

The relevance of epistasis to genome-wide prediction in wheat

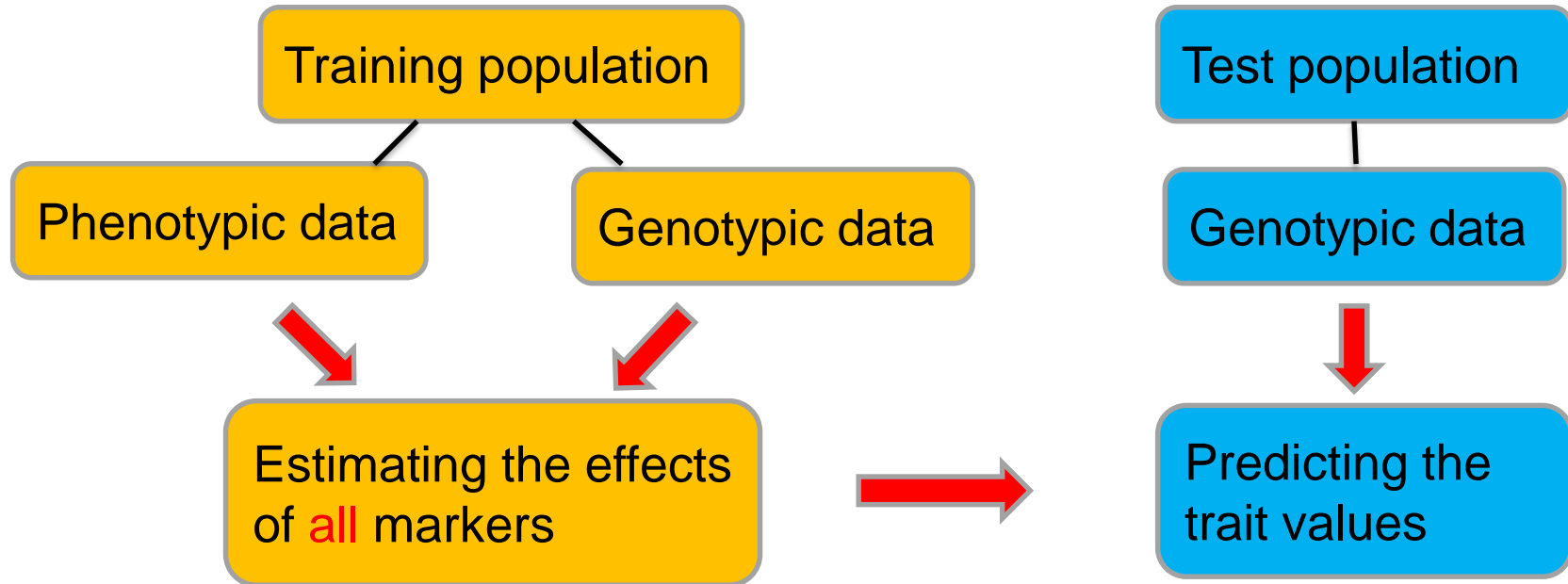
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Epistasis

- *Epistasis*: The non-additivity in the contributions of several loci to a trait.
- Interaction effects among alleles in different loci
- The role of epistasis in genomic prediction for complex traits has been debated
- The effectiveness of including epistasis in genomic prediction model seems depending on species and traits

Genomic prediction models I



RR-BLUP, Bayes A, Bayes B, ...

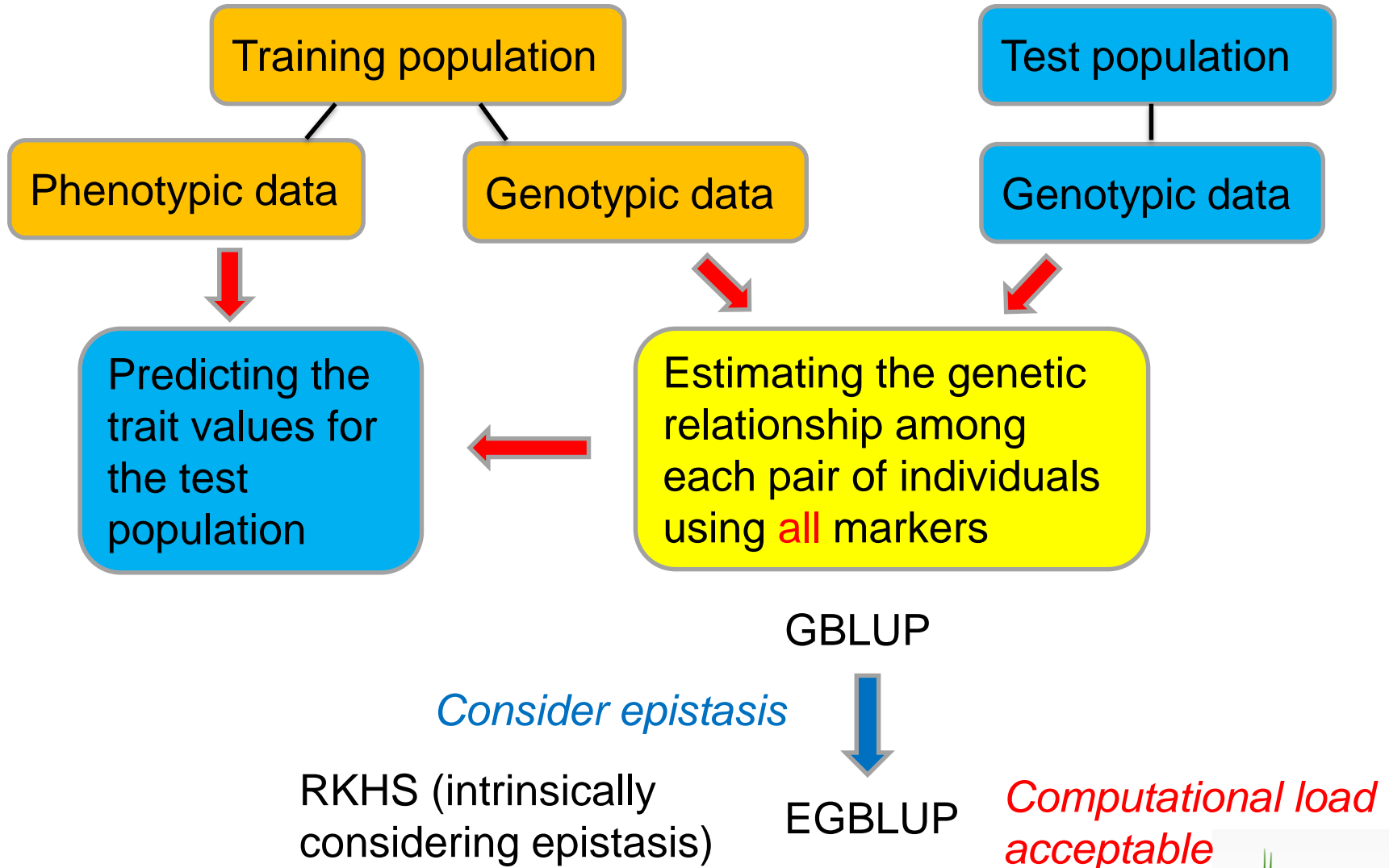


Consider epistasis

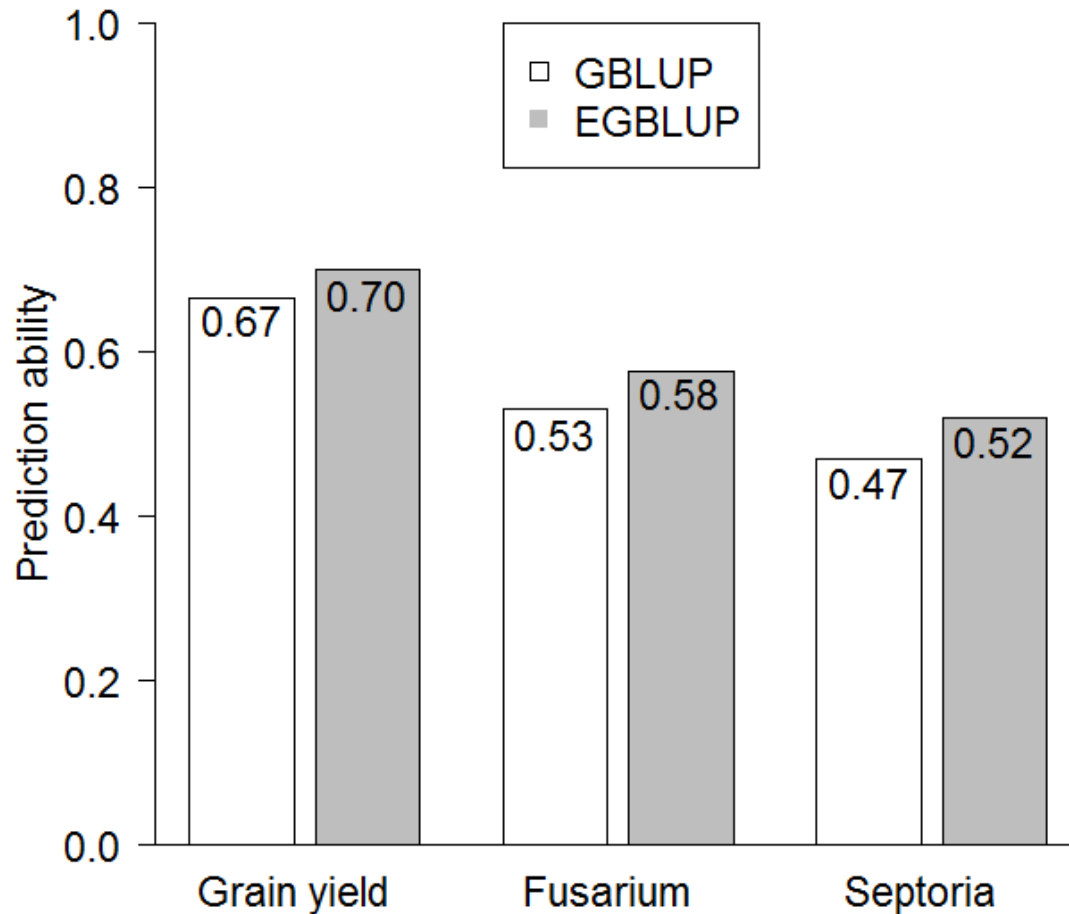
Extended RR-BLUP, Bayes models, ...

High computational load !

Genomic prediction models II



Genomic prediction for grain yield in a large winter wheat population



Data set

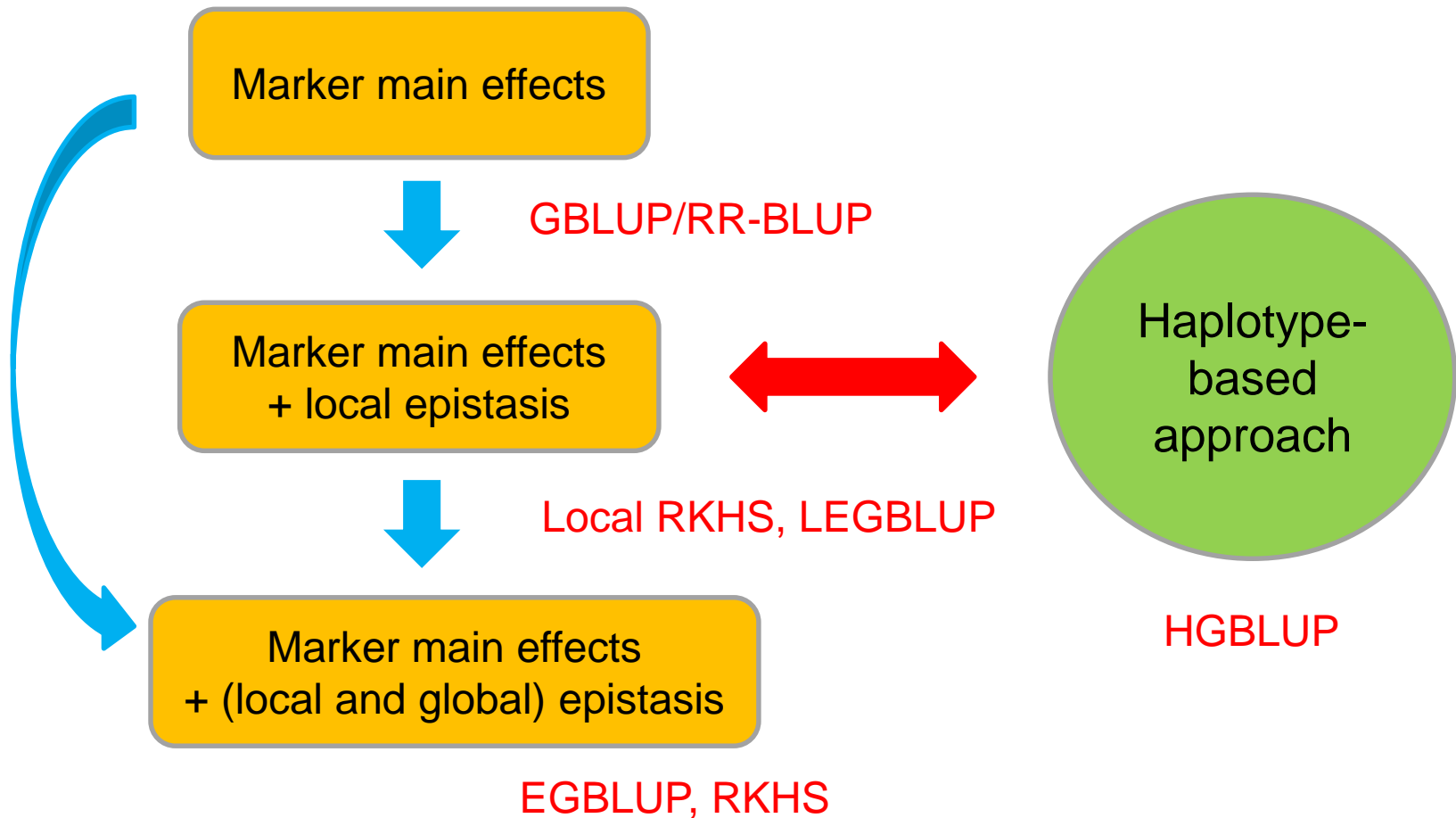


Trait	No. of lines	h^2
Grain yield	3,816	0.71
Fusarium	2,325	0.56
Septoria	2,325	0.32

Can a breeder make use of epistasis?

- Epistatic effects may disappear after generations due to recombination
- It may be beneficial to focus on epistatic interactions that span short map segments (*local epistasis*), e.g. 20 cM.
- Can we efficiently exploit local epistasis in genomic prediction models?

Genomic prediction models taking local epistasis into account



A trip from Haplotype-based model to marker-based model

HGBLUP

$$y = 1_n \mu + Xh + e$$
$$h \sim N(0, I\sigma_h^2)$$

Inbred population

Hybrid population

There exists a matrix V such that $X = ZV$

There does NOT exist any matrix V such that $X = ZV$

Let $\beta = Vh$

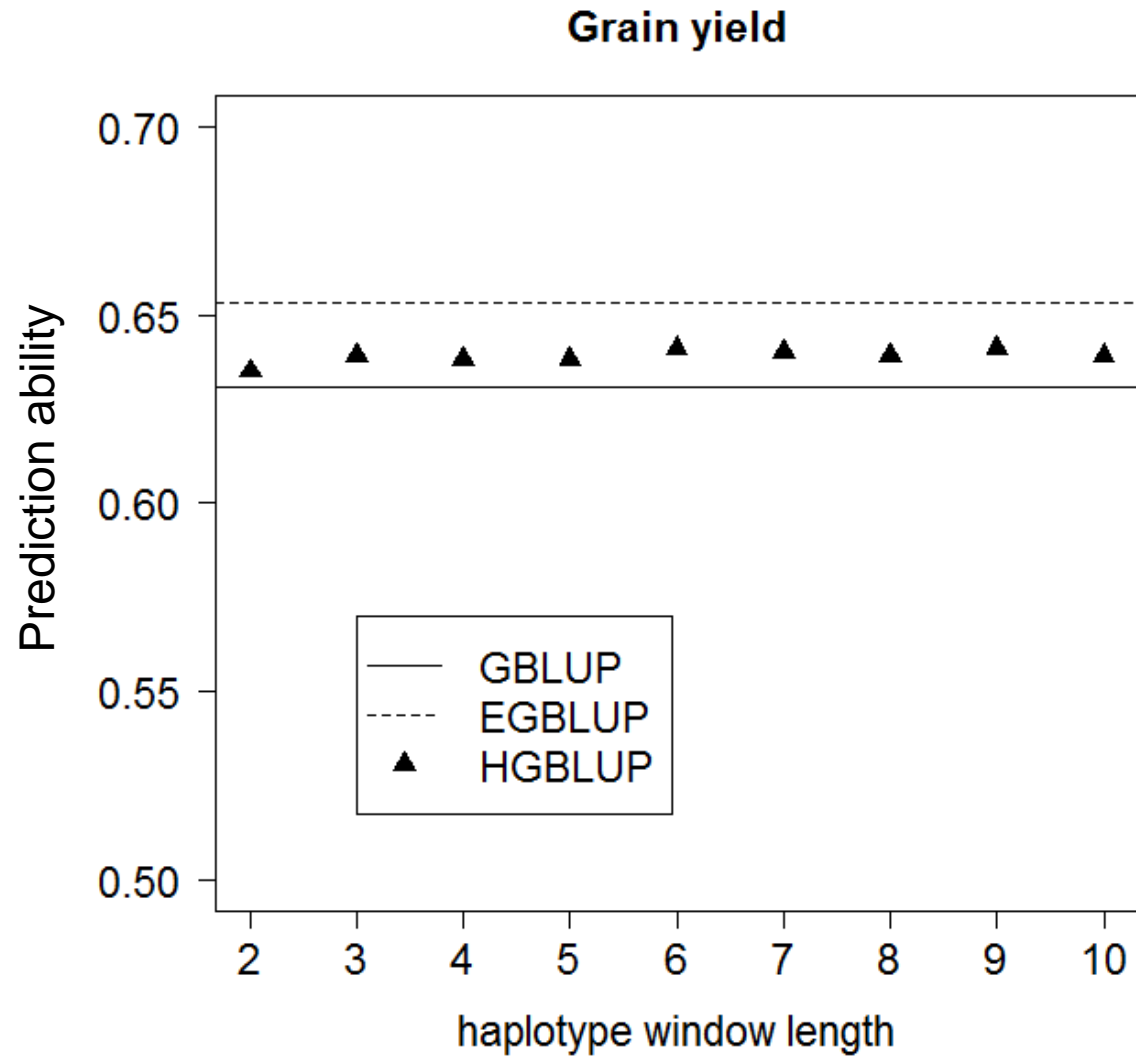
$$y = 1_n \mu + Z\beta + e$$
$$\beta \sim N(0, VV^T \sigma_h^2)$$

LEGBLUP

$$y = 1_n \mu + Z\alpha + e$$
$$\alpha \sim N(0, I\sigma_\alpha^2)$$

This result does NOT depend on the methods defining haplotypes

Haplotype-based genomic prediction



Summary

- Considering epistasis in genomic prediction can potentially increase prediction accuracy for complex trait such as grain yield in wheat
- Haplotype-based genomic prediction models intrinsically exploit local epistasis and hence can be attractive tools for breeders

Aknowledgement

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