Joint Approximation

In the context of LGMs, the true joint posterior for a set of observations \( y = \{y_i, i \in I\} \) and a joint set \( (x, \theta) \) of latent field and hyperparameters respectively is given by

\[
\pi(x, \theta | y) \propto \pi(\theta | y) \pi(x | \theta) \prod_{i \in I} \pi(y_i | x_i, \theta)
\]

The following posterior marginals are computed internally in INLA[4] using nested Laplace approximations

\[
\tilde{\pi}(y | \theta) \propto \tilde{\pi}(x, \theta | y) \big|_{x = \tilde{x}}
\]

\[
\tilde{\pi}(\theta | y) = \int \tilde{\pi}(\theta | y) \tilde{\pi}(y | \theta) d\theta.
\]

The joint \( \pi(x, \theta | y) \) can be approximated through numerical integration

\[
\tilde{\pi}(x, \theta | y) \approx \sum_k \tilde{\pi}_c(x | \theta, y) \tilde{\pi}(\theta | y) 1(\theta = \theta_k) \Delta_k
\]

where \( k \) describes the number of points in the grid exploration for achieving \( \tilde{\pi}(\theta | y) \).

Methodology for the Joint

How we get the approximation \( \tilde{\pi}(x, \theta | y) \)?

1. the hyperparameters are sampled from the integration points \( \{\theta, i = 1, \ldots, k\} \)
2. for each sampled configuration point a sample is drawn from \( \tilde{\pi}_c(x | \theta, y) \)

We can also extend the joint approximation \( \tilde{\pi}(x, \theta | y) \) exploiting Skew-Normal marginals \( \tilde{\pi}_c(x | \theta, y) \) for the approximation \( \tilde{\pi}(x | \theta) \) through a Gaussian copula [3]. This leads to new transformed values

\[
\tilde{x}_i = \sigma_i(\theta) F^{-1}_i \left[ \phi \left( \frac{x_i - \mu_i(\theta)}{\sigma_i(\theta)} \right) + \tilde{\mu}_i(\theta) \right]
\]

where \( x_i \sim N(\mu_i(\theta), \sigma_i(\theta)^2) \). This describes a Skewness Correction within the internal function inla.posterior.sample which extends the default mean correction applying the Standard Skew-Normal cumulative function.

Validating the Joint with SBC

Algorithm 1 SBC[1] applied on a subset \( x_S \)

**Input:** The joint posterior density \( \pi(x, \theta | y) \) with \( k \) fixed; number of replicated data sets \( M \) and dimension \( S \) for \( x_S = \{x_i, i \in S\} \)

**Output:** p-value for testing if the joint approximation is biased in the \( i^{th} \) marginal of \( x_S 

1. for \( j = 1 : M \) do
2. Solve \( Q \Sigma = I \);
3. Extract \( \Sigma_{SS} \) and solve \( \Sigma_{SS} \Sigma_{SS} = I_{SS} \);
4. Draw \( x_S^{(1)} \sim N(\mu_S, Q_S) \);
5. Generate a data set \( y \) from \( \pi(y | x_S, \theta_k) \);
6. Run the sampler on dataset \( y \) and get an approximation for the joint subset \( \pi_S(i) \);
7. for \( i = 1 : S \) do
8. Label \( \pi_S(i) \) as the \( i^{th} \) marginal component of \( x_S(i) \);
9. Label \( x_S^{(0)} \) as the \( i^{th} \) marginal component of \( x_S(0) \);
10. Get \( p_{ij} = Pr(x_S^{(0)} < x_S^{(1)} | x_S^{(0)} \sim \pi_S(i)) \);
11. end for
12. end for
13. for \( i = 1 : S \) do
14. Test the symmetry of the distribution of \( \{p_{ij}\} \);
15. If rejected the \( i^{th} \) marginal is biased
16. end for

References


