JULIUS-MAXIMILIANS UNIVERSIÄT WÜRZBURG

DOCTORAL THESIS

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

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A thesis submitted in fulfillment of the requirements

for the degree of Ph.D.

in the

Research group for evolutionary genomics

GSLS

October 23, 2019

Declaration of Authorship

I, Jan Alexander FREUDENTHAL, declare that this thesis titled, "Quantitative genetics - from genome assemblies to neural network aided omics based prediction of quantitative traits" and the work presented in it are my own. I confirm that:

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- Where I have consulted the published work of others, this is always clearly attributed.
- Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work.
- I have acknowledged all main sources of help.
- Where the thesis is based on work done by myself jointly with others, I have made clear exactly what was done by others and what I have contributed myself.

Signed:

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_____

"Wit beyond measure is man's greatest treasure"

Rawenclaw

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Abstract

Faculty Name

GSLS

Ph.D.

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

by Jan Alexander FREUDENTHAL

The Thesis Abstract is written here (and usually kept to just this page). The page is kept centered vertically so can expand into the blank space above the title too...

Acknowledgements

The acknowledgments and the people to thank go here, don't forget to include your project advisor…

Contents

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List of Abbreviations

Adadelta	**Ada**ptive **delta**
Adagrad	**Ada**ptive **Grad**ient Algorithm
Adam	**Ada**ptive **M**oment estimation
ANN	**A**rtificial **N**eural **N**etwork
AUC	**A**rea **U**nder the **C**urve
BLUE	**B**est **L**inear **U**nbiased **E**stimator
BLUP	**B**est **L**inear **U**nbiased **P**redictor
BP	**B**ase **P**air
CPU	**C**ore **P**rocessing **U**nit
DH	**D**oubled **H**aploid
DNA	**D**eoxyribo**N**ucleic **A**cid
DNA	**R**ibo**N**ucleic **A**cid
EMMA	**E**fficient **M**ixed **M**odel **A**ssociations
FCL	**F**ully **C**onnected **L**ayer
GBLUP	**G**enomic **B**est **L**inear **U**nbiased **P**redictor
GD	**G**radient **D**escent
GP	**G**enomic **P**rediction
GPU	**G**raphical **P**rocessing **U**nit
GS	**G**enomic **S**election
GUI	**G**raphical **U**ser **I**nterface
GWAIS	**G**enome **W**ide **I**nteraction **A**ssociation **S**tudies
GWAS	**G**enome **W**ide **A**ssociation **S**tudies
HDF	**H**ierarchical **D**ata **F**ormat
IR	**I**nverted **R**epeat
LCL	**L**ocally **C**onnected **L**ayer
LD	**L**inkage **D**isequilibrium
LMM	**L**inear **M**ixed **M**odel
LSC	**L**arge **S**ingle **C**opy
MLP	**M**ulti **L**ayer **P**erceptron
ML	**M**achine **L**earning
MSE	**M**ean **S**quare **E**rror
Nadam	**N**esterov-**a**ccelerated **A**daptive **M**oment **E**stimation
NAG	**N**esterov **A**ccelerated **M**omentum
QTL	**Q**uantitative **T**rait **L**ocus
ReLU	**Re**ctified **L**inear **U**nits
RKHS	**R**eproducing **K**ernel **H**ilbert **S**paces
RMSE	**R**oot **M**ean **S**quare **E**rror
RMSProp	**R**oot **M**ean **S**quare **Prop**agation
ROC	**R**eceiver **O**perating **C**haracteristics
RSS	**R**esidual **S**um of **S**quares

SGD	**S**tochastic **G**radient **D**escent
SNP	**S**ingle **N**ucleotide **P**olymorphism
SSC	**S**mall **S**ingle **C**opy
TRN	**TR**ai**N**ing subset
TST	**T**e**ST**ing subset
WGS	**W**hole **G**enome **S**equencing
XOR	e**X**clusive **OR**

For/Dedicated to/To my...

1 Benchmarking of Chloroplast Genome Assembly tools

1.1 Introduction

Here I will but the introduction to from the paper

1.2 Material and Methods

1.2.1 Methods

1.2.2 Tools

1.2.3 Evaluation

Quantitative

$$score = \frac{1}{4} \cdot \left(cov_{ref} + cov_{qry} + min \left\{ \frac{cov_{qry}}{cov_{ref}}, \frac{cov_{ref}}{cov_{qry}} \right\} + \frac{1}{n_{contigs}} \right) \cdot 100 \qquad (1.1)$$

Qualitative

Consisteny

1.2.4 Data

Simulated

Real data set

Novel data set

1.3 Results

1.3.1 Qualitative

1.3.2 Quantitatve

Simulated data

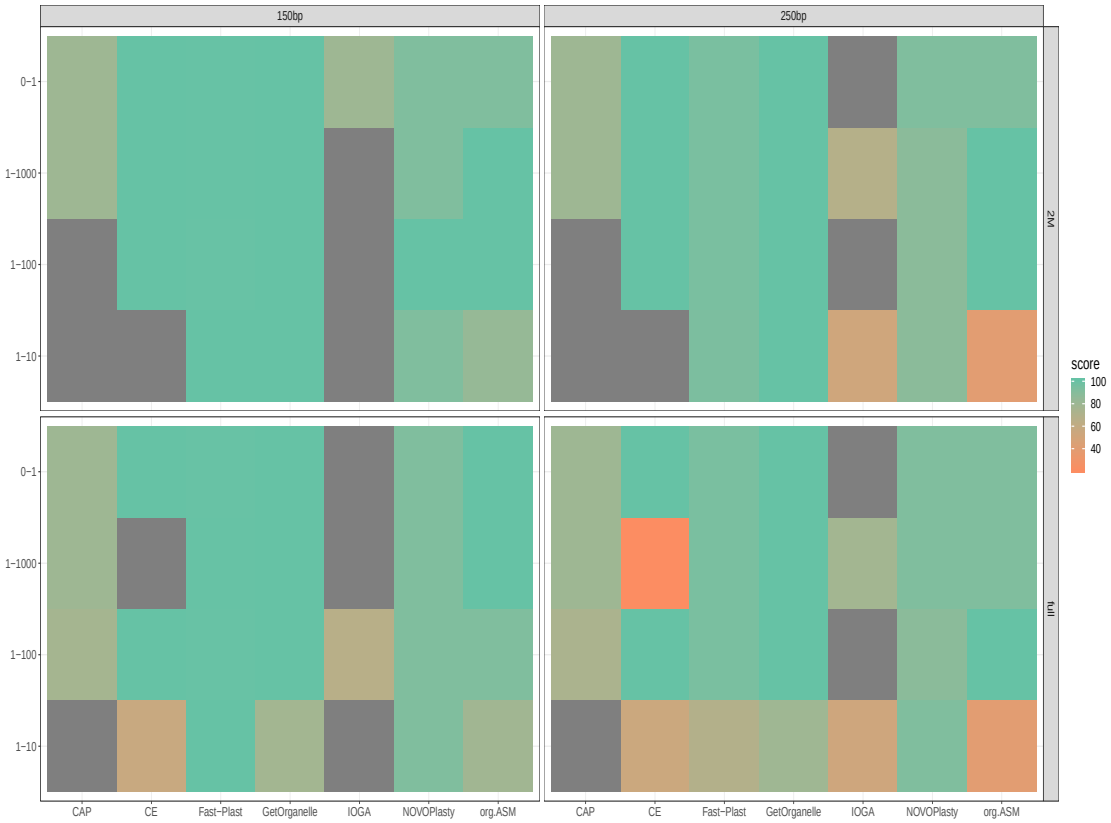

FIGURE 1.1: Results of assemblies exectuted with simulated data sets.

TABLE 1.1: **Scores of assemblies of simulated data**

	data set	CAP	CE	Fast-Plast	GetOrganelle	IOGA	NOVOPlasty
1	sim_150bp.0-1	79.10	100.00	99.48	100.00		91.52
2	sim_150bp.0-1.2M	79.10	100.00	99.72	100.00	79.10	91.52
3	sim_150bp.1-10		56.44	100.00	76.98		91.52
4	sim_150bp.1-10.2M			99.97	100.00		91.52
5	sim_150bp.1-100	75.72	100.00	99.48	100.00	66.09	91.52
6	sim_150bp.1-100.2M		100.00	99.47	100.00		100.00
7	sim_150bp.1-1000	79.10		99.72	100.00		91.52
8	sim_150bp.1-1000.2M	79.10	100.00	99.72	100.00		91.52
9	sim_250bp.0-1	79.10	100.00	93.82	100.00		91.52
10	sim_250bp.0-1.2M	79.10	100.00	93.83	100.00		91.52
11	sim_250bp.1-10		54.98	68.45	78.89	52.71	91.52
12	sim_250bp.1-10.2M			93.00	100.00	52.67	87.40
13	sim_250bp.1-100	72.81	100.00	93.82	100.00		87.40
14	sim_250bp.1-100.2M		100.00	93.83	100.00		87.40
15	sim_250bp.1-1000	79.10	21.30	93.83	100.00	76.96	91.52
16	sim_250bp.1-1000.2M	79.10	100.00	93.83	100.00	67.55	87.40

Real data sets

TABLE 1.2: **Mean scores of chloroplast genome assemblers**

	assembler	Median	IQR	N_perfect	N_tot
1	CAP	45.25	50.19	0	369
2	CE	56.55	71.50	14	369
3	Fast-Plast	92.80	23.59	113	369
4	GetOrganelle	99.83	20.94	210	360
5	IOGA	71.10	11.21	0	338
6	NOVOPlasty	75.95	48.69	58	369
7	org.ASM	67.35	91.69	46	348

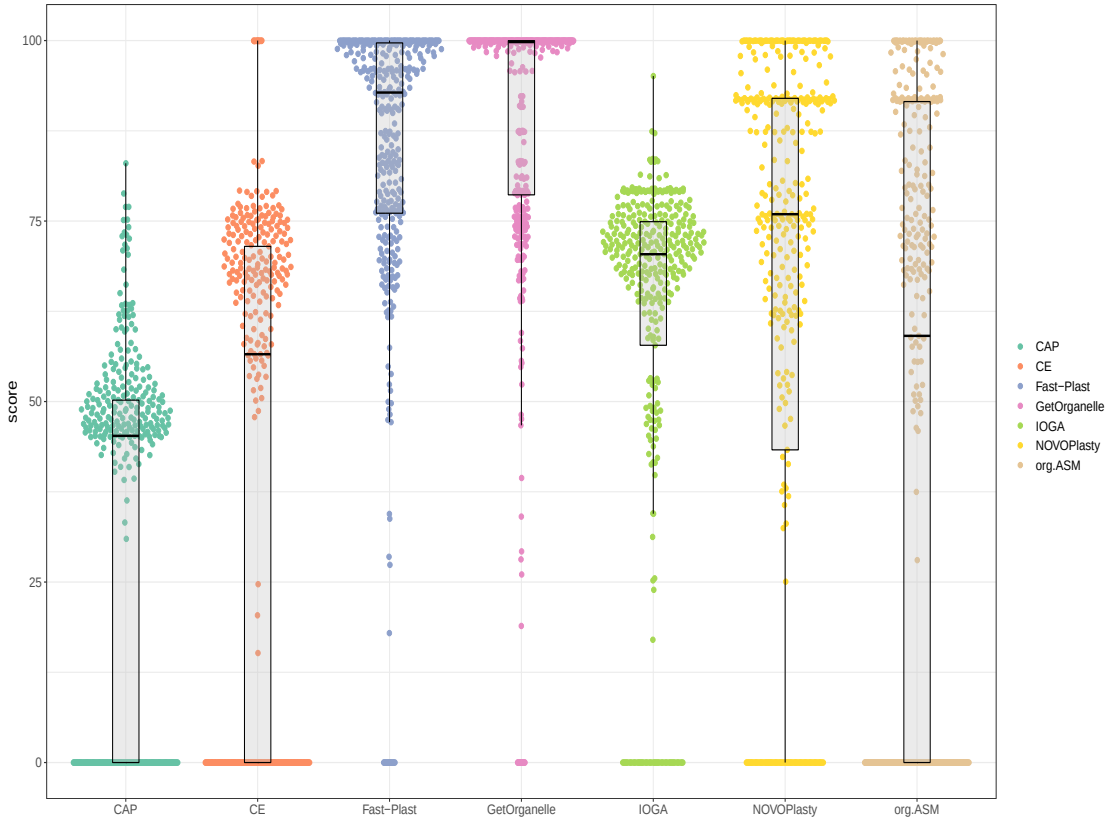

FIGURE 1.2: Box and swarm plots depict the resluts from the scoring shown in 1.1

Consistency

Real data sets

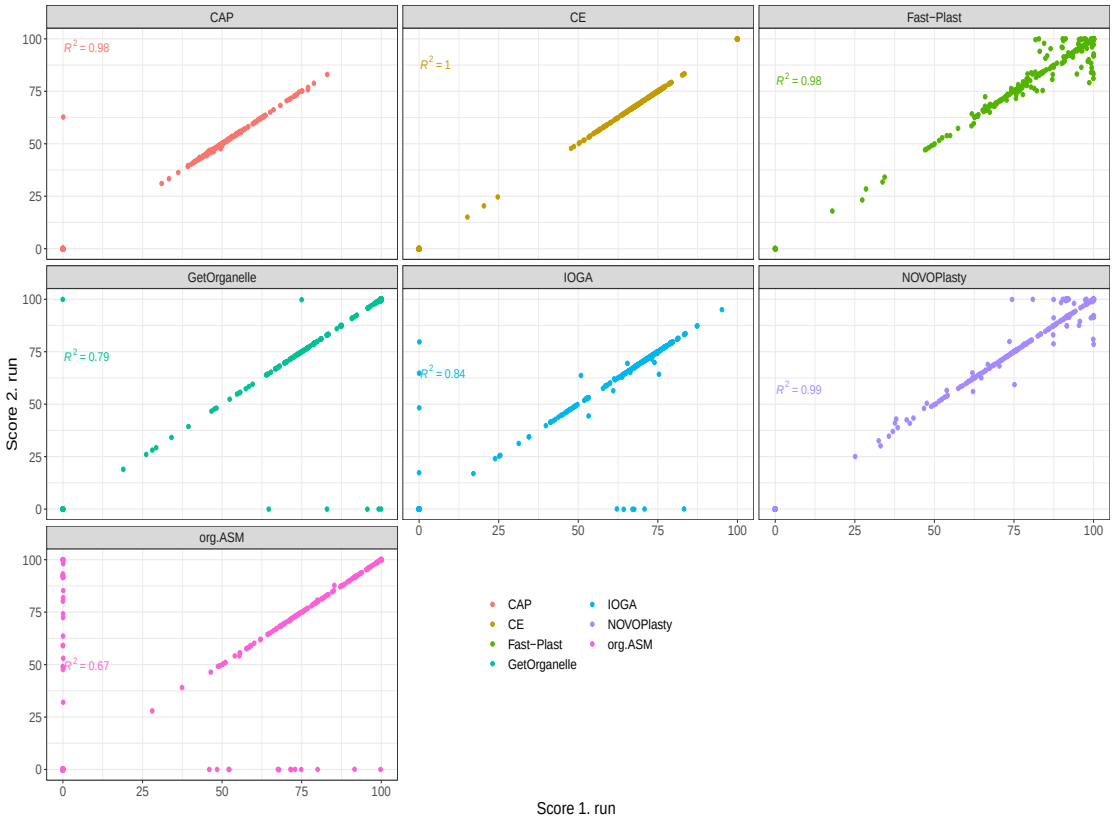

FIGURE 1.3: Swarm plots depict the resluts from the scoring shown in 1.1 for two independet runs for each assembler on each of the datasets

Novel

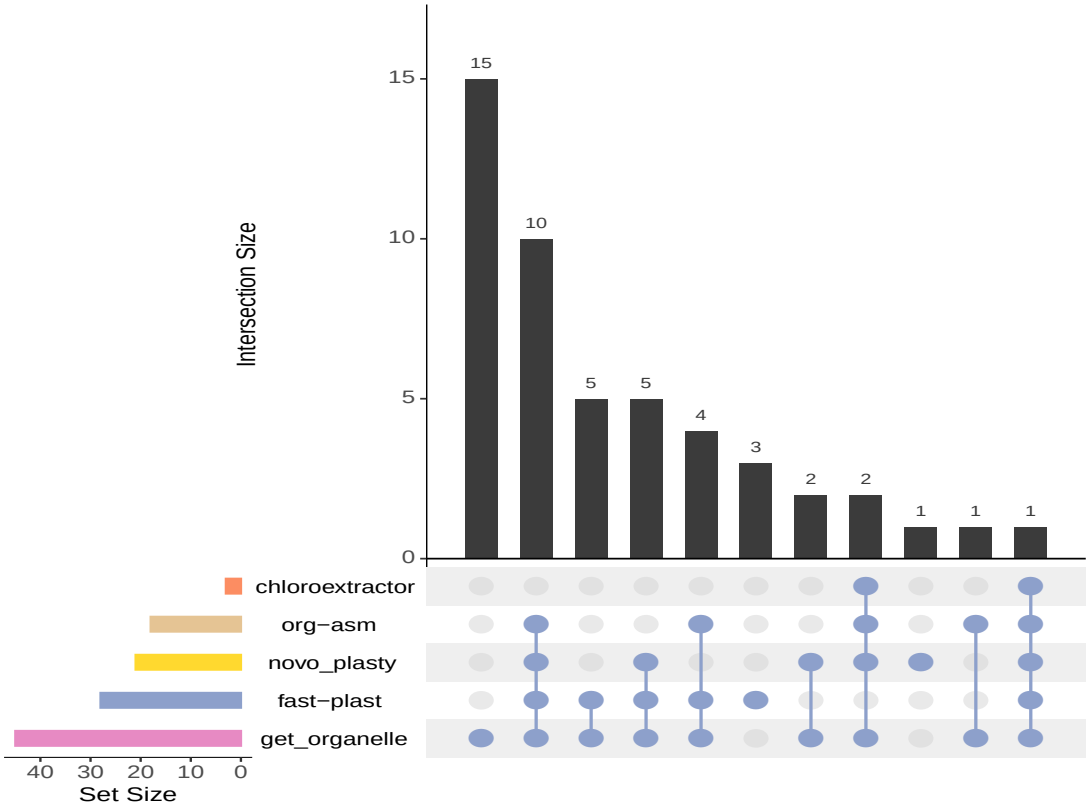

FIGURE 1.4: nls

1.4 Disucssion

FIGURE 1.5: Upset plot showing the intersections of sucess rates between assemblers. A successful assembly was defined with a score > 99 according to equation 1.1

2 Understanding the hapoltype structure of Arabidopisis thaliana

2.1 Introduction

2.2 Haplotyping of A. thaliana

2.3 Results

2.4 Disucssion

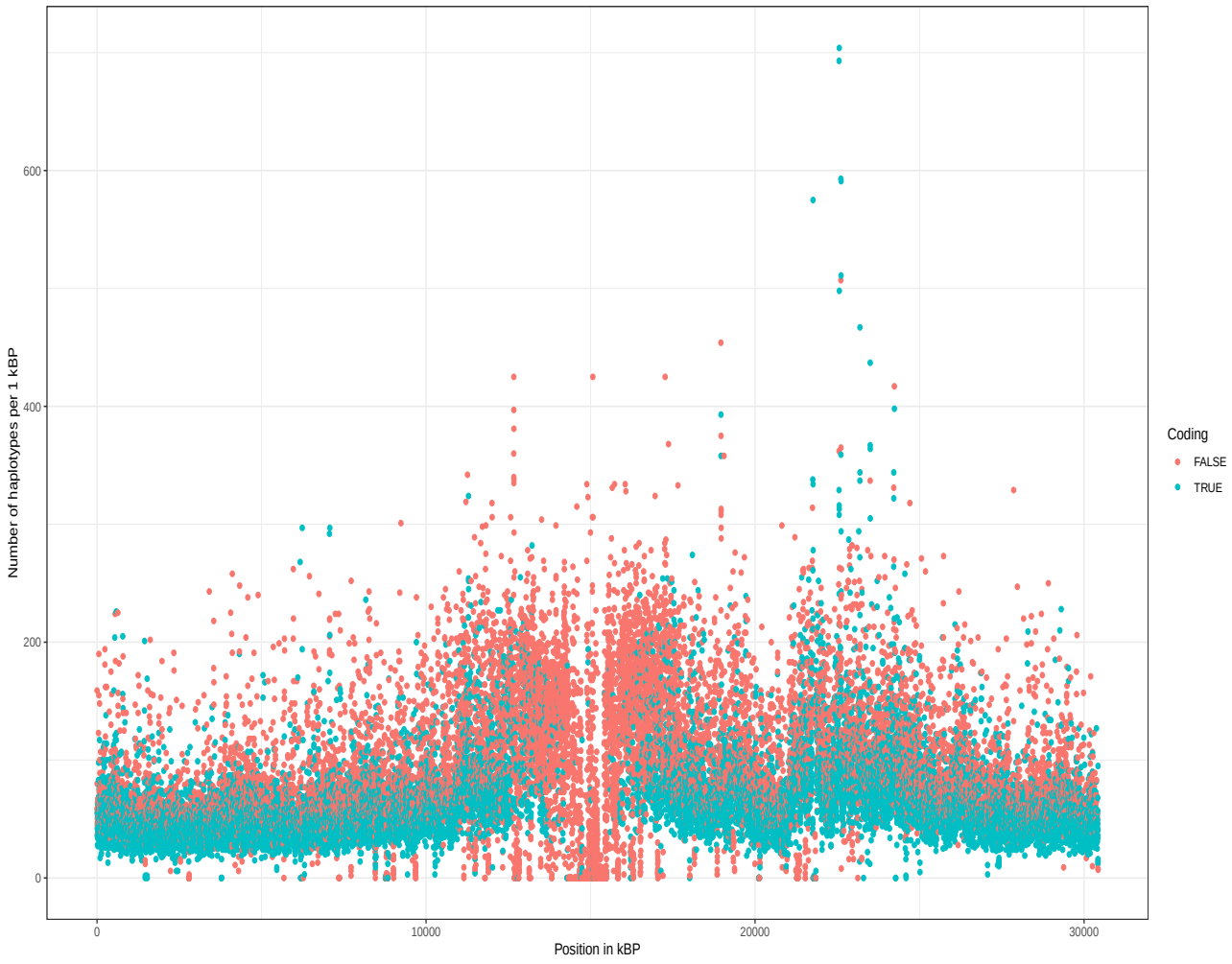

FIGURE 2.1: The number of segregating haplotypes with a polymorphism in at least one position over a stretch of 1 kBP.

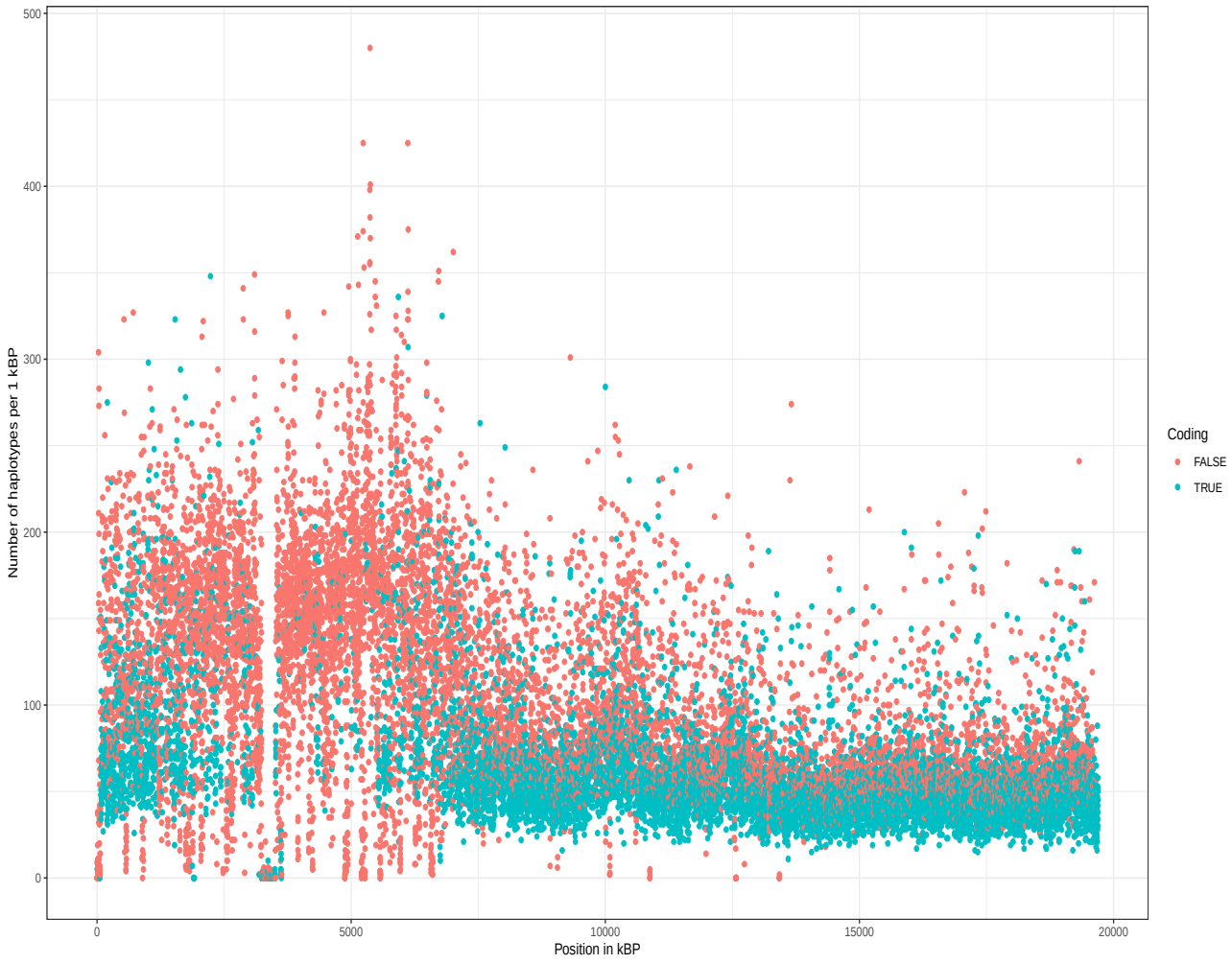

FIGURE 2.2: Number of segregating haplotypes with a polymorphism in at least one position over a stretch of 1 kBP.

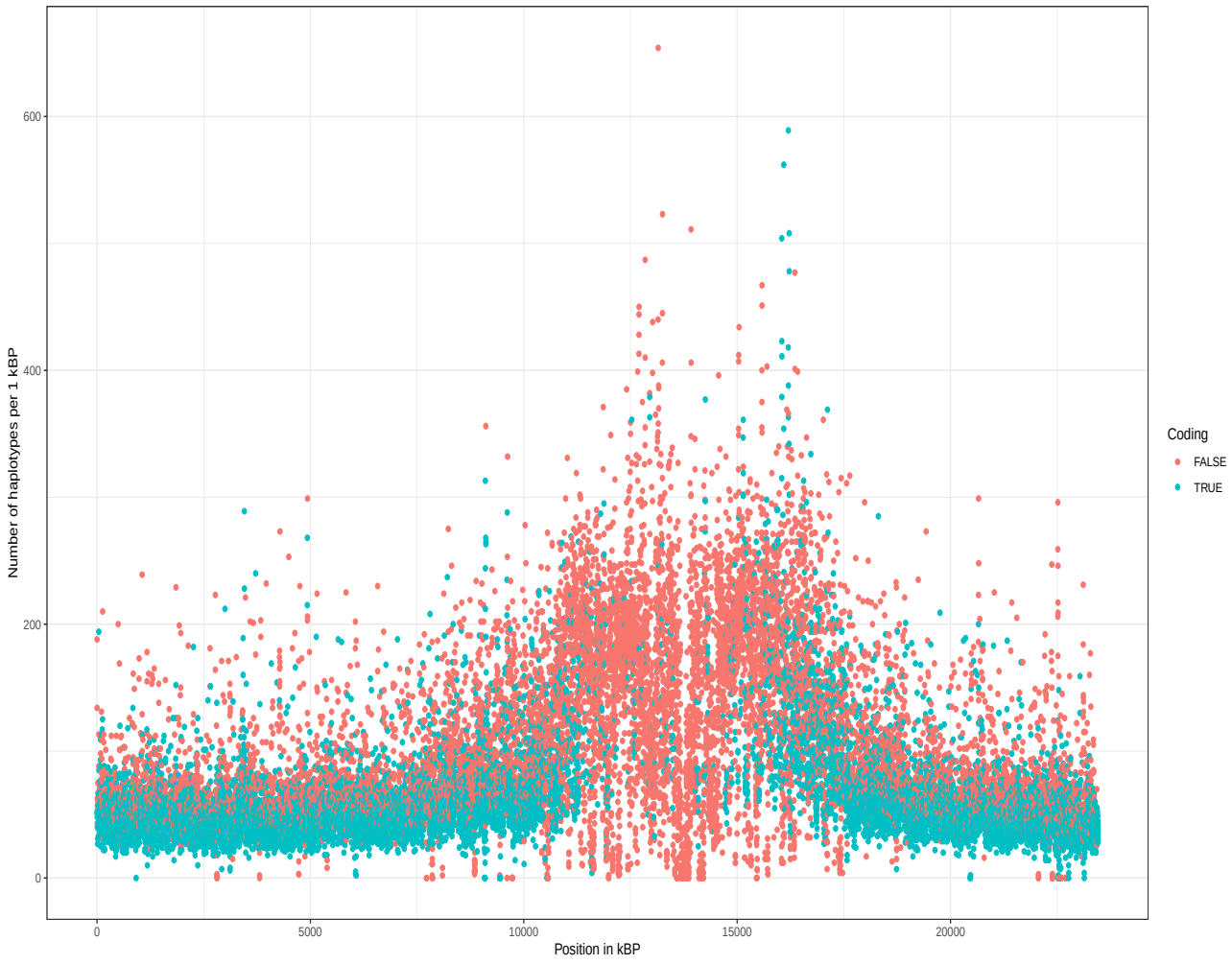

FIGURE 2.3: Number of segregating haplotypes with a polymorphism in at least one position over a stretch of 1 kBP.

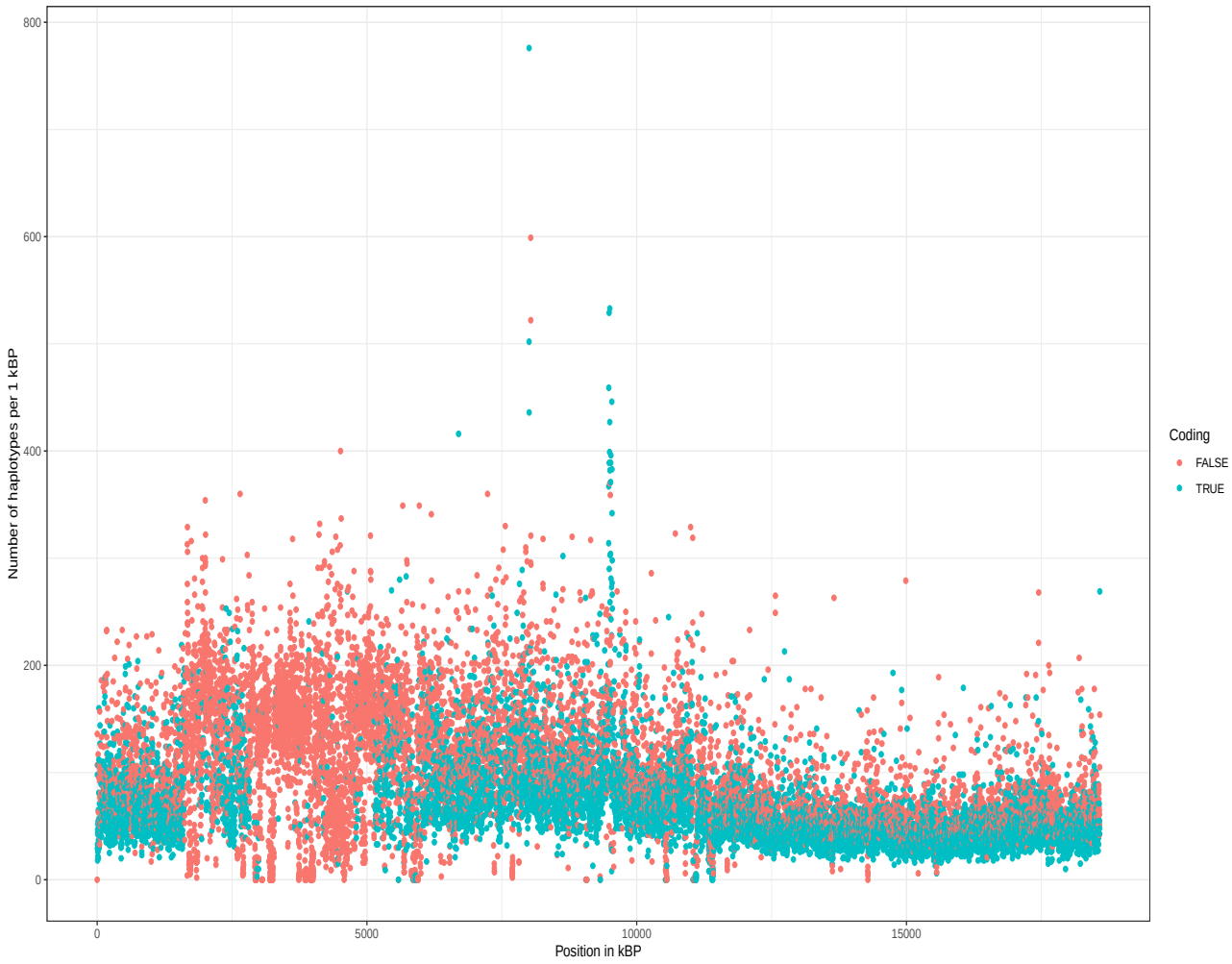

FIGURE 2.4: Number of segregating haplotypes with a polymorphism in at least one position over a stretch of 1 kBP.

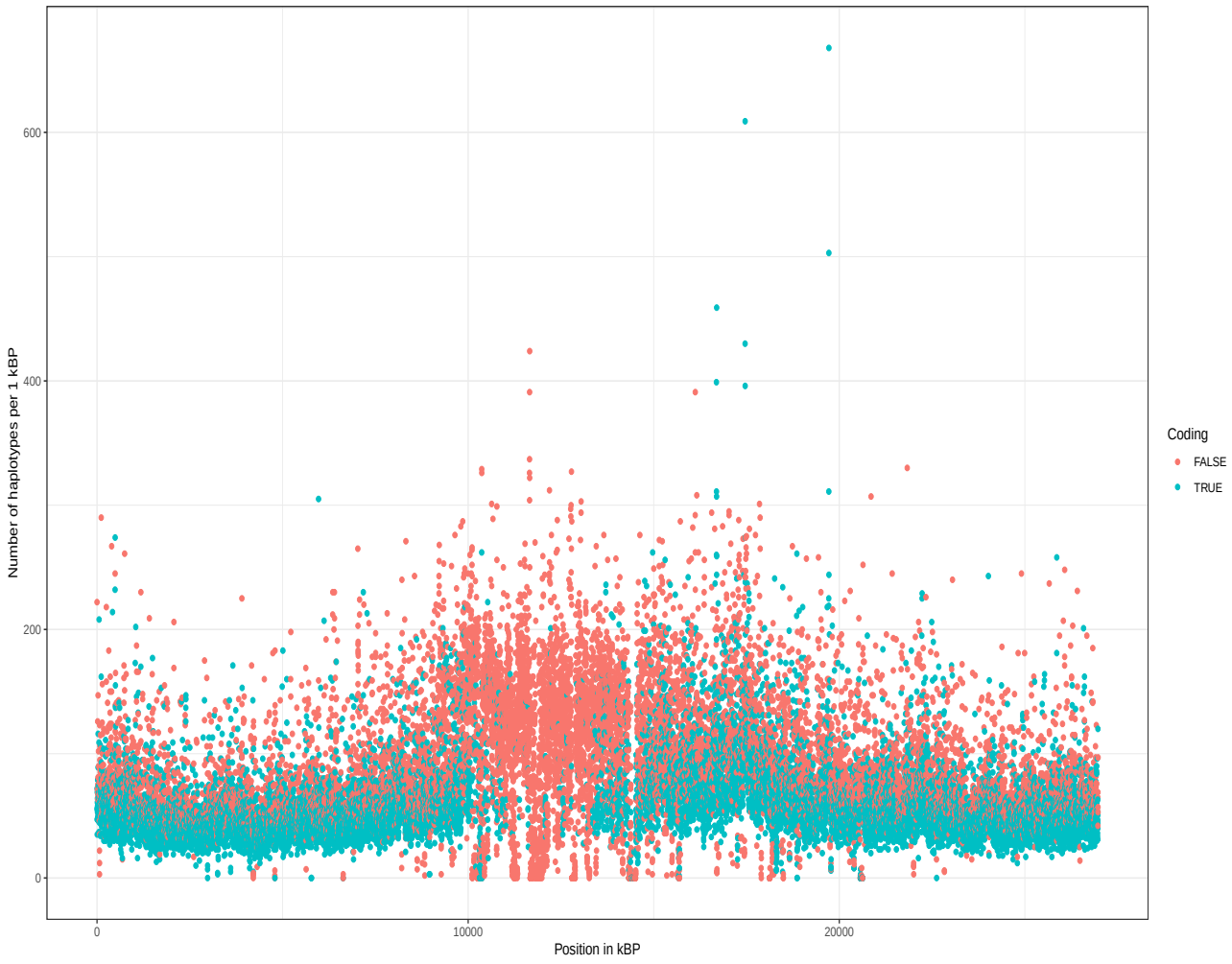

FIGURE 2.5: Number of segregating haplotypes with a polymorphism in at least one position over a stretch of 1 kBP.

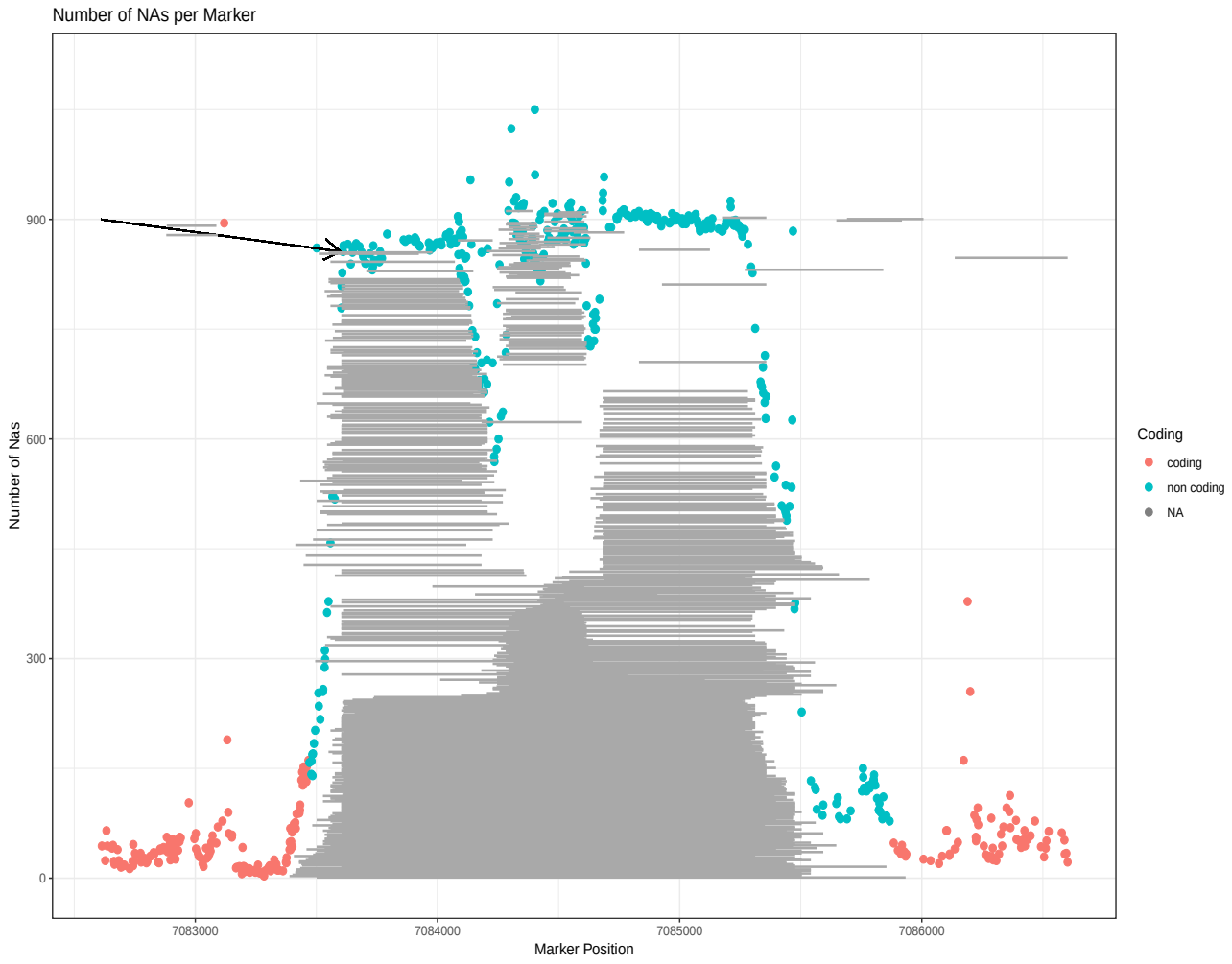

FIGURE 2.6: Number of segregating haplotypes with a polymorphism in at least one position over a stretch of 1 kBP.

3 GWAS-Flow a gpu-accelerated software for large-scale genome-wide association studies

The following chapter has been published in a similar version on the bioχiv preprint server *Freudenthal* et al., 2019 and has been submitted for publication to Oxford Bioinformatics. The experiments and the software have been designed and conducted author. The manuscript has been prepared by the author, with minor corrections from Prof. Arthur Korte & Dominik Grimm. All authors approved of the final manuscript.

3.1 Introduction

Genome-wide association studies, pioneered in human genetics *Hirschhorn* and *Daly*, 2005 in the last decade, have become the predominant method to detect associations between phenotypes and the genetic variations present in a population. Understanding the genetic architecture of traits and mapping the underlying genomic polymorphisms is of paramount importance for successful breeding both in plants and animals, as well as for studying the genetic risk factors of diseases. Over the last decades, the cost for genotyping have been reduced dramatically. Early GWAS consisted of a few hundred individuals which have been phenotyped and genotyped on a couple of hundreds to thousands of genomic markers. Nowadays, marker density

for many species easily exceed millions of genomic polymorphisms. Albeit commonly SNPs are used for association studies, standard GWAS models are flexible to handle different genomic features as input. The *Arabidopsis* 1001 genomes project features for example 1135 sequenced *Arabidopsis thaliana* accessions with over 10 million genomic markers that segregate in the population *Alonso-Blanco* et al., 2016. Other genome projects also yielded large amounts of genomic data for a substantial amount of individuals, as exemplified in the 1000 genomes project for humans *Siva*, 2008, the 2000 yeast genomes project or the 3000 rice genomes project *Li*, *Wang*, and *Zeigler*, 2014. Thus, there is an increasing demand for GWAS models that can analyze these data in a reasonable time frame. One critical step of GWAS is to determine the threshold at which an association is termed significant. Classically the conservative Bonferroni threshold is used, which accounts for the number of statistical tests that are performed, while many recent studies try to significance thresholds that are based on the false-discovery rate (FDR) *Storey* and *Tibshirani*, 2003. An alternative approach are permutation-based thresholds *Che* et al., 2014. Permutation-based thresholds estimate the significance by shuffling phenotypes and genotypes before each GWAS run, thus any signal left in the data should not have a genetic cause, but might represent model mis-specifications or uneven phenotypic distributions. Typically this process is repeated hundreds to thousands of times and will lead to a distinct threshold for each phenotype analyzed *Togninalli* et al., 2017. The computational demand of permutation-based thresholds is immense, as per analysis not one, but at least hundreds of GWAS need to be performed. Here the main limitation is the pure computational demand. Thus, faster GWAS models could easily make the estimation of permutation-based thresholds the default choice.

3.2 Methods

GWAS Model

The GWAS model used for `GWAS-Flow` is based on a fast approximation of the linear-mixed-model described in *Kang* et al., 2010; *Zhang* et al., 2010, which estimates the variance components σ_g and σ_e only once in a null model that includes the genetic relationship matrix, but no distinct genetic markers. These components are thereafter used for the tests of each specific marker. Here, the underlying assumption is, that the ratio of these components stays constant, even if distinct genetic markers are included into the GWAS model. This holds true for nearly all markers and only markers which posses a big effect will alter this ratio slightly, where now σ_g would become smaller compared to the null model. Thus, the p-values calculated by the approximation might be a little higher (less significant) for strongly associated markers.

The GWAS-Flow Software

The `GWAS-Flow` software was designed to provide a fast and robust GWAS implementation that can easily handle large data and allows to perform permutations in a reasonable time frame. Traditional GWAS implementations that are implemented using Python *Van Rossum* and *Drake Jr*, 1995 or R *R Core Team*, 2019 cannot always meet these demands. We tried to overcome those limitations by using TensorFlow *Abadi* et al., 2015, a multi-language machine learning framework published and developed by Google. GWAS calculations are composed of a series of matrix computations that can be highly parallelized, and easily integrated into the architecture provided by TensorFlow. Our implementation allows both, the classical parallelization of code on multiple processors (CPUs) and the use of graphical processing units (GPUs). `GWAS-Flow` is written using the Python TensorFlow API. Data import is done with *pandas McKinney*, 2010 and/or *HDF5* for Python *Collette*, 2013. Preprocessing of the data (e.g filtering by minor Allele count (MAC)) is performed with *numpy*

Oliphant, 2006. Variance components for residual and genomic effects are estimated with a slightly altered function based on the Python package *limix Lippert* et al., 2014. The GWAS model is based on the following linear mixed model that takes into account the effect of every marker with respect to the kinship:

$$Y = \beta_0 + X_i\beta_i + u + \epsilon, u \sim N(0, \sigma_g K), \epsilon \sim N(0, \sigma_e I) \tag{3.1}$$

From this LMM the residual sum of squares for marker i are calcucated as descirebed in 3.2

$$RSS_i = \sum Y - (X_i\beta_0 + I_i\beta_1) \tag{3.2}$$

The residuals are used to calculate a p-value for each marker according to an overall F-test that compares the model including a distinct genetic effect to a model without this genetic effect:

$$F = \frac{RSS_{env} - R1_{full}}{\frac{R1_{full}}{n-3}} \tag{3.3}$$

Apart from the p-values that derive from the F-distribution, `GWAS-Flow` also report summary statistics, such as the estimated effect size (β_i) and its standard error for each marker.

Calculation of permutation-based thresholds for GWAS

To calculate a permuation-based threshold, we essentially perform n repetitions ($n > 100$) of the GWAS on the same data with the sole difference that before each GWAS we randomize the phenotypic values. Thus any correlation between the phenotype and the genotype will be broken and indeed for over 90% of these analyses the estimated pseudo-heritability is close to zero. On the other hand, the phenotypic distribution will stay unaltered by this randomization. Hence, any remaining signal in the GWAS has to be of a non-genetic origin and could be caused by e.g. model mis-specifications. Now we take the lowest p-value (after filtering for the

desired minor allele count) for each permutation and take the 5% lowest value as the permutation-based threshold for the GWAS.

Benchmarking

For benchmarking of `GWAS-Flow` we used data from the *Arabidopsis* 1001 Genomes Project *Alonso-Blanco* et al., 2016. The genomic data we used were subsets between 10,000 and 100,000 markers. We chose not to include subsets that exceed 100,000 markers, because there is a linear relationship between the number of markers and the computational time demanded, as all markers are tested independently. We used phenotypic data for flowering time at ten degrees (FT10) for *A. thaliana*, published and downloaded from the AraPheno database *Seren* et al., 2016. We down- and up-sampled sets to generate phenotypes for sets between 100 and 5000 accessions. For each set of phenotypes and markers we ran 10 permutations to assess the computational time needed. All analyses have been performed with a custom R script that has been used previously *Togninalli* et al., 2017, `GWAS-Flow` using either a CPU or a GPU architecture and *GEMMA Zhou* and *Stephens*, 2012. *GEMMA* is a fast and efficient implementation of the mixed model that is broadly used to perform GWAS. All calculations were run on the same machine using 16 i9 virtual CPUs. The GPU version ran on an NVIDIA Tesla P100 graphic card. Additionally to the analyses of the simulated data, we compared the times required by *GEMMA* and both `GWAS-Flow` implementations for $>$ 200 different real datasets from *A. thaliana* that have been downloaded from the AraPheno *Seren* et al., 2016 database and have been analyzed with the available fully imputed genomic dataset of ca. 10 million markers, filtered for a minor allele count greater five.

3.3 Results

The two main factors influencing the computational time for GWAS are the number of markers incorporated in such an analysis and the number of different accessions, while the latter has an approximate quadratic effect in classical GWAS implementations *Zhou* and *Stephens*, 2012. Figure 1A shows the time demand as a function of the number of accessions used in the analysis with 10,000 markers. The quadratic increase in time demand is clearly visible for the custom R implementation, as well as for the CPU-based `GWAS-Flow` implementation and *GEMMA*. The `GWAS-Flow` implementation and *GEMMA* clearly outperforms the R implementation in general, while for a small number of accessions `GWAS-Flow` is slightly faster then *GEMMA*. For the GPU-based implementation the increase in run-time with larger sample sizes is much less pronounced. While for small ($<$ 1,000 individuals) data, there is no benefit compared to running `GWAS-Flow` on CPUs or running *GEMMA*, the GPU-version clearly outperforms the other implementations if the number of accessions increases. Figure 1B shows the computational time in relation to the number of markers and a fixed amount of 2000 accessions for the two different `GWAS-Flow` implementations. Here, a linear relationship is visible in both cases. To show the performance of `GWAS-Flow` not only for simulated data, we also run both implementations on more than 200 different real datasets downloaded from the AraPheno database. Figure 1C shows the computational time demands for all analyses comparing both `GWAS-Flow` implementation to *GEMMA*. Here, the CPU-based `GWAS-Flow` performs comparable to *GEMMA*, while the GPU-based implementation outperforms both, if the number of accessions is above 500. Importantly all obtained GWAS results (p-values, beta estimates and standard errors of the beta estimates) are nearly (apart from some mathematical inaccuracies) identical between the three different implementations.

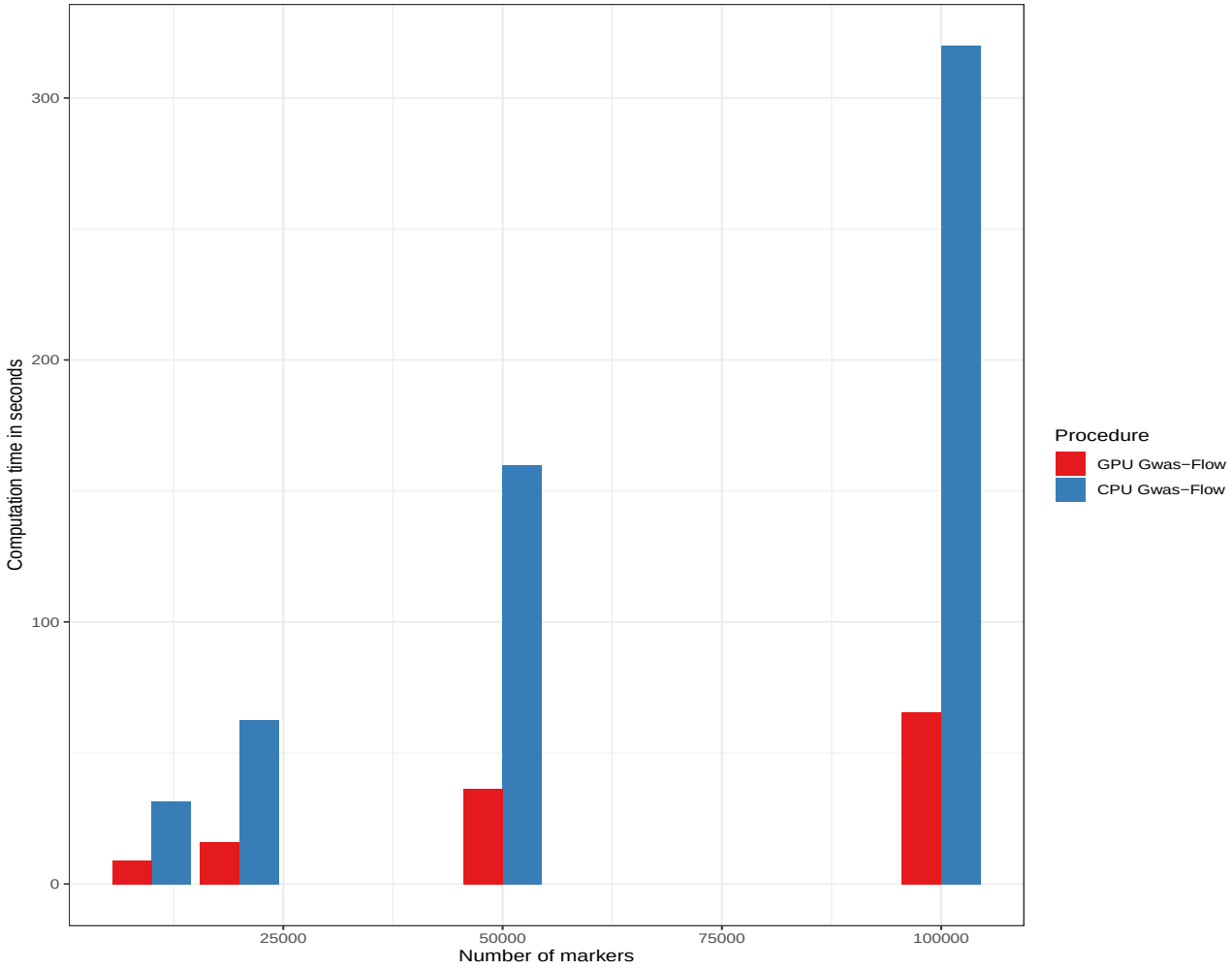

FIGURE 3.1: Computational time as a function of the number of genetic markers with constantly 2000 accessions for both `GWAS-Flow` versions

3.4 Disucssion

We made use of recent developments of computational architecture and software to cope with the increasing computational demand in analyzing large GWAS datasets. With `GWAS-Flow` we implemented both, a CPU- and a GPU-based version of the classical linear mixed model commonly used for GWAS. Both implementations outperform custom R scripts on simulated and real data. While the CPU-based version performs nearly identical compared to *GEMMA*, a commonly used GWAS implementation, the GPU-based implementation outperforms both, if the number of individuals, which have been phenotyped, increases. For analyzing big data, here the

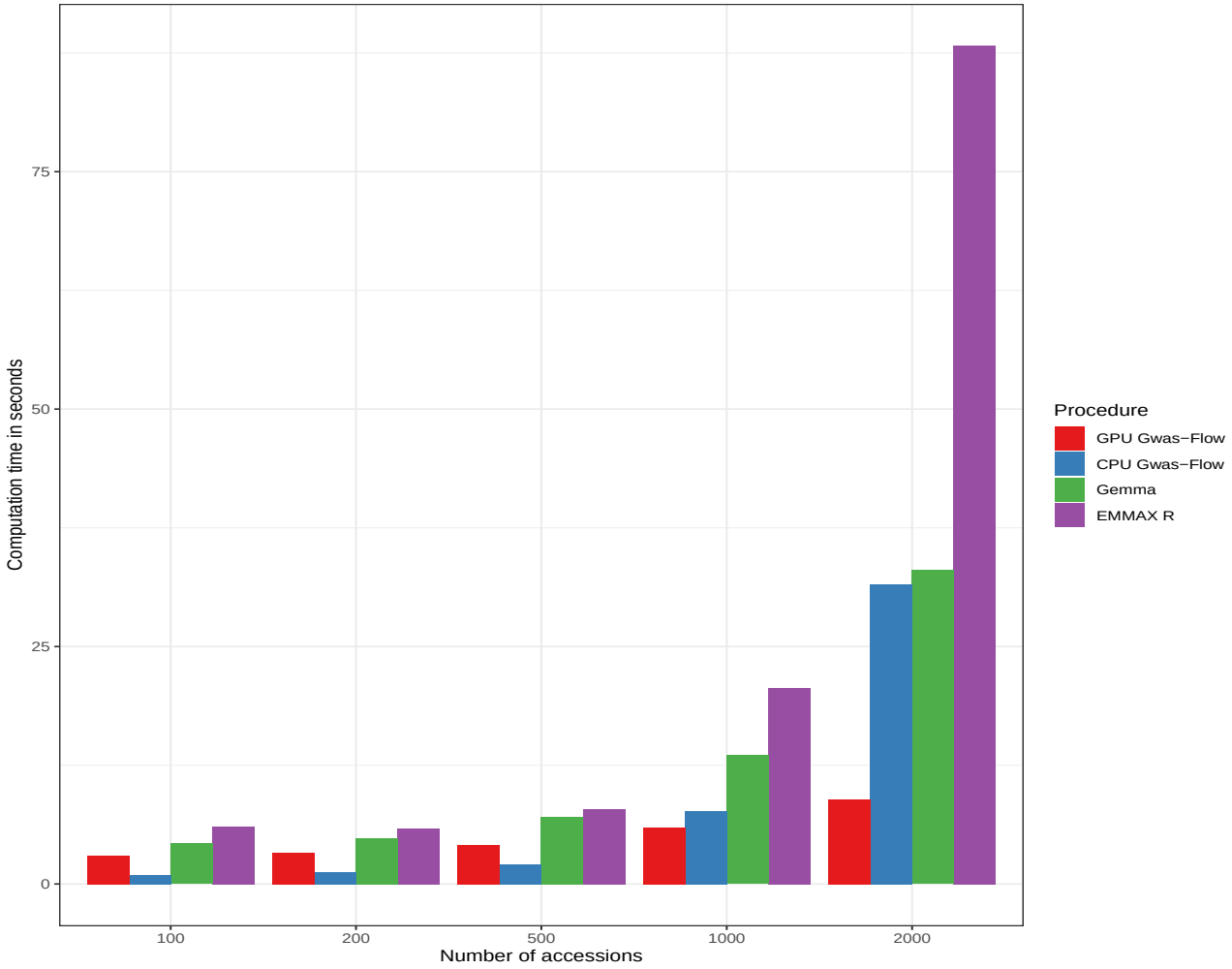

FIGURE 3.2: Computational time as a function of the number of accessions with 10000 markers each.

main limitation would be the RAM of the GPU, but as the individual test for each marker are independent, this can be easily overcome programmatically. The presented `GWAS-Flow` implementations are markedly faster compared to custom GWAS scripts and even outperform efficient fast implementations like *GEMMA* in terms of speed. This readily enables the use of permutation-based thresholds, as with `GWAS-Flow` hundred permutations can be performed in a reasonable time even for big data. Thus, it is possible for each analyzed phenotype to create a specific, permutation-based threshold that might present a more realistic scenario. Importantly the permutation-based threshold can be easily adjusted to different minor allele counts, generating different significance thresholds depending on the allele

count. This could help to distinguish false and true associations even for rare alleles. `GWAS-Flow` is a versatile and fast software package. Currently `GWAS-Flow` is and will remain under active development to make the software more versatile. This will e.g. include the compatibility with TensorFlow v2.0.0 and enable data input formats, such as PLINK *Purcell* et al., 2007. The whole framework is flexible, so it is easy to include predefined co-factors e.g to enable multi-locus models *Segura* et al., 2012 or account for multi-variate models like the multi-trait mixed model *Korte* et al., 2012. Standard GWAS are good in detecting additive effects with comparably large effect sizes, but lack the ability to detect epistatic interactions and their influence on complex traits *Mckinney* and *Pajewski*, 2012; *Korte* and *Farlow*, 2013. To catch the effects of these gene-by-gene or SNP-by-SNP interactions, a variety of genome-wide association interaction studies (GWAIS) have been developed, thoroughly reviewed in *Ritchie* and *Van Steen*, 2018. Here, `GWAS-Flow` might provide a tool that enables to test the full pairwise interaction matrix of all SNPs. Although this might be a statistic nightmare, it now would be computationally feasible.

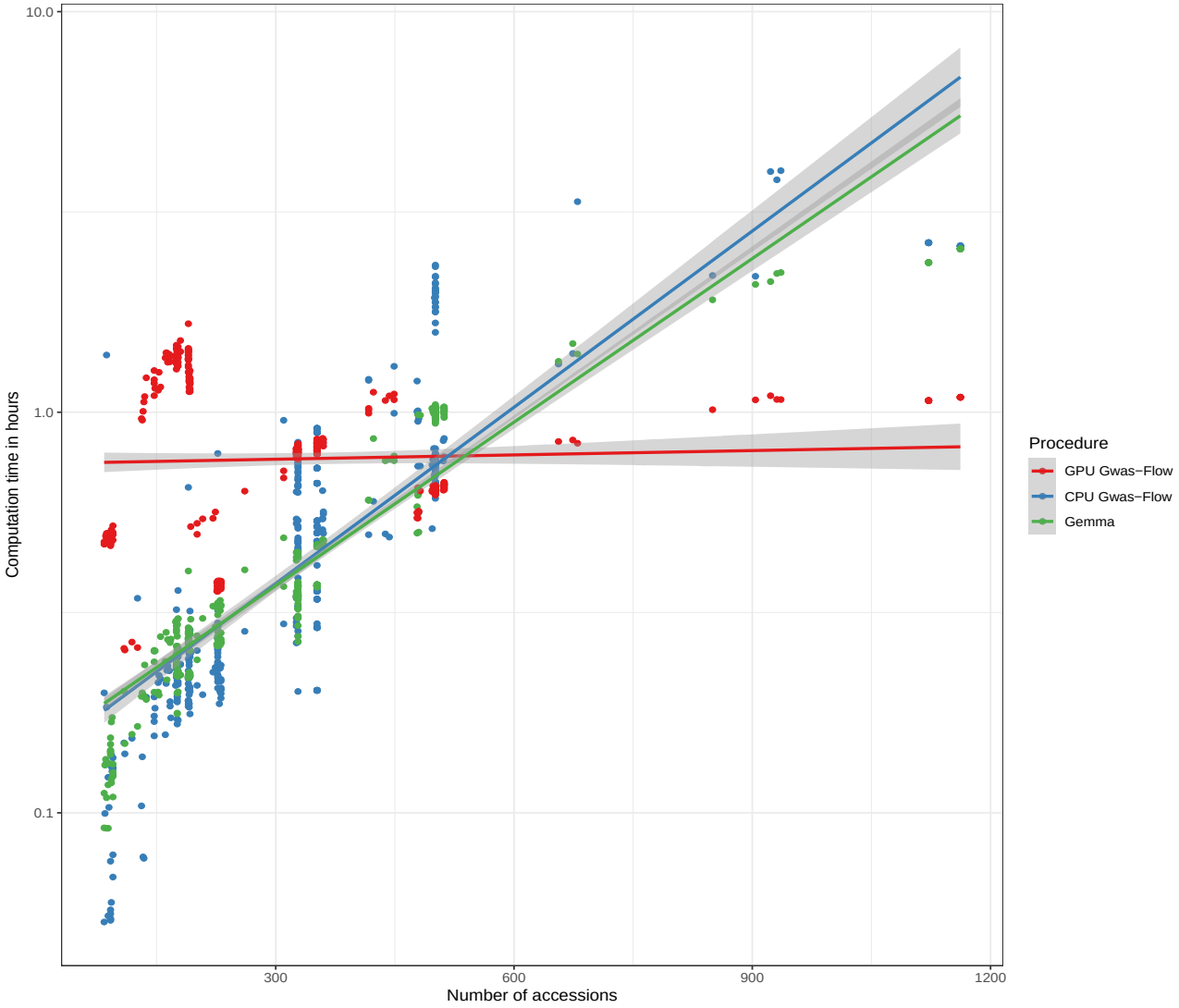

FIGURE 3.3: Comparison of the computational time for the analyses of $>$ 200 phenotypes from *Arabidopsis thaliana* as a function of the number of accessions for *GEMMA* and the CPU- and GPU-based version of `GWAS-Flow`. GWAS was performed with a fully imputed genotype matrix containing 10.7 M markers and a minor allele filter of MAC $>$ 5

4 Genomic prediction of phenotypic values of quantitative traits using Artificial neural networks

4.1 Introduction

4.1.1 A brief history of machine learning

Basic perceptron model

While machine learning, neural networks, deep learning became essential tools for many applications in more recent years, their mathematical principals date back to the early 1950s and 1960s. Figure 4.1 schematically show the basic perceptron model as proposed by Rosenblatt, which was designed to mimic the information flow in biological nervous systems *Rosenblatt*, 1961

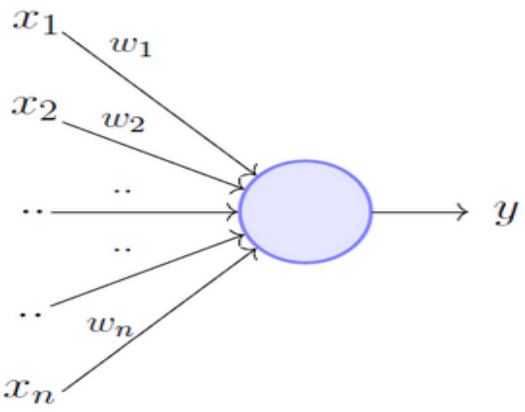

FIGURE 4.1: Basic perceptron model as proposed by Rosenblatt

This basic perceptron, which contrary to perceptrons used nowadays does not have an activation function, takes n binary inputs $x_1, x_2....x_n$ and produces a single, likewise binary, output y after being processed by the perceptron or neuron. To achieve this Rosenblatt introduced the concept of weights which indicated a certain relative importance to the outcome of the output. $w_1, w_2...w_n$. The output y is determined by the weighted sum of the weights and biases $\sum_i w_i x_i$. If a certain threshold value is met the neuron is either activated and outputs 1 or not and outputs 0. This is algebraically represented in 4.1

$$0 = \text{if } \sum_i^n w_j x_i - \theta \leq 0 \tag{4.1a}$$

$$1 = \text{if } \sum_i^n w_i x_i - \theta > 0 \tag{4.1b}$$

Next to the weights w_n and the inputs x_n a third term θ is introduced in equation 4.1 which represents the activation threshold in per definition is negative. A single perceptron is a linear classifier and can only be trained on linearly separable functions and can used as shown by *Rosenblatt*, 1961 to solve simple logical operations as AND, OR and not. The simple perceptron fails, due to non-linearity, to perform XOR operations as shown by *Marvin* and *Seymour*, 1969. This discovery let to a near still stance in the research of artificial neural networks in the 1970s. This time period as now often referred to as the first AI-winter. Another reason that massively hindered the applications and research of machine learning during that time, was the compared to modern times incredibly small amount of computational power available *Nguyen* and *Widrow*, 1990.

More complex decision making, like solving XOR problems, requires more complex structures than a single perceptron. Continuing the trend of mimicking human neural networks, multiple artificial neurons are stacked into layers and these layers, are connected to each other allowing communication between the many perceptrons

in a such generated network. Figure 4.2 shows schematically the basic structure of such a network, now container three types of layers. (i) the input layer, (ii) one or more hidden layers and (iii) one output layer, which in this case only consists of one neuron.

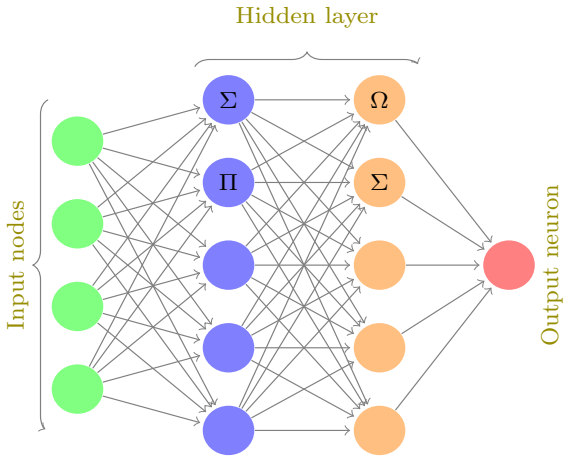

FIGURE 4.2: Schematic layout of a simple multi-layer perceptron

In the sample layout of figure 4.2 the neurons in the first column weigh the inputs and pass those the the neurons on the second layer. In this case all neurons on the first layer or connected to all neurons on the second layer, such layers are referred to fully-connected layers (FLC) , and their resulting networks are often called multi-layer perceptrons (MLP). This architecture enables the network to perform more complex calculations and result in more abstract decisions than single neurons or single layer architectures.

Activation functions

The neurons discussed so far are only capable of outputting binary results. Either 0 or 1, depending on the threshold values being met or not. For more complex estimations it is desirable that small changes in the input also result in small changes of the output. This requirement can not be met with binary outputs. Activation functions for a given node provides rules for the output in accordance to the inputs *Žilinskas*, 2006.

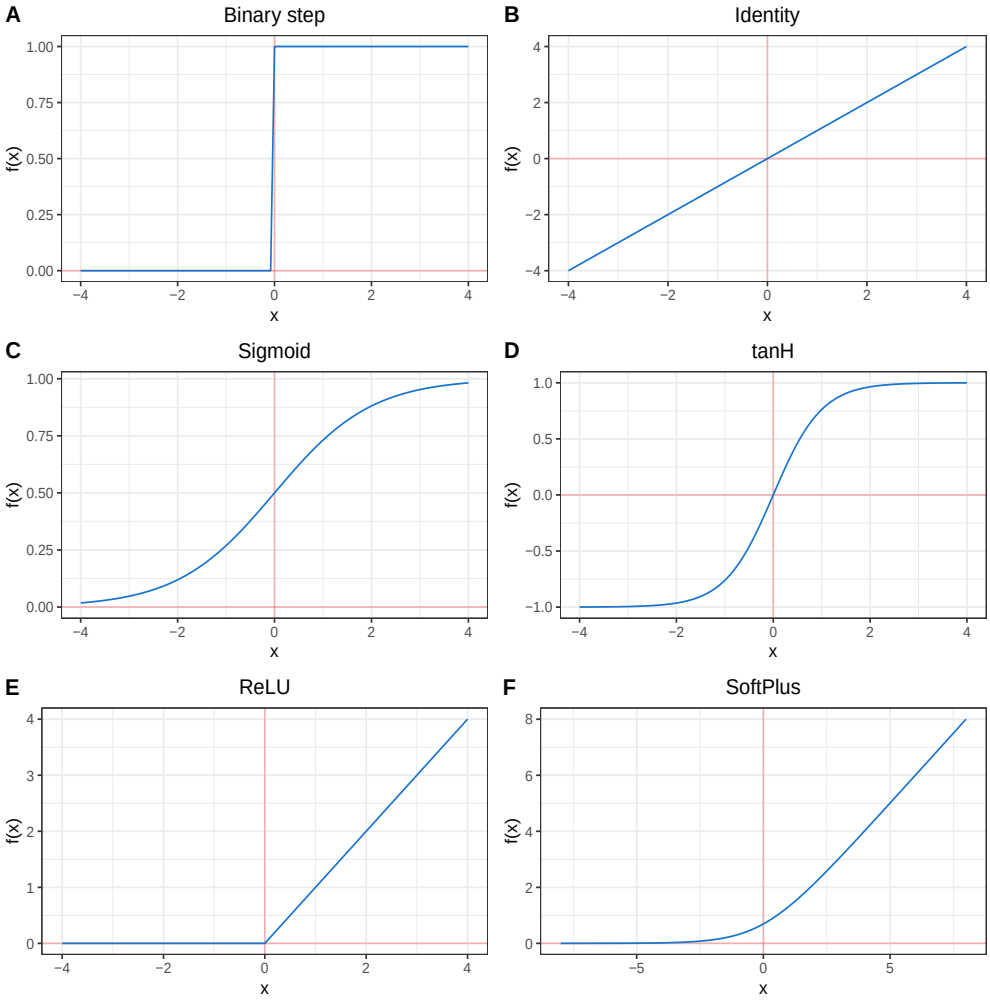

FIGURE 4.3: Popular activation functions used in neural networks. **A** Binary step activation function. **B** Identity activation function. **C** Sigmoid or logistic activation function. **D** tangens hyperbolicus activation function. **E** rectified linear units activation function . **F** SoftPlus activation function.

Figure 4.3 **A** shows six of the most commonly used activation functions *Warner and Misra*, 1996. The simplest one was introduced, is the binary step activation function equation 4.2, which properties have been discussed along the perceptron model. All other activation produce continuous outputs from any given input. Basically any mathematical function can serve as an activation function in neural nets, starting with a simple identity function 4.3 , 4.3 **B**. Sigmoid figure 4.3 **C**, equation 4.4 and tanh figure 4.3 **D**, equation 4.5, when $x \to \infty$ or $x \to -\infty$ they have similar properties to the binary function, but produce continuous output around 0.

$$f(x) = \sigma(x) = \begin{cases} 0 \; for \; x < 0 \\ 1 \; for \; x \geq 0 \end{cases} \tag{4.2}$$

$$f(x) = \sigma(x) = x \tag{4.3}$$

$$f(x) = \sigma(x) = \frac{1}{1 + e^{-x}} \tag{4.4}$$

$$f(x) = \sigma(x) = \frac{e^{x} - e^{-x}}{e^{x} + e^{-x}} \tag{4.5}$$

$$f(x) = \sigma(x) = \begin{cases} 0 \; for \; x < 0 \\ x \; for \; x \geq 0 \end{cases} \tag{4.6}$$

$$f(x) = ln(1 + e^{x}) \tag{4.7}$$

ReLU (equation 4.6) and the softplus (equation 4.7) share similar properties as well, the latter one being a smoothed version of ReLU. Rectifiers as activation functions have been introduced in 2000s *Hahnloser* et al., 2000 and have since then overtaken all others as the most popular activations functions in neural networks and deep learning today *LeCun*, *Bengio*, and *Hinton*, 2015 and they have proven to be superior in deep-learning algorithms that sigmoid or logistic functions. One of the advantages leading to the superiority of ReLUs is that with randomly initialized weights only half of the ReLU neurons are activated, compared to tanh and sigmoid activation *Glorot*, *Bordes*, and *Bengio*, 2011. All activation functions shown in figure 4.3, but the binary step function, share one common property: a small change of the input weight will result in small changes in the output, while a small change of the input for the binary step function leads to either no or a complete change of the output. This property is, as described below, is an important prerequisite for networks being able to learn.

Gradient descent algorithm

Let the network shown in 4.2 be for the classification of a arbitrary phenotype like blue petals with $x_1 ... x_4$ on the input layers being genetic markers as features. And the output layer displaying a value from 0 to 1, meaning yes: blue petals from 0 - 0.5 and no blue petals from 0.5 to 1. To quantify how well the network performs on achieving that goal a loss function is applied *Schmidhuber*, 2015. There is a large variety of different loss functions available for neural networks like mean squared error (MSE), root mean squared error (RMSE), cross-entropy and many others. In general MSE, MSE are commonly used for regression problems, with the latter being less popular and cross-entropy also called log loss is used for binary or multi-class classification problems *Janocha* and *Czarnecki*, 2017. Since all problems presented in due course or regression problems, that use MSE as their loss function, this will be the only one emphasized.

$$MSE = \frac{1}{n} \sum_{i=1}^{n} (y_i - \widetilde{y})^2 \tag{4.8}$$

Equation 4.8 shows the MSE function which is the sum of the squares of the differences of all the predicted and the real values. The same function can be rewritten with the previously used terminology of weights and biases in equation 4.8.

$$L(w, b) = \frac{1}{2n} \sum_{x} \|y(x) - \widetilde{y}\|^2. \tag{4.9}$$

With w and b as the collection of all the weights and the biases in the network used to optimize the function $y(x)$. Giving the quadratic nature of the function the $L(w, b)$ will always be positive. And if $L(w, b) \rightarrow 0$ the loss is minimal, meaning that the real and predicted values are close together and the network found weights and biases that explain the output well.

A widely used function to find the optimum for such a loss function is gradient descent. Its objective is to fine the minimum for the loss function *Bottou*, 1991. The behind gradient descent or other optimizing algorithms is start with randomly initialized weights and biases and repeatedly move them in direction Δw and Δb. This results in a change of the loss function as shown in equation 4.10, making use of partial derivatives.

$$\Delta L = \frac{\partial L}{\partial w}\Delta w + \frac{\partial L}{\partial b}\Delta b \tag{4.10}$$

Ideally ΔL is negative and the optimization algorithm found Δw and Δb that lead to a reduction of the loss. To simplify this problem let Δd be the vector of changes: $\Delta d = (\Delta w, \Delta b)^T$ and ∇L the vector of the partial derivatives: equation 4.11

$$\nabla L = \left(\frac{\partial L}{\partial w}, \frac{\partial L}{\partial w}\right)^T \tag{4.11}$$

Having defined ∇L and Δd the term 4.10 can be simplified as equation 4.12

$$\Delta C = \nabla L * \Delta d \tag{4.12}$$

Now the task of gradient descent or any other optimizer is to find Δd that results in ΔC being negative as shown in equation 4.13

$$\Delta d = -\eta \nabla L \tag{4.13}$$

In this case η is a small positive decimal number, commonly referred to as the learning rate, which usually, but not exclusively ranges from 0.1 to 0.001. However it can be larger or much smaller in some cases. Having found a way to ensure that ΔL always decreases according to equation 4.13 it is utilized to repeatedly update the gradient ∇L. To make the gradient descent algorithm efficient the learning rate η must be chosen correctly. If η is too large, the gradient ΔL might end up being larger than zero, leading to an increase of the loss, and if the step size is too small

convergence will either take too long or not take place at all *Bergstra* et al., 2011. In practical machine learning approaches different learning rates are tested. There are also algorithmic approaches. While equation 4.10 only accounts for two inputs features, it can be generalized to compute n inputs shown in equation 4.14.

$$\nabla L = \left(\frac{\partial L}{\partial w_1}, \ldots, \frac{\partial L}{\partial w_n} \right)^T \tag{4.14}$$

Equation 4.15 shows the gradient descent how it is used to repetitively update the weights and biases to optimize the loss function $L(c, w)$ with w and b as the weight and bias matrices and the learning rate η. In machine learning each iterational update of the network is often called epoch or training epoch.

$$w = w_i - \eta \frac{\partial}{\partial w} L(w) \tag{4.15a}$$

$$b = b_i - \eta \frac{\partial}{\partial b} L(b) \tag{4.15b}$$

$$\tag{4.15c}$$

Substituting the partial differentials with ∇L equation 4.15 a simplifies to:

$$w = w_i - \eta \nabla L \tag{4.16}$$

Optimizers

The previous section introduced the concept of gradient descent, an algorithm to minimize the loss function of the weights and biases of a neural network. All other optimizers introduced here, are either variations or extensions of the basic gradient descent algorithm (GD) shown in 4.15. One disadvantage of gradient descent is that

if the data sets grow larger, the demand in memory for computation increases exponentially. Taking into consideration machine learning is a popular method ind big data applications this is a serious drawback. Methods to overcome that are stochastic gradient descent and mini-batch gradient descent. The idea behind the latter is to randomly divide the entity of the training data in sub-samples called mini-batches *Bottou* and *Bousquet*, 2008. The network is then trained iteratively over the mini batches. The batch size influences the accuracy and the training speed and is another hyperparameter which has to be tuned. If the batch size is 1 mini batch GD is also referred to as stochastical gradient descent (SGD). During the optimization process optimizers can find local minima in the cost function without being able to overcome them to find the desired global minimum. An algorithm extending GD to accelerate the search of the global minimum is momentum. Which allows the GD to speed up when the loss is decreasing and to slow down when going in the wrong direction - increasing the loss function $L(w, b)$. This is achieved by accounting for the gradient of the previous step in the calculation of the current step. This concept was introduced by *Polyak*, 1964 and re-popularized alongside backpropagation learning by *Rumelhart*, *Hinton*, and *Williams*, 1988.

$$w = w_i - \eta \nabla L + \alpha \Delta w \tag{4.17}$$

Equation 4.17 shows how the momentum is mathematically represented in GD to update the weights w or likewise the biases the delta of the weights multiplied by the coefficient α - the momentum, which usually ranges from 0.1 to 0.9 and is another parameter to tuned for successful training. If the momentum is two small the GD will not be able to overcome local minima and if α is two large the loss functions tends to oscillate without finding an optimum *LeCun*, *Bengio*, and *Hinton*, 2015. For both of the momentum and the learning rate it is impractical to remain on the same level during all training epochs. Because after each epoch the loss function is either closer or further away from its global minima and depending on the distance to that

minimum it is desirable to have larger or smaller learning rates and momenta. This can be achieved with naive approaches for example using a step function to gradually decrease those values after each iteration, or to utilize algorithmic approaches *Michie*, *Spiegelhalter*, and *Taylor*, 1994. There is a large variety of optimizers trying to find optimal values for α and η and till today this field is under active research *Goodfellow*, *Bengio*, and *Courville*, 2016. Popular among those are: RMSprop *Hinton*, *Srivastava*, and *Swersky*, 2012; Nesterov momentum *Dozat*, 2016; Adadelta *Zeiler*, 2012; Adagrad *Ruder*, 2016 and Adam *Kingma* and *Ba*, 2014. With Adam being the most widely used optimizer today. Nesterov momentum is slight change to the normal momentum capable of having huge impacts in practical applications, because it helps avoiding oscillations around the minimum by using intermediate information to adapt the momentum.

RMSProp - root mean square propagation - is a method aiming to adapt the learning rate algorithmically, by choosing η for each parameter. And lastly the wide-spread Adam optimizer combines both of the features of momentum and RMSProp and adapts the learning rate as well as the momentum iteratively *Kingma* and *Ba*, 2014.

Backpropagation

maybe i will leave out backpropagation $\odot$

Backpropagation *Rumelhart*, *Hinton*, and *Williams*, 1988

Regularization parameters

When applying the combined aforementioned algorithms and optimizers to find global minima of a loss function of a neural network a problem arises, because optimizers like Adam work "too" well. This issues is due to the fact that neural networks have 100s of thousand of free parameters to be trained, deep neural networks have billions and trillions of parameters. If training of the neural net continues for enough epochs eventually. The loss function will approach a minimum and as $L(w, b) \rightarrow 0$ the initial conclusion could be that the training was quite successful,

but when trying to apply the network trained on the training data set (TRN) to a testing data set (TST). The loss and accuracy of the prediction of TST and TST are very large or accordingly small. This phenomenon is know as overfitting and a lot of fine tuning of hyperparameters is devoted to minimizing this effect *Tetko*, *Livingstone*, and *Luik*, 1995. Figure 4.4 visualizes the effects of overfitting during training *Goodfellow*, *Bengio*, and *Courville*, 2016.

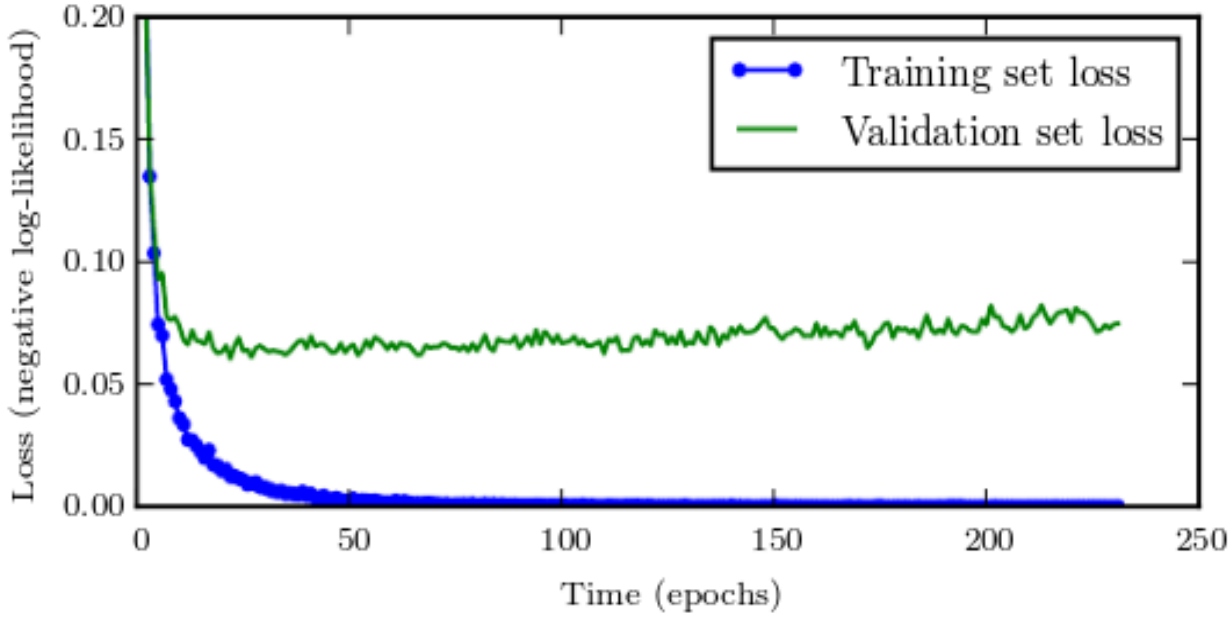

FIGURE 4.4: Learning curves showing how a loss function changes during training in the loss and validation data set. While the training loss approaches 0 the validation loss starts increasing after hitting a minimum. This effect is due to overfitting on the training data set. Figure from *Goodfellow*, *Bengio*, and *Courville*, 2016.

Cross-validation

A method that is used in basically every training of neural network is splitting up the data sets in multiple sub-sets. More specifically a training set (TRN) and a testing set (TST). The training set is used to minimize the loss functions and its success is evaluated on the TRN set, by comparing the predicted values $\hat{y}$ with the

real values in TST y. For all neural nets in this study person's correlation coefficient was chosen as performance metric, as in equation 4.18 *Soper* et al., 1917.

$$\rho(y, \hat{y}) = \frac{cov(y, \hat{y})}{\sigma_y \sigma_{\hat{y}}} \tag{4.18}$$

There are other popular performance metrics, especially for classification problems, like AUC (area under the curve) and ROC (receiver operating characteristics), which basically evaluate by weighing sensitivity and specificity. In cross-validation compared to single validation the initial data set is split into TRN and TST multiple times e.g. if the ratio is 80:20 5 times, and each TRN-TST pair is evaluated individually. Sometimes it becomes necessary to use a third subset - the validation data. Because hyperparameter tuning is performed with the TRN and TST sets, a third portion of the data needs to be assessed to check whether the neural network is able to generalize on global data.

L1 and L2 loss

L1 and L2

Dropout

4.1.2 On the nature of quantitative traits

According to the omnigenic model which is an extension of the polygenic model proposed by *Boyle*, *Li*, and *Pritchard*, 2017 and thoroughly reviewed in *Timpson* et al., 2018 all traits or phenotypic values are influenced by a great number or all genes in the genome. Therefore resulting in traits following certain gradual statistical distributions instead of being binned in classes or even binary. Intuitively this might be contradicting with the foundation of modern Genetics - Mendel's three laws. That where derived from observations with where mainly influenced by one locus. But staying with one of Mendel's examples the round or wrinkled surfaces of peas

Pisum sativum, an assessment of a couple of thousands peas, would most likely inevitably lead to the conclusion that form the "roundest" to the "wrinkliest" pea any gradual step between those is possible and observable. Mendel's third law of independent segregation also only holds true under certain assumptions. The most simplest one being that the traits under investigation have to be located on different linkage groups. Otherwise for the 7 traits used in Mendel's initial studies would not have segregated independently. The odds of 7 randomly selected traits being on 7 different linkage groups are rather small, especially taking into account, that the genome of the *P. sativum* consists of only 7 chromosomes itself *Kalo* et al., 2004. Mendel probably new about traits not following its own laws, as well as being aware of the quantitative nature of traits such as the constitution of surfaces of peas or the color of petals. But being the pioneer of a then rather unexplored field of science, some of which big questions we fail to satisfactory answer today, he did not have the resources or the knowledge to explain behavior's not "mendeling", that were only able to be deciphered in later decades and centuries based on his ground-breaking work.

Initially thought to be contradicting to Mendel's ideas Darwin proposed the concept's of evolution due to natural selection which also introduce the idea of traits following a gradual distribution *Darwin*, 1859. This contrast led to a long lasting debate in the scientific community in the early 1900s, between the Mendelians and the biometricians who believed in the quantitative nature of continuous traits. This conflict has eventually been solved by Fisher's fundamental work published in 1918 *Fisher*, 1919. His theories combined the then in all fields of science popular research of distributions with genomics. He he mathematically proved that traits influenced by many genes, with randomly-sampled alleles follow a continuous normal distribution in a population. While this combined the ideas of Mendel and the biometricians it opened an other long debated question of effect size and the overall architecture of complex traits. While in the theory of monogenic traits the effect size of the single gene on the trait is 1 or 100 % with an increasing number of genes

influencing a complex traits the *per sè* contribution of single gene has to decrease with an increasing number of loci determining the value a given trait. In the 1990s it has been thought, that complex traits are predominantly controlled from few genes with a large to medium effect size, while others had a minimal influence *Zhang* et al., 2018.

With the upcoming popularity of GWAS as the favored method to decipher genetic architectures of traits, or having pioneered in human genetics in became clear that the majority of the effect sizes are tiny < 1 % while there are very few loci which have a moderate effect on the phenotypic variance of a population with around 10 % or less *Korte* and *Farlow*, 2013, *Stringer* et al., 2011. This nature of quantitative traits present great challenges to animal *Goddard* and *Hayes*, 2009 and plant breeding *Würschum*, 2012, in further improving crop or livestock performances, as well complicating the decomposition of genomic causes for diseases like schizophrenia or autism in human medicine *De Rubeis* et al., 2014, *Purcell* et al., 2014.

While the complex nature of the architecture of quantitative traits provide enough challenges as is, all traits will also be influenced by the environment from which an individual originates. Therefore the distribution of trait values in a given population can be expressed as the addition of the variances of its genetic and the environmental effects 4.19.

$$\sigma_P = \sigma_G + \sigma_E \tag{4.19}$$

The genomic and the environmental effects not only influence the phenotypic variance directly, but the environment also has an influence on gene expression methylation of DNA bases etc. and therefore the equation 4.19 needs to be extend by the variance of the gene-environment interactions σ_{GxE} 4.20 , *Lynch* and *Walsh*, 1998, *Walsh* and *Lynch*, 2018.

$$\sigma_P = \sigma_G + \sigma_E + \sigma_{GxE} \tag{4.20}$$

Equation 4.20 shows the decomposition of the phenotypic variance, to thoroughly understand complex genetic architectures of traits the genetic variance needs to be decomposed further in its additive, dominance and epistatic components 4.21

$$\sigma_G = \sigma_A + \sigma_D + \sigma_I \tag{4.21}$$

The additive effects are caused by single, for this model mostly homozygous, loci while the variance caused by dominance effects, is caused by heterozygous loci and their resulting interactions being full-, over- , co- or underdominant. And lastly the interaction effects that are a result of two or more genes only having an impact if the involved genes co-occur in a certain state. The resulting variance is commonly known as gene-gene interactions and/or epistasis *Falconer* and *Mackay*, 1996.
Since possible interactions in a genome can happen between additive or dominant or a combination of those loci. The variance due to interaction effects σ_I can be further dissembled in the variance resulting from additive-additive σ_{AA} dominant-dominant σDD and additive-dominant $sigmaAD$ terms as represented in equation 4.22.

$$\sigma_I = \sigma_{AxA} + \sigma_{DxD} + \sigma_{AxD} \tag{4.22}$$

Knowledge of the variance components involved in the expression of a trait in population, lead up to the estimation of the total influence of all genetic variances and the environmental variance one the phenotypic distribution. This concept if called heritability. The heritability of a trait H^2 accounts for the proportion of the phenotypic variance controlled by the total genetic variance as shown in equation 4.23. This is also referred to as broad sense heritability, because all genetic effects including additive, dominance and epistatic effects are included *Brooker*, 1999.

$$H^2 = \frac{\sigma_A + \sigma_D + \sigma_I}{\sigma_P} \tag{4.23}$$

The concept of narrow-sense heritability 4.24 is similar to the broad-sense heritability, but only the additive genetic effects are included in the genetic part of the equation. This differentiation is import for natural and artificial selection and thus is commonly used in evolutionary genomics and breeding. Because in diploid species each parent only passes down on a single a allele of a give locus. Dominance effects or interaction effects are not commonly inherited from one parent. Therefore the it is mainly the additive genetic effects of a parent that influences its offspring. While the dominance and epistatic variances are controlled by the combination of the parents *Falconer* and *Mackay*, 1996, *Walsh* and *Lynch*, 2018.

$$h^2 = \frac{\sigma_A}{\sigma_P} \tag{4.24}$$

4.1.3 Artificial selection in plant and animal breeding in the genomics era

Genomic prediction has been applied to almost all relevant crop and model species. Including: *A. thaliana Hu* et al., 2015; *Shen* et al., 2013. Alfalfa (*Medicago sativa*) *Li* and *Brummer*, 2012; *Annicchiarico* et al., 2015; *Li* et al., 2015; *Biazzi* et al., 2017; *Hawkins* and *Yu*, 2018. Barley *Neyhart*, *Lorenz*, and *Smith*, 2019; *Oakey* et al., 2016; *Zhong* et al., 2009. Cassava (*Manihot esculenta*) *Elias* et al., 2018a; *Elias* et al., 2018b. Cauliflower (*Brassica olearacea spp*) *Thorwarth*, *Yousef*, and *Schmid*, 2018. Cotton (*Gossiypium spp. Gapare* et al., 2018. Maze (*Zea mays*) *Moeinizade* et al., 2019; *Allier* et al., 2019; *Brauner* et al., 2018; *Schrag* et al., 2018; *Schopp* et al., 2017b; *Sousa* et al., 2017; *Schopp* et al., 2017a; *Kadam* et al., 2016; *Bustos-Korts* et al., 2016a; *Montesinos-López* et al., 2015; *Owens* et al., 2014; *Lehermeier* et al., 2014; *Technow* et al., 2014; *Peiffer* et al., 2014; *Riedelsheimer* et al., 2013; *Guo* et al., 2013; *Technow*, *Bürger*, and *Melchinger*, 2013; *Windhausen* et al., 2012; *Rincent* et al., 2012. Potato (*Solanum tuberosum*); *Enciso-Rodriguez* et al., 2018; *Endelman* et al., 2018. Rape seed (*Brassica naps*) *Würschum*, *Abel*, and *Zhao*, 2014; *Jan* et al., 2016; *Luo* et al., 2017; *Werner* et al., 2018; *Snowdon* and *Iniguez Luy*,

2012; *Qian, Qian*, and *Snowdon*, 2014. Rice (*Oryza sativa*) *Momen* et al., 2019; *Hassen* et al., 2018; *Xu*, 2013; *Grenier* et al., 2015. Rye (*Secale cerale*) *Auinger* et al., 2016; *Bernal-Vasquez* et al., 2014; *Wang* et al., 2014; *Bernal-Vasquez* et al., 2017; *Marulanda* et al., 2016. Soybean (*Glycine max*) *Stewart-Brown* et al., 2019; *Jarquin, Specht*, and *Lorenz*, 2016; *Xavier, Muir*, and *Rainey*, 2016. Switchgrass (*Panicum virgatum*) *Poudel* et al., 2019; *Ramstein* and *Casler*, 2019; *Ramstein* et al., 2016. Wheat (*Triticum aestivum*) *Cuevas* et al., 2019a; *Howard* et al., 2019; *Krause* et al., 2019; *Rincent* et al., 2018; *Norman* et al., 2018; *Belamkar* et al., 2018; *Ovenden* et al., 2018; *Sukumaran* et al., 2016; *Bustos-Korts* et al., 2016b; *Gianola* et al., 2016; *Crossa* et al., 2016; *Thavamanikumar, Dolferus*, and *Thumma*, 2015; *Lopez-Cruz* et al., 2015. As well as various tree species *Almeida Filho* et al., 2019; *Rincent* et al., 2018; *Kainer* et al., 2018; *Ratcliffe* et al., 2017; *El-Dien* et al., 2016; *Kumar* et al., 2015; *Jaramillo-Correa* et al., 2014; *Zapata-Valenzuela* et al., 2013; *Holliday, Wang*, and *Aitken*, 2012; *Resende* et al., 2012.

4.1.4 Genomic selection using artificial neural networks

Genomic selection (GS) has been successfully applied in animal *Gianola* and *Rosa*, 2015, *Hayes* and *Goddard*, 2010 and plant breeding *Crossa* et al., 2010, *Desta* and *Ortiz*, 2014, *Heffner* et al., 2010, *Crossa* et al., 2017a as well as in medical applications, since it was first reported *Hayes* and *Goddard*, 2001. Since then the repertoire of methods for predicting phenotypic values has increased rapidly e.g.*De Los Campos* et al., 2009, *Habier* et al., 2011, *Gianola*, 2013 , *Crossa* et al., 2017b. The most commonly applied methods include GULP and a set of related algorithms known as the bayesian alphabet *Gianola* et al., 2009. Genomic prediction in general has repeatedly been shown to outperform pedigree-based methods *Crossa* et al., 2010, *Albrecht* et al., 2011 and is nowadays used in many plant and animal breeding schemes. It has also been shown that using whole-genome information is superior to using only feature-selected markers with known QTLs for a given trait *Bernardo* and *Yu*, 2007, *Heffner*,

Jannink, and *Sorrells*, 2011 in some cases. A more recent study *Azodi* et al., 2019 compared 11 different genomic prediction algorithms with a variety of data sets and found contradicting results, indicating that feature selection can be usefull in some cases the when the whole genome regression is performed by neural nets 1 While every new method is a valuable addition to the tool-kits for genomic selection, some fundamental problems remain unsolved, of which the n»p problematic stands out. Usually in genomic selection settings the size of the training population (TRN) with n phenotypes is substantially smaller than the number of markers (p) *Fan*, *Han*, and *Liu*, 2014. Making the number of features immensely large, even when SNP-SNP interactions are not considered. Furthermore each marker is treated as an independent observation neglecting collinearity and linkage disequilibrium (LD). Further difficulties arise through non-additive, epistatic and dominance marker effects. The main problem with epistasis issue quantitative genetics is the almost infinite amount of different marker combinations, that cannot be represented within the size of TRN in the thousands, the same problems arises for example in GWA studies *Korte* and *Farlow*, 2013. With already large p the number of possible additive SNP-SNP interactions potentiates to $p^{(p-1)}$. Methods that attempt to overcome those issues are EG-BLUP, using an enhanced epistatic kinship matrix and reproducing kernel Hilbert space regression (RKHS) *Jiang* and *Reif*, 2015, *Martini* et al., 2017.

In the past 10 years, due to increasing availability of high performance computational hardware with decreasing costs and parallel development of free easy-to-use software, most prominent being googles library TensorFlow *Abadi* et al., 2016 and Keras *Chollet*, 2015, machine learning (ML) has experienced a renaissance. ML is a set of methods and algorithms used widely for regression and classification problems. popular among those are e.g. support vector machines, multi-layer perceptrons (MLP) and convolutional neural networks. The machine learning mimics the architecture of neural networks and are therefore commonly referred to as artificial neural networks (ANN). Those algorithms have widely been applied in many biological fields *Min*, *Lee*, and *Yoon*, 2017 , *Lan* et al., 2018, *Mamoshina* et al., 2016,

Angermueller et al., 2016 , *Webb*, 2018, *Rampasek* and *Goldenberg*, 2016.

A variety of studies assessed the usability of ML in genomic prediction *González-Camacho* et al., 2018, *González-Camacho* et al., 2016, *Ogutu*, *Piepho*, and *Schulz-Streeck*, 2011, *Montesinos-López* et al., 2019a, *Grinberg*, *Orhobor*, and *King*, 2018 , *Cuevas* et al., 2019b, *Montesinos-López* et al., 2019b, *Ma* et al., 2017, *Qiu* et al., 2016, *González-Camacho* et al., 2012 *Li* et al., 2018. Through all those studies the common denominator is that there is no such thing as a gold standard for genomic prediction. No single algorithm was able to outperform all the others tested in a single of those studies, let alone in all. While the generally aptitude of ML for genomic selection has been repeatedly shown, how no evidence exists that neural networks can outperform or in many cases perform on that same level as mixed-model approaches as GBLUP *Hayes* and *Goddard*, 2001. While in other fields like image classification neural networks have up to 100s of hidden layers *He* et al., 2016 the commonly used fully-connected networks in genomic prediction of 1 - 3 hidden layers. With 1 layer networks often being the most successful among those. Contradicting to the idea behind machine learning in genomic selection 1 hidden layer networks will be inapt to capture interactions between loci and thus only account for additive effects. As shown in *Azodi* et al., 2019 convolutional networks perform worse than fully-connected networks in genomic selection, which again is contradicting to other fields where convolutional layers are applied successfully, e.g natural language processing *Dos Santos* and *Gatti*, 2014 or medical image analysis *Litjens* et al., 2017. Instead of using convolutional layers and fully-connected layers only, as show in Pook et al 2019, we also propose to use locally-connected layer in combination with fully-connected layers. While CL and LCL are closely related they have a significant difference. While in CL weights are shared between neurons in LCLs each neuron as its own weight. This leads to a reduced number of parameters to be trained in the following FCLs, and should therefore theoretically lead to a decrease in overfitting a common problem in machine learning. To evaluate the results of Pook et al. 2019 accomplished with simulated data we used the data sets generated in the scope of the 1001 genome

project of *Arabidopsis thaliana Alonso-Blanco* et al., 2016

4.2 Proof of concept for ANN-based genomic selection

Having established the quantitative architecture of traits in section 4.1.2 an the basics of machine learning and neural nets in section 4.1.1, that knowledge can be used to provide a proof of concept that neural networks are a candidate for GP. Table 4.1 provides also the possible genotypes that can be derived by two bi-allelic markers $G_1 \ldots G_4$ on a fictional haploid organism. In this simulation the effect sizes for each marker β_1 and β_2 are constant with a value of 1.

TABLE 4.1: Simple simulated phenotypes and genotypes for genomic prediction with genotypes $G_1 \ldots G_4$, M_1 and M_2 and phenotypes based on additive effects or *and*, *or*, *xor* logic gates.

	M_1	M_2	Y_{ADD}	Y_{AND}	Y_{OR}	Y_{XOR}
G_1	0	0	0	0	0	0
G_2	0	1	1	0	1	1
G_3	1	0	1	0	1	1
G_4	1	1	2	1	1	0

The four phenotypes Y_{ADD}, Y_{AND}, Y_{OR} and Y_{XOR} , which were derived from their respective marker effects. Y_{ADD} is a phenotype with purely additive effects. So in the nomenclature introduced in chapter 4.1.2 $\sigma_A = \sigma_G$ and $\sigma_I = 0$. Since the hypothetical organism is haploid there are dominance effects to be accounted for $\sigma_D = 0$. Since all the genetic effects are caused by additive effects and there are now environmental effects σ_E, the narrow sense heritability h^2 - equation 4.24 - and the broad sense heritability H^2 - equation 4.23 - are equally 1. The other three phenotypes are base on epistatic effects σ_I generated by passing the markers M_1 and M_2 through their respective logic gates. This theoretically in results in $h^2 = 0$ and $H^2 = 1$, because there are no additive effects. For y_{AND} however $h \approx 0.5$, because

there is a correlation between Y_{ADD} and Y_{AND}. In practical applications this allows methods like GBLUP, designed to account for additive genetic effects to capture some of the epistatic effects of σ_I *Vieira* et al., 2017.

According to chapter 4.1.1 a single perceptron would fail to solve *xor* gates. While a network with multiple nodes and layers should be able to overcome that deficit. A relatively simple neural network with two fully-connected hidden layers with 10 and 5 nodes, was trained for the prediction of each phenotypes. To keep the simulation as possible, no regularization parameters, dropout etc. was included. The activation function was ReLU (4.6) with an Adam optimizer. The results of the prediction are shown in table 4.2.

TABLE 4.2: Results of genomic prediction from phenotypes and genotypes in table 4.1

	M_1	M_2	$\hat{Y}_{ADD}$	$\hat{Y}_{AND}$	$\hat{Y}_{OR}$	$\hat{Y}_{XOR}$
G_1	0	0	0.01	0.00	0.00	0.01
G_2	0	1	0.99	0.01	0.99	0.98
G_3	1	0	0.99	0.00	0.99	1.01
G_4	1	1	1.99	0.98	1.01	0.02

4.3 Material

4.3.1 DH populations derived from MAZE landraces

4.3.2 A. thaliana

4.4 Methods

4.4.1 ANN

4.4.2 GBLUP

4.5 Results

4.6 Discussion

5 GWAS

5.1 Reevalulation of 463 phenotypes from the AraPheno database

5.1.1 Introduction

5.1.2 Material and Methods

5.1.3 Results

5.1.4 Results

5.1.5 Disucssion

5.2 GWAS in DH landrace populatios of maze across and within environments

5.2.1 Introduction

5.2.2 Material and Methods

5.2.3 Results

5.2.4 Results

5.2.5 Disucssion

A Source code GWAS-Flow

A.1 gwas.py

```
import os
import sys
import time
import numpy as np
import pandas as pd
import main
import h5py

# set defaults
mac_min = 1
batch_size =  500000
out_file = "results.csv"
m = 'phenotype_value'
perm = 1
mac_min= 6

X_file = 'gwas_sample_data/AT_geno.hdf5'
Y_file = 'gwas_sample_data/phenotype.csv'
K_file = 'gwas_sample_data/kinship_ibs_binary_mac5.h5py'



for i in range (1,len(sys.argv),2):
    if sys.argv[i] == "-x" or sys.argv[i] == "--genotype":
        X_file = sys.argv[i+1]
    elif sys.argv[i] == "-y" or sys.argv[i] == "--phenotype":
        Y_file = sys.argv[i+1]
    elif sys.argv[i] == "-k" or sys.argv[i] == "--kinship":
```

```
29          K_file = sys.argv[i+1]
30      elif sys.argv[i] == "-m":
31          m = sys.argv[i+1]
32      elif sys.argv[i] == "-a" or sys.argv[i] == "--mac_min":
33          mac_min = int(sys.argv[i+1])
34      elif sys.argv[i] == "-bs" or sys.argv[i] == "--batch-size":
35          batch_size = int(sys.argv[i+1])
36      elif sys.argv[i] == "-p" or sys.argv[i] == "--perm":
37          perm  = int(sys.argv[i+1])
38      elif sys.argv[i] == "-o" or sys.argv[i] == "--out":
39          out_file = sys.argv[i+1]
40      elif sys.argv[i] == "-h" or sys.argv[i] == "--help":
41          print("-x , --genotype :file containing marker information in
    csv or hdf5 format of size")
42          print("-y , --phenotype: file container phenotype information
    in csv format"  )
43          print("-k , --kinship : file containing kinship matrix of size
     k X k in csv or hdf5 format")
44          print("-m : name of columnn containing the phenotype : default
     m = phenotype_value")
45          print("-a , --mac_min : integer specifying the minimum minor
    allele count necessary for a marker to be included. Default a = 1"
     )
46          print("-bs, --batch-size : integer specifying the number of
    markers processed at once. Default -bs 500000" )
47          print("-p , --perm : single integer specifying the number of
    permutations. Default 1 == no perm ")
48          print("-o , --out : name of output file. Default -o results.
    csv  ")
49          print("-h , --help : prints help and command line options")
50          quit()
51      else:
52          print('unknown option ' + str(sys.argv[i]))
53          quit()
54
55
56
57  print("parsed commandline args")
```

```
58
59 start = time.time()
60
61 X,K,Y_,markers = main.load_and_prepare_data(X_file,Y_file,K_file,m)
62
63
64 ## MAF filterin
65 markers_used , X , macs = main.mac_filter(mac_min,X,markers)
66
67 ## prepare
68 print("Begin performing GWAS on ", Y_file)
69
70 if perm == 1:
71     output = main.gwas(X,K,Y_,batch_size)
72     if( X_file.split(".")[-1] == 'csv'):
73         chr_pos = np.array(list(map(lambda x : x.split("- "),
    markers_used)))
74     else:
75         chr_reg = h5py.File(X_file,'r')['positions'].attrs['
    chr_regions']
76         mk_index= np.array(range(len(markers)),dtype=int)[macs >=
    mac_min]
77         chr_pos = np.array([list(map(lambda x: sum(x > chr_reg[:,1]) +
     1, mk_index)), markers_used]).T
78         my_time = np.repeat((time.time()-start),len(chr_pos))
79     pd.DataFrame({
80         'chr' : chr_pos[:,0] ,
81         'pos' : chr_pos[:,1] ,
82         'pval': output[:,0] ,
83         'mac' : np.array(macs[macs >= mac_min],dtype=np.int) ,
84         'eff_size': output[:,1] ,
85         'SE' : output[:,2]}).to_csv(out_file,index=False)
86 elif perm > 1:
87     min_pval = []
88     perm_seeds = []
89     my_time = []
90     for i in range(perm):
91         start_perm = time.time()
```

```
92          print("Running permutation ", i+1, " of ",perm)
93          my_seed  = np.asscalar(np.random.randint(9999,size=1))
94          perm_seeds.append(my_seed)
95          np.random.seed(my_seed)
96          Y_perm = np.random.permutation(Y_)
97          output = main.gwas(X,K,Y_perm,batch_size)
98          min_pval.append(np.min(output[:,0]))
99          print("Elapsed time for permuatation",i+1 ," with p_min",
    min_pval[i]," is",": ", round(time.time() - start_perm,2))
100         my_time.append(time.time()-start_perm)
101      pd.DataFrame({
102         'time': my_time ,
103         'seed': perm_seeds ,
104         'min_p': min_pval }).to_csv(out_file,index=False)
105
106 print("done")
107
108 end = time.time()
109 eltime = np.round(end -start,2)
110
111 if eltime <= 59:
112     print("Total time elapsed",  eltime, "seconds")
113 elif eltime > 59 and eltime <= 3600:
114     print("Total time elapsed",  np.round(eltime / 60,2) , "minutes")
115 elif eltime > 3600 :
116     print("Total time elapsed",  np.round(eltime / 60 / 60,2), "hours"
    )
117
118
```

A.2 main.py

```
1     import pandas as pd
2     import numpy as np
3     from scipy.stats import f
4     import tensorflow as tf
5     import limix
6     import herit
```

```
    import h5py
    import limix
    import multiprocessing as mlt

    def load_and_prepare_data(X_file,Y_file,K_file,m):
    type_K = K_file.split(".")[-1]
    type_X = X_file.split(".")[-1]

    ## load and preprocess genotype matrix
    Y = pd.read_csv(Y_file,engine='python').sort_values(['accession_id
'']).groupby('accession_id').mean()
    Y = pd.DataFrame({'accession_id' :  Y.index, 'phenotype_value' : Y
[m]})
    if type_X == 'hdf5' or type_X == 'h5py'  :
        SNP = h5py.File(X_file,'r')
        markers= np.asarray(SNP['positions'])
        acc_X =  np.asarray(SNP['accessions'][:],dtype=np.int)
    elif type_X == 'csv' :
        X = pd.read_csv(X_file,index_col=0)
        markers = X.columns.values
        acc_X = X.index
        X = np.asarray(X,dtype=np.float32)/2
    else :
        sys.exit("Only hdf5, h5py and csv files are supported")

    if type_K == 'hdf5' or type_K == 'h5py':
        k = h5py.File(K_file,'r')
        acc_K = np.asarray(k['accessions'][:],dtype=np.int)
    elif type_K == 'csv':
        k = pd.read_csv(K_file,index_col=0)
        acc_K = k.index
        k = np.array(k, dtype=np.float32)

    acc_Y =  np.asarray(Y[['accession_id']]).flatten()
    acc_isec = [isec for isec in acc_X if isec in acc_Y]

    idx_acc = list(map(lambda x: x in acc_isec, acc_X))
    idy_acc = list(map(lambda x: x in acc_isec, acc_Y))
```

```
43      idk_acc = list(map(lambda x: x in acc_isec, acc_K))
44
45      Y_ = np.asarray(Y.drop('accession_id',1),dtype=np.float32)[idy_acc
        ,:]
46
47      if type_X == 'hdf5' or type_X == 'h5py' :
48          X = np.asarray(SNP['snps'][0:(len(SNP['snps'])+1),],dtype=np.
        float32)[:,idx_acc].T
49          X = X[np.argsort(acc_X[idx_acc]),:]
50          k1 = np.asarray(k['kinship'][:])[idk_acc,:]
51          K  = k1[:,idk_acc]
52          K = K[np.argsort(acc_X[idx_acc]),:]
53          K = K[:,np.argsort(acc_X[idx_acc])]
54      else:
55          X  = X[idx_acc,:]
56          k1 = k[idk_acc,:]
57          K  = k1[:,idk_acc]
58
59
60      print("data has been imported")
61      return X,K,Y_,markers
62
63
64  def mac_filter(mac_min, X, markers):
65      ac1 = np.sum(X,axis=0)
66      ac0 = X.shape[0] - ac1
67      macs = np.minimum(ac1,ac0)
68      markers_used  = markers[macs >= mac_min]
69      X = X[:,macs >= mac_min]
70      return markers_used, X, macs
71
72  def gwas(X,K,Y,batch_size):
73      n_marker = X.shape[1]
74      n = len(Y)
75      ## REML
76      K_stand = (n-1)/np.sum((np.identity(n) - np.ones((n,n))/n) * K) *
        K
```

```
77      vg, delta, ve  = herit.estimate(Y,"normal",K_stand,verbose = False
    )
78      print(" Pseudo-heritability is " , vg / (ve + vg + delta))
79      print(" Performing GWAS on ", n , " phenotypes and ", n_marker ,"
    markers")
80      ## Transform kinship-matrix, phenotypes and estimate intercpt
81      Xo = np.ones(K.shape[0]).flatten()
82      M = np.transpose(np.linalg.inv(np.linalg.cholesky(vg * K_stand +
    ve  * np.identity(n)))).astype(np.float32)
83      Y_t = np.sum(np.multiply(np.transpose(M),Y),axis=1).astype(np.
    float32)
84      int_t = np.sum(np.multiply(np.transpose(M),np.ones(n)),axis=1).
    astype(np.float32)
85      ## EMMAX Scan
86      RSS_env = (np.linalg.lstsq(np.reshape(int_t,(n,-1)) , np.reshape(
    Y_t,(n,-1)))[1]).astype(np.float32)
87      ## calculate betas and se of betas
88      def stderr(a,M,Y_t2d,int_t):
89            x = tf.stack((int_t,tf.squeeze(tf.matmul(M.T,tf.reshape(a,(n
    ,-1))))),axis=1)
90            coeff = tf.matmul(tf.matmul(tf.linalg.inv(tf.matmul(tf.
    transpose(x),x)),tf.transpose(x)),Y_t2d)
91            SSE = tf.reduce_sum(tf.math.square(tf.math.subtract(Y_t,tf.
    math.add(tf.math.multiply(x[:,1],coeff[0,0]),tf.math.multiply(x
    [:,1],coeff[1,0])))))
92            SE = tf.math.sqrt(SSE/(471-(1+2)))
93            StdERR = tf.sqrt(tf.linalg.diag_part(tf.math.multiply(SE , tf
    .linalg.inv(tf.matmul(tf.transpose(x),x))))[1]
94            return tf.stack((coeff[1,0],StdERR))
95      ## calculate residual sum squares
96      def rss(a,M,y,int_t):
97            x_t = tf.reduce_sum(tf.math.multiply(M.T,a),axis=1)
98            lm_res = tf.linalg.lstsq(tf.transpose(tf.stack((int_t,x_t),
    axis=0)),Y_t2d)
99            lm_x = tf.concat((tf.squeeze(lm_res),x_t),axis=0)
100           return tf.reduce_sum(tf.math.square(tf.math.subtract(tf.
    squeeze(Y_t2d),tf.math.add(tf.math.multiply(lm_x[1],lm_x[2:]), tf.
    multiply(lm_x[0],int_t)))))
```

```
    ## loop over the batches
    for i in range(int(np.ceil(n_marker/batch_size))):
        tf.reset_default_graph()
        if n_marker < batch_size:
            X_sub = X
        else:
            lower_limit = batch_size * i
            upper_limit = batch_size * i + batch_size
            if upper_limit <= n_marker :
                X_sub = X[:,lower_limit:upper_limit]
                print("Working on markers ", lower_limit , " to ",
upper_limit, " of ", n_marker )
            else:
                X_sub = X[:,lower_limit:]
                print("Working on markers ", lower_limit , " to ",
n_marker, " of ", n_marker )
        config = tf.ConfigProto()
        n_cores = mlt.cpu_count()
        config.intra_op_parallelism_threads = n_cores
        config.inter_op_parallelism_threads = n_cores
        sess = tf.Session(config=config)
        Y_t2d = tf.cast(tf.reshape(Y_t,(n,-1)),dtype=tf.float32)
        y_tensor =  tf.convert_to_tensor(Y_t,dtype = tf.float32)
        StdERR = tf.map_fn(lambda a : stderr(a,M,Y_t2d,int_t), X_sub.T
)
        R1_full = tf.map_fn(lambda a: rss(a,M,Y_t2d,int_t), X_sub.T)
        F_1 = tf.divide(tf.subtract(RSS_env, R1_full),tf.divide(
R1_full,(n-3)))
        if i == 0 :
            output = sess.run(tf.concat([tf.reshape(F_1,(X_sub.shape
[1],-1)),StdERR],axis=1))
        else :
            tmp = sess.run(tf.concat([tf.reshape(F_1,(X_sub.shape
[1],-1)),StdERR],axis=1))
            output = np.append(output,tmp,axis=0)
        sess.close()
        F_dist = output[:,0]
    pval  = 1 - f.cdf(F_dist,1,n-3)
```

```
133     output[:,0] = pval
134     return output
135
136
137
```

A.3 herit.py

```
1
2 def estimate(y, lik, K, M=None, verbose=True):
3     from numpy_sugar.linalg import economic_qs
4     from numpy import pi, var, diag
5     from glimix_core.glmm import GLMMExpFam
6     from glimix_core.lmm import LMM
7     from limix._data._assert import assert_likelihood
8     from limix._data import normalize_likelihood, conform_dataset
9     from limix.qtl._assert import assert_finite
10    from limix._display import session_block, session_line
11    lik = normalize_likelihood(lik)
12    lik_name = lik[0]
13    with session_block("Heritability analysis", disable=not verbose):
14        with session_line("Normalising input...", disable=not verbose)
      :
15            data = conform_dataset(y, M=M, K=K)
16        y = data["y"]
17        M = data["M"]
18        K = data["K"]
19        assert_finite(y, M, K)
20        if K is not None:
21           # K = K / diag(K).mean()
22            QS = economic_qs(K)
23        else:
24            QS = None
25        if lik_name == "normal":
26            method = LMM(y.values, M.values, QS, restricted=True)
27            method.fit(verbose=verbose)
28        else:
29            method = GLMMExpFam(y, lik, M.values, QS, n_int=500)
```

```
30              method.fit(verbose=verbose, factr=1e6, pgtol=1e-3)
31          g = method.scale * (1 - method.delta)
32          e = method.scale * method.delta
33          if lik_name == "bernoulli":
34              e += pi * pi / 3
35          v = var(method.mean())
36          return g , v , e
```

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