Perfect sampling for posterior landmark distributions
with an application to the detection of disease clusters

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Abstract

We study perfect sampling for the posterior distribution in a class of spatial point process models introduced by Baddeley and van Lieshout (1993). For Neyman–Scott cluster models, perfect sampling from the posterior is shown to be computationally feasible via a coupling-from-the-past type algorithm of Kendall and Møller. An application to data on leukemia incidence in upstate New York is presented.

1 Introduction

Bayesian cluster models based on spatial point processes were originally introduced by Baddeley and van Lieshout (1993), primarily for applications in computer vision. Disease clustering applications have also played a prominent role in the development of these models, as surveyed by Lawson and Clarke (1999). An important special case is the Neyman–Scott process in which the observations arise from a superposition of inhomogeneous Poisson processes associated with underlying landmarks (Neyman and Scott, 1972); van Lieshout (1995) focused on this case.

Markov chain Monte Carlo (MCMC) techniques are indispensable for the application of point process models in statistics, see, e.g., the survey of Møller (1999). Following the seminal work of Propp and Wilson (1996), Kendall and Møller (2000) developed a version of perfect simulation for locally stable point processes; see the article of Møller (2001) in this volume. This raises the possibility of constructing perfect samplers for the posterior distribution in Bayesian cluster models. Perfect samplers deliver an exact draw from the target distribution; this is a distinct advantage over traditional