note0501

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5.4 Example: A Genomic Model

Improper Uniform Prior Distributions for the Variance Components

On page 229, the prior distribution of $(\mu, \sigma_g^2, \sigma_g^2)$ of the genomic model is assumed to be improper uniform. As indicated in the book, this leads to a posterior distribution of the form

$$p(\mu, \alpha, \sigma_g^2, \sigma_e^2 | y) \propto p(\alpha | \sigma_g^2) p(y | \mu, \alpha, \sigma_e^2). \tag{5.45}$$

The fully conditional posterior distribution of σ_g^2 is

$$
\begin{aligned}
p(\sigma_g^2 | D) &\propto p(\alpha | \sigma_g^2) \\
&\propto (\sigma_g^2)^{-\left(\frac{n-1}{2}\right)} \exp\left(-\frac{\alpha' \Lambda^- \alpha}{2\sigma_g^2}\right),
\end{aligned}
\tag{5.51}
$$

as shown on page 232, that is proportional to the density of a scaled inverted chi-square distribution with $v_g = n - 3$ degrees of freedom and scale $S_g = (\alpha' \Lambda^- \alpha / v_g)$. A Monte Carlo extraction from this distribution is obtained by drawing from a chi-square distribution with v_g degrees of freedom and computing

$$\frac{\alpha'_{-n} \Lambda^{-1} \alpha_{-n}}{\chi^2(v_g)}.$$

Similarly, for σ_e^2, the fully conditional posterior distribution is of the form

$$
\begin{aligned}
p(\sigma_e^2 | D) &\propto p(y | \mu, \alpha, \sigma_e^2) \\
&= (\sigma_e^2)^{-\frac{n}{2}} \exp\left[-\frac{1}{2\sigma_e^2}(y - 1\mu - U\alpha)'(y - 1\mu - U\alpha)\right].
\end{aligned}
$$

This is proportional to the density of a scaled inverted chi-square distribution with $v_e = n - 2$ degrees of freedom and scale $S_e = (y - 1\mu - U\alpha)'(y - 1\mu - U\alpha)/v_e$. A Monte Carlo extraction from this distribution is obtained by drawing from a chi-square distribution with v_e degrees of freedom and computing

$$\frac{(y - 1\mu - U\alpha)'(y - 1\mu - U\alpha)}{\chi^2(v_e)}.$$

Scaled Inverted Chi-Square Prior Distributions for the Variance Components

A slightly different parametrisation that has the advantage of mitigating potential problems due to impropriety of posterior distributions that may arise with the use of improper priors of variance components (Hobert and Casella, 1996), is to assume the alternative prior specification

$$
\begin{aligned}
[\mu] &\propto \text{ constant,} \\
[\sigma_g^2 | S_g, v_g] &\sim \chi^{-2}(S_g, v_g), \\
[\sigma_e^2 | S_e, v_e] &\sim \chi^{-2}(S_e, v_e),
\end{aligned}
$$

where $\chi^{-2}(S_i, v_i)$, $i = g, e$, is the scaled inverted chi-square distribution with v_i degrees of freedom and scale parameter S_i whose density function is

$$
\begin{aligned}
p(\sigma_i^2 | S_i, v_i) &= \frac{(v_i/2)^{(v_i/2)}}{\Gamma(v_i/2)} S_i^{(v_i/2)} (\sigma_i^2)^{-\left(\frac{v_i}{2}+1\right)} \exp\left(-\frac{v_i S_i}{2\sigma_i^2}\right) \\
&\propto (\sigma_i^2)^{-\left(\frac{v_i}{2}+1\right)} \exp\left(-\frac{v_i S_i}{2\sigma_i^2}\right), \quad v_i, S_i > 0.
\end{aligned}
$$

This specification leads to the posterior density

$$
p(\mu, \alpha, \sigma_g^2, \sigma_e^2 | y) \propto p(\alpha|\sigma_g^2) p(y|\mu, \alpha, \sigma_e^2) p(\sigma_g^2 | S_g, v_g) p(\sigma_e^2 | S_e, v_e).
$$

The fully conditional posterior distribution of σ_g^2 is now

$$
\begin{aligned}
p(\sigma_g^2 | D) &\propto p(\alpha|\sigma_g^2) p(\sigma_g^2 | S_g, v_g) \\
&\propto (\sigma_g^2)^{-\left(\frac{n-1}{2}\right)} \exp\left(-\frac{\alpha'\Lambda^-\alpha}{2\sigma_g^2}\right) (\sigma_g^2)^{-\left(\frac{v_g}{2}+1\right)} \exp\left(-\frac{v_g S_g}{2\sigma_g^2}\right) \\
&= (\sigma_g^2)^{-\left(\frac{v_g^*}{2}+1\right)} \exp\left(-\frac{v_g^* S_g^*}{2\sigma_g^2}\right),
\end{aligned}
$$

where $v_g^* = (n-1) + v_g$ and $S_g^* = (\alpha'\Lambda^-\alpha + v_g S_g)/v_g^*$. A Monte Carlo extraction from this distribution is obtained by drawing from a chi-square distribution with v_g^* degrees of freedom and computing

$$
\frac{\alpha'_{-n}\Lambda^{-1}\alpha_{-n} + v_g S_g}{\chi^2(v_g^*)}.
$$

The fully conditional posterior distribution of σ_e^2 is

$$
\begin{aligned}
p(\sigma_e^2 | D) &\propto p(y|\mu, \alpha, \sigma_e^2) p(\sigma_e^2 | S_e, v_e) \\
&\propto (\sigma_e^2)^{-\frac{n}{2}} \exp\left[-\frac{1}{2\sigma_e^2}\varepsilon'\varepsilon\right] (\sigma_e^2)^{-\left(\frac{v_e}{2}+1\right)} \exp\left(-\frac{v_e S_e}{2\sigma_e^2}\right) \\
&= (\sigma_e^2)^{-\left(\frac{v_e^*}{2}+1\right)} \exp\left(-\frac{v_e^* S_e^*}{2\sigma_e^2}\right),
\end{aligned}
$$

where $\varepsilon = (y - 1\mu - U\alpha)$, $v_e^* = v_e + n$ and $S_e^* = (\varepsilon'\varepsilon + v_e S_e)/v_e^*$. A Monte Carlo extraction from this distribution is obtained by drawing from a chi-square distribution with v_e^* degrees of freedom and computing

$$\frac{\varepsilon'\varepsilon + v_e S_e}{\chi^2(v_e^*)}.$$

The `R`-code CODE1313 has been modified to specify scaled inverted chi-square prior distributions for the variance components of the genomic model as an option; the updated code can be found at https://github.com/SorensenD/SLGDS in the folder `Codes`.

References

Hobert, J. P. and G. Casella (1996). The effect of improper priors on Gibbs sampling in hierarchical linear models. *Journal of the American Statistical Association 91*, 1461–1473.