WGBLUP MODEL IMPROVES ACCURACY OF BREEDING VALUES PREDICTION IN A COMMERCIAL LINE OF BROILERS

H. Romé, T. T. Chu, R. Hawken, J. Henshall, J. Jensen

Project

Accuracy of prediction => Major component to maximize genetic gain in poultry

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Genomic information into prediction models => ↗ Accuracy of predicted BV

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→ Large genotypic and phenotypic datasets

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Genomic information into prediction models => ↗ Accuracy of predicted BV

- ↪ Improvement in accuracy is trait dependent
- ↪ No clear domination of one genomic prediction models over other ones
- ➡ Large genotypic and phenotypic datasets

Could we use GWAS results to improve accuracy of predicting breeding values (BV) in broilers?

Project

Accuracy of prediction => Major component to maximize genetic gain in poultry

Genomic information into prediction models => ↗ Accuracy of predicted BV

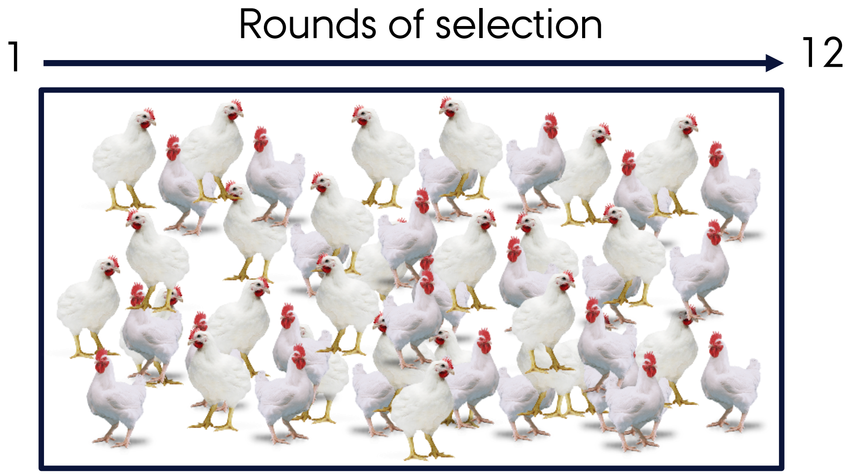
- Improvement in accuracy is trait dependent **Body weight**
- No clear domination of one genomic prediction models over other ones **"BLUP alphabet"**

→ Large genotypic and phenotypic datasets

Could we use GWAS results to improve accuracy of predicting breeding values (BV) in broilers?

Data

- Population of commercial pure lines of broilers

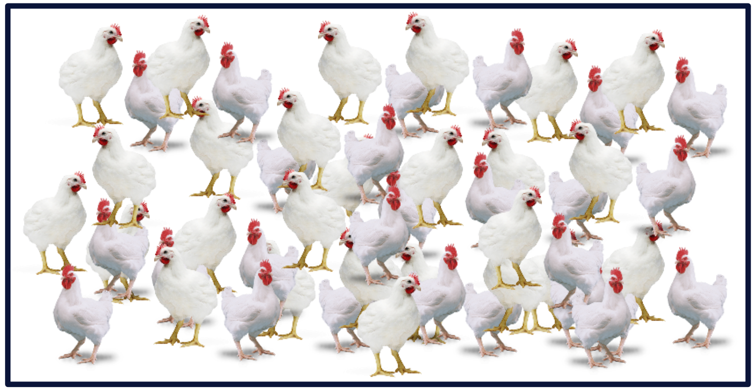


Data

- Population of commercial pure lines of broilers
- Both sexes

Rounds of selection

1 → 12

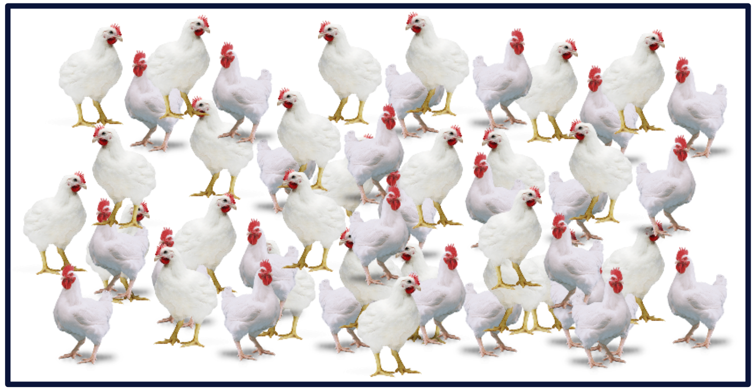


Data

- Population of commercial pure lines of broilers
- Both sexes
- BW recorded for 5 successive weeks

Rounds of selection

1 → 12



Data

- Population of commercial pure lines of broilers
- Both sexes
- BW recorded for 5 successive weeks

10 traits

Data

- Population of commercial pure lines of broilers
- Both sexes
- BW recorded for 5 successive weeks
- All genotyped and phenoyped
    - Around 8000 individuals per traits

10 traits

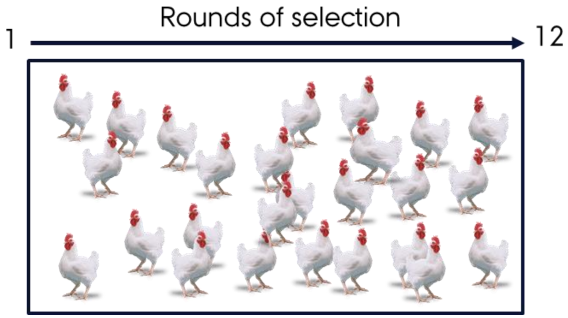
Data

- Population of commercial pure lines of broilers
- Both sexes
- BW recorded for 5 successive weeks
- All genotyped and phenoyped

10 traits

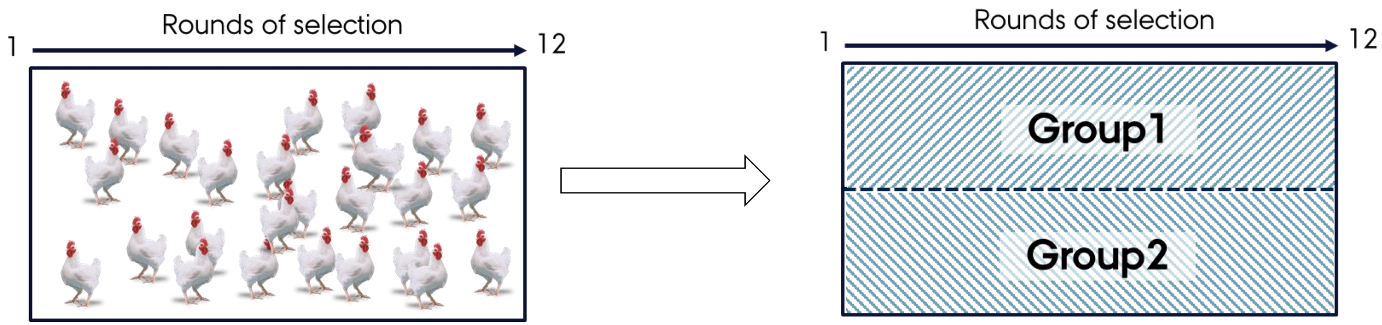
Illumina 60k array => after quality control : 46502 SNP

Method



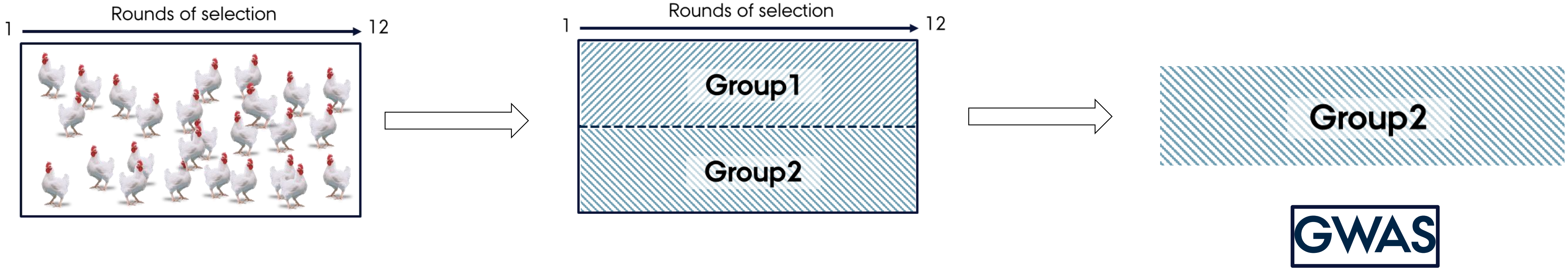
Estimation of SNP effect on a different population than the one we want to estimate

Method



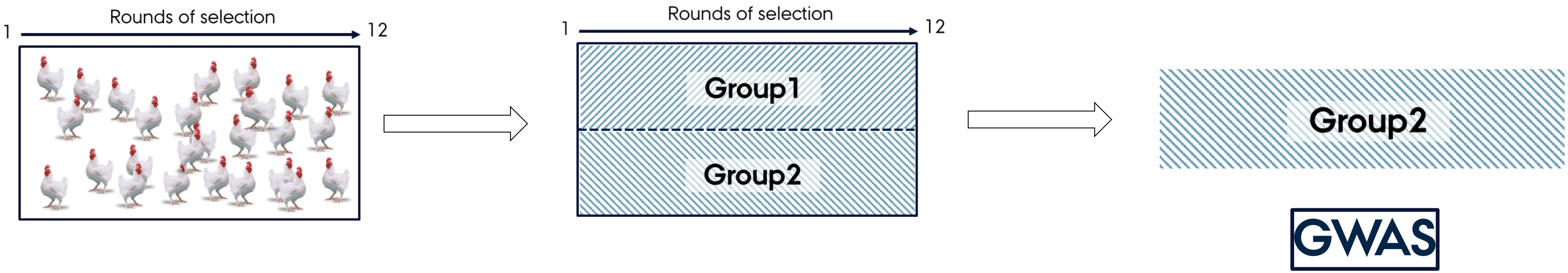
Individuals were assigned randomly to a group within round of selection

Method



$$y = \mathbf{X}b + \beta_1{*}SNP_{ia} + \beta_2{*}SNP_{id} + \mathbf{Z}u + \mathbf{W}m + \mathbf{W}c + \mathbf{e}$$

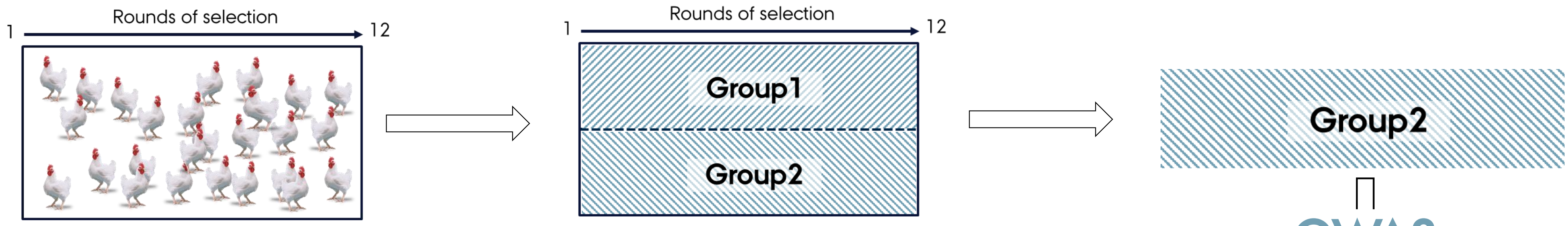
Method



$$y= \mathbf{X}b + \beta_1 {*}SNP_{ia} + \boxed{\beta_2 {*}SNP_{id}} + \mathbf{Z}u + \mathbf{W}m + \mathbf{W}c + \mathbf{e}$$

Correcting for the size effect

Method



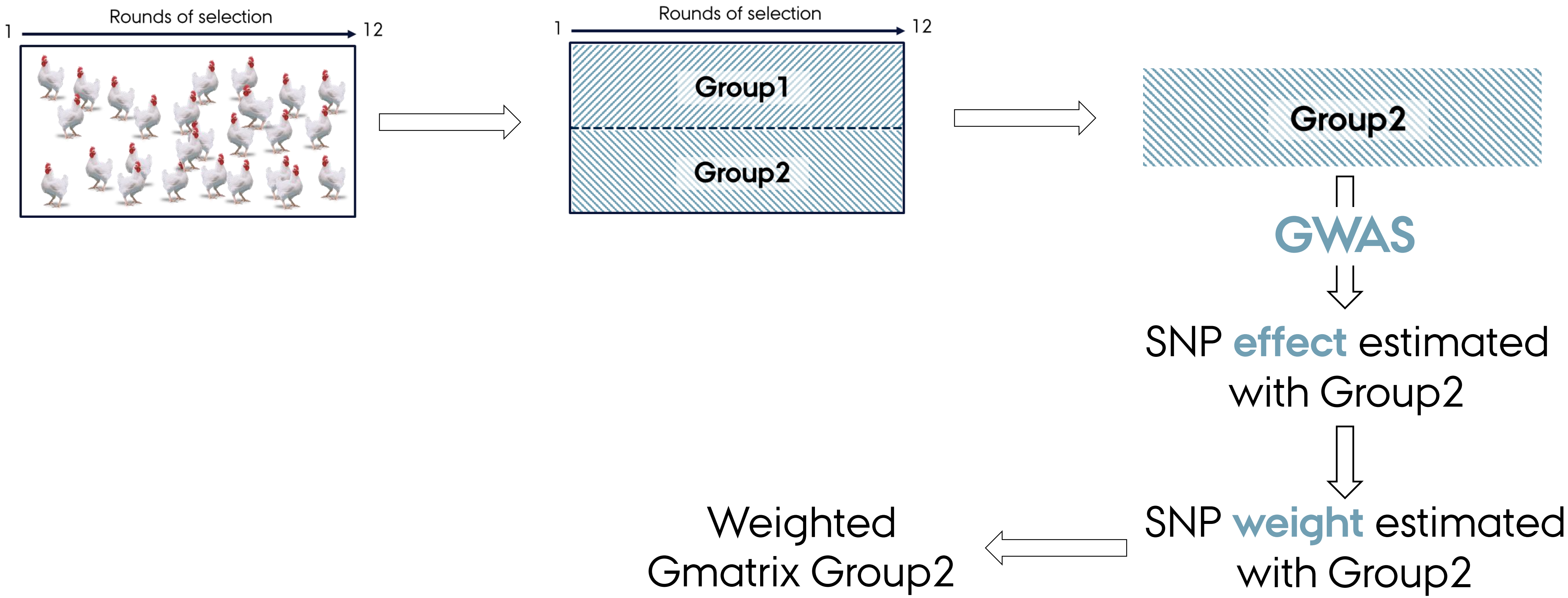
GWAS

SNP **effect** estimated with Group2 = β1

SNP **weight** estimated with Group2

$$w = \frac{\hat{\beta}_{1i}^{2} / \overline{\beta 1}}{\sum 2p_i q_i} \text{ where } \overline{\beta_1} = \frac{\sum 2p_i q_i * \hat{\beta}_{1i}^{2}}{\sum 2p_i q_i}.$$

Method



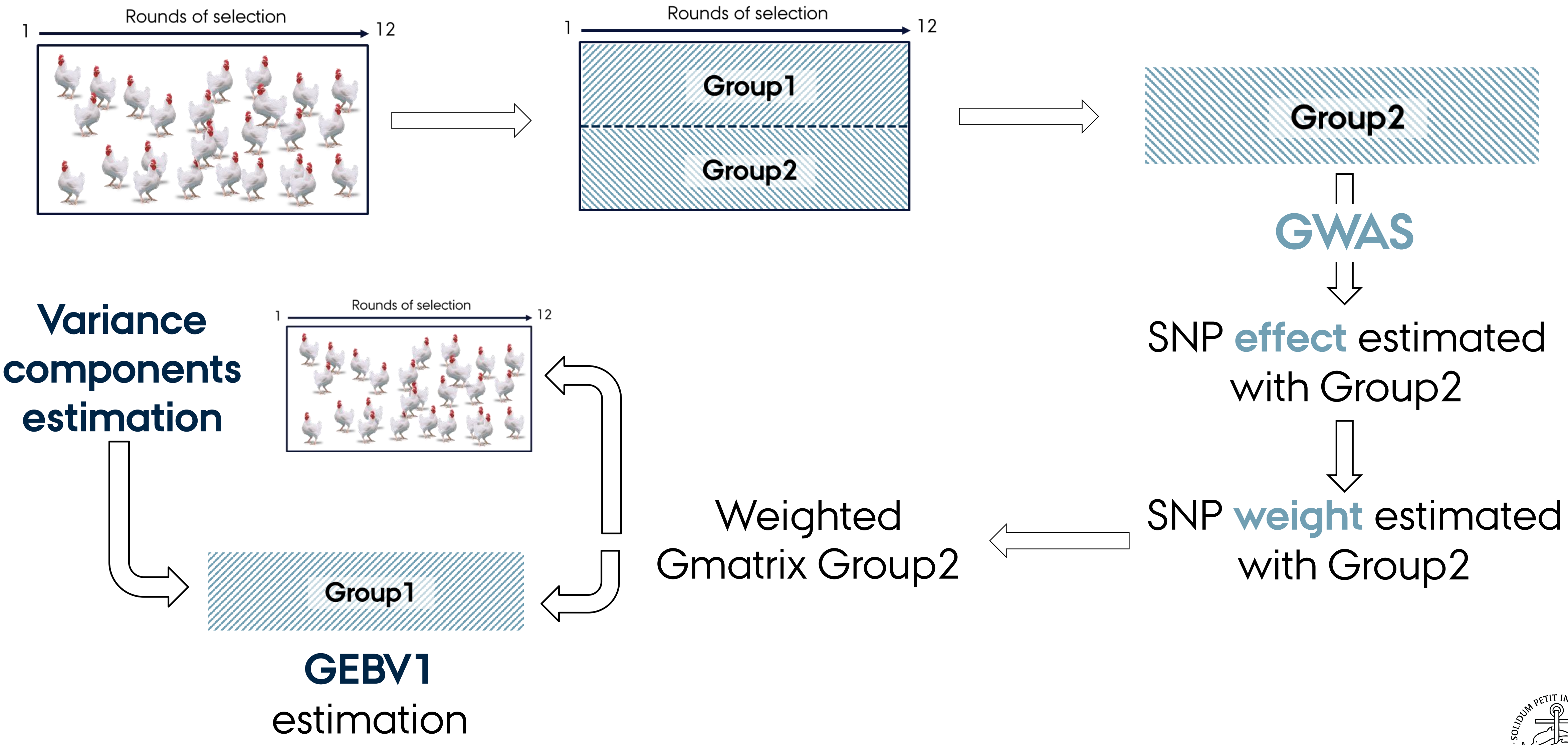
GWAS

SNP **effect** estimated with Group2

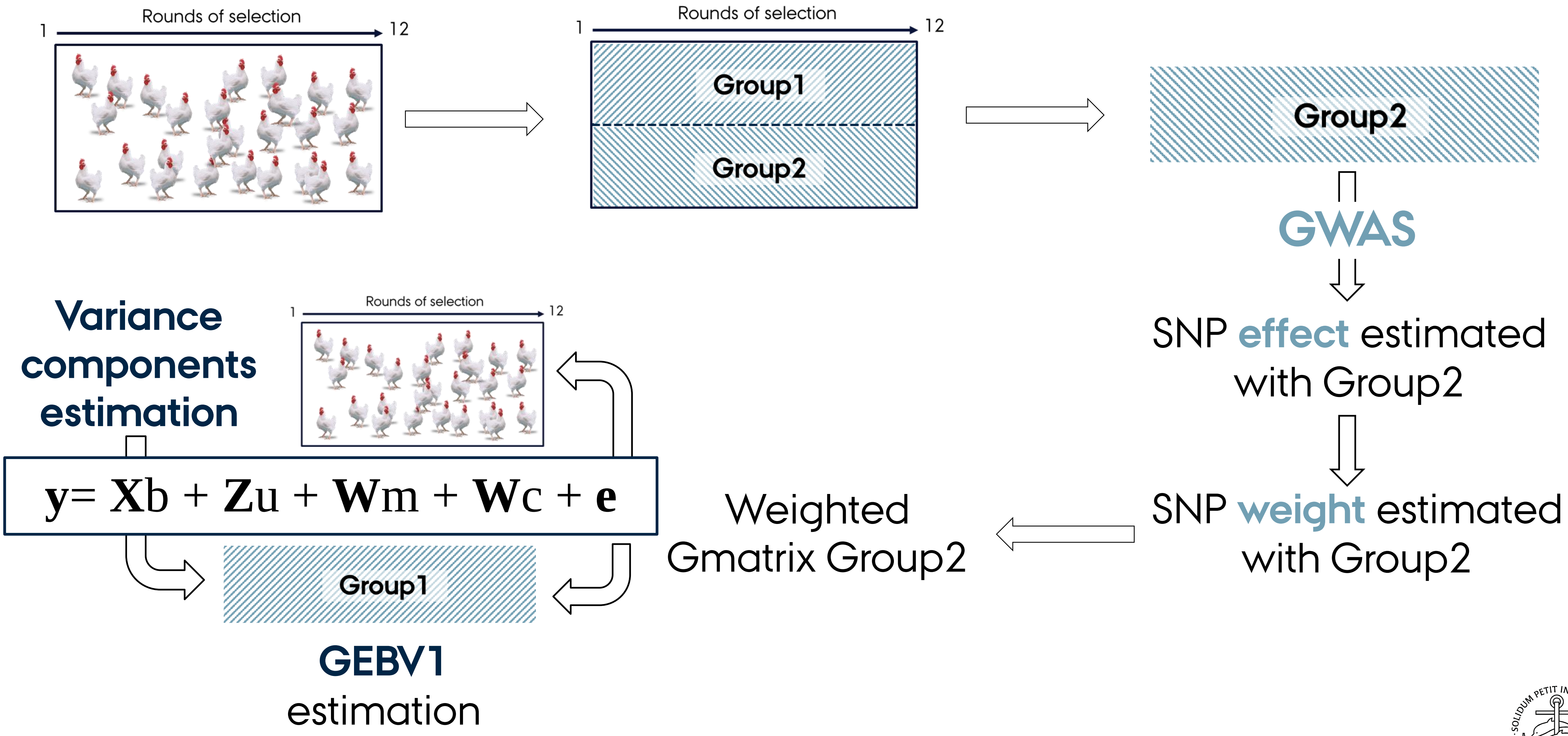
SNP **weight** estimated with Group2

Weighted Gmatrix Group2

Method


Rounds of selection
1
12
Rounds of selection
1
12
Group1
Group2
Group2
GWAS
SNP effect estimated with Group2
SNP weight estimated with Group2
Weighted Gmatrix Group2
Variance components estimation
Rounds of selection
1
12
Group1
GEBV1 estimation

Method



Rounds of selection
1
12

Rounds of selection
1
12

Group1

Group2

Group2

GWAS

SNP **effect** estimated
with Group2

SNP **weight** estimated
with Group2

Weighted
Gmatrix Group2

**Variance
components
estimation**

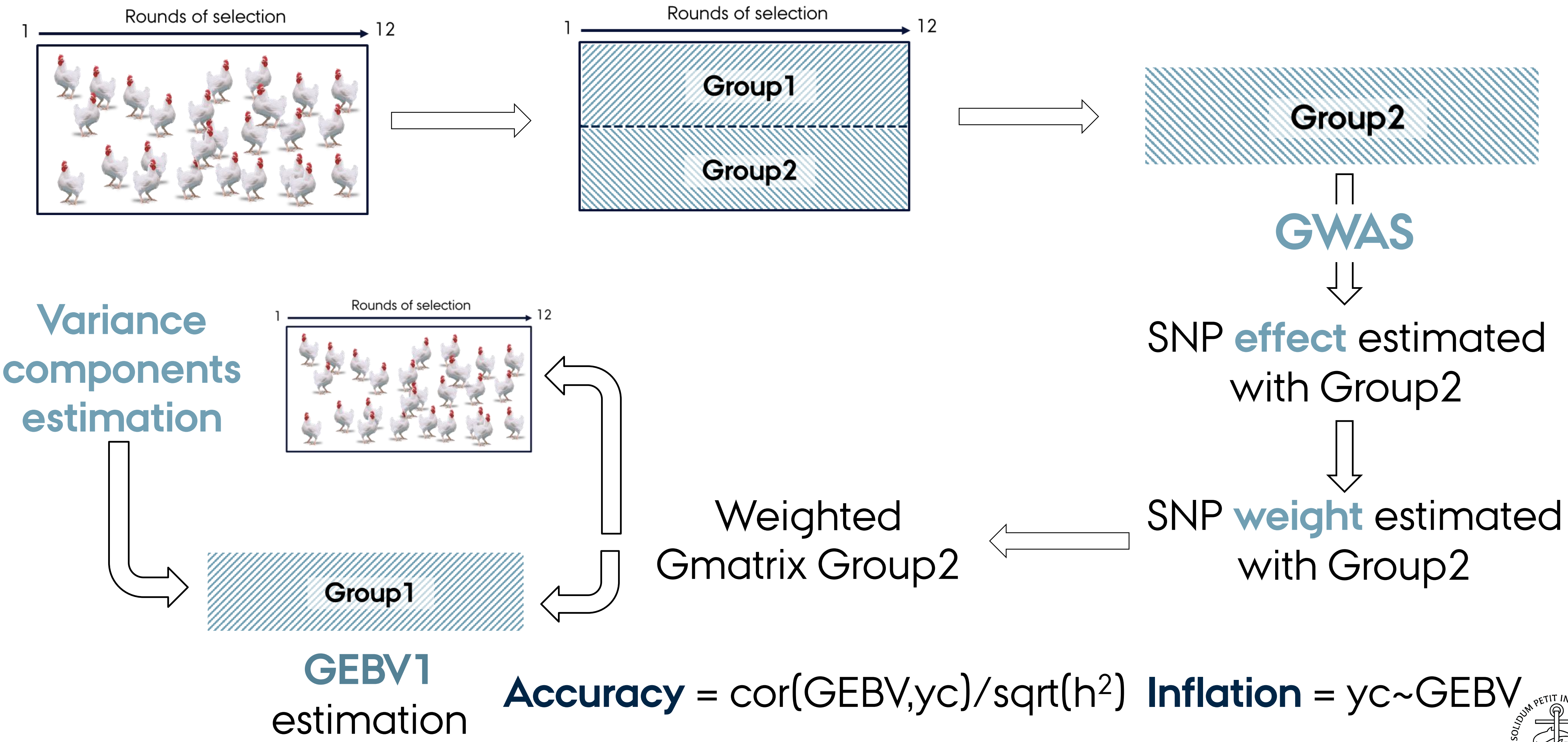
Rounds of selection
1
12

$$\mathbf{y}= \mathbf{X}\mathrm{b} + \mathbf{Z}\mathrm{u} + \mathbf{W}\mathrm{m} + \mathbf{W}\mathrm{c} + \mathbf{e}$$

Group1

GEBV1
estimation

Method



GWAS

SNP **effect** estimated with Group2

SNP **weight** estimated with Group2

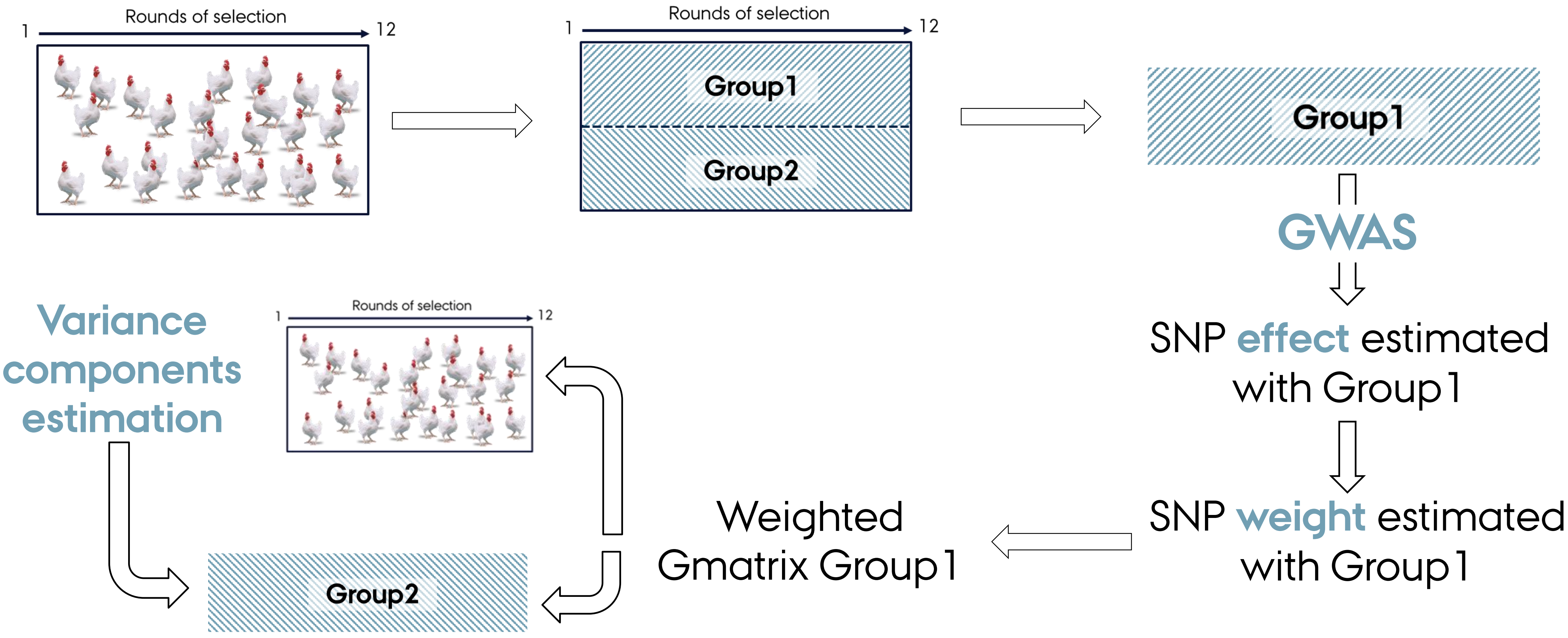
Weighted Gmatrix Group2

Variance components estimation

GEBV1 estimation

Accuracy = cor(GEBV,yc)/sqrt(h^2) **Inflation** = yc~GEBV

Method



Rounds of selection
1
12

Rounds of selection
1
12
Group1
Group2

Group1

GWAS

SNP **effect** estimated with Group1

SNP **weight** estimated with Group1

Weighted Gmatrix Group1

Rounds of selection
1
12

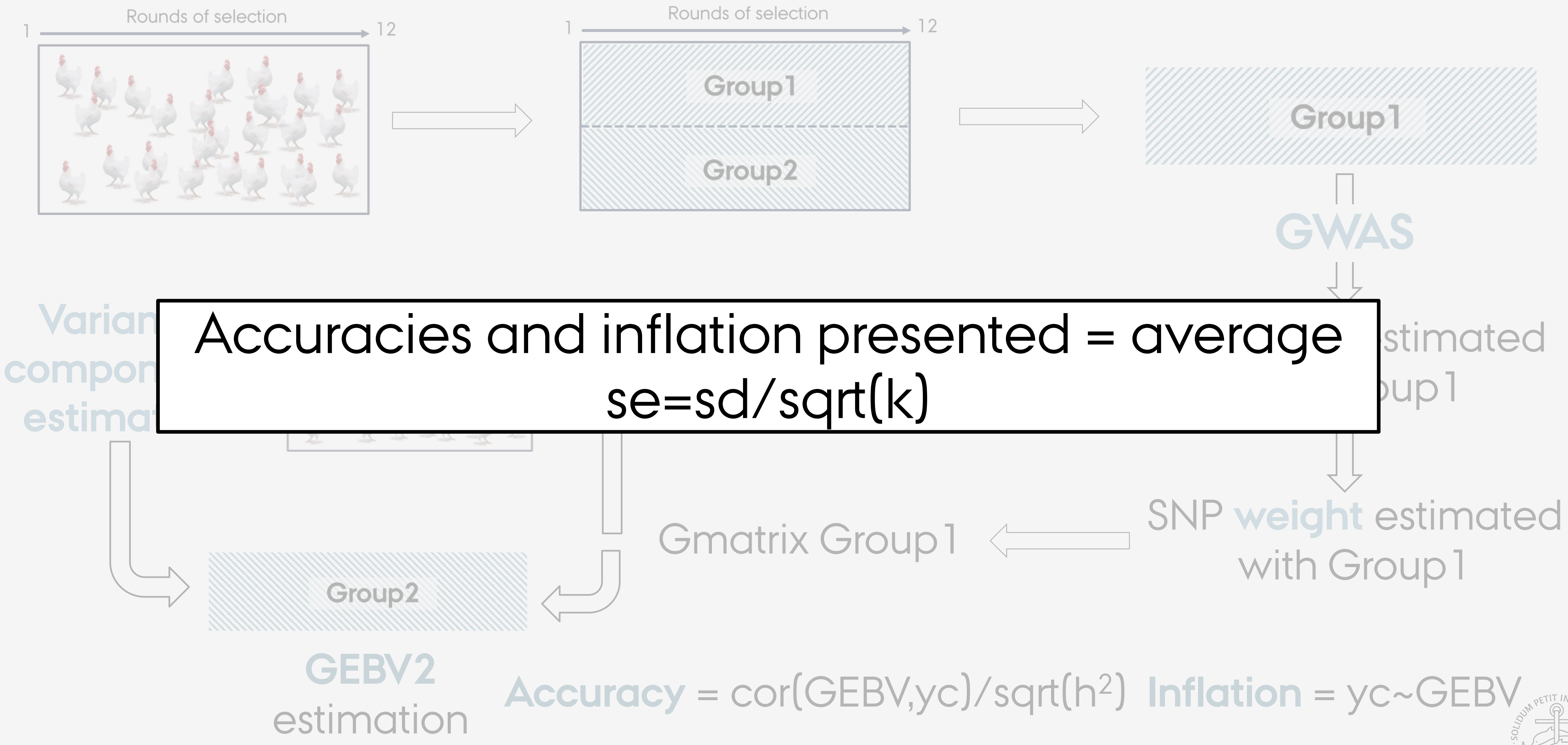
Variance components estimation

Group2

GEBV2 estimation

Accuracy = cor(GEBV,yc)/sqrt(h^2) **Inflation** = yc~GEBV

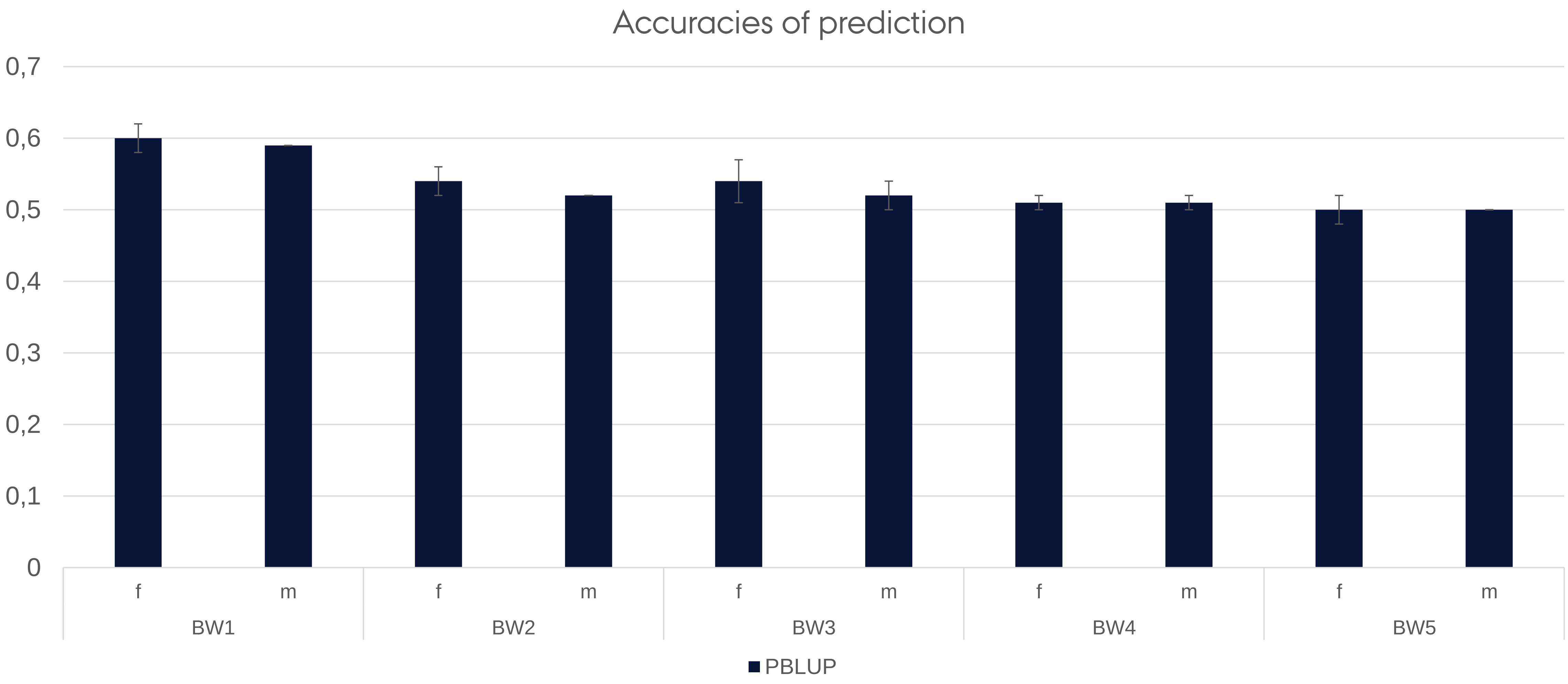
Method



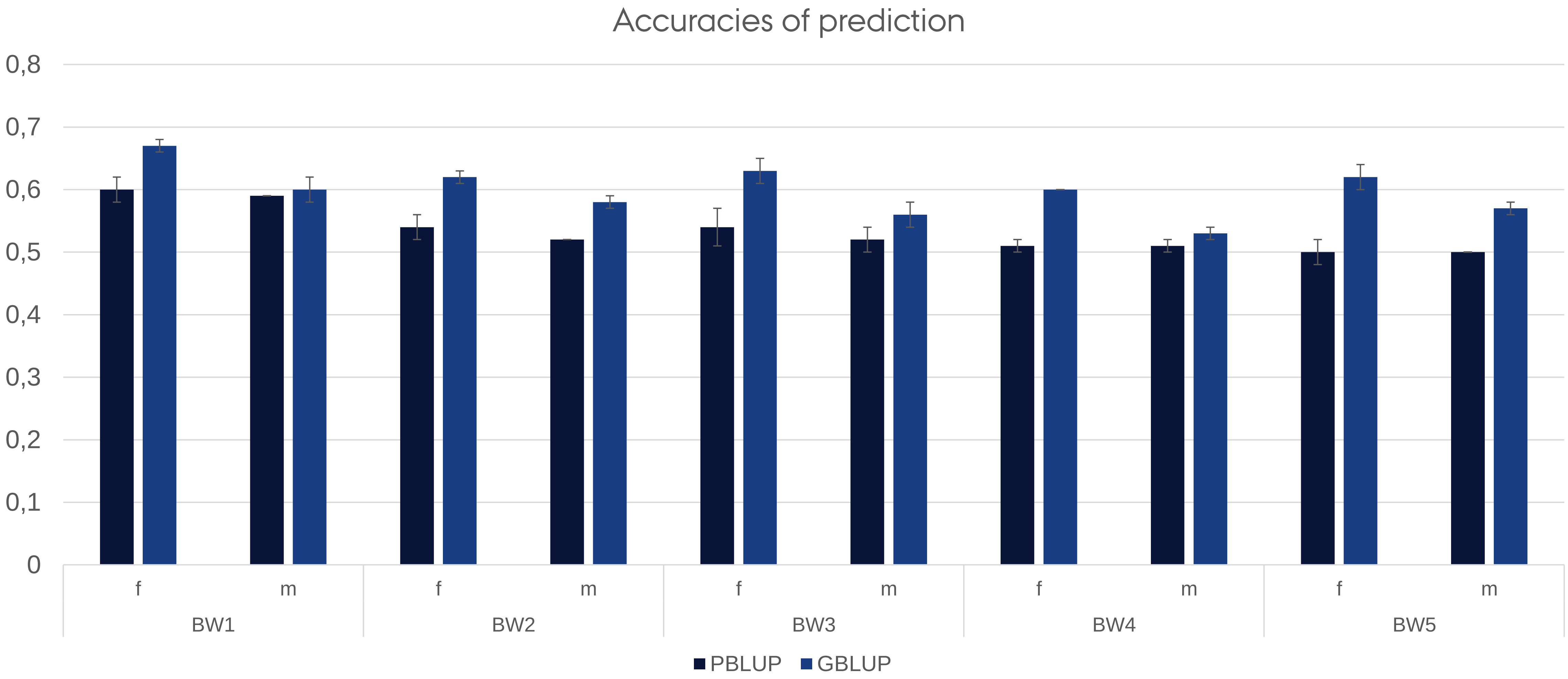
Accuracies and inflation presented = average
se=sd/sqrt(k)

Accuracy = cor(GEBV,yc)/sqrt(h^2) **Inflation** = yc~GEBV

Results - Accuracies



Results - Accuracies



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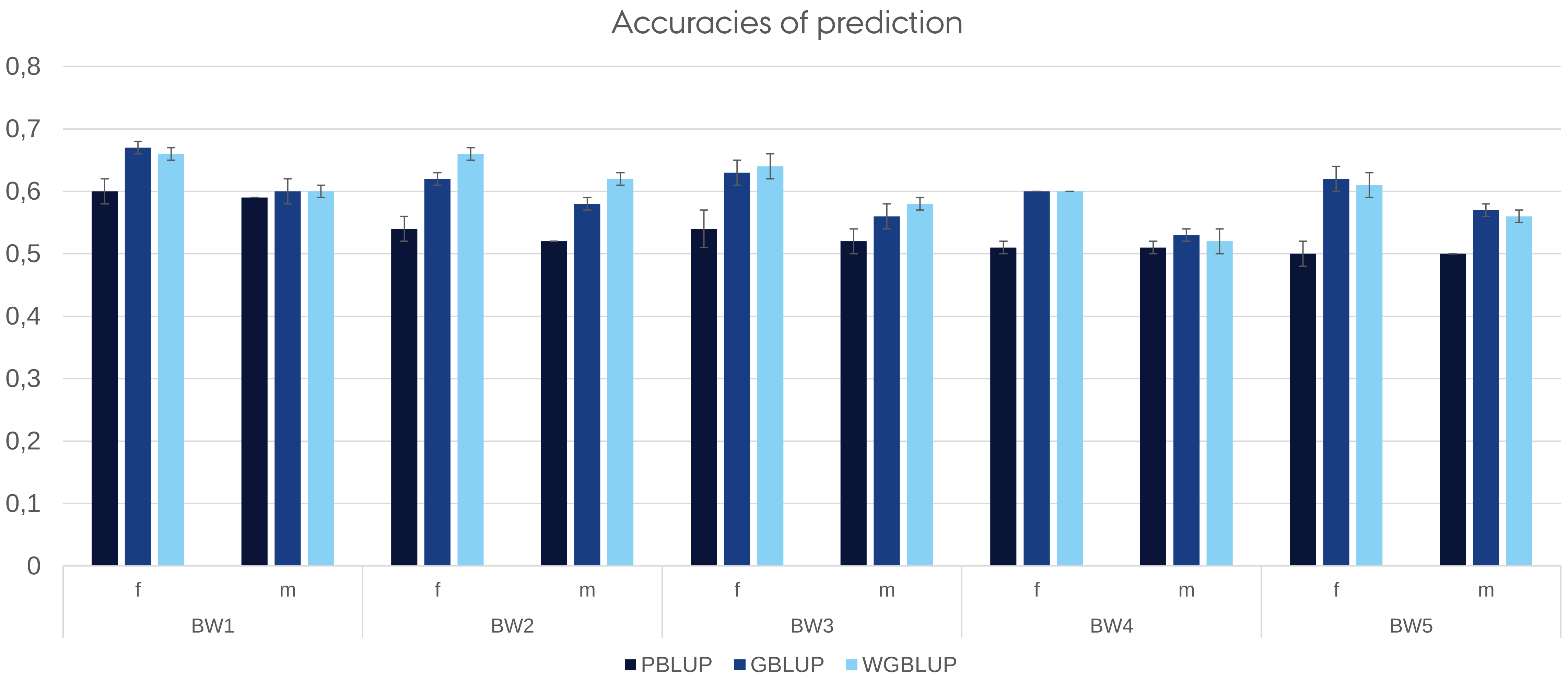
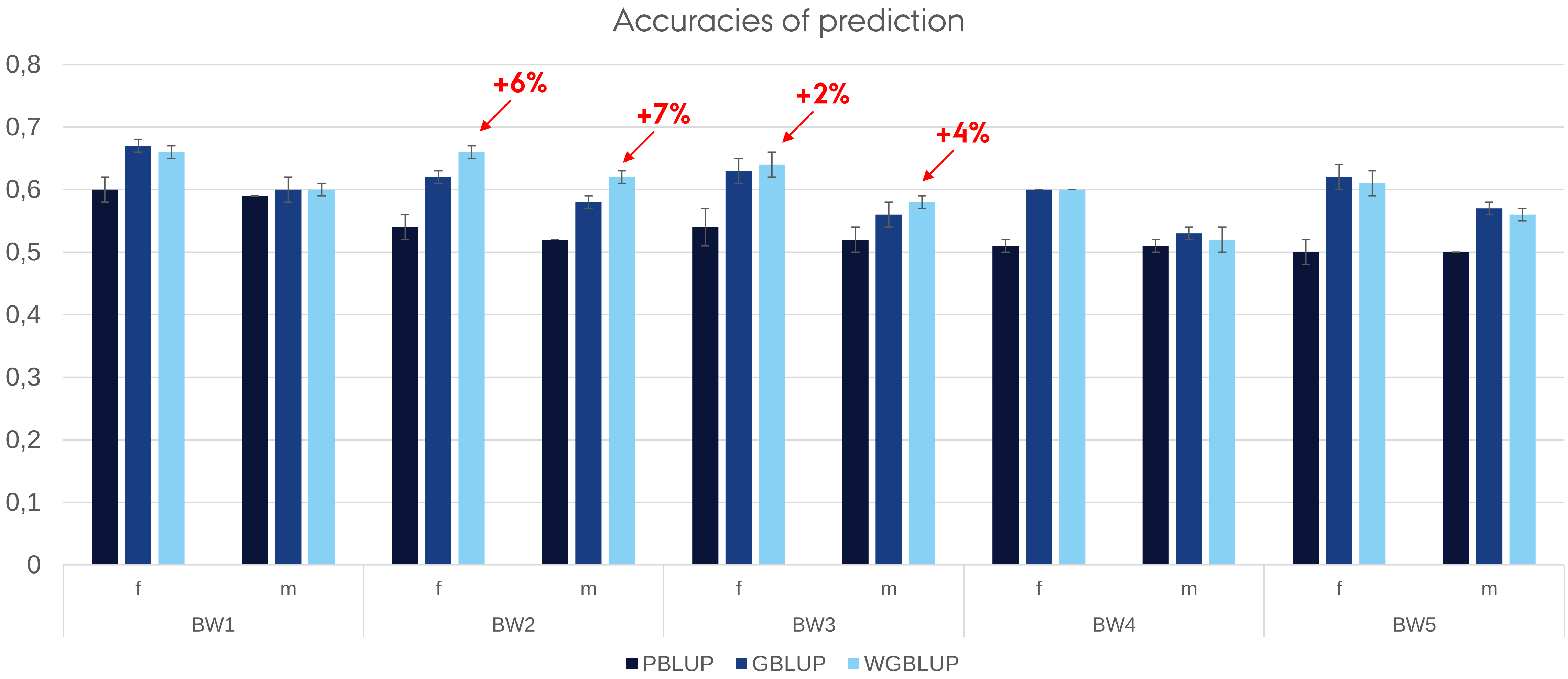
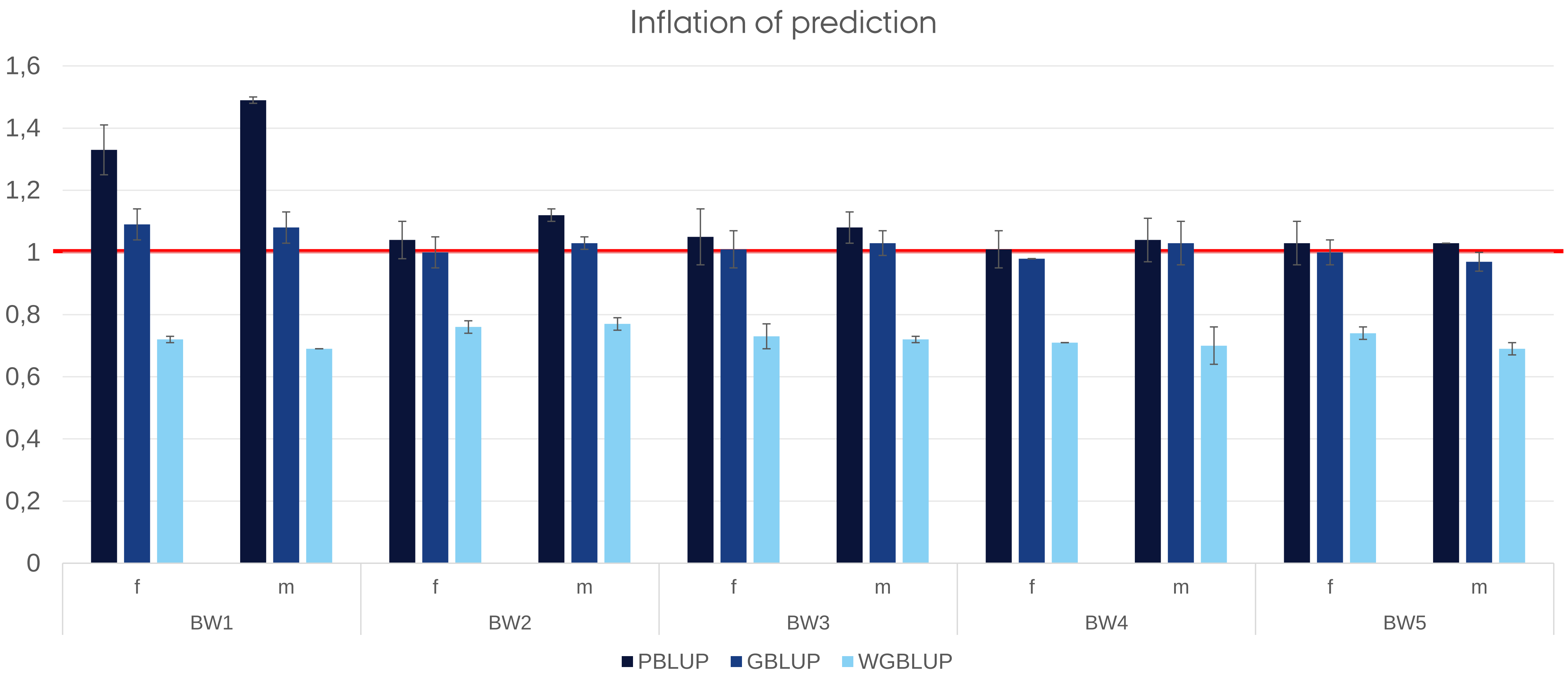


Results - Accuracies



Results - Inflation



Discussion

- Genomic information into prediction model ↗ accuracies from 2% to 22%
  - ↳ Quite small compared to literature
    - ↳ PBLUP is already highly accurate (0.5 to 0.6) compared to maximum expected 0.71

Discussion

- Genomic information into prediction model ↗ accuracies from 2% to 22%
- GWAS information into prediction model ↗ accuracies from 2% to 7%
  - ⤷ Only for few traits => the ones controlled by few large QTL
  - ⤷ Could be improve by weighting windows and not individual SNP
  - ⤷ Other models to estimate SNP effect

Discussion

- Genomic information into prediction model ↗ accuracies from 2% to 22%
- GWAS information into prediction model ↗ accuracies from 2% to 7%
- WGBLUP increases accuracies but also inflation
  - ↪ Has to be consider for selection index

Discussion

- Genomic information into prediction model ↗ accuracies from 2% to 22%
- GWAS information into prediction model ↗ accuracies from 2% to 7%
- WGBLUP increases accuracies but also inflation
- Accuracies of prediction were higher in females than in males
    - ↪ Could be link with maternal effect

Discussion

- Genomic information into prediction model ↗ accuracies from 2% to 22%
- GWAS information into prediction model ↗ accuracies from 2% to 7%
- WGBLUP increases accuracies but also inflation
- Accuracies of prediction were higher in females than in males
- Persistency => How often should SNP effect be re-estimated?

Conclusion

- **WGBLUP** model **improves accuracy** of breeding values prediction for BW in broilers
    - This gain in accuracy is **moderate** compared to the one observed by adding genomic information
        - But it does **not require extra cost**, just computation time
- **No gain in accuracy** was observed for trait closer to **targeted age**
    - Not enough power to estimate SNP effect?
- **WGBLUP** model **improves accuracy** but **increased inflation**

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