Alternative computing strategies

Simulate a small number of animals (no more than 10) for more markers than there are animals. This ensures that the genomic relationship matrix will be full rank.

Assume some variances for the markers and residual (e.g. 3 and 1).

Fit the marker effects model and obtain posterior means for the marker effects. You could do this using MCMC or by directly solving the mixed model equations.

Premultiply the posterior means for the marker effects by the genotype matrix in order to obtain predictions of the genomic breeding values for the animals.

Now form the genomic relationship matrix as $\mathbf{MM'}$. Invert this matrix (it should be full rank if you have more markers than animals). Fit the GBLUP equations which would be the same as the PBLUP equations except that $\mathbf{G^{-1}}$ is used in place of $\mathbf{A^{-1}}$.

Solve the GBLUP equations using MCMC or direct solution. You should obtain the same solutions for the animals as you obtained from the marker effects model.

Now compute the reliabilities for the breeding values of the animals from each of the marker effects and breeding values models. You should find that the reliabilities are not the same. This is the case because these models are not strictly equivalent. That is, they have different first and second moments.

Now compute the reliabilities for some linear functions that represent comparisons between the animals. You should find that these reliabilities are invariant to the choice of models.

Now try scaling the marker covariates in some other way. For example, use ($\mathbf{2\text{-}M}$) instead of $\mathbf{M}$, or $\mathbf{M\text{-}1}$ instead of $\mathbf{M}$. You should find that the reliabilities of linear functions of animals are invariant to these transformations. However, the approximations of reliabilities for models using genomic relationships are sensitive to the manner in which $\mathbf{M}$ is defined.

Centering $\mathbf{M}$ so that $\mathbf{M'1=0}$ will lead to a singular $\mathbf{G}$ so cannot be used in GBLUP unless $\mathbf{G}$ is regressed towards $\mathbf{A}$ or some other approach is used to remove the singularities. Similar ad-hoc tricks are sometimes used when there are more animals genotyped than there are markers.