GxE with high-dimensional environmental data: correlated herd effects

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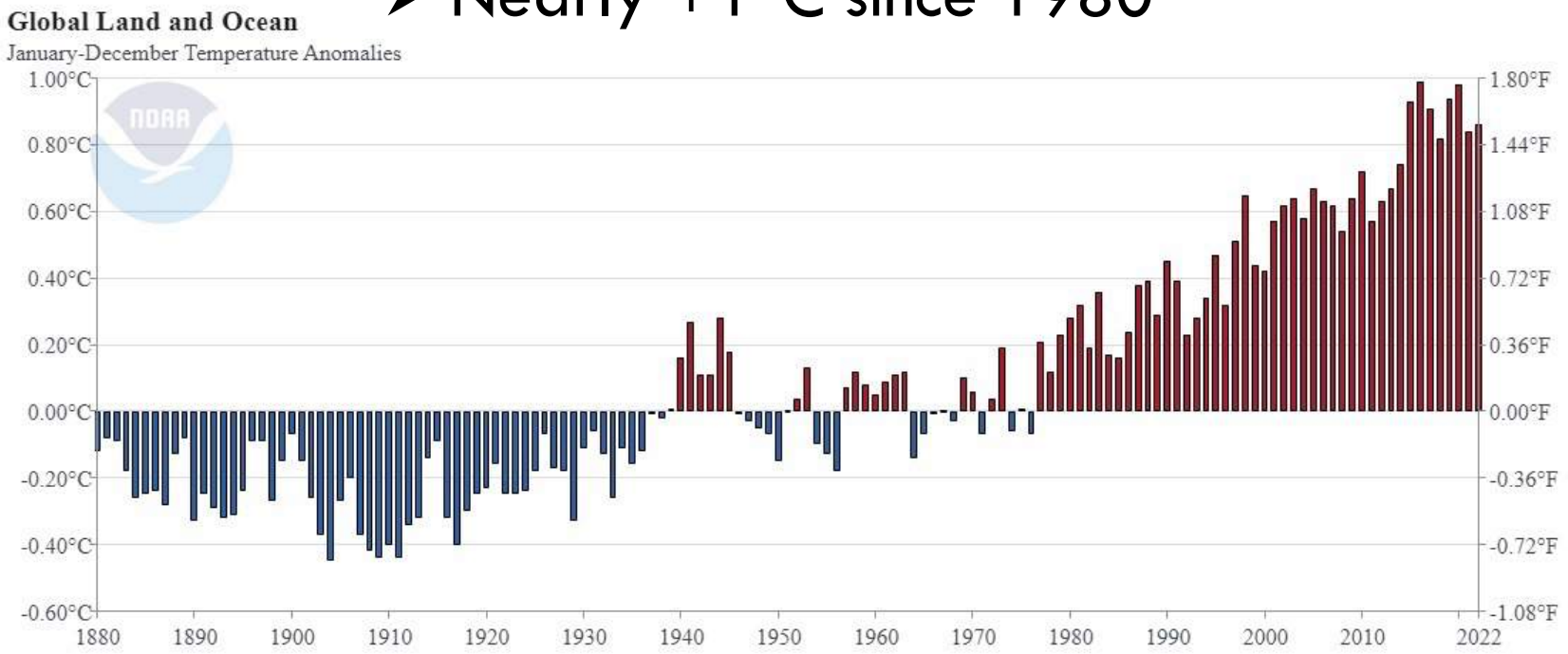
Introduction

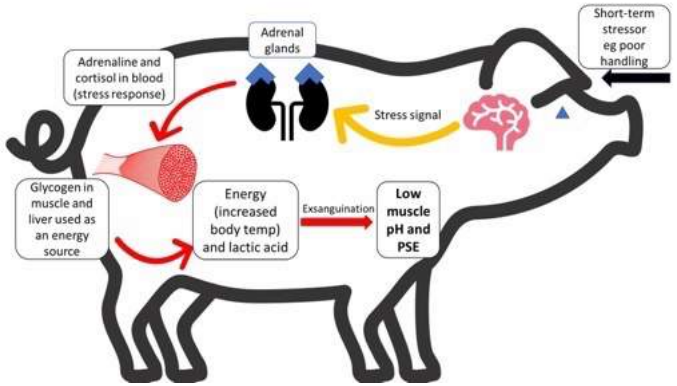
- Nearly +1°C since 1980



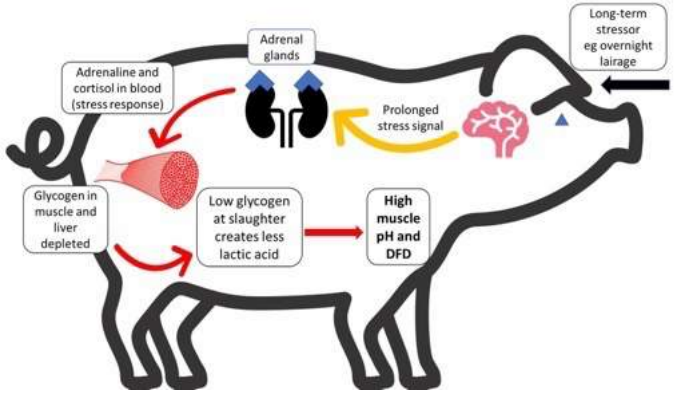
National Centers for Environmental Information: https://www.ncei.noaa.gov/access/monitoring/monthly-report/global/202213

Introduction

- Environmental effect:
  - Seasonal productivity fluctuations
  - Heat Stress



Short-term



Long-term

- $299 million loss

  (St-Pierre et al., 2003)

- Welfare

- Diseases

The Pig Site: https://www.thepigsite.com/articles/what-are-the-impacts-of-stress-on-pork-quality

Introduction

- Environmental effect:
  - Seasonal productivity fluctuations
  - Heat Stress
    - Sweat glands are not stimulated (Ingram, 1967)
    - Max 50 % heat production dissipated by respiratory evaporation (Renaudeau et al., 2012)
    - Evidences of worsening with selection (Brown-Brandl et al., 2001)

Introduction

- Environmental effect:
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    - Sweat glands are not stimulated (Ingram, 1967)
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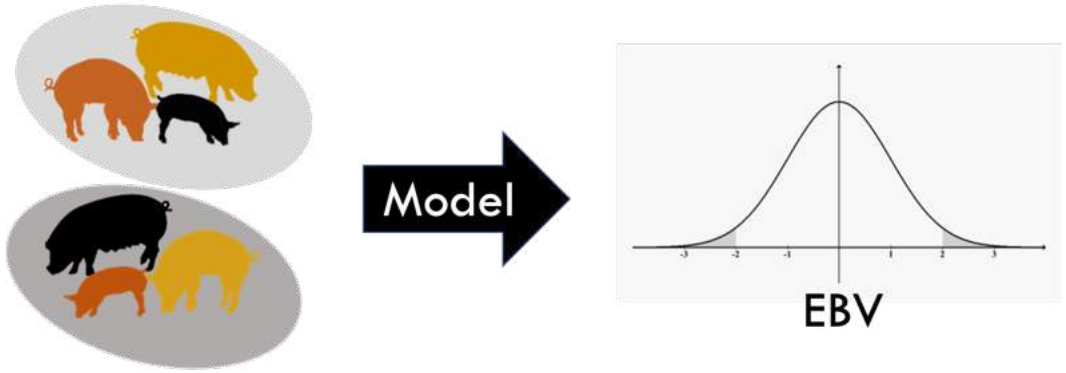
    - Evidences of worsening with selection (Brwon-Brandl et al., 2001)
    - Statistically



- Fixed
- Random
- Uncorrelated

Introduction

- What if:
  - Herds are geographically close?
  - Climate conditions are similar?
  - Management/manager is the same?
  - …
  - Correlated random herd effects

    (Tiezzi et al., 2017; Selle et al., 2020; Cuyabano et al., 2021; Makanjuola et al., 2022)

Introduction

- Heat stress and climate effect:
  - Temperature and Humidity → THI
  - Heat Load → f(THI)
    - Same THI for all locations – need to adapt (Bohmanova et al., 2007)
    - Temperature as good as THI (Dikmen and Hansen, 2009; Dado-Senn et al., 2023)

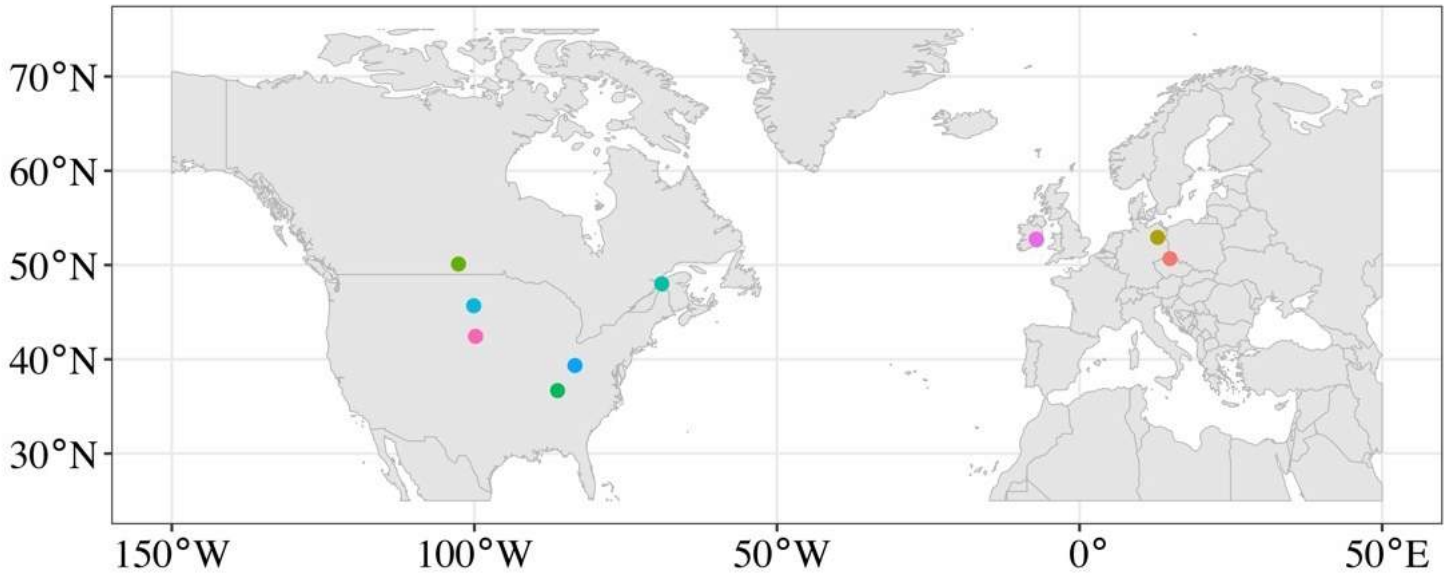
- Jarquín et al., 2014
  - To accommodate environmental covariates (EC) by (co)variance structures
    - Reduces number of parameters
    - Better characterization of the environment

Objective

- To investigate GxE by using the (co)variances approach to model correlated herd effects and their impact on the prediction accuracy of genomic evaluation in pigs

Datasets Provided

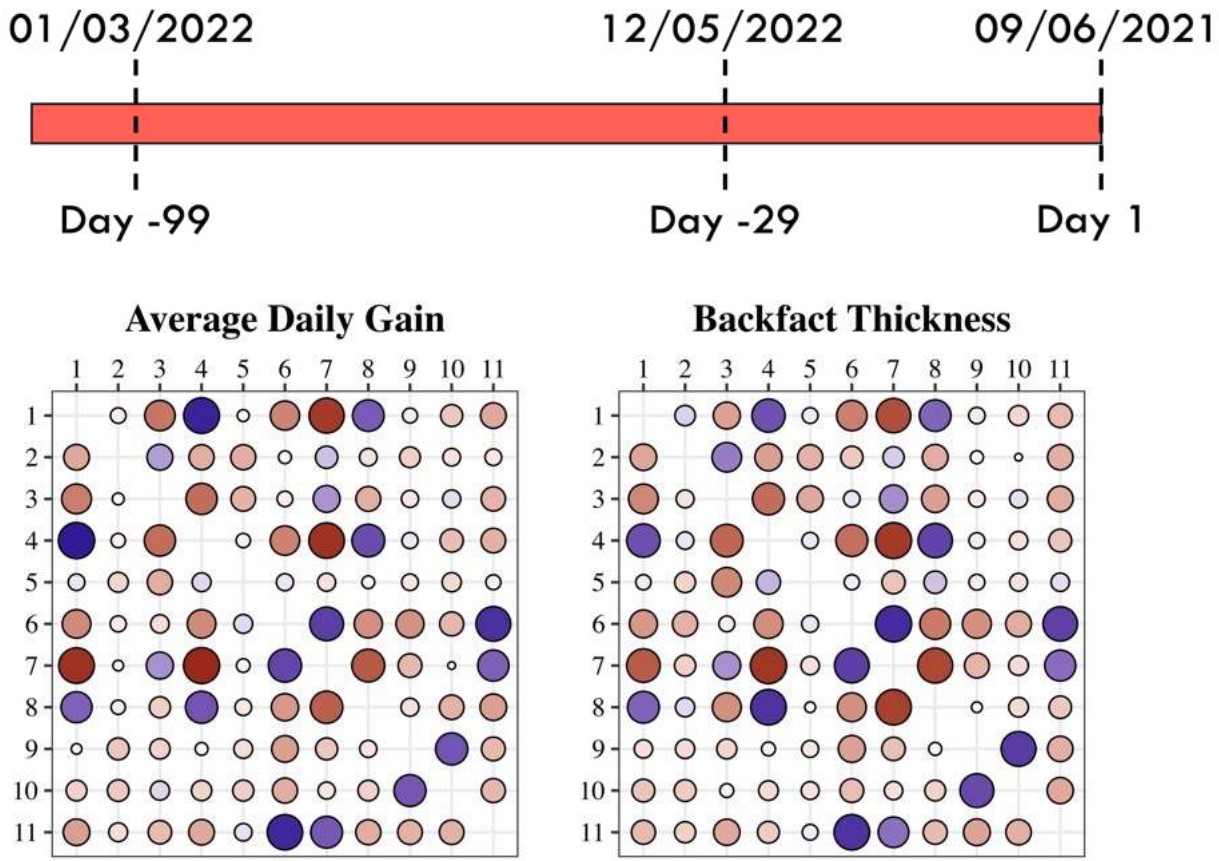
- Growth Purebred Pigs:
  - Average Daily gain (ADG)
    - 35,597 records
    - All genotyped
    - 11 farms
  - Backfat Thickness (BFT)
    - 32,105
    - All genotyped
    - 11 farms



Environmental Data

- NASA POWER (https://power.larc.nasa.gov/data-access-viewer/) - EC
  - T (Temperature - °C)
  - Td (Dew/Frost temperature - °C)
  - Tw (Wet-bulb temperature - °C)
  - Ts (Earth surface temperature - °C)
  - H (Relative humidity - %)
  - R (Rainfall – mm/day)
  - Ws (Wind speed – m/s)
  - Md (Wind direction - °)

- Linear Regression every 10 days



Model of Analysis

- $ADG_{ijkl} = \mu + CG_i + l_j + g_k + e_l + \epsilon_{ijkl}$
- $BFT_{ijkl} = \mu + \beta_1 EW_k + CG_i + l_j + g_k + e_l + \epsilon_{ijkl}$
- $\mathbf{y} = \mathbf{X\beta} + \mathbf{Z}_1\mathbf{l} + \mathbf{Z}_2\mathbf{g} + \mathbf{Z}_3\mathbf{e} + \boldsymbol{\epsilon}$
  - $\mathbf{l} \sim MVN(\mathbf{0}, I\sigma_l^2)$
  - $\mathbf{g} \sim MVN(\mathbf{0}, G\sigma_g^2)$
  - $\mathbf{e} \sim MVN(\mathbf{0}, I\sigma_e^2)$ → $\mathbf{e} \sim MVN(\mathbf{0}, \mathbf{E}_{30}\sigma_e^2)$ → $\mathbf{e} \sim MVN(\mathbf{0}, \mathbf{E}_{100}\sigma_e^2)$
  - $\boldsymbol{\epsilon} \sim MVN(\mathbf{0}, I\sigma_\epsilon^2)$

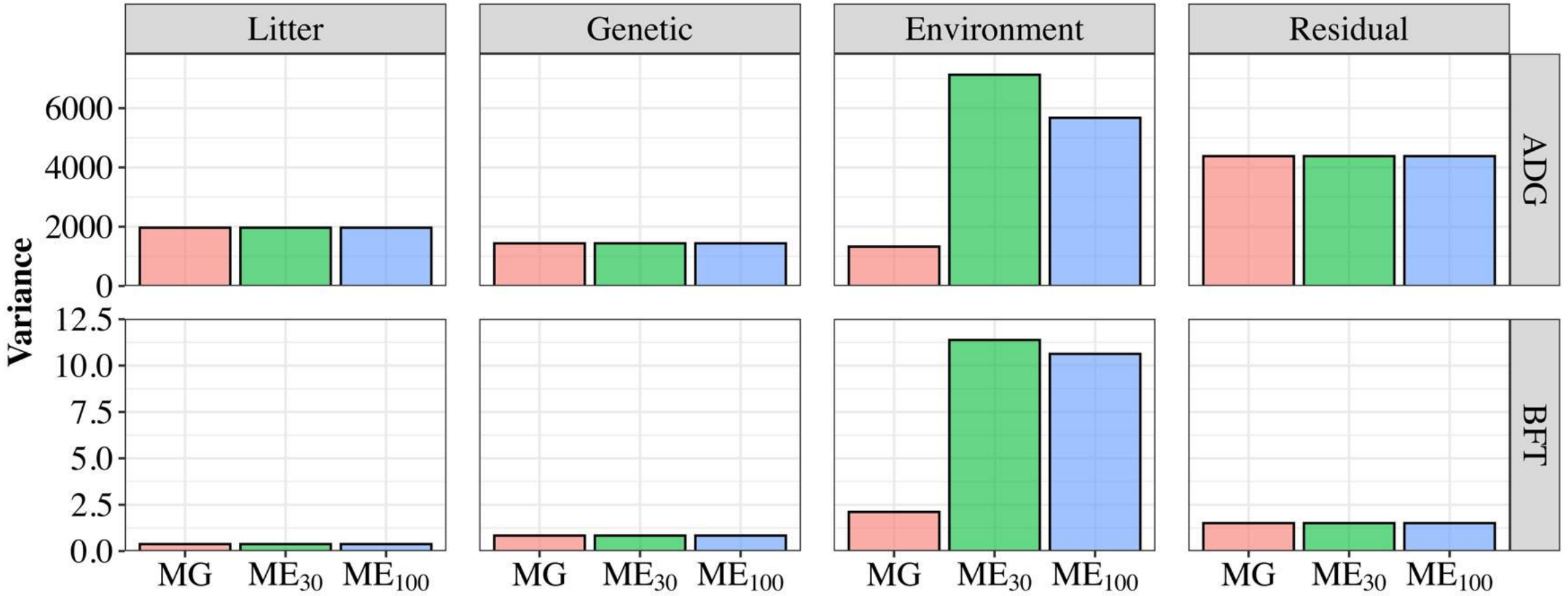
MG ME_{30} ME_{100}

Validation

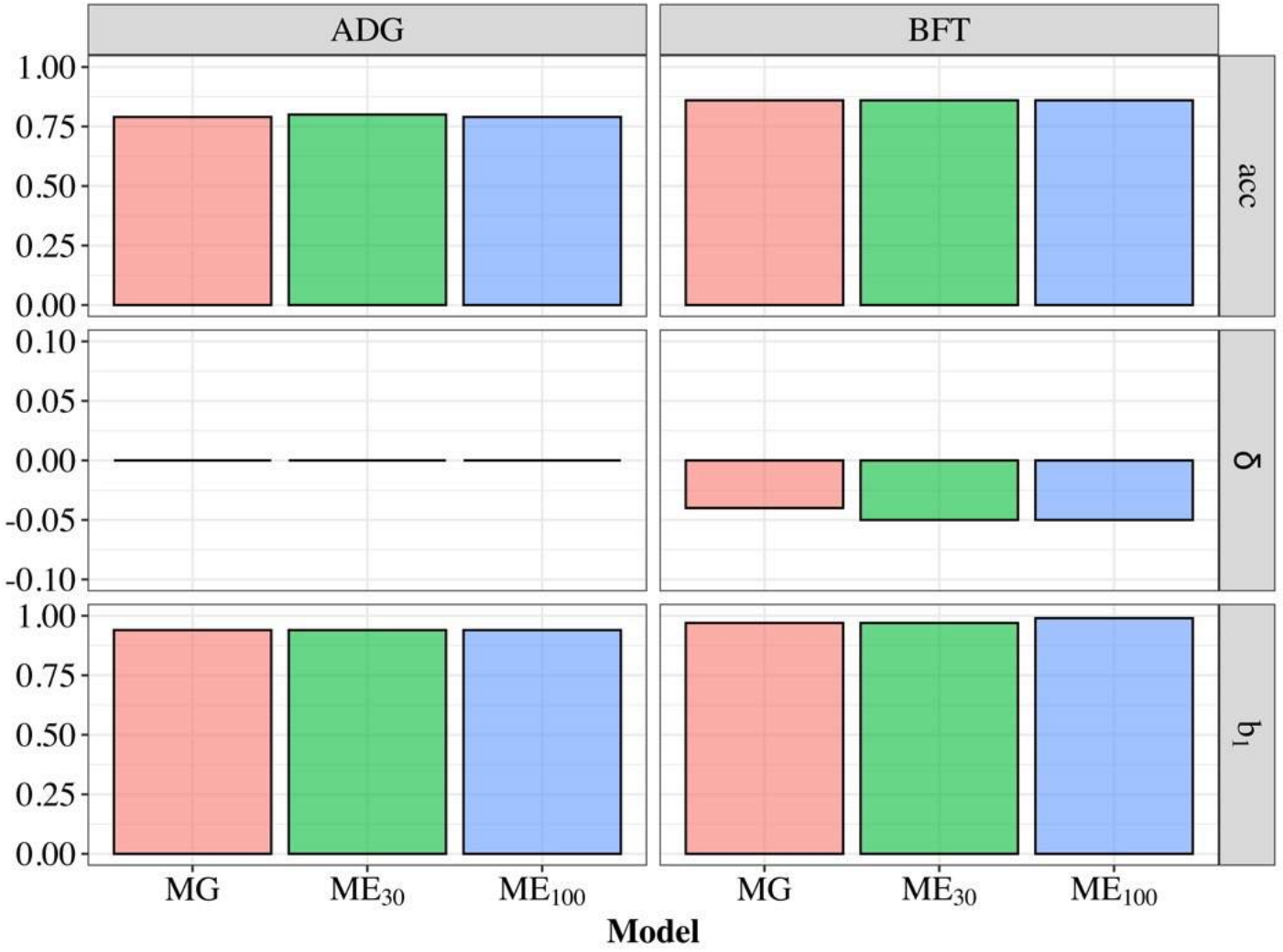
- Focal animals - born in 2020
  - One whole (w, from 2009 to 2020) and one partial (p, from 2009 to 2019) datasets

- LR (Legarra and Reverter, 2018)
  - $\text{acc} = \sqrt{\text{cov}(\hat{\mathbf{g}}_p, \hat{\mathbf{g}}_w)/(1-\bar{F})\sigma_g^2}$
  - $\delta = (\bar{\hat{\mathbf{g}}}_p - \bar{\hat{\mathbf{g}}}_w)/\sigma_g$
  - $b_1 = \text{cov}(\hat{\mathbf{g}}_p, \hat{\mathbf{g}}_w)/\text{var}(\hat{\mathbf{g}}_p)$

Variance Components



Validation Statistics



- No improvement in acc, bias, and dispersion
- What if within environment?
  - No improvement also

Model of Analysis

- $\text{Var}\begin{bmatrix}\mathbf{l}\\ \mathbf{g}\\ \mathbf{e}\\ \boldsymbol{\epsilon}\end{bmatrix} = \begin{bmatrix}\mathbf{I}\sigma_l^2 & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ & \mathbf{G}\sigma_g^2 & \mathbf{0} & \mathbf{0}\\ & & \mathbf{E}_i\sigma_e^2 & \mathbf{0}\\ \text{sym.} & & & \mathbf{I}\sigma_\epsilon^2\end{bmatrix}$ $\text{Cov}(\mathbf{g},\mathbf{e}) = (\mathbf{G}\odot\mathbf{Z}_4\mathbf{E}_i\mathbf{Z}_4')\sigma_{ge}^2$

- $\mathbf{y} = \mathbf{X\beta} + \mathbf{Z}_1\mathbf{l} + \mathbf{Z}_2\mathbf{g} + \mathbf{Z}_3\mathbf{e} + \mathbf{Z}_4\mathbf{ge} + \boldsymbol{\epsilon}$
  - $\mathbf{l}\sim\text{MVN}(\mathbf{0}, \mathbf{I}\sigma_l^2)$
  - $\mathbf{g}\sim\text{MVN}(\mathbf{0}, \mathbf{G}\sigma_g^2)$
  - $\mathbf{e}\sim\text{MVN}(\mathbf{0}, \mathbf{E}_i\sigma_e^2)$
  - $\mathbf{ge}\sim\text{MVN}[\mathbf{0}, (\mathbf{G}\odot\mathbf{Z}_4\mathbf{E}_i\mathbf{Z}_4')\sigma_{ge}^2]$
  - $\boldsymbol{\epsilon}\sim\text{MVN}(\mathbf{0}, \mathbf{I}\sigma_\epsilon^2)$

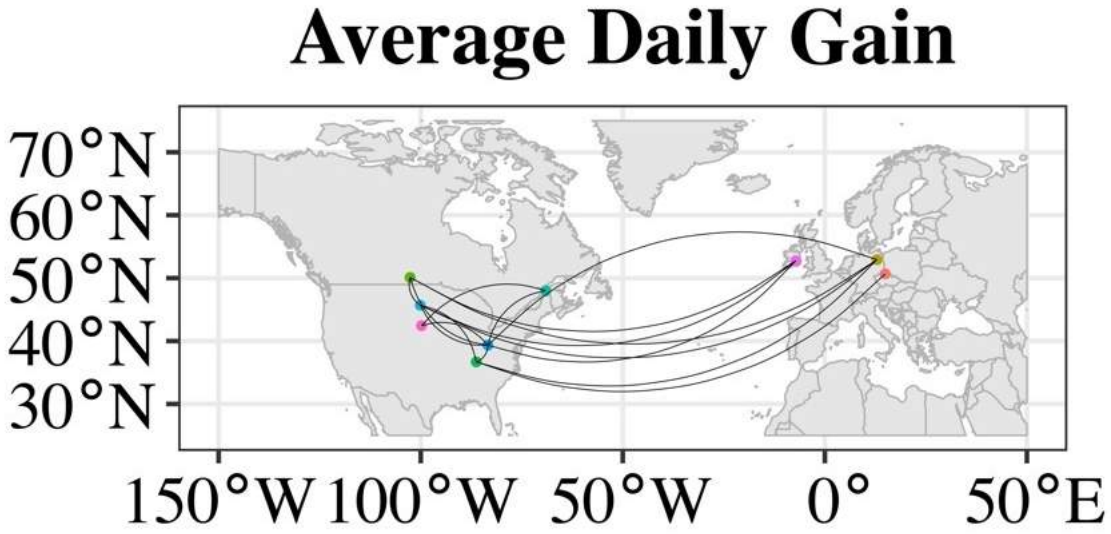
→ $\mathbf{e}\sim\text{MVN}(\mathbf{0}, \mathbf{E}_{30}\sigma_e^2)$
$\mathbf{ge}\sim\text{MVN}[\mathbf{0}, (\mathbf{G}\odot\mathbf{Z}_4\mathbf{E}_{30}\mathbf{Z}_4')\sigma_{ge}^2]$ MGE_{30}

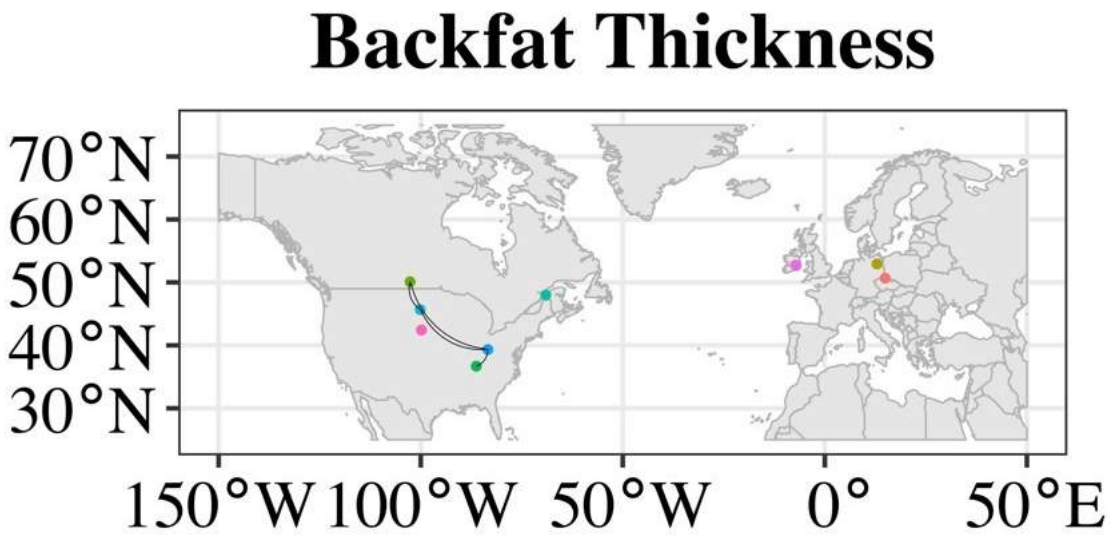
→ $\mathbf{e}\sim\text{MVN}(\mathbf{0}, \mathbf{E}_{100}\sigma_e^2)$
$\mathbf{ge}\sim\text{MVN}[\mathbf{0}, (\mathbf{G}\odot\mathbf{Z}_4\mathbf{E}_{100}\mathbf{Z}_4')\sigma_{ge}^2]$ MGE_{100}

Two Questions

- Is there GxE?
  - MTM
  - $r_{g_{eiej}} < 0.80$
    - Bending
    - Number or records/environment
    - Feeding and measurement systems

- Can we improve accuracy by including GxE?





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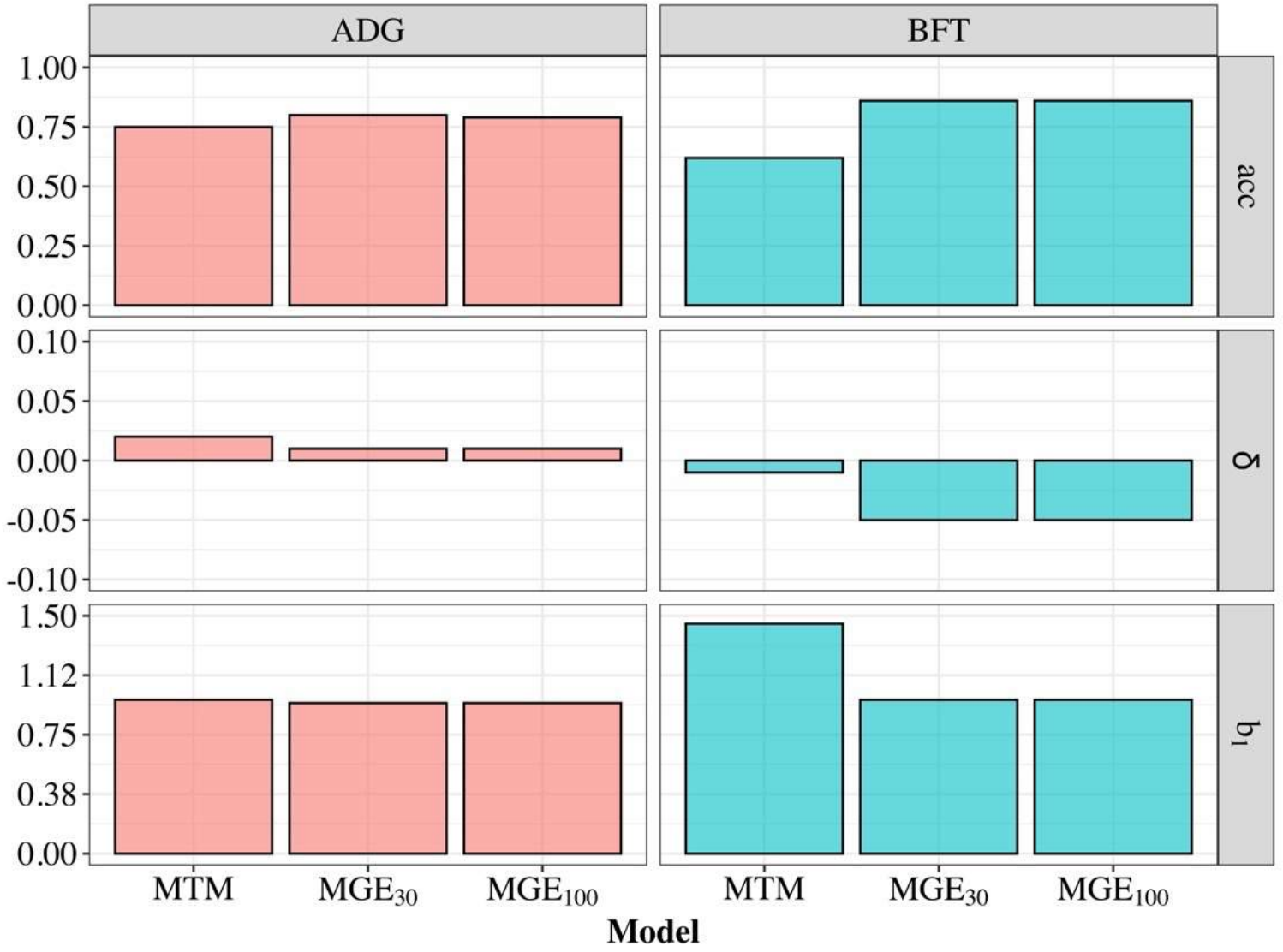
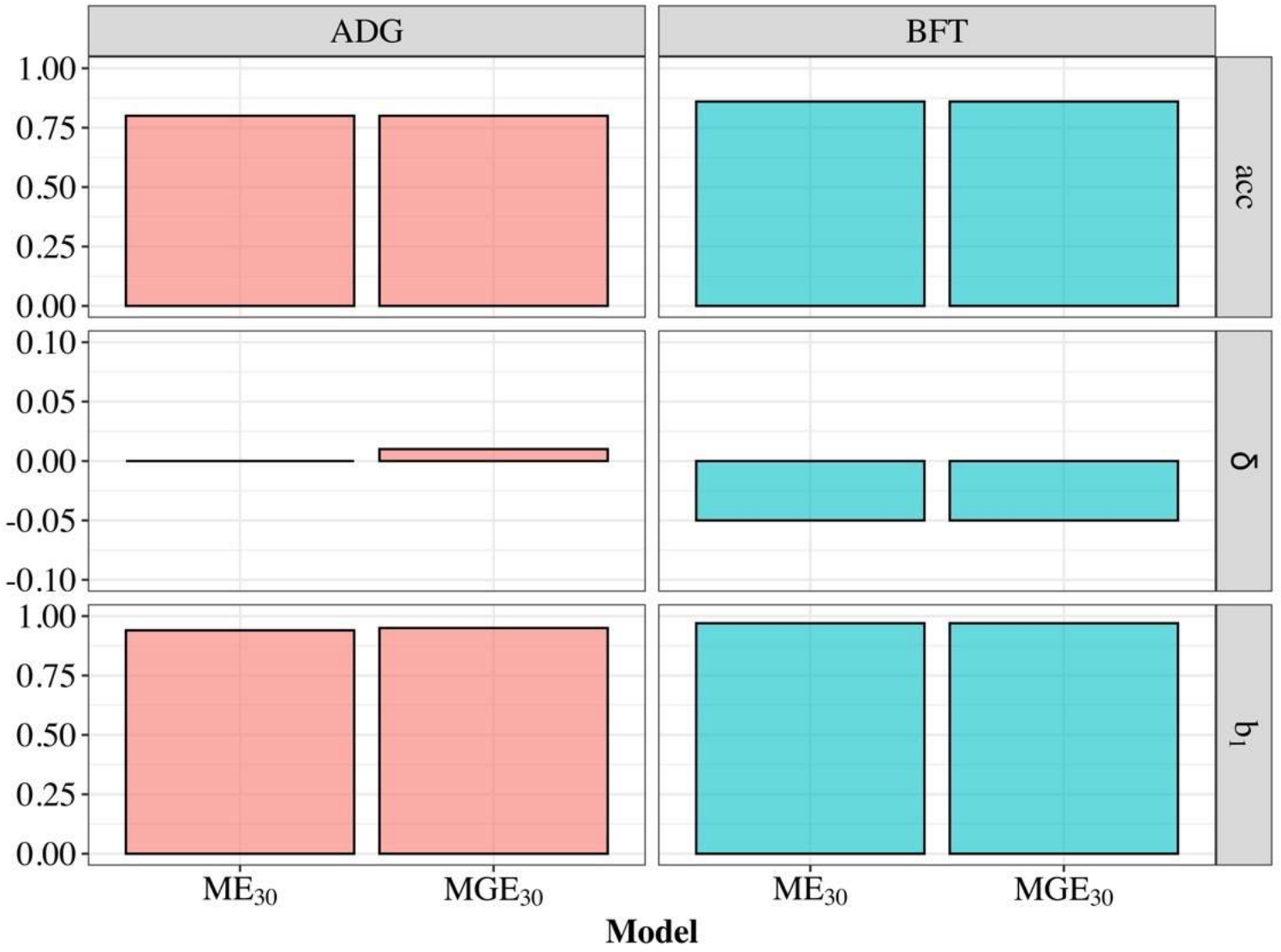


ME_{30} vs MGE_{30}

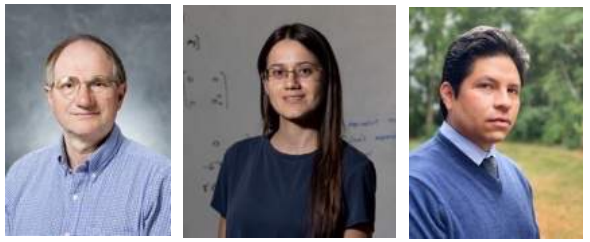
- No improvement in acc, bias, and dispersion
- MGE = ME?
  - Possibly no reranking



Remarks

- The (co)variances approach could increase accuracy when environment accounts for a lower proportion of phenotypic variance
  - fixed herd effect is usually enough
- Considering GxE where E is a correlated effect does not improve accuracy
- (Co)variances approach had higher accuracy than MTM for BFT
- This model provides a "ge" breeding value – specific environmental change on the genotype (recalling MGE_i are analogous to a reaction norm, "g" acts a b_0 and "ge" as a b_1)
- Overall…
  - Using outdoor EC to correlate environments has little benefit for genomic predictions
  - MGE would be better if "g" was observed in each different "e"
  - MTM performs as good if there is borrowing of information

Acknowledgements



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