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REVIEW

A systematic review of Bayesian spatial–temporal models on cancer incidence and mortality

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Abstract

Objectives This study aimed to review the types and applications of fully Bayesian (FB) spatial–temporal models and covariates used to study cancer incidence and mortality.

Methods This systematic review searched articles published within Medline, Embase, Web-of-Science and Google Scholar between 2014 and 2018.

Results A total of 38 studies were included in our study. All studies applied Bayesian spatial–temporal models to explore spatial patterns over time, and over half assessed the association with risk factors. Studies used different modelling approaches and prior distributions for spatial, temporal and spatial–temporal interaction effects depending on the nature of data, outcomes and applications. The most common Bayesian spatial–temporal model was a generalized linear mixed model. These models adjusted for covariates at the patient, area or temporal level, and through standardization.

Conclusions Few studies (4) modelled patient-level clinical characteristics (11%), and the applications of an FB approach in the forecasting of spatial–temporally aligned cancer data were limited. This review highlighted the need for Bayesian spatial-temporal models to incorporate patient-level prognostic characteristics through the multi-level framework and forecast future cancer incidence and outcomes for cancer prevention and control strategies.

Keywords Bayesian · Spatio-temporal · Cancer · Systematic review

Abbreviations

PRISMA	Preferred reporting items for systematic review and meta-analysis
PQL	Penalized quasi-likelihood
EB	Empirical Bayes
FB	Fully Bayesian
MCMC	Markov chain Monte Carlo
INLA	Integrated nested Laplace approximations
IQR	Interquartile range
GLMM	Generalized linear mixed models
CAR	Conditional autoregressive
BYM	Besag, York and Mollie
APC	Age–period cohort
AFT	Accelerated failure time
ANOVA	Analysis of variance
SLA	Second-level area
ESM	Electronic supplementary material

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00038-020-01384-5) contains supplementary material, which is available to authorized users.

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Introduction

Globally, cancer is still the leading cause of mortality (Cancer Research UK 2019). In 2018, over 17 million new cancer cases were diagnosed, and its incidence is projected to increase by 62% by 2040 with a growing ageing population (Cancer Research UK 2019). Cancer incidence and outcomes vary over space (geographical areas) and time, but there are still challenges in understanding this variation

(Goodman et al. 2014). Key obstacles for cancer modelling involve wide year-to-year fluctuations and a small number of cases in sparsely populated areas leading to unstable estimates.

The traditional statistical approach, frequentist inference, is based on the likelihood function, which is used to derive parameter estimates. Bayesian approaches use probability to measure uncertainty in predictions or inference estimates and incorporate spatial and temporal dependencies through the specification of prior distributions (Austin et al. 2002). Bayesian approaches can overcome modelling issues prevalent in cancer research (non-normality, small sample size, missing data, clustered data structure). Spatio-temporal analyses that simultaneously investigate space–time variation can identify disease patterns that persist or evolve systematically over time across spatial units, through series of maps to identify areas or periods with extreme risks (Bernardinelli et al. 1995). Understanding this variation and its attributable factors will help to contribute to our understanding of disease aetiology and prevention, monitor healthcare access and plan healthcare interventions. Bayesian spatial–temporal models have proved to be beneficial and provide more convincing evidence of true variations than separate spatial or time-series or cross-sectional analysis (Bernardinelli et al. 1995; Carroll et al. 2016, 2018; Knorr-Held 2000; Lawson et al. 2017; Waller et al. 1997). Misleading results could be obtained using traditional non-spatial models in data which reveal a spatial or temporal correlation since individuals in the same area or year tend to have similar characteristics, and these need to be accounted for in the analysis (Banerjee and Dey 2005; Dormann 2007). In the last two decades, due to improvements in the quality and maturity of clinical registries and advancements in computing speed and capacities over the years, studies have developed Bayesian spatial–temporal models which incorporate spatial correlation, temporal correlation and space–time interaction. Thus, Bayesian spatial–temporal models investigating variation in cancer incidence and mortality outcomes across areas over time are integral in contributing to cancer control and management as they provide a unified approach to the modelling process. However, to the best of our knowledge, there exists no systematic evaluation of the use of these models in the literature. Therefore, this study aimed to review the types and applications of Bayesian spatial–temporal models and covariates used to study cancer incidence and mortality outcomes between 2014 and 2018. Our a priori hypothesis was that there is a lack of studies incorporating individual patient data as well as use of these models for forecasting.

Methods

Search strategy

The methodology of this review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (Moher et al. 2009). We employed a broad selection strategy of these databases, MEDLINE, EMBASE, Web of Science, in February 2019, with few restrictions to minimize the risk of bias (Electronic supplementary material/ESM-1). A manual search was also undertaken through a reference list of articles and Google Scholar.

The titles and abstracts of articles were screened, and then, the papers identified were evaluated and selected after reading the full text and the inclusion criteria (WW). Studies were included after any disagreements on the inclusion of a particular study were resolved between the two authors (AE, WW).

Selection criteria

This systematic review focused on the use of Bayesian spatial–temporal models as the study design. It included studies utilizing a fully Bayesian (FB) approach that applied spatial–temporal models on cancer incidence and mortality outcomes in area and time and published between 2014 and 2018. The spatial–temporal model was defined as the model, which includes a geographic index for locations and a time index to estimate disease risk over space and time with spatial and temporal terms or spatial–temporal interaction terms (Bernardinelli et al. 1995). The ESM-2 displays the model formula of all included studies. Studies were excluded if their models were applied on non-cancer, purely spatial models or time-series models, utilized non-Bayesian inference, or studies which did not mention any use of spatial–temporal model terms. Articles were also excluded if they were a review, had no English full-text access and were Conference abstracts and Editorial materials or studies which primarily used penalized quasi-likelihood (PQL) estimation (empirical Bayes/EB approach). We focused on peer-reviewed articles published between 1 January 2014 and 31 December 2018 to ensure this review was undertaken based on most recent literature due to a near doubling of articles published particularly in the last five years and continual development of recent models upon earlier models (Bernardinelli et al. 1995; Waller et al. 1997; Knorr-Held 2000). EB approach using PQL estimation is performed under a frequentist perspective (Ugarte et al. 2015b), and this review focused only on studies with FB approach which generally uses Markov chain Monte Carlo (MCMC) or integrated nested Laplace

approximations (INLA) techniques (Ugarte et al. 2014). In FB approach, the prior distribution is completely specified before any data is observed, which considers the uncertainty of model parameters (Ugarte et al. 2014). EB approach is an approximation of the FB approach, and the prior parameters are estimated from the data which conditions the estimation on point estimates of model parameters (Ugarte et al. 2014).

Quality assessment

All included studies were scored using a standardized item list to assess the quality and risk of bias (Harris et al. 2016). The checklist comprises eight questions with scores ranging from 0 to 2 for each question (0 = Poor, 1 = Moderate, 2 = Good) and a maximum overall score of 16. The quality level of the overall score ranges from low to very high (quality level—Low < 8, Medium = 8–10, High = 11–13, Very high > 13). Assessment of quality of included studies was done by one reviewer (WW) first, and the second reviewer (AE) independently checked each study to quantify the scoring and overall evaluation of quality. Any disagreement was resolved through discussion between the two scorers.

Data extraction

Descriptive details were author name, publication year, data collection design, cancer incidence/outcomes, areal units, temporal units, objectives, key findings and applications. Methodological details such as whether the model adjusted for patient-, area- or temporal-level covariates, standardized for demographic covariates, analytical models used, model structures (spatial, temporal and space–time models), were also collected.

Results

Data

Figure 1 depicts a PRISMA flow chart for the selection process. After reviewing the abstracts from databases and searching of reference lists and Google Scholar, 217 articles were assessed for full-text review, and of these, 38 studies were finally included.

Table 1 shows the summary characteristics of all included studies. All studies made use of observational data from registries. Incidence rates were more commonly studied than mortality rates or survival time. All studies were applied to explore spatial patterns over time (ESM-3). Twenty (53%) studies aimed to study the association between outcomes and risk factors. The areal units studied in these spatial–temporal models varied from large areas at the state level to the smaller grid (30×30 km) level (ESM-4). The number of areas ranged from 18 to 8073 (median = 94, interquartile range/IQR = 48–478). Studies used different levels of temporal aggregation, including annual cases (5–43 years) to periods (0.5- to 8-year groups).

Covariates

Studies incorporated a wide range of covariates, most commonly demographics (82%), socio-economics (37%), lifestyle (8%), clinical (11%), meteorological (11%), environmental (8%) and access to healthcare (8%) (Table 1, ESM-4). These models adjusted for covariates at the patient level (18%), area or temporal level (58%) and through standardization of patients' demographic characteristics (45%). Four studies included patient-level clinical characteristics, stage, grade, radiation therapy, surgery, cancer subtype, previous cancer history (Carroll et al. 2018; Cramb et al. 2016; Hurtado Rua and Dey 2016; Carroll and Zhao 2018).

Analytical methods

ESM-5 shows a summary structure of spatial–temporal models.

Twenty-six (68%) studies used generalized linear mixed models (GLMM) over space and time.

GLMM with spatial, spatial–temporal random effects, temporal fixed/random effects

The earliest (Bernardinelli et al. 1995) and majority of spatial–temporal GLMM models for areal data have been extended from the spatial Besag, York and Mollie/BYM model, through a pair of unstructured and structured random effects (Besag et al. 1991). The unstructured random-effects term in the BYM model accounts for over-dispersion and allows for unknown factors, and the spatially structured random effects account for spatial or temporal dependence by allowing for correlated heterogeneity between areas or years using spatially or temporally structured random-effects, through conditional autoregressive/CAR prior. These studies used CAR prior in the spatial (Adin et al. 2017; Carroll and Zhao 2018; Cramb et al. 2017; Herrmann et al. 2015, 2018; Jafari-Koshki et al. 2014, 2017; Kang et al. 2015; López-Abente et al. 2014; Ocaña-Riola et al. 2016; Sharafi et al. 2018; Sparks 2015; Ugarte et al. 2015a; Vicens et al. 2014; Yin et al. 2014) and temporal (Yin et al. 2014) random effects to smooth risk estimates across areas and years with adjacent boundaries and also in the spatial–temporal interaction (Cramb et al.

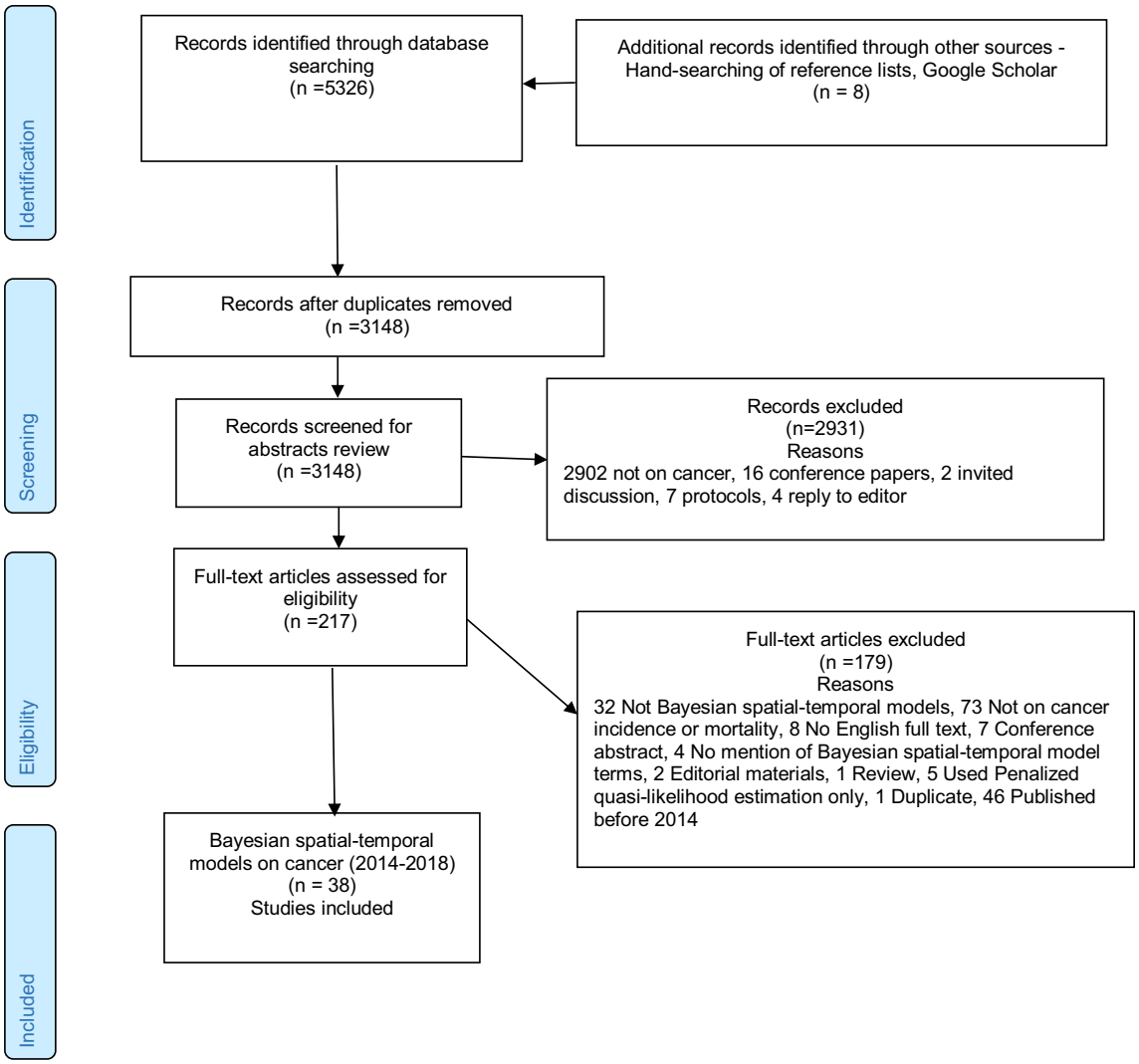

Fig. 1 Flow diagram of selection of included studies

2017; Jafari-Koshki et al. 2014, 2017; Kang et al. 2015; López-Abente et al. 2014; Ocaña-Riola et al. 2016; Sharafi et al. 2018) to allow spatially correlated area-specific differences in trends). Other studies (Goicoa et al. 2016, 2018; Ugarte et al. 2014, 2016, 2017) used Leroux CAR to overcome negative correlations between far-apart areas arising from CAR prior (Leroux et al. 2000).

Some studies included time as fixed-effect covariates (Herrmann et al. 2015, 2018), thus stratifying time into a few blocks of time and estimating the effect of each block independently from the others. Other studies allowed each areal unit for a separate linear (Bernardinelli et al. 1995; Cramb et al. 2017; Jafari-Koshki et al. 2014, 2017; Kang et al. 2015; López-Abente et al. 2014; Ocaña-Riola et al. 2016; Sharafi et al. 2018) and quadratic terms (Ocaña-Riola et al. 2016) or flexible, dynamic first- or second-order random walks (Adin et al. 2017; Kang et al. 2015; López-Abente et al. 2014; Sparks 2015; Ugarte et al. 2014, 2015a, Vicens et al. 2014) in the temporal random effects.

The following studies (Adin et al. 2017; Carroll and Zhao 2018; Goicoa et al. 2016, 2018; Kang et al. 2015; López-Abente et al. 2014; Sparks 2015; Ugarte et al. 2014, 2015a, 2016) applied the Knorr-Held (2000) model to account for spatial–temporal interactions (varying area-specific trends in disease risk) besides spatial (CAR) and temporal trends (first- or second-order random walks) adjustment. Four different types of interactions with structured matrices were constructed as the Kronecker product of the corresponding structure matrices of the main spatial and temporal random effects. When spatial–temporal evolution patterns of cancer were not the same among all age groups, interactions of age with area and time were incorporated in the Knorr-Held (2000) model to detect different regional and temporal effects on age groups (Goicoa et al. 2016).

Table 1 Summary of characteristics of included studies

Item	Category	*n* (%)
Design of data collection	Existing registry	38 (100%)
Cancer incidence/outcomes[a]	Incidence	19 (50%)
	Mortality/survival (dichotomous)	19 (50%)
	Survival time	3 (8%)
Applications[a]	Explore spatial–temporal patterns	38 (100%)
	Identify association with risk factors	20 (53%)
Covariates[a]	Demographic	31 (82%)
	Socio-economic	14 (37%)
	Life styles	3 (8%)
	Clinical	4 (11%)
	Meteorological	4 (11%)
	Environmental	3 (8%)
	Health care access	3 (8%)
Covariates adjustment in models[a]	Patient level	7 (18%)
	Area or temporal level	22 (58%)
	Standardization of patients' demographic characteristics	17 (45%)
Statistical models[a]	Generalized linear mixed models	26 (68%)
	Spatio-temporal Multivariate mixture models	4 (11%)
	P-spline and B-spline models	3 (8%)
	Spatial–temporal survival accelerated failure time models	2 (5%)
	Spatio-temporal flexible parametric relative survival models	2 (5%)
	Two-stage spatially dependent variable selection models	1 (3%)
	Poisson log-linear model with clustering and smoothing components	1 (3%)
	Latent process spatio-temporal autoregressive model	1 (3%)
	Besag, York and Mollié moving average model	1 (3%)
	Spatio-temporal moving average risk smoothing model	1 (3%)
	Transformation class of spatio-temporal cure rate CAR survival models	1 (3%)

[a]Study used more than 1 categories

To overcome identifiability issues due to confounding effects among spatial, temporal main and interaction terms in four different types of spatial–temporal interactions in GLMM (Knorr-Held 2000) and B-spline models (Ugarte et al. 2017), Goicoa et al. (2018) suggested to reparametrize the spatial, temporal and spatial–temporal random effects using the spectral decompositions of their precision matrices. This is to ensure that the appropriate identifiability constraints will be well defined to achieve plausible results with a less extra-computing time required to fit the reparametrized models.

GLMM with two-level spatial and spatial–temporal effects (Ugarte et al. 2015a, 2016) were used when small areas were aggregated in larger regions, and the frequency of disease was very low. Their simulation results showed the two-level model with second-level interaction was better than the single-level spatial models. These models were appropriate to identify potential differences in the implementation of health policies at each level of spatial aggregation. They had a shorter computational time when second-level area/SLA interactions instead of the first-level area were used since the number of restrictions needed for model identifiability was significantly reduced. These models could be difficult to fit if the number of SLA was too large due to a complex computation of the posterior marginal of the hyper-parameters.

The spatial–temporal model with the spatially varying random effects allowed for spatially structured variation in risk over time to measure disparities in cancer incidence between two small subpopulations by varying their risk differences between areas over time (Sparks 2015).

GLMM with shared spatial, temporal and spatial–temporal random effects

Following a shared component, joint modelling framework, joint models (shared spatial, temporal and spatial–temporal random-effects) showed a better performance than the

separate models with an independent set of random effects (Knorr-Held and Best 2001). Without having the actual risk factor data, these shared-components models were demonstrated to identify some common unmeasured or unknown risk factors among multiple population groups like gender, race, birth cohorts (Cramb et al. 2015; Dreassi 2018; Yin et al. 2014), or shared and divergent geographic and temporal patterns of various diseases with common risk factors (Mahaki et al. 2018; Raei et al. 2018). Since cancer has a complex aetiology and long latency, these studies considered a temporal lag association and sensitivity analyses with residential history, data sparseness and remoteness groupings. However, these models had a limitation assuming independence between the shared components and the impossibility of assessing interaction among covariates.

GLMM with spatial, age, period, cohort and space–period random effects

These studies used the multivariate spatial–temporal age–period cohort (APC) models to analyse the gender-specific impact of age, time, date of birth and area on stomach and pancreatic cancer mortality trends (Etxeberria et al. 2017; Papoila et al. 2014). APC models were suitable to exhibit effects of cohort trends in cancer aetiology and mortality but assumed minimal migration between areas and had restraint on spatially varying covariates.

Nautiyal and Holford (2018) developed the spatial–temporal APC models to incorporate spatial uncertainty in cancer survival estimates at a smaller spatial resolution and smooth back-calculated cancer incidence from survival estimates in a spatial–temporal sparse setting. Models detected varying time trends in lung cancer risk across areas. Piece-wise exponential survival models were used to estimate cause-specific hazards while assuming incident cases die from cancer or other causes or migrate out of an area.

Latent process spatio-temporal autoregressive models

To adjust for spatial–temporal interactions in Bayesian hierarchical models, Utazi et al. (2018) developed the latent process spatio-temporal autoregressive model to characterize a spatio-temporal dependence dynamically with a temporal autoregressive random-effect and a spatial autocorrelation captured via Leroux CAR. The first-order autoregressive term corresponds to the random effects at each time point being dependent on the value of the random effect at the previous time point to enable correlation between consecutive time periods. This model was shown to be at least effective as CAR-based priors for modelling the latent process of spatial–temporal interactions and appropriate to detect the overall spatial pattern in the risk estimates and characterize the presence of heterogeneity due to the clustering of areas with distinct risks. But, when spatially varying covariates are included, those models for a latent process may change as these explain residual autocorrelation in the data.

Spatio-temporal flexible parametric relative survival models

Due to possible uncertain accuracy of the recorded cause of death in population-based cancer studies, the Bayesian spatial–temporal flexible parametric relative survival models allowed to measure net survival with time-dependent and continuous covariates and obtain smooth survival predictions (Cramb et al. 2016, 2017). These models determined temporal changes in relative survival differ by areas while adjusting for individual-level risk factors, spatial, time-varying and spatial–temporal interaction components. Restricted cubic splines were used to flexibly smooth the cumulative baseline excess hazard with improved model fit.

Spatial–temporal accelerated failure time (AFT) models

When the Cox-proportional hazards model assumptions (proportionality of hazard/survival odds with covariates) did not hold, AFT models were used to enable a direct relationship with the logarithm of survival time with both the risk factors, spatial, temporal and spatial–temporal random effects (Carroll and Zhao 2018; Carroll et al. 2018). AFT models with spatial and temporal frailties were demonstrated to study unmeasured confounders beyond known individual demographic and clinical risk factors and to detect changes in survival over time due to a major disaster or health policy legislation. Despite multiple temporal random effects in a single linear predictor, the model did not experience identifiability issues due to appropriately recovered parameters.

Transformation class of spatio-temporal cure rate CAR survival models

Hurtado Rua and Dey (2016) developed the transformation class of cure rate survival models to adjust for the dependent survival times in the same area and year-of-diagnosis and incorporated a cure fraction (proportion of patients who never experience an event of death) while considering assumptions of the time-varying proportional effect of the hazard function and a time constant odds ratio between two covariates sets. This model included a nonparametric baseline survival function and modelled cure rates through a covariate specification to capture the effect of covariates

on spatial–temporal survival function. It allowed for the inclusion of patient-level covariates and interaction between those covariates in the cure rate specification.

Spatio-temporal multivariate mixture models

Compared to the Knorr–Held spatio-temporal interaction model, the mixture models within the model selection setting were shown to have an improved model fit of rare diseases by borrowing information from related, more common diseases while accounting for unmeasured exposures like health service availability, behavioural, environmental and demographic factors shared among multiple-related diseases with different rarity and common aetiology (Carroll et al. 2016, 2017a, b, Lawson et al. 2017). The mixture model selection methods applied a model probability to linear predictors in distinguishing whether the most appropriate linear predictor was spatial, spatial–temporal or a mixture of two, to indicate a difference in aetiology between diseases. These models can overcome some issues (collinearity, excess parameters than a possible number of MCMC iterations) in variable selection approach which usually requires one to choose a fixed-set of predictors before final model fit and incorporates collinear predictors lowering the required number of modelling parameters with improved model fit. The limitation involved a lack of flexibility with linear predictors and some identification issues arising from the model selection process (model mis-specification and collinearity between fixed and random effects).

Two-stage spatially dependent variable selection models

Choi and Lawson (2018) developed the two-stage spatially dependent variable selection models to detect the spatially varying subset of covariates with common temporal dependence. Two-stage framework separately estimates the regression coefficients with a temporal trend depending on both space and space–time random components. It could reduce the confounding bias where covariate varying in space and time correlated with spatial–temporal random effects when estimating the regression coefficients of that covariate on outcomes. It showed better goodness-of-fit performance than the covariates-only model in a simulation study.

Poisson log-linear model with clustering and smoothing components

Standard Bayesian spatial–temporal models for risk estimation used the spatial–temporal autocorrelation to estimate smoothed disease risk, whereas scan statistics identified clusters of areas with higher risks compared to adjacent areas. The integrated clustering and smoothing components model allowed areal units in different clusters with different baseline levels of disease risk and detected both cluster congregations and average risk levels variation over time (Lee and Lawson 2014). It yielded better performance in risk estimation than the Knorr-Held 2000; Rushworth et al. 2014 models. However, limitations to model performance could arise when a disease is rare, and clustering models did not adjust for covariates to estimate the unexplained risk component for unknown aetiologic covariates and model multiple diseases simultaneously.

P-spline and B-spline models

One-, two- and three-dimensional B-splines were used to model space–time interactions (Ugarte et al. 2017). The one-dimensional P-splines were appropriate when the number of small areas was not large since they incorporated CAR spatial random effects via a covariate matrix to produce local smoothing considering adjacent regions with a shared border and outperformed the two-dimensional P-splines models to handle spatial heterogeneity. The two- and three-dimensional P-splines (interaction P-spline and ANOVA-type P-spline) offered large-scale smoothing because splines consider distance through B-spline basis using some knots and were computationally better alternatives when the number of small regions was high. Interactions with age, space and time in the one- and two-dimensional P-spline models were flexible to capture different mortality trends by age groups (Goicoa et al. 2017). The simulation study with different spatial–temporal scenarios showed three-dimensional P-spline models as a good alternative to Knorr–Held (2000), CAR, BYM moving average and spatial moving average risk-smoothing models particularly in the analysis of highly sparse spatial–temporal data (Adin et al. 2017).

Assessment of quality

Based on the modelling study quality assessment checklist, scores ranged from 9 to 16 (ESM-6). Twenty-four were considered very high quality, eleven high quality and three medium quality. The median quality score across 38 studies was relatively very high, 15 out of 16.

Discussion

The applications of FB spatial–temporal models were mainly for exploring spatial–temporal patterns, followed by studying the association of risk factors with cancer incidence or mortality outcomes. However, few models included patient-level data and applications in terms of

forecasting of spatial–temporally arranged cancer incidence and mortality outcomes were limited. With regards to forecast uncertainty, Bayesian spatial-temporal models are particularly suitable since they can potentially embed different sources of error in a joint probabilistic forecasting model (Bennett et al. 2015). FB methods are preferable where complete and accurate estimations of uncertainty are warranted (Ugarte et al. 2014). Schmid and Held (2004) demonstrated an APC model using a random walk prior in period or cohort effects for prediction of future stomach cancer mortality rates while allowing for space–time interaction. Other studies developed spatial–temporal P-splines models using PQL estimation in the EB approach for future forecasts of cancer mortality (Etxeberria et al. 2014; Ugarte et al. 2012). FB spatio-temporal models with age, birth cohort, time and space components were developed to forecast mortality and life expectancy at the small-area level in England and Wales (Bennett et al. 2015). Projections of cancer incidence and outcomes using FB spatio-temporal models at the small-area level are of significant interest to health services planning, health policy decision-making and appropriate resource utilization.

In the spatial–temporal modelling context, few studies accounted for patient-level clinical characteristics which are of prognostic importance. These clinical risk factors were included as fixed-effect covariates in the studies that modelled spatio-temporally clustered cancer survival data using AFT, flexible parametric relative survival and transformation class of cure survival modelling frameworks while accounting for spatial and temporal correlation. The studies generally used a two-stage approach in which individual-level conditional probabilities of disease were modelled first and then used as offset terms to adjust for the spatial–temporal models. Combining individual information from direct surveys and aggregated data from other sources have shown to improve the quality of small-area indicators and provide better results than purely area-level models (Jackson et al. 2008). The ability to incorporate both individual- and area-level information in the Bayesian spatial–temporal model in a multi-level framework could improve the causal inference on the relationship while reducing ecological fallacy. Thus, the spatial–temporal models incorporating individual clinical characteristics and underlying biology could explore potential aetiologic factors. Future studies would be useful to identify how known individual risk factors can be included as spatially and temporally varying coefficients in the spatial–temporal models. Thus, exploring clinical variation across geographic and temporal units is useful to explore the latent combination of unmeasured risk factors beyond known risk factors.

A large variety of modelling methods were used to study cancer incidence or mortality outcomes, within the Bayesian spatial–temporal modelling framework. This depended on data types, outcomes and applications, and there is currently no consensus on which modelling approach is preferable. Most Bayesian spatial–temporal models have been done within a GLMM framework including fixed effects and spatial, temporal and spatial–temporal random effects spanning the wide variety of distributional characteristics. Most studies used a spatial CAR model to account for spatial and temporal trends and area-specific differences in trends, which was relevant for the investigation of local risk factors. First- or second-order random walk terms were commonly used in temporal random effects, but they may not capture the complexity of the temporal trends over longer time periods. Spline models allowed a more flexible estimation of complex temporal patterns particularly in applications covering extended periods, large-scale spatial smoothing like investigating a source of pollution dispersing with a distance and highly sparse spatial–temporal data. In the non-parametric approach in the spatial–temporal interactions, area-specific one-, two-, three-dimensional B-splines and P-splines models were modelled for each region to allow nonlinear area-specific trends for varying disease risk.

The majority of studies were scored as very high quality. Most studies which developed novel methods carried out a sensitivity analysis for changes in the prior and hyper-prior distribution and that informed the reliability and robustness of results. Simulation studies which investigated the performance of new method comprehensively reported the conduct of uncertainty and sensitivity analysis in different spatial–temporal scenarios. However, studies that applied the existing models could have included comprehensive uncertainty and sensitivity analyses. Besides data quality, the validity of the outcome of spatial–temporal analyses was greatly dependent on the spatial scale and aggregation. Different aggregation level of temporal random-effects had a negligible impact on model goodness of fit and estimation of fixed effects, whereas spatial aggregation had an influence (Kang et al. 2015). Thus, future spatial–temporal models should consider a multi-level framework and prediction uncertainty in different clinical and spatial–temporal scenarios using validation and simulation studies. These FB spatial–temporal models could be useful for public health researchers to detect changing time trends in risk across regions to quantify effects of regional policies and formulate a hypothesis for cancer aetiology and forecasting of cancer burden to guide efforts to reduce disparities.

Studies commonly undertook model fitting and inference using MCMC followed by INLA. MCMC (exact method for Bayesian inference) is widely used as the posterior distributions cannot be obtained in closed form in an FB approach (Ugarte et al. 2014). The INLA approach

(approximate method) reduces the computational burden of Bayesian inference taking advantage of sparse precision matrices. It provides accurate results in substantially less computing time than MCMC algorithms due to a lower number of constraints needed to identify the model (Ugarte et al. 2017).

The strength of the review was the assessment of bias following the PRISMA guidelines and a quality checklist, screening of relevant articles through 3 databases and Google Scholar. This review might have missed studies published in other languages. Despite the screening and extraction of data by one reviewer, duplication of this process by a primary reviewer and validation with another reviewer could have reduced the likelihood of missing relevant studies. Significant variations in methodology, covariate inclusion, cancer types and outcomes within the included studies precluded a meta-analysis. Finally, publication bias cannot be entirely avoided.

Conclusion

Studies used a diverse range of modelling approaches with different prior distributions in spatial, temporal and spatial–temporal interaction effects depending on nature of data, outcomes and applications. Few studies (11%) modelled patient-level clinical characteristics, and the applications of an FB approach in the forecasting of spatial–temporally arranged cancer data was limited. Therefore, this review highlighted the need for future Bayesian spatial-temporal models to incorporate patients-level prognostic characteristics through the multi-level framework and predict future cancer incidence and outcomes for prevention and control strategies.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Research involving human participants and animals Not applicable.

Informed consent Not applicable.

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