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.)

Statistical models

<table>
<thead>
<tr>
<th>Model</th>
<th>Single trait</th>
<th>Multi-trait</th>
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</thead>
<tbody>
<tr>
<td>Threshold</td>
<td>Growth and feed efficiency traits</td>
<td></td>
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<tr>
<td></td>
<td>Mortality and disorder traits</td>
<td>All traits</td>
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<tr>
<td>Threshold-linear</td>
<td>-</td>
<td>Realized accuracy comparison with and without genotype</td>
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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 + THRGIBBSF90: estimate (co)variance components POSTGIBBSF90: test convergence for threshold models PPUBLIF90 + THRGIBBSF90 with fixed variance components: estimate EBV

References