Combining environmental and genomic information in artificial neural networks for phenotypic prediction

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Artificial neural networks (ANNs)

- Promising for phenotypic and genomic predictions
- Ability to
  - learn non-linear relationships
  - handle high-dimensional data

- However
  - Inconsistent predictive performances with genomic data
  - Usually trained on pre-corrected phenotypes

Aim

To evaluate the feasibility and predictive ability of ANNs

using both environmental and genomic information

for phenotypic prediction

➔ To eliminate the need for pre-correction, and leveraging non-linear relationships among effects

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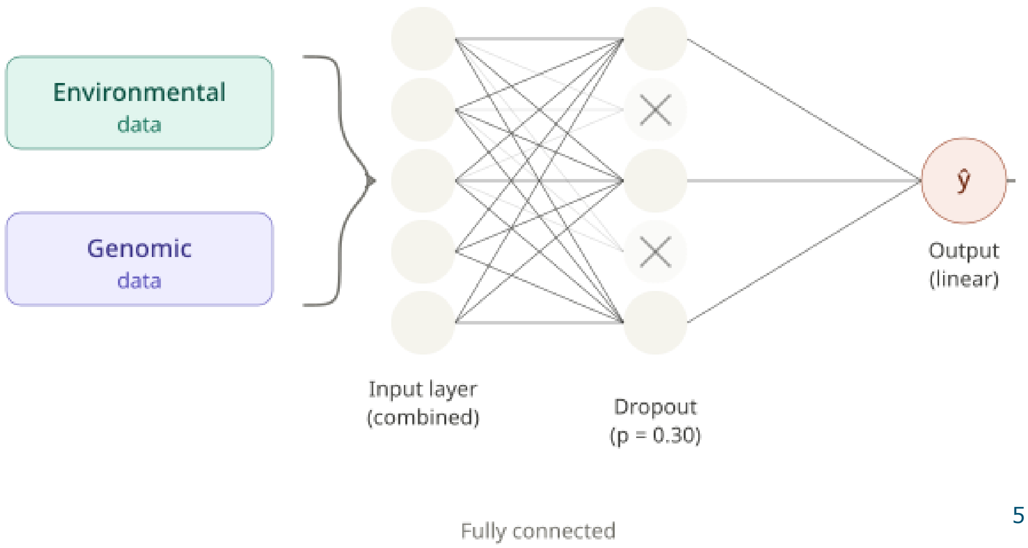
Tools

- MiXBLUP
  - Program for solving large-scale mixed model equations
- mixnn
  - Fortran program that trains a set of ANNs
    - Based on the library neural-fortran https://github.com/modern-fortran/neural-fortran
  - Input
    - Sparse incidence matrices (“fixed” effects)
    - SNP genotype matrices
  - Output: phenotypes

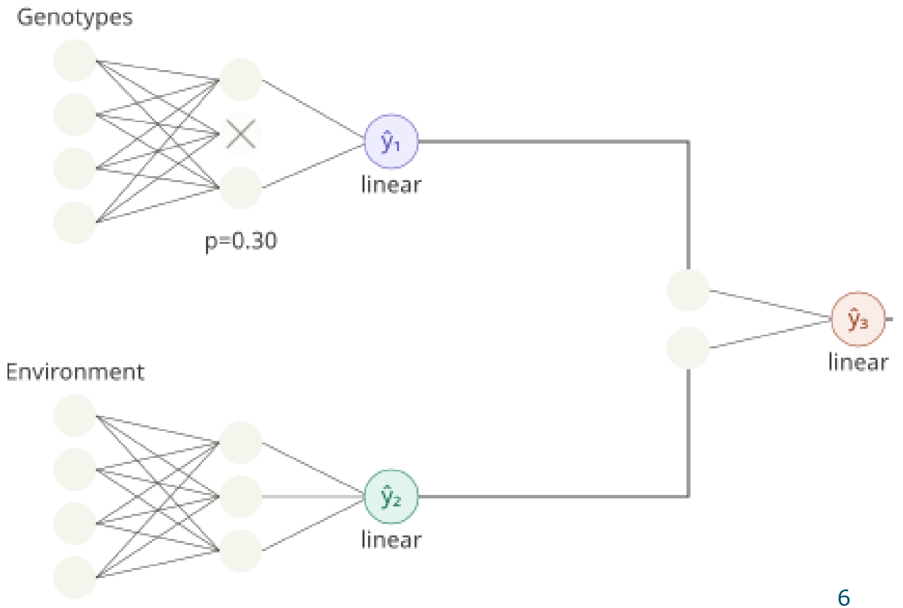
Models – ANN 1

- ANN
  - 1 input layer combining environmental and genomic data
  - Fully connected (output=1, linear)
  - Dropout (0.30)
  - Optimizer: Adam



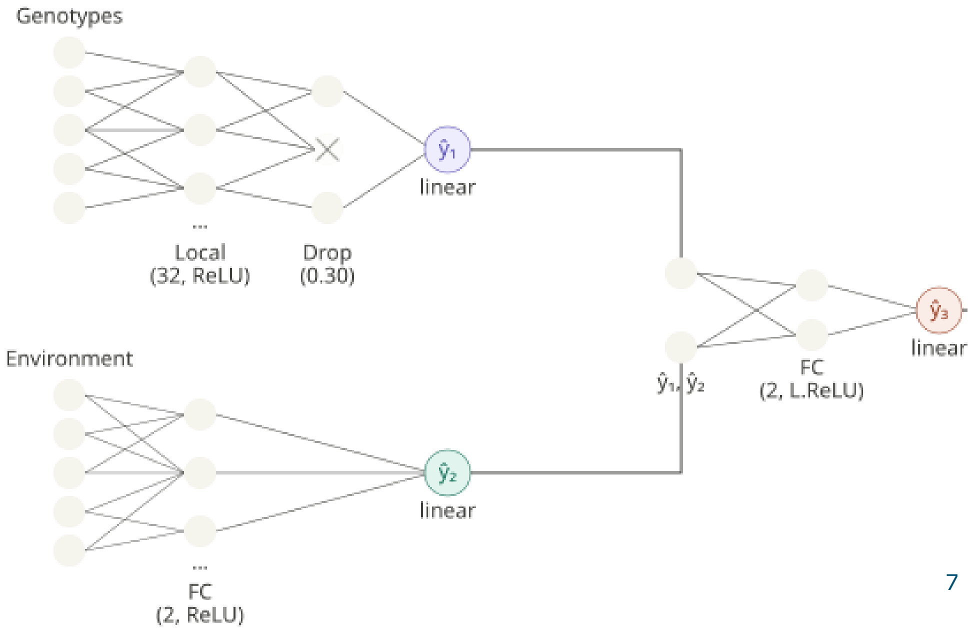
Models – ANN 2

- Set of 3 ANNs
  - ANN 1 (genotypes)
    - Dropout (0.30)
    - FC (output=1, linear)
  - ANN 2 (environment)
    - FC (output=1, linear)
  - ANN 3
    - FC (1, linear)



Models – ANN 3

- Set of 3 ANNs
- ANN 1 (genotypes)
  - Locally connected (3, 32, ReLU)
  - Dropout (0.30)
  - FC (1, linear)
- ANN 2 (environment)
  - FC (2, ReLU)
  - FC (1, linear)
- ANN 3
  - FC (2, Leaky ReLU)
  - FC (1, linear)



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Data

- Data
  - Dutch DMI routine genetic evaluation
  - Dutch CH_4 routine genetic evaluation

- 3 subsets
  - Training: training & validation datasets
  - Inference: test dataset (not used in the training phase)

- Predictive abilities presented for the best performing model

Data – DMI evaluation

- 1415 first-parity genotyped cows
- 25,153 DMI records
  - Effects: experiment, herd, month, year, parity*age at calving, DIM (2^{nd} Legendre), permanent environment

- Training, validation and test sets based on herds

Dataset	Training	Validation	Test
Animals	1149	122	144
Phenotypes	20,388	2253	2512

Predictive ability – DMI evaluation

Pearson correlations between true and predicted phenotypes

Dataset	SNPBLUP	ANN 1	ANN 2	ANN 3
Training	0.96	0.65	0.95	0.94
Validation	0.87	0.47	0.82	0.85
Test	0.87	0.46	0.83	0.85
Time (s)	111	1455	1393	55,708

➔Modelling environmental and genomic information separately improves the predictive ability

➔NN do not outperform SNPBLUP

Data – CH_4 evaluation

- 7284 first-parity genotyped cows
- 166,224 sniffer CH_4 records
  - Effects: herd, year, week, parity*DIM(2nd Legendre), breed composition, perm. env., perm. env. within parity

- Training, validation and test sets based on the year of measurement

Dataset	Training	Validation	Test
Year of measurement	<2022	2023	2024
Animals	6453	2675	4186
Phenotypes	45,995	105,442	14,787

Predictive ability – CH4 evaluation

Pearson correlations between true and predicted phenotypes

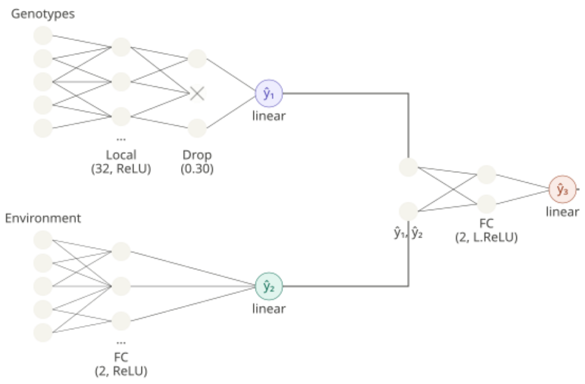
Dataset	SNPBLUP	ANN 1	ANN 2	ANN 3
Training	0.86	0.50	0.60	0.75
Validation	0.30	0.20	0.30	0.31
Test	0.22	0.16	0.17	0.30
Time (s)	741	12,488	12,114	220,859

➔Modelling environmental and genomic information separately improves the predictive ability

➔Some ANNs outperform SNPBLUP

Conclusions

- Set of ANNs
  - 1 ANN dedicated to each source of information
    - Environmental & Genomic
  - 1 ANN to combine the separate predictions into phenotypic predictions



→Might improve phenotypic predictions compared to linear models

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Thank you for your attention!

To explore the potential of nature to improve the quality of life

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