

Joint spatial modeling of gender-specific cancer data at subregional level

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Introduction

Reference area

- Lower Saxony (German state):
 - ▶ ~47 624km²
 - ▶ ~8 million inhabitants
 - ▶ Division in 384 RMUs (regional monitoring units, see Fig. 1)

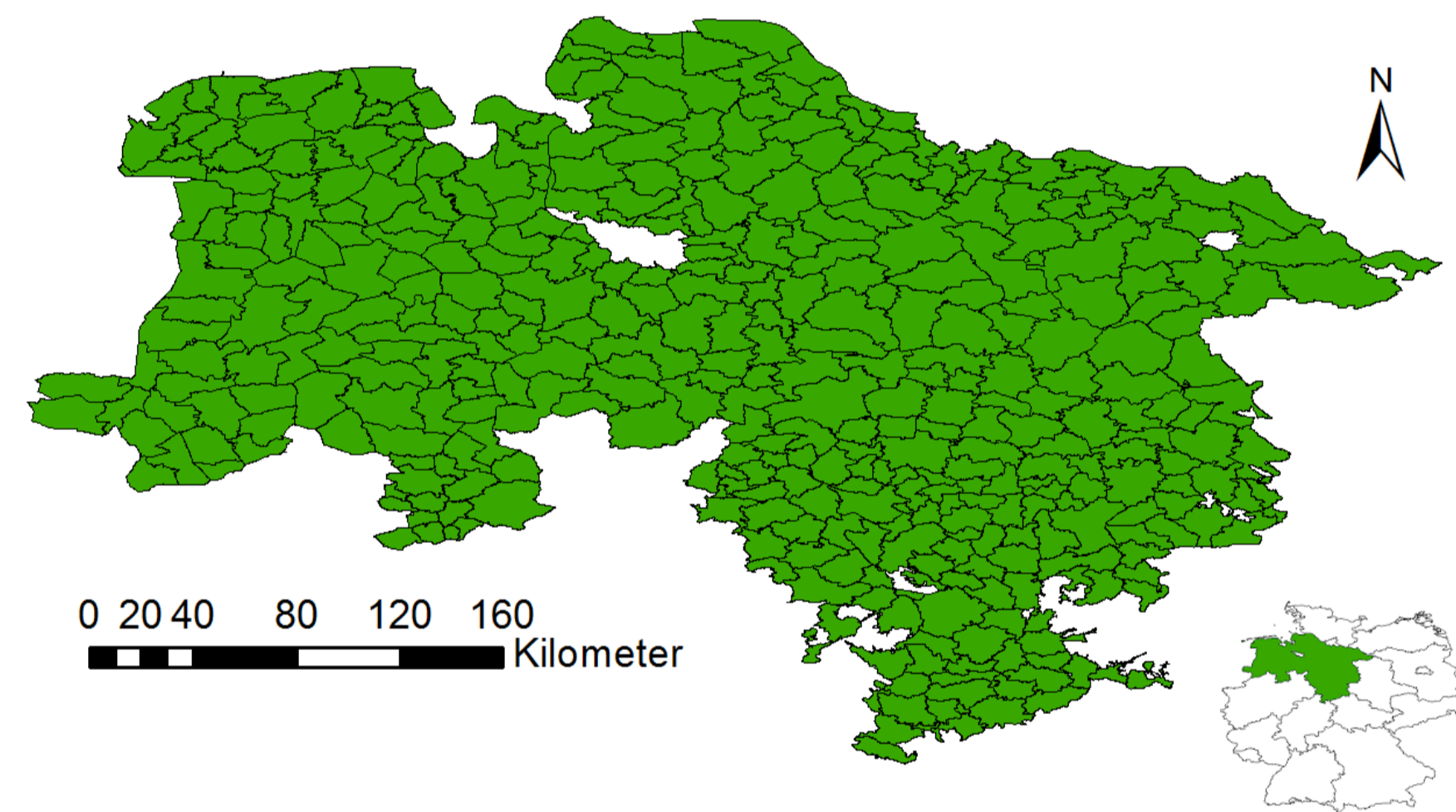


Figure 1: Lower Saxony, division in RMUs.

Conditions studied

- Breast cancer (ICD-10 C50)
 - ▶ Most common cancer diagnosed in females in Lower Saxony (32.1% of all cancers diagnosed, in 2011)[1]
 - ▶ Among others, reproductive and genetic factors increase the risk
 - ▶ Mammography screening started in 2005
- Prostate cancer (ICD-10 C61)
 - ▶ Most common cancer diagnosed in males in Lower Saxony (28%, in 2011)
 - ▶ Hormonal and genetic factors increase the risk, but risk factors in general not well studied
 - ▶ High incidence might be due to PSA (prostate-specific antigen) screening
- Similarities between breast and prostate cancer and common risk factors have been reported (e.g. genetic mutations) [2]
- Implementation and access to screening are potential determinants of the spatial and temporal distributions [3, 4]

Data source

- Age-specific (5-year age groups) female breast and male prostate cancer cases at RMU level during 2008–2012
- Age-specific population data at RMU level during 2008–2012
- Shapefiles, defining the neighbouring structure of the RMUs

Objective

- Analyse potential common spatial pattern for gender-specific (female breast and male prostate) cancer risk by joint spatial modeling of gender-specific cancer in Lower Saxony during 2008–2012

Methods

- Indirect age-standardization using overall population of Lower Saxony as a reference
- Jointly model disease-specific incidence in space by *shared-component model* [5, 6, 7]
 - ▶ Model formulation covers disease-specific spatially structured and unstructured random effects and a shared component measuring the geographical association between the two diseases
 - ▶ Bayesian spatial Poisson regression model

$$y_{ij} \sim \text{Pois}(E_{ij}\theta_{ij})$$

$$\log(\theta_{i1}) = \alpha_1 + \varphi_{i1} + \phi_i \delta$$

$$\log(\theta_{i2}) = \alpha_2 + \varphi_{i2} + \frac{\phi_i}{\delta}$$

where y_{ij} are the observed number of cancer cases in the i^{th} RMU ($i=1, \dots, 384$) for the j^{th} disease ($j=1$ for prostate and $j=2$ for breast cancer), E_{ij} the corresponding expected cases, θ_{ij} the relative risk, α_j the disease-specific intercept, φ_{ij} the convolution prior [8] (the sum of a disease-specific spatially structured and an unstructured random effect), ϕ_i the spatial shared-component and δ a scaling factor.

- Spatial random effects were assumed to follow a conditional autoregressive prior distribution
- Model formulation and fitting based on Markov chain Monte Carlo was done in WinBUGS (Imperial College and MRC, London, UK)

Results

- Minor shared spatial pattern but considerable amount of spatial breast cancer incidence variation explained by shared component
- Greater contribution of shared component to breast cancer incidence (indicated by relative risk ratio estimate <1)
- Disease-specific and shared variability higher for breast cancer
- Information of urbanization level (defined by population density) did not improve model performance (indicated by the Deviance Information Criterion)

Outlook

- Refined study of areas showing common risk distribution
- Consideration of information on hospital density or screening services/accessibility as covariates
- Joint modeling at larger geographical scale such as country level

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