

Genomic evaluation for harvest and residual carcass weight in channel catfish using single-step genomic BLUP

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Introduction

- Harvest weight: 0.8 to 1 kg
 - Sexual maturity between 2 and 3 years old
 - Spawning season in the Spring/Summer
 - About 20,000 eggs/year
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- Channel catfish (*Ictalurus punctatus*)
 - Blue catfish (*Ictalurus furcatus*)
 - Hybrid



Breeding program

- USDA Warmwater Aquaculture Research Unit
- Pedigree based evaluation since 2006 (Harvest weight and carcass yield)
- Genotypes available early 2017

Genomic selection

- Increases accuracy
- Reduces generation interval
- Explore within family variation

Objectives

- Investigate feasibility of implementing genomic selection by using ssGBLUP
- Identify major SNP associated with harvest weight and residual carcass weight

Material and Methods

Data

- USDA-ARS Warmwater Aquaculture Research Unit
 - Records from 2008 to 2015

 - Pedigree information: 36,365 animals
 - Harvest weight (HW): 27,160 records ($h^2 = 0.27$)
 - Residual carcass weight (RCW)*: 6,020 records ($h^2 = 0.34$)
- * Carcass weight adjusted to a common body weight

Genotypes

- 55k panel developed by the USDA Warmwater Aquaculture Research Unit
- 2,911 genotyped animals
 - 2,826 with harvest weight records
 - 969 with carcass weight records
- 54k SNP after quality control

Single-step GBLUP (ssGBLUP)

- Includes all animals
- Combines genotypes, phenotypes and pedigree
- Integrated genomic/pedigree relationship matrix (H)

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + H^{-1}\lambda \end{bmatrix} \begin{bmatrix} \beta \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

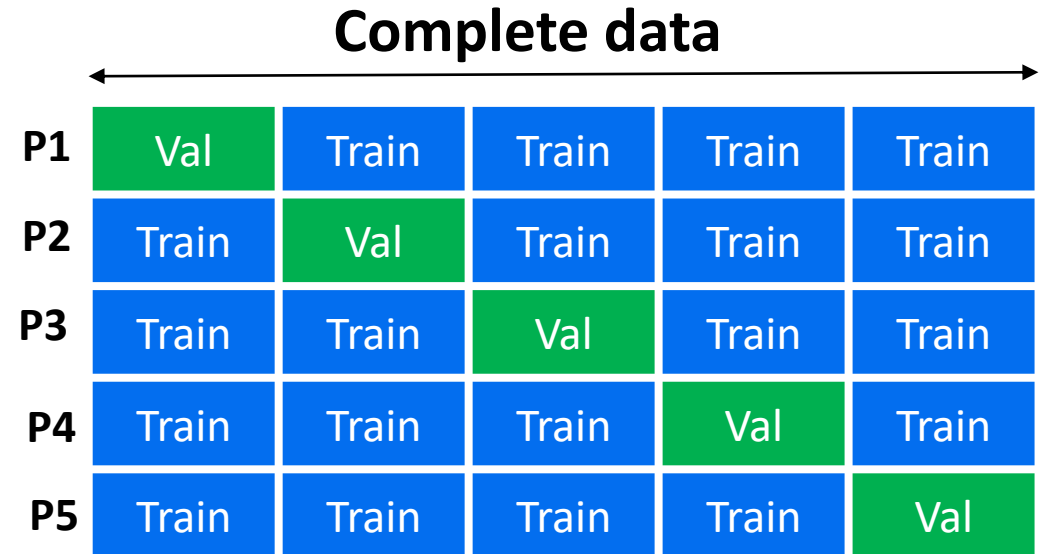
$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$

- A = pedigree relationship matrix
- A_{22} = pedigree relationship matrix for genotyped animals
- G = genomic relationship matrix
- $\lambda = \sigma_e^2 / \sigma_a^2$

Validation Study

Validation

- Method to compare traditional and genomic evaluation
- ✓ Adjusted phenotypes based on complete data (\hat{Y})
- ✓ 5-fold cross validation
- ✓ 10-fold cross validation
- Genotyped animals randomly divided in 5/10 mutually exclusive groups
- 5 replicates



- BLUP and ssGBLUP performed using BLUPF90 family of programs

- ✓ Predictive ability: ability to predict future performance

$$\text{cor}((G)EBV, \hat{Y})$$

- ✓ Accuracy:

$$\text{acc} = \frac{\text{predictive ability}}{\sqrt{h^2}}$$

- ✓ Inflation: $b_1 < 1.0$

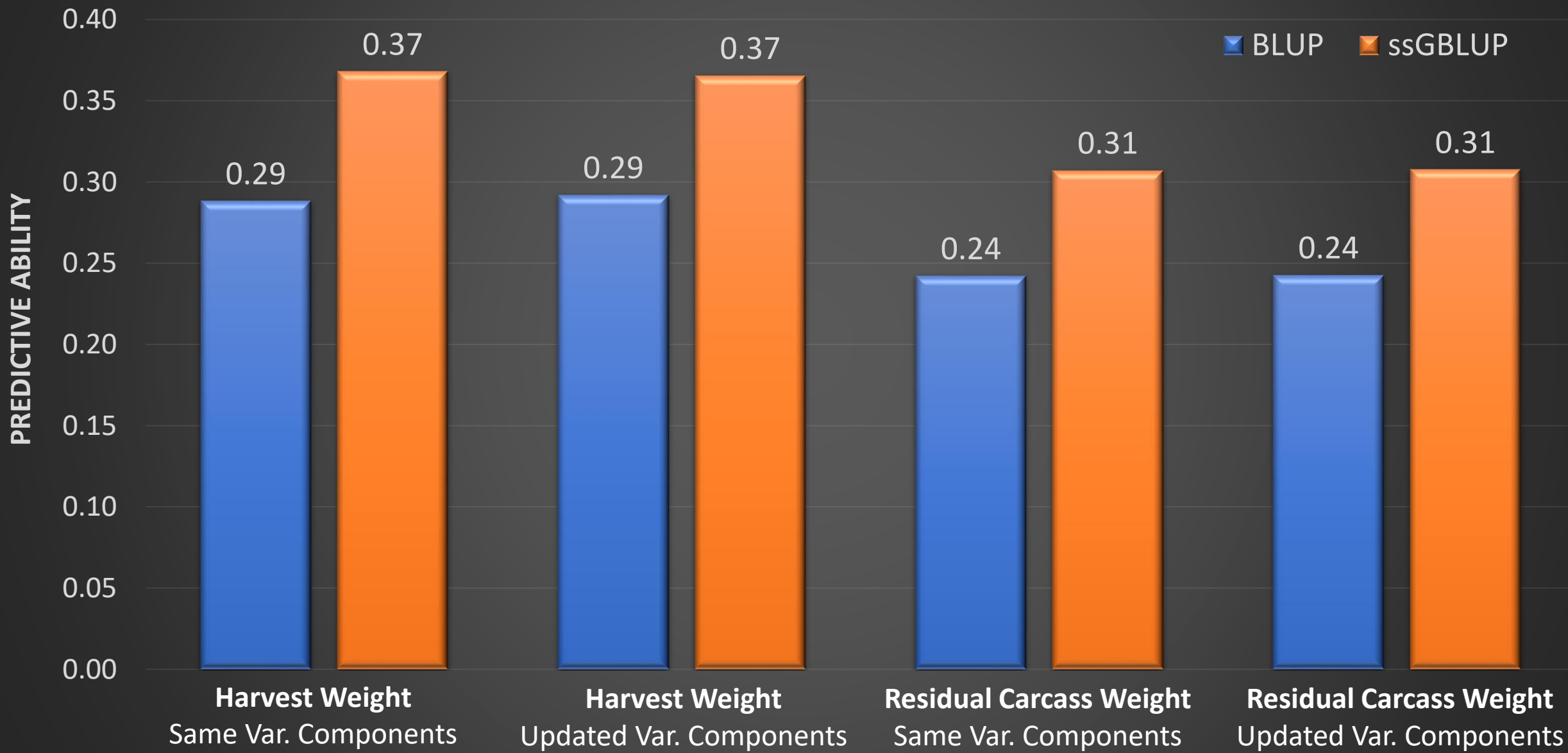
$$\hat{Y}_c = b_0 + b_1 \times (G)EBV$$

- ✓ Updated variance components

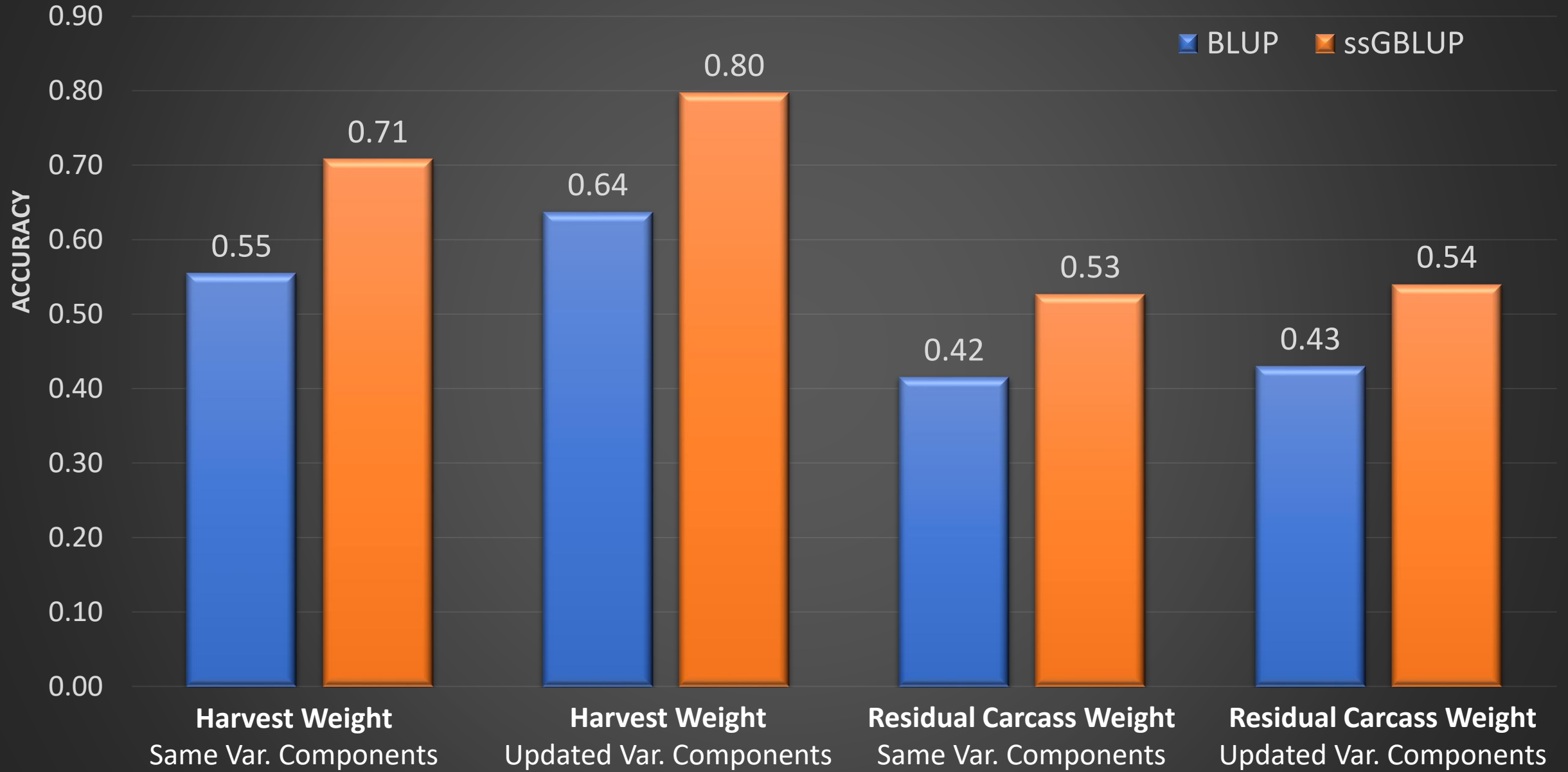
Results

5-Folds Cross Validation

Predictive Ability

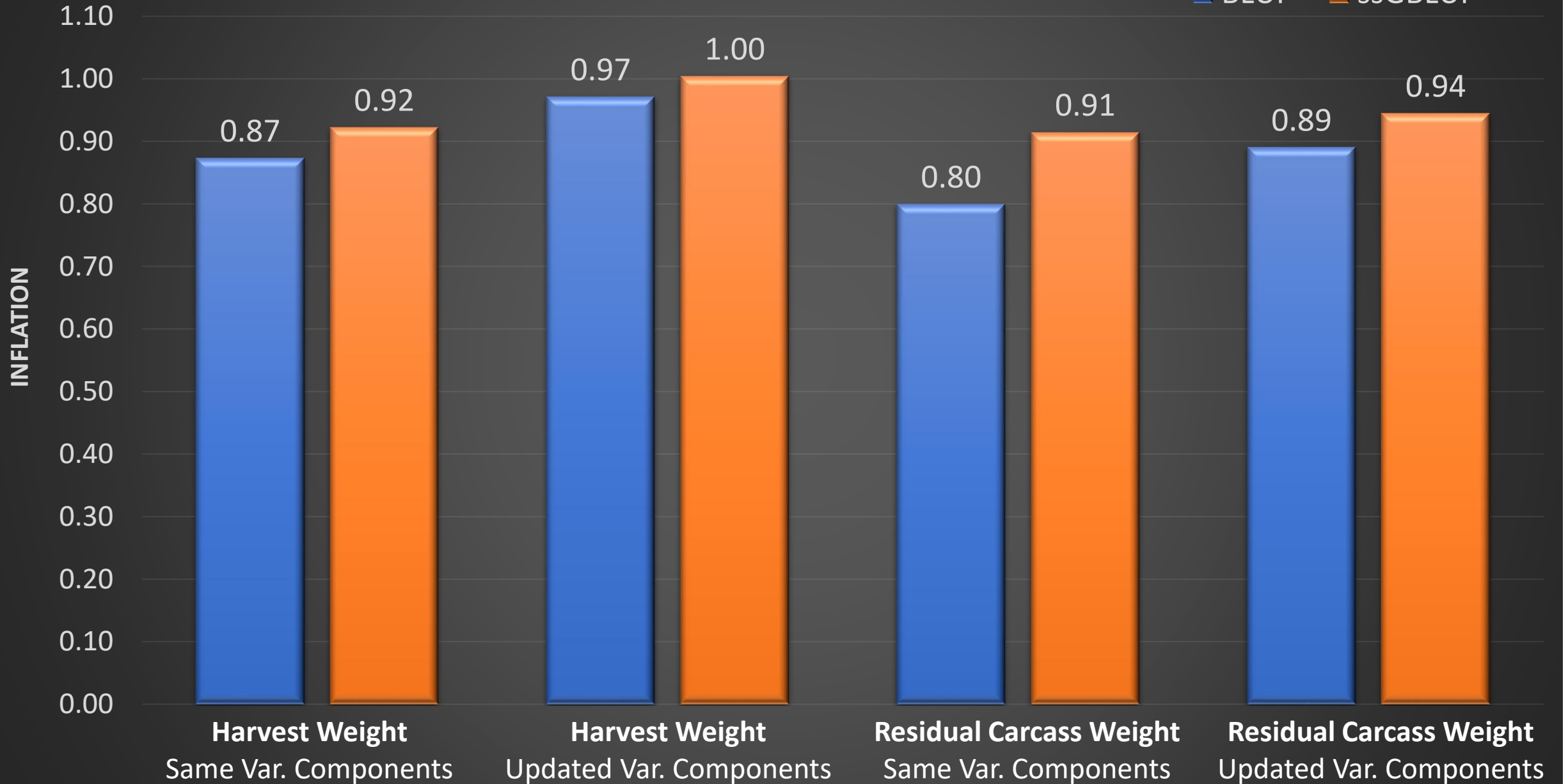


Accuracy



Inflation

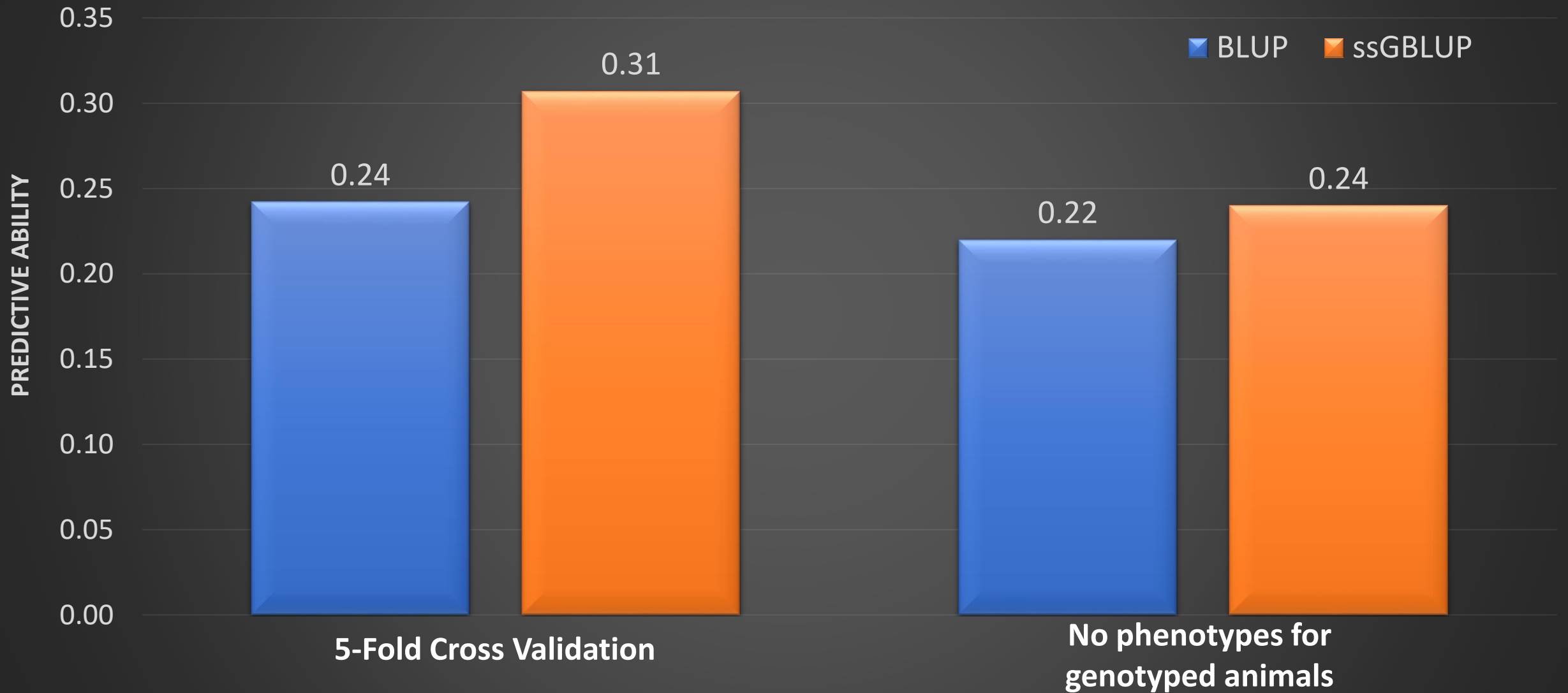
BLUP ssGBLUP



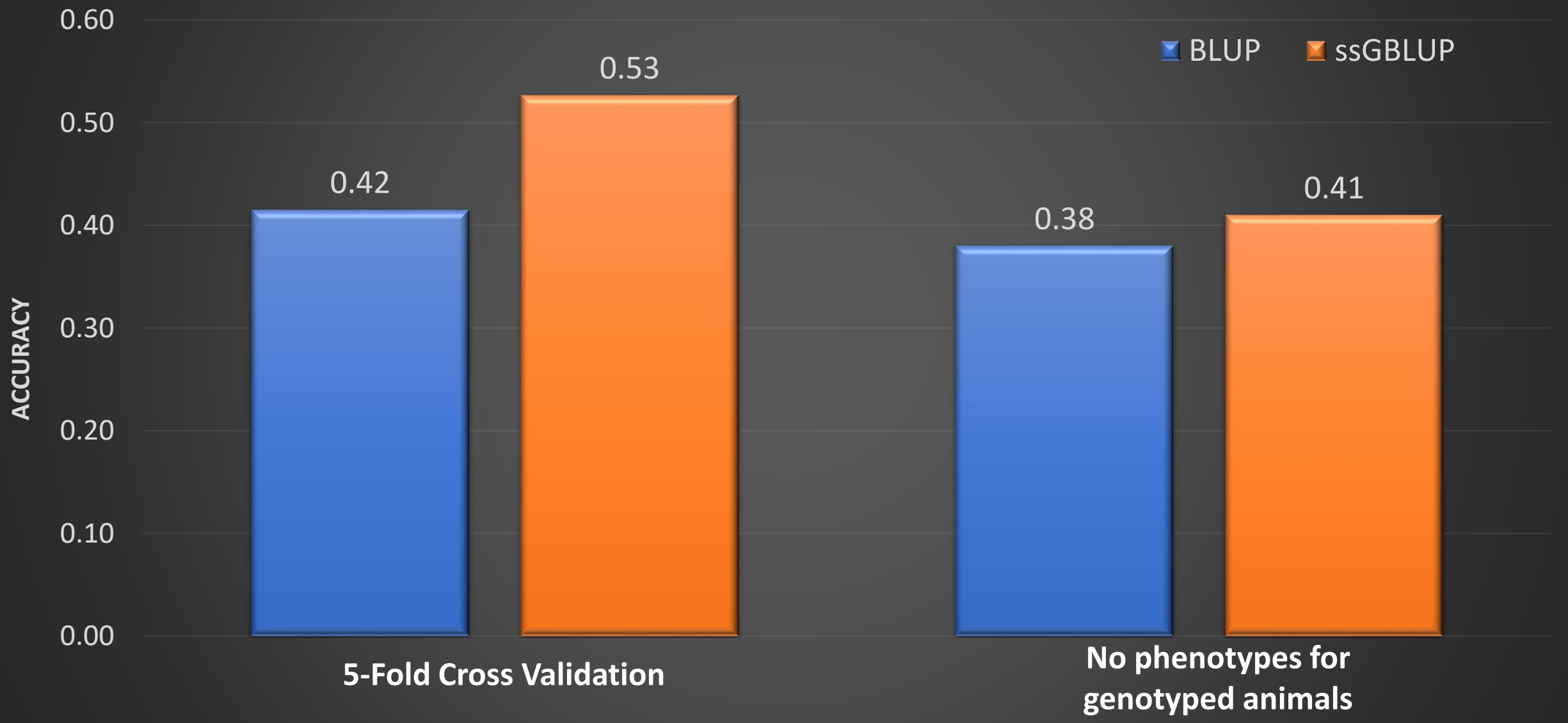
Is it important to genotype processed fish?

- Remove phenotypes only for genotyped animals
- New validation data set
- Calculate predictive ability and accuracy
- Compare BLUP and ssGBLUP

Predictive Ability for RCW



Accuracy for RCW



Weighted ssGBLUP Study

Weighted ssGBLUP

- Iterative process

1. $D = I$

2. $G = \frac{ZDZ'}{2\sum p_i(1-p_i)}$

3. GEBV from ssGBLUP

4. $\hat{u} = \delta DZ'G^{-1}\hat{a}$

5. $d_i = \hat{u}_i^2 2p_i(1-p_i)$

6. Iterate from 2

- G = genomic relationship matrix

- $\lambda = \sigma_e^2 / \sigma_a^2$

- $\delta = \sigma_u^2 / \sigma_a^2$

- D = diagonal matrix for SNP weights

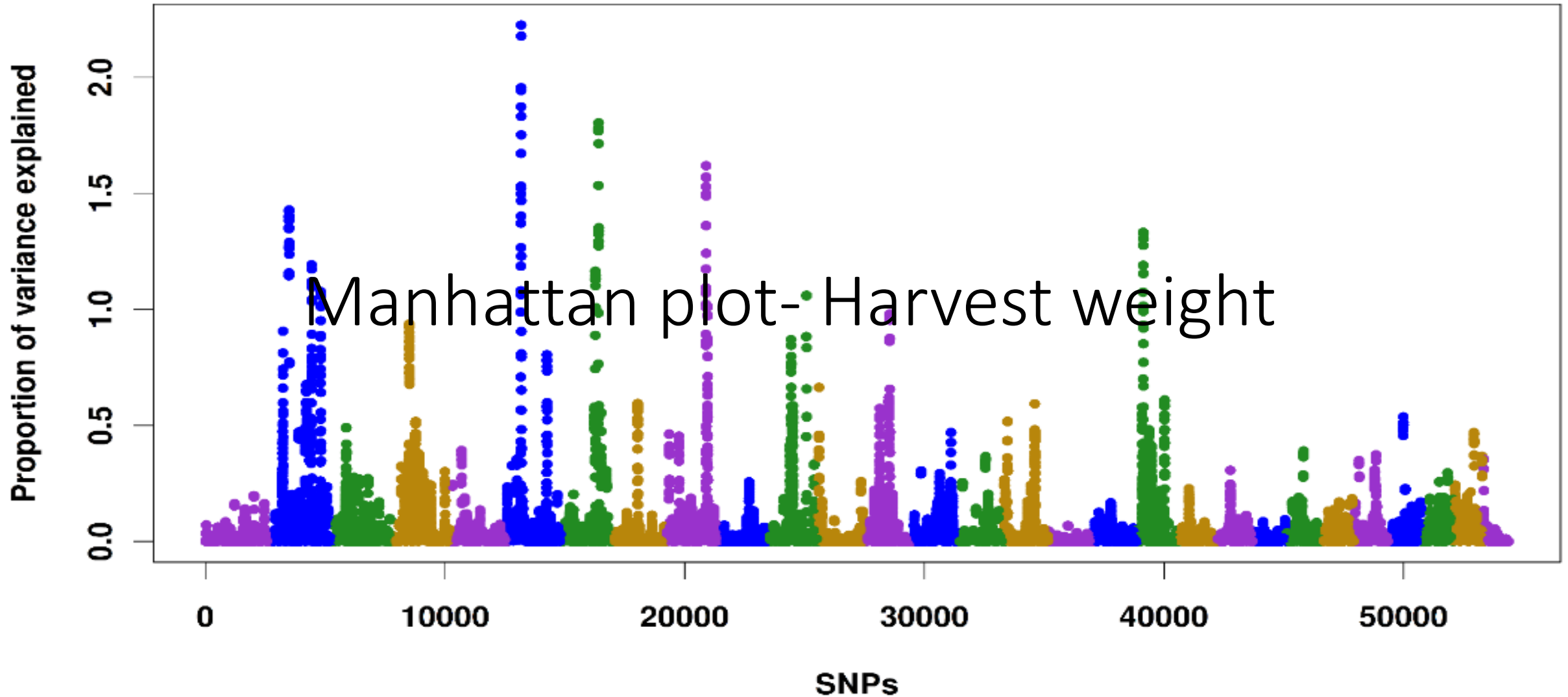
- Z = matrix of SNP markers centered for current allele frequencies

- u = SNP effect

- d_i = Weight for SNP markers

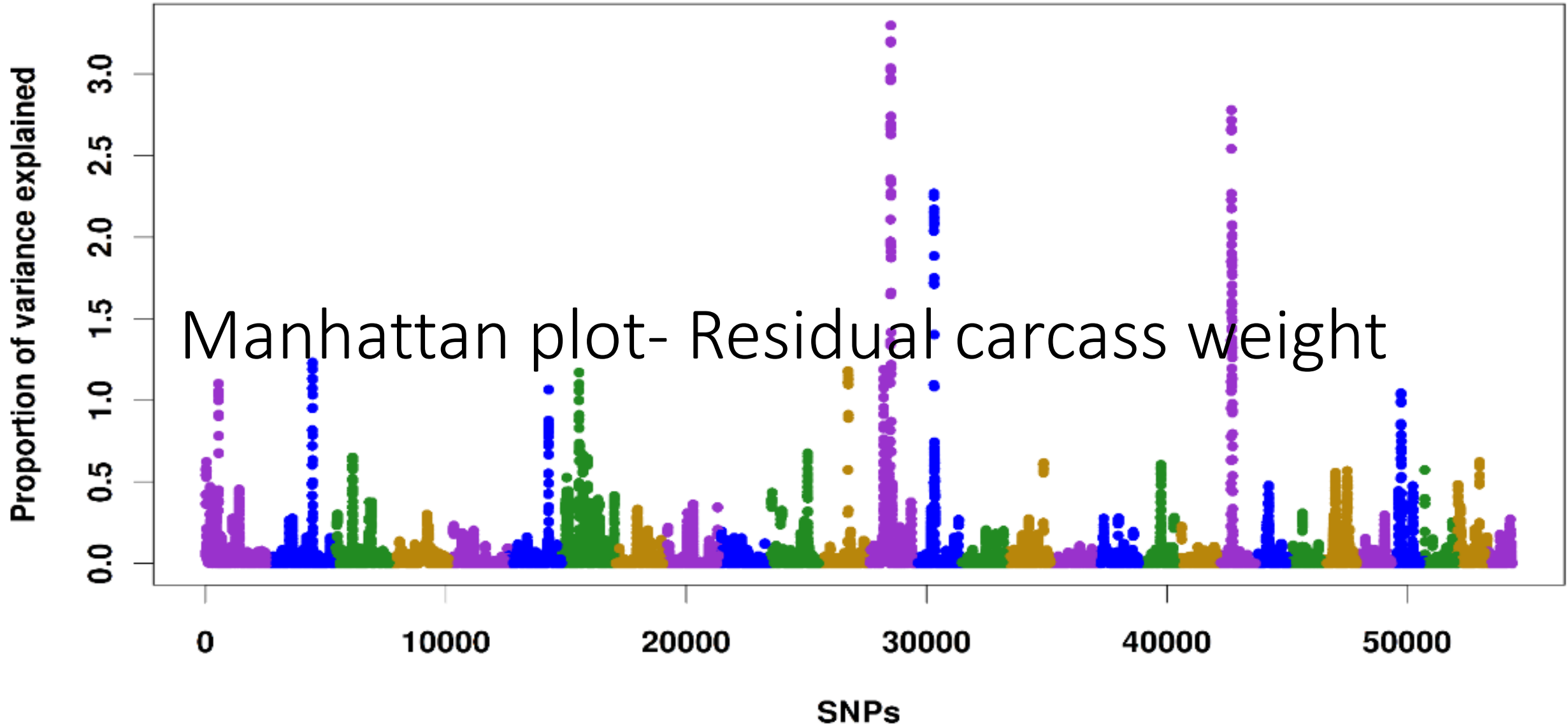
- p_i = allele frequency

Variance explained by 20 adjacent SNP



- 2.2% at most

Variance explained by 20 adjacent SNPs



- 3.3% at most

Conclusions

- Genomic information improved ability to predict future performance
- Estimated variance components for training data sets reduced inflation
- It is important to genotype processed fish for carcass traits
- No major SNP were found in both traits, indicating the need of using all the markers available for evaluation purposes

Acknowledgements



Thank you!

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