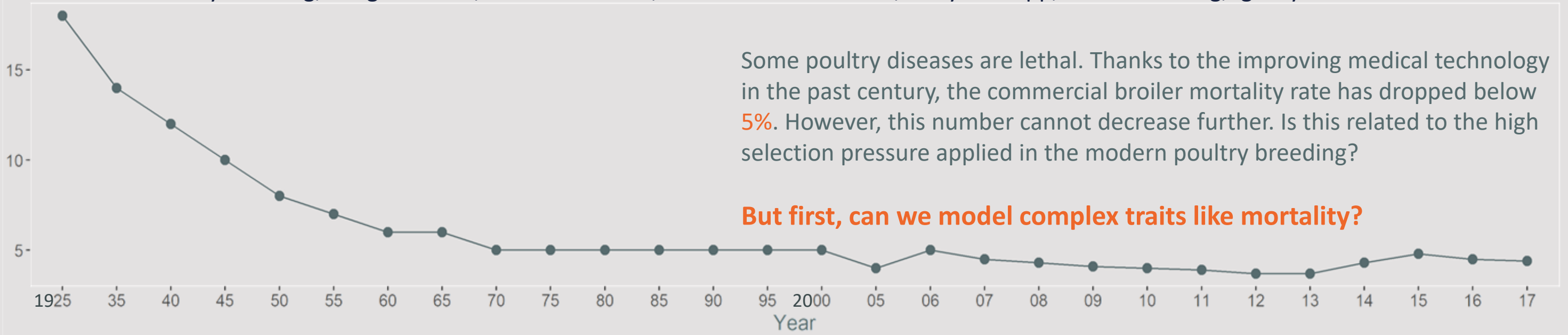


Genetics of performance and disorder traits of broiler chicken

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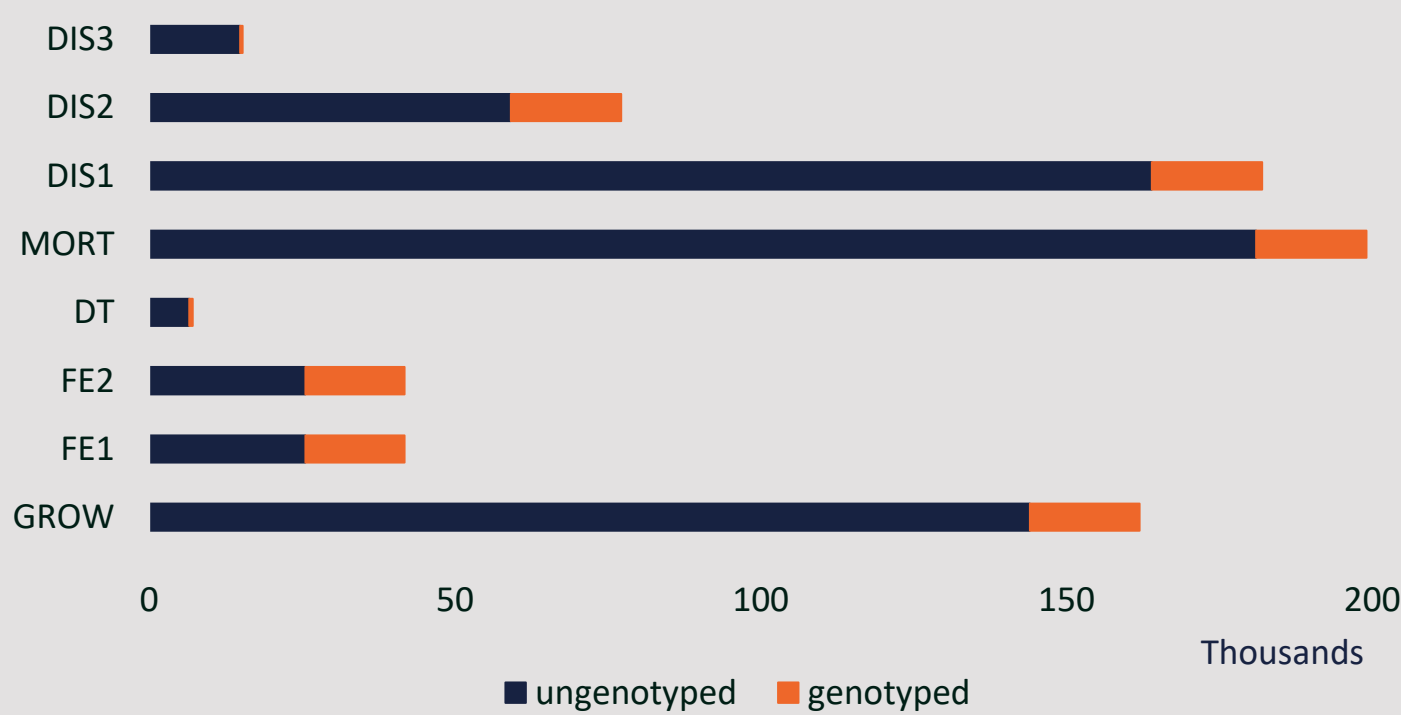
Questions with analyses of health data

- Can we model multiple continuous and categorical traits together, with both phenotypes and genotypes?
- Is genotype information helpful in predicting future breeding values?
- For broilers: Is mortality affected by selection on growth and feed efficiency?

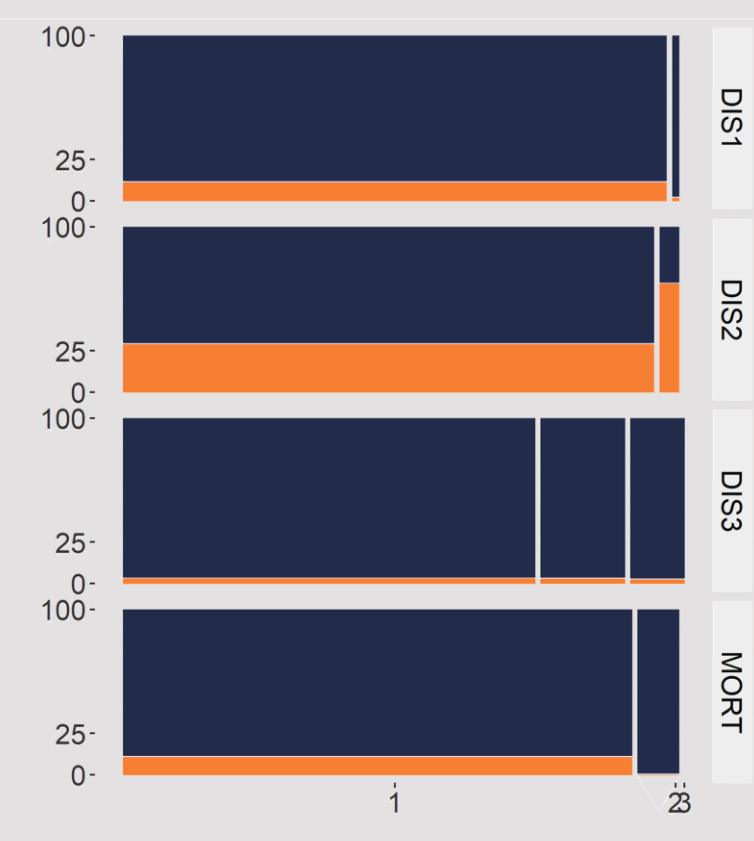
Data

- 4 continuous traits: growth(**GROW**), feed efficiency (**FE1** and **FE2**), dissection trait(**DT**), likely causes of disorders.
- 4 categorical traits: mortality(**MORT**), disorders(**DIS1**, **DIS2** and **DIS3**). Disorder traits are likely causes of mortality.
- Genotypes were obtained using 60k Illumina (San Diego, CA) SNP BeadChip arrays.

Number of broiler chickens in the data set (Cobb-Vantress Inc.)



Percentage (%) of broilers by trait and category



Mortality and disorder traits are either binary or categorical. **1** = alive or healthy, **2** = died or sick. In **DIS3**, 1 to 7 is the score of the disease progress with 1 being normal and 7 being severe disorder. Categories **3-7** were grouped together as there were few records in each category.

Statistical models

Model	Number of traits	
	Single trait	Multi-trait
Linear	Growth and feed efficiency traits	
Threshold	Mortality and disorder traits	
Threshold-linear	-	All traits

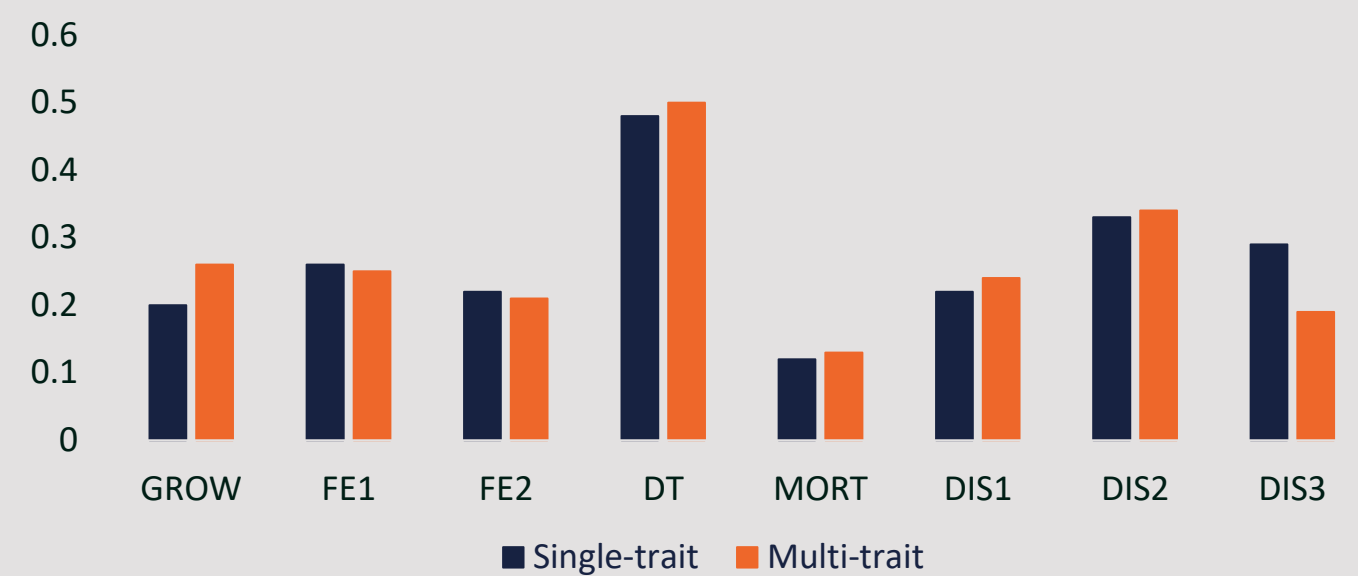
Validation scheme

1. Remove the last generation, split the rest data into 2 equal-sized subsamples.
2. Apply the same model to the 2 separated data, obtain the prediction of the EBV on the last generation.
3. Compute the correlation between the 2 sets of EBV as the realized accuracy.
4. Repeat the randomization for 10 times, average the realized accuracy.

Computation and software

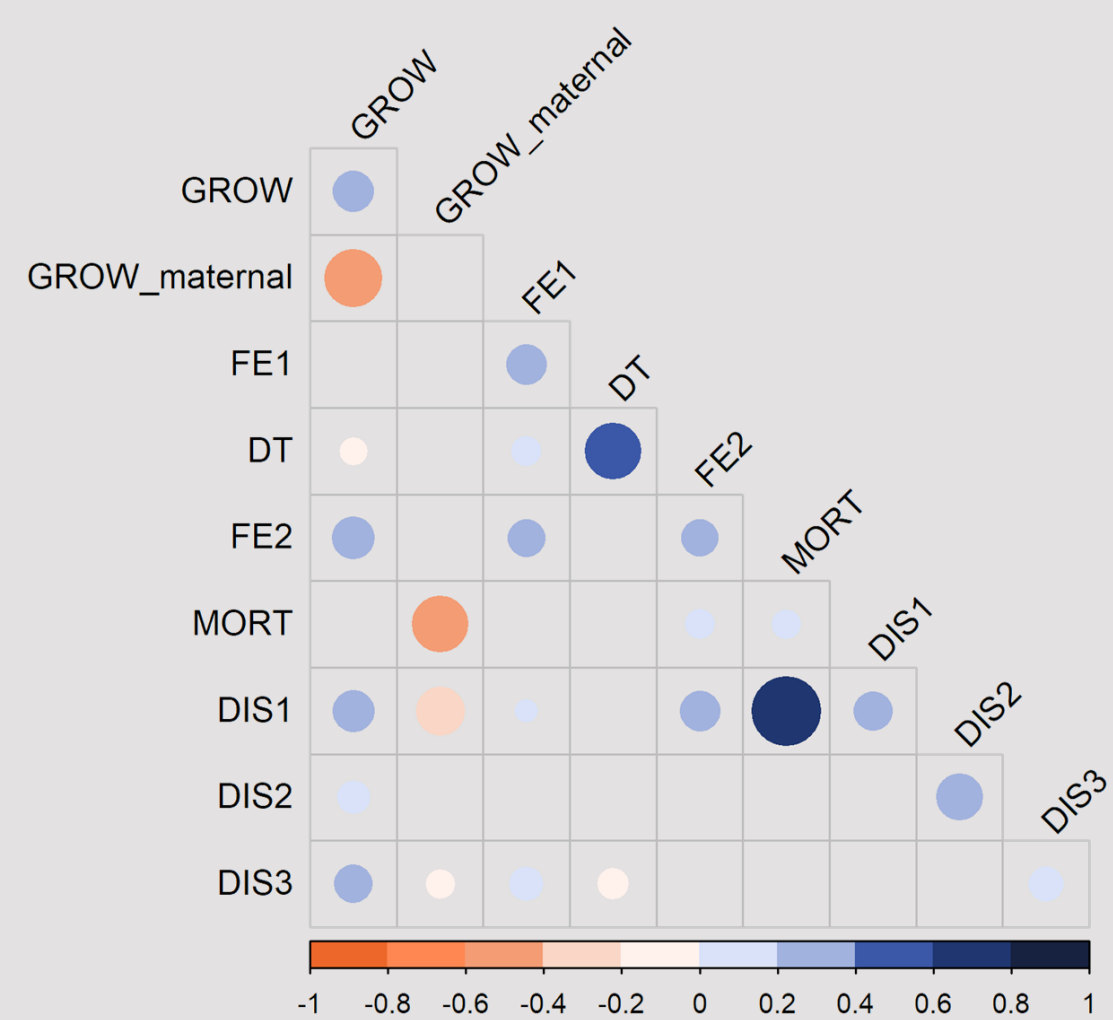
AIREMLF90 + THRGIBBS1F90: estimate (co)variance components
 POSTGIBBSF90: test convergence for threshold models
 BLUPF90 + THRGIBBS1F90 with fixed variance components: estimate EBV

Heritability comparison between the two models



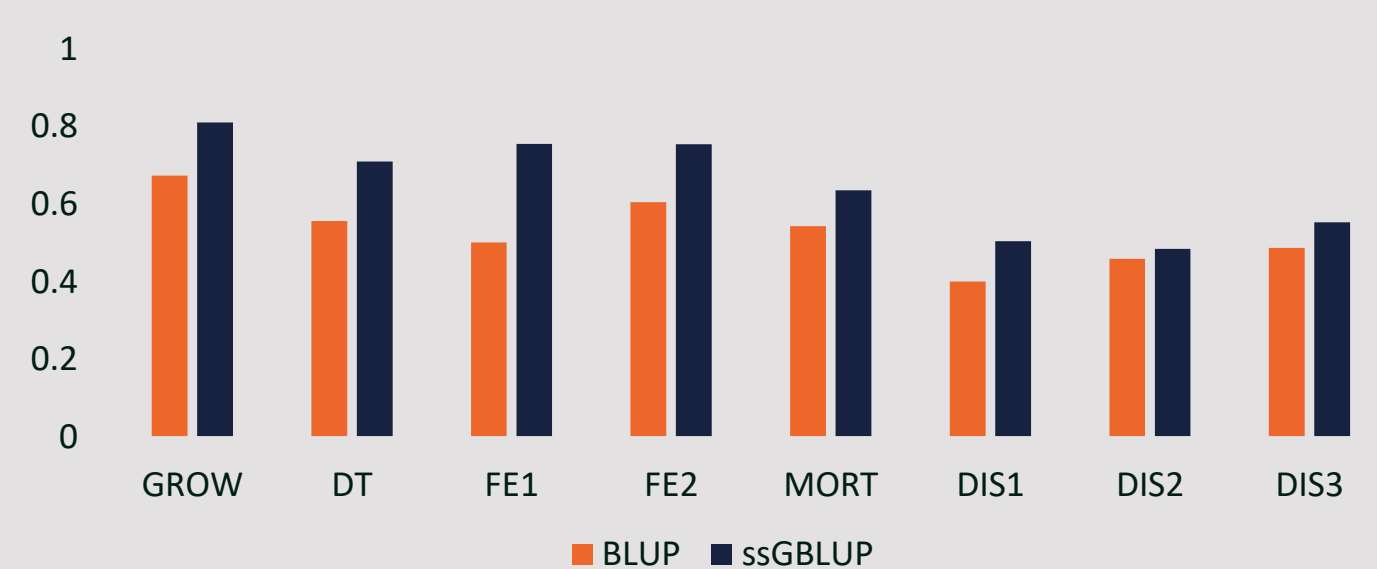
- Most traits have moderate to high heritability except **MORT** and **DIS3**.
- Multi-trait threshold-linear model better accounts for selection bias compared to single trait models.
- Heritabilities obtained using multi-trait threshold-linear model are more realistic and independent of incidences in location over time.

Heritabilities (diagonal) and correlations (off-diagonal) from the multi-trait threshold-linear model



- Selection for heavier and more efficient animals will likely **not** increase the incidence of **MORT** and disorders, since performance traits have **weak** correlation with disorders and mortality traits. Therefore, it's possible to select broilers on **GROW**, **FE1**, **FE2** and **MORT** together.
- Offspring **MORT** can be **reduced** by selecting for heavier maternal **GROW**.

Realized accuracy comparison with and without genotype



Modeling with genotypes boosted the prediction accuracy of EBV.

Conclusions

- Meaningful quantitative genetics analysis of health related traits requires good modeling to account for correlated traits, binary nature of health traits, and genomic info.
- This is possible with the ssGBLUP methodology and BLUPF90 software.

References

Groenen, M. A., et al. 2011. The development and characterization of a 60k SNP chip for chicken. *BMC genomics*. 12(1): 274.
 Misztal, I., et al. 2002. BLUPF90 and related programs (BGF90). *Proc. 7th World Congr. Genet. Appl. Livest. Prod.*, Montpellier, France. Communication 28-07.
 Misztal, I., et al. 2016. Inexpensive computation of the inverse of the genomic relationship matrix in populations with small effective population size. *Genetics*. 202(2): 401-409.
 Ramirez-Valverde, R., et al. 2001. Comparison of threshold vs linear and animal vs sire models for predicting direct and maternal genetic effects on calving difficulty in beef cattle. *J. Anim. Sci.* 79: 333-338.
 Tsuruta, S., and I. Misztal. 2006. THRGIBBSF90 for estimation of variance components with threshold and linear models. *Proc. 8th World Congr. Genet. Appl. Livest. Prod.*, Belo Horizonte, Brazil. Communication 27-31.
 Zhang, X., et al. 2015. Efficiency of Single-step GBLUP in Genomic Evaluation and GWAS in Broiler Chickens (Doctoral dissertation, University of Georgia).
 Zhang, X., et al. 2015. Comparison of traditional vs. genomic, and single vs. multiple trait analyses of broiler chicken mortality. *J. Anim. Sci.* 93(E-Suppl. 2): 844. (Abstr.)
<http://www.nationalchickencouncil.org/about-the-industry/statistics/u-s-broiler-performance>

