Quantitative genetics from genome assemblies to neural network aided omics-based prediction of complex traits

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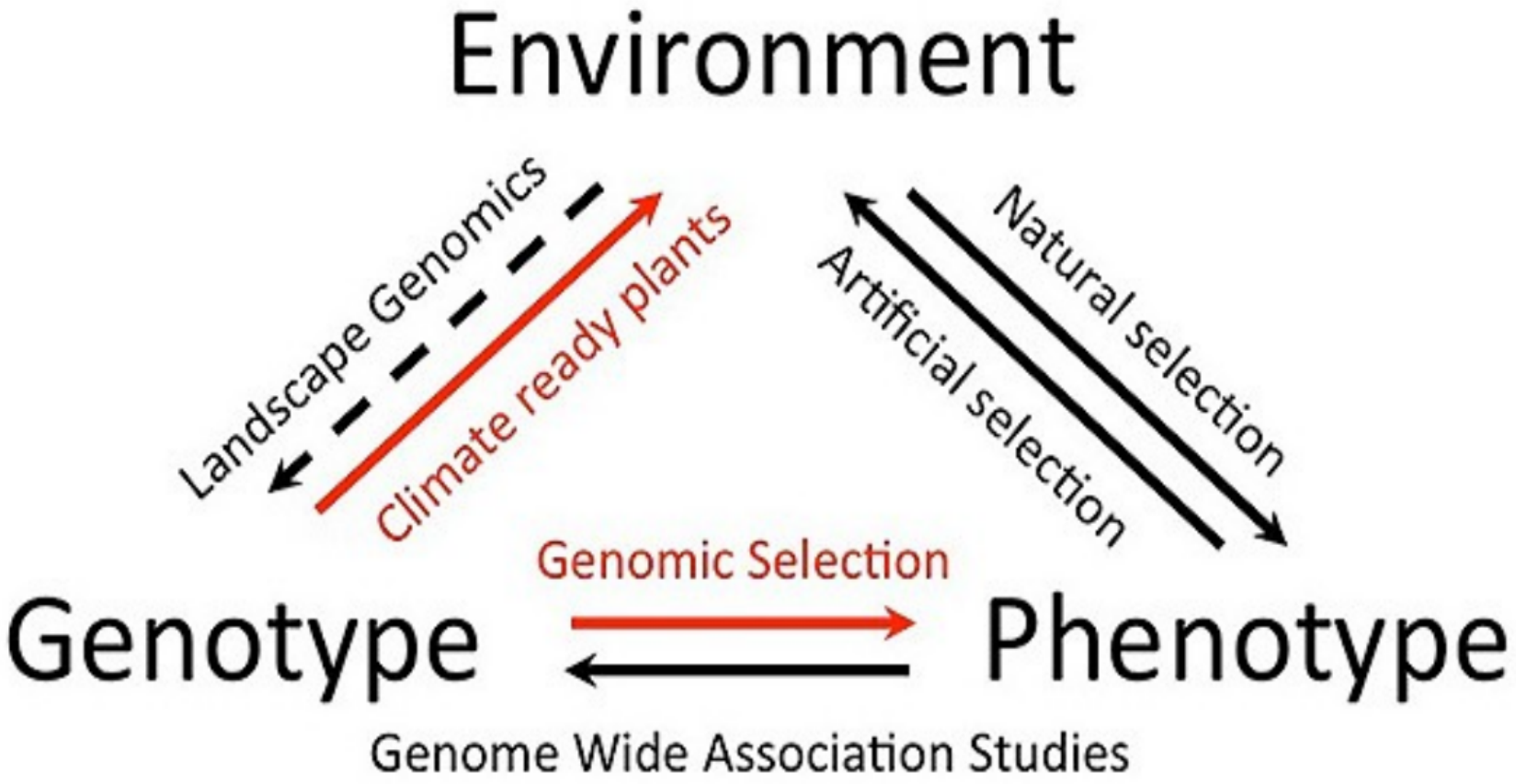
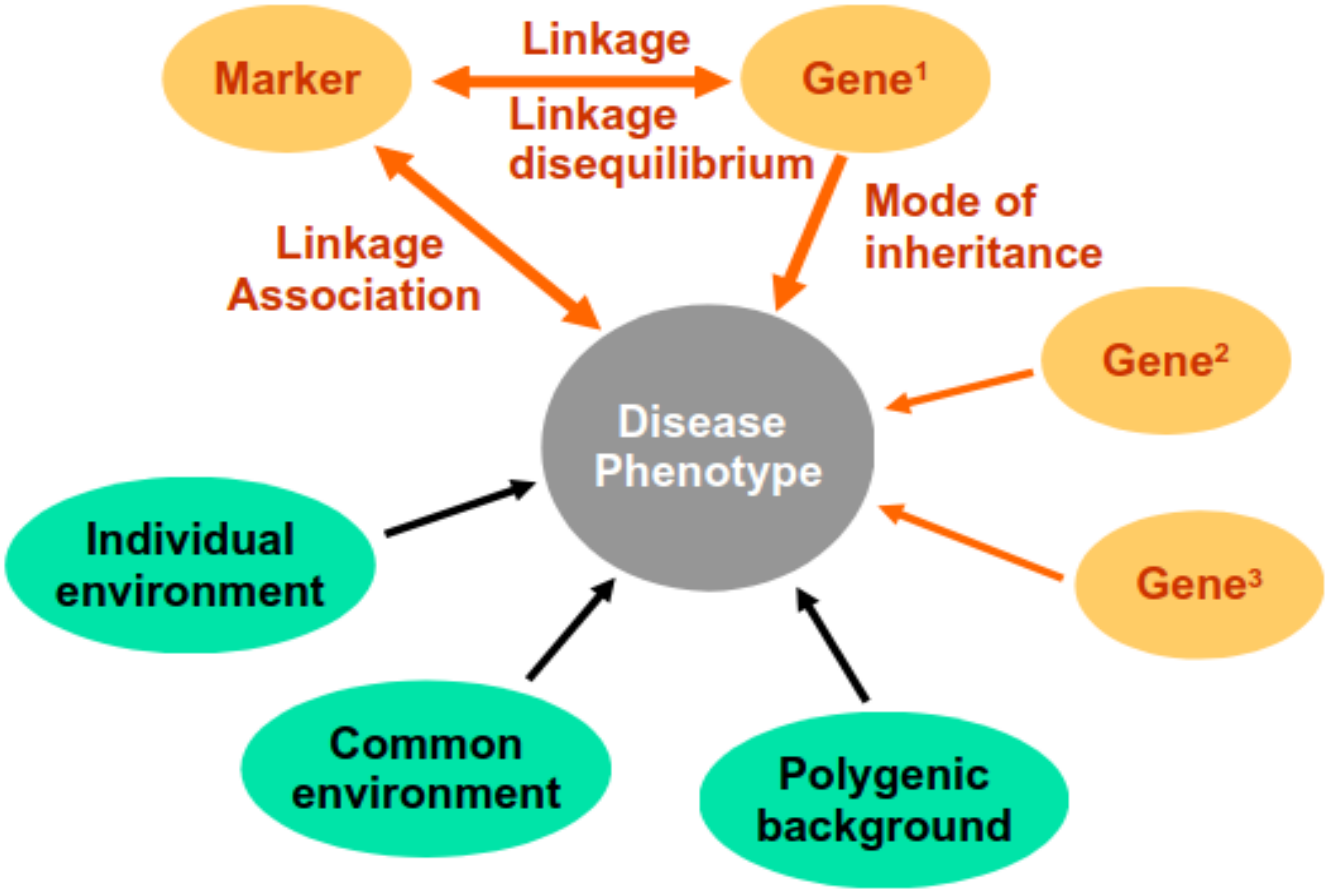
Quantitative genetics

Quantitative genetics aims to explain the heritable parts of traits that follow certain statistical distributions.

Quantitative genetics



Complex trait



Quantitative genetics

Decomposition of phenotypic variance

$$\sigma_P = \sigma_G + \sigma_E + \sigma_{GxE}$$

$$\sigma_G = \sigma_A + \sigma_D + \sigma_I$$

$$\sigma_I = \sigma_{AA} + \sigma_{AD} + \sigma_{DD}$$

$$h^2 = \frac{\sigma_A}{\sigma_P}$$

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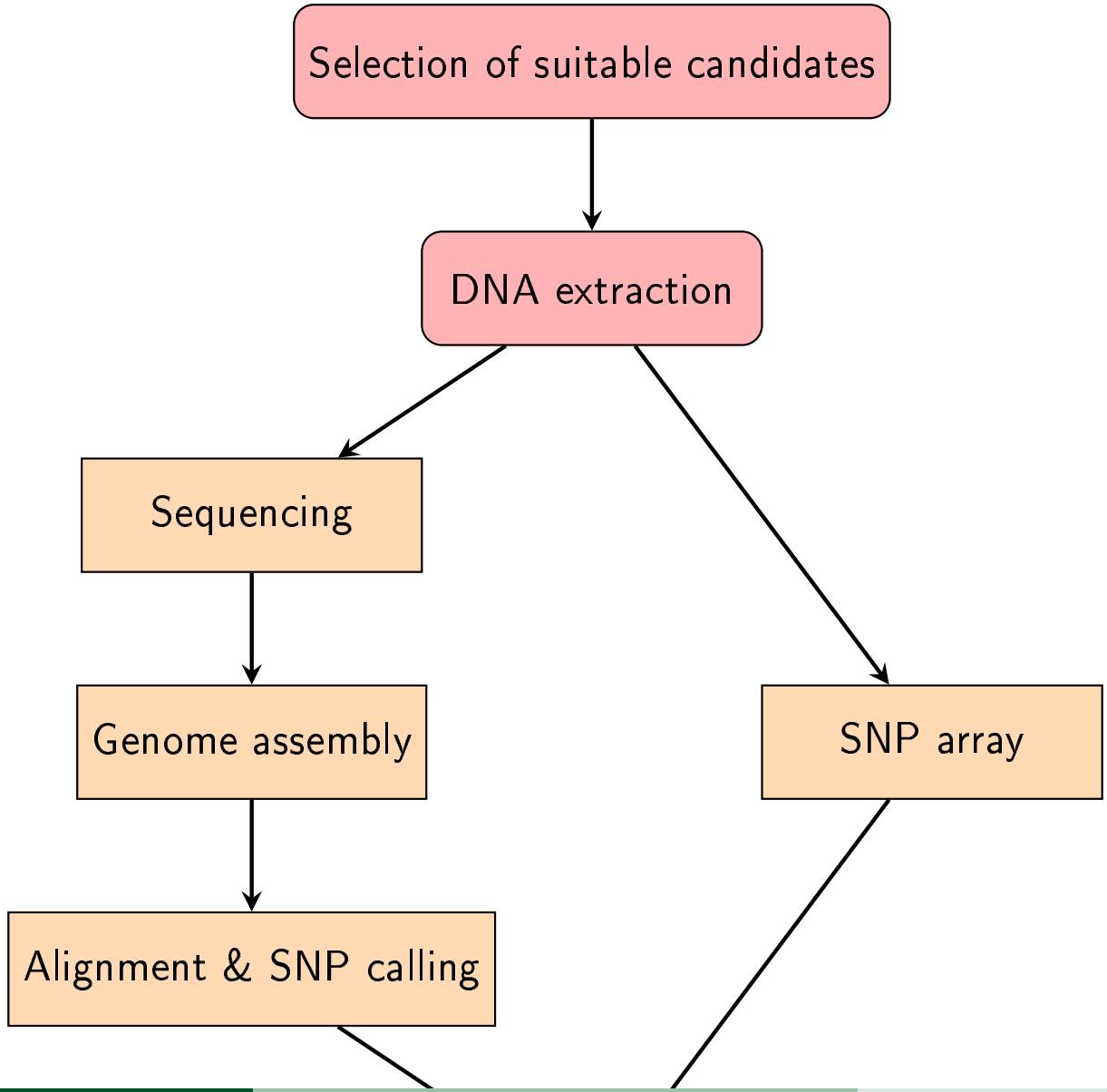
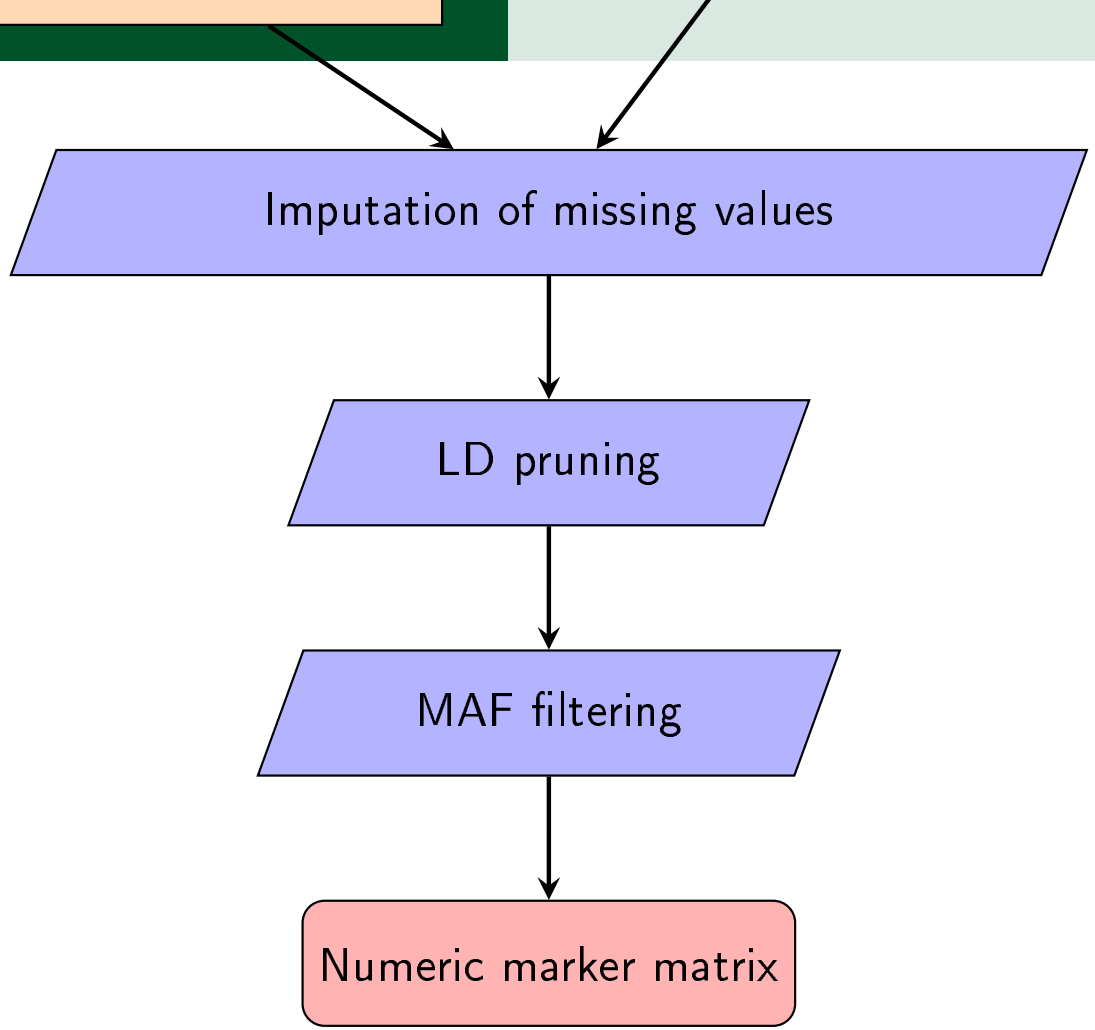
Workflow in quantitative Genetics





Schematic process of genotyping for quantitative genetics analyses with its crucial steps

Numeric marker matricies

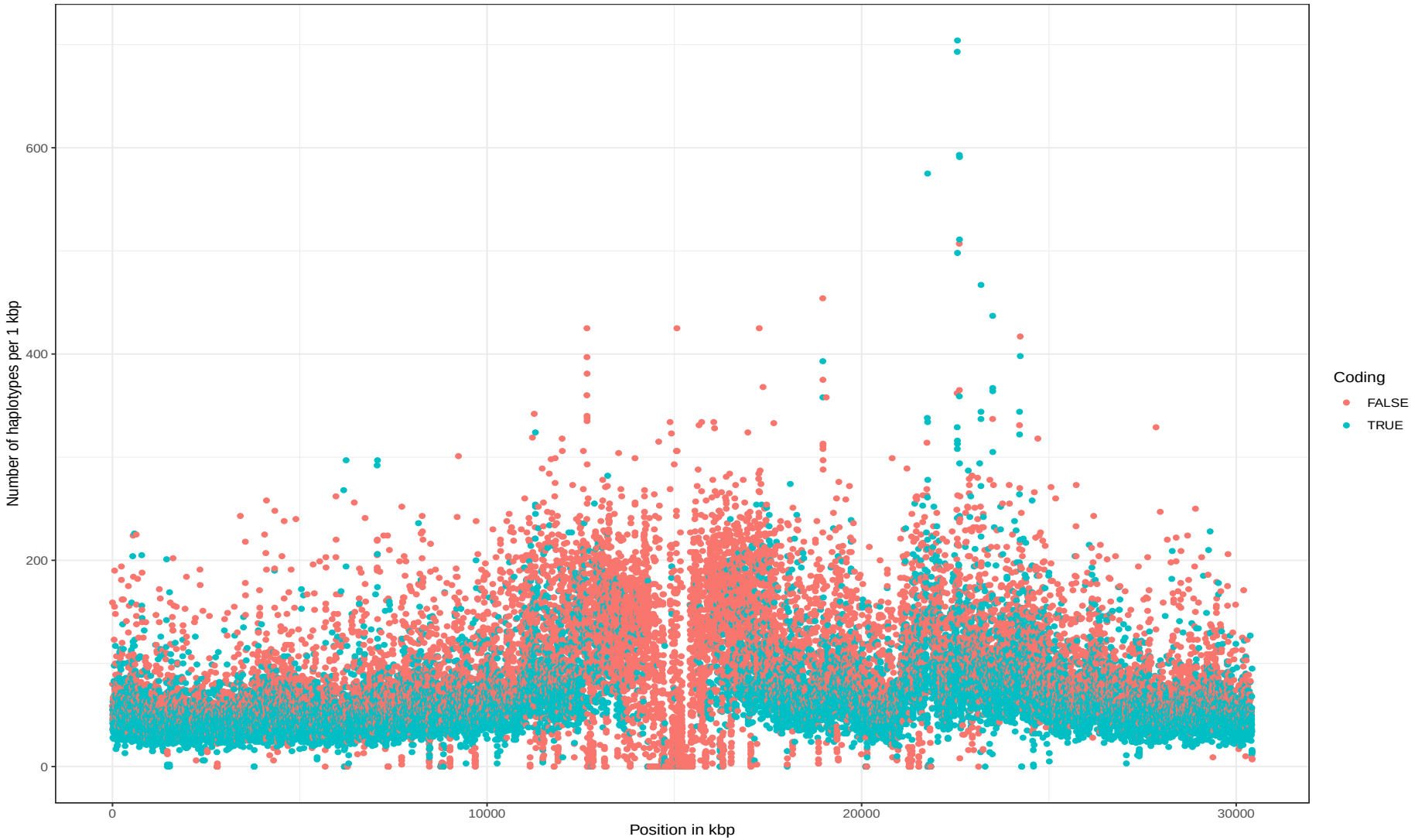


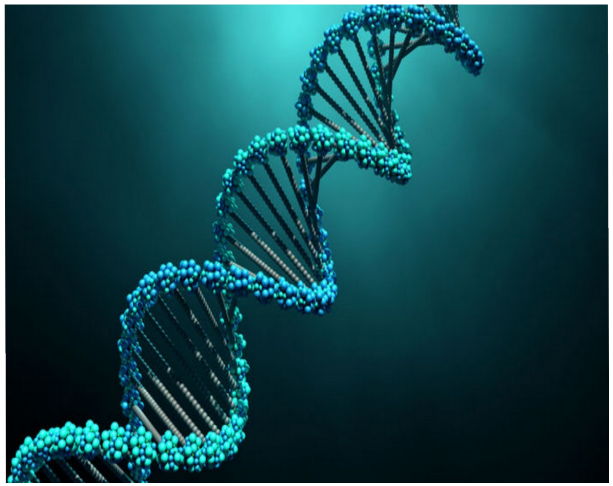
Tabelle: Schematic representation of the enhanced genotype matrix for across environment prediction of maize phenotypes with DHs 1-2 with markers M 1-2 in environments E1-2

	M-1	M-2	M-3	M-4
Acc1	0	1	1	0
Acc2	1	0	1	0
Acc3	0	1	0	1
Acc4	1	0	0	1

Methods in quantitative genetics

GWAS

Genomic Selection



Objectives

1. Improve GWAS methodology
2. Apply non-parametric statistical methods to genomic selection

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- Significant testing is commonly done with bonferroni thresholds

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Problems with GWAS and bonferroni correction

- With increasing phenotypes and markers the computational time increases exponentially
- Bonferroni assumes independent testing
- Due to LD markers are not independent from each other
- Permutation based thresholds are better suited to account for LD and structured population
- Permutations have to be repeated 100 times with shuffled phenotypes

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GWAS Flow

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Performance of GWAS-FLow