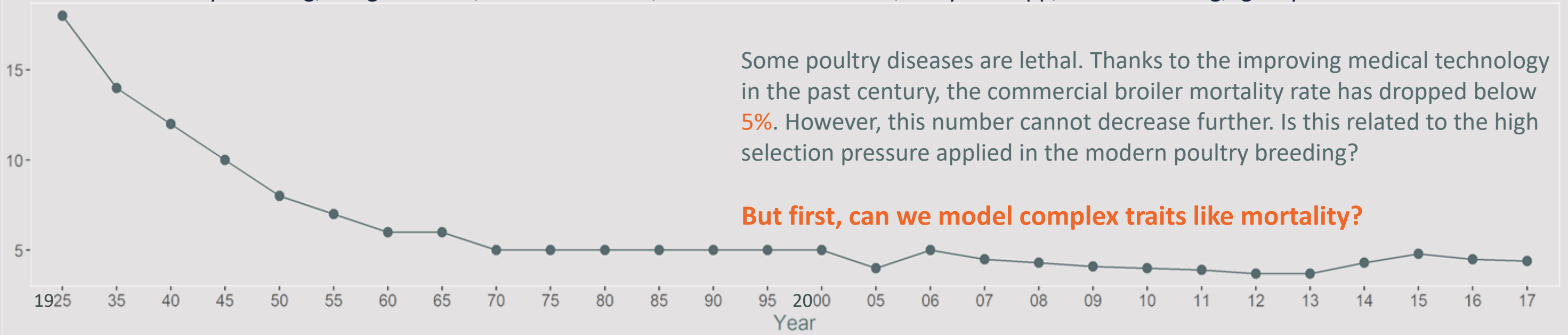


# Genetics of performance and disorder traits of broiler chicken

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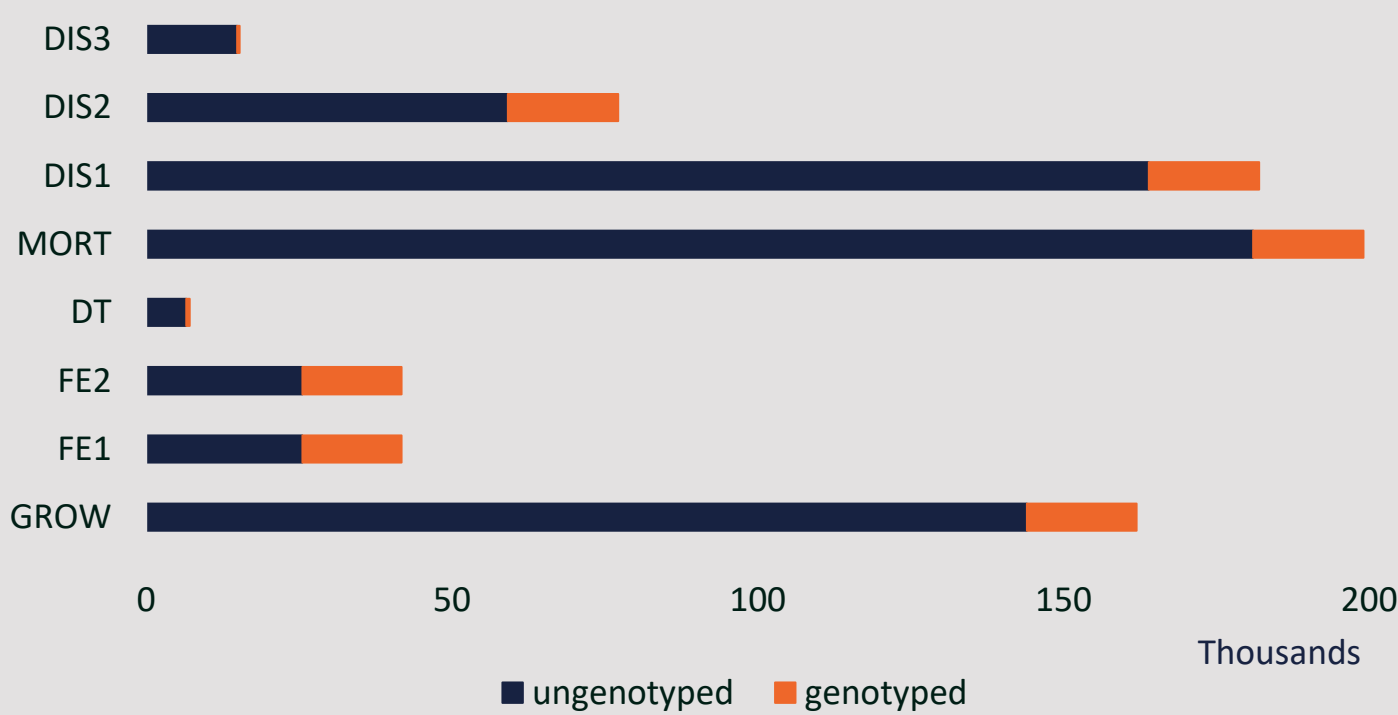
## Questions with analyses of health data

- 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?

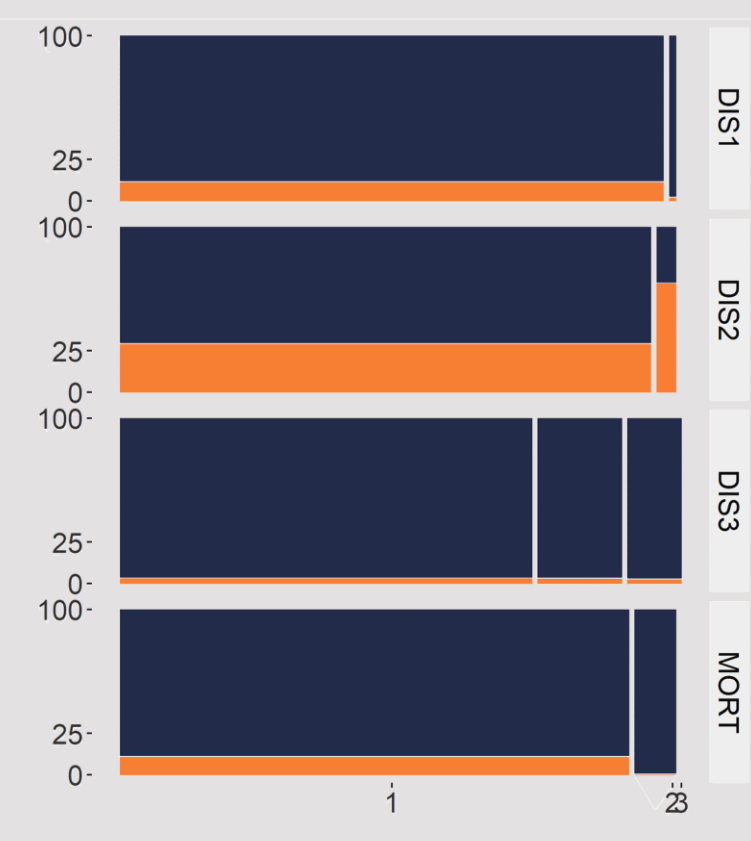
## Data

- 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

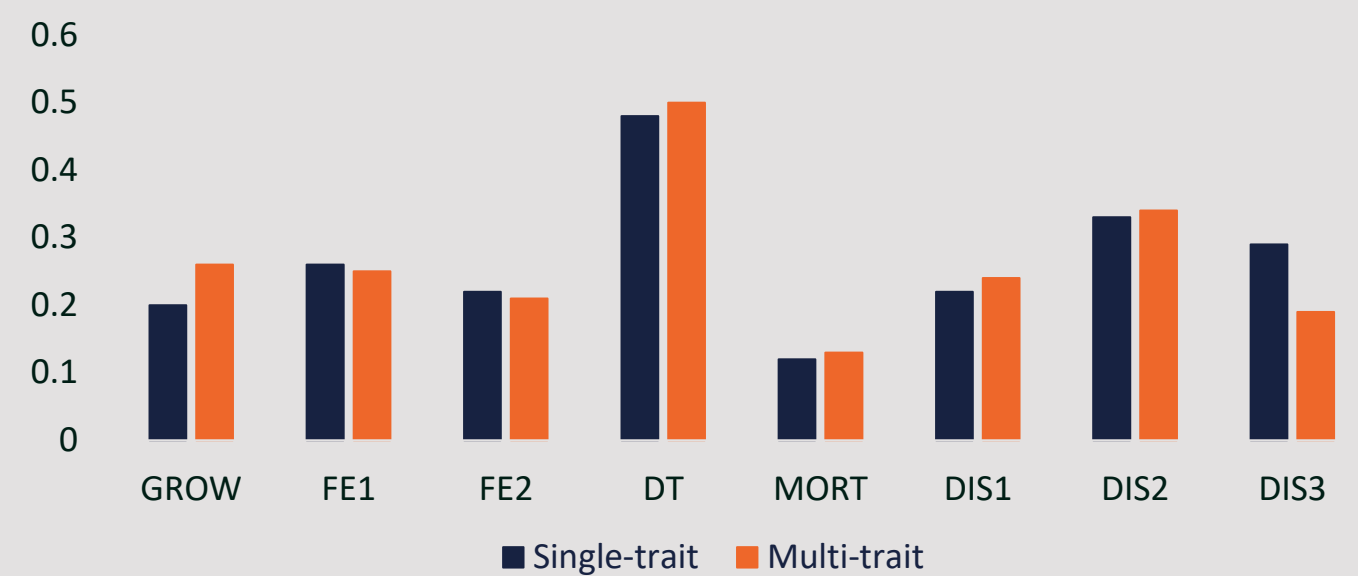
## Validation scheme

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

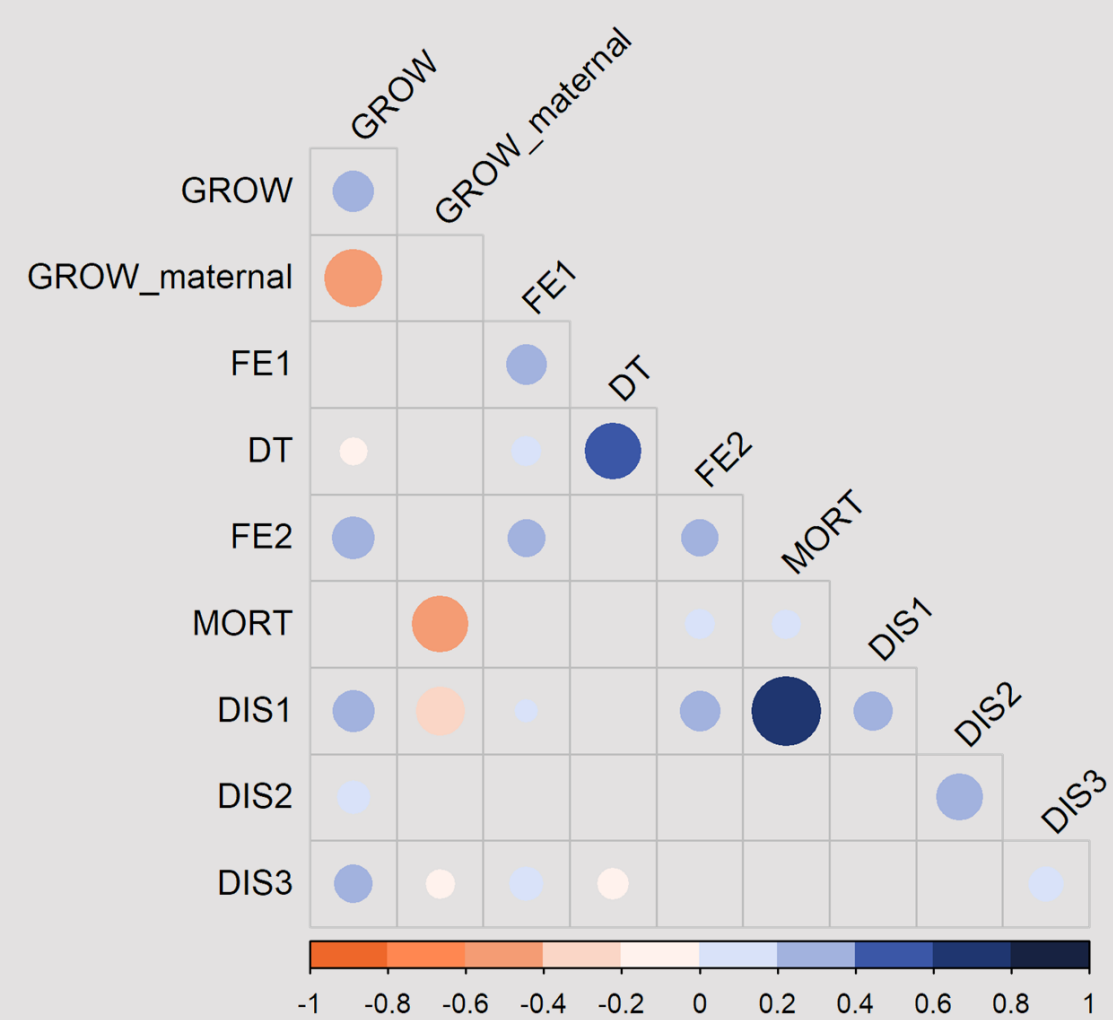
AIREMLF90 + THRGIBBS1F90: estimate (co)variance components  
 POSTGIBBSF90: test convergence for threshold models  
 BLUPF90 + THRGIBBS1F90 with fixed variance components: estimate EBV

Heritability comparison between the two models



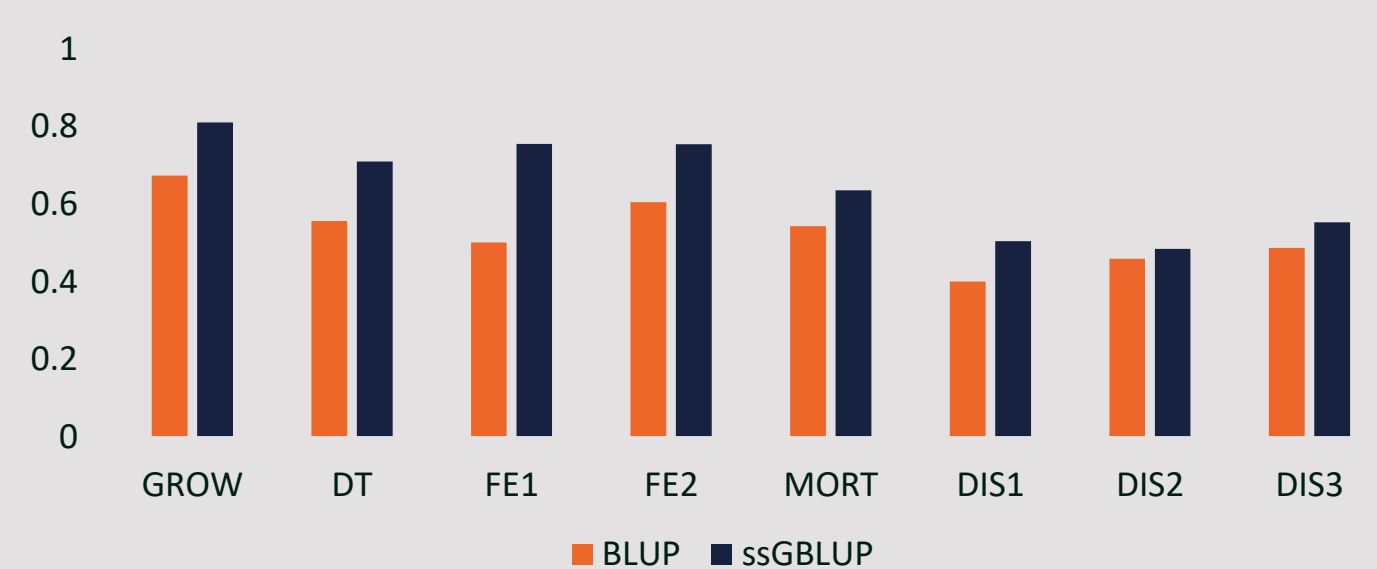
- Most traits have moderate to high heritability except **MORT** and **DIS3**.
- Multi-trait threshold-linear model better accounts for selection bias compared to single trait models.
- Heritabilities obtained using multi-trait threshold-linear model are more realistic and independent of incidences in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

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