



# THE IMPACT OF SINGLE NUCLEOTIDE POLYMORPHISM SELECTION ON PREDICTION OF GENOMEWIDE BREEDING VALUES

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## **1. Data**

## **2. Models**

## **3. Results**

- **mean, SD**
- **individual differences**
- **SNP effects**
- **correlations**

## **4. Conclusions**



## 1. QTL workshop simulated data set

## 2. Animals with genotypes and phenotypes

## 3. SNP data sets

- all 6 000
- $MAF \geq 0.3$  3 328
- every 5<sup>th</sup> 1 200
- every 10<sup>th</sup> 600
- every 20<sup>th</sup> 300



**EBV**

$$\mathbf{y} = \boldsymbol{\mu} + \mathbf{Z}\boldsymbol{\alpha} + \mathbf{e}$$

$$\boldsymbol{\alpha} \sim N(0, \mathbf{A}\sigma_{\alpha}^2)$$

$$\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$$

**GBV**

$$\sum_{i=1}^{N_{SNP}} z_i q_i$$

1.  $\mathbf{y} = \boldsymbol{\mu} + \mathbf{X}\mathbf{q} + \mathbf{e}$

$$x \in \{0,1,2\}$$

2.  $\mathbf{y} = \boldsymbol{\mu} + \mathbf{Z}\boldsymbol{\alpha} + \mathbf{X}\mathbf{q} + \mathbf{e}$

$$\boldsymbol{\alpha} \sim N(0, \mathbf{A}\hat{\sigma}_{\alpha}^2)$$

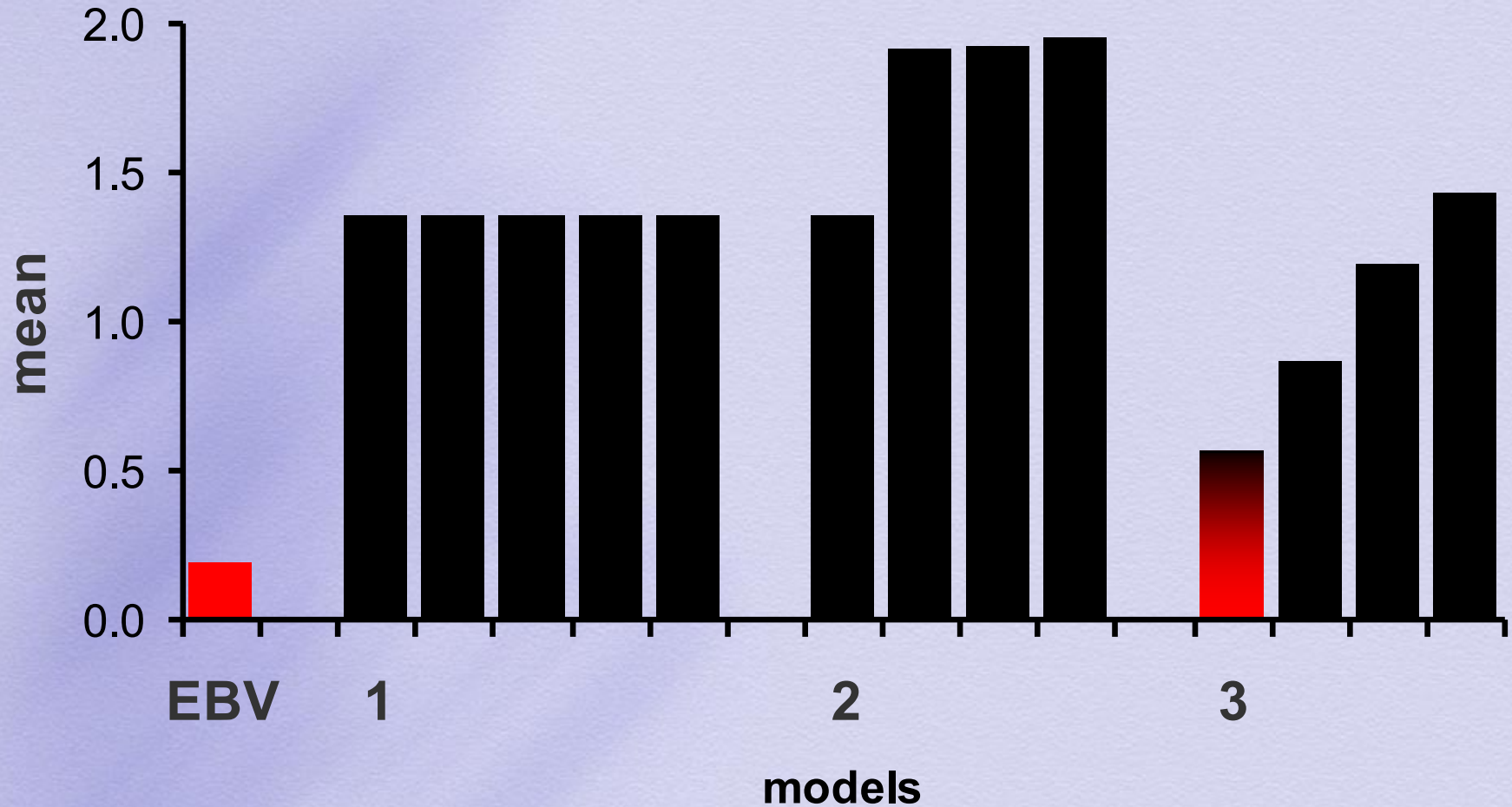
3.  $\mathbf{y} = \boldsymbol{\mu} + \mathbf{Z}_q\mathbf{q} + \mathbf{e}$

$$z \in \{0,1,2\}$$

$$\mathbf{q} \sim N(0, \mathbf{I}\hat{\sigma}_{\alpha}^2)$$

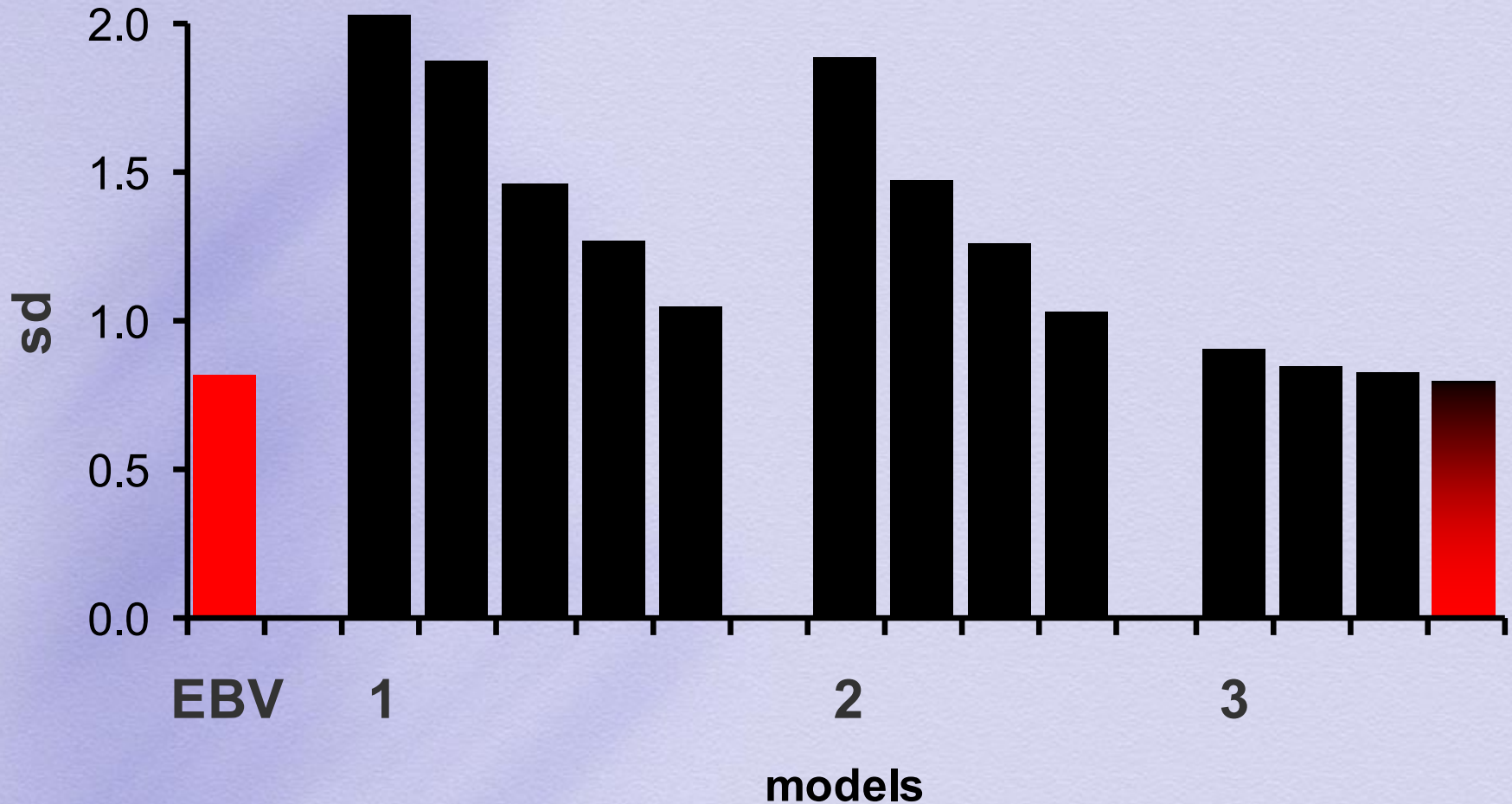
## Mean GBVs

for models 1, 2, 3 and various SNP data sets



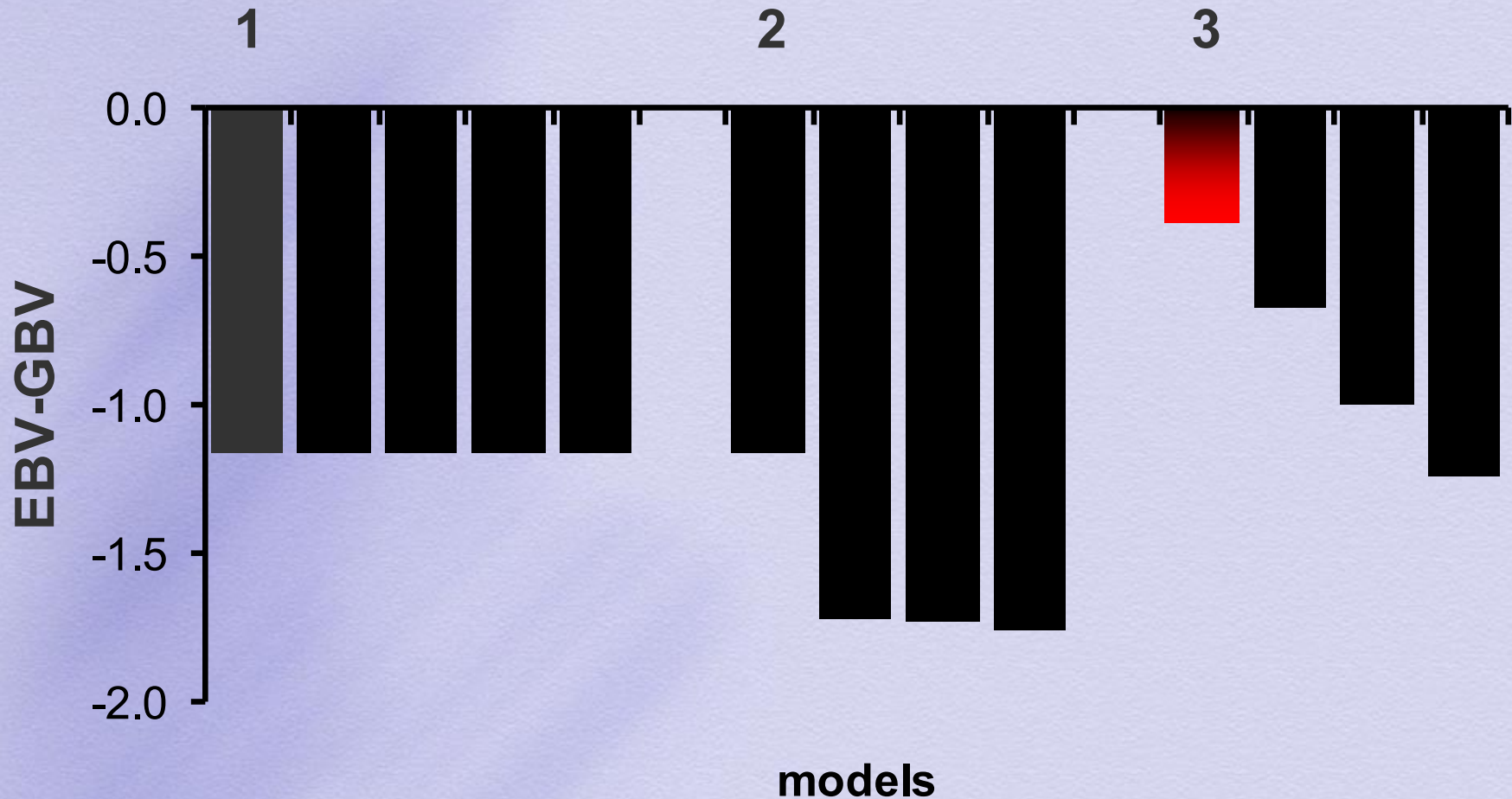
## Standard deviations of GBVs

for models 1, 2, 3 and various SNP data sets



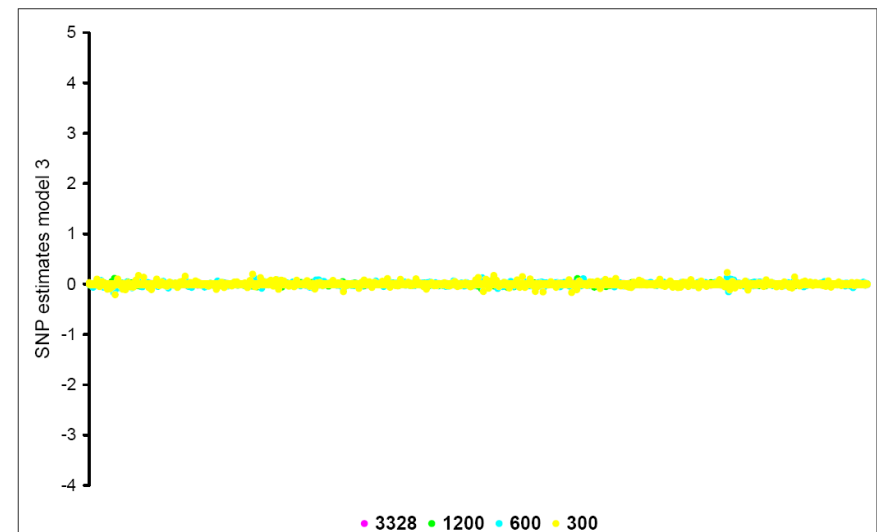
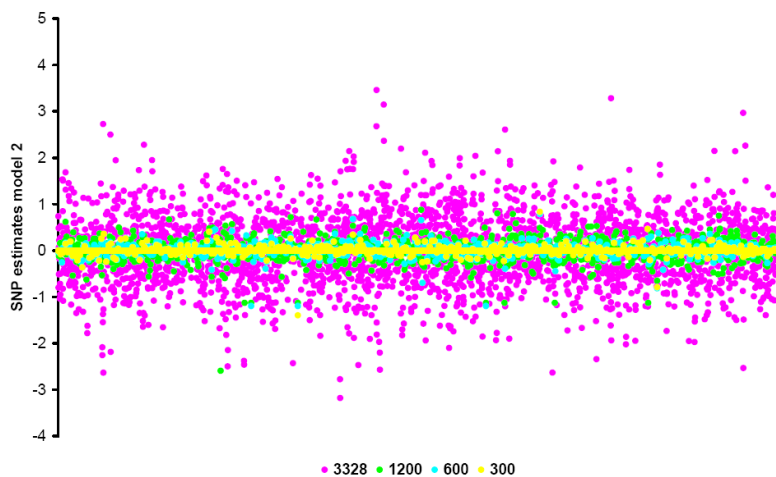
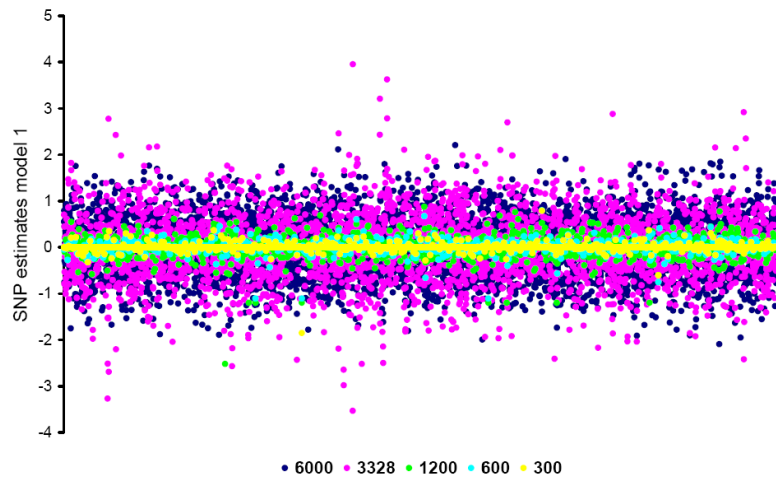
## Mean EBV-GBV

for models 1, 2, 3 and various SNP data sets



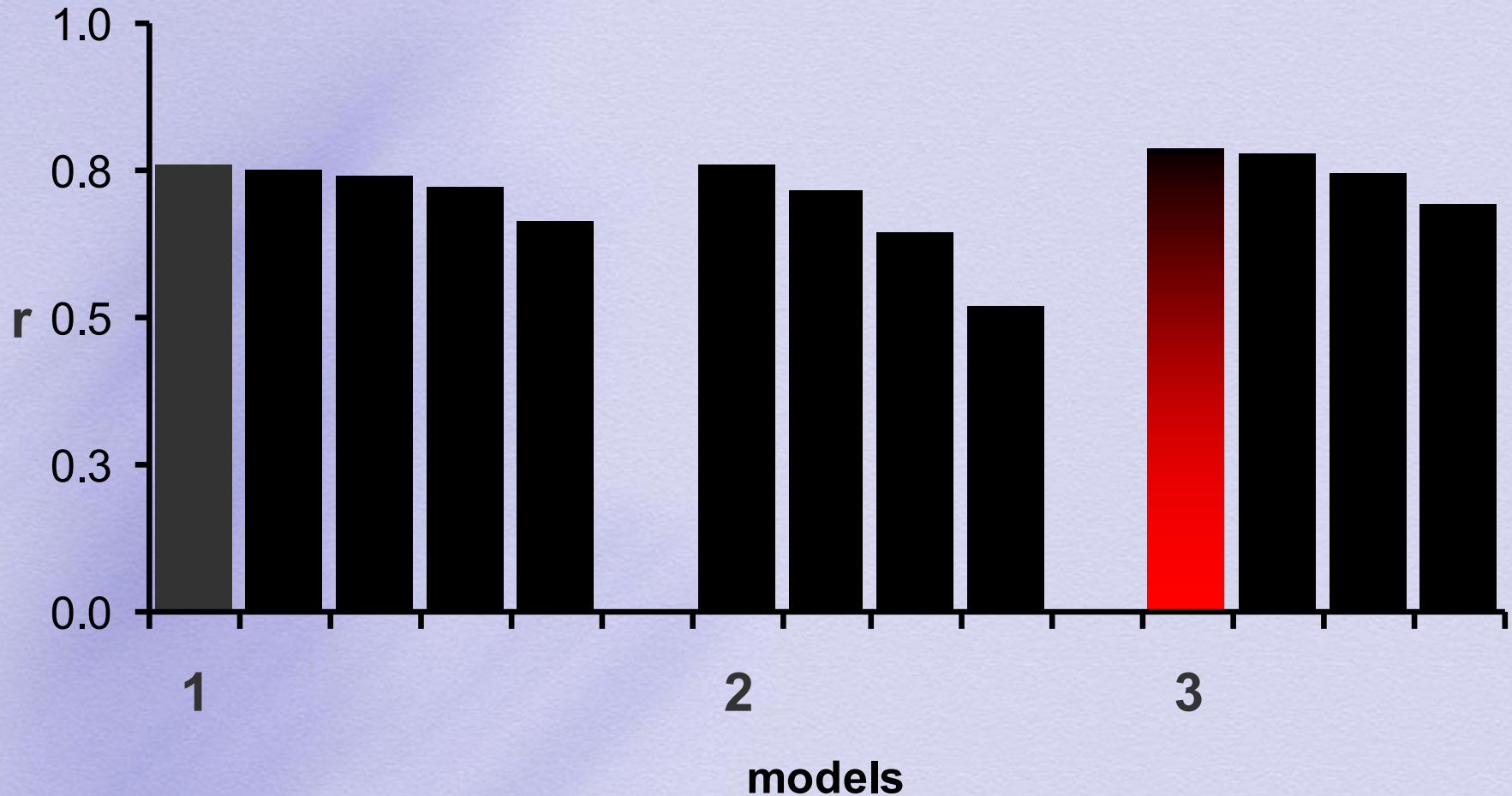
## SNP additive effects

for models 1, 2, 3 and various SNP data sets



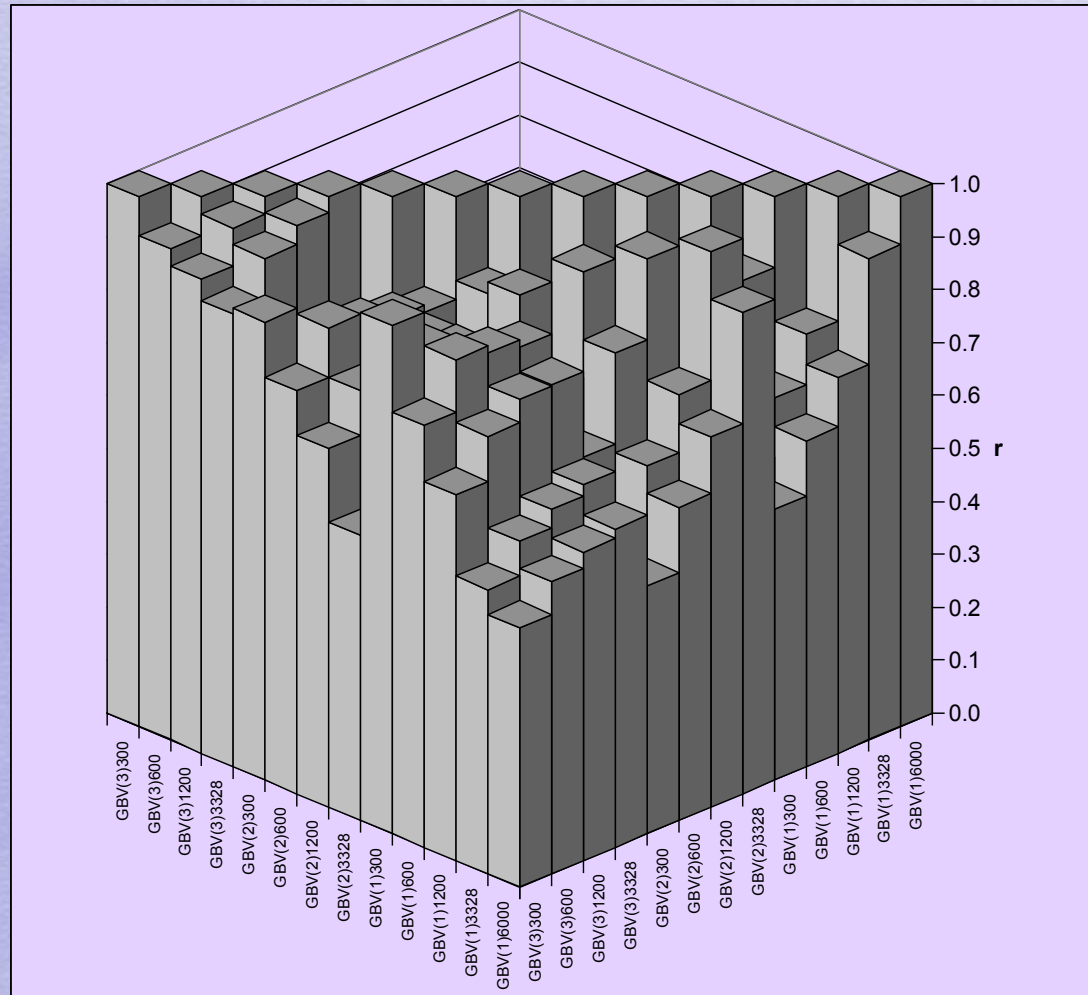
## Correlation EBV-GBV

for models 1, 2, 3 and various SNP data sets



# Correlation GBV-GBV

for models 1, 2, 3 and various SNP data sets





1. Low correlations EBV-GBV
2. Low correlations GBV-GBV
3. GBV overestimates EBV
4. SNP estimates differ across models
  - GBV → model with random SNP
  - QTL → model with fixed SNP



**audience**



**collaborators**