BayesAS and GBLUP models for genomic selection in Mink

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Genomic tested mink

- **Foulum brown line**

- **Phenotypes**
  - **Weight**, quality, under wool density, silketness
  - **Pelt length**, pelt quality, pelt density, pelt silketness

- **Genotypes**
  - 1800 mink
  - 28,336 markers

Accuracies and Conclusions

5-fold cross validation, 2014

Trait	ST-GBLUP	MT-GBLUP	ST-BayesAS	MT-BayesAS
Live weight	0.490	0.500	0.516	0.523
Pelt length	0.480	0.489	0.618	0.624

- Relatively high accuracies

- BayesAS better than BLUP
  - Indicates genes with large effects

- Not a clear tendency that MT is better than ST
  - We might have to few data