GEroNIMO and RUMIGEN Joint Final Event

Breeding the Future

Genomics, Epigenomics & Societal

Acceptability for Sustainability in Livestock

Including methylation in genomic prediction (Part 1)

Improvement of predictive breeding models in monogastrics

Levi Ayres

WAGENINGEN UNIVERSITY & RESEARCH

IRTA

UNIVERSITY OF COPENHAGEN

Funded by the European Union

GEroNIMO and RUMIGEN Joint Final Event

Breeding the Future

Genomics, Epigenomics & Societal

Acceptability for Sustainability in Livestock

Can epigenomics and transcriptomics help us better predict traits?

WAGENINGEN UNIVERSITY & RESEARCH

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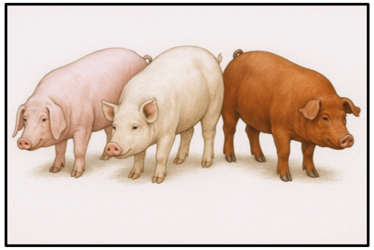
Genomic prediction

DANBRED

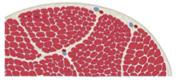
- 443 DanBred pigs
  - Duroc
  - Landrace
  - Yorkshire



- Traits
  - Average daily gain
  - Residual feed intake
  - Backfat thickness

BLUP

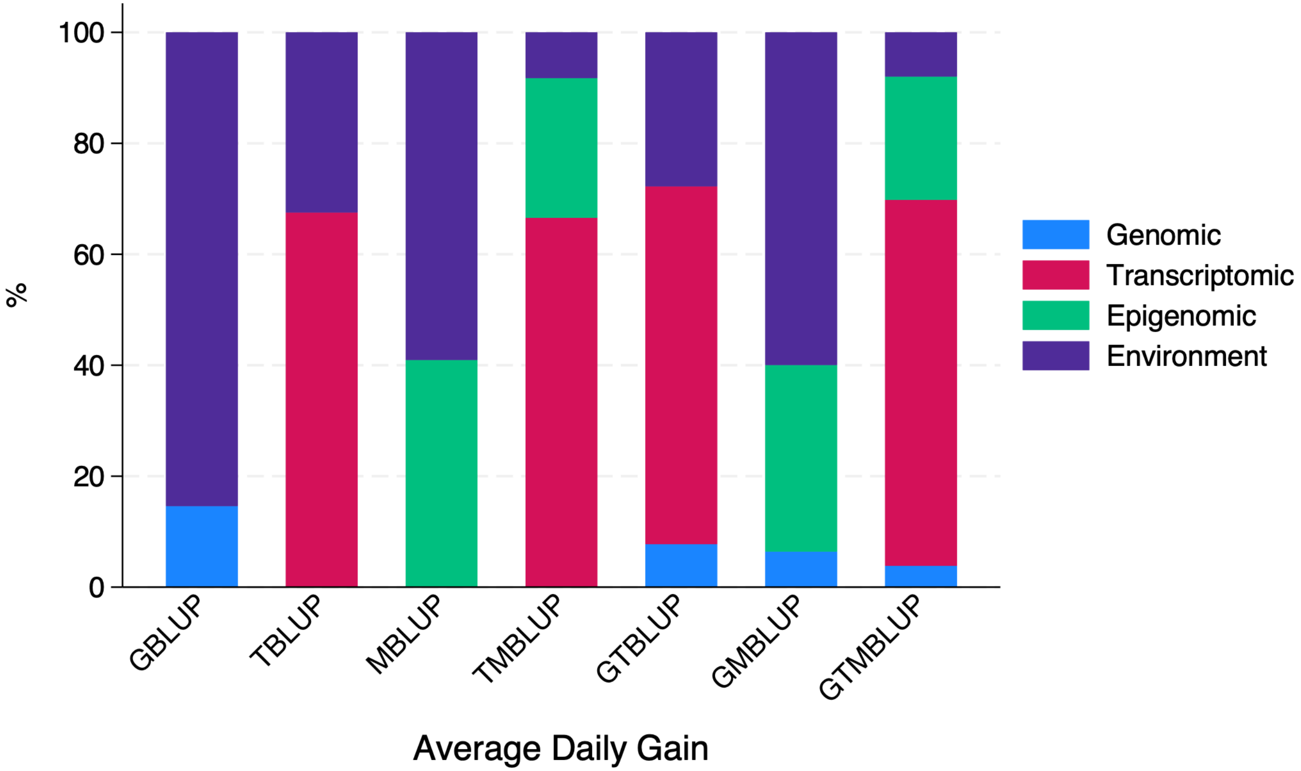
- Genotypes
- Muscle tissue



  - Epigenomics (DNA methylation)
  - Transcriptomics (gene expression)

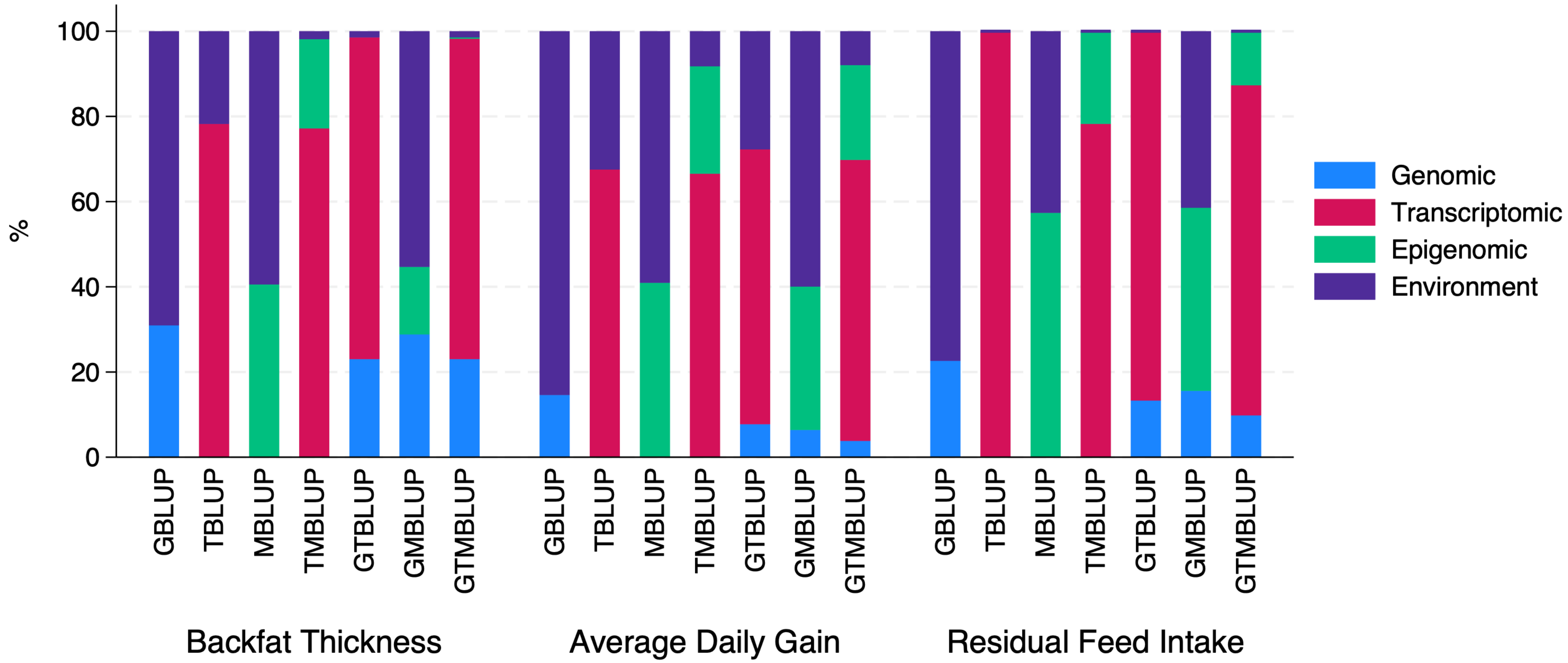
* *We thank LF, Breeding & Genetics (DAFC F.m.b.A.) for the study data*

Sources of variation



The GERoNIMO project has received funding from European Union’s Horizon 2020 research and innovation program under Grant Agreement No 101000236. This project is part of EuroFAANG (https://eurofaang.eu).

Sources of variation



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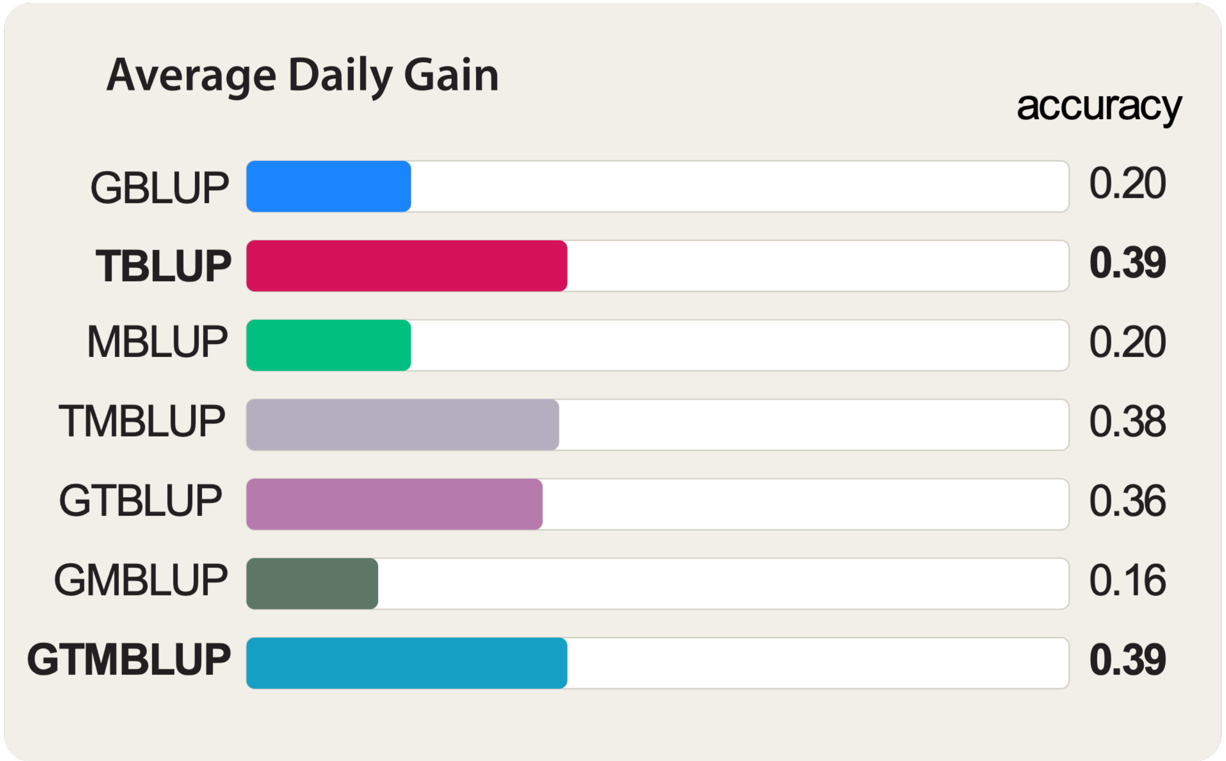
Multi-breed prediction accuracies



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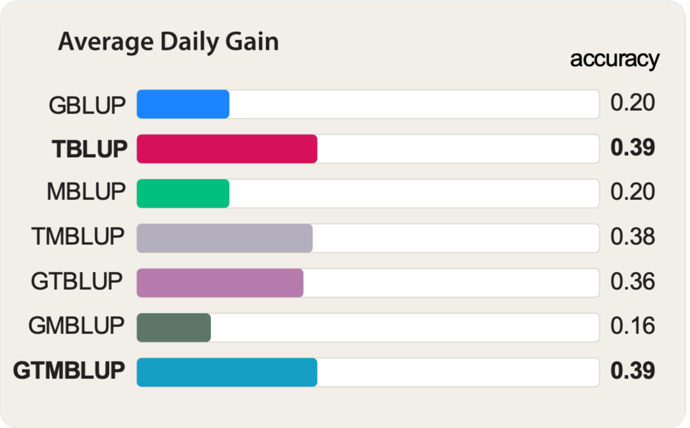

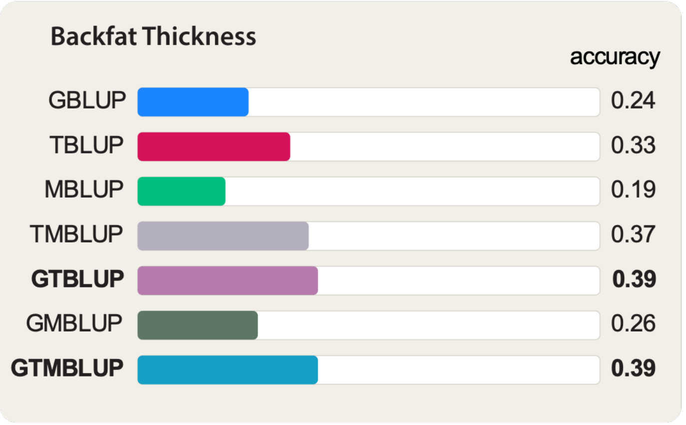

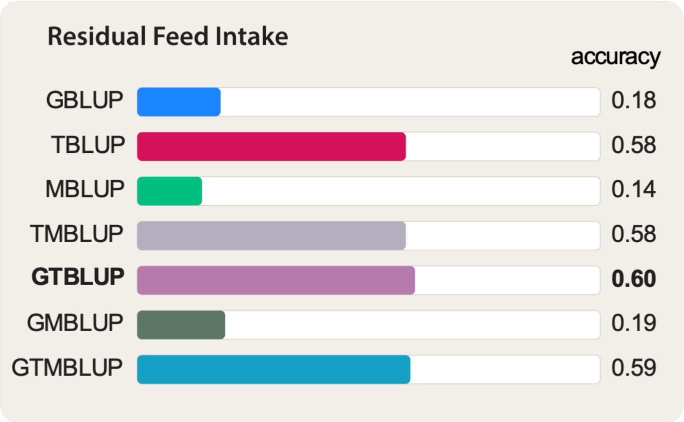

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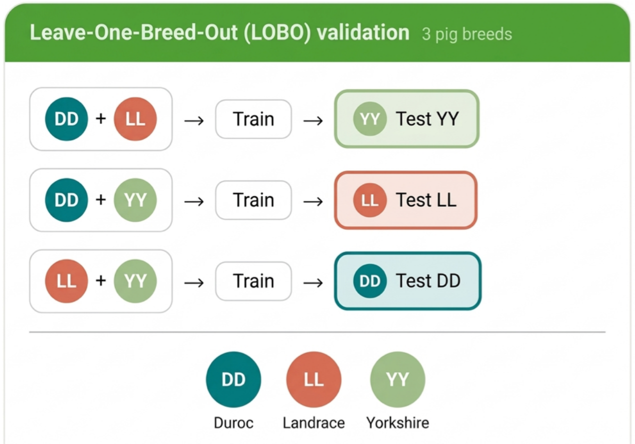
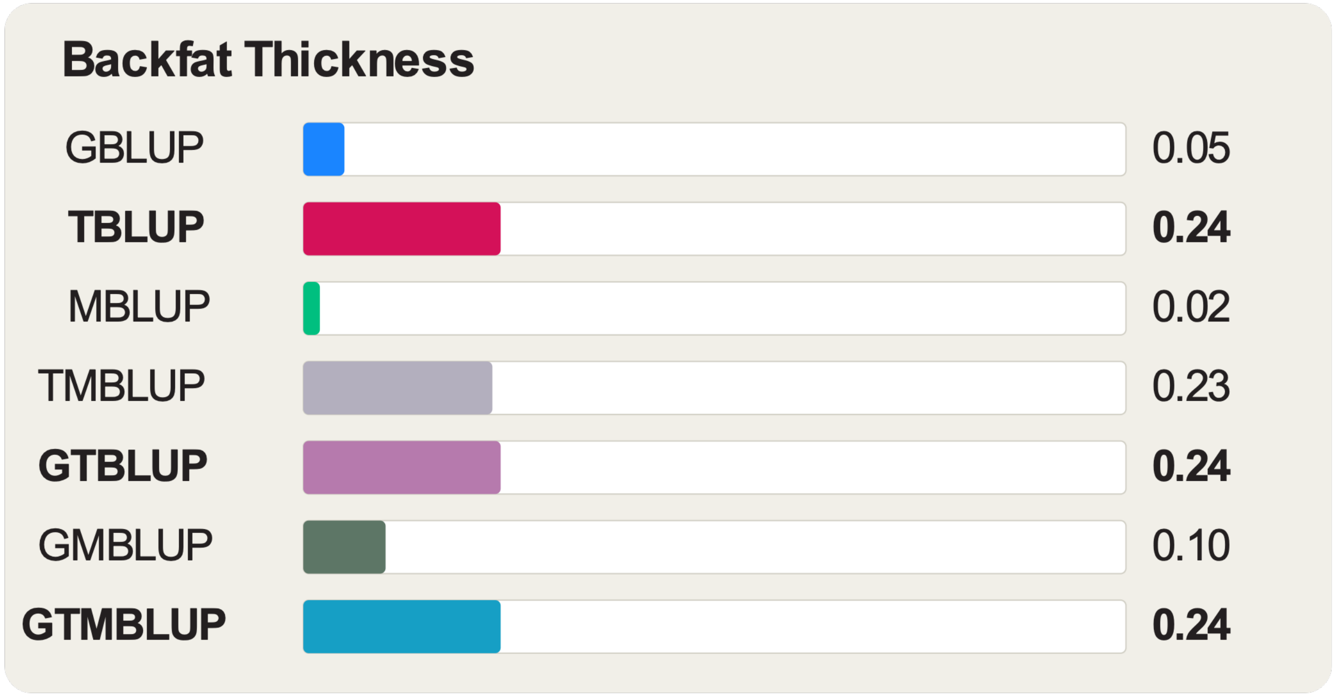
Across-breed prediction accuracies



Duroc



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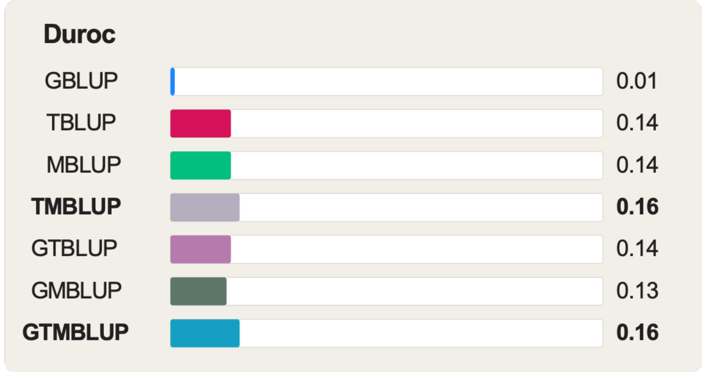
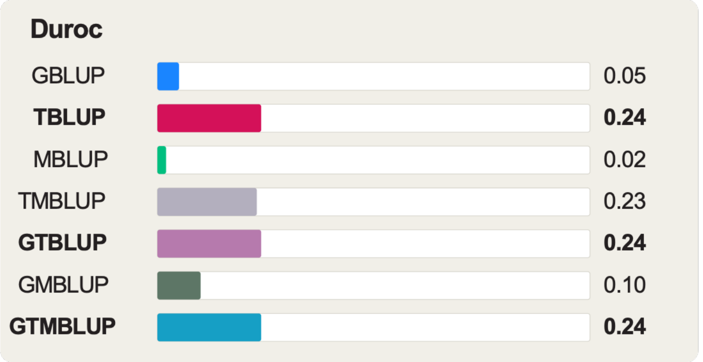
Across-breed prediction accuracies

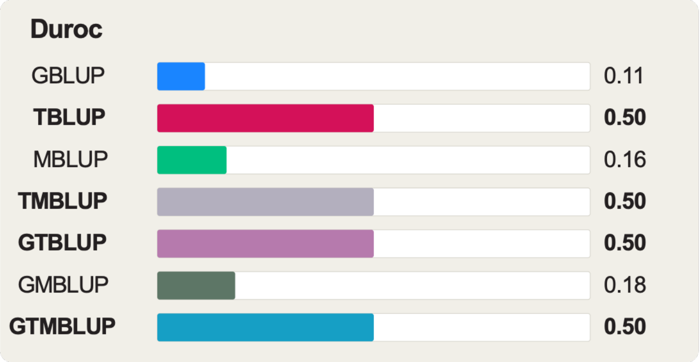
Average Daily Gain



Backfat Thickness



Residual Feed Intake



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Conclusions

1. **Transcriptomics provided the greatest improvement in prediction.**

2. **DNA methylation also showed a predictive signal, but its contribution was smaller.**

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