Comment on paper:
"Bayesian analysis of agricultural field experiments"
by Julian Besag and David Higdon

Carmen Fernández and Peter Green (University of Bristol):

We congratulate the authors for their insightful perspective on the use of spatially smoothing stochastic models for agricultural field experiments, and for demonstrating the host of opportunities for inference that the Bayesian setting provides.

In current research with Sylvia Richardson (INSERM, France), we are developing stochastic models for geographical epidemiology, where spatial patterns are often an issue. Part of our work focusses on mixture modelling with spatially correlated allocation variables, and we wonder whether this could provide an interesting alternative to the approach in this paper. As an illustration, we reexamine the "El Batán" dataset. We model the response (yield) as

$$y_{ij} = \tau_{t_{ij}} + \beta_i + \mu_{z_{ij}} + \sigma\,\varepsilon_{ij}\,;\; i = 1, \ldots, 3\,;\, j = 1, \ldots, 50,$$

where i indexes the column, j the plot within the column, t_{ij} the variety employed, and $\tau_1, \ldots, \tau_{50}$ and $\beta_1, \ldots, \beta_3$ respectively denote the centred variety and column effects. The difference with the authors' formulation is that in place of a fertility surface plus noise, we aim to explain the remaining variability in the data through a mixture of k normally distributed components, with means $\mu_1 < \ldots < \mu_k$ and common variance σ^2, which captures both plot error and the non-spatial component of fertility. Separation of the last two elements could be done through prior assumptions, but will be avoided here. All the parameters are assigned weakly informative priors. The allocation variables $\{z_{ij}\}$ are assumed independent for different columns. Within each column, the use of a limiting case of a logistic auto-normal multinomial allocation scheme, controlled by a smoothing parameter $h > 0$, ensures that the prior probability that two plots are allocated to the same component decreases as they are further apart. Although here we apply a one-dimensional adjustment, our methodology is directly applicable to arbitrary graphs. In addition, it allows borrowing strength from all plots allocated to the same component, regardless of their location.

Figures 1-3 display results from our analysis, using the authors' hierarchical-t formulation as benchmark for comparison. Fertility patterns are smoother with the hierarchical-t model, although the posterior means for fertility effects are not entirely comparable with the quantities $E(\beta_i + \mu_{z_{ij}}|y)$ plotted for the spatial mixture specifications, as explained in the previous paragraph. Inference on variety effects is very similar in all cases.

Although this is not how we would interpret our model, it is formally equivalent to a block model where the allocations of plots to blocks (*i.e.* components) are not asserted a priori but data-dependent. Model averaging leads to the relatively smooth fertility patterns we have displayed.

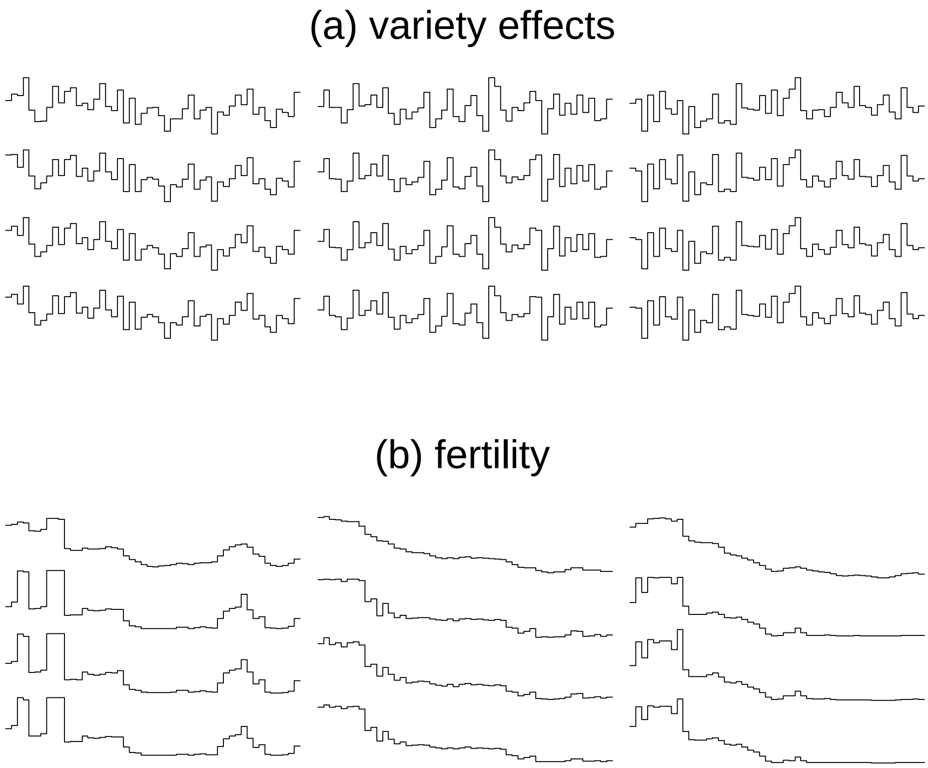

Fig. 1. Hierarchial-t (top line) versus spatial mixture (three bottom lines), respectively using $(k = 3, h = 100)$, $(k = 6, h = 100)$ and $(k = 6, h = 1000)$: (a) posterior means for variety effects; (b) posterior means for fertility effects (hierarchical-t) and $E(\beta_i + \mu_{z_{ij}}|y)$ (spatial mixtures)

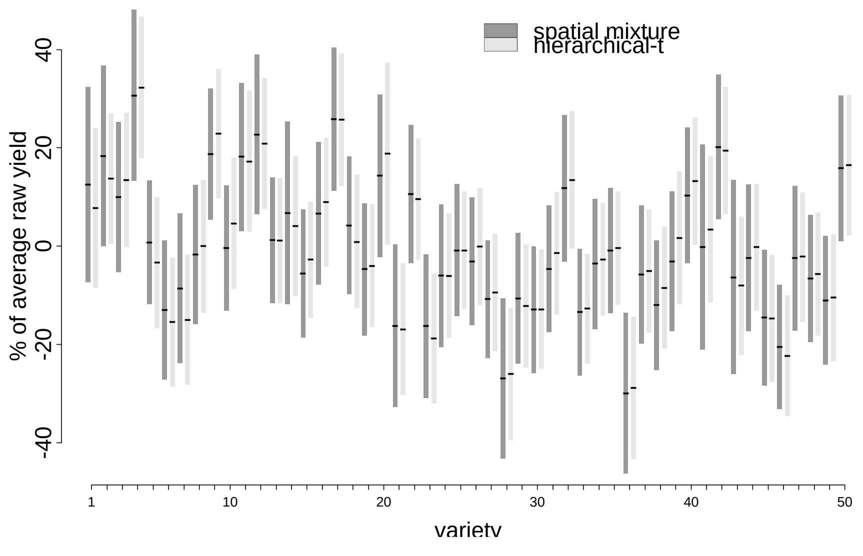

Fig. 2. Posterior 90% credible intervals for variety effects under hierarchical-t and spatial mixture with $k = 6, h = 100$

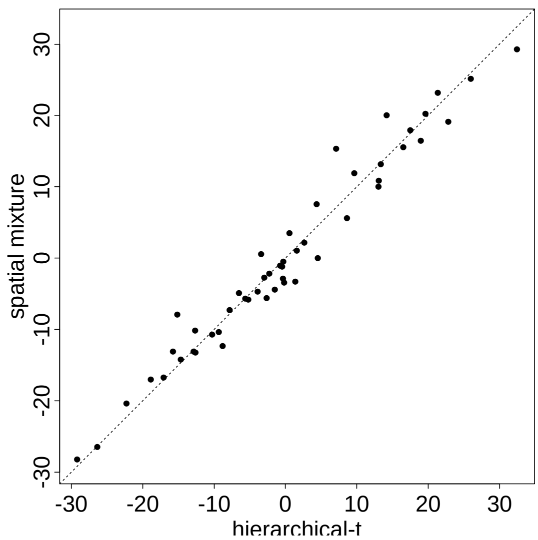

Fig. 3. Posterior means of variety effects under hierarchical-t and spatial mixture with $k = 6, h = 100$