Bayesian inference model with nested effects to perform differential gene expression analysis from multi-level spatial transcriptomics data with multiple conditions

Lira Pi[1], Matt Ryals[1], Jialie Luo[1], Jake Gagnon[2]

[1]PharmaLex-US, 5280 Corporate Drive Suite C200, Frederick, MD 21703, USA.
[2]Analytics and Data Sciences, Biogen, Inc., 225 Binney St., Cambridge, MA 02142, USA.

Many cutting-edge statistical methods have been proposed to detect SVG (Spatially Variable Gene) from spatial transcriptomics (ST) data that consist of single or multiple tissue section(s). But the development of comparisons to identify DEG (Differentially Expressed Gene) has been relatively limited. Although a novel Bayesian technique called Splotch suggested a robust estimation of DE analysis by taking spatial-temporal coordinate into account, the complex model via MCMC implementation is computationally very expensive and hence infeasible to test large numbers of genes. To enable efficient, large-scale DE testing on spatial data, we propose a design for DE analysis using multi-level Bayesian inference model with nested effects by adopting R-INLA (Integrated Nested Laplace Approximation) scheme.