Map Comparison for the Evaluation of Spatial Bayesian Models

C. Robertson[1], J.A. Long[2], T.A. Nelson[3], F. Nathoo[4]

[1]Wilfrid Laurier University, 3rd Floor Arts Bldg,
75 University Ave West, Waterloo, ON, Canada, N2L 3C5
Telephone: (+1.519.884.0710 ext.4757)
Email:crobertson@wlu.ca

[2]University of Victoria,
Victoria, BC, Canada
Telephone: (+1.250.853.3271)
Email: jlong@uvic.ca

[3]University of Victoria,
Victoria, BC, Canada
Telephone: (+1.250.472.5620)
Email: trisalyn @uvic.ca

[4]University of Victoria,
Victoria, BC, Canada
Telephone: (+1.250.472.4693)
Email: nathoo@uvic.ca

1. Introduction

Spatial Bayesian models are increasingly developed to model spatially explicit processes in ecology and epidemiology. Spatial models of ecological spread processes, such as an infectious disease propagating through a human population or an invasive species spreading through a landscape, often have spatially distributed model parameters that account for variation spread rate (i.e., deviations from a global model such as a travelling wave)(e.g., Smith et al. 2002, Wheeler & Waller 2008). Local parameters are spatially varying coefficients with an estimated value at each spatial unit. In Bayesian models, each spatial parameter has a full posterior distribution available for inference. One advantage of aforementioned models is that each spatial unit has parameter estimates that can be used to provide spatial context about the spread process.

Validation of spatial models presents unique challenges. Typical validation approaches include some form of spatially global comparison between observed and expected values, such as the chi-squared (χ^2) test (e.g., Dice 1945). One initial problem with a global approach is that obtaining the true value for a theoretical spatial parameter describing some property of a complex ecological process is often difficult. Typically, assumptions are made based on results of field experiments taken over limited spatial scales (e.g., dispersal range in mark-recapture studies). Second, there may be spatial structure in the way that parameters themselves fit the data, and understanding the spatial structure of parameter estimates may reveal systematic errors that can be used to further refine the model. These two issues form the basis for the current research.

We employ a spatially explicit approach to the evaluation of spatial parameters in a Bayesian model-checking framework. Two approaches, posterior predictive checks

(Gelman 2005) and map comparison (Wang et al. 2004) are combined to provide evidence of model fit that includes information on spatial structure. We examine spatial structure when comparing maps of parameter estimates from a spatially local model describing the rate of spread across a study area. Our appraoch addresses the second problem of evaluating spatially local models. The first problem, knowing the true values of the parameters, is handled via Bayesian model checking. Simulation-estimation is a common approach whereby the fitted model is used to estimate new data which are then used to test model fit via a measure of discrepancy (Gelman et al. 1996). A case study using simulated data describing different spatial-temporal spread patterns is used to highlight our methodology.

2. Methods

2.2 Simulation-Estimation

In Bayesian modelling , uncertainties in parameter estimates are evident in the properties of the posterior distribution. If values are tightly clustered around the mean, there is strong evidence that the mean is a good estimate. Checking the model as a whole is more complicated. Posterior predictive checking is an approach whereby random draws from the posterior distributions of all model parameters are used to simulate new data sets, generally denoted as Y_{rep}, which we define as simulated replicates of the observed data. The Y_{rep} can be used to measure model fit with a general discrepancy measure such as the Deviance Information Criterion (Spiegelhalter et al. 2002), or more specific model test statistics. We re-estimate the model using the Y_{rep} datasets and compare the parameter estimates with known true values (i.e., those used to simulate the data). The comparison of these values at each spatial location forms the central problem of this research.

2.3 Map Comparison

The objective of map comparison here is to uncover similarities (or differences) in the spatial structure of expected and observed parameter maps. Examining spatial structure provides improved confidence in observed parameter estimates over purely aspatial comparisons. We selected the structural similarity (SSIM) index as an exploratory statistic for comparing maps (Wang et al. 2004). SSIM incorporates a Gaussian weighting function, to assess similarity across spatially local *regions*. SSIM does not require direct pixel to pixel comparisons, which ignore spatial structure and often produces overly critical comparison statistics (Pontius 2000). SSIM considers three components for map comparison: luminance, contrast, and structure, relating to local differences in mean, variance, and covariance respectively (Wang et al. 2004). Note that these three components are relatively independent, and changes in one component will not necessarily affect others (Wang et al. 2004). SSIM takes the following spatially local form, computing a similarity statistic for each spatial unit:

$$SSIM\,(x,y) = [l(x,y)]^{\alpha} \cdot [c(x,y)]^{\beta} \cdot [s(x,y)]^{\gamma} \quad (1)$$

where (x,y) denotes the spatial unit, l the luminance component, c the contrast component, and s the structure component (Wang et al. 2004). The exponents α, β, and γ can be used to weight individual components, with default values taken as $\alpha = \beta = \gamma = 1$. We report a mean global statistic for each of the three components and overall similarity. When two maps are identical, SSIM = 1, and values decrease as similarity decreases.

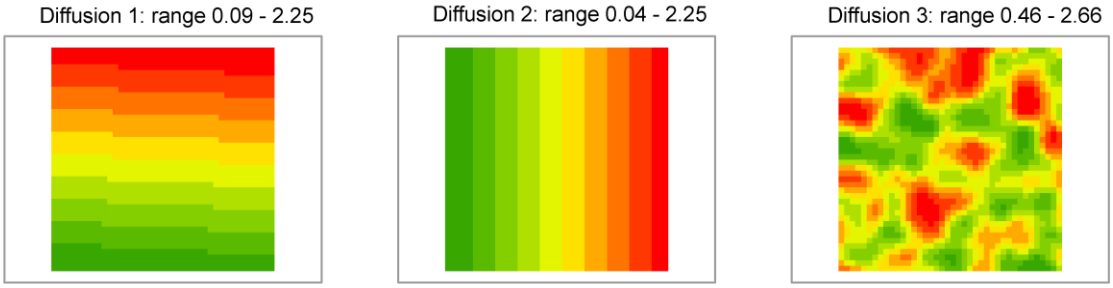
Expected and observed maps with low similarity in the luminance component are interpreted differently from those low in the structure component.

2.4 Case Study

To demonstrate the importance of spatial structure in model validation we implement the SSIM statistic comparison of data simulated from a model with spatially local parameters describing a spreading process. We specify a logistic model for a spatial spread process similar to Smith et al. (2002) where the logistic probability of an uninfected region (i) becoming infected at time t is defined as:

$$log\{p_{it}/(1- p_{it})\} = \mu_t + \lambda_i NN_{[i,t-1]} \quad (2)$$

Here μ_t is a time varying parameter representing a baseline probability of infection; $NN_{[i,t-1]}$ is the number of infected neighbors of region i at time $t-1$; and λ_i is a spatially varying parameter quantifying the impact of infected regions on their uninfected neighbors. Our research here focuses on investigating the spatial structure of differences between the true values for λ and those estimated by the model. Values for spread were simulated as in Figure 1.These values were used to simulate data describing a spreading process on 40x40 grids over 100 time periods. As such, these represent the true values against which model estimates from the Y_{rep} data are compared via map comparison



a) b) c)

Figure 1. True values of diffusion parameters (λ) in three scenarios of a spatial spread process: a) Λ_1, b) Λ_2, c) Λ_3. A range of μ-scenarios (M_1, M_2, M_3) were also used (not shown), generating nine spread scenario combinations.

3. Preliminary Results

Results of map comparison analysis on three types of diffusion spread represented in Figure 1.

	M	Luminance	Contrast	Structure	SSIM
	1	0.924	0.864	0.889	0.710
Λ_1	2	0.231	0.739	0.890	0.152
	3	0.951	0.881	0.899	0.753
	1	0.681	0.870	0.898	0.532
Λ_2	2	0.214	0.872	0.930	0.174
	3	0.824	0.858	0.897	0.634
	1	0.974	0.827	0.697	0.561
Λ_3	2	0.903	0.726	0.692	0.454
	3	0.972	0.856	0.720	0.599

Table 1. Map comparison analysis results comparing estimated diffusion to the true diffusion used to simulate data.

3. Discussion

Map comparison revealed that in some cases observed spread values were different from expected in terms of magnitude but the general spatial pattern of spread (structure component) was retrieved. The SSIM method enables creation of maps of local differences in mean, variance, and covariance, providing information on the spatial structure and differences in each which can be further explored to reveal systematic deficiencies in model development. Models that fit well based on aspatial validation tests do not always demonstrate good spatial agreement, warranting such a spatial approach. The approach we present for model evaluation is relatively simple and can be easily implemented with existing models (not exclusively Bayesian) providing valuable and unique insight on how the spatial structure of parameters relate to model performance.

4. References

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