Julius-Maximilians-
UNIVERSITÄT
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:::::: Faculty of Biology
Center for Computational and
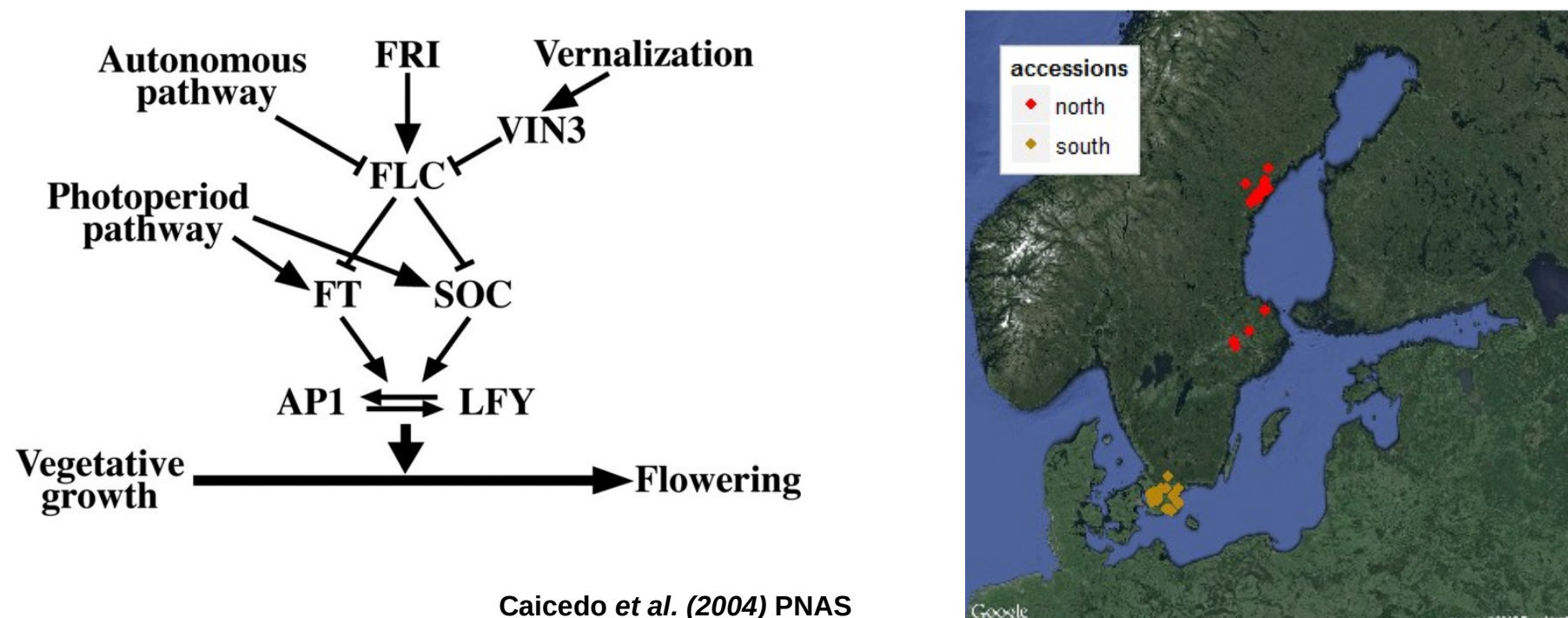Theoretical Biology

CTB

Natural Variation of Gene Regulatory Networks

Jan Freudenthal, Ammarah Anwar, William López and Arthur Korte
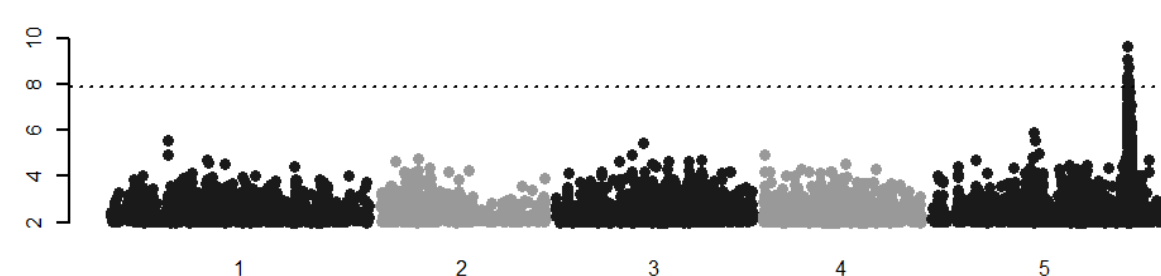
Center for Computational and Theoretical Biology, University Würzburg, 97074 Würzburg, Germany.

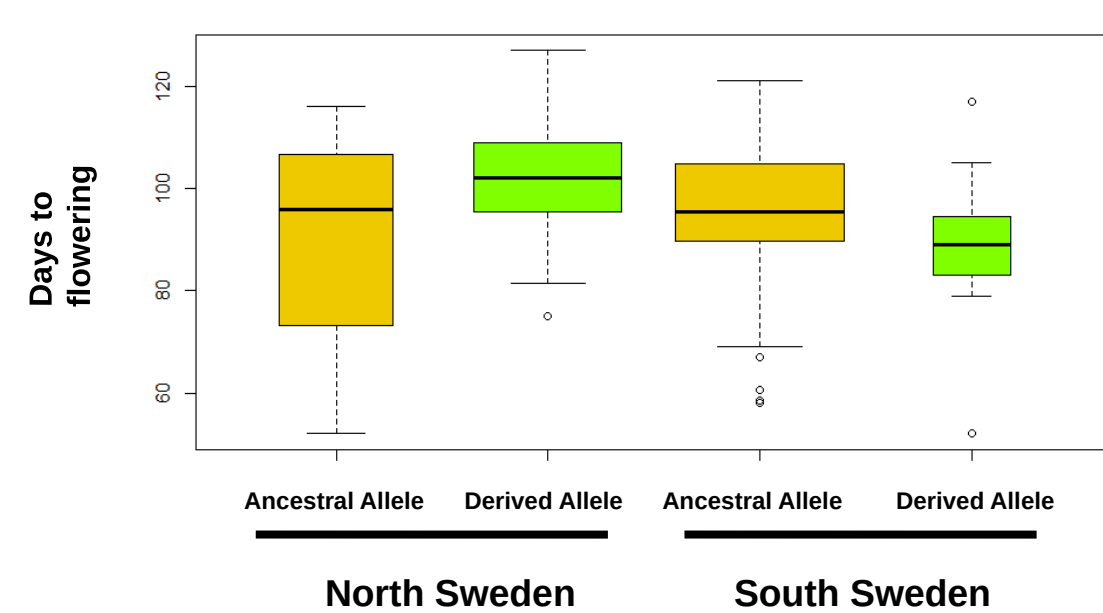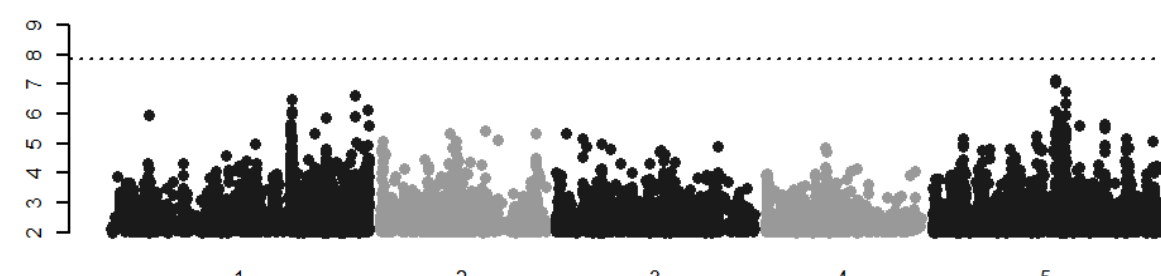## Natural variation in the flowering time pathway in *Arabidopsis thaliana*

Autonomous pathway FRI Vernalization
VIN3
FLC
Photoperiod pathway
FT SOC
AP1 LFY
Vegetative growth → Flowering

Caicedo et al. (2004) PNAS

accessions
• north
• south

GWAS in local populations

North Sweden

South Sweden

Days to flowering

Ancestral Allele Derived Allele Ancestral Allele Derived Allele
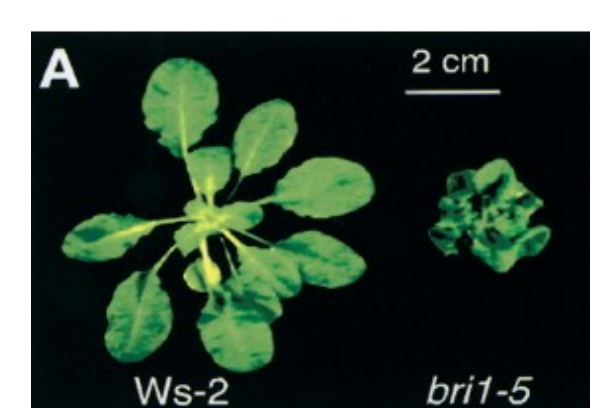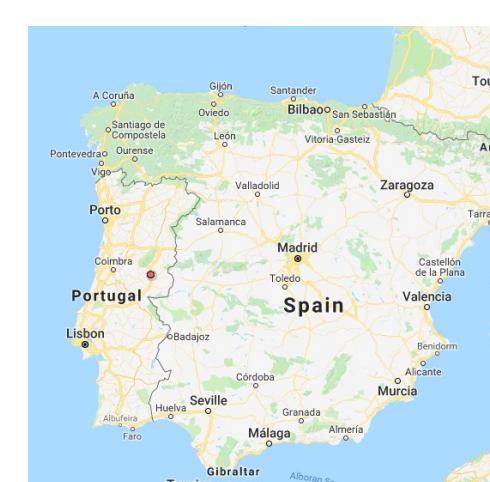North Sweden   South Sweden

The effect of the respective allele depends on the genetic background

Effect of gene knock-out is depending on the genetic background

Natural BRI1 knock out in an accession from Portugal (IP-Alo-0)

2 cm
Ws-2   bri1-5

Santiago Mora-García et al. 2004, Genes Dev.

Co-occurrence of premature STOP codons

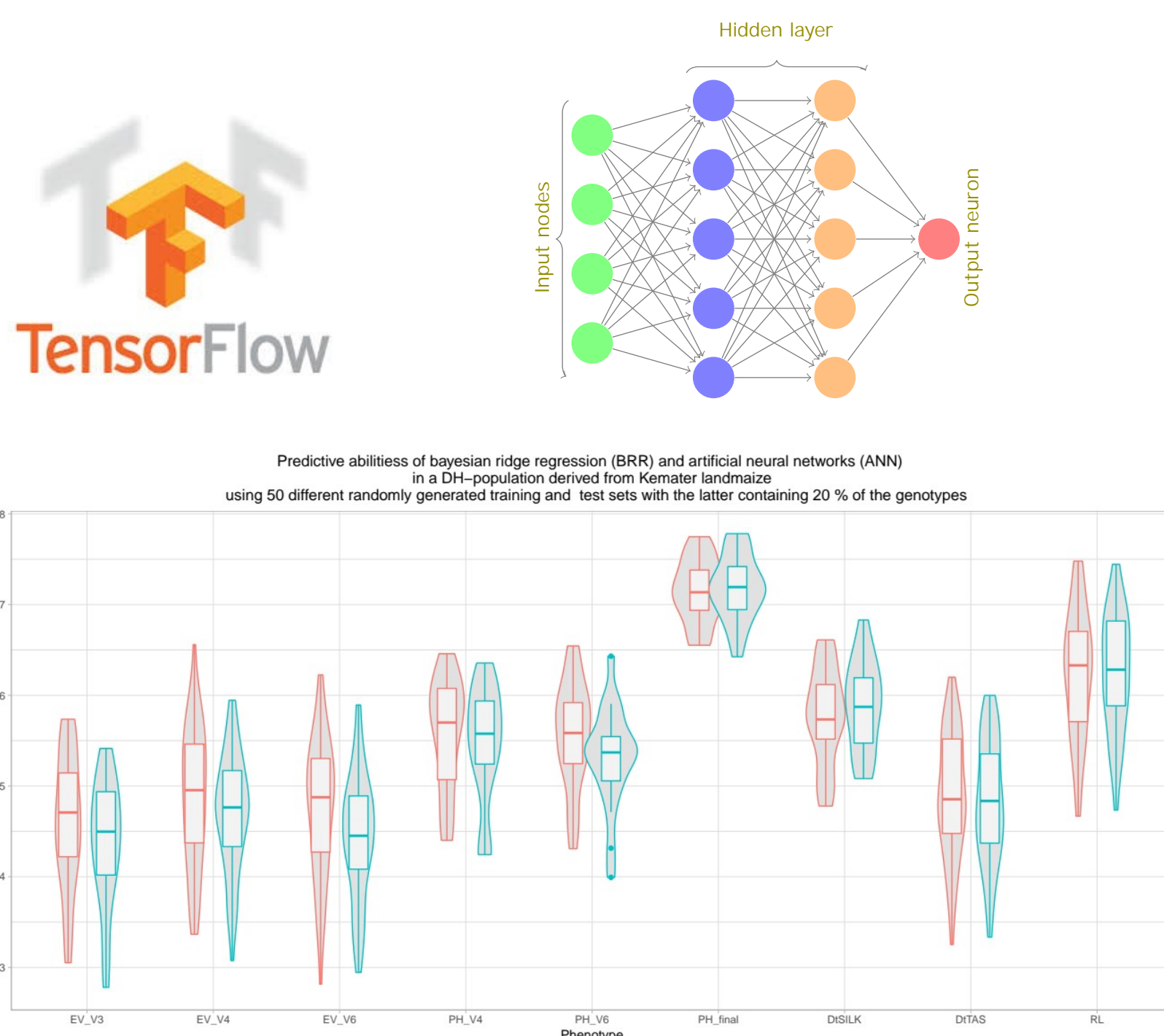| Gene 1	Gene 2	gene1_count	gene2_count	Co - occurrence	Lower border	Upper border	P-value
AT1G66920	AT3G59750	341	251	122	100	157	0.03
AT4G36140	AT5G45150	312	356	266	138	196	1.7e-57
AT3G05685	AT3G63320	444	114	38	55	96	5.6e-16

Many genes are knocked out together more (or less) often then exspected by chance

Genomic prediction

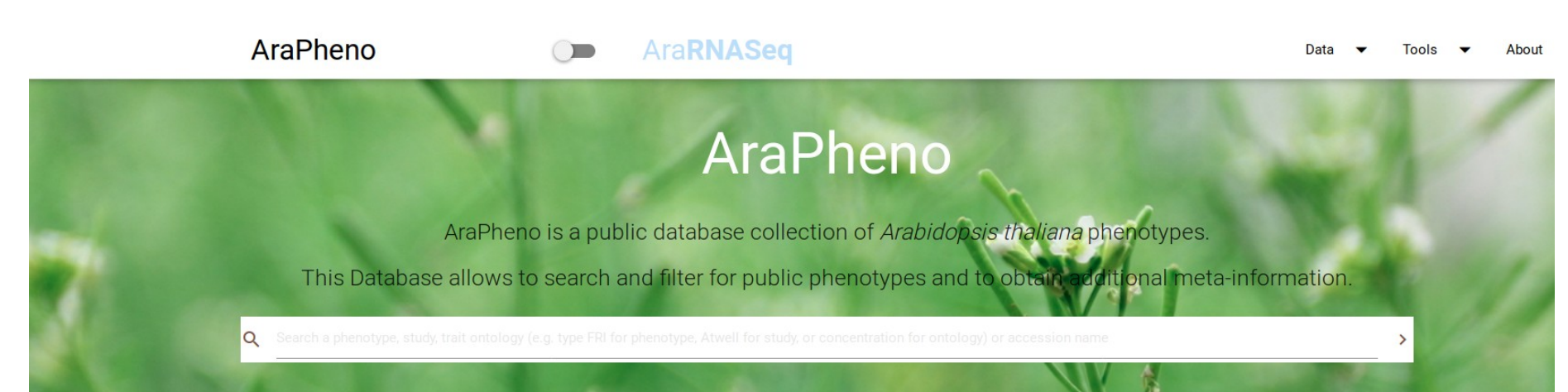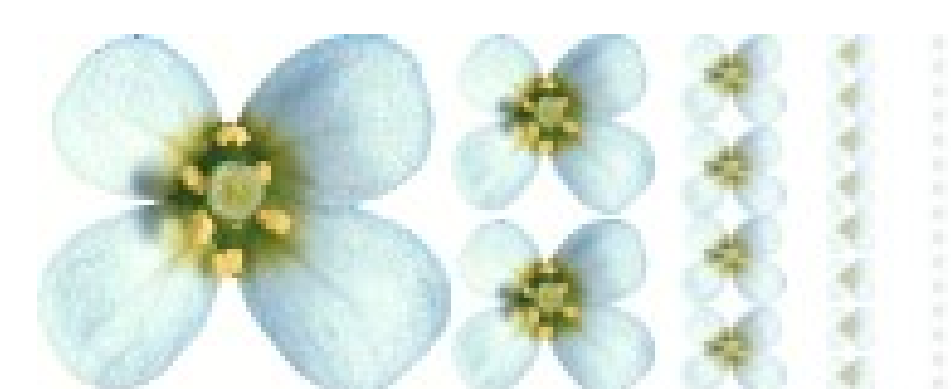**MAZE - Accessing the genomic and functional diversity of maize to improve quantitative traits**
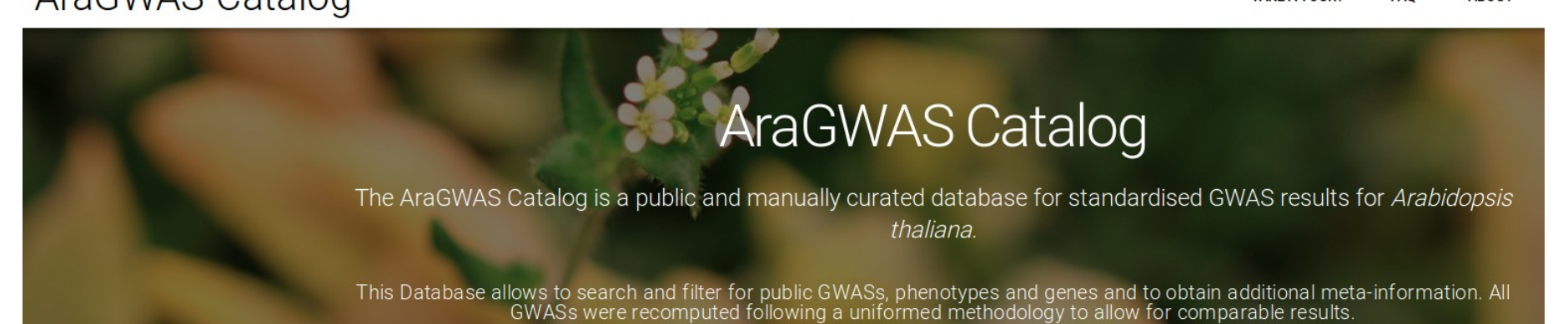
GP with artificial neural networks

TensorFlow

Hidden layer
Input nodes
Output neuron

Predictive abilities of bayesian ridge regression (BRR) and artificial neural networks (ANN)
in a DH-population derived from Kemater landmaize
using 50 different randomly generated training and test sets with the latter containing 20 % of the genotypes

Predictive ability

EV_V3 EV_V4 EV_V6 PH_V4 PH_V6 PH_final DtSILK DtTAG RL
Phenotype

method
ANN
BRR

www.europeanmaize.net

SPONSORED BY THE
Federal Ministry of Education and Research

The 1,001 Genomes project

AraPheno   AraRNASeq   Data Tools About

AraPheno

AraPheno is a public database collection of *Arabidopsis thaliana* phenotypes.
This Database allows to search and filter for public phenotypes and to obtain additional meta-information.

Quick Stats

22 Studies
471 Phenotypes total
462 Phenotypes published
Last Update: Sep/04/2019

AraGWAS Catalog   TAKE A TOUR! FAQ ABOUT

AraGWAS Catalog

The AraGWAS Catalog is a public and manually curated database for standardised GWAS results for *Arabidopsis thaliana*.

This Database allows to search and filter for public GWASs, phenotypes and genes and to obtain additional meta-information. All
GWASs were recomputed following a uniformed methodology to allow for comparable results.

www.1001genomes.org