Joint Analysis of Multivariate Spatial Count and Zero-Heavy Count Outcomes

Using Common Spatial Factor Models

Cindy Feng  
U Saskatchewan

Charmaine Dean  
U Western Ontario

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Outline

- Introduction
- Joint outcome analysis
- Testing for common spatial structure
- Precision gains through joint modeling
- Concluding remarks
Introduction

- Joint modelling
  - Account for dependence between longitudinal and time-to-event outcomes

- Scientific objectives for joint modelling
  - Inferences about longitudinal outcome, while accounting for informative drop-out time
  - Inferences about survival outcome, while accounting for association between the two outcomes
  - Interested in the relationship between the two outcomes
## General model formulation

### Longitudinal model

\[ Y_i(t) = \mu_i(t) + W_{1i}(t) + \varepsilon_i(t) \]

### Survival model

\[ \lambda_i(t) = \lambda_0(t) \exp \{ X_i \beta + W_{2i}(t) \} \]

- **\( \mu_i(t) \)** - mean response
- **\( \varepsilon_i(t) \)** - measurement error
- **\( X \)** - covariate
- **\( W(t)=[W_{1i}(t) \ W_{2i}(t)] \)** - bivariate latent Gaussian process
General model formulation

<table>
<thead>
<tr>
<th>Longitudinal model</th>
<th>[ Y_i(t) = \mu_i(t) + W_{1i}(t) + \varepsilon_i(t) ]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Survival model</td>
<td>[ \lambda_i(t) = \lambda_0(t) \exp { X_i \beta + W_{2i}(t) } ]</td>
</tr>
</tbody>
</table>

- **Shared Frailties**

  \[ W_{2i}(t) = \gamma W_{1i}(t) + V_i \]
Shared Frailties

- Used in a variety of contexts
- Dunson (2009), for example, for linking glmms
Let $y_{ij} | \mu_{ij} \sim \text{Poisson}(\mu_{ij})$ for $i = 1, \cdots, n$ regions and $j = 1, \cdots, J$ outcomes. The model can be written as:

$$\log(\mu_{ij}) = \alpha_j + \log(E_{ij}) + \gamma_j b_i + h_{ij}$$

- $b = (b_1, \cdots, b_n)' \sim \text{MVN}(0, \sigma_b^2 (D - W)^{-1})$: spatially correlated random effects.
- $\gamma_j$: factor loading for the shared spatial component with $\gamma_1 \equiv 1$.
- $h_j = (h_{1j}, \cdots, h_{nj})' \sim \text{MVN}(0, \sigma_h^2 I)$: spatially uncorrelated random effects.
The joint posterior distribution is expressed as

\[
p(\alpha, b, h, \gamma, \sigma_b^2, \sigma_{h_1}^2, \cdots, \sigma_{h_J}^2|Y) \propto L(Y|\alpha, b, h, \gamma)p(b|\sigma_b^2)p(h|\sigma_h^2)
\]

\[
p(\alpha)p(\gamma)p(\sigma_b^2)p(\sigma_{h_1}^2) \cdots p(\sigma_{h_J}^2).
\]

The first term is the conditional likelihood,

\[
L(Y|\alpha, b, h, \gamma) \propto \exp \left[ - \sum_{i=1}^{n} \sum_{j=1}^{J} E_{ij} \exp(\alpha_j + \gamma_j b_i + h_{ij}) \right]
\]

\[
\times \prod_{i=1}^{n} \prod_{j=1}^{J} [E_{ij} \exp(\alpha_j + \gamma_j b_i + h_{ij})]^{y_{ij}}.
\]

The second and third terms are the distributions of \( b \) and \( h \) respectively and the remaining terms are the prior distributions.
Ontario Lung Cancer

- **Outcome:** total observed counts of mortality from lung cancer for males and females over the period 1995 to 2002.
- **Sub-regions:** 37 local health areas (LHA) in Ontario.
Let $m$ and $f$ index males and females, respectively. The common spatial factor model is,

$$\begin{align*}
\log(\mu_{im}) &= \alpha_m + \log(E_{im}) + b_i + h_{im} \\
\log(\mu_{if}) &= \alpha_f + \log(E_{if}) + \gamma \cdot b_i + h_{if}
\end{align*}$$

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Mean</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\gamma$</td>
<td>1.145</td>
<td>(0.866, 1.466)</td>
</tr>
<tr>
<td>$\sigma^2_b$</td>
<td>0.059</td>
<td>(0.032, 0.116)</td>
</tr>
<tr>
<td>$\sigma^2_h_m$</td>
<td>0.0038</td>
<td>(0.0018, 0.0094)</td>
</tr>
<tr>
<td>$\sigma^2_h_f$</td>
<td>0.0050</td>
<td>(0.0023, 0.0129)</td>
</tr>
</tbody>
</table>
Ontario Lung Cancer

**Table**: $p_D$ and DIC for competing models in the analysis of Ontario lung cancer incidence.

<table>
<thead>
<tr>
<th>Type</th>
<th>Model</th>
<th>$p_D$</th>
<th>DIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shared</td>
<td>M1</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;i&lt;/sub&gt; + h&lt;sub&gt;im&lt;/sub&gt;</td>
<td>56.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + γ · b&lt;sub&gt;i&lt;/sub&gt; + h&lt;sub&gt;if&lt;/sub&gt;</td>
<td></td>
</tr>
<tr>
<td></td>
<td>M2</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;i&lt;/sub&gt;</td>
<td>56.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + γ · b&lt;sub&gt;i&lt;/sub&gt; + h&lt;sub&gt;if&lt;/sub&gt;</td>
<td></td>
</tr>
<tr>
<td></td>
<td>M3</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;i&lt;/sub&gt; + h&lt;sub&gt;im&lt;/sub&gt;</td>
<td>56.6</td>
</tr>
<tr>
<td></td>
<td></td>
<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + γ · b&lt;sub&gt;i&lt;/sub&gt;</td>
<td></td>
</tr>
<tr>
<td></td>
<td>M4</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;i&lt;/sub&gt;</td>
<td>38.8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + γ · b&lt;sub&gt;i&lt;/sub&gt;</td>
<td></td>
</tr>
<tr>
<td>Separate</td>
<td>M5</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;im&lt;/sub&gt; + h&lt;sub&gt;im&lt;/sub&gt;</td>
<td>68.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + b&lt;sub&gt;if&lt;/sub&gt; + h&lt;sub&gt;if&lt;/sub&gt;</td>
<td></td>
</tr>
<tr>
<td></td>
<td>M6</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;im&lt;/sub&gt;</td>
<td>68.8</td>
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<td></td>
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<td></td>
</tr>
<tr>
<td></td>
<td>M7</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;im&lt;/sub&gt; + h&lt;sub&gt;im&lt;/sub&gt;</td>
<td>69.4</td>
</tr>
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<td></td>
<td></td>
<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + b&lt;sub&gt;if&lt;/sub&gt;</td>
<td></td>
</tr>
<tr>
<td></td>
<td>M8</td>
<td>log(μ&lt;sub&gt;im&lt;/sub&gt;) = α&lt;sub&gt;m&lt;/sub&gt; + logE&lt;sub&gt;im&lt;/sub&gt; + b&lt;sub&gt;im&lt;/sub&gt;</td>
<td>70.1</td>
</tr>
<tr>
<td></td>
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<td>log(μ&lt;sub&gt;if&lt;/sub&gt;) = α&lt;sub&gt;f&lt;/sub&gt; + logE&lt;sub&gt;if&lt;/sub&gt; + b&lt;sub&gt;if&lt;/sub&gt;</td>
<td></td>
</tr>
</tbody>
</table>
Power of the Test of Common Spatial Structure

Hypothesis test: $H_0 : \gamma = 0$ versus $H_1 : \gamma \neq 0$. 

![Graph 1](image1.png)

![Graph 2](image2.png)
Table: The average absolute relative bias (ABIAS) of estimated risks, as well as their average standard deviation (ASE) and average root mean squared error (ARMSE), along with average exceedance probability (APREX) for regions with true relative risks greater than one. The expected disease counts are scaled by the inverse of \( \delta \). The true value of \( \sigma^2_h \) is 0.01.

<table>
<thead>
<tr>
<th>( \delta )</th>
<th>( \sigma^2_{b} = 0.1 )</th>
<th>( \sigma^2_{b} = 0.5 )</th>
<th>( \sigma^2_{b} = 1 )</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Joint</td>
<td>Separate</td>
<td>Joint</td>
</tr>
<tr>
<td>( \delta = 1 )</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABIAS</td>
<td>0.073</td>
<td>0.073</td>
<td>0.135</td>
</tr>
<tr>
<td>ASE</td>
<td>0.044</td>
<td>0.047</td>
<td>0.044</td>
</tr>
<tr>
<td>ARMSE</td>
<td>0.099</td>
<td>0.099</td>
<td>0.174</td>
</tr>
<tr>
<td>APREX</td>
<td>0.767</td>
<td>0.757</td>
<td>0.790</td>
</tr>
<tr>
<td>( \delta = 50 )</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABIAS</td>
<td>0.113</td>
<td>0.122</td>
<td>0.155</td>
</tr>
<tr>
<td>ASE</td>
<td>0.132</td>
<td>0.136</td>
<td>0.190</td>
</tr>
<tr>
<td>ARMSE</td>
<td>0.196</td>
<td>0.205</td>
<td>0.296</td>
</tr>
<tr>
<td>APREX</td>
<td>0.567</td>
<td>0.560</td>
<td>0.634</td>
</tr>
<tr>
<td>( \delta = 100 )</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABIAS</td>
<td>0.130</td>
<td>0.136</td>
<td>0.199</td>
</tr>
<tr>
<td>ASE</td>
<td>0.143</td>
<td>0.145</td>
<td>0.221</td>
</tr>
<tr>
<td>ARMSE</td>
<td>0.219</td>
<td>0.225</td>
<td>0.349</td>
</tr>
<tr>
<td>APREX</td>
<td>0.528</td>
<td>0.523</td>
<td>0.590</td>
</tr>
</tbody>
</table>
Zero Inflation

- The presence of excess zeros is a special case of overdispersion,
- Excess zeros may arise from unsuitable habitat or immunity of individuals,
- Difference in excess zeros and sampling zeros.

Zero-inflated Models for Count Data

- Mixture model and two-part model.

Zero-inflated Models for Correlated Data

- GEE or random effect model.

Zero-inflated Models for Spatially Correlated Data

- Spatial correlation in the counts and in the probabilities for subjects coming from the component of excess zeros.
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Zero-inflated Models for Spatially Correlated Data

- Spatial correlation in the counts and in the probabilities for subjects coming from the component of excess zeros.
Suppose the response variable $Y_{ij}$ is distributed as

$$Y_{ij} | z_{ij} = \begin{cases} 0 & \text{if } z_{ij} = 1, \\ \text{Poisson}(\mu_{ij}) & \text{if } z_{ij} = 0 \end{cases}$$

The probability distribution functions are

$$Pr(Y_{ij} = y_{ij} ) = \begin{cases} \pi_{ij} + (1 - \pi_{ij})e^{-\mu_{ij}} & \text{if } y_{ij} = 0, \\ (1 - \pi_{ij})\frac{e^{-\mu_{ij}}\mu_{ij}^{y_{ij}}}{y_{ij}!} & \text{if } y_{ij} > 0 \end{cases}. $$
The common spatial factor model is

\[ \log(\mu_{ij}) = \alpha_j + \gamma_j b_i + h_{ij}, \quad \logit(\pi_{ij}) = \zeta_j + \omega_j d_i, \]

where

\[ b = (b_1, \cdots, b_n)^T \sim \text{MVN}(0, \sigma_b^2 (D - W)^{-1}), \]
\[ d = (d_1, \cdots, d_n)^T \sim \text{MVN}(0, \sigma_d^2 (D - W)^{-1}), \]
\[ h_j = (h_{1j}, \cdots, h_{nj})^T \sim \text{MVN}(0, \sigma_{h_j}^2 I) \]
Common Spatial Factor Model for Zero-Inflated Data

The joint posterior distribution of the parameters is:

\[ p(\alpha, \zeta, b, d, h, \gamma, \omega, \sigma_b^2, \sigma_d^2|Y) \propto L(Y|\alpha, \zeta, b, d, h, \gamma, \omega) p(\alpha)p(\zeta)p(\gamma)p(\omega) \]

\[ p(b|\sigma_b^2)p(d|\sigma_d^2)p(h|\sigma_h^2)p(\sigma_b^2)p(\sigma_d^2)p(\sigma_h^2), \quad (1) \]

The first term is the conditional likelihood,

\[ L(Y|\alpha, \zeta, b, d, h, \gamma, \omega) \propto \prod_{i=1}^{n} \prod_{j=1}^{J} \left[ l(y_{ij} = 1) \{ \pi_{ij} + (1 - \pi_{ij})e^{\mu_{ij}} \} \right. \]

\[ + \left. l(y_{ij} = 0) \left\{ (1 - \pi_{ij})\frac{e^{-\mu_{ij}}(\mu_{ij})^{y_{ij}}}{y_{ij}!} \right\} \right], \quad (2) \]

To avoid computational instability, normal priors can be assigned on \( \alpha, \zeta, \gamma \) and \( \omega \) with a moderately large variance and uniform distribution with again moderately large variance for \( \sigma_b, \sigma_d \) and \( \sigma_h \).
Comandra blisters rust (CBR) is a disease of hard pines that is caused by a fungus growing in the inner bark; CBR infects pines but needs an alternate host plant (AHP) to spread from one pine to another.

- Plantation of lodgepole pine trees over a $124 \times 64$ grid;
- Each grid is 1.5 meters $\times$ 1.5 meters;
- 1000 trees susceptible to CBR infection were randomly sampled over the field;
- In each grid cell, two outcomes:
  1. counts of lesions on each tree,
  2. counts of disease host plants in each grid cell.
Comandra Blister Rust Study

[Images of Comandra Blister Rust on plants and a person holding a map next to a small tree in a forest.]
Comandra Blister Rust Study

Lesion Counts

Counts of Disease Host Plants
Comandra Blister Rust Study

Lesion counts

<table>
<thead>
<tr>
<th>Frequency</th>
<th>Counts</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0</td>
<td>66.6%</td>
</tr>
<tr>
<td>0.1</td>
<td>33.3%</td>
</tr>
</tbody>
</table>

Counts of disease host plants

<table>
<thead>
<tr>
<th>Frequency</th>
<th>Counts</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00</td>
<td>81.1%</td>
</tr>
<tr>
<td>0.05</td>
<td>18.9%</td>
</tr>
<tr>
<td>0.10</td>
<td>6.1%</td>
</tr>
</tbody>
</table>
Let $L$ and $H$ index counts of lesion and counts of disease host plants, respectively. The zero-inflated common spatial factor model is then,

\[
\begin{align*}
\log(\mu_{Hi}) &= \alpha_H + b_i + h_{Hi} \\
\log(\mu_{Li}) &= \alpha_L + \gamma \cdot b_i + h_{Li}
\end{align*}
\]

where

\[
\begin{align*}
b &= (b_1, \cdots, b_n)^T \sim \text{MVN}(0, \sigma_b^2(D - W)^{-1}), \\
d &= (d_1, \cdots, d_n)^T \sim \text{MVN}(0, \sigma_d^2(D - W)^{-1}), \\
h_L &= (h_{1L}, \cdots, h_{nL})^T \sim \text{MVN}(0, \sigma_{h_L}^2 I), \\
h_H &= (h_{1H}, \cdots, h_{nH})^T \sim \text{MVN}(0, \sigma_{h_H}^2 I),
\end{align*}
\]
### Table: Posterior summaries

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Mean</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\gamma$</td>
<td>0.25</td>
<td>(0.23, 0.33)</td>
</tr>
<tr>
<td>$\omega$</td>
<td>1.42</td>
<td>(0.03, 5.88)</td>
</tr>
<tr>
<td>$\sigma_b^2$</td>
<td>532.49</td>
<td>(354.53, 793.72)</td>
</tr>
<tr>
<td>$\sigma_{hH}^2$</td>
<td>0.89</td>
<td>(0.35, 2.57)</td>
</tr>
<tr>
<td>$\sigma_{hL}^2$</td>
<td>0.20</td>
<td>(0.11, 0.37)</td>
</tr>
</tbody>
</table>

**Remark:** Spatial similarity of the random process exists across the spatial maps through a latent random effect and zero mass components of the two distributions are also correlated though a latent spatially varying process.
Posterior Medians of the Shared Random Effects

posterior median for $b$

posterior median for $d$
## Joint Modeling of Tree Infection and Host Plants

### Table: pD and DIC for competing models

<table>
<thead>
<tr>
<th>Type</th>
<th>Model</th>
<th>Poisson distribution</th>
<th>Excess Zero</th>
<th>pD</th>
<th>DIC</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Shared</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
| M1       | log(\(\mu_{ih}\)) = \(\alpha_H + b_i + h_{ih}\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + \gamma_b \cdot b_i + h_{il}\) | logit(\(\pi_{ih}\)) = \(\zeta_H + d_i\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L + \gamma_d \cdot d_i\) | 530.0  | 3457.5 |
| M2       | log(\(\mu_{ih}\)) = \(\alpha_H + b_i + h_{ih}\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + \gamma_b \cdot b_i + h_{il}\) | logit(\(\pi_{ih}\)) = \(\zeta_H\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L\) | 534.8  | 3462.6 |
| M3       | log(\(\mu_{ih}\)) = \(\alpha_H + b_i\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + \gamma_b \cdot b_i\) | logit(\(\pi_{ih}\)) = \(\zeta_H + d_i\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L + \gamma_d \cdot d_i\) | 461.0  | 3505.5 |
| M4       | log(\(\mu_{ih}\)) = \(\alpha_H + b_i\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + \gamma_b \cdot b_i\) | logit(\(\pi_{ih}\)) = \(\zeta_H\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L\) | 462.4  | 3508.7 |
| **Separate** |       |                      |             |       |       |
| M5       | log(\(\mu_{ih}\)) = \(\alpha_H + b_{ih} + h_{ih}\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + b_{il} + h_{il}\) | logit(\(\pi_{ih}\)) = \(\zeta_H + d_{ih}\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L + d_{il}\) | 658.0  | 3645.0 |
| M6       | log(\(\mu_{ih}\)) = \(\alpha_H + b_{ih} + h_{ih}\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + b_{il} + h_{il}\) | logit(\(\pi_{ih}\)) = \(\zeta_H\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L\) | 654.9  | 3659.8 |
| M7       | log(\(\mu_{ih}\)) = \(\alpha_H + b_{ih}\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + b_{il}\) | logit(\(\pi_{ih}\)) = \(\zeta_H + d_{ih}\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L + d_{il}\) | 513.6  | 3721.7 |
| M8       | log(\(\mu_{ih}\)) = \(\alpha_H + b_{ih}\)  
          |       | log(\(\mu_{il}\)) = \(\alpha_L + b_{il}\) | logit(\(\pi_{ih}\)) = \(\zeta_H\)  
          |       |                       | logit(\(\pi_{il}\)) = \(\zeta_L\) | 547.2  | 3723.7 |
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Spatio-temporal extension of the common spatial factor model would be interesting.

Gains may be obtained by assuming the shared frailty term is spatially uncorrelated, when it is not clear what neighborhood spatial structure is appropriate.

Shared frailty models have found utility in many applications.
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