

# Singular Value Decomposition of the Genotype Matrix

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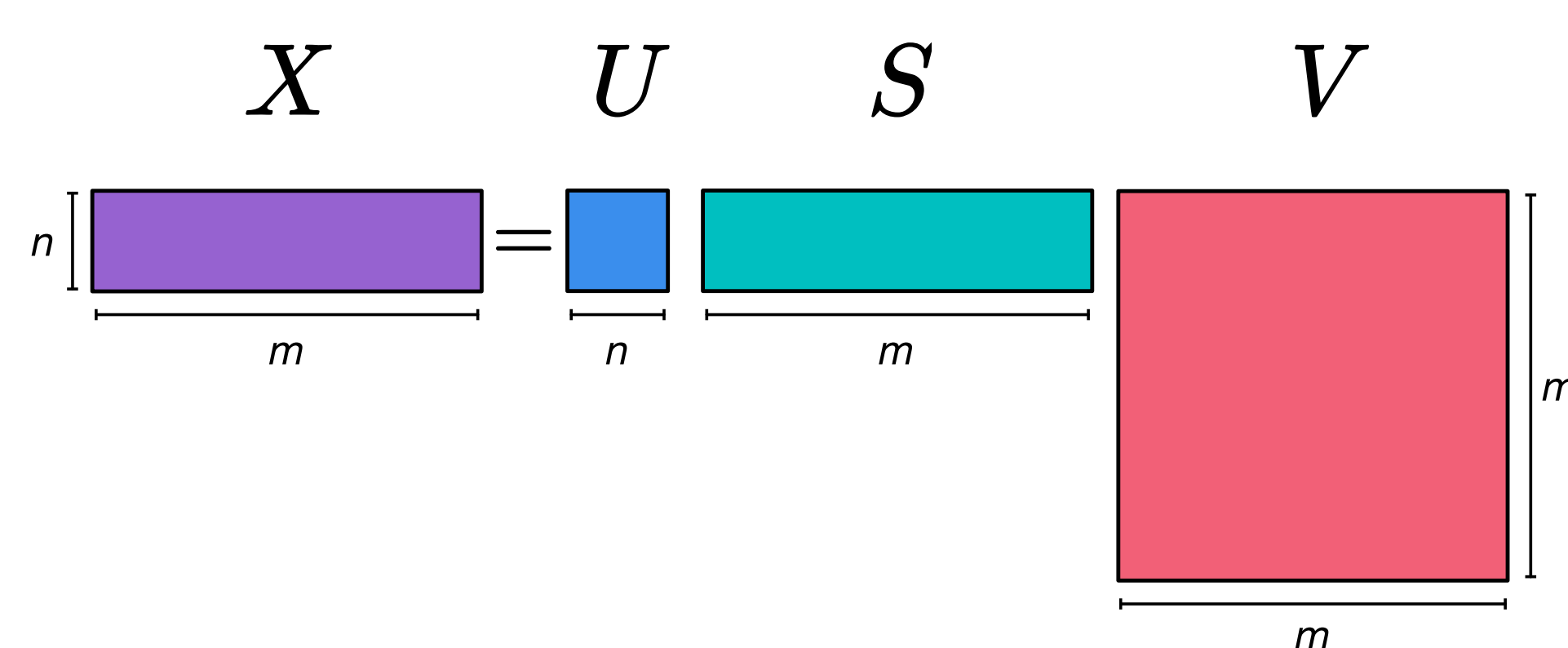
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## Aim

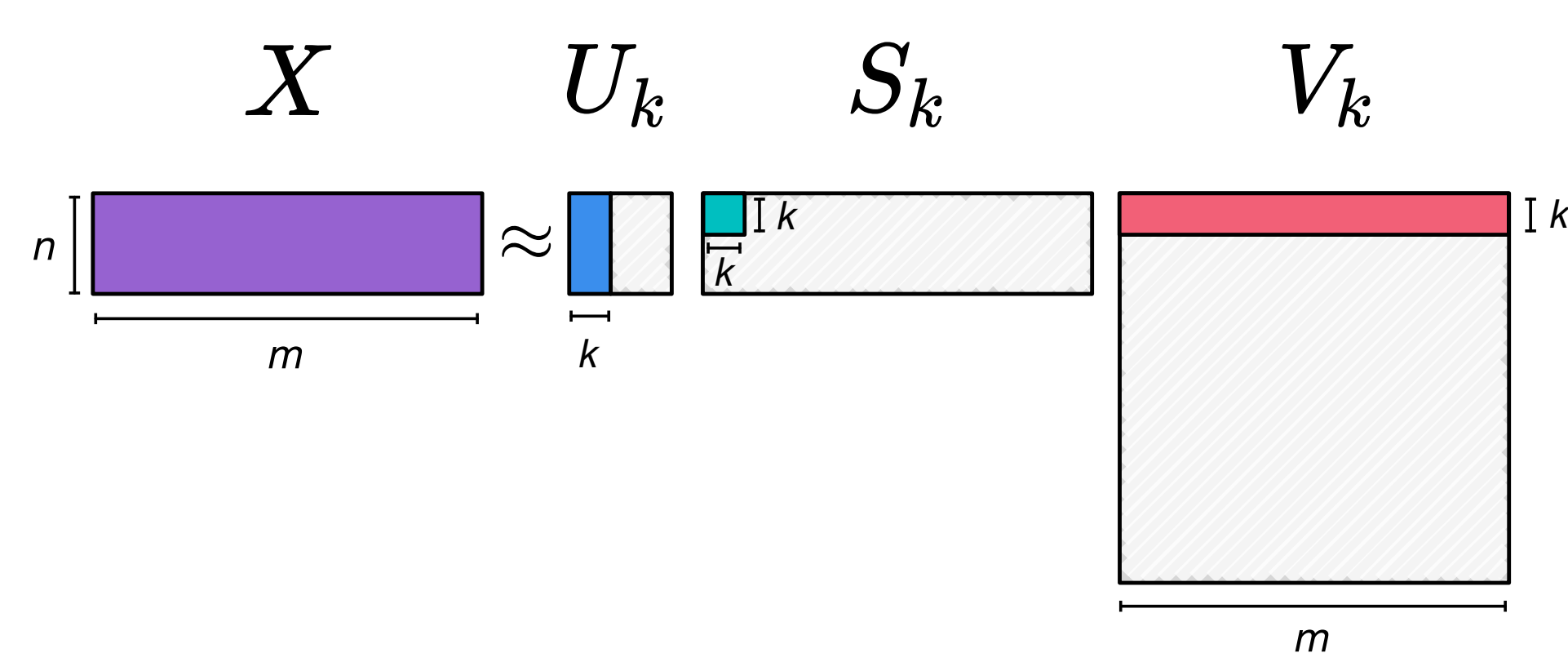
Evaluate the accuracy of prediction when varying the number of components in the truncated-SVD approximation of the genotype matrix.

## SVD

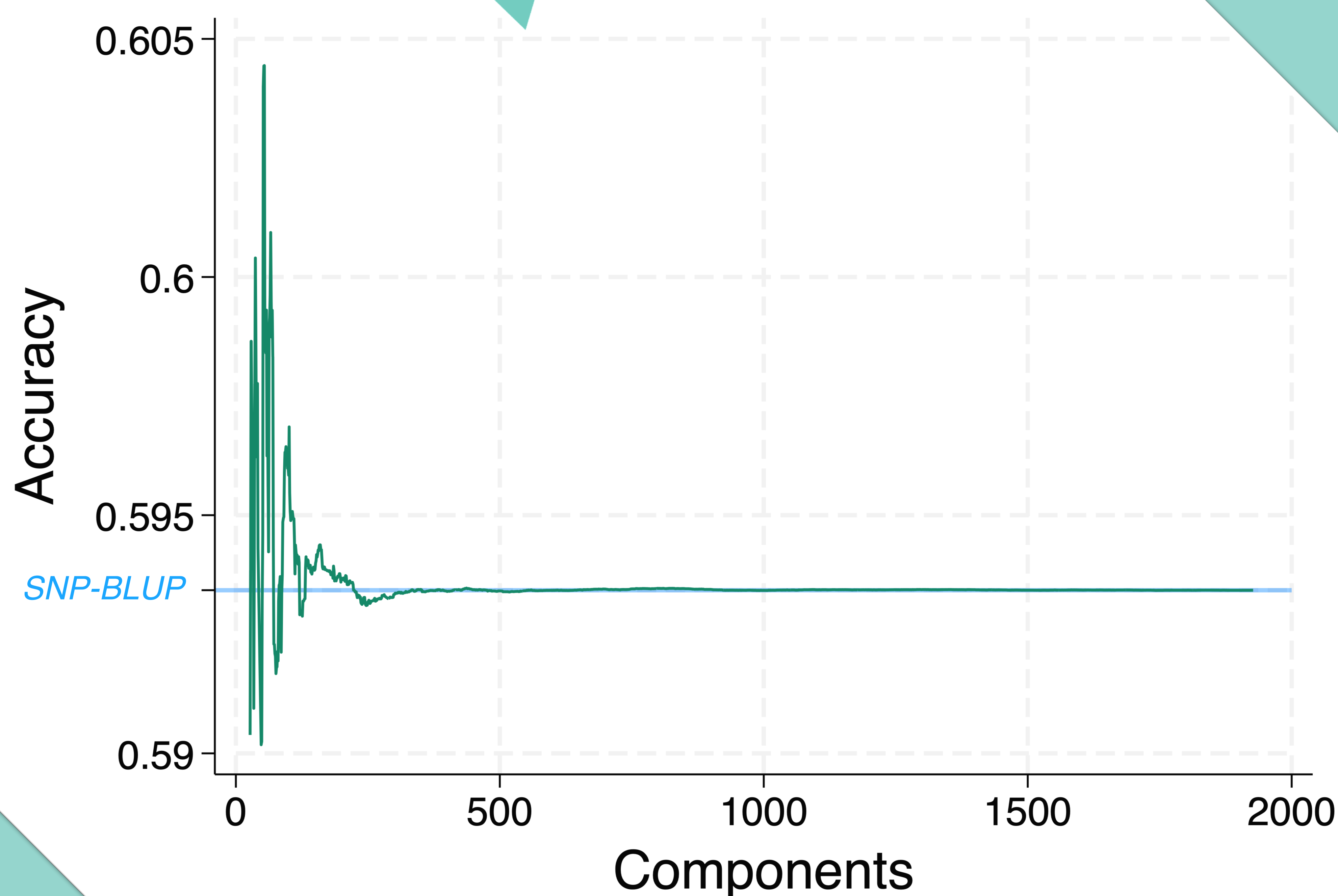
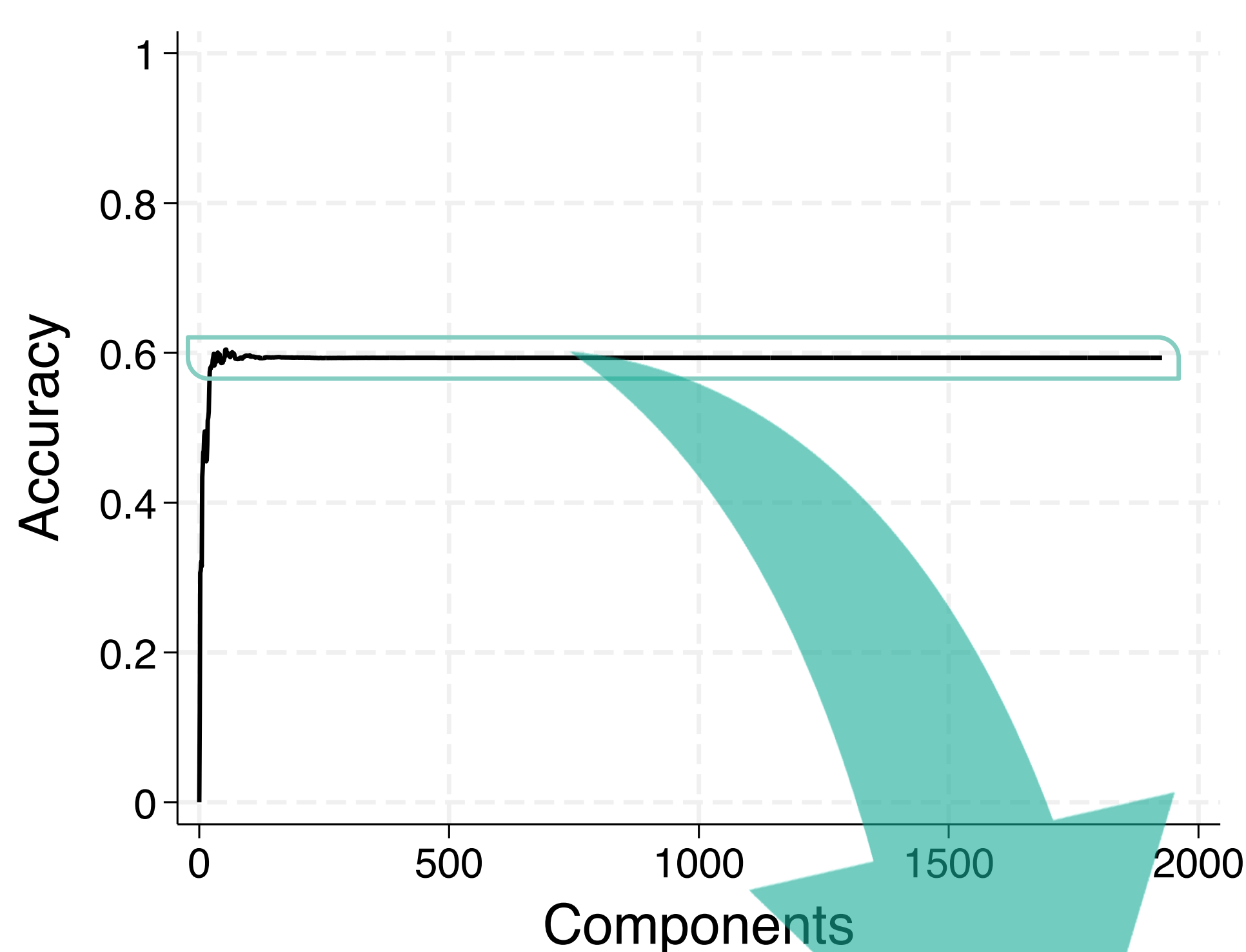
### Singular Value Decomposition



### Truncated SVD



## Results



## Simulation

- 1,000 QTL along 16,454 SNPs (1,927 Atlantic Salmon individuals)
- QTL effects sampled from normal distribution  $b_1, \dots, b_{1000}$  i.i.d.  $b_i \sim N(0, V_m)$

$$V_m = \frac{h^2}{2 \sum_{i=1}^{1000} p_i(1 - p_i)}$$

- QTLs masked from genotype matrix  $X$

- True breeding values  $g$  calculated

$$g = Xb$$

- Breeding values predicted by PCRR

$$\hat{g} = X\hat{b} = X V_k \hat{S}_k$$

(10-fold cross-validation)

- Correlation coefficients estimated

$$\hat{r} = \frac{Cov(g, \hat{g})}{\hat{\sigma}_g \hat{\sigma}_{\hat{g}}}$$

## Conclusions

- SVD is useful for data reduction of genotype matrices
- Good accuracies with few components
- SVD can yield higher accuracies than SNP-BLUP

## QR code for supplement

