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

Jan Freudenthal

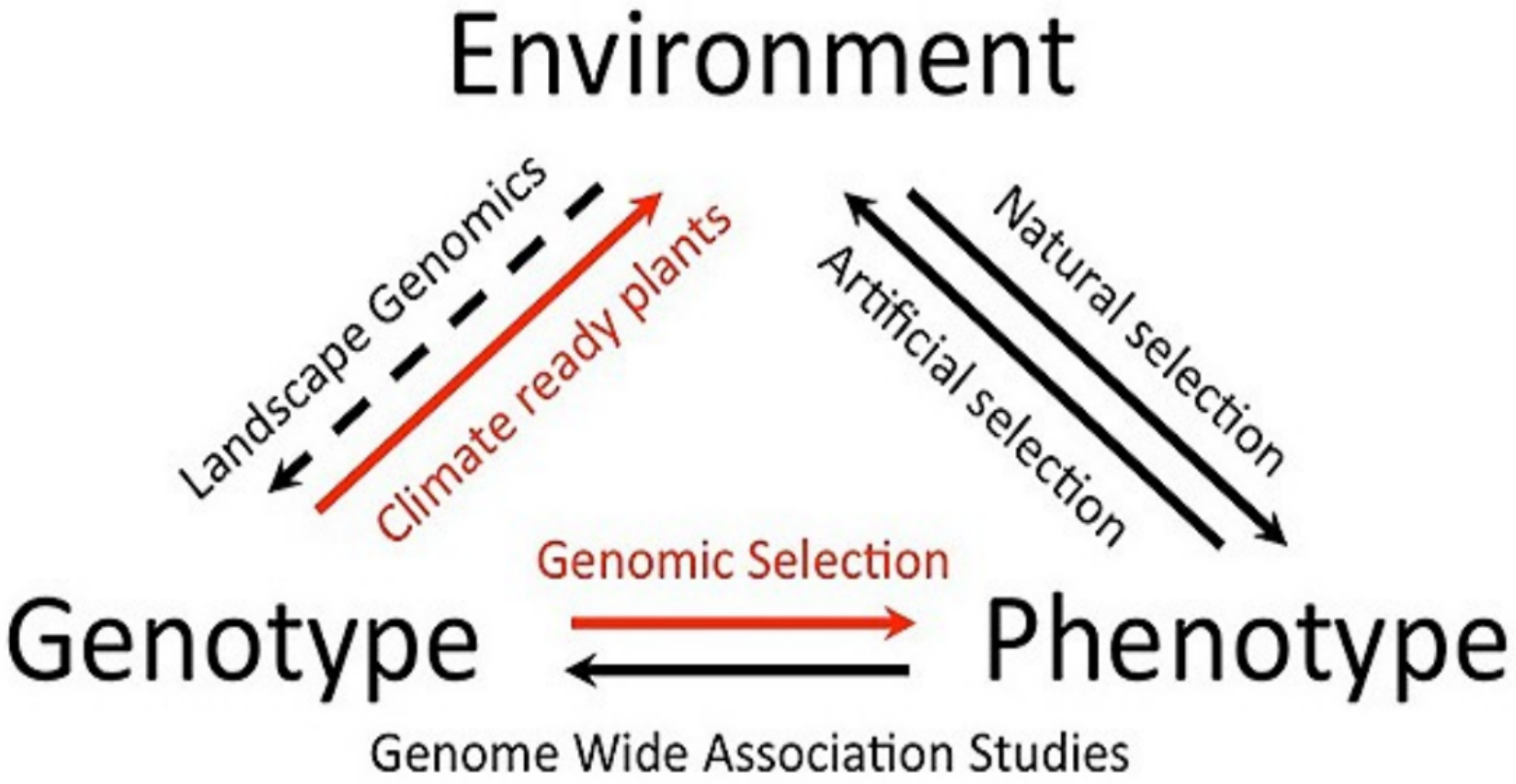
CCTB
Evolutionary genomics
Julius-Maximilians-Universität Würzburg

31. Jan 2020

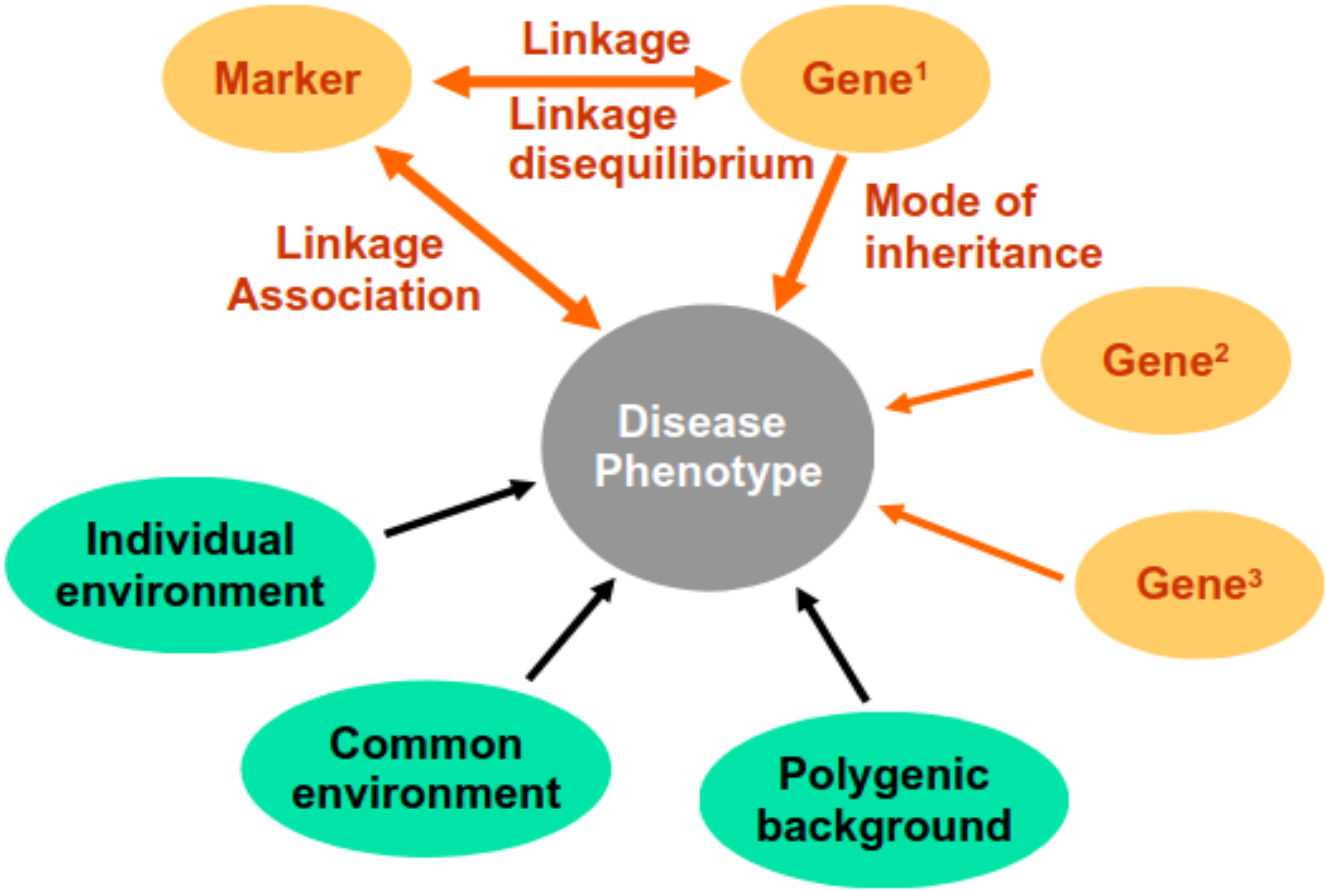
Quantitative genetics

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

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

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

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

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

Decomposition of phenotypic variance

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

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

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

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

Decomposition of phenotypic variance

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

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

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

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

Decomposition of phenotypic variance

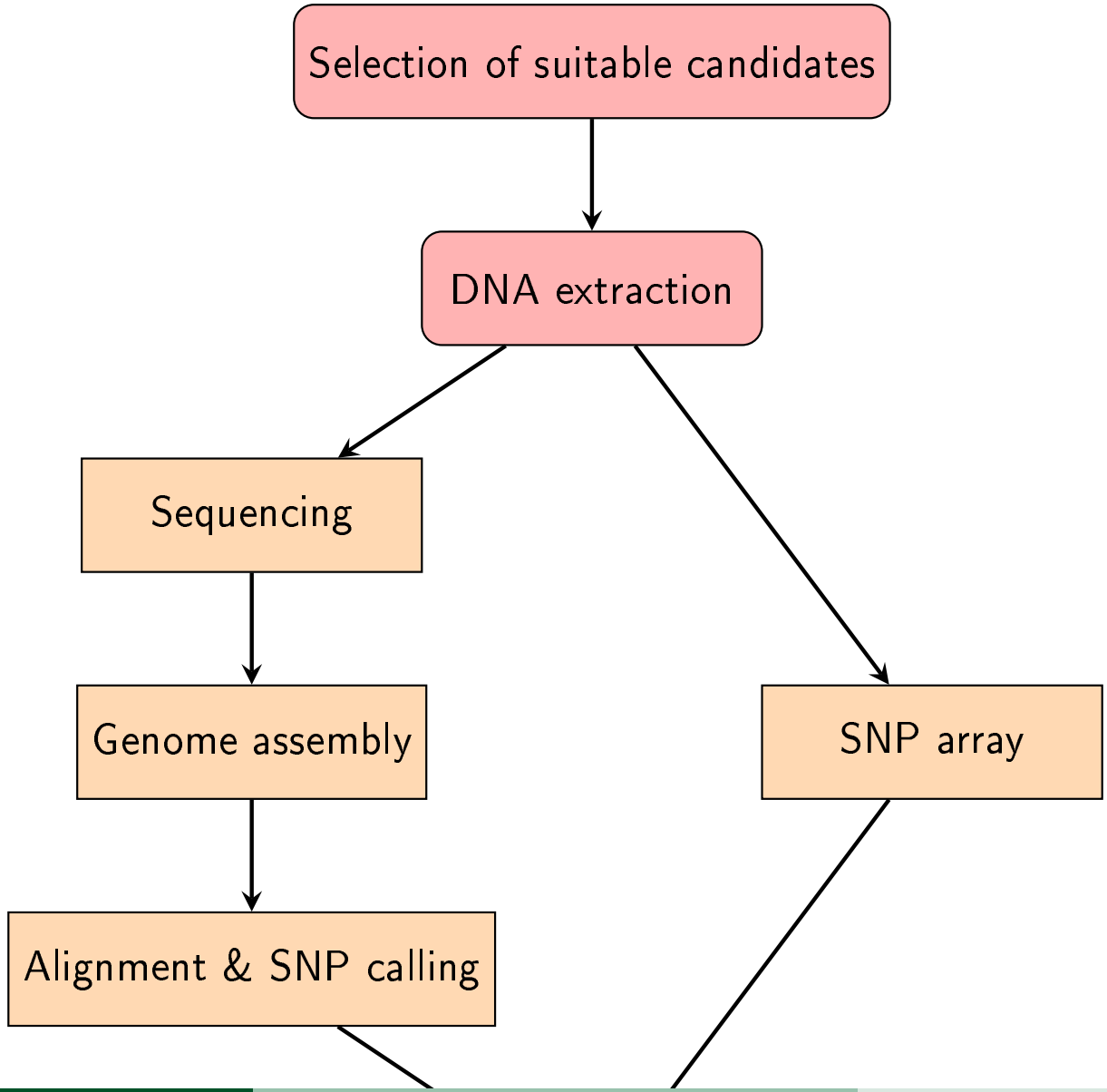
$$\sigma_P = \sigma_G + \sigma_E + \sigma_{GxE}$$

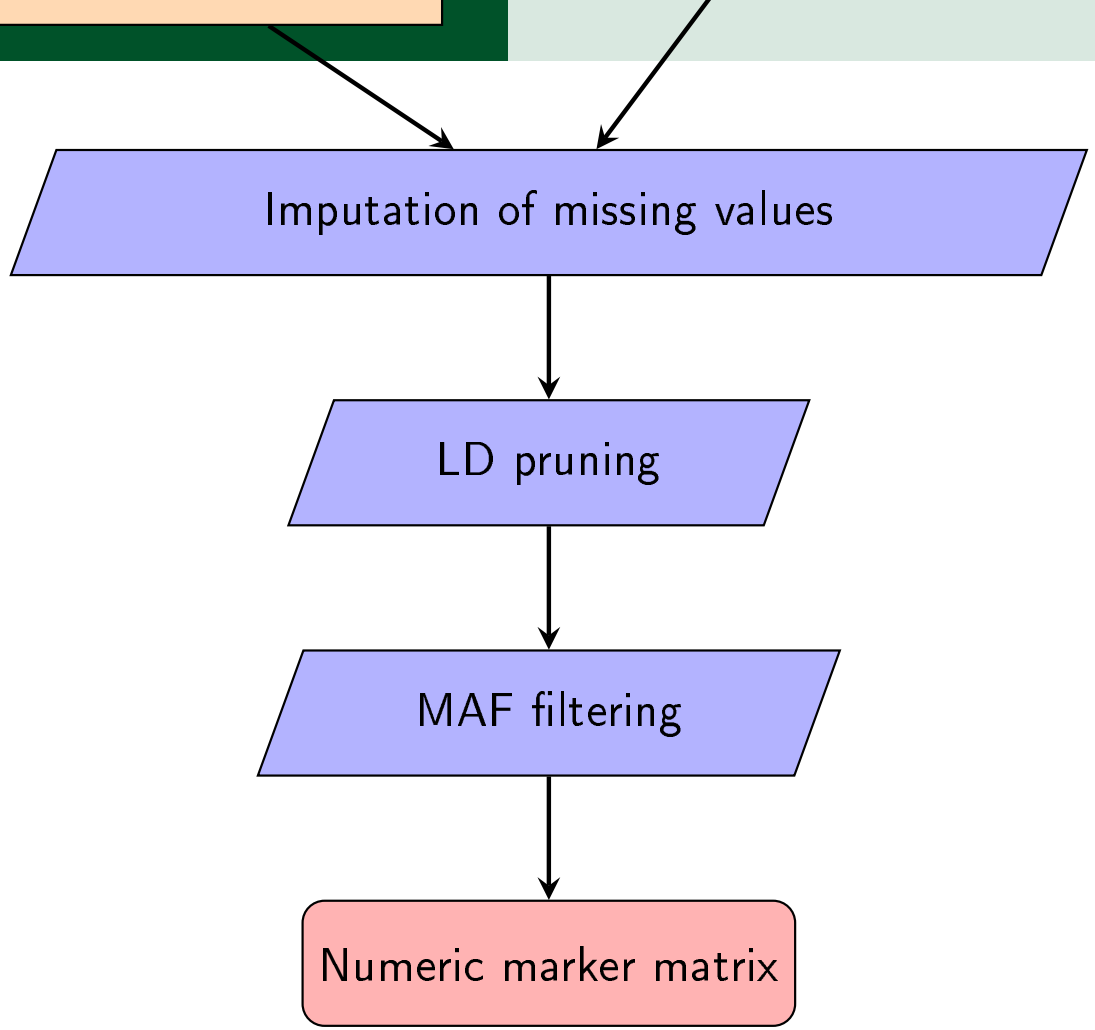
$$\sigma_G = \sigma_A + \sigma_D + \sigma_I$$

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

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

Workflow in quantitative Genetics





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

Numeric marker matricies

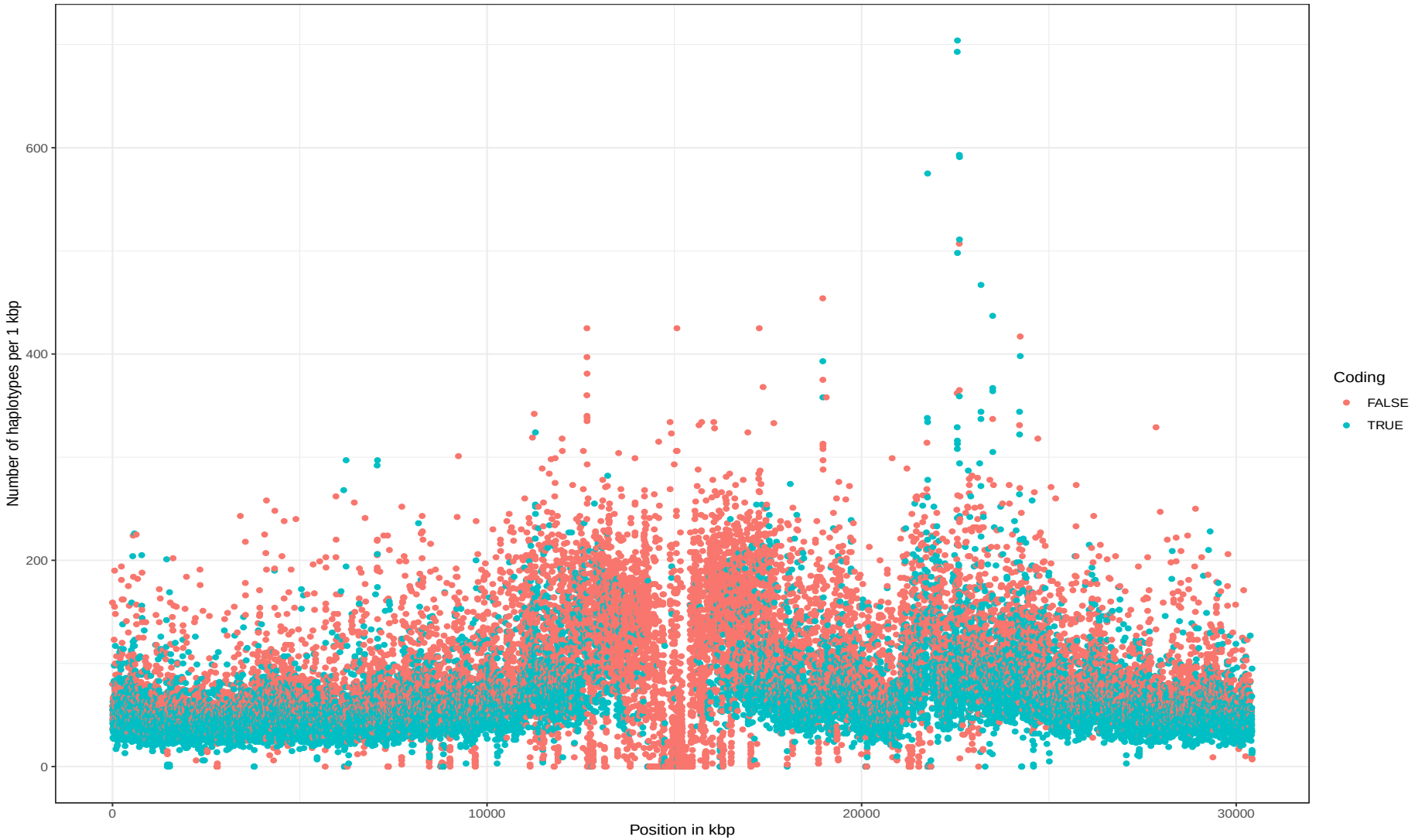


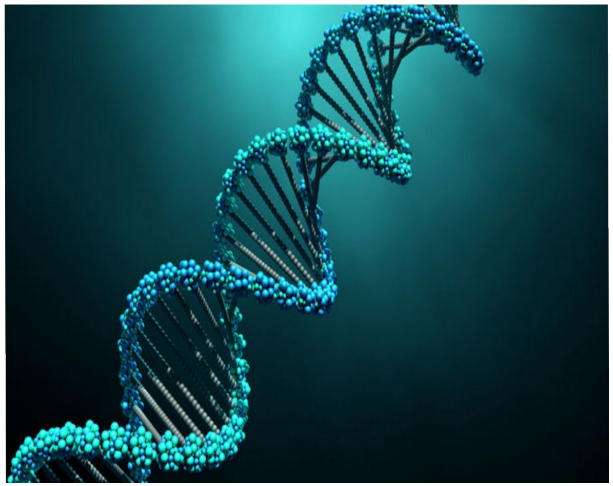
Tabelle: Schematic representation of the enhanced genotype matrix for across environment prediction of maize phenotypes with DHs 1-2 with markers M 1-2 in environments E1-2

	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

Objectives

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

GWAS

- GWAS is the main method used to link traits/phenotypes to genetic polymorphisms
- GWAS utilizes mixed-model linear equations to account for structured populations
- Significant testing is commonly done with bonferroni thresholds

GWAS

- GWAS is the main method used to link traits/phenotypes to genetic polymorphisms
- GWAS utilizes mixed-model linear equations to account for structured populations
- Significant testing is commonly done with bonferroni thresholds

GWAS

- GWAS is the main method used to link traits/phenotypes to genetic polymorphisms
- GWAS utilizes mixed-model linear equations to account for structured populations
- Significant testing is commonly done with bonferroni thresholds

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

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

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

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

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

GWAS Flow

- GWAS consists of a series of matrix operations that can be highly parallelized
- GWAS Flow uses the TensorFlow's Python API
- The calculations can be run on both GPU and CPU

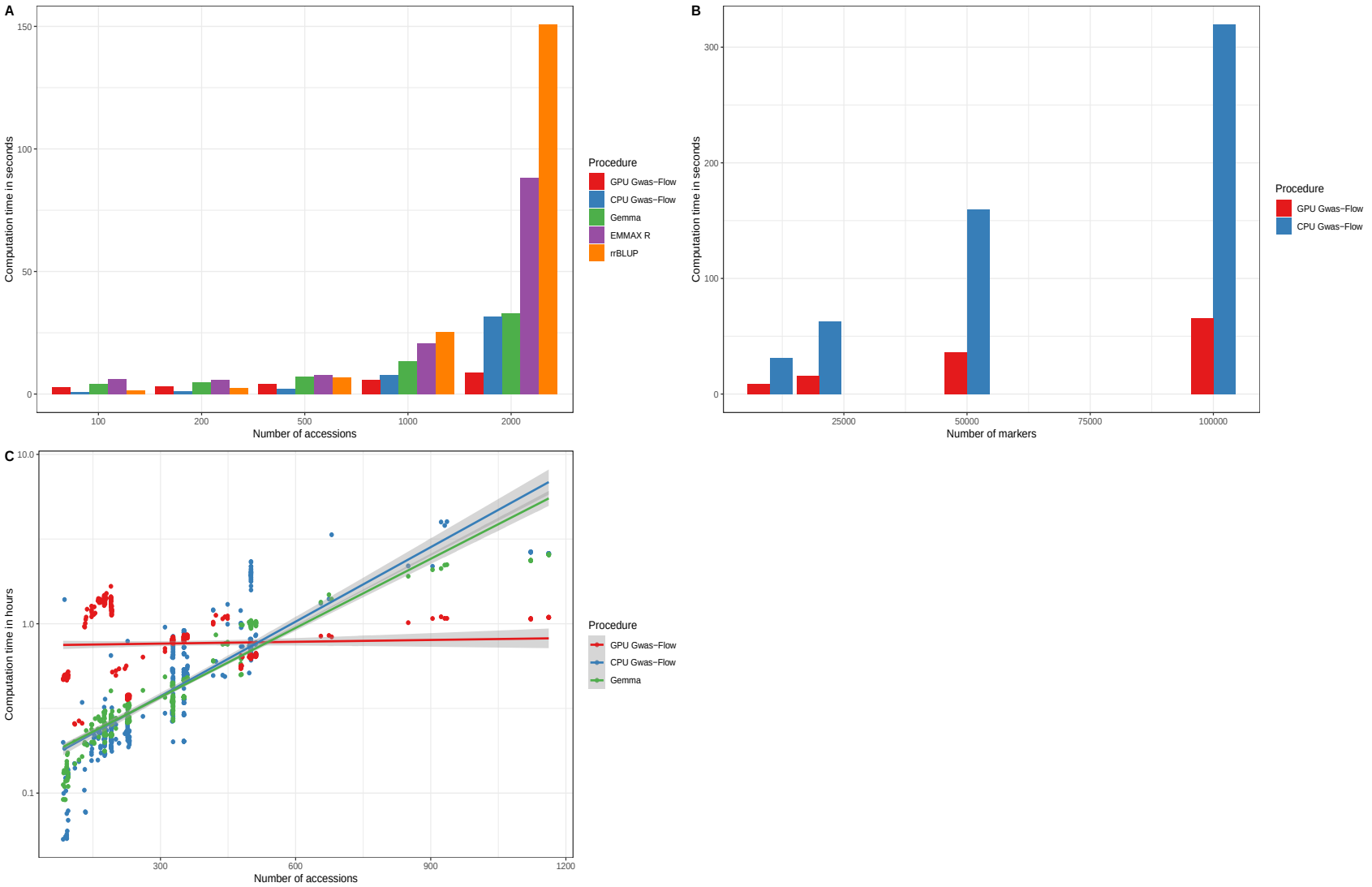
GWAS Flow

- GWAS consists of a series of matrix operations that can be highly parallelized
- GWAS Flow uses the TensorFlow's Python API
- The calculations can be run on both GPU and CPU

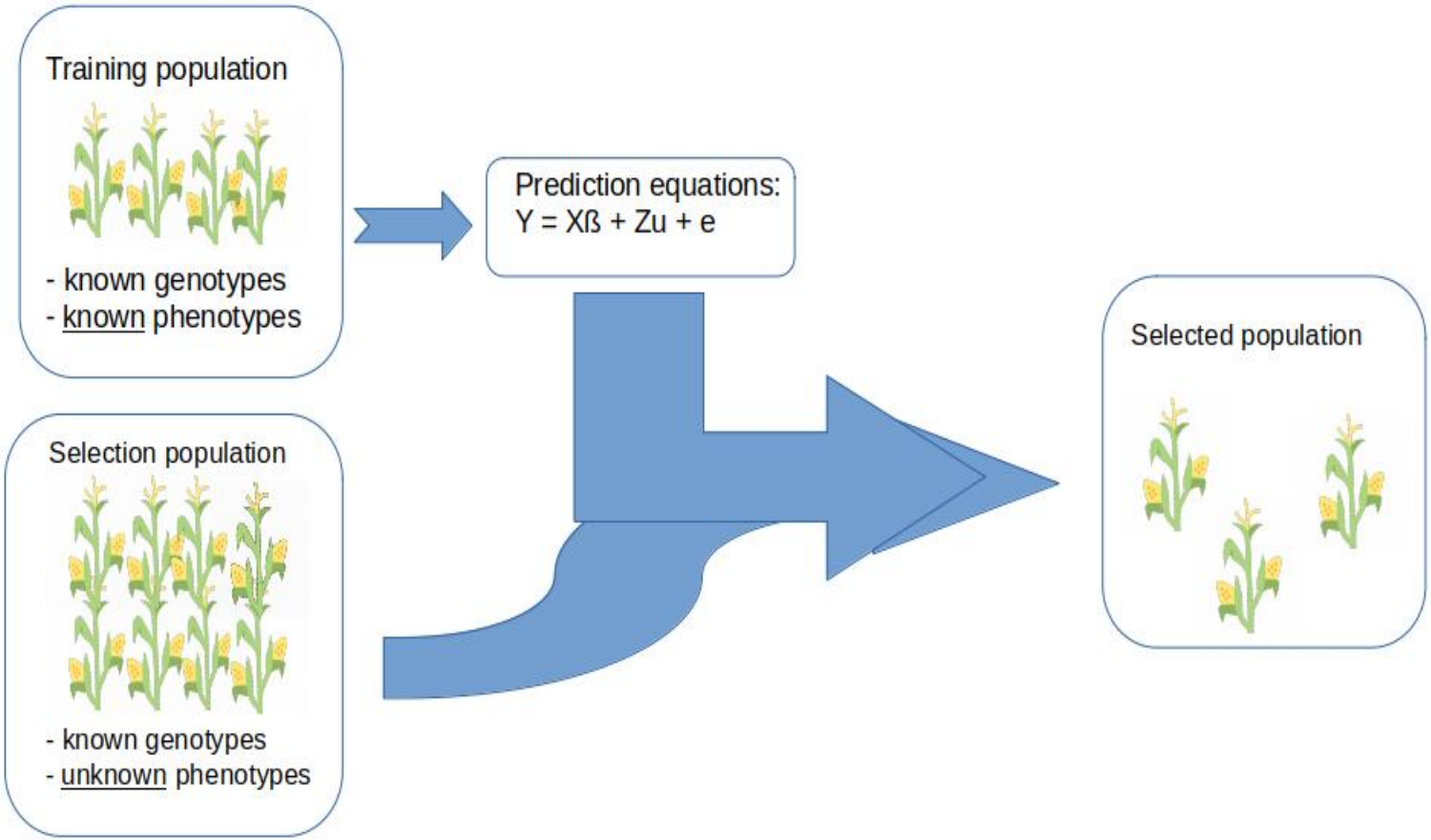
GWAS Flow

- GWAS consists of a series of matrix operations that can be highly parallelized
- GWAS Flow uses the TensorFlow's Python API
- The calculations can be run on both GPU and CPU

Performance of GWAS-Flow



Genomic selection



Advantages of genomic selection

1. Selection from larger populations
2. Stricter selection intensity
3. Acceleration of the breeding cycle
4. Reduction in phenotyping costs

Advantages of genomic selection

1. Selection from larger populations
2. Stricter selection intensity
3. Acceleration of the breeding cycle
4. Reduction in phenotyping costs

Advantages of genomic selection

1. Selection from larger populations
2. Stricter selection intensity
3. Acceleration of the breeding cycle
4. Reduction in phenotyping costs

Advantages of genomic selection

1. Selection from larger populations
2. Stricter selection intensity
3. Acceleration of the breeding cycle
4. Reduction in phenotyping costs

Prediction methods in genomic selection