

The WinBUGS [1] code accompanies the paper “Bayesian models for pooling microarray studies with multiple sources of replications” by Erin M. Conlon, Joon J. Song and Jun S. Liu, *BMC Bioinformatics* (2006), **7**:247. Questions regarding this code can be addressed to the corresponding author Erin M. Conlon.

The simulated data for Example1 corresponds to a two-study model. In total there are 9 microarray slides, 3,000 genes and 10% differentially expressed genes. The first 300 genes are differentially expressed. The first 5 slides are for Study 1 as follow: slides 1-3 are for experiment 1, slide 4 is for experiment 2 and slide 5 is for experiment 3. Slides 6-9 are for Study 2 as follow: slides 6 and 7 are for experiment 1, slide 8 is for experiment 2 and slide 9 is for experiment 3.

The following model parameters were used to simulate the data using the *R* statistical language [2]. Study 1:  $\eta_{1g_0}^2 = 0.015$ , and  $c_1 = 66.67$ ; Study 2:  $\eta_{2g_0}^2 = 0.055$ , and  $c_2 = 15.45$ . For Study 1, the variance across slides was 0.0734 and across experiments was 0.0279. For Study 2, the variance across slides was 0.0200 and across experiments was 0.0203. The variance between studies was 0.0732 for all 3,000 genes and 0.3379 for the top 10% of genes.

In the WinBUGS code, the parameter  $T$  represents the parameter  $D_g$  in the paper. The posterior mean of  $T$  is used as the basis for inference. The  $dgamma(\alpha, \beta)$  distribution for the precision of the Normal distribution is equivalent to a Scaled-inverse-chi-square distribution for the variance with parameters  $\left(\alpha = \frac{\nu}{2}, \beta = \frac{\nu}{2} s^2\right)$ , where  $\nu$  = degrees of freedom and  $s^2$  = scale parameter.

#### References:

[1] The BUGS Project [<http://www.mrc-bsu.cam.ac.uk/bugs>].

[2] Ihaka R, Gentleman, R (1996) A language for data analysis and graphics. *J. Comput. Graphical Statist.* **5**: 299 - 314.