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Deep learning – an alternative for genomic prediction?

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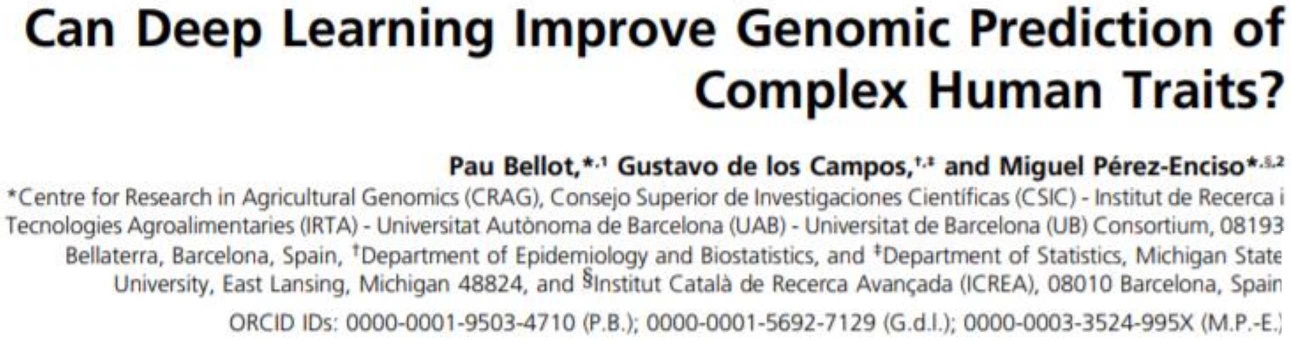
Lots of people starting to use them!



Can Deep Learning Improve Genomic Prediction of Complex Human Traits?

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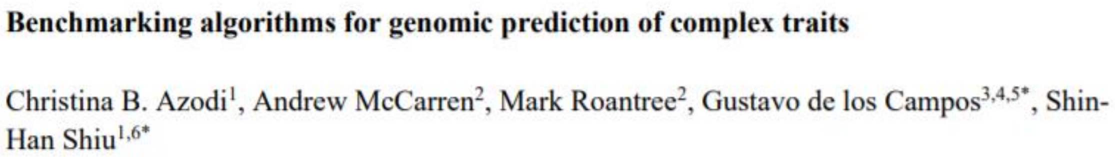
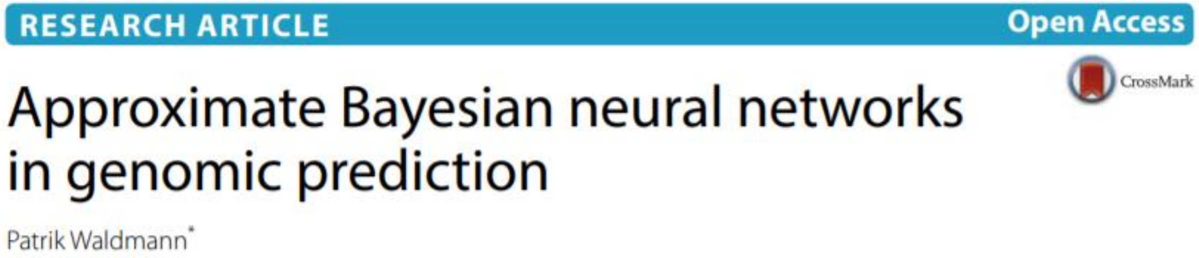


Benchmarking algorithms for genomic prediction of complex traits

Christina B. Azodi[1], Andrew McCarren[2], Mark Roantree[2], Gustavo de los Campos[3,4,5*], Shin-Han Shiu[1,6*]



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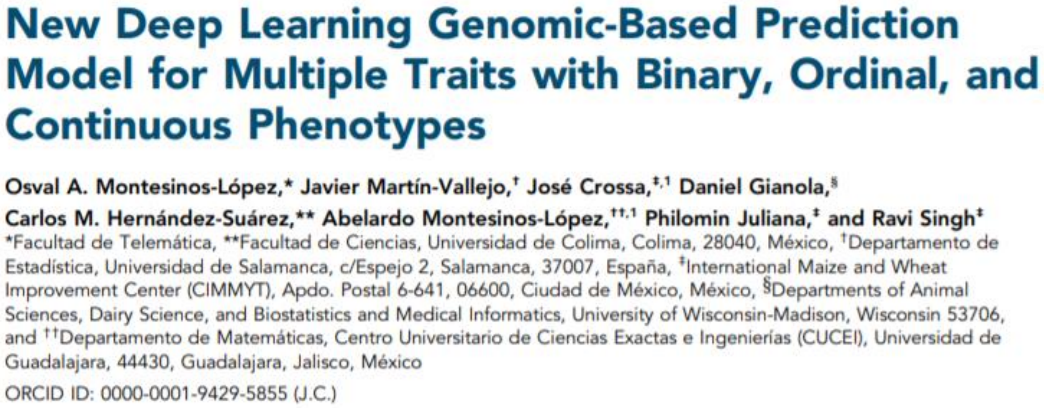
Approximate Bayesian neural networks in genomic prediction

Patrik Waldmann[*]



New Deep Learning Genomic-Based Prediction Model for Multiple Traits with Binary, Ordinal, and Continuous Phenotypes

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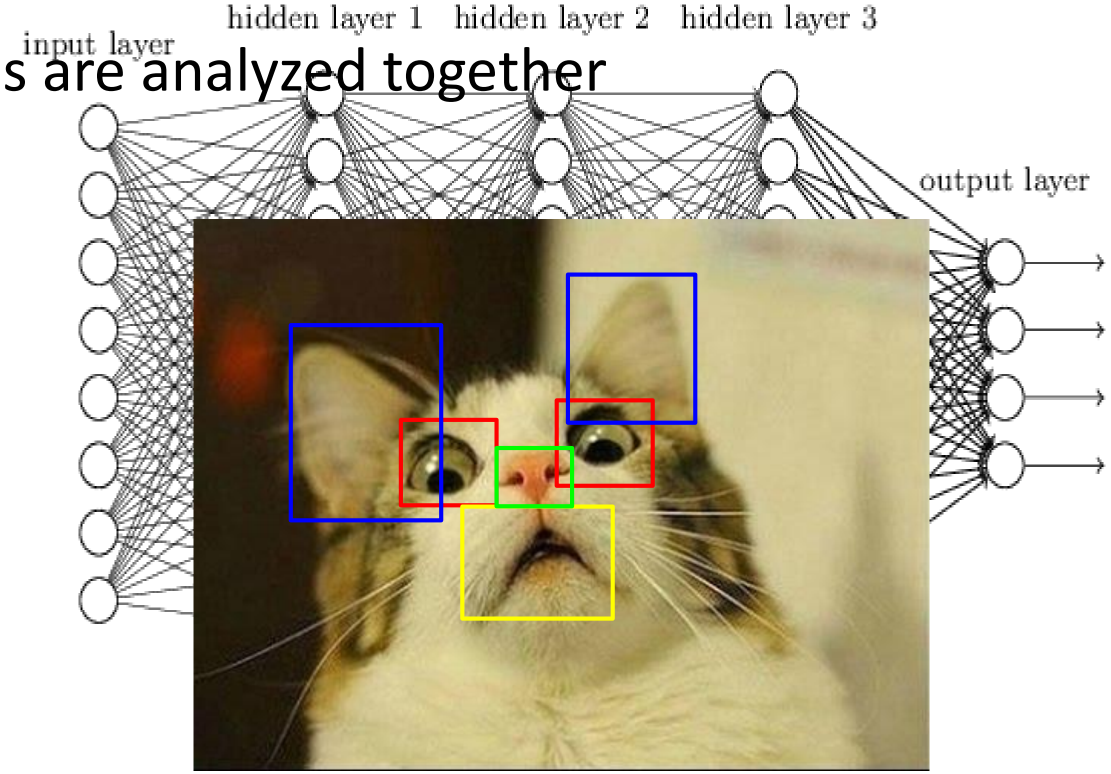
- Convolutional neural networks (CNN) do not work in this context!
- Other fields: CNN are the biggest reason for the rise of neural networks!

Neural networks are no black-box

- Fully-connected-layer
  - Nodes are connected to all nodes of the previous layer
- Convolutional-layer
  - Adjacent nodes are analyzed together

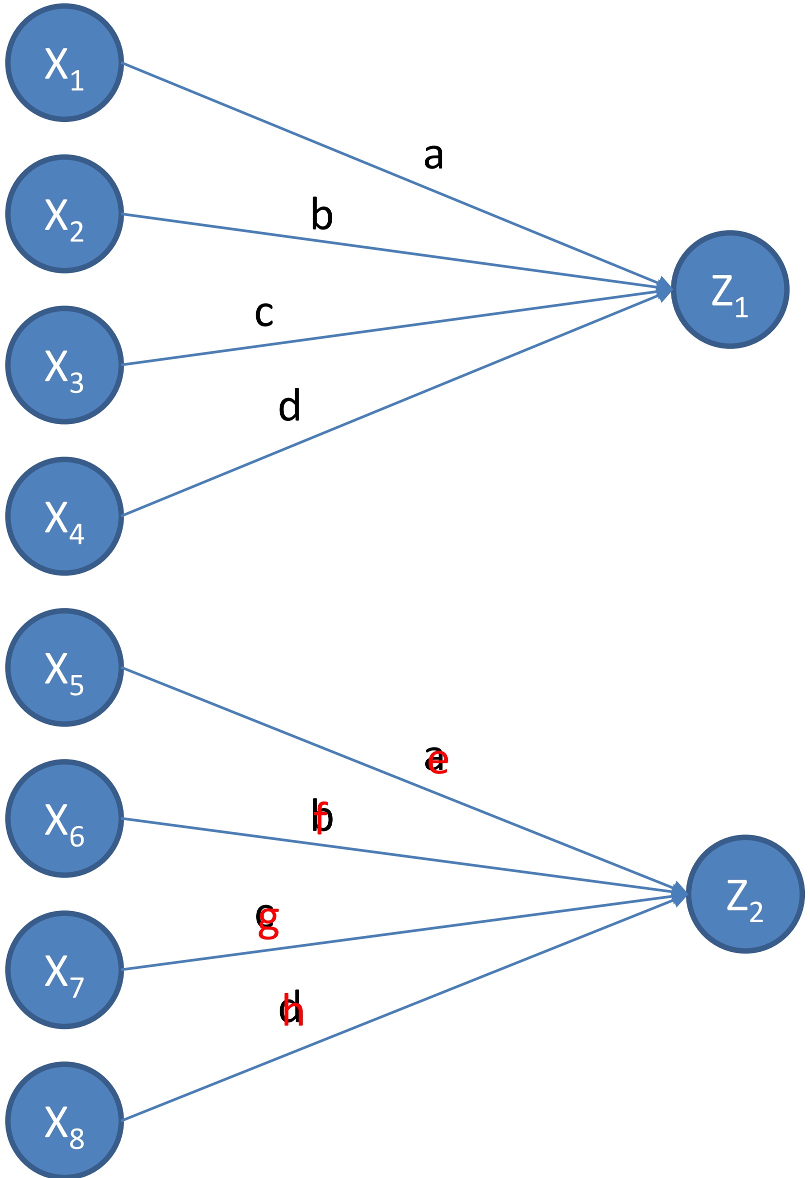


Problem with CNN

- Effects are assigned to specific sequences
  - e.g. for SNP-datasets 2201220
- BUT
  - Same sequences in different regions have different effects
  - Sequence is coding dependent (ancestral allele? / frequency based?)
  - What is between markers?

Our solution: Local convolutional layer

- Instead of using the same filter everywhere use local weightings
- For 50‘000 SNPs and 32 Nodes of a fully-connected-layer (FCL)
  - No CNN:
    - 1‘600‘000 parameters in the FCL
  - CNN (10 SNPs):
    - 10 parameters in the CNN
    - 160‘000 parameters in the FCL
  - Local CNN (10 SNPs):
    - 50‘000 parameters in the CNN
    - 160‘000 parameters in the FCL

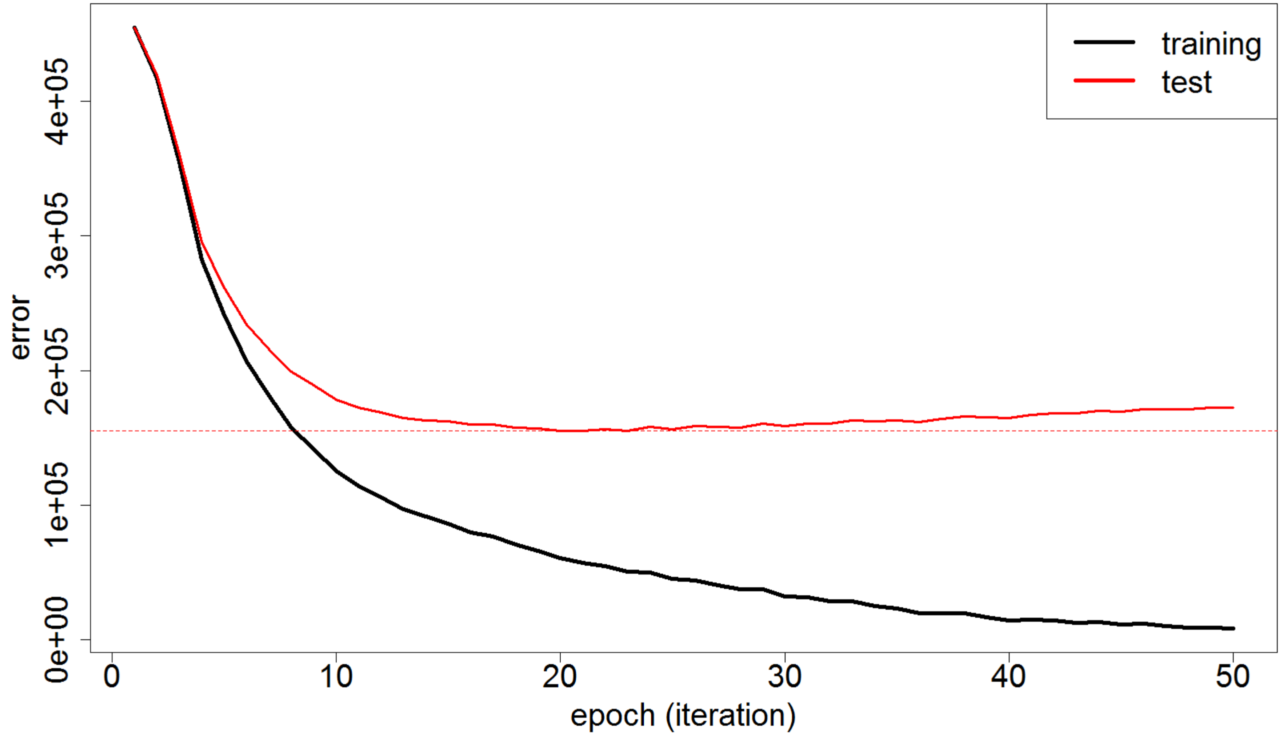


Data

- 10’501 bulls genotyped using a 50k chip
- Deregressed breeding values:
  - Milk yield (h^2 = 0.49)
  - Fat-kg (h^2 = 0.48)
  - Protein-kg (h^2 = 0.48)
  - Somatic cell score (h^2 = 0.23)
  - Non-Return-Rate (h^2 = 0.015)

Our model

- Local convolutional layer (15 SNPs, stride length = 10)
- Fully connect
- Fully connect



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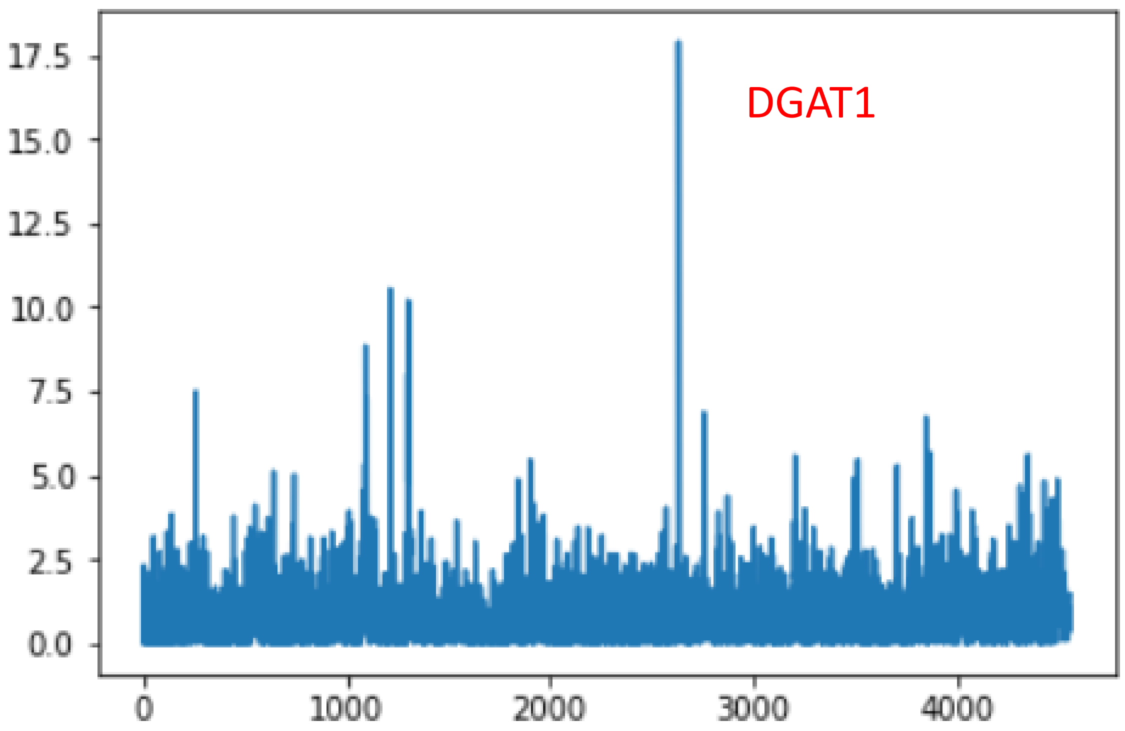
501)

- Use validatior n
  - How man
  - How many layers / nodes should be used
  - Target/optimization-function

Comparison to GBLUP

	GBLUP	Deep Learning	Change
Milk yield	0.830	0.834	+ 0.4 %
Fat-kg	0.809		
Protein-kg	0.822		
Somatic cell score	0.770		
Non-Return-Rate	0.658		



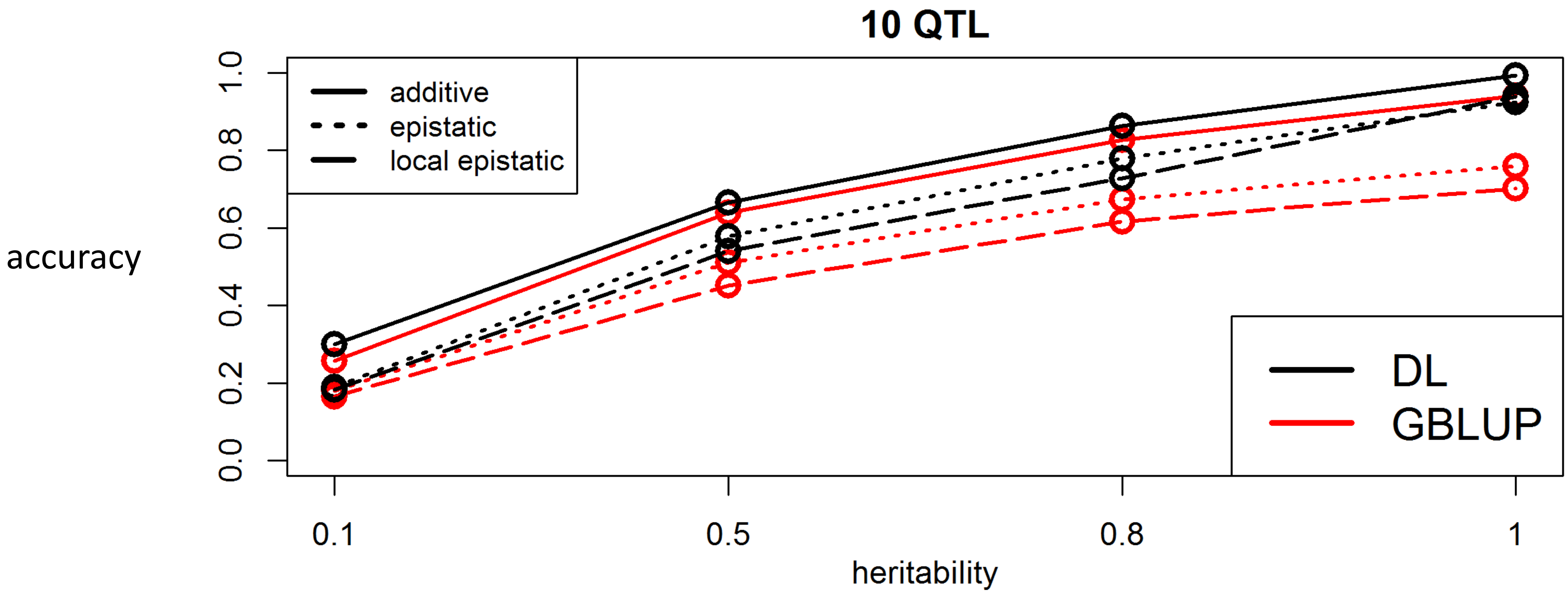
- Correlation of estimated breeding values a the test set
- DL is much worse for smaller training sets

Simulation study

- On what type of effect structures does Deep Learning work?
- Simulation of 10’000 animals
- 17 Traits of different complexity
  - 10 additive single marker QTL
  - 1’000 gamma distributed QTL caused by multiple physically linked QTL

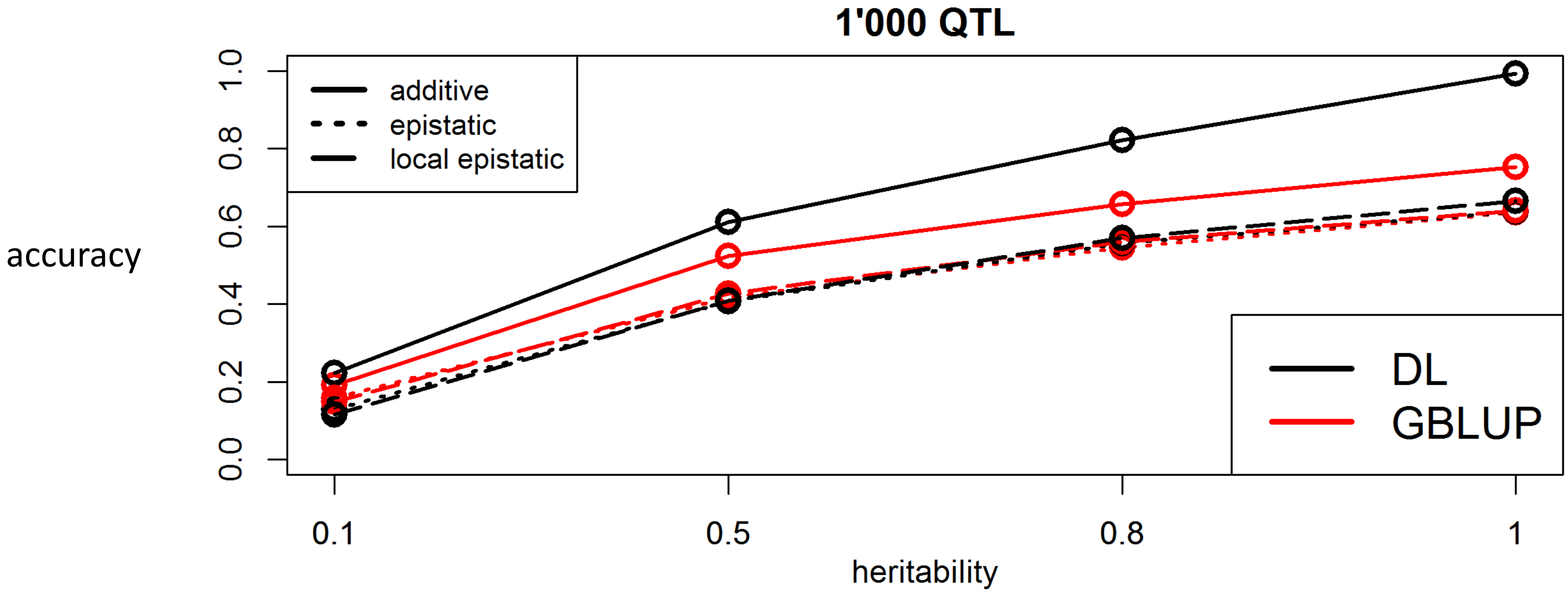
Low number of QTL

- Best performance for high heritability



High number of QTL

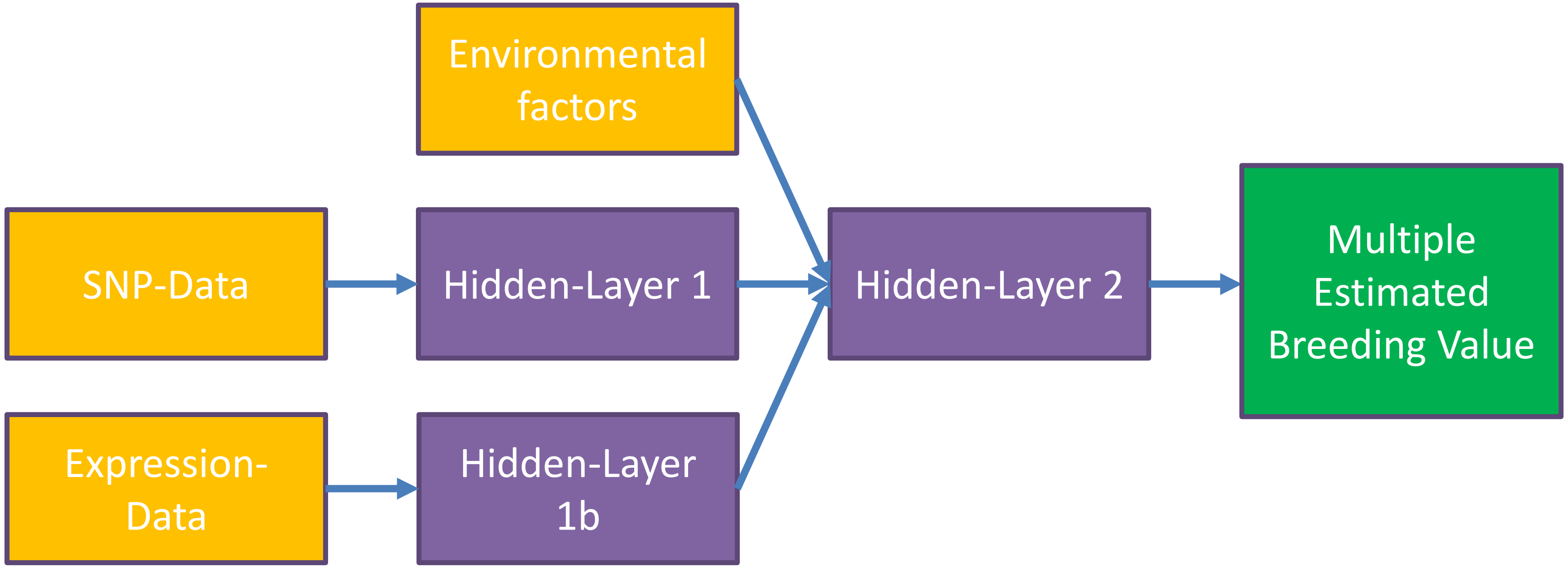
- Training set to small for highly complex traits?
- CNN do not excel in the local epistatic case



Further potential in genomic prediction

- Breeding values are additive by design!
- Genotypes of all individuals are needed!

- Phenotype prediction
- Expression data so far of limited usefulness
- High flexibility of input and output structure
- Linear scaling in computing time!



Acknowledgments

- MAZE: “Accessing the genomic and functional diversity of maize to improve quantitative traits”, BMBF Grant ID 031B0195
- FBF e.V. & vit

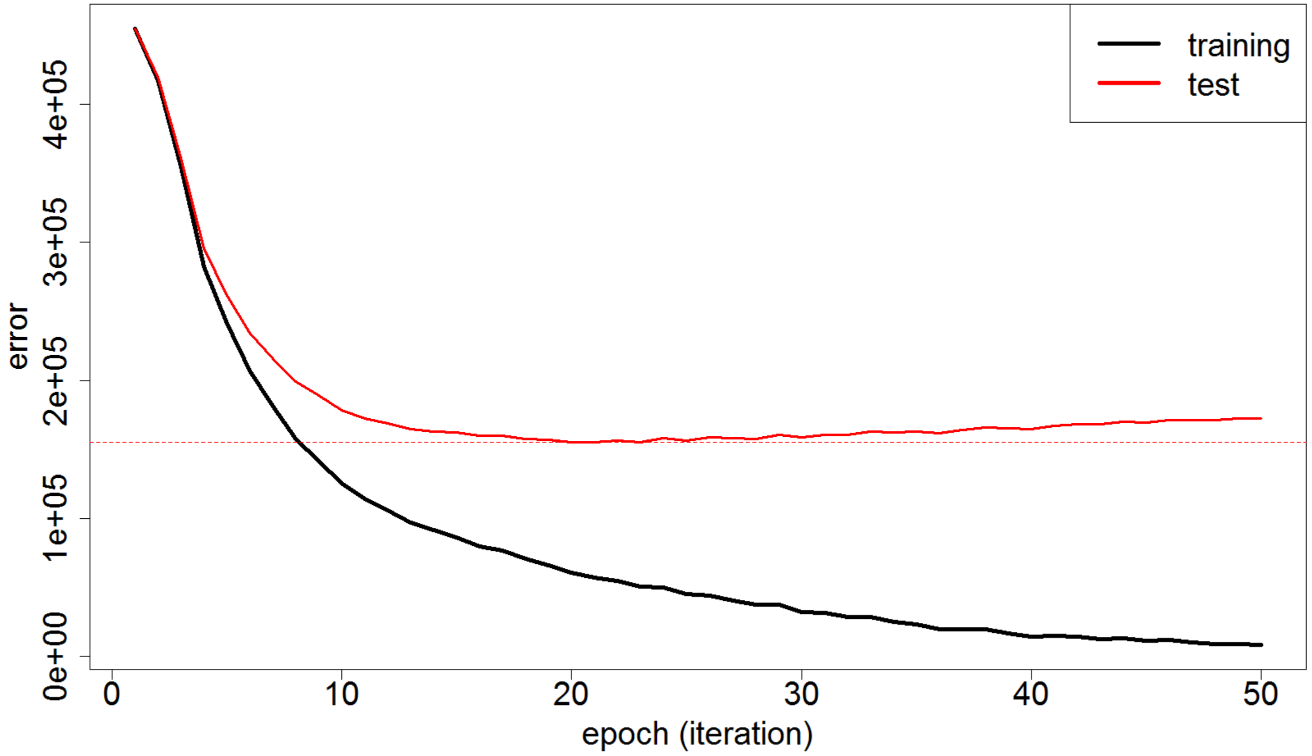
FBF Förderverein Bioökonomieforschung e.V.

vit Service & Daten aus einer Quelle

European Maize

Bundesministerium für Bildung und Forschung

Results



- Our current model contains 240.000 parameters
- Tendency of overfitting
- How to reduce overfitting or figure out when to stop

How to

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2. Use ar lo some minor
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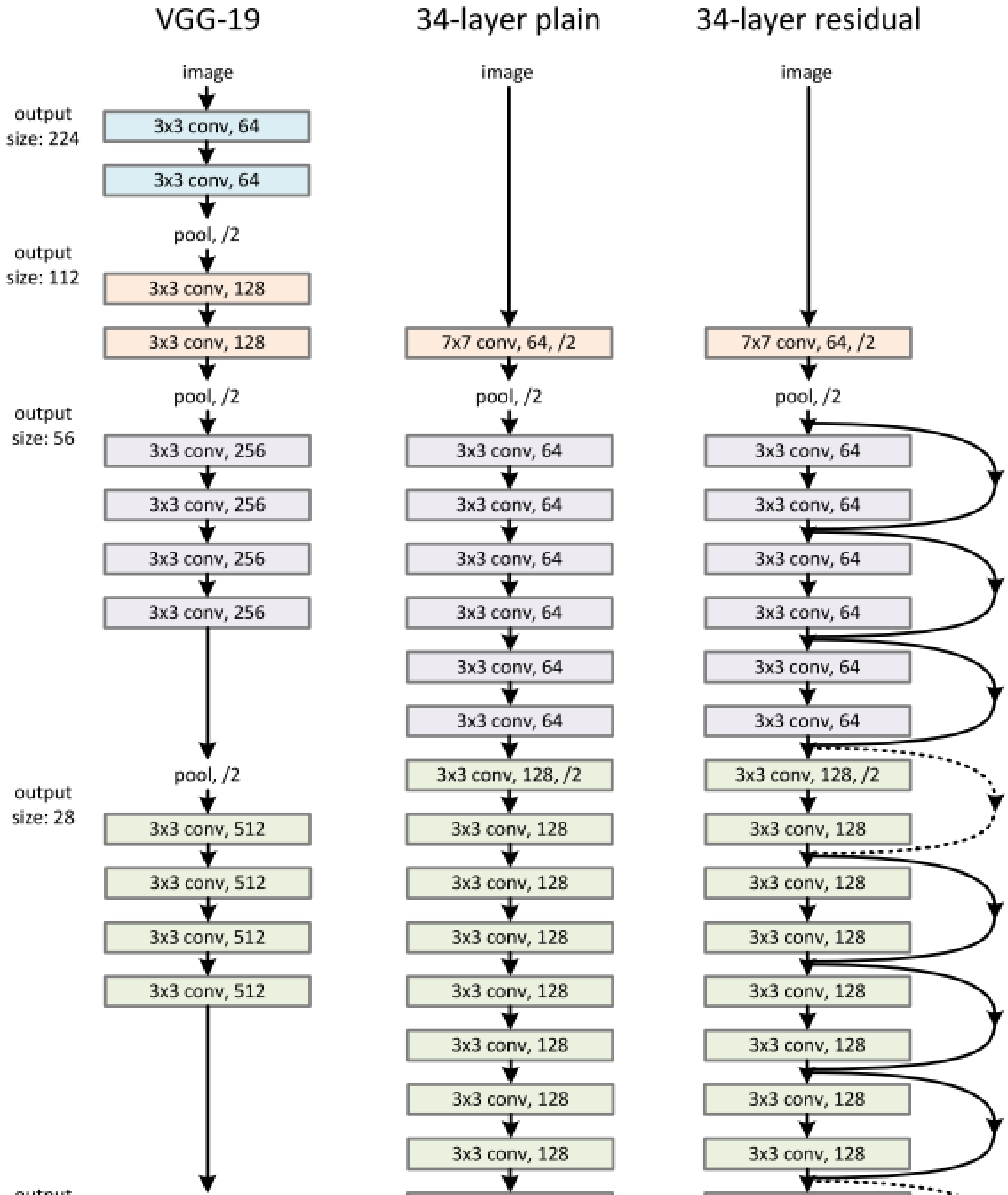

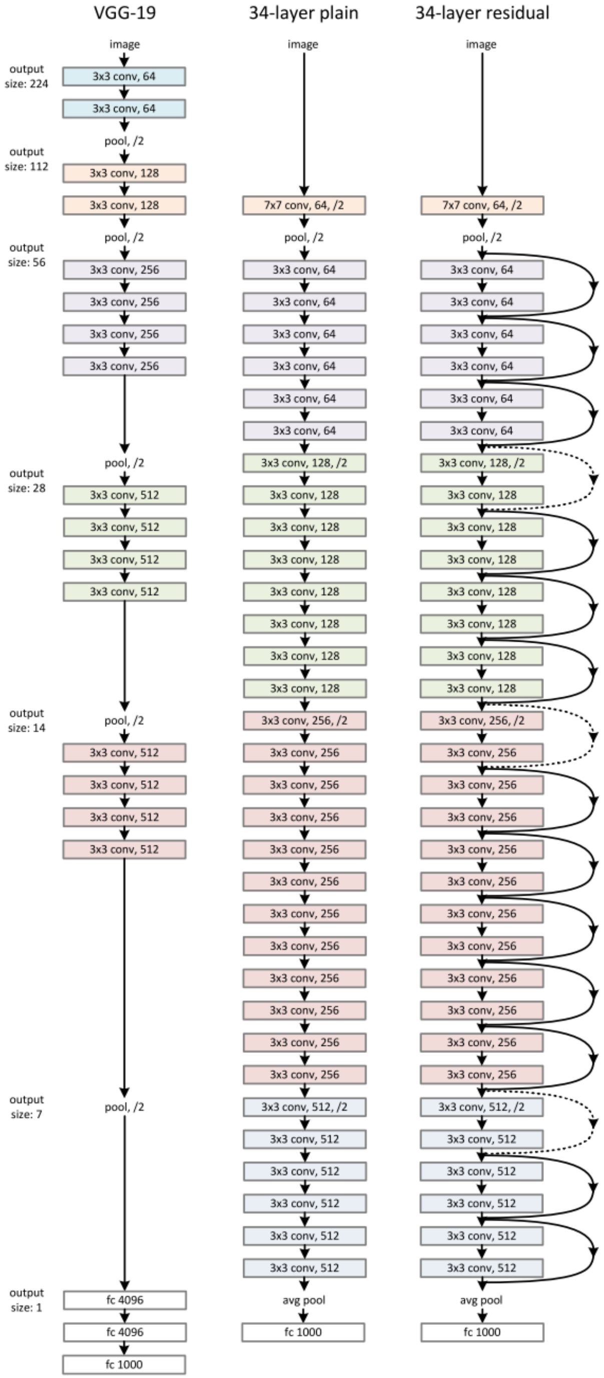
VGG-19
34-layer plain
34-layer residual
output size: 224
output size: 112
output size: 56
output size: 28
output size: 14
output size: 7
output size: 1
image
3x3 conv, 64
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3x3 conv, 128
3x3 conv, 128
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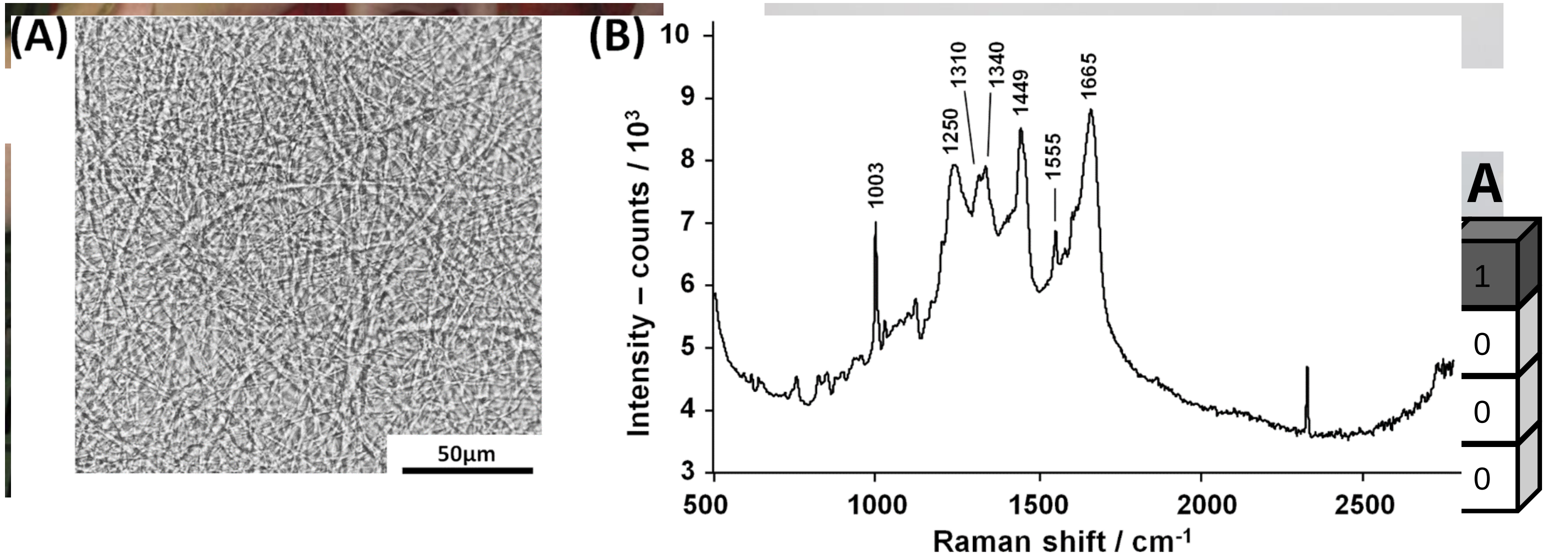
3x3 conv, 512
avg pool
fc 1000

Application in genetics in general

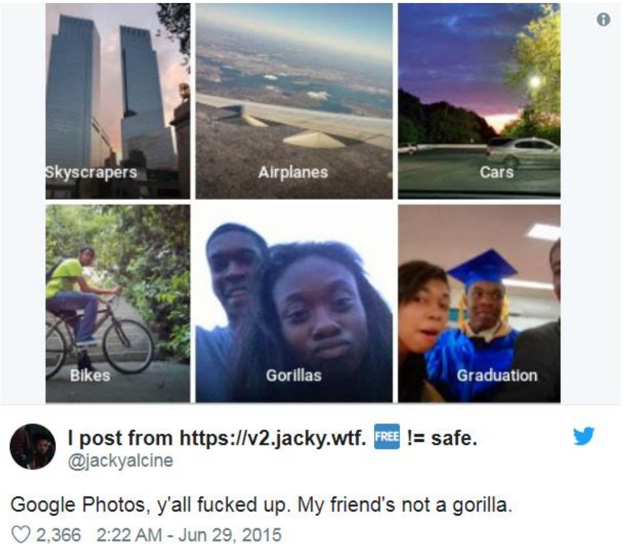
- Complex input and/or effect structure
- Spectral data (sexing of chicken, Galli et al. 2018)
- Phenotyping (Image and video analysis)
- Basically everything when working on sequence data
- Prediction of expression level (Washburn et al. 2019)



Expression levels?

Problem for genomic prediction

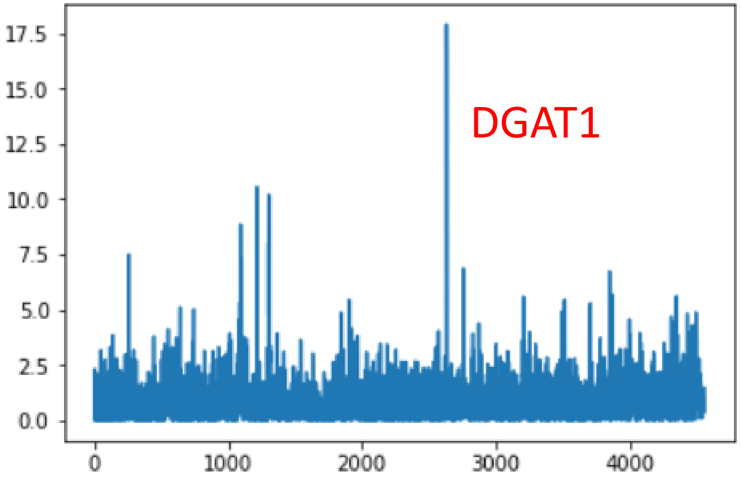
- No major gains when just using a SNP-dataset
- Old pipelines are already established
  - Model structure is far less understood // Black-Box
  - No reliabilities etc.
  - Goodness of fit outside of the training set
- Breeding for non-additive-effects in a random mating setting is not maximizing genetic gain



I post from https://v2.jacky.wtf. FREE != safe.
@jackyalcine

Google Photos, y'all fucked up. My friend's not a gorilla.

♡ 2,366 2:22 AM - Jun 29, 2015



Increasing the sample size

- Models are extremely data hungry:
- Generate additional data based on the already existing
- “Simple” way here:
  - Use same phenotype and some random mutations
  - Simulate a mating, use mean as phenotype
- Data augmentation
- Generative adversarial network:
  - Generate new data
  - Let the network determine which observation are simulated/real
  - Generate new data that would not be classified as fake in the previous model