



# Weighted ssGBLUP enhances the genomic prediction accuracy for milk citrate predicted by milk mid-infrared spectra of Holstein cows in early lactation

**Y. Chen<sup>1</sup>**, H Atashi<sup>1</sup>, C. Grelet<sup>2</sup>, N. Gengler<sup>1</sup>  
<sup>1</sup>:Ulege-GxABT; <sup>2</sup>:CRAW

04/09/2024

yansen.chen@uliege.be

# Background

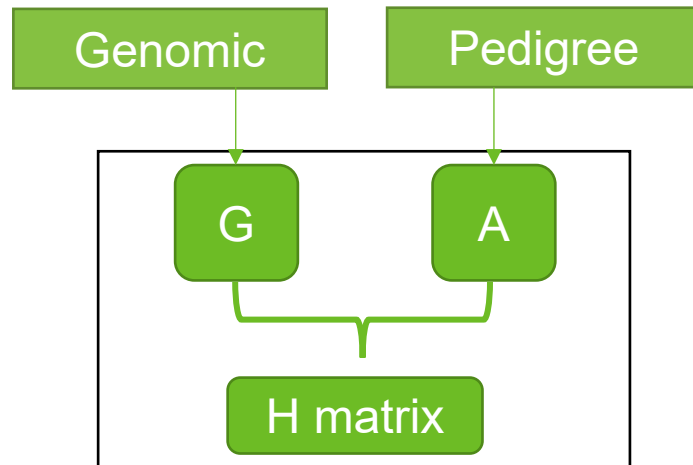


- ✓ Genomic prediction → animal breeding
- ✓ Methods
  - ✓ Bayesian: Bayes A, B, ...
  - ✓ BLUP: SNP-BLUP, GBLUP, **ssGBLUP**

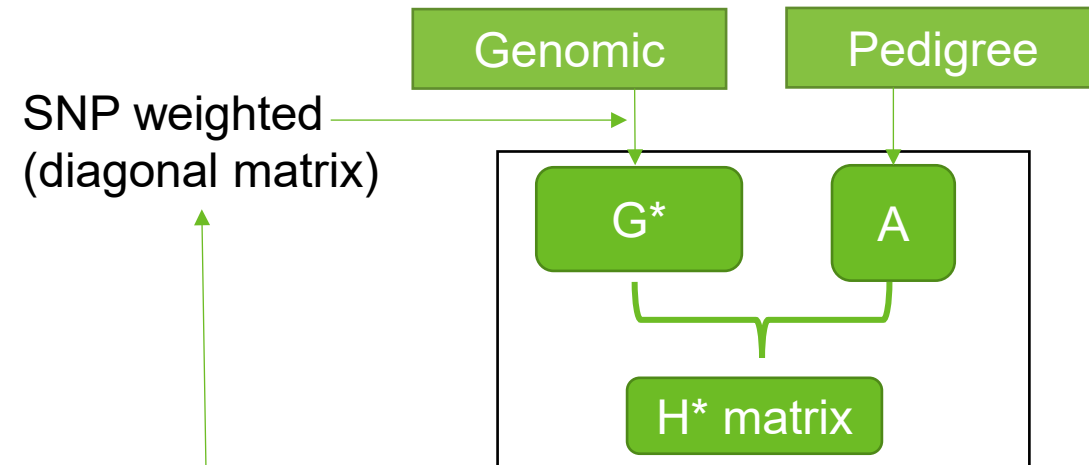
# Background



## ✓ ssGBLUP



## ✓ Weighted ssGBLUP



$$\text{Weight} = \text{CT}^{\frac{|\text{SNP effects}|}{\text{sd}(\text{SNP effects})} - 2} \text{ (nonlinear A method)}$$

where CT: distribution of SNP effects variance;  
SNP effects: back-solving the animals' GEBV

(Wang et al., 2012; VanRaden, 2008)

# Background



Weighted ssGBLUP

Small genotyped population  
(local breed or novel traits)

Few QTLs effect traits

# Background



- ✓ Negative energy balance
- ✓ High-producing dairy cows
- ✓ Early lactation

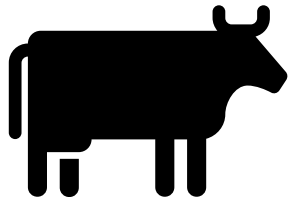


Reproduction

Metabolism

Infectious

Disease



Welfare

Decrease

€



# Background



- ✓ Negative energy balance (NEB)

- ✓ Hardly measure directly

- ✓ Biomarkers ← good ideas

Citrate

- ✓ Respond fast to NEB

- ✓ Predicted by milk mid-infrared

# Background

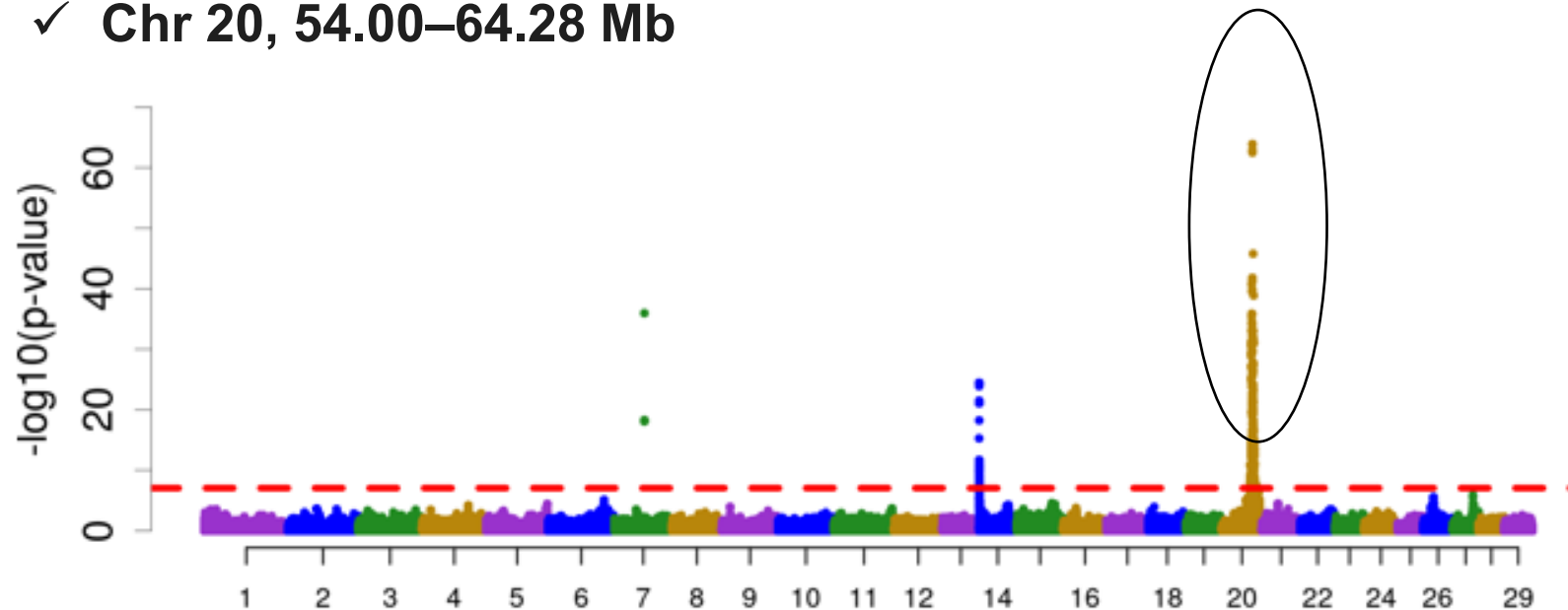
## ✓ Citrate

✓ Heritability: 0.35 - 0.40

✓ Chromosome (Chr) 7, 68.569–68.575 Mb

✓ Chr 14, 0.15–1.90 Mb

✓ **Chr 20, 54.00–64.28 Mb**



(Chen et al., 2024)



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## Genetic analysis of milk citrate predicted by milk mid-infrared spectra of Holstein cows in early lactation

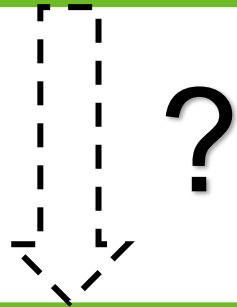
Yansen Chen,<sup>1\*</sup> Hongqing Hu,<sup>1</sup> Hadi Atashi,<sup>1,2</sup> Clément Grelet,<sup>3</sup> Katrien Wijnrocx,<sup>1</sup> Pauline Lemal,<sup>1</sup> and Nicolas Gengler<sup>1</sup>



# Aim



Weighted ssGBLUP



Genomic prediction  
for citrate

# Data



## Whole dataset

- ✓ 134,517 records
- ✓ 52, 198 Holstein cows
- ✓ 122,218 animals in pedigree
- ✓ 4,479 animals with genotypic (566,170 SNP)
- ✓ Parity: 1-5
- ✓ Days in milk: **First 50**
- ✓ Test year: **2012-2019**

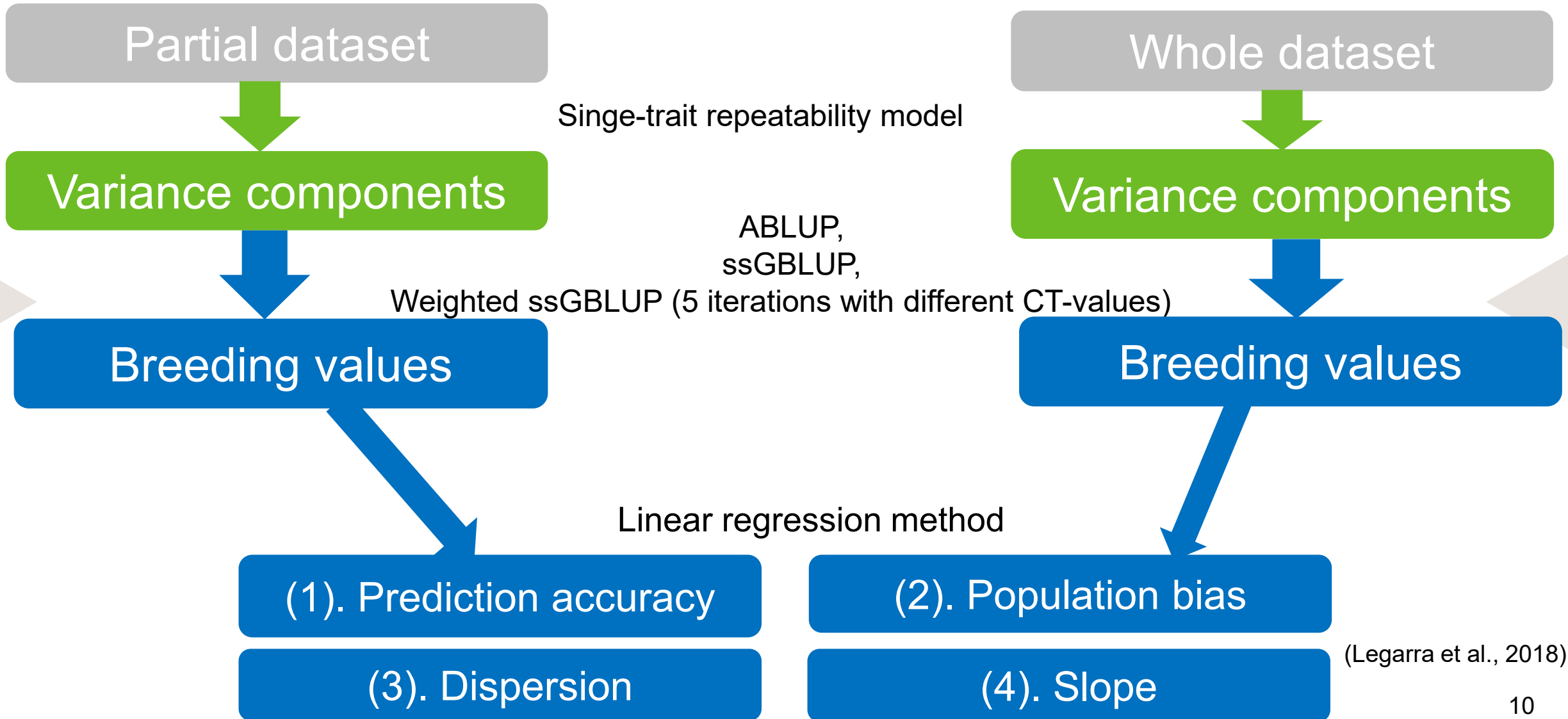
## Partial dataset

- ✓ Same as the whole dataset, excepted **records from 2017 to 2019** were set as **missing** values

## Validation population

- ✓ 181 youngest cows with genotype born after 2015

# Workflow



# Workflow



Expected value

(1). Prediction accuracy

1

$$\sqrt{\frac{cov(\hat{u}_p, \hat{u}_w)}{(1 - \bar{f})\sigma_u^2}}$$

(2). Population bias

0

$$\overline{\hat{u}_p} - \overline{\hat{u}_w}$$

(3). Dispersion

1

$$\frac{cov(\hat{u}_w, \hat{u}_p)}{var(\hat{u}_p)}$$

(4). Slope

1

$$\frac{Reliability_p}{Reliability_w} = \frac{cov(\hat{u}_p, \hat{u}_w)}{var(\hat{u}_w)}$$

(Legarra et al., 2018)

# Results



| LR statistic        | ABLUP | ssGBLUP | Increase (%) |
|---------------------|-------|---------|--------------|
| Prediction accuracy | 0.42  | 0.70    | 66.67        |
| Bias                | 0.04  | -0.03   | -25.00       |
| Dispersion          | 0.95  | 1.05    | 0.00         |
| Slope               | 0.41  | 0.76    | 85.37        |



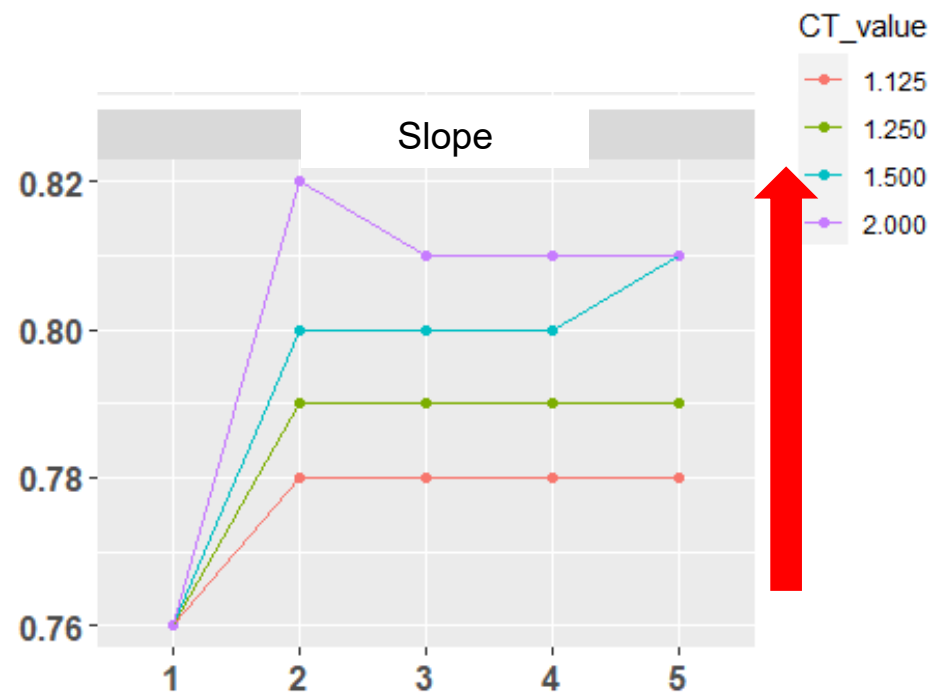
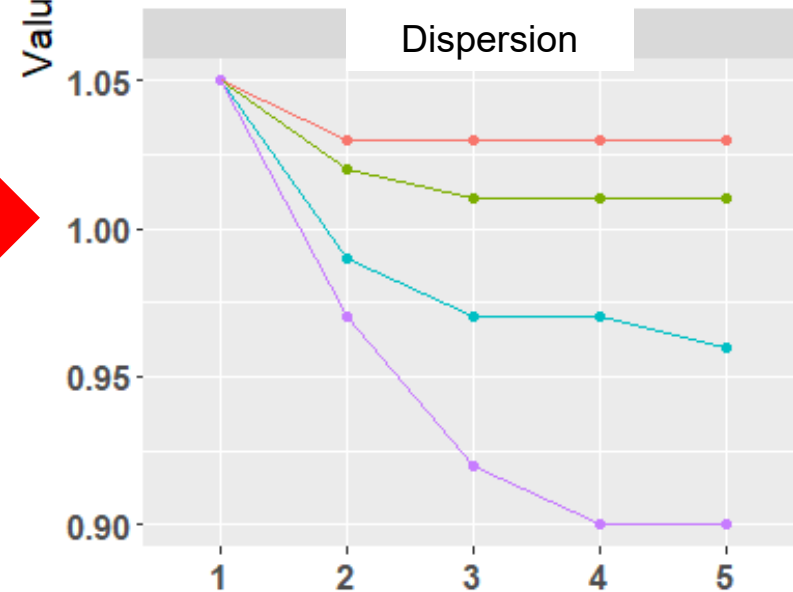
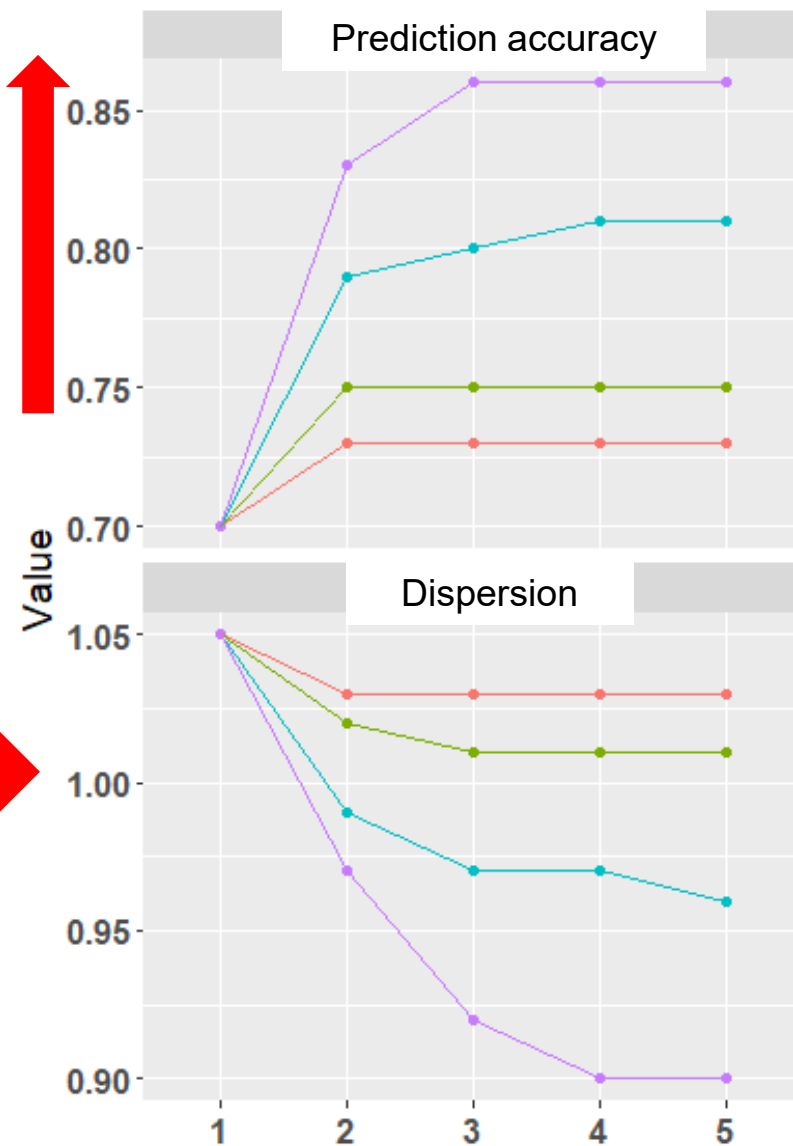
Genomic information

# Results

Two parameters:

- ✓ CT
- ✓ Iteration

First iteration is  
ssGBLUP



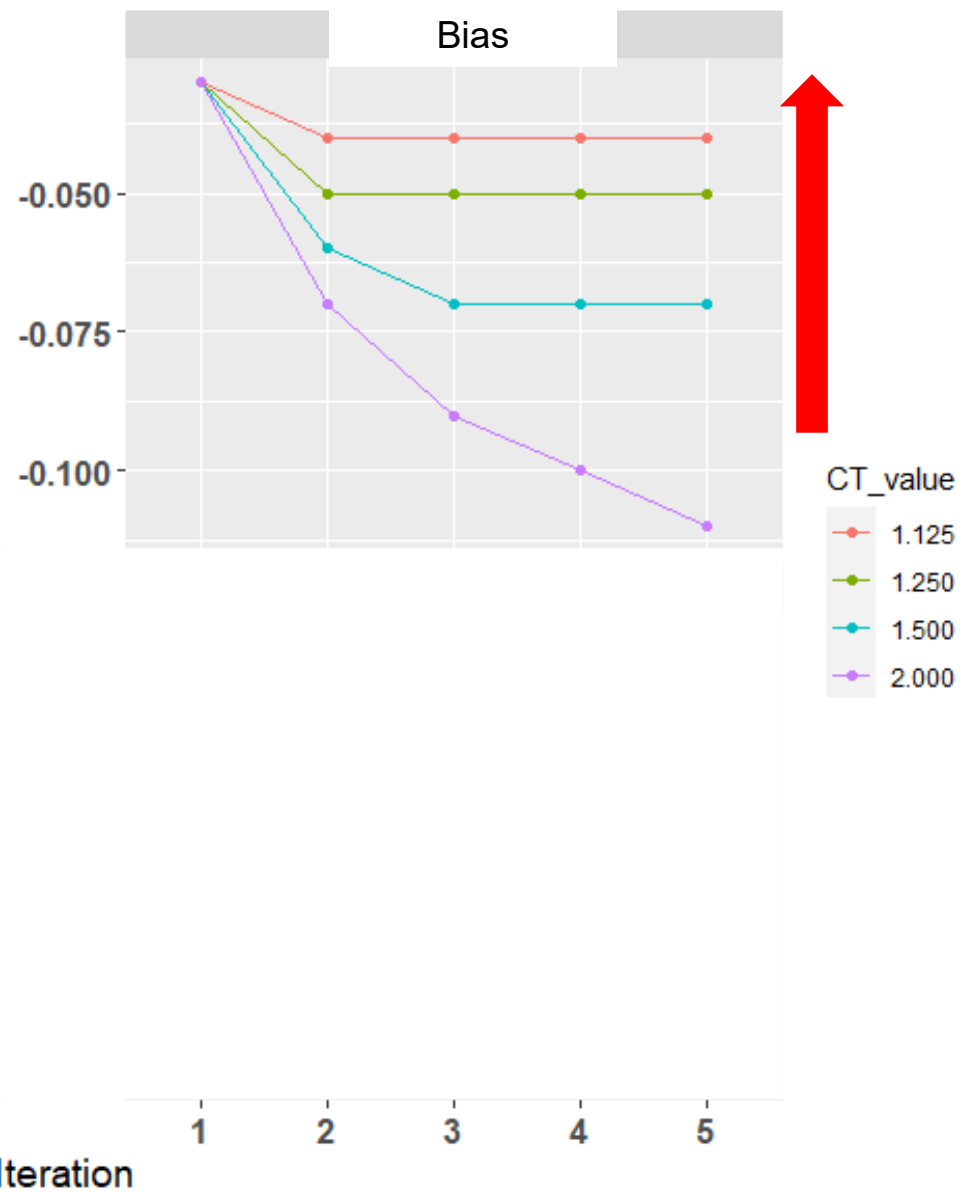
# Results

Two parameters:

- ✓ CT
- ✓ Iteration

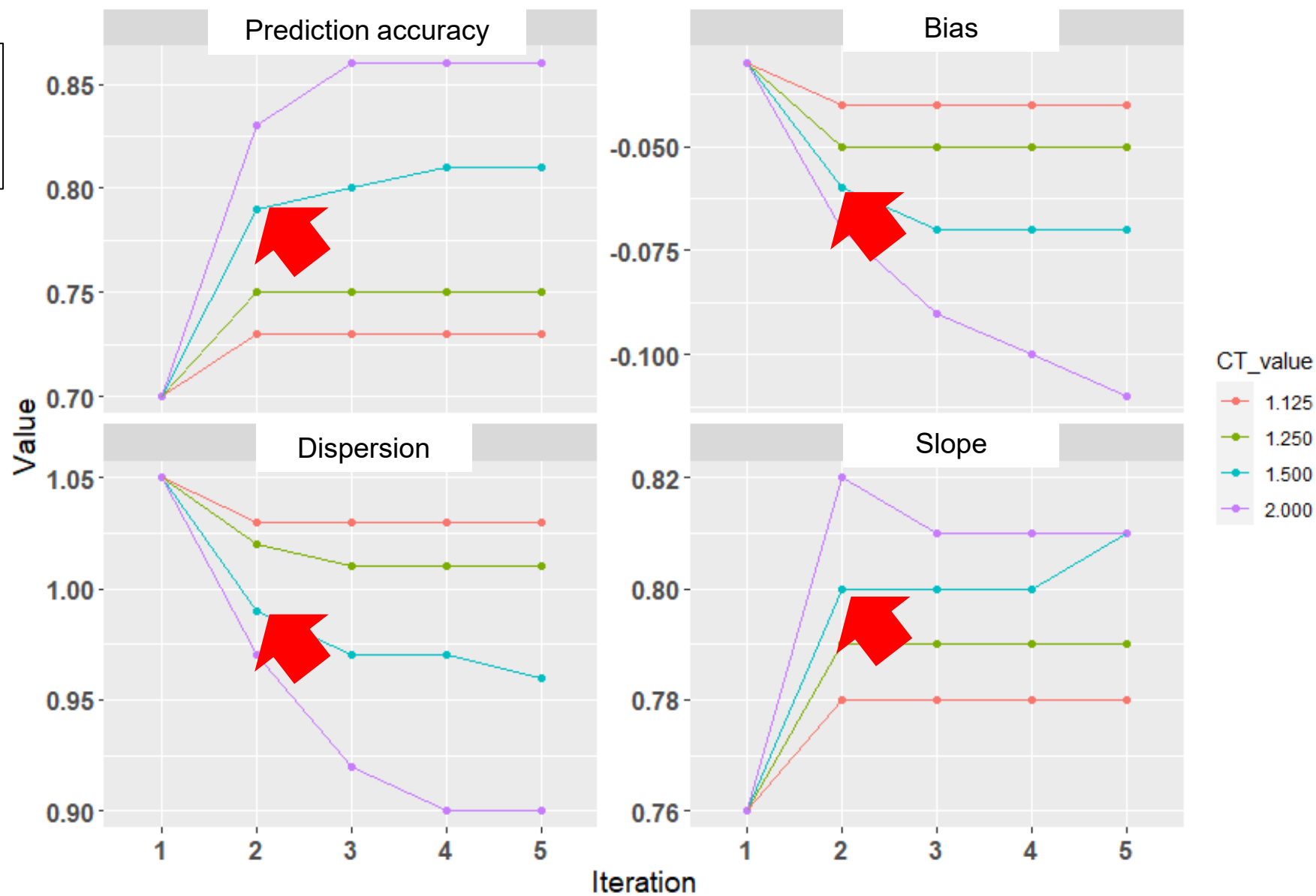
First iteration is  
ssGBLUP

Value



# Results

Optimize results:  
**CT=1.500**  
**Iteration = 2**



# Conclusions



Genomic prediction for citrate

Genomic prediction for citrate

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Genomic prediction  
for citrate



# Thank you for your attention!

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