

Supplementary Materials

Legends

Table 1: Simulated log-normal survival data – marginal posterior probability of inclusion of relevant variables, $p(\gamma_j|\mathbf{X})$, at correlation levels of 0, 0.5 and 0.8 among covariates, with 20 true variables and small to medium regression coefficients.

Table 2: Simulated log-normal survival data – marginal posterior probability of inclusion of relevant variables, $p(\gamma_j|\mathbf{X})$, at correlation levels of 0, 0.5 and 0.8 among covariates, with 10 true variables and small regression coefficients.

Figure 1: Breast cancer microarray data – non-parametric estimation of log-survival distribution for uncensored cases.

Figure 2: Breast cancer microarray data – concordance of results across four MCMC runs. Each plot shows the difference in relative frequencies of inclusion for single genes between two MCMC chains.

β_j	$n = 100$			$n = 50$		
	$\rho = 0$	$\rho = 0.5$	$\rho = 0.8$	$\rho = 0$	$\rho = 0.5$	$\rho = 0.8$
0.3619	0.0165	0.0300	0.0363	0.0190	0.0147	0.0150
-0.4660	0.0157	0.0189	0.0205	0.0526	0.0247	0.0242
2.8749	1.0000	1.0000	0.9377	0.1353	0.1278	0.2042
-0.6910	0.0440	0.0238	0.0300	0.0293	0.0458	0.0302
0.1137	0.0126	0.0279	0.0234	0.0176	0.0316	0.0552
1.8491	0.0856	0.3112	0.0679	0.0263	0.1174	0.0363
2.0855	0.3696	0.1511	0.1242	0.2346	0.0807	0.0233
-1.5926	0.9546	0.9899	0.9846	0.0197	0.0199	0.0190
-2.8595	0.7469	0.7502	0.3622	0.5384	0.2262	0.1712
1.2526	0.0482	0.0232	0.0150	0.1508	0.0955	0.2442
-2.2763	0.8359	0.3481	0.6588	0.0361	0.0742	0.1637
2.9377	0.9953	0.9901	0.9244	0.0886	0.1181	0.0614
-0.8548	0.0665	0.1572	0.0770	0.0225	0.0218	0.0223
-1.9454	0.7513	0.7194	1.0000	0.0350	0.0188	0.0185
-1.8206	0.7100	0.4678	0.1612	0.0189	0.0224	0.0187
2.2215	0.8521	0.9852	0.3287	0.0174	0.0531	0.0983
-1.5112	0.0394	0.1322	0.0206	0.0162	0.0171	0.0104
2.2324	0.8149	0.9477	0.1587	0.4014	0.0934	0.2243
-1.2628	0.7229	0.4290	0.3771	0.0213	0.0464	0.0262
1.5962	0.1908	0.2210	0.0302	0.0687	0.6928	0.1835

Table 1: Simulated log-normal survival data: Marginal posterior probabilities of inclusion of relevant variables under different maximum correlation, ρ , among covariates. Case with 20 predictive variables and small to medium regression coefficients.

β_j	$n = 100$		
	$\rho = 0$	$\rho = 0.5$	$\rho = 0.8$
-0.7687	0.4859	0.5049	0.9908
-0.3275	0.0195	0.0065	0.0247
0.2412	0.0110	0.0081	0.0071
0.4747	0.7380	0.0151	0.0211
-0.6857	0.7769	0.5833	0.7925
0.1846	0.0159	0.0108	0.0216
0.5050	0.4084	0.0236	0.7810
-0.4189	0.0994	0.9302	0.0913
-0.4525	0.8251	0.0416	0.8679
0.8822	0.9906	1.0000	1.0000

Table 2: Simulated log-normal survival data: Marginal posterior probabilities of inclusion of relevant variables under different maximum correlation, ρ , among covariates. Case with 10 predictive variables and small regression coefficients.

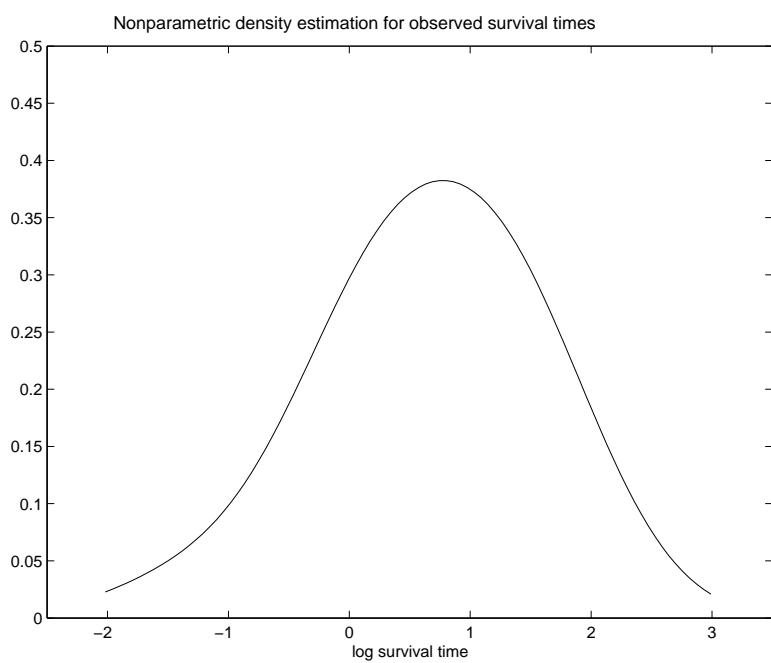


Figure 1: Breast cancer microarray data: non-parametric estimation of log-survival distribution for uncensored cases.

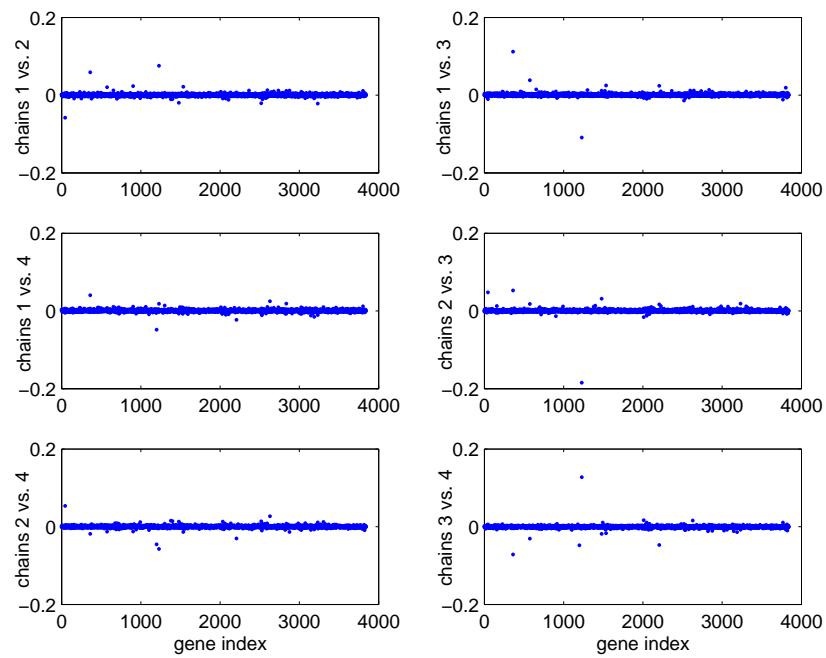


Figure 2: Breast cancer microarray data: concordance of results across four MCMC chains – differences in relative frequencies of inclusion for single genes.