

Weighted Multi-Trait GBLUP

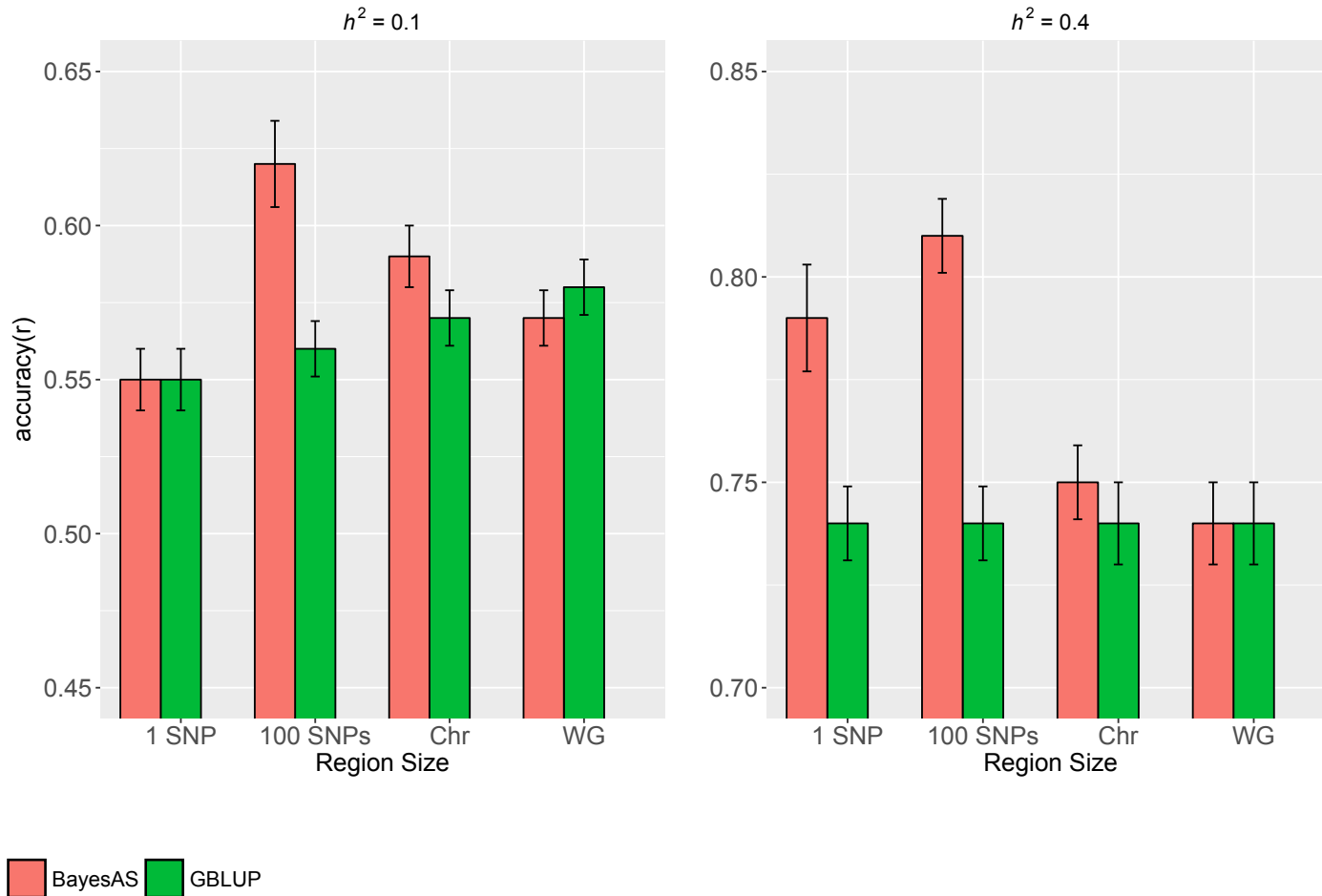
Using (co)variance estimates from Bayesian models

E Karaman*, MS Lund, MT Anche, L Janss & G Su

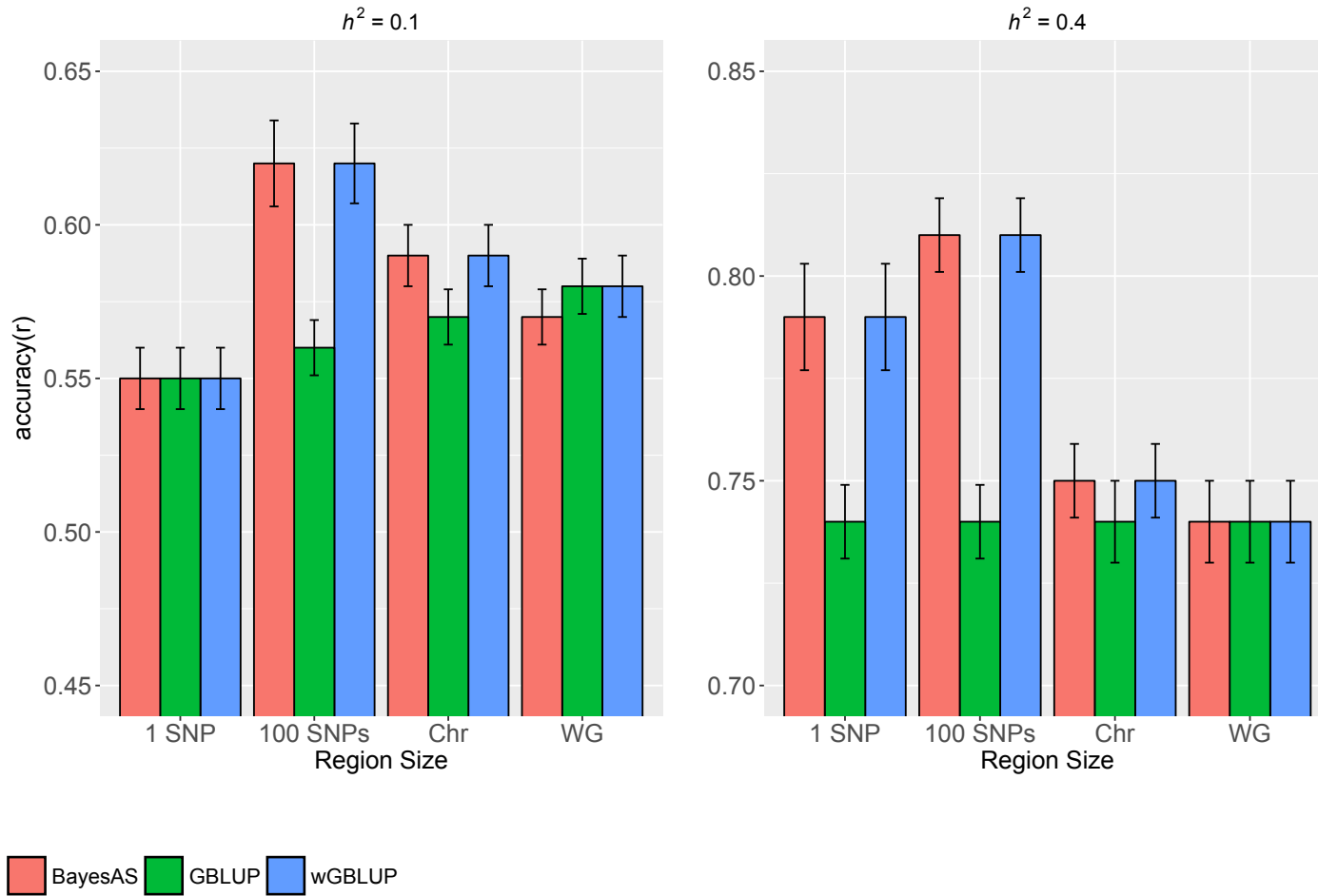
Centre for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University (DK)
*emre@mbg.au.dk

- Genetic correlation between traits:
 - a result of shared QTL
 - varies across the genome
- **GBLUP** assumes a constant correlation over the genome
- **Bayesian** multi-trait method accounting for heterogeneous (co)variances can provide higher accuracies
 - Can be *transferred* to GBLUP with weighted relationship matrices, **wGBLUP**

Bayesian method assuming region specific (co)variances improved accuracies



wGBLUP yielded similar accuracies to Bayesian method



Weighted Multi-Trait GBLUP

Using (co)variance estimates from Bayesian models

- Bayesian methods are computationally intensive
- GBLUP can yield accuracies as high as Bayesian methods when SNPs are weighted accordingly