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

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**Introduction**

**Reference area**
- Lower Saxony (German state):
  - \(47,624 \text{ km}^2\)
  - \(8\) million inhabitants
  - Division in \(384\) RMUs (regional monitoring units, see Fig. 1)

**Conditions studied**
- Breast cancer (ICD-10 C50)
  - Most common cancer diagnosed in females in Lower Saxony (32.1\% of all cancers diagnosed, in 2011\cite{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) \cite{2}
- Implementation and access to screening are potential determinants of the spatial and temporal distributions \cite{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**

**Methods**
- Indirect age-standardization using overall population of Lower Saxony as a reference
- Jointly model disease-specific incidence in space by shared-component model \cite{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
  
  \[ y_{ij} \sim \text{Pois}(E_i \theta_j) \]

  \[ \log(\theta_i) = \alpha_1 + \phi_1(i) + \phi_0 \]

  \[ \log(\theta_j) = \alpha_2 + \phi_2(j) + \phi_0 \]

  where \(y_{ij}\) are the observed number of cancer cases in the \(i\)th RMU in the \(j\)th disease (\(j=1\) for prostate and \(j=2\) for breast cancer), \(E_i\) the corresponding expected cases, \(\theta_i\) the relative risk, \(\alpha_j\) the disease-specific intercept, \(\phi_0\) the convolution prior \(\Phi\) (the sum of a disease-specific spatially structured and an unstructured random effect), \(\phi_1\) the spatial shared-component and \(\phi_2\) a scaling factor.

**Results**
- 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)

**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

**References**

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