Multiresolution Decomposition of Areal Count Data

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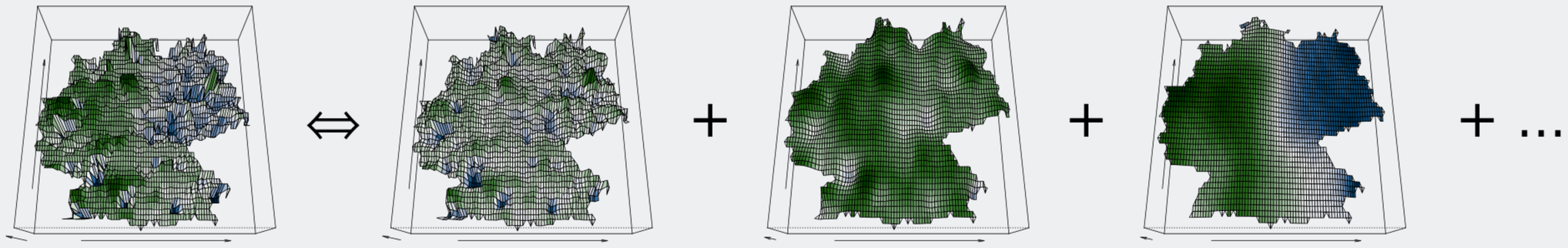
Multiresolution Decomposition, an Image Processing Method to Answer:

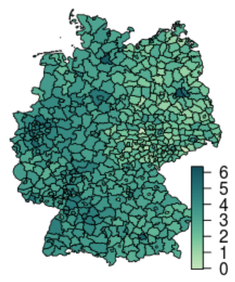
- Can we identify different features on different scales in regularly gridded data?
- Where are the predominant scale-dependent features located?



Rasterized areal count data.

Approach to Decompose Areal Count Data

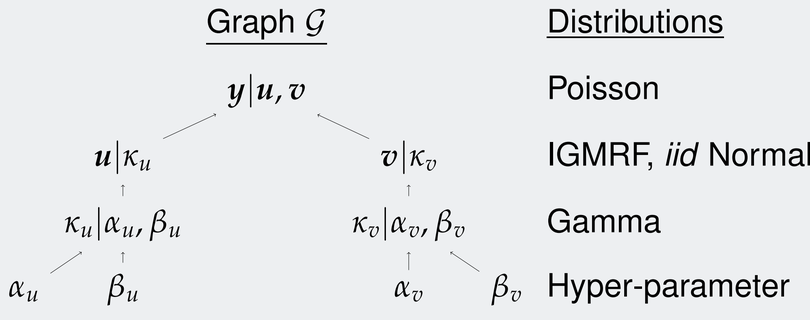
- Extending an image processing method[1] for incomplete, discrete and irregularly gridded data.
- Incorporating the Besag–York–Mollié model, to model count data and add a priori demographic knowledge.[2]
- Exploiting the sparse structure of the precision matrix for efficient computing.[3]
- Showing the method's feasibility on the oral cavity cancer log-counts per district in Germany.[4]
- The extended method consists of the three steps outlined below.



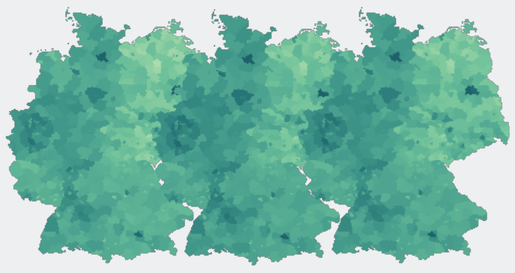
Oral cavity cancer log-counts in Germany. The counts were collected over 1986–1990.

1. Spatial Field Resampling

- Assume the observed field $\boldsymbol{y}$ compounds of the true field $\boldsymbol{x}$ and additive noise $\boldsymbol{\varepsilon}$.
- Let $\boldsymbol{y}$ be the observed and $\boldsymbol{e}$ the known expected counts. The Poisson's rate is defined as $\boldsymbol{e} \cdot \exp(\boldsymbol{u} + \boldsymbol{v})$, whereat u is the spatially correlated log-relative risk and v a noise term.
- Resample $\boldsymbol{u}$ and $\boldsymbol{v}$ with a Metropolis-Hastings procedure.
- Reconstruct the log-counts with $\boldsymbol{e} \cdot \exp(\boldsymbol{u} + \boldsymbol{v})$, since the Poisson rate is equivalent to its mean.



Besag–York–Mollié (BYM) model.



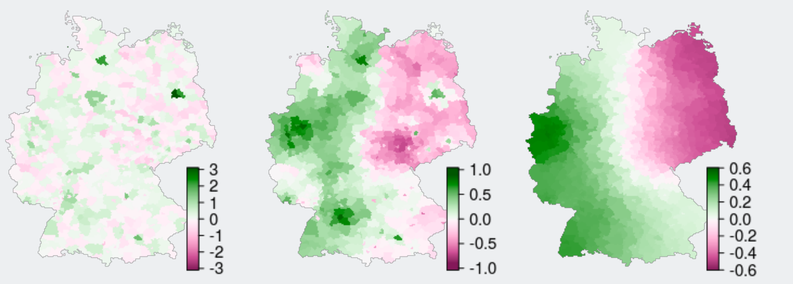
Reconstructed log-counts.

2. Calculating Differences Between Smooths

- We use a penalty smoother $\boldsymbol{S}_\lambda = (\mathbf{I} + \lambda \boldsymbol{R})^{-1}$.
  $\boldsymbol{R}$ is the sparse precision matrix from the IGRMF (BYM model) based on adjacency relations.
  λ denotes the smoothing parameter such that $0 = \lambda_1 < \lambda_2 < \ldots < \lambda_L = \infty$.
- The spatial field $\boldsymbol{x}$ can be written as differences of smooths, say details $\boldsymbol{z}_i$,

$$\boldsymbol{x} = \sum_{i=1}^{L-1} (\boldsymbol{S}_{\lambda_i}\boldsymbol{x} - \boldsymbol{S}_{\lambda_{i+1}}\boldsymbol{x}) + \boldsymbol{S}_{\lambda_L}\boldsymbol{x} = \sum_{i=1}^{L} \boldsymbol{z}_i.$$

- λ's are chosen such that the differences between smooths are maximal.



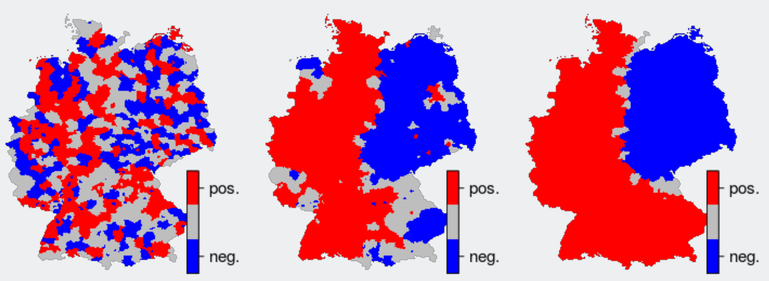
Scale dependent details summarized by their posterior means: $\mathrm{E}(z_1|\boldsymbol{y})$, $\mathrm{E}(z_2|\boldsymbol{y})$ and $\mathrm{E}(z_3|\boldsymbol{y})$ (left to right).

3. Credibility Analysis

In pointwise probability maps, for each detail z_i, the locations s are divided into three different subsets in which the components $z_{i,s}$ differ jointly credible from zero, with credibility level $\alpha = 95\%$.

$$I^{\text{blue}} = \{s|\mathrm{P}(\boldsymbol{z}_{i,s} > 0|\text{data}) \geq \alpha\}, \quad I^{\text{red}} = \{s|\mathrm{P}(\boldsymbol{z}_{i,s} < 0|\text{data}) \geq \alpha\} \quad \text{and} \quad I^{\text{gray}} = I \setminus \left(I^{\text{blue}} \cup I^{\text{red}}\right).$$

The corresponding maps indicate with blue jointly credible negative and with red jointly credible positive areas.



Pointwise probability maps for details z_1, z_2 and z_3 (left to right).

References

[1] Holmström L., Pasanen L., Furrer R., Sain S. R. (2011).Scale space multiresolution analysis of random signals. *Computational Statistics & Data Analysis* **55**, 2840–2855.

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[3] Furrer R., Sain. S. R. (2010). A sparse matrix R package with emphasis on MCMC methods for Gaussian Markov random fields. *Journal of Statistical Software* **36**, 1–25.

[4] Knorr-Held L., Raßer G. (2000). Bayesian detection of clusters and discontinuities in disease maps. *Biometrics* **56**, 13–21.