Simulation of phenotypic values (100 iterations)

\[ y = X_1 \beta_1 + X_2 \beta_2 + X_3 \beta_3 + Zu + e, \text{ (Eq. 1)} \]

- \( y \): phenotypic values
- \( X_1 \beta_1, X_2 \beta_2, X_3 \beta_3 \): fixed effects (marker effects)
- \( Zu \): random effects (polygene effects)
- \( e \): residuals

- \( X_1 \) and \( X_2 \) belong to the same haplotype block.

We assumed 2 scenarios.

1. **Coupling**: \( \text{cor}(X_1, X_2) > 0 \) \( \rightarrow \beta_1 = \beta_2 \), \( \text{cor}(X_1, X_2) < 0 \) \( \rightarrow \beta_1 = -\beta_2 \)
2. **Repulsion**: \( \text{cor}(X_1, X_2) > 0 \) \( \rightarrow \beta_1 = -\beta_2 \), \( \text{cor}(X_1, X_2) < 0 \) \( \rightarrow \beta_1 = \beta_2 \)

Perform GWAS with 4 methods.

1. Our proposed method, **RAINBOW** (R package RAINBOWR)
2. The **single-SNP** method (R package rrBLUP)
3. **Haplotype-based** method introduced by Yano *et al.*, 2016
4. **SNP-set** method, SKAT (R package SKAT)

Evaluate the results with the following summary statistics

1. \(-\log_{10}(p)\) and \(-\log_{10}(p_a)\), correspond to the **detection power**
2. **Recall**, **Precision**, and **F-measure**
3. **AUC** (area under the curve) for **regions around causals**