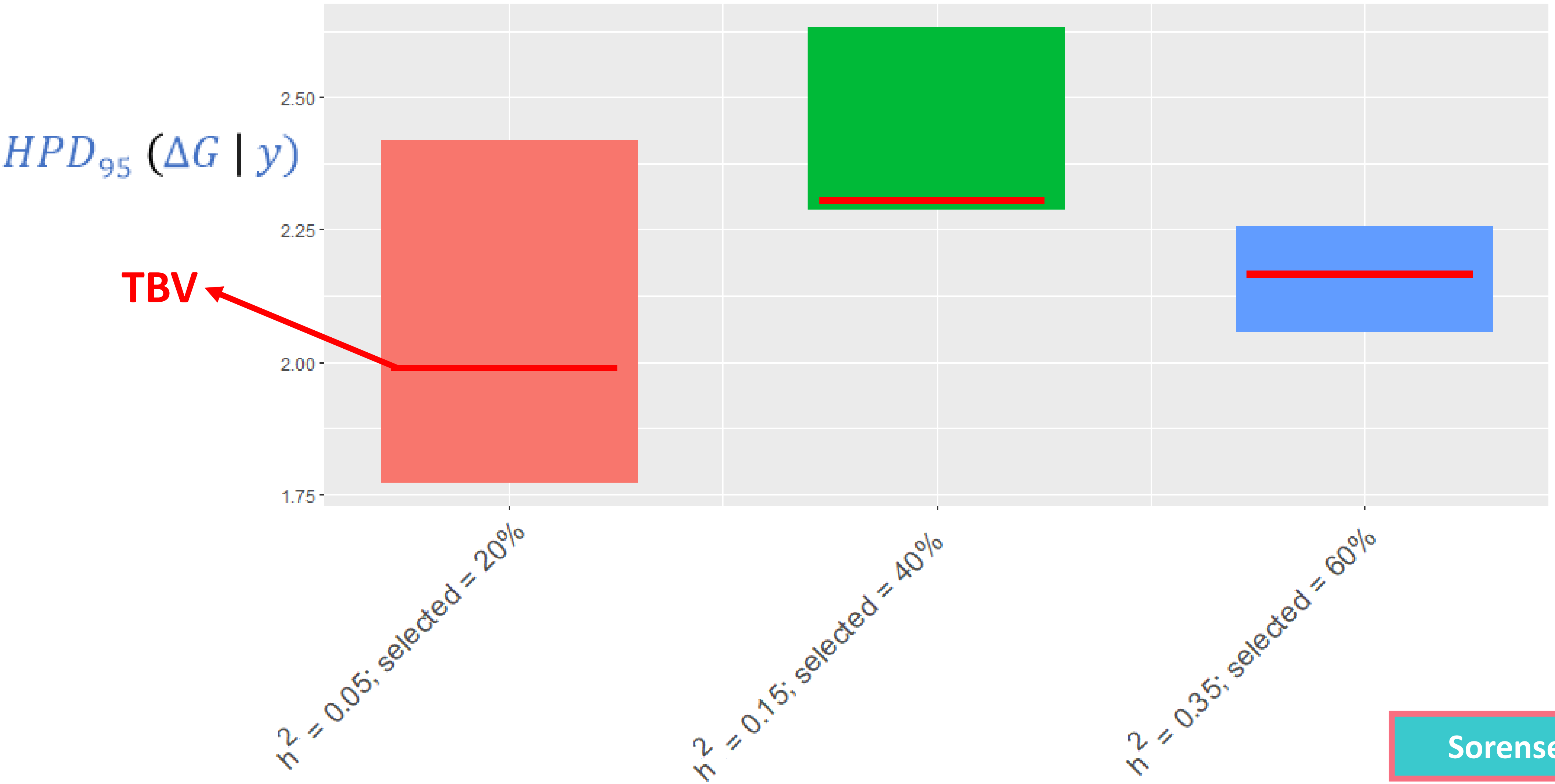
How?

- TM (Legarra et al., 2008) modified version

For each iteration!



First objective: Genetic gain analysis



TBV

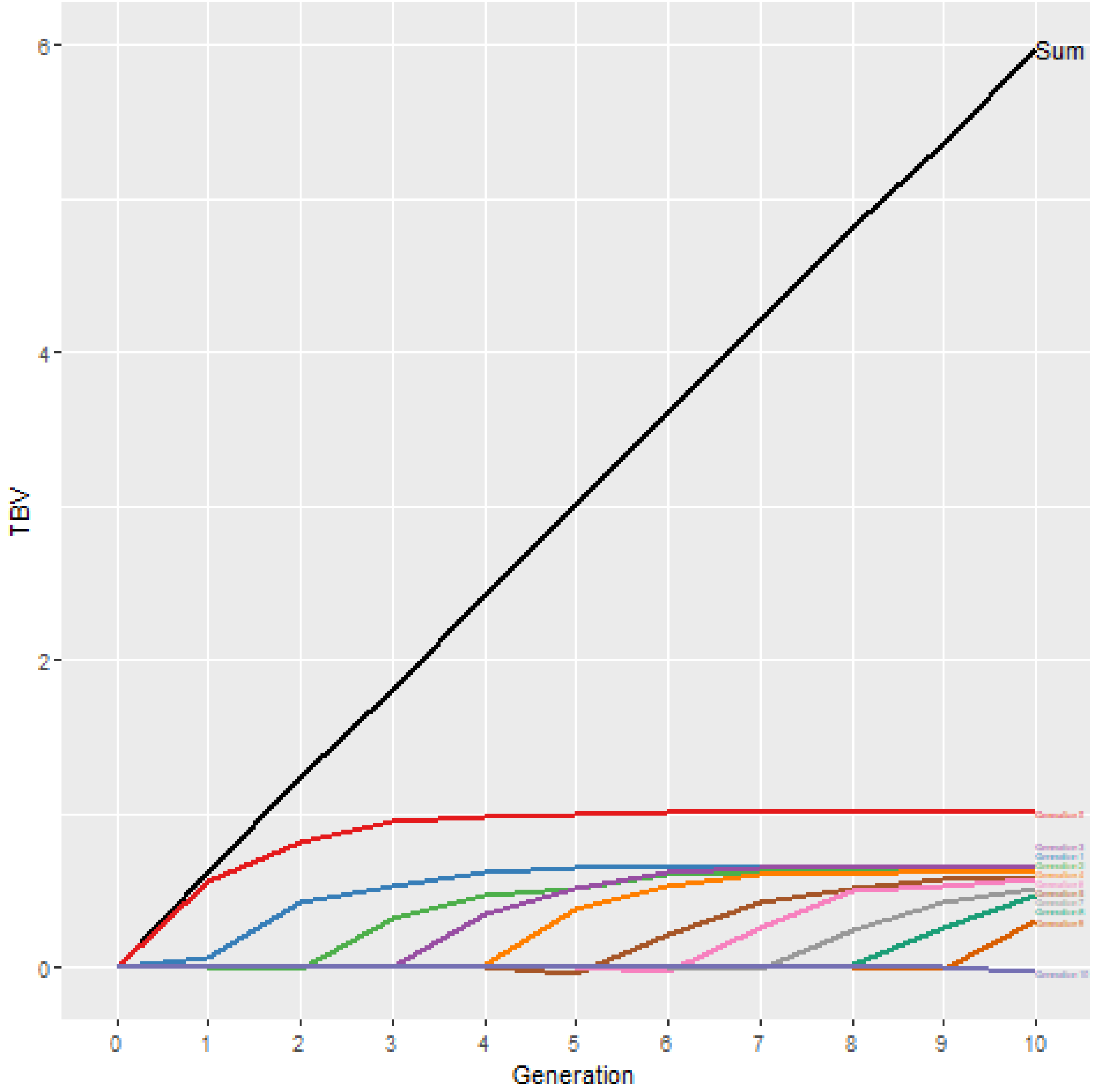
Sorensen et al., 1994

Simulation: AlphaSimR

- Generation 0: Founder population (500 males and 500 females)
- Generations 1-4: **Selection** of 100 males and 200 females **on phenotype**
- Generations 5-10 : **Selection** of 100 males and 200 females **on EBV**

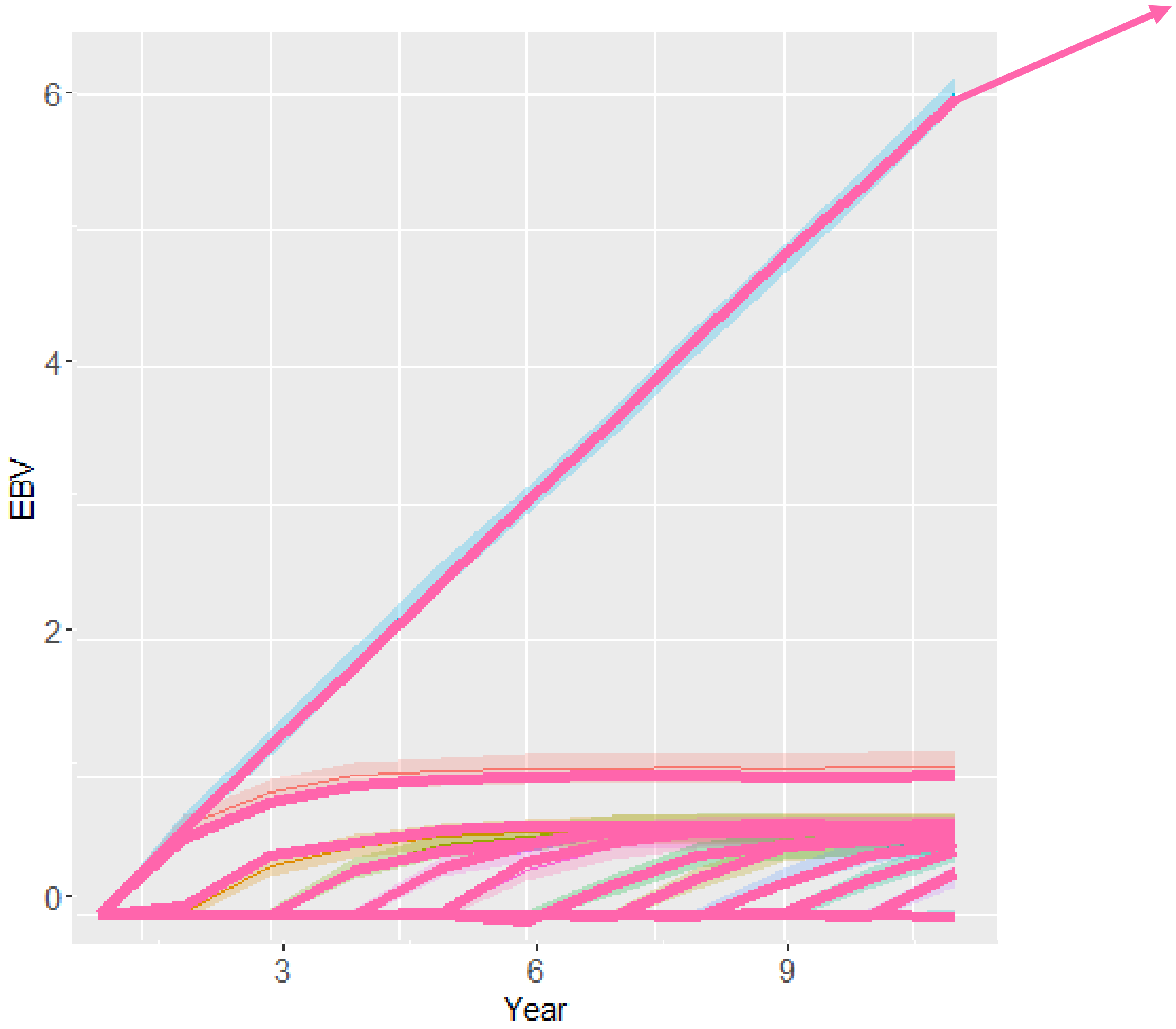
- Each generation 1,000 individuals are generated
- EBV calculated using TM software

Genetic trends



Genetic trends

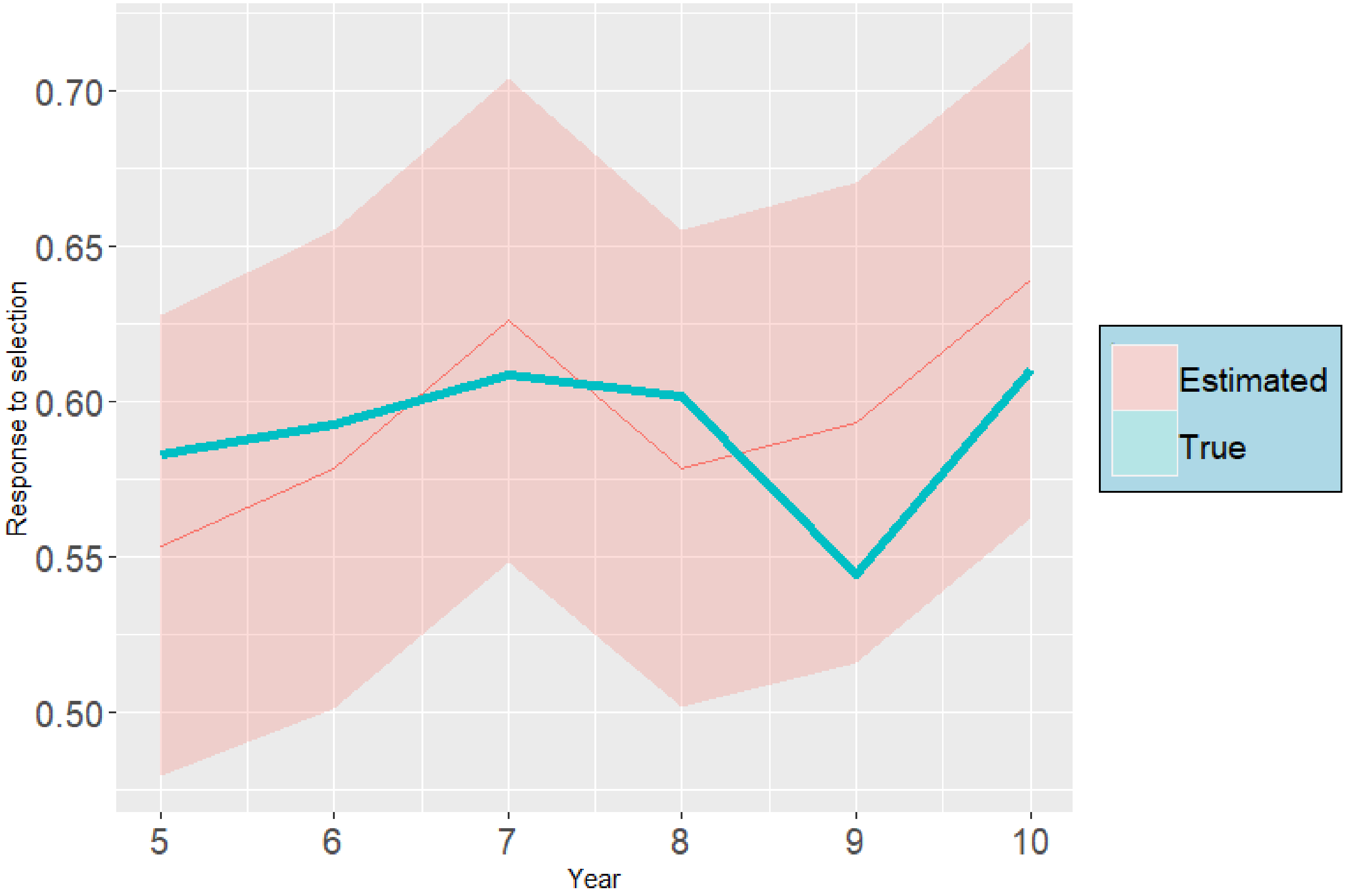
$_{95}(\mathit{Genetic\ trends}_{EBV} \mid y)$



TBV

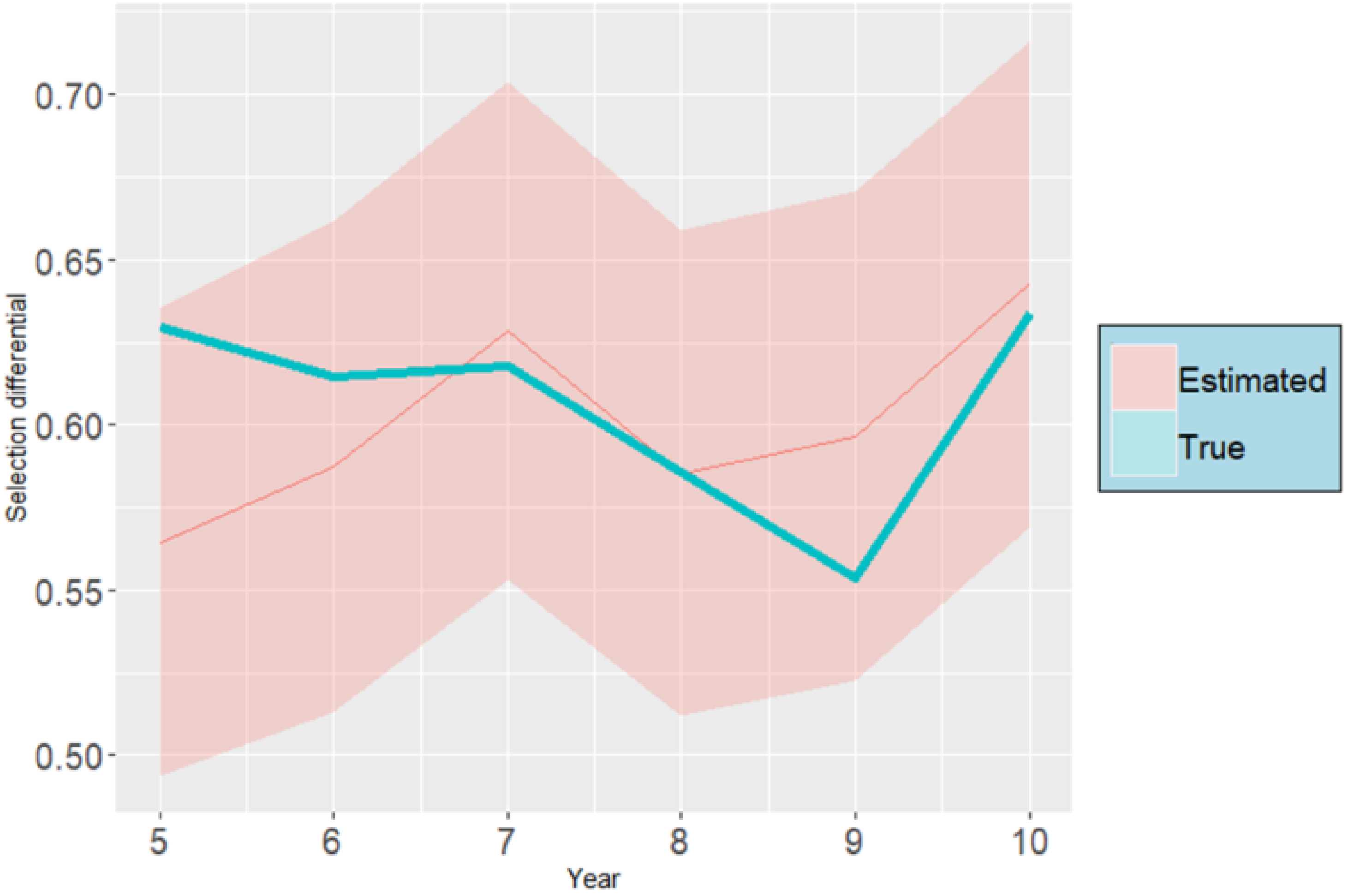
Breeder’s equation analysis:

$$\Delta G = \widehat{BV}_2 - \widehat{BV}_1$$



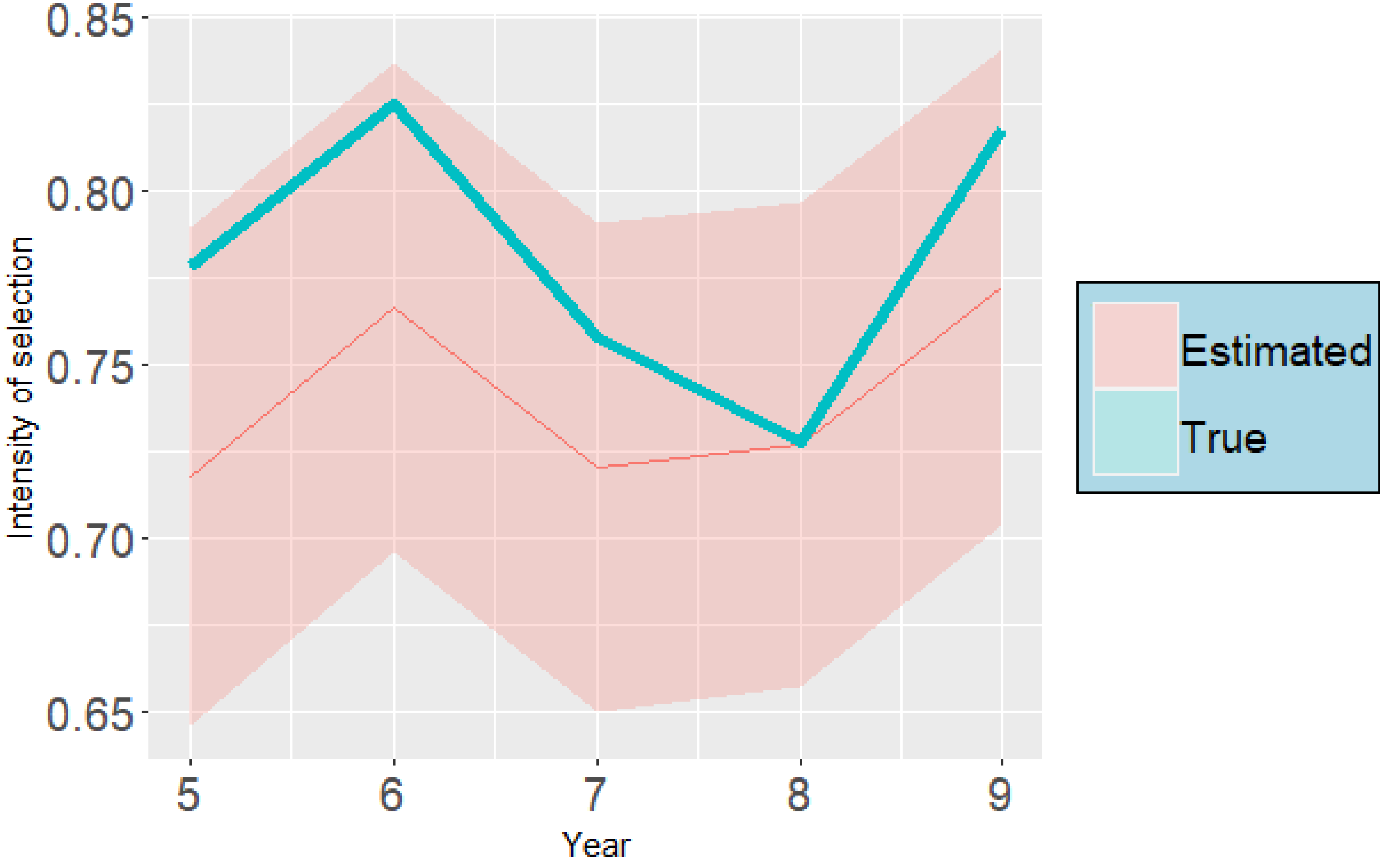
Breeder’s equation analysis:

$SelDiff = \widehat{BV_{S1}} - \widehat{BV}_1$



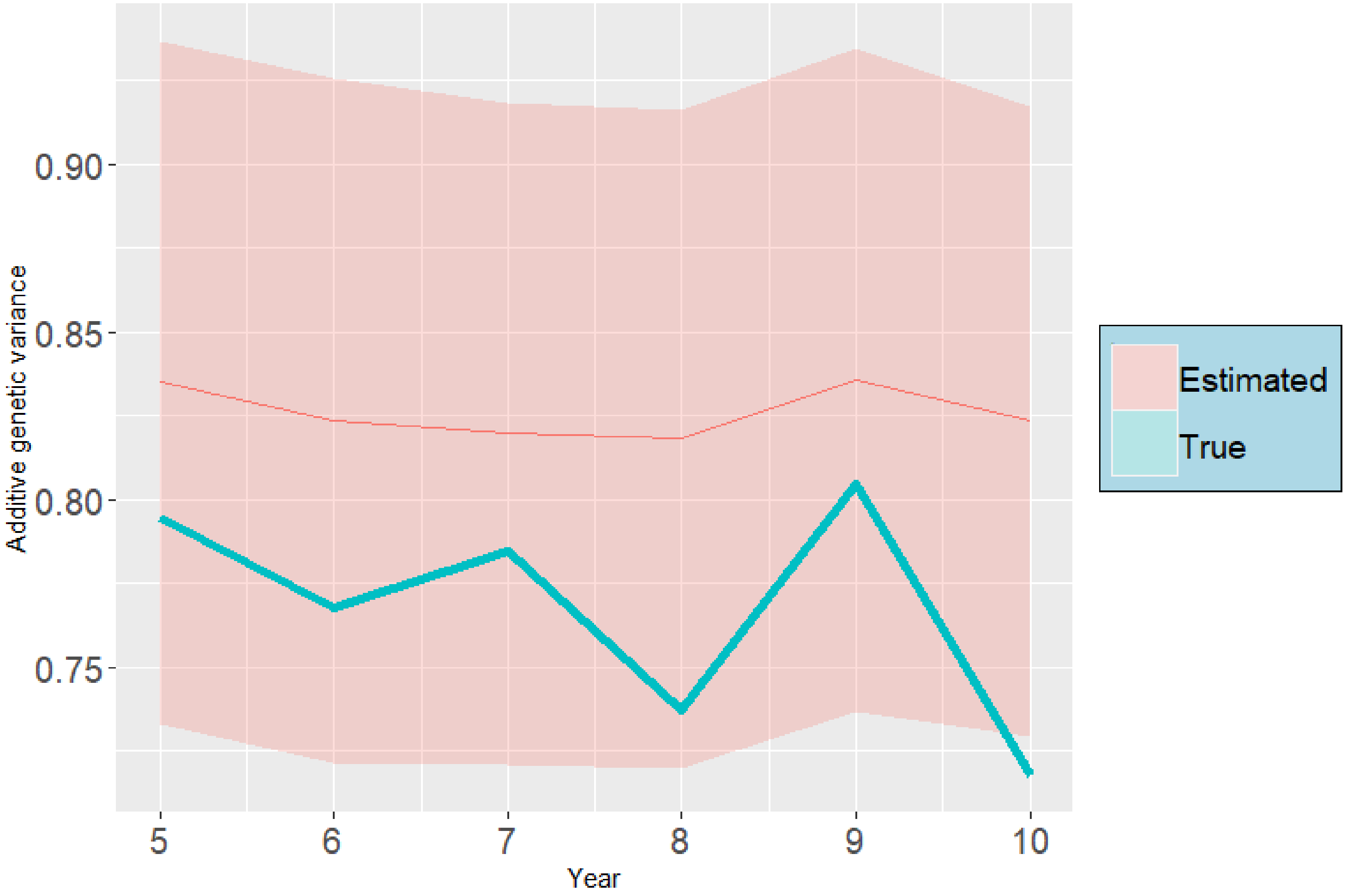
Breeder’s equation analysis:

$Intensity\ of\ selection$



Breeder's equation analysis:

Additive genetic variance of selection candidates

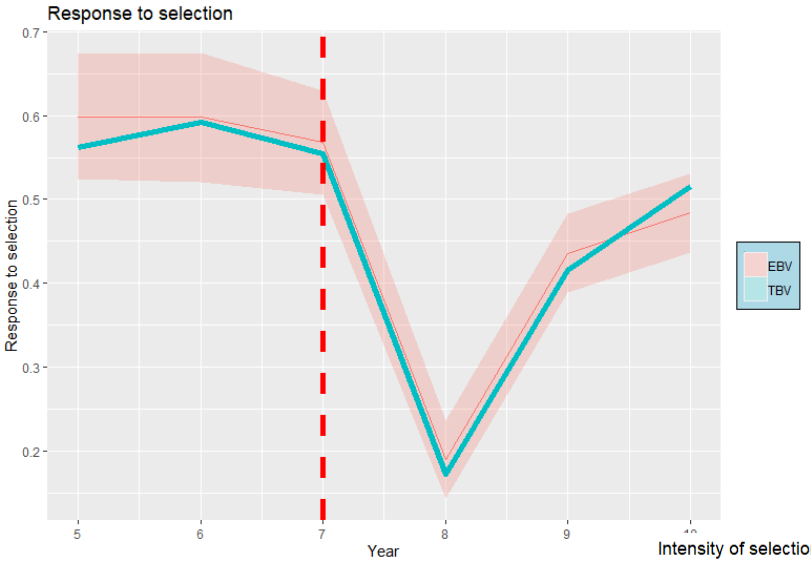


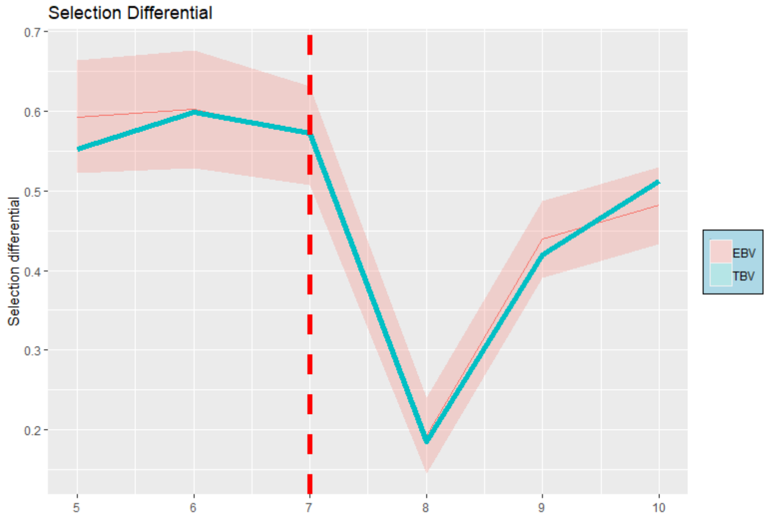
Changing the simulation

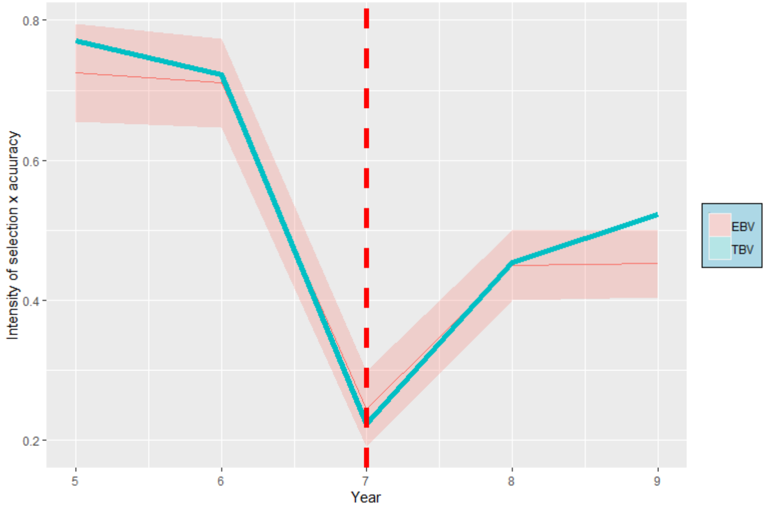
- Increasing the progeny

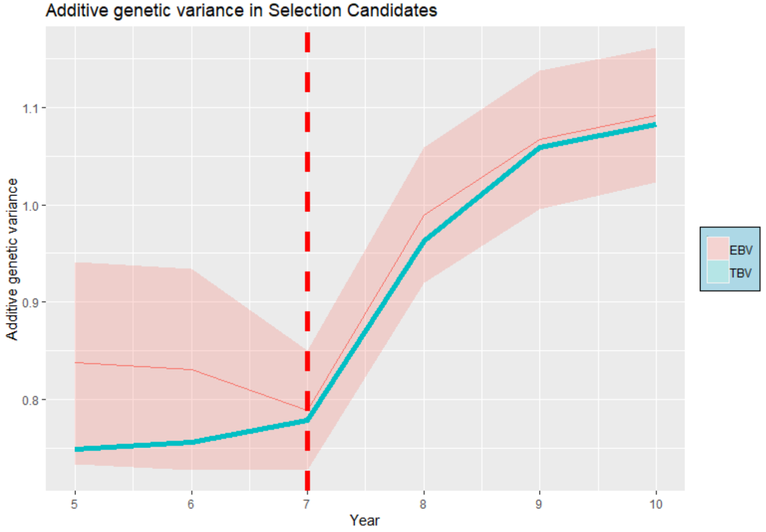
- Decreasing the selection intensity

Changing the number of progeny

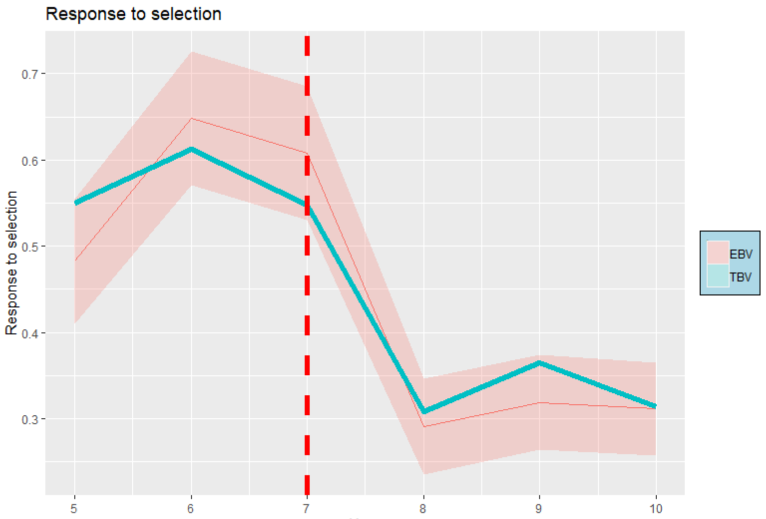

Response to selection

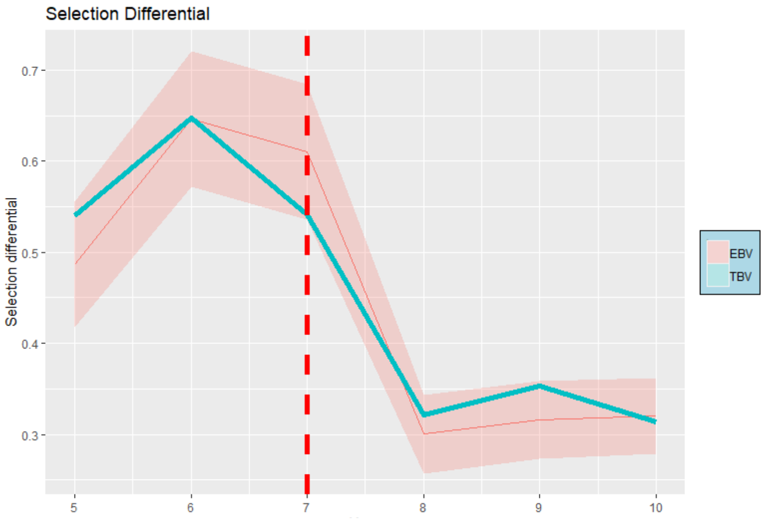

Selection Differential

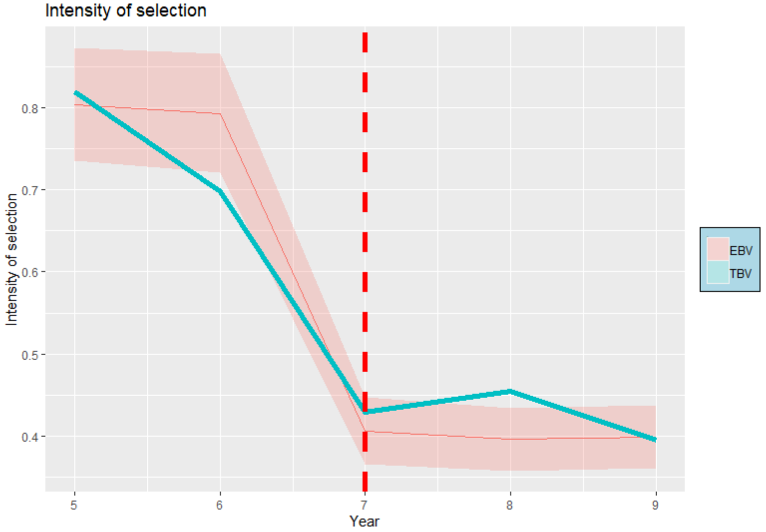

Intensity of selection

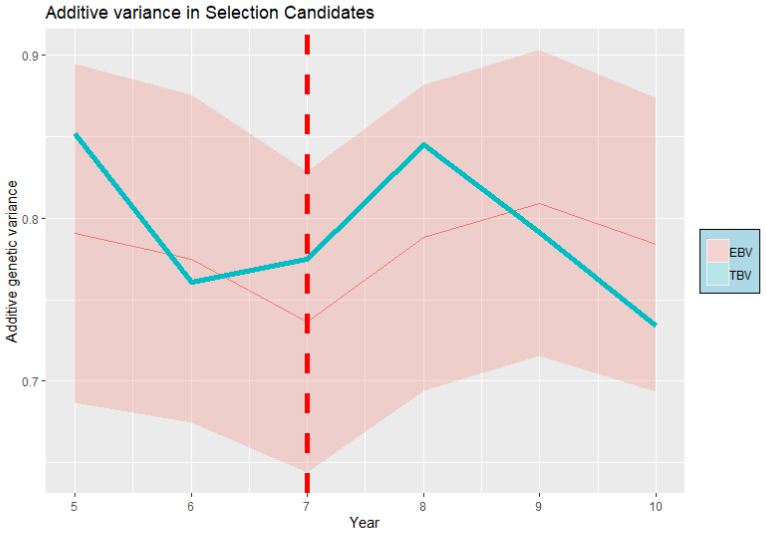

Additive genetic variance in Selection Candidates

Changing the intensity of selection

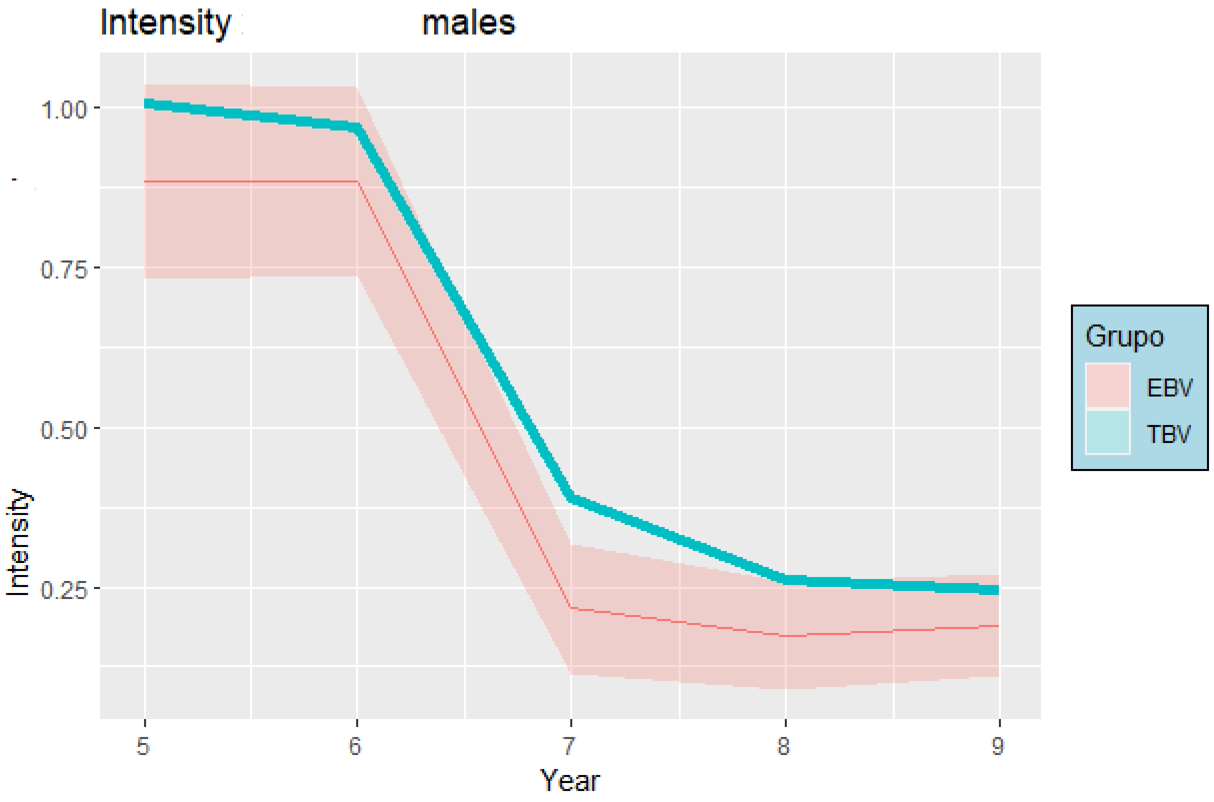

Response to selection


Selection Differential

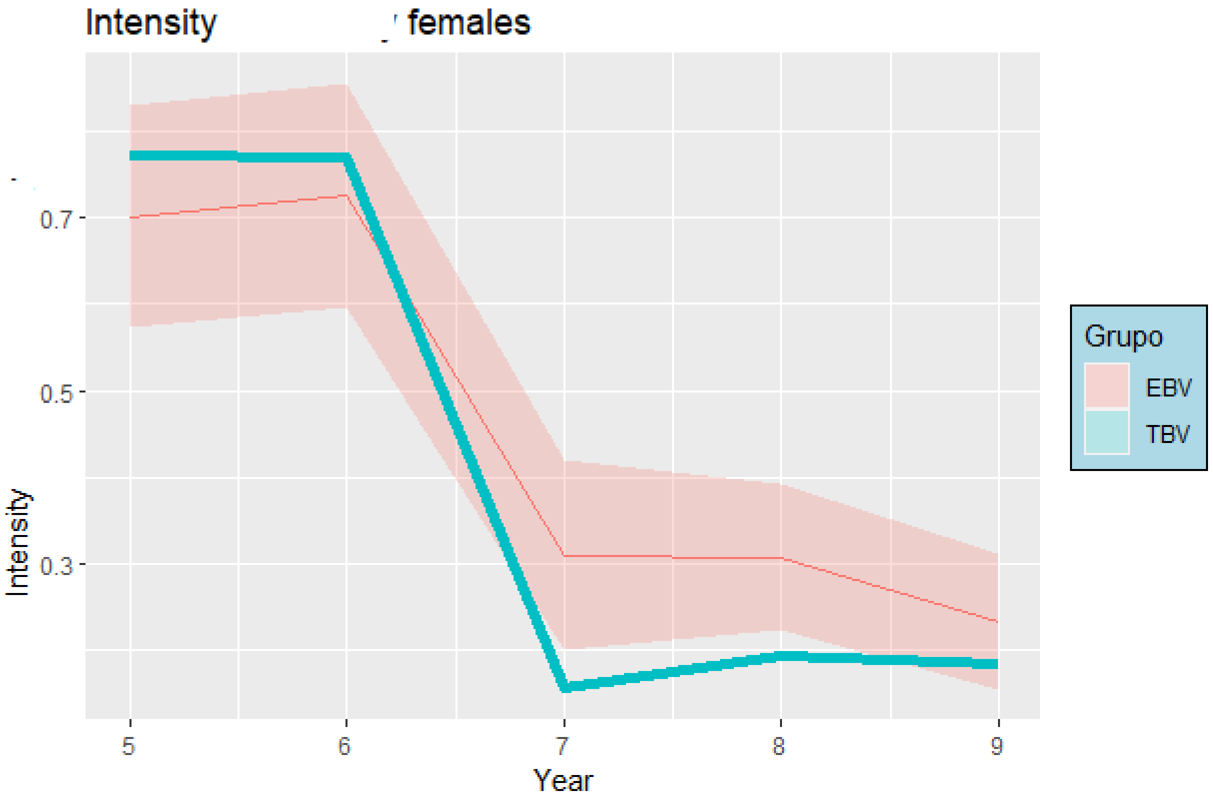

Intensity of selection


Additive variance in Selection Candidates

Analysis by groups (Sex)



Intensity males



Intensity females

Conclusions

- This Bayesian approach allow us to evaluate genetic trends using a HPD_{95} interval
- It can be used to analyse Breeder's Equation parameters -> Prospective analysis
- Breeder's Equation parameters decomposed by groups

Scan me to receive the software

Thanks for your attention

David López Carbonell

davidlc@unizar.es

QUANTITATIVE GENETICS LAB

Universidad Zaragoza

HLab