Gelman and Rubin Diagnostics

Gelman and Rubin diagnostics (Gelman and Rubin; 1992; Brooks and Gelman; 1997) are based on analyzing multiple simulated MCMC chains by comparing the variances within each chain and the variance between chains. Large deviation between these two variances indicates nonconvergence.

Define $\{\theta^t\}$, where t = 1, ..., n, to be the collection of a single Markov chain output. The parameter θ^t is the tth sample of the Markov chain. For notational simplicity, θ is assumed to be single dimensional in this section.

Suppose you have M parallel MCMC chains that were initialized from various parts of the target distribution. Each chain is of length n (after discarding the burn-in). For each θ^l , the simulations are labeled as θ^l_m , where $t = 1, \ldots, n$ and $m = 1, \ldots, M$. The between-chain variance B and the within-chain variance B are calculated as

$$B = \frac{n}{M-1} \sum_{m=1}^{M} (\bar{\theta}_{m}^{\cdot} - \bar{\theta}_{.}^{\cdot})^{2}, \text{ where } \bar{\theta}_{m}^{\cdot} = \frac{1}{n} \sum_{t=1}^{n} \theta_{m}^{t}, \ \bar{\theta}_{.}^{\cdot} = \frac{1}{M} \sum_{m=1}^{M} \bar{\theta}_{m}^{\cdot}$$

$$W = \frac{1}{M} \sum_{m=1}^{M} s_m^2$$
, where $s_m^2 = \frac{1}{n-1} \sum_{t=1}^{n} (\theta_m^t - \bar{\theta}_m^t)^2$

The posterior marginal variance, $var(\theta | \mathbf{y})$, is a weighted average of W and B. The estimate of the variance is

$$\widehat{V} = \frac{n-1}{n}W + \frac{M+1}{nM}B$$

If all M chains have reached the target distribution, this posterior variance estimate should be very close to the within-chain variance W. Therefore, you would expect to see the ratio \widehat{V}/W be close to 1. The square root of this ratio is referred to as the *potential scale reduction factor* (PSRF). A large PSRF indicates that the between-chain variance is substantially greater than the within-chain variance, so that longer simulation is needed. If the PSRF is close to 1, you can conclude that each of the M chains has stabilized, and they are likely to have reached the target distribution.