Spatio-temporal Markov Random Field approach to risk mapping

Lamiae Azizi[1,2], Florence Forbes[1], Doyle Senan[1], Myriam Charras-Garrido[2] & David Abrial[2]

[1] *INRIA Rhône-Alpes & Laboratoire Jean Kuntzmann, Equipe Mistis, Inovallée, 655 av. de l'Europe, Montbonnot, 38334 Saint-Ismier Cedex.*
[2] *INRA, Unité dÉpidémiologie Animale, Centre de recherche de Clermont-Ferrand-Theix, 63122 Saint-Genès Champanelle.*

Abstract

Recent developments of statistical methodology have contributed to the rapid evolution of disease mapping in the last few decades. Most of the proposed methods focus on spatial models that perform risk smoothing. The risk estimates provided by the spatial models are supposed to be static in time, which is usually not realistic from a disease mapping point of view. Recent advances in disease mapping have focused on extending these models to the spatio-temporal context. Taking into account the spatio-temporal interactions allows us to obtain maps that can be compared in space and time. This comparison can give important information about the disease spread mechanisms. Within this framework, we propose to extend usual two-dimensional spatial MRF to three-dimensional spatio-temporal MRF. Our spatio-temporal MRF is a three-dimensional model in which the neighborhood is defined by a graph taking simultaneously into account the spatial and the temporal neighbors for each region of the domain under study. This approach allows to derive groups of geographical units homogeneous both in space and time. To encode the fact that two neighboring regions are similar, we propose a variant of the standard Potts model as the latter is not always appropriate in the disease mapping context. Estimation of the model parameters and partionning into homogeneous regions are accomplished simultaneously, using a Variational Expectation Maximisation (EM) algorithm based on a Mean-Field approximation. We also address the problem of finding good initial parameter values for this algorithm, in particular to deal with rare diseases for which with risk values and numbers of observed cases can be very small. To illustrate our procedure, we perform tests on simulated data with properties similar to the targeted real data.