Bayesian Inference of Multiple-Traits in a House Sparrow
Population using the Animal Model

Ingelin Steinsland & Henrik Jensen
Norwegian University of Science and Technology, Trondheim, Norway

Why Bayesian?
- Can easily access uncertainty for all quantities of interest, e.g. for heritability and genetic correlation estimates as well as response to selection.
- Uncertainty of estimated parameters are considered in the further analysis.

Data
- Most house sparrows of six islands off the coast of Northern Norway are ringed and measured since 1993.
- Blood samples taken ⇒ Genotyping of 9 microsatellites ⇒ Pedigree
- Traits measured on adult birds: tarsus length, wing length, bill depth, bill length, body mass, total badge and visual badge.

The Animal Model
For bird $i$ ($i = 1, \ldots, 1004$):

observed traits \(= \text{fixed} + \text{genetic} + \text{environmental} \)

\[ y_i = \beta_i + u_i + \epsilon_i \]

- \( y_i \): observations (traits), \( y_i = (y_{\text{tarsus}}, y_{\text{wing}}, \ldots) \)
- \( \beta_i \): “fixed effects” (sex, hatch year and hatch island), \( \beta_i \sim N(0, \sigma_{\beta}^2) \)
- \( u_i \): genetic effects, \( u_i \sim N(0, \Sigma_u) \)
- \( \epsilon_i \): Environmental effects: \( \epsilon_i \sim N(0, \Sigma_{\epsilon}) \)
- Conjugate prior for the genetic and environmental covariance matrices \( \Sigma_u \) and \( \Sigma_{\epsilon} \) (inverted Wishart).

Full conditional distributions:
- \( \beta_i, u_i, \epsilon_i \mid y_i, \Sigma_u, \Sigma_{\epsilon} \sim \text{MGMRF} \), a multivariate Gaussian Markov Random Field with constraints.
- \( \Sigma_u, \Sigma_{\epsilon} \mid \beta_i, u_i, \epsilon_i \sim \text{Inverted Wishart} \) (if no constraints)

Gibbs sampler
Use a Gibbs sampler with two blocks for making inference.

Algorithm
- For each iteration
  1. Sample \( (\beta_i, u_i, \epsilon_i) \) of dimension 25000!
  2. Sample \( (\Sigma_u, \Sigma_{\epsilon}) \) (Metropolis-Hasting step because of constraints)

Step 1 is the challenge:
- Sparse \( A^{-1} \Rightarrow \) cheaper calculations.
- Complexity \( \mathcal{O}(n^{1.7}) \), use GMRFLib.

Results
PS. This is ongoing work, the software is still tested
- The Gibbs sampler ran for 55000 iterations.
- All environmental correlation estimates are positive.
- Genetic correlation estimates for traits with low heritability (body mass) and/or many missing data (badges) are uncertain.

Summary
- Animal model of multiple traits = MGMRF model.
- Use a Gibbs sampler with only two blocks.
- Able to find uncertainty in heritability and genetic correlation.
- Can handle constraints, e.g. in “fixed effects”.

Further work
- Extend methodology to make inference about response to selection with uncertainty.