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Abstract book

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Contents

Workshop 1

Spatio-temporal analysis of epidemic data using the R package 'surveillance'

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Abstract:

This workshop provides an introduction to the spatio-temporal analysis of infectious disease spread using the R package surveillance. We will give an overview of the theory and applications of the endemic-epidemic modelling framework for areal count time series, followed by several programming exercises using real-world data. We will cover univariate and multivariate models with various assumptions on spatial coupling, the inclusion of covariates and the generation of short-term forecasts. We will conclude with a quick overview of other functionalities of the surveillance package, such as an endemic-epidemic point process model for individual-level data.

Workshop 2

Spatial Modeling with Stan

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Abstract:
The goals of this workshop are twofold:

- To introduce new users to existing implementations of spatial models in Stan and the corresponding tools and workflow for model validation and comparison.
- To provide researchers with the necessary understanding of Stan language syntax and computation so that they can develop custom models and extend existing ones.

We will provide both R and Python Jupyter notebooks and use publicly available datasets.

Part 1: To show how statistical models are expressed in the Stan probabilistic programming language, we start with simple linear and multi-level regression models. Next we present the ICAR model developed by Besag (1973), which uses an intrinsic Gaussian Markov random field to model spatial correlation between areal units, and the corresponding generative but computationally expensive Conditional Autoregressive (CAR) model. Throughout we use tools from the Stan ecosystem to validate and visualize the model fit and inferences.

Part 2: To show how to build complex models using the elements from part 1, we focus on the Besag York Mollié model (1991), which accounts for both spatial and random variation in observed per-area disease data. We work through the Stan implementation of the BYM2 model of Riebler et al (2016), a reparameterization of the BYM model which provides independent hyperparameters for the spatial and random effects components. We then present several extensions of this model developed during the SARS-Cov-19 pandemic.

Keynote 1

Mapping ‘last-mile’ populations

Authors:
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Abstract:

Substantial resources are being invested into ‘last mile’ delivery of health interventions, aiming to reach those populations that are often vulnerable and hard-to-reach. Campaigns to provide bednets to households or vaccines to children require small area data on the numbers and locations of those populations to effectively and efficiently deliver life-saving interventions. Moreover, the universal provision of routine healthcare services needs reliable and recent data on target populations to ensure access and that no one is left behind. Such population data are typically sourced through a national census, and then updated through administrative data sources - but in many of the settings with the highest disease burdens, or last remaining pockets of transmission, the most recent census was more than a decade ago and administrative sources are lacking.

Such data gaps have prompted the development of inter-disciplinary geospatial approaches to estimate population distributions, demographics and dynamics at small area scales. As part of the work of WorldPop, Bayesian spatial modelling approaches have been co-developed with governments around the World to meet a variety of demographic data needs around healthcare and intervention delivery. These range from mapping zero-dose children for vaccine delivery and filling gaps in census enumeration, to accounting for biases in satellite mapping of settlements and integrating surveys on population displacement. Professor Tatem will present an overview of these efforts to quantify small area population distributions through geospatial data integration and support last mile healthcare and intervention delivery.

Keynote 2

A Bayesian hierarchical framework to evaluate policy effects through quasi-experimental designs in a longitudinal setting

Authors:
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1: Imperial College London

Abstract:

The use of quasi-experimental designs has proven popular to establish causal links in observational studies, where randomised clinical trials are not feasible. In the context of longitudinal data, Interrupted Time Series (ITS) can be used to evaluate the effects of interventions. In an ITS study, a time series of a particular outcome of interest is “interrupted” by an intervention at a known point in time (e.g. smoking bans, changes in alcohol trading laws, etc.). Such methods have been extensively used in several research areas, most notably econometrics and more recently in epidemiology and in public health, where they are often (heavily) modified to accommodate specific data requirements (for instance the presence of non-linear time trends or the need to adjust for controls).

In this talk I will present some recent work on the extension of the ITS design to a Bayesian hierarchical framework, aiming to build a flexible, comprehensible, and generalisable statistical modelling framework to evaluate the individual and cumulative impact of “shocks” (e.g. government policies or unpredictable events) on health outcomes over time and specifically when there is some dependency in space. To highlight this, I will show two applications of this approach (i) to evaluate the effect of municipal waste incinerator openings on adverse birth outcomes in England and (ii) to evaluate the impact of two governmental policies on mental-ill health on the whole population and specifically on minoritised ethnic groups in England.

Keynote 3

A Journey Through Spatial Epidemic Modelling

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Abstract:

In recent years, there has been an understandable increase in the interest in the mathematical and statistical modelling of infectious disease epidemics. In this talk, we will journey through the landscape of epidemic models that allow for spatial heterogeneity in the underlying population. Along this journey, we will explore simple meta-population models through to individual-level models, and spend some time discussing recent developments such as models which allow for change in population behavior to be accounted for.

Typically, statistical inference for these models is carried out in a Bayesian context using computational techniques such as Markov chain Monte Carlo (MCMC). This is in part due to the non-standard form of the models, but also due to the fact that we often have missing or uncertain data – for example, infection times are rarely directly observed – and Bayesian data augmentation provides a natural framework for allowing for such uncertainty.

However, the computational burden associated with fitting spatially explicit individual-level models to large data sets can be intense. We will therefore touch on some of the approximate computational techniques widely employed when using such models.

Invited 1: Challenges to harmonize data along time

Local distribution of cattle over Guadeloupe archipelago: an adapted method for disaggregating census data

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Abstract:

High resolution gridded livestock distribution data are produced since many years and find applications in diverse sectors such as epidemiology, livestock impact assessment or territory management. Those data are based on census conducted at national/sub-national scale downscaled using machine learning algorithm and relevant spatial predictors. Most known of livestock dataset is Gridded Livestock of the World (GLW; Da Re et al. 2020) who produce 1km resolution maps at continental scale. We propose here an adaptation of the GLW methodology at finer scale for the Guadeloupe archipelago. Cattle census data were collected from local authorities for the 32 municipalities. The Random Forest (RF) algorithm was retained from the previous methodology and Geographical Random Forest (GRF; Georganos et al. 2021) was implemented to compare predictions of both algorithms. Environmental factors and expert identified predictors were collected or created. A high-resolution land cover database (Karucover 2017) was used to create predictor and suitability rasters. Steps were introduced to the data preparation to deal with potential bias of census data. In order to manage suitability hypothesis on possible breeding area and predictor variability within municipal area, an innovative predictor sampling method is also proposed. Cattle distribution maps were produced with a spatial resolution of 225 m for the whole Guadeloupean archipelago. GRF algorithm does performed significantly better than RF but with higher processing time. Newly developed predictor sampling methodology also showed advantages over existing models. Importance of predictors was analyzed. The methodology needs to be further explored and possibly applied to other Caribbean islands.

Invited 1: Challenges to harmonize data along time

Promoting healthy urban environments: the importance of integrate data and methods in the urban planning system

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Abstract:

Urban territories play a crucial role in the health of the populations that live in them. The urban environment can directly influence the quality of life and well-being of individuals, impacting their physical and mental health. Several factors present in cities, such as air pollution, lack of green areas, limited access to health services, precarious housing conditions and other social determinants, can contribute to the emergence of disease, contributing to existing health problems.

Therefore, it is essential that local public policies take into account the importance of the urban environment in promoting the health of the population. To this end, it is important to recognize and reinforce the role of information and monitoring systems, as well as the possibility of using assessment methodologies, which are integrated into the various urban planning instruments, contributing to a vision of health in all policies.

Invited 1: Challenges to harmonize data along time

Addressing methodological challenges of boundary changes in longitudinal spatial epidemiology

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Abstract:

Longitudinal studies in spatial epidemiology encounter challenges due to boundary changes in areal units over time.

Our aim is to transform data from previous census to raster surfaces and aggregate cells to the more recent census boundaries (our target). To validate the method, we correlated population counts per areal unit generated by interpolation, and population counts from Census in the same areal unit.

The study focuses on Argentina, Brazil, and Mexico. Population from censuses 1991, 2001, and 2010 for Argentina; 1991, 2000, and 2010 for Brazil; and 1990, 2000, and 2010 for Mexico were used (IPUMS-International database). Inverse Distance Weighting (IDW) interpolator with 125-meter cell size was used to generate population grids by country/census and age groups (60-69, 70-79 and > 79 years-old). To validate, we calculated the Pearson´s correlation coefficient (r) between population counts by IDW and by IPUMS.

Then, we overlaid each census/year/age group grid onto target boundaries and sum cells within each boundary to align all data from previous censuses to the more recent census.

Coefficient r between the population counts from IPUMS and from IDW were: Argentina -0.83 to 0.99 in 1991; 0.83 to 0.99 in 2001; 0.82 to 0.99 in 2010 ($p<0.01$). Brazil - 0.98 to 0.99 in 1991; 0.97 to 1.0 in 2000/2010 ($p<0.01$). Mexico - 0.91 to 0.99 in 1990/2000 and 0.86 to 0.98 in 2010.

The results demonstrated that interpolating areal data to grid and retransforming it to areal unit is an effective method to address incompatible area boundaries over time.

Invited 2: Disease mapping: methods, data analyses and practical tools

Scalable Bayesian disease mapping models with bigDM: a divide-and-conquer approach for analyzing high-dimensional data

Authors:
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Abstract:

The use of statistical models that incorporate spatial or spatio-temporal dependence is crucial for analyzing areal data in research areas such as cancer epidemiology. These models allow us to obtain smoothed estimates of mortality or incidence risks (or rates) in small areas, mitigating the huge variability associated with classical risk estimation measures such as standardized mortality ratios or crude rates. Despite the proliferation of statistical models and computational techniques for studying the temporal evolution of the geographical patterns of areal data, the development of scalable models for high-dimensional areal data still remains limited.

The R package bigDM (https://cran.r-project.org/web/packages/bigDM/index.html) implements several scalable spatial and spatio-temporal disease mapping models for high-dimensional areal count data using the well-known INLA (integrated nested Laplace approximation) technique for approximate Bayesian inference in latent Gaussian models. The modelling approach relies on the principle of "divide-and-conquer," enabling the simultaneous fitting of local models. Adapting this idea to the context of disease mapping proves suitable when dealing with a large number of small areas, mainly for three reasons: (1) it is a natural and simple strategy, (2) the larger the spatial domain, the less likely it is for the data to be stationary across the whole map, and (3) it provides a scalable modelling scheme that substantially reduces the RAM/CPU memory usage and computational time by performing both parallel and distributed computation strategies.

Invited 2: Disease mapping: methods, data analyses and practical tools

On Bayesian disease mapping and pandemic management

Authors:
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Affiliations:
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Abstract:

Bayesian disease mapping methods, such as Gaussian Markov random fields and their adaptive extensions, provide important tools for research into spatial epidemiology of disease and complex dynamics of infectious disease risks and infection outbreaks. The methodological applications are seen in the large and still growing literature on spatial and spatiotemporal analysis of COVID-19 infection and related health outcomes. In the contexts of pandemic monitoring and public policy for pandemic management, I discuss spatial and spatiotemporal disease mapping models and related methods for prediction and forecasting infection and infection risks, including modeling infection underreporting and excess mortality.

Invited 2: Disease mapping: methods, data analyses and practical tools

Demystifying spatial confounding

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Abstract:

Spatial regression models, i.e. regression models for data that have been collected at different geographical locations, use spatial random effects to approximate unmeasured spatial variation in the response variable. However, as spatial random effects are typically not independent of the covariates in the model, this can lead to significant bias in covariate effect estimates of interest. This fundamental problem, which makes covariate effect estimation in all spatial regressions potentially unreliable, is referred to as spatial confounding. There has been much interest in spatial confounding, particularly in recent years, not least because the most established methods for dealing with the problem were proven to be ineffective. However, research into the topic has sometimes led to puzzling and seemingly contradictory results. Here, we develop a broad theoretical framework that brings mathematical clarity to the mechanisms of spatial confounding, providing explicit and interpretable analytical expressions for the resulting bias. From these, we see that it is a problem directly linked to spatial smoothing, and we can identify exactly how the features of the model and the data generation process affect the size and occurrence of bias. Our framework can also be used to understand and generalise some of the existing results on spatial confounding, including suggested methods for bias adjustment.

Invited 2: Disease mapping: methods, data analyses and practical tools

Joint outcome modelling of spatial COVID-19 incidence data for the senior population of Ontario, Canada, using a shared component model

Authors:
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Abstract:

Adverse COVID-19 outcomes such as hospitalizations and death counts are key in quantifying an outbreak that can jointly account for the high proportion of morbidity among seniors. Furthermore, the burden attributed to the adverse outcomes from COVID-19 in seniors may be due to various health, socioeconomic and demographic risk factors. This study aims to quantify and map the geographical variation in the incidence of deaths, multiple hospitalizations and single hospitalization counts to understand the risk of multiple adverse outcomes among senior residents over 65 years in Ontario, Canada. The data for this study were obtained from the Ministry of Health's Ontario Health Data Platform (OHDP) supported by the Institute for Clinical Evaluative Sciences (ICES). A Bayesian hierarchical spatial model using Integrated Nested Laplace Approximation (INLA) is used to estimate the joint burden of adverse COVID-19 outcomes between January 2020 – March 2022 among the senior residents of Ontario at the forward sortation area level. The multivariate outcomes include count data in which the outcomes are combined with the shared and the outcome-specific components using a shared component model to improve the precision of our estimates over space. The results can provide the baseline against which to assess the need for area-specific support to protect the senior population of Ontario by identifying the forward sortation areas with elevated risks and risk factors. The findings of this study can also be used for effectively monitoring and evaluating current public health policies and programmes targeted toward senior residents across Ontario and for better preparedness for future outbreaks.

Invited 3: Environmental modelling for health impact assessment

A comparison of statistical and machine learning models for spatio-temporal prediction of ambient air pollutant concentrations in Scotland

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Stoner, Oliver

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Abstract:

The spatio-temporal prediction of air pollutant concentrations is vital for assessing regulatory compliance and for producing exposure estimates in epidemiological studies. Numerous approaches have been utilised for making such predictions, including land use regression models, additive models, spatio-temporal smoothing models and machine learning prediction algorithms. However, relatively few studies have compared the predictive performance of these models thoroughly, which is one of the novel contributions of this paper. For the specific challenge of predicting monthly average concentrations of NO2, PM10 and PM2.5 in Scotland, we find that random forests typically outperform (or are as good as) more traditional statistical prediction approaches. Additionally, we utilise the best performing model to provide a new data resource, namely, predictions of monthly average concentrations (with uncertainty quantification) of the above pollutants on a regular 1 km2 grid for all of Scotland between 2016 and 2020.

Invited 3: Environmental modelling for health impact assessment

Estimation of a Proportional Hazards Model with Spatially-Dependent Errors through Presmoothing

Authors:
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Abstract:

This paper delves into the proportional hazards model, renowned for its adaptability in handling censored data and incorporating covariate effects without the need to define the baseline hazard function explicitly. Unlike traditional approaches that might not account for spatial dependencies, this research introduces a semiparametric proportional hazards model that integrates an underlying continuous spatial process to consider correlations between points based on proximity. The novel method explored involves a two-step procedure: initially adopting a nonparametric approach to estimate the underlying spatial process via the partial likelihood method, followed by a regression analysis to ascertain the parametric functional mean and covariance function of the process, a strategy referred to as presmoothing. We discuss the asymptotic behavior of our estimator and validate our approach with an empirical example. This research significantly enriches the existing body of knowledge by offering a nuanced method to handle spatial dependencies in survival data.

Invited 3: Environmental modelling for health impact assessment

Source apportionment of PM2.5 species data collected over space and time

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Abstract:

The health burden associated with particulate matter exposure is now well documented and recognized,. Recently, various research efforts have been undertaken to better understand the health impacts of individual components of particulate matter. While evidence in this regard is still forming, it appears clear that some of the species of PM2.5 are particularly noxious to human health. Thus, reduction of PM2.5 species' concentration is fundamental for improving public health. To ensure that mitigation efforts are well directed and more effective, it is important to understand what are the major sources for PM2.5 species. In this presentation, we propose a Bayesian hierarchical model to perform source apportionment of six PM2.5 components observed in California in year 2023.

Specifically, adopting a functional data framework, we represent the observed log concentration of the 6 PM2.5 components using a Bayesian latent factor model with site-specific latent source profiles modeled to be spatially dependent and linked to a global source profile.

We applied our proposed model to simulated data, successfully retrieving the pollution sources and contribution of the sources to each pollutant. We also applied our model to observed concentrations of aluminum, sulfur, organic carbon, elemental carbon, nitrate and sulfate in California during the year 2023, identifying 4 major sources.

Invited 3: Environmental modelling for health impact assessment

Flexible scan statistic with restricted likelihood ratio for optimized COVID-19 surveillance

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2: University of Environment and Sustainable Development

Abstract:

Disease surveillance remains important for early detection of new COVID-19 variants. For this purpose, the WHO recommends integrating COVID-19 surveillance with other respiratory diseases. This requires knowledge of areas with elevated risk, which in developing countries is lacking from the routine analyses. Focusing on Ghana, this study employed scan statistic cluster analysis to uncover the spatial patterns of incidence and case fatality rates (CFR) of COVID-19 based on reports covering the four pandemic waves in Ghana. Applying the flexible spatial scan statistic method with a restricted ratio, we examined the incidence and CFR clusters before and after adjustment for covariates. We used distance to the epicenter, the proportion of the population aged >65, the male proportion, and the urban proportion of the population as the covariates. We identified 56 significant spatial clusters for incidence and 26 for CFR for all four waves. The most likely clusters (MLCs) of incidence occurred in the districts in south-eastern Ghana, while the CFR ones occurred in districts in the central and the north-eastern parts of the country. These districts could serve as sites for sentinel or genomic surveillance. Spatial relationships were identified between COVID-19 incidence covariates and the CFR ones. We observed closeness to the epicenter and higher proportions of urban populations increased COVID-19 incidence, while high proportions of those aged >65 years increased the CFR. Accounting for the covariates resulted in changes in the distribution of the clusters.

Invited 4: Geospatial methods for global public health

Leveraging spatial accessibility and catchment areas models to improve disease mapping

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6: Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, UK

Abstract:

Due to resource constraints, information on the precise spatial location of exposure to a disease is rarely collected during school-based sample surveys for malaria, neglected tropical diseases, and other diseases. Consequently, when mapping prevalence using such school-based survey data, the school location is often used as the exposure location in standard geostatistical methods to model spatial correlation. This is questionable since exposure to the disease is more likely to occur in residential locations.

We propose a modelling framework that accounts for the uncertainty in the location of the residence of the students when modelling malaria prevalence. Specifically, the framework relies on cost distance and allocation algorithms to model school catchment areas, describing the population of students that use a particular school. The catchment areas are derived based on three travel scenarios (walking only, walking & bicycling, and walking & motorised) and informed by factors that affect travel (road network, land use, protected areas, water bodies, and travel speed).

The modelling framework is illustrated using two case studies of malaria in Kenya and compared with the standard approach that uses school locations to build geostatistical models. The framework presents several inferential benefits, such as dealing with ecological bias when estimating the effects of malaria risk factors. The results show that invalid assumptions on the modes of travel to school can worsen the predictive performance of geostatistical models. Future research should focus on collecting granular information on the modes of travel to school to better parametrize catchment area models.

Invited 4: Geospatial methods for global public health

Small Area Estimation in Low- and Middle-Income Countries

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Abstract:

Small Area Estimation (SAE) in Low- and Middle-Income Countries (LMICs) is fundamentally more difficult than in high income countries, in part because of the lack of good auxiliary information, with census data often being unreliable and/or outdated. In this talk I will discuss models and software for carrying out SAE in LMICs, using examples from the work of my collaborators and I with the United Nations (UN) and the World Health Organization (WHO). These examples include child mortality, vaccianation coverage and fertility. I will discuss the pros and cons of both area-level and unit-level models. Area-level (Fay-Herriot) models rely on less assumptions but require sufficent data to obtain a weighted estimator and an associated variance. Unit-level models need to acknowledge the survey design, and require a tricky aggregation step but can be used with sparse data. The SUMMER and surveyPrev R packages (with an accompanying Shiny app) will be described, along with new SAE functions within the module within the survey package. Other topics to be discussed include benchmarking, variance modeling, combining different data sources and the use of machine learning models within Bayesian SAE models.

Invited 4: Geospatial methods for global public health

Disentangling the effects of fine-scale mobility on leptospirosis infection using telemetry data

Authors:
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Eyre, Max (3);
Read, Jonathan (1);
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Abstract:

Human movement is linked to risk for infectious diseases, especially those with strong environmental drivers. Telemetry data collected using GPS trackers is one way to record these movements. Previous methods for analysing telemetry data have not been able to quantify the fine-scale interactions with the environment. In this project we used step-selection functions, a spatio-temporal point process model used in animal movement ecology, to estimate selection coefficients for different environmental rasters in urban slums in Salvador, Brazil. We analysed if differences in these selection coefficients could be associated with risk for leptospirosis, a zoonotic bacterial infection with strong environmental risk factors. Furthermore, we wanted to assess if changes existed between genders and as people aged. A total of 130 individuals participated in this study across four study areas. Study areas were matched by socio-demographic and environmental factors. Individuals wore GPS trackers for 24 to 48 hours, with locations being recorded every 35 seconds. Movement analysis was performed on day-time active hours (5 am – 9 pm), morning hours (5 am – 9 am), midday hours (9 am – 1 pm), afternoon hours (1 pm – 5 pm) and evening hours (5 pm – 9 pm). We found women were more likely to move closer to the central stream in their community than men. We also found that women were likely to move away from open sewers compared to men. This project presents a novel method to analyse human telemetry data in the context of infectious disease epidemiology.

Invited 4: Geospatial methods for global public health

Design and analysis of randomised trials to estimate spatiotemporally heterogeneous treatment effects

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Abstract:

We consider randomized trial design to evaluate interventions with spatially or spatio-temporally heterogeneous effects. A common approach in this setting is the cluster randomized trial. In many cases, clusters are consituted as discrete subdivisions of a contiguous area of interest. However, cluster trials designed in this way may suffer from issues of contamination and may fail to capture the relevant spatial and temporal effects. Alternative designs and analyses may therefore be preferable. We define possible randomisation schemes and consider the identifiability of the causal effects of the intervention and the required trial design assumptions. We develop mixed model and treatment effect function specifications that can satisfy the required assumptions. We show that causal “dose response functions” are identifiable under certain randomisation schemes. Finally, we present design examples, including a re-analysis of data from a trial of an interventions to reduce the risk of malaria.

Invited 5: Challenges and advances in areal data statistical modeling

Assessing the Impact of the Modifiable Areal Unit Problem

Authors:
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Abstract:

The Modifiable Areal Unit Problem (MAUP) introduces variability in statistical outcomes based on the spatial resolution and partition of geographical units. For instance, correlations between variables X and Y may differ significantly when computed at the county level versus the Census block level. In this study, we propose a method to quantitatively measure the magnitude of the MAUP effect in specific spatial analyses. Our approach adapts the SKATER algorithm to construct computationally efficient bound curves for the statistic T across various geographical levels. We derive an index from these bound curves to gauge the strength of the MAUP influence in the data analysis.

Invited 5: Challenges and advances in areal data statistical modeling

Computationally efficient inference in disease mapping using anisotropic basis functions

Authors:
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Abstract:

The population-level risk of disease varies spatially, and is estimated from data relating to K areal units using Bayesian hierarchical models that account for spatial autocorrelation. This autocorrelation is typically captured by Conditional autoregressive (CAR) random effects models, which assume that neighbouring units exhibit similar risks. However, this smoothing ignores disease risk boundaries, where neighbouring units exhibit a step-change between their risks. While CAR models have been extended to account for this localised spatial smoothness, these approaches are computationally prohibitive for big data. This talk proposes a novel computationally efficient approach for localised spatial smoothing, using a set of $Q << K$ anisotropic spatial basis functions. Each basis function is centred at a different areal unit, and is constructed using its geodesic distance to all other units and a vector of ancillary data. The latter allows each basis function to exhibit either smooth or step change transitions in its value between neighbouring areal units, thus allowing for localised spatial smoothing. The central locations of the basis functions are determined by a spatial partitioning algorithm, and model fitting utilises computationally efficient generalised linear modelling algorithms. The methodology is motivated by a new study of respiratory ill health in England, which is partitioned into K=32,754 Lower Super Output Areas. The aims of the study are to: (i) understand the drivers of respiratory ill health; (ii) identify the locations of high-risk regions; and (iii) quantify the magnitude of the socio-economic health inequalities.

Invited 5: Challenges and advances in areal data statistical modeling

Trivariate shared Bayesian models to estimate ovarian cancer deaths attributable to asbestos exposure in Lombardy (Italy) in 2000-2018

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Mensi, Carolina (2);
Fazzo, Lucia (3);
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Manno, Valerio (4);
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3: Italian National Institute of Health, Italy;
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5: Italian Workers' Compensation Authority (INAIL), Italy

Abstract:

Background: There is sufficient evidence for a causal association between exposure to asbestos and ovarian cancer.

Aims: We aimed to estimate deaths from ovarian cancer attributable to asbestos exposure in Lombardy region, Italy.

Methods: This ecological study is based on Italian National Institute of Statistic (ISTAT) mortality data. We formulate a trivariate Bayesian joint disease model to estimate the attributable fraction (AF) and the number of ovarian cancer deaths attributable to asbestos exposure, from the geographic distribution of ovarian, pleural and breast cancer mortality at municipality level from 2000 to 2018. Expected deaths and standardized mortality ratios were calculated using regional rates.

Results: We found shared dependencies between ovarian and pleural cancer, which capture risk factors common to the two diseases (asbestos exposure), and a spatially structured clustering component shared between ovarian and breast cancer, capturing other risk factors. Based on 10462 ovarian cancer deaths, we estimated that 574 (95% Credibility Interval 388-819) were attributable to asbestos (AF 5.5%; 95% Credibility Interval 3.7-7.8). In some municipalities with heavy asbestos pollution, AF was as high as 34-47%.

Conclusions: The impact of asbestos on ovarian cancer occurrence can be relevant, particularly in areas with high asbestos exposure. Estimating attributable cases was possible only by using advanced Bayesian modelling to consider other risk factors for ovarian cancer. These findings

are instrumental in tailoring surveillance programs and implementing compensation and prevention policies.

Invited 5: Challenges and advances in areal data statistical modeling

Model validation for small area estimation models using complex survey data

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University of California, Santa Cruz, United States of America

Abstract:

Small area estimation (SAE) has been extensively used in official statistics to estimate quantities of interest in small domains with few or no samples available. A wide variety of methods have been proposed in the SAE literature from different philosophical views. However, model validation, checking, and comparison has been lacking the SAE literature. We discuss different approaches and scoring metrics to model validation in this talk, with the focus on estimating prevalence of a binary indicator at different levels of granularity. The work is motivated by the routine task of prevalence estimation using Demographic Health Surveys (DHS) in low- and middle-income country context, where data is sparse and auxiliary information usually does not exist.

Invited 6: Beyond the Basics: advanced use of INLA for spatial analysis

Bayesian modelling for the integration of spatially misaligned health and environmental data

Authors:
Moraga, Paula

Affiliations:
KAUST, Saudi Arabia

Abstract:

Spatially misaligned data is increasingly common primarily due to advancements in data collection and management. In this talk, I will present a flexible and fast Bayesian modelling framework for the combination of data available at different spatial resolutions and from various sources. Inference is performed using INLA and SPDE, which provides a fast approach to fit latent Gaussian models. The approach is flexible and can be applied in preferential sampling and spatio-temporal settings. The Bayesian modelling approach is demonstrated in a range of health and environmental settings. Specifically, a spatial model is developed to combine point and areal malaria prevalence data, and to integrate air pollution data from different sources. The approach presented provides a useful tool in a wide range of situations where information at different spatial scales needs to be combined, and provides valuable insights for decision-making in health and environmental fields.

Invited 6: Beyond the Basics: advanced use of INLA for spatial analysis

Multivariate Models to Explore Gender-Based Violence in Areal Data

Authors:
Ugarte, Lola;
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Abstract:

Univariate spatio-temporal models have been widely used in disease mapping, mainly to study the evolution of geographical patterns of chronic diseases such as cancer.

However, and despite their potential, multivariate models are not so widespread in practice due to computational burden and difficulties in implementation.

In this work, we present multivariate spatio-temporal P-spline models to analyze several crimes against women in

the districts of Maharashtra (India).

The joint modelling of the different crimes improves the precision of the estimates in comparison to univariate models and provides between-crime correlations. We will

briefly discuss other modelling appproaches when the number of areas increases significantly.

Invited 6: Beyond the Basics: advanced use of INLA for spatial analysis

Addressing Positional Anonymisation in Geostatistial Analyses of DHS Data

Authors:
Fuglstad, Geir-Arne;
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Paige, John;
Riebler, Andrea

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Abstract:
Geostatistical models using fine-scale covariate rasters are routinely applied for mapping demographic and health indicators in low- and middle-income countries. However, a key data source is household surveys from the Demographic and Health Surveys (DHS) program, where the GPS coordinates are intentionally jittered for privacy purposes. This jittering means that both the geographical coordinates of observations and the associated covariates have random errors. We demonstrate that ignoring jittering, which is almost always done, can lead to biases in the coefficients of the covariates and reduced predictive power, and propose a computationally efficient approach to account for the jittering. The approach uses Laplace approximations through Template Model Builder and is implemented in the R package GeoAdjust.

Invited 6: Beyond the Basics: advanced use of INLA for spatial analysis

Combining Laplace and VB for fast approximate Bayesian inference

Authors:
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Rue, Haavard

Affiliations:
KAUST, Saudi Arabia

Abstract:

Integrated nested Laplace approximations (INLA) provided a tool for efficient approximate Bayesian inference for many models, including spatial and spatio-temporal models. In this work however, we improve this methodology by proposing a novel hybrid approach that uses a low-rank variational Bayes correction to a high-dimensional Laplace approximation. The methodology can be applied to latent Gaussian models (the class of models for INLA) as well as non-latent Gaussian models of GAMM type. This new proposal enables us to essentially circumvent the "N" step in INLA, which was the most time-consuming. Now, we can do spatial modeling for discrete as well as continuous domains, in almost linear time with improved prediction performance. The method is implemented in the INLA R library.

Invited 7: Challenges and open problems in health surveillance and environmental epidemiology

Climate vulnerability and nutritional status variability in school-aged children and adolescents across the communities in the Mount Meru Ecosystem (Tanzania)

Authors:
Pirani, Monica

Affiliations:
Imperial College London, United Kingdom

Abstract:
The impact of environmental changes and climatic variability in Tanzania is highly heterogeneous among local communities, heavily affecting, among the others, food and water availability and access. In this study we present a spatiotemporal analysis of the nutritional status of 26,086 school-aged children and adolescents from 18 villages spread over the slopes of Mount Meru (Northern Tanzania), which is an active volcano located along the Eastern branch of the East African Rift Valley. The ecosystem of this region is characterised by sub-ecosystems which differ for rainfall, temperature, and soil quality. Population density is higher than the national average, although lower in the dryer portion of the landscape, dominated by rangelands and pastoral systems.

We characterise the nutritional status using anthropometric data (height, weight and the derived body mass index) collected over the years 2010-2015, as part of a series of development projects (overall five waves) aiming at improving food security across communities of Mount Meru ecosystem, which were implemented by a nongovernmental Tanzanian organization Oikos East Africa in partnership with the Italian Institute Oikos ETS. We assess the space-time trends in children and adolescents' nutritional status in relationship to the community-prevalent livelihood strategy (pastoralist, agropastoralist and farmers), socio-demographic characteristics, agro-environmental conditions and climate trends. Our analytical approach is grounded in a Bayesian setting and adopts a space-time geostatistical modelling framework.

Invited 7: Challenges and open problems in health surveillance and environmental epidemiology

Challenges and opportunities in global spatiotemporal modeling of seasonal and pandemic influenza.

Authors:
Naumova, Elena

Affiliations:
Tufts University

Abstract:

The combination of enhanced analytic capabilities and global surveillance systems for seasonal infections has created new opportunities to advance statistical methodology and deepen our understanding of global disease dynamics. We developed a framework to analyze the seasonality of infectious diseases using publicly available global health surveillance data. Specifically, our goals were to estimate seasonal characteristics and their uncertainties through mixed-effects models with harmonic components and the δ-method, and to create multi-panel visualizations that display the complex interplay of seasonal peaks across different geographic locations. For this study we compiled 2,422 weekly time series of 14 reported outcomes from 173 Member States, sourced from the World Health Organization's (WHO) international influenza virological surveillance system, FluNet, covering the period from January 1995 to June 2021. We estimated dominant seasonal peaks for spatially homogeneous counties from different climate zones and common travel patterns. We also develop a series of data visualizations to describe the global traveling waves of influenza, addressing issues of data completeness and credibility. Our results provide guidance for improving data collection, reporting, analysis, and the development of statistical methodologies and predictive approaches for spatiotemporal modeling. These steps will help to compile both structured and unstructured data for advancing AI-powered applications.

Invited 7: Challenges and open problems in health surveillance and environmental epidemiology

Modeling seasonality of malnutrition and effects of extreme weather on global food security.

Authors:
Venkat, Aishwarya

Affiliations:
Tufts University

Abstract:

Reduction of wasting or low weight-for-height is a key target towards the Zero Hunger Sustainable Development Goal. In 2022, approximately 45 million children under five suffered from wasting, with 93% of the global burden in low- or lower-middle-income countries. Despite the recognition of this inter-sectoral priority, accounting for locally specific seasonal patterns of wasting remains a “missing piece” of the nutrition puzzle. Short-term fluctuations in weight and weight-for-height measures render nutrition surveillance of relevant indicators particularly challenging. We demonstrated potential solutions to address current data and analytical limitations in both spatial and temporal domains by pooling data from existing cross-sectional data sources and aligning spatial and temporal boundaries to facilitate seasonality analysis. We compiled 15 years of child-level anthropometry from Standardized Monitoring and Assessment of Relief and Transition (SMART) surveys, the USAID Demographic and Health Surveys (DHS), which has been collecting household data in 90 countries for over 30 years, and the UNICEF Multiple Indicator Cluster Survey, which has been collecting a slate of public health indicators from households in 120 countries for 29 years. Pooling data from all three sources and aligning health records with the specially designed climate zones and extreme weather repository provided a foundation for extensive data analytics. We demonstrated the challenges and findings from this study.

Invited 7: Challenges and open problems in health surveillance and environmental epidemiology

Linking spatial data sets with LLMs to enable global nutrition modeling.

Authors:
Monahan, Kyle

Affiliations:
Tufts University

Abstract:

In establishing research programs to enable global nutrition modeling we need to assemble data set with matched spatial boundaries. In common global surveys collected location fields typically have variable spatial resolution, but generally classify the surveyed region into increasingly smaller administrative units or geographic boundaries (e.g. country, region, state, county, etc.). If the survey extent covers a large area and includes variable population densities, the survey may also include information about whether the surveyed area was urban, sub-urban, or rural. Once standardized, these fields can be utilized to match the survey location to a representative digital spatial feature. To facilitate spatial analysis, we must match survey outcomes with environmental, demographic, or socioeconomic characteristics extracted from various sources. We outline a workflow to facilitate this matching for large cross-sectional surveys spanning multiple countries with different spatial data collected in each survey. We illustrate a LLM-based approach to facilitate the linkages for several projects, including spatiotemporal modeling of cholera and nutritional outcomes in Yemen during the civil war of 2016-19 and malnutrition in Sahel region of Africa. We will also discuss the process of training, code and data sharing for such applications.

Invited 8: Advances in spatial epidemiology and ecology

The effect of spatio-temporal sample imbalance in epidemiologic surveillance using opportunistic samples: A case and simulation study using self-reported COVID-19 Symptoms Data

Authors:
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Neyens, Thomas (1,2)

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2: DSI, Hasselt University, Belgium

Abstract:

Online open surveys, commonly used to complement surveillance programs, often yield opportunistically sampled data with spatial and temporal imbalance. This can compromise the applicability of traditional models assuming randomised study designs. Our study used Flemish and Brussels' self-reported COVID-19 symptoms data from the Great Corona Study, a Belgian large-scale online open survey, to explore the performance of spatio-temporal statistical models in detecting and describing epidemiological trends despite spatial and/or temporal sample imbalance.

We first compared incidence trend estimates derived from spatio-temporal modelling with self-reported data to those from test-confirmed cases; a modest correlation of 0.25 was found, with a 26.6% average weekly agreement in the top 20 municipalities with the highest incidences. In a simulation study, we simulated self-reported COVID-19 symptoms incidences under different sampling scenarios to explore the impact of spatio-temporal sample imbalance, along with sample size and disease incidence, and on-trend detection via spatio-temporal modelling.

Our findings suggest that for most cases, spatial, temporal, or spatio-temporal sample imbalance in open surveys does not significantly impair model performance in trend estimation and high-risk area detection. However, maintaining balance in either space or time is crucial for low-incidence diseases to ensure accurate results. Furthermore, the study emphasises the importance of large sample sizes, asserting that investing in collecting substantial samples generally outweighs the need for spatio-temporal balance, especially when dealing with high-incidence diseases. Overall, the models highlight the resilience of spatio-temporal statistical approaches in handling imbalanced survey data for effective epidemiological trend analysis.

Invited 8: Advances in spatial epidemiology and ecology

Towards Integrated Spatial Health Surveillance

Authors:
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Abstract:

Statistical methods for near-real-time spatial analysis of incidence/prevalence data have been available for at least 20 years but, to the authors' knowledge, have not yet been incorporated into routine public health surveillance. A possible explanation is that even in wealthy countries, the pro-active collection of comprehensive, spatio-temporally resolved data on incident cases of a particular disease can be prohibitively expensive. The ongoing COVID-19 epidemic, has led to growing interest, in the UK and elsewhere, in the use of affordable alternatives to traditional epidemiological study-designs and disease metrics, including mobile symptom-reporting apps (Fry et al, 2020, J. Med. Informatics) and biochemical analysis of wastewater samples (Cianella et al, 2023, Sci.Tot.Env.).

Analogous problems arise in low-income country settings, where surveys of so-called Neglected Tropical Diseases (Feasey et al, 2010,Brit.Med.Bull.) have typically been carried out for a single disease, with little or no consideration of the efficiency gains that could be obtained from combining surveys of multiple diseases with overlapping spatial distributions.

The statistical challenge in all of these cases is to exploit the potential efficiency gains from integrating multiple data-sources whilst identifying and adjusting for their potential biases. In this talk, we will describe several approaches that have been used to address this challenge, with a particular focus on the potential for combining high-volume, low-cost proxies for disease incidence/prevalence with relatively small-scale gold-standard randomised incidence/prevalence surveys (Elliott et al, 2021, Science).

Invited 8: Advances in spatial epidemiology and ecology

A spatio-temporal latent factor model for sparse multivariate time series in ecology

Authors:
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3: Leuven Biostatistics and Statistical Bioinformatics Centre (L-BioStat), Department of Public Health and Primary Care, KU Leuven, Leuven, Belgium

Abstract:
Anthropogenic pressure is influencing the way species assemble into communities across the globe. Among others, changing climatological conditions, altered nutrient fluxes, land use changes and invasive species have become key drivers determining how species perform and interact, in addition to natural dynamics. Quantifying changes in community composition requires a substantial amount of data, often restricting the spatial, temporal and taxonomic scope and resolution of such efforts. Furthermore, existing methods typically require highly structured datasets, leaving other data sources unexploited. We developed a Bayesian hierarchical model that ordinates species communities through space and time, using a latent factor approach in which the site-loadings are spatiotemporally structured by means of Gaussian processes. As such, information is efficiently shared across space, time and species, mediating data sparseness. To flexibly accommodate opportunistically collected data, the broadest and most available class of biodiversity data, we embedded this construct within an occupancy-detection model structure to address false positives arising from imperfect and heterogeneous detection, e.g. due to seasonal or observer-induced effects. We applied our model to a large dataset of historical butterfly records in Flanders, enabling us to quantify changes in butterfly community composition at high spatial resolution in over a century’s time.

Invited 8: Advances in spatial epidemiology and ecology

Joint geostatistical modelling of lymphatic filariasis antigenaemia and microfilariae prevalence

Authors:
Fronterre, Claudio

Affiliations:
CHICAS, Lancaster University, United Kingdom

Abstract:

Lymphatic filariasis (LF) is a mosquito-borne neglected tropical disease targeted for global elimination by 2020. In recent years, the mapping of LF has been greatly facilitated by the use of simple and rapid detection tests based on the immuno-chromatographic test (ICT), which avoids the need to collect blood at night and the time-consuming preparation and examination of blood slides. Even if the scientific output of interest is the prevalence of microfilaraemia, the number of mapping surveys that measure MF is low, and it is decreasing due to the diffusion and cost-effectiveness of ICT tests. We develop a geostatistical model that exploits the abundance of ICT prevalence surveys and the relationship between ICT and MF prevalence to predict microfilaraemia prevalence at unobserved locations. We use LF data from West-Africa to show how this modelling framework can be used to produce relevant output for control and elimination programmes.

Contributed 01: Environmental exposures

Geostatistical analysis of geomasked PFAS food contamination data in Veneto Region (Italy)

Authors:
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Zamboni, Michela (2);
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3: Lancaster Medical School, Lancaster University, Lancaster, United Kingdom

Abstract:
Introduction: The Veneto Region conducted a PFAS food contamination monitoring campaign in 2016-2017, but faced legal challenges due to data non-disclosure, leading to citizen committees initiating legal action. We aim to employ a geomasking technique to determine an appropriate displacement distance that safeguards confidentiality, allows data disclosure and assures the integrity of geostatistical inference.

Methods: We analysed 886 samples (430 vegetables, 456 animals) collected from 692 agro-livestock in the study area. Model-based geostatistics was performed to predict the probability of positive sample specimens in 24 municipalities with contaminated water. A simulation study was conducted to balance privacy protection and analytical accuracy. We calculated the relative percentage difference of the rootmean-integrated-square error (RMISE) criterion using uniform geomasking at different maximum displacements (50 m, 100 m, 1 km, 2 km, 3 Km, 4 Km, 10 km, 15 km) and the original unperturbed coordinates.

Results: There was a higher probability of being positive in the towns in the north-central part of the contaminated aquifer. The simulation study shows that up to 3 km RMISE Relative Percent Difference is close to zero, thus suggesting negligible differences between the predictive probability generated using the geomasked and unperturbed data.

Discussion: When carefully implemented case-by-case, geographical masking protects geoprivacy while making georeferenced, individual-level data available to researchers. We proposed a simple procedure, applicable in various settings, through a simulation study to calculate the displacement required for georeferenced data to protect privacy and ensure the right to access information.

Contributed 01: Environmental exposures

Long-term effects of air pollution on adolescents' mental health: A two-stage Bayesian approach including exposure uncertainty

Authors:
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Blangiardo, Marta (1);
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2: University College London, United Kingdom

Abstract:

Investigating the extent of the health effects of air pollution exposure is a global mission, however, there are limited studies on mental health outcomes, especially in adolescents. This study aims to quantify the mental health effects (depression and anxiety) of long-term exposure to fine air particles (PM2.5) and nitrogen dioxide (NO2) in a London-based prospective cohort of adolescents.

The two-stage Bayesian hierarchical modelling approach is designed to propagate uncertainty from the first-stage air pollution exposure model to the second-stage mental health model. The exposure estimates derive from a new high-resolution 1km monthly spatiotemporal model for air pollution across Greater London. This uses the Stochastic Partial Differential Equation (SPDE) approach with computation based on the Integrated Nested Laplacian Approximation (INLA). Assimilating multiple sources of air pollution data, including satellite-derived observations and a numerical model, as well as predictive covariates, e.g., meteorology and population. We compared different modelling structures, considering different temporal terms, spatially-varying coefficients, and additional data sources, to select the final model.

Using the best prediction model for PM2.5 and NO2, we estimate air pollution exposure at the residence and school for each adolescent, bringing through a measure of uncertainty from the model. We investigate the complex relationship between air pollution and questionnaire-based depression and anxiety scores, considering proximity and access to greenspaces as a potential effect modifier of this relationship. We also account for the participants' socioeconomic background, such as parents' jobs and education, and underlying physical health, including respiratory health conditions.

Contributed 01: Environmental exposures

A distributed-lag non-linear model for predictors with interacting effects

Authors:
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Abstract:

Background:

High temperatures are recognized for impacting human health and increasing mortality rates. Distributed lag non-linear models (DLNMs) offer flexibility in modelling both immediate and delayed temperature effects. Usually, a single summarizing temperature measure is used, such as maximum or minimum temperature. However, including both temperature measures simultaneously might enhance model performance and epidemiological insights. Current DLNM implementations permit joint modelling of two lagged effects, typically treated additively. However, epidemiological research suggests that their effects may interact.

Methods:

This study introduces an extended DLNM, allowing for interacting lagged effects between two predictors. Examining all-cause mortality in Flanders (2000–2019) during summer (May 15 to September 30), we compare our model to traditional DLNM parametrizations. These include modelling the lagged effect of temperature based on: solely maximum, solely minimum and the additive combination of both. The effect is studied for different age and sex groups. The selected model is used to perform a spatial risk-analysis at municipality level.

Results:

Results indicate that the model allowing for interaction effects between maximum and minimum temperatures provides flexibility towards the analysis of two interacting predictors with time-delayed effects on an outcome of interest. Through this, we show that both temperatures impact mortality but based on age, sex and temperature distribution, attributable fractions differ between municipalities.

Conclusion:

Typically only a single temperature measure is used in research. Our new modelling approach, however, provides a flexible way to correct for interacting time-delayed effects in a DLNM context.

Contributed 02: Data science tools for spatial modeling

Measuring geographic access to emergency obstetric care: a comparison of travel time estimates modelled using Google Maps Directions API and AccessMod in three Nigerian conurbations

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8: University of Geneva, Geneva, Switzerland;
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10: Maternal and Reproductive Health Research Collective, Lagos, Nigeria

Abstract:

Google Maps Directions Application Programming Interface (API) and AccessMod tools are increasingly being used to estimate travel time to healthcare. However, no formal comparison of estimates using both tools has been conducted. We model and compare median travel time (MTT) to comprehensive emergency obstetric care (CEmOC) using both tools in three Nigerian conurbations. We compiled spatial layers of CEmOC healthcare facilities, road network, elevation, and land cover in Kano, Port-Harcourt, and Lagos conurbations, Nigeria, and used a least-cost path algorithm within AccessMod to estimate MTT to the nearest CEmOC facility. Comparable MTT estimates were extracted using the API for peak and non-peak travel scenarios. We investigated the relationship between MTT estimates generated by both tools at pixel-level (0.6km2). We aggregated the pixel estimates to generate an administratively relevant ward-level MTT. We compared ward-level estimates and identified within-conurbation wards falling into different 15-minute incremental categories (<15/15-30/30-45/45-60/+60). Of the 189, 101, and 375 wards, 72.0%, 72.3% and 90.1% were categorised in the same 15-minute category in Kano, Port-Harcourt, and Lagos, respectively. Concordance decreased in wards with longer MTT. AccessMod MTT were longer than API's in areas with longer travel times (~45min). At the pixel-level, MTT had a strong positive correlation (≥0.8) in all conurbations. Adjusted R2 from a linear model (0.624-0.723) was also high, increasing marginally in a piecewise linear model (0.677-0.807). In conclusion, at shorter travel times,

ward-level estimates from API and AccessMod are marginally different, however, at longer travel times substantial differences exist, which are amenable to derived conversion factors.

Contributed 02: Data science tools for spatial modeling

Spatial distribution of poultry farms using point pattern modelling: a method to address livestock environmental impacts and disease transmission risks

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5: Royal Veterinary College, UK;
6: INRAE, France

Abstract:

Information on the location and size of farms is essential for monitoring the spread of diseases, particularly when livestock production intensifies and farms cluster near cities. However, those data are not available in many countries, their generation being resource-intensive. Here, we develop a farm distribution model (FDM), which allows the prediction of locations and sizes of poultry farms in countries with scarce data. The model combines a Log-Gaussian Cox process model to simulate the farm distribution as a spatial Poisson point process, and a random forest model to simulate farm sizes (i.e. the number of animals per farm). Spatial predictors were used to calibrate the FDM on intensive broiler and layer farm distributions in Bangladesh, Gujarat (Indian state) and Thailand. The FDM yielded realistic farm distributions in terms of spatial clustering, farm locations and sizes, while providing insights on the factors influencing these distributions. Finally, we illustrate the relevance of modelling realistic farm distributions in the context of epidemic spread by simulating pathogen transmission on an array of spatial distributions of farms. We found that farm distributions generated from the FDM yielded spreading patterns consistent with simulations using observed data, while random point patterns underestimated the probability of large outbreaks. Indeed, spatial clustering increases vulnerability to epidemics, highlighting the need to account for it in epidemiological modelling studies. As the FDM maintains a realistic distribution of farm location and sizes, its use to inform mathematical models of disease transmission is particularly relevant for regions where these data are not available.

Contributed 02: Data science tools for spatial modeling

Analyzing urban landscapes through satellite data to predict abundance of Aedes mosquito breeding sites

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Abstract:

The spread of mosquito-transmitted diseases such as dengue is a major public health issue worldwide. Aedes aegypti mosquitoes, one of the primary vectors for dengue, thrive in urban environments and breed mainly in artificial and natural water containers. A better understanding of the relationship between urban landscapes and potential breeding sites would help mitigate the risks associated with these diseases. This study examines the relationship between urban landscape characteristics derived from remote sensing and the abundance and type of potential breeding sites in cities of French Guiana, South America, provided by the surveys carried out by the regional vector control service. A Multiple Factor Analysis revealed variables associated with the abundance of breeding sites, including building area, landscape form index, number of buildings, and texture indices. We obtained a good fit between predicted and observed values of breeding sites abundance using Random Forest models, with varying effectiveness depending on the type of breeding site. Since in-situ breeding site data were not specifically acquired for the purpose of this study, the dataset showed some limitations. However, we were able to apply this model in areas where entomological data were not available. This approach also has the potential to be used as input in the modelling of mosquito dynamics. This research highlights the usefulness of urban characteristics based on satellite data for improving vector control strategies.

Contributed 03: COVID-19 Epidemiology and Response

Capturing the spatiotemporal spread of COVID-19 in 30 EU/EEA countries during 2020 – 2022

Authors:
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2: Centre for Health Economic Research and Modelling Infectious Diseases, Vaccine and Infectious Disease Institute, University of Antwerp, Belgium

Abstract:

Background: In Europe, significant evidence points to key factors shaping COVID-19 transmission within the region. However, these factors vary among countries, leading to a gap in understanding how the disease evolves and spreads across countries as a whole. We endeavor to understand the spatiotemporal spread of COVID-19 epidemics in 30 EU/EEA countries between 2020-2022.

Method: We employed a space-time endemic-epidemic model to analyze weekly COVID-19 cases across countries during the specified period. We considered the discrepancies in the population size, vaccine coverage encompassing primary and booster doses with presumed waning immunity, the Stringency Index, and the circulation of various viral variants while integrating the power law approach for movement approximation.

Results: Unsurprisingly, we found that intra-country transmission dominated across all countries over the three years, from approximately 82% to 99% at certain time points. Nevertheless, the contribution of inter-country transmission to the epidemics was remarkably low and can be neglected since the second half of 2021, when it remained consistently below 0.1%. We also observed early signs of the transition to endemicity starting from January 2022, with the endemic proportion rising from 2.5% to 17.6% by September 2022. Simulations derived from the model fit yielded similar results.

Conclusion: We presented a comprehensive view of the spatiotemporal dynamics of SARS-CoV-2 in the EU/EEA region. Our study also opens the question of whether cross-country transmission plays a greater or lesser role in epidemics. The study aids in anticipating the post-pandemic trajectory of SARS-CoV-2 and facilitating the adaptation of suitable control strategies.

Contributed 03: COVID-19 Epidemiology and Response

Spatio-temporal dynamic of the COVID-19 epidemic and the impact of imported cases in Rwanda

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4: University of Hasselt

Abstract:

Introduction

Africa was threatened by the coronavirus disease 2019 (COVID-19) due to the limited health care infrastructure. Rwanda has consistently used non-pharmaceutical strategies, such as lockdown, curfew, and enforcement of prevention measures to control the spread of COVID-19. Despite the mitigation measures taken, the country has faced a series of outbreaks in 2020 and 2021.

In this paper, we investigate the nature of epidemic phenomena in Rwanda and the impact of imported cases on the spread of COVID-19 using endemic-epidemic spatio-temporal models. Our study provides a framework for understanding the dynamics of the epidemic in Rwanda and monitoring its phenomena to inform public health decision-makers for timely and targeted interventions.

Results

The findings provide insights into the effects of lockdown and imported infections in Rwanda's COVID-19 outbreaks. The findings showed that imported infections are dominated by locally transmitted cases. The high incidence was predominant in urban areas and at the borders of Rwanda with its neighboring countries. The inter-district spread of COVID-19 was very limited due to mitigation measures taken in Rwanda.

Conclusion

The study recommends using evidence-based decisions in the management of epidemics and integrating statistical models in the analytics component of the health information system.

Contributed 03: COVID-19 Epidemiology and Response

Social inequalities and the COVID-19 epidemic in France: territorial analyses by epidemic waves and metropolitan areas

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Abstract:

Context:

Previous studies highlighted relationships between socioeconomic inequalities and COVID-19 epidemic. In France, metropolitan areas show diverse socioeconomic heterogeneities, which could explain the differences observed in terms of incidence and testing rates. We assessed the variability of socioeconomic inequality impacts on COVID-19 through metropolitan areas and waves.

Methods:

For the 22 metropolitan areas (7187 neighborhoods), we defined socioeconomic profiles based on deprivation variables derived from census data, using classification on principal component. We analyzed associations between profiles, testing rates and incidences by epidemic wave, using spatialized generalized additive mixed models.

Results:

We highlighted the diversity of socio-economic profiles characterizing metropolitan areas (deprived or privileged suburbs or urban centers, privileged semi-rural areas).

Testing rates were on average 14% lower in the most deprived neighborhoods compared to the most privileged. Testing rates ratio (TRR) varied across metropolitan areas and waves (Quartile1 TRR=0.80; Quartile3 TRR=0.96). The Nice metropolitan area was an exception (Quartile1 TRR=1.17; Quartile3 TRR=1.45) as testing rate between these profiles were similar during the summer-autumn 2021 (wave4) (Median TRR=1.00).

Incidence rates were on average 29% higher in the most deprived neighborhoods compared to the most privileged between July-2020 and October-2021 (waves2-4). Incidence rates ratio (IRR) between deprived and privileged neighborhoods differed across metropolitan areas during these waves (Quartile1 IRR=1.17; Quartile3 IRR=1.40).

Conclusion:

The impact of social inequalities on the COVID-19 epidemic was driven by the specificities of metropolitan areas and epidemic waves. This may be explained by differences in prevention measure implementation (lockdown, vaccination…), different population behaviors, and specific socioeconomic contexts.

Contributed 03: COVID-19 Epidemiology and Response

Multiscale Spatio-temporal Modeling of Covid-19 case incidence and mortality

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Abstract:
During the Covid-19 pandemic many attempts were made to model state or national level time series of case counts or mortality

To a much lesser extent, some effort was focused on spatial aspects of the pandemic and there are a few example of spatio-temporal modeling at finer spatial scales.

It is clear that spatial aspects are important in pandemic spread at a variety of scales (both spatial and temporal)

Usually, the different scales are modelled separately. However there could easily be shared impact of linkages between levels.

In this talk we outline the basic linkage models which can be set up across spatial scales and their potential linkages (mainly)via random effects.

CDC in the US now has public domain data at county level weekly mortality and case incidence for Covid19 pandemic for all US states.

We give an example of modeling Covid19 mortality where weekly data is available now for 173 week periods at county level and state level in the US.

A simple example of one state with associated counties is given. At the state level we have time series models and at the county level spatio-temporal modeling.

Linkage is by shared effects. In principal, spatio-temporal models at state level can also be used. Comparison of models with and without linkage is made.

The approach can be extended to multivariate multiscale modeling for Covid19 data whereby case incidence, mortality and hopitalizations could be examined.

Contributed 04: Health inequalities and care

Spatial variation in inequality distribution of all-cause and cause-specific premature mortality in Belgium since 2000

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Abstract:
The risk of premature mortality varies across different sub-populations over both space and time, influenced by numerous factors, including levels of socioeconomic deprivation. Our study assesses the spatio-temporal variations of all-cause and cause-specific premature risk of dying between 2000 and 2019 at the subnational level in Belgium. We use a hierarchical Bayesian spatio-temporal model to study the variation of standardized mortality ratios (SMRs) and their association with deprivation, measured by the Belgian Index of Multiple Deprivation 2011 (BIMD2011). The results show that a unit increase in deprivation score raises the chances of dying prematurely by about 13%, equally for men and women. The majority of cause-specific SMRs have increased over time, suggesting an increase in inequality, the magnitude of which differs by sex, cause-of-death, and period. Throughout the study period, municipalities with the highest SMRs are primarily situated in Wallonia, while municipalities with the lowest SMRs are found in Flanders.

Contributed 04: Health inequalities and care

Socio-economic inequalities and access to healthcare during the COVID-19 pandemic: analyses in rural areas in southern France

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Abstract:
Context:

Previous studies highlighted the impact of socioeconomic inequalities and disparities in healthcare access during the COVID-19 epidemic, but few investigated rural areas specifically. Focusing on rural areas of Provence-Alpes-Côte-d'Azur (PACA), a geographically diverse region in Southern France, we aimed to determine factors associated to COVID-19 testing and incidence at the finest geographic scale (neighbourhoods, total=666).

Methods:

We created different socioeconomic, environmental, healthcare and testing access profiles with >60 variables from national databases using principal component analyses and classifications. We analysed the relationship between these profiles and testing and incidence rates per epidemic wave using spatialized generalized additive mixed models, to consider confounding factors.

Results:

We observed various profiles within the region’s rural areas, with a significant gradient between access to healthcare and testing rates. Testing rates were lower in neighbourhood with the highest distance to testing facilities and the lowest access to healthcare in general compared to the neighbourhoods with the highest access (example: wave 2 from july-2020 to january-2021, TRR (Testing Rate Ratio) =0.72[0.67-0.78]). During waves 4 to 7 (July-2021 to August-2022), less privileged neighbourhoods were less tested than the most privileged (average TRR=0.93). During the 5th wave (October-2021 to March-2022), incidence rate was higher in natural high-altitude neighbourhoods compared to agricultural and artificial land areas (IRR (Incidence Rate Ratio) =1.09[1.03-1.15]), similarly to wave 8 (autumn 2022, IRR=1.11[1-1.23]).

Conclusion:

Our study highlighted the impact of healthcare accessibility on testing in rural areas. It showed that significant differences can be identified within rural areas of the PACA region.

Contributed 04: Health inequalities and care

Model-based disease mapping using primary care registry data

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Abstract:

Background. Spatial modeling of disease risk using primary care registry data is promising for public health surveillance. However, it remains unclear to which extent challenges such as spatially disproportionate sampling and practice-specific reporting variation affect statistical inference.

Methods. Using lower respiratory tract infection data from the INTEGO registry, modeled with a logistic model incorporating patient characteristics, a spatially structured random effect at municipality level, and an unstructured random effect at practice level, we conducted a case and simulation study to assess the impact of these challenges on spatial trend estimation.

Results. Even with spatial imbalance and practice-specific reporting variation, the model performed well. Performance improved with increasing spatial sample balance and decreasing practice-specific variation.

Conclusion. Our findings indicate that, with correction for reporting efforts, primary care registries are valuable for spatial trend estimation. The diversity of patient locations within practice populations plays an important role.

Contributed 05: Wastewater based surveillance

Utilisation of wastewater-based epidemiology in the post-pandemic era: a data integration approach

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Abstract:

During the COVID-19 pandemic, wastewater-based epidemiology (WBE), a suite of methods to detect and measure viral contents in wastewater, has been recognised as an efficient surveillance tool to monitor the disease. In this talk, we consider the use of WBE in the post-pandemic setting, in which data collection through national randomised surveys is run at a reduced scale but wastewater data, a spatially refined and low-cost disease metric, can be used to complement the reduced health data for disease monitoring in a cost-effective manner. Using measurements collected from a network of sewage treatment works, we construct a space-time geostatistical model to predict wastewater viral load at a fine spatial-temporal scale for the whole of England. We develop a data integration framework to combine these wastewater viral predictions with prevalence estimates obtained from public health data collected through randomised surveys and community testing. The data integration framework aims to produce prevalence nowcast at a fine spatial scale when prevalence estimates can only be derived at a coarse spatial level due to the scaled-down health data collection. The results from our cross-validation demonstrate the added-values of wastewater data, not only improving the accuracy of the prevalence nowcast but also reducing the nowcast uncertainty. Our investigation also highlights the critical role of the coarse-level prevalence estimates in anchoring the wastewater data, thus calling for the need to maintain some form of reduced-scale national prevalence survey in the non-pandemic periods.

Contributed 05: Wastewater based surveillance

Estimating sub-national surveillance sensitivity for wild poliovirus in Nigeria to inform declaration of elimination

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Abstract:

The global eradication of wild poliovirus is now in its final stages. As this initative approaches its goal, in remaining endemic countries we see extended periods of absence of detected virus, prompting debate around declaring elimination. Premature declaration and cessation of vaccination could result in catastrophic resurgence, and it is uncertain how long is necessary to wait to be confident of the absence of circulating infection.

Confidence in elimination is dependent on data collected and assumptions about sensitivity and consistency of the surveillance system over time and space. We present a statistical framework to estimate time-varying sensitivity of two central components of polio surveillance - wastewater sampling and clinical cases - for detecting infection on a sub-national level. We then estimate the probability of freedom from infection (FFI) at a critical prevalence level, given absence of detected virus. This allows us to explore how variability in surveillance data influences our interpretation of elimination attainment on a national level.

We applied this framework to the period of absence observed in Nigeria from 2013-2016, ascertaining the FFI probability that would have accumulated at the point when WPV1-positive cases were again detected in July 2016. We find substantial spatial heterogeneity in surveillance coverage and sensitivity, and conclude that re-observing WPV1 infection after 30 months of absence was not surprising given the extent of surveillance activity during this period. This analysis demonstrates that timelines for declaring elimination could, and should, be informed by local, time-updated estimates of surveillance sensitivity within the setting of interest.

Contributed 05: Wastewater based surveillance

Spatial-temporal Modelling Using Wastewater for Norovirus Surveillance

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Abstract:

Wastewater-based epidemiology is a valuable surveillance tool that has recently emerged as a cost-effective method for early detection and surveillance of viral outbreaks. Extensive research was conducted during the COVID-19 pandemic. However, there remains a notable gap in the development of spatially explicit models to predict wastewater concentrations of other pathogens, such as norovirus, at fine spatio-temporal resolutions covering entire regions or countries. This research considers norovirus, the most common cause of acute gastroenteritis globally. Norovirus surveillance in the UK relies on clinical samples from confirmed outbreaks in hospitals, excluding mild and asymptomatic cases, which underestimates the true disease burden. Wastewater-based epidemiology can overcome this issue though being virtually free from selection bias, thereby improving the estimates of norovirus activity.

In this study, we address this through specifying a geostatistical model that quantifies the relationship between fortnightly norovirus concentration in sewage treatment works' (STWs) catchment areas and relevant covariates including viral genogroup, indices of deprivation, demographic factors (including proportion of Black, Asian, and Minority Ethnic populations and age structure), land use and population mobility. We used data on fortnightly average of flow-normalized norovirus concentration, reported as the number of viral gene copies per 100 000 people, collected from 152 STWs between 27-5-2021 and 30-3-2022. We accounted for spatial and temporal correlations to map fortnightly norovirus concentrations at desired levels of spatial resolution. We then extended the model to predict norovirus activity using public health surveillance data, which is important for policy makers.

Contributed 05: Wastewater based surveillance

Spatial modelling of viral loads in wastewater: an evaluation of sampling strategies for comprehensive surveillence programs

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Abstract:

Wastewater based surveillance of respiratory pathogens has become popular since SARS-CoV-2 RNA was successfully detected in municiple wastewater systems in 2020. Monitoring wastewater does not suffer from some limitations of clinical surveillance strategies such as variability in case ascertainment rate and delays between infection and reporting, but raises different challenges.

In this work we approach two important challenges. Firstly, the geographical 'catchments' that feed waste to each treatment plant frequently have boundaries that differ from administrative areas, making comparison to clinical outcome data challenging. Secondly, it is not clear how many and which treatment plants to monitor to provide sufficient resolution to make clinically relevant epidemiological inferences. We analyed viral loads measured in SARS-CoV-2 monitoring program between January 2022 and January 2023, with samples from 120 treatment plants in Switzerland.

First, we generated treatment plant sampling strategies, selecting sub-sets of monitored treatment plants under different frameworks, making use of geographical proximity, mobility data and by applying timeseries clustering to the measured viral load timeseries. Secondly, we developed a spatio-temporal model of viral loads to predict viral loads at postcode level. We aggregated predicted viral loads to evaluate the predictive power of different sampling strategies when imputing viral concentrations in the excluded treatment plant catchments. We also evaluated the predictive value of the modelled viral loads at canton level by quantifying the translation etropy between our estimates and hospitalisations at a contonal level.

Contributed 06: Advancements in disease mapping

Assessing the impact of neighborhood structures in Bayesian disease mapping

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Abstract:
Background: In Bayesian disease mapping, defining the neighborhood structure is a key step when fitting the conditional auto-regressive model. Yet, there has been little assessment of how different neighborhood structures affect the model performance in case of fine-resolution scale data. This paper rigorously explores this gap.

Methods: In a case study examining COVID-19 pandemic effects, 2020 mortality is contrasted with pre-pandemic rates (2009-2019) in small areas in Limburg (Belgium). Mortality data is modeled using BYM and BYM2, with three broadening neighborhood structures and two weight schemes. A simulation study assesses model performance in reproducing spatial correlation. In addition, models are compared in terms of WAIC, goodness-of-fit, parameter estimates, and computation time.

Results: In our study, the BYM model appears to outperform the BYM2 model and the order-based weight matrix performs better than the binary matrix. The simple first-order neighborhood structure shows comparable performance to larger structures with higher-order neighbors while requiring much less computation time. Our findings suggest minimal advantages in employing higher-order neighborhood matrices.

Conclusions: Our study indicates that opting for a simple first-order neighborhood structure is a pragmatic and suitable choice when applying a conditional auto-regressive model to fine-scale data in Bayesian disease mapping.

Contributed 06: Advancements in disease mapping

Disease mapping: What if Tobler's First Law of Geography doesn't hold?

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Abstract:

Identifying areas with extreme or unusual disease risks (compared to nearby areas) allows public health administration to implement targeted interventions in high-risk areas to reduce the population's health disparities and identify possible drivers of low-risk areas. Since an area's true disease risk cannot be observed directly, practitioners often fit statistical models to obtain spatially smoothed risk estimates from noisy standardised incidence ratios. These spatial smoothing models are fitted under the assumption that Tobler's First Law of Geography holds: "Everything is related to everything else, but near things are more related than distant things". However, the standardised incidence ratios of areas with extreme or unusual disease risks will likely differ substantially from those of nearby areas, and this possible violation of the spatial smoothness assumption could result in spatially smoothed estimates that do not accurately estimate the true underlying extreme or unusual disease risks. Therefore, in this talk, we outline tools to identify outliers for further investigation. We evaluate relative density-based outlier scores of the standardised incidence ratios in a formal hypothesis testing framework to identify areas where the spatial smoothness assumption of the true underlying risks might be violated. We then fit a spatial smoothing model with a locally relaxed spatial smoothness assumption for these extreme or unusual observations to obtain more accurate estimates of the underlying risks. We evaluate the efficacy of our method with a simulation study and present an application of our method using English small-area mental health data.

Contributed 06: Advancements in disease mapping

Optimizing the use of exceedance probabilities in disease mapping: a simulation study

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Abstract:

Model-based disease mapping often employs exceedance probabilities (EPs) to detect areas of high risk. The EP of an areal unit usually represents the probability that the relative risk within that areal unit is greater than a given threshold value. In a Bayesian context, this is equal to the proportion of the relative risk's posterior distribution that lies above that threshold value c. High-risk areas are typically defined as those with EPs larger than a certain critical probability, e.g., 0.95. It is however unclear to which extent the choices regarding c and the critical probability affect EPs' sensitivity and specificity in detecting high-risk areas, and if the optimal choices vary under different circumstances, such as the number areal units the studio region consists of, the severity of the disease risk, etc.

Using a random forest classifier approach, we develop a decision rule, based on the best combination of threshold values and critical probabilities to detect high-risk areas. In a simulation study, we test specificity and sensitivity of several threshold values and critical probabilities under multiple scenarios that differ in the characteristics of spatial patterns of increased risks, the magnitude of elevated risks and the magnitude of the overall disease risk throughout the region. The goal is to provide recommendations for researchers interested in employing EP at their full potential for high-risk area detection in disease mapping.

Contributed 06: Advancements in disease mapping

Analysing time trends for cognitive impairment across the U.S.A states.

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Abstract:

Cognitive impairment (CI)is when a person has trouble remembering, learning new things, concentrating, or making decisions. CI is costly, people with CI report more than three times as many hospital stays as people hospitalized for some other condition. It is estimated that more than 16 million people in the United States live with CI, still little is known about its prevalence at the state level and its temporal development.

In this study, we consider data from 15 consecutive cross-sectional waves (2008-2022) of the American Community Survey (ACS), an annual survey which replaced the decennial census, and that uses a representative sample of the US population including those living in the community and institutions. Our goal is to study the development, in space and time, of CI for 50 US states. While most study focuse on CI for oldeg ages, here we consider people between 18 and 85.

We develop a Bayesian version of the Lee-Carter model where, in order to capture the space-time dynamics, some the components (age or time effects) are allowed to vary in space according to a CAR model. We fit the model using the recently developed inlabru software package. inlabru extends the types of models that can be fitted using the popular INLA methodology, by allowing the latent predictor to be non-linear in its parameters, moving beyond the additive linear predictor framework to allow more complex functional relationships. We show how our model can be used both to understand space-time patterns and for predictions

Contributed 07: Vector-borne diseases and spatial data integration

A novel approach to mapping Japanese encephalitis virus in Asia with convolutional neural networks

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Abstract:

Japanese encephalitis virus (JEV), a mosquito-borne virus endemic to Asia and the western Pacific, is the leading cause of vaccine-preventable encephalitis in these regions, causing over 20,000 deaths in 2019. Despite its impact, detailed JEV occurrence data is sparse due to frequent misdiagnosis, low levels of serological confirmation, and epidemiological reporting typically occurring at the state or national level. We conducted a literature review to identify geocodable records of JEV occurrence, yielding 1,322 data points over the past 30 years with 68% of these records on the Indian subcontinent. We use these occurrence data with high-resolution remotely sensed covariates and a convolutional neural network (CNN)-based approach to model probability of JEV occurrence at 100m x 100m resolution, a first for the region and a significant improvement over past research. Our model incorporates 13 covariates, including remotely sensed climate and environmental data, as well as population, land use, vector habitat, and animal density. Initial results are promising, with a 0.79 probability of occurrence predicted for the validation dataset, comprised of 15% of our JEV observations withheld from model training and testing. Bangladesh, India, and mainland Southeast Asia have some of the highest probabilities of occurrence, above 0.9, with large patches of high predicted occurrence through eastern China and Indonesia despite a lack of existing data, indicating potential burden in these areas. This approach not only offers a more detailed understanding of JEV distribution but also supports the development of targeted intervention strategies, aiming to mitigate the disease's impact in endemic areas.

Contributed 07: Vector-borne diseases and spatial data integration

Use of syndromic surveillance data in the design of climate-driven early warning systems for dengue epidemics: feasibility study in Cambodia

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Abstract:
Dengue is a mosquito-borne viral disease that causes recurrent epidemics in Cambodia, a Southeast Asian country where the disease is endemic. Climate has a major impact on vector spread and human behavior, so the importance of climate indicators in the design of early warning systems is crucial. While climate data are becoming increasingly qualitative and accessible, the health data needed to feed such models remain limited in quality, spatial resolution, access and latency. Primarily based on clinical factors, syndromic data are typical health data from low-income countries and offer timely and regularly reported information, serving as a valuable foundation for establishing health surveillance information systems. Acute hemorrhagic fever, i.e. the clinical diagnosis of dengue, is a notifiable syndrome in Cambodia. This study aims to investigate the potential use of acute hemorrhagic fever data, in designing climate-driven early warning systems for dengue epidemics. Machine learning models based on climate indicators obtained from publicly available satellite images have been set to estimate the weekly dynamics of acute hemorrhagic fever in Cambodia. The same framework was tested at the province scale to inform at a larger resolution. Our results highlight the impact of extreme climate events on dengue epidemics at different scales and investigate the limitations and robustness of syndromic data. It supports the importance of linking climate indicators and health data in implementing operational early warning systems and defining appropriate warning thresholds to facilitate decision-making by public health services.

Contributed 07: Vector-borne diseases and spatial data integration

Spatiotemporally Explicit Epidemic Model for West Nile Virus Outbreak in Germany

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Abstract:

Since 2018 after the first autochthonous transmission of West Nile Virus in Germany (WNV) was detected, it has become endemic in several parts of Germany and has continued to spread due to the attainment of a suitable environment for vector occurrence and pathogen transmission. Increasing temperature associated with a changing climate has been identified as a potential driver of mosquito-borne disease in temperate regions. This scenario justifies the need for the development of a spatially and temporarily explicit model that describes the dynamics of WNV transmission in Germany.We developed a process based mechanistic epidemic model driven by environmental, entomological, and epidemiological data. Functional traits of mosquitoes and birds of interest were used to parameterize our compartmental model appropriately. Air temperature, precipitation, and relative humidity were the key climatic forcings used to replicate the fundamental niche responsible for supporting mosquito population and infection transmission risks in the study area. An inverse calibration method was used to optimize our parameter selection. Our model was able to generate spatially and temporally explicit basic reproductive number (R0) maps showing dynamics of the WNV occurrences across Germany, which was strongly associated with the deviation from daily means of climatical forcings, signaling the impact of a changing climate in vector-borne disease dynamics. Epidemiological data for human infections were used to validate model simulated transmission rates. The study presents a path for developing an early warning system for vector-borne diseases driven by climate change.

Contributed 07: Vector-borne diseases and spatial data integration

Enhancing Epidemic Intelligence with the MOOD Platform: Integration and Application in Public Health Surveillance

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Abstract:
The MOOD project is pioneering a transformative trajectory in epidemic intelligence (EI). The uniqueness lies in the synergistic integration of indicator-based and event-based surveillance, leveraging a blend of structured and unstructured data streams.

The MOOD platform centers on six case studies: West Nile virus infection, tick-borne encephalitis, antimicrobial resistance, COVID-19, Leptospirosis, Chikungunya, Dengue, and highly pathogenic avian influenza.

The platform features a central database with covariates, vector and disease data. The innovative use of these technologies in epidemiological contexts sets the MOOD platform apart from conventional tools.

The MOOD GeoNetwork meticulously catalogue comprehensive metadata used and produced by the MOOD experts as well as tools and models.

This presentation showcases the innovative MOOD information system architecture and its advanced features through practical examples. The platform is uniquely equipped with

advanced techniques for standardizing thematic, temporal, and spatial data, enabling the seamless integration and insightful spatial and temporal analysis of diverse pan-European datasets. The platform provides decision-makers with actionable intelligence, enhancing the precision of public health responses and shortens the response time in crisis situations. Key questions that can readily be explored include: Where is there a risk, which covariates are key to defining it, and how do they evolve over time? This reinvention of the EI landscape allows for a leap forward in health security and emergency preparedness.

To ensure its long-term sustainability once the project is closed the platform will be hosted, maintained and further developed as the ‘MOOD Epidemiological Platform Non-Profit Association’, with key-members of the MOOD consortium.

Contributed 08: Disease mapping and clustering

Geospatial patterns of excess mortality in Belgium: Insights from the first year of the COVID-19 pandemic

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Abstract:
Belgium experienced multiple COVID-19 waves that hit various groups in the population, which changed the mortality pattern compared to periods before the pandemic. In this study, we investigated the geographical excess mortality trend in Belgium during the first year of the COVID-19 pandemic. We retrieved the number of deaths and population data in 2020 based on gender, age, and municipality of residence, and we made a comparison with the mortality data in 2017--2019 using a spatially discrete model. Excess mortality was significantly associated with age, gender, and COVID-19 incidence, with larger effects in the second half of 2020. Most municipalities had higher risks of mortality with some exceptions in the northeastern part of Belgium. Some discrepancies in excess mortality were observed between the north and south regions. This study offers useful insight into excess mortality and will aid local and regional authorities in monitoring mortality trends.

Contributed 08: Disease mapping and clustering

Spatial distribution and determinants of tuberculosis incidence in Mozambique: A nationwide Bayesian disease mapping study

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Abstract:
Background

Mozambique is a high-burden country for tuberculosis (TB). International studies show that TB is a disease that tends to cluster in specific regions. Although Mozambique has a higher burden of TB, its spatial distribution is unknown. Therefore, we aimed to analyze the spatial distribution and determinants of tuberculosis incidence in Mozambique and identify the hotspot areas.

Method

We conducted an ecological study with the district as a unit of analysis (n = 154), where we included all new cases of tuberculosis diagnosed in Mozambique between 2016 and 2020. We obtained the data from the Mozambique Ministry of Health and other publicly available sources. The parameters were estimated using Bayesian hierarchical Poisson regression models and Markov chain Monte Carlo simulations.

Results

A total of 512,877 people were diagnosed with tuberculosis in Mozambique during our study period. We found high variability in the incidence of tuberculosis; the highest rates were concentrated in the south and the country's central region, while lower incidence rates were mainly in the north. Sixty-two districts out of 154 were identified as hotspot areas. We found

that TB incidence increased with an increase in HIV prevalence (RR: 1.23; 95% CrI: 1.13 to 1.34) and a reduced annual average temperature (RR: 0.83; 95% CrI: 0.74 to 0.94).

Conclusion

The incidence of tuberculosis is unevenly distributed in Mozambique. Lower temperatures and high HIV prevalence seem to increase TB incidence. Targeting interventions in higher-risk areas and collaboration between HIV and TB programs is paramount to ending tuberculosis in Mozambique.

Contributed 08: Disease mapping and clustering

Detecting Co-Occurring Clusters of Coronary Heart Disease and Depression in New England: A Neighborhood-Level Analysis

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Abstract:

Background: There is increasing evidence for the comorbidity of mental health disorders among coronary heart disease (CHD) patients due to similar etiologies and shared risk factors. This relationship has been studied among individuals, but few studies have examined co-occurrence at the neighborhood level.

Methods: Spatial scan statistics were used to detect potential co-occurring geographic clusters of CHD and depression among adults ages 18 and older in New England in 2019. Data for analyses were linked by location and included the CDC's PLACES dataset, Census estimates, EPA air quality, and other publicly available sources. Negative binomial regression models were used to adjust cluster analyses for relevant covariates, including age, sex, race, social vulnerability, urbanicity, pollution, walkability, greenspace, blue space, physical activity, healthcare utilization, and access to mental health facilities.

Results: Sixteen significant adjusted clusters were identified, including nine multivariate clusters and seven univariate clusters for depression (none for CHD). The highest multivariate relative risk (RR) was seen in the cluster around Bristol County, Massachusetts (22 Census Tracts, Depression RR=1.05, CHD RR=1.08). Among the univariate clusters for depression, the cluster with the highest RR was in southern Maine (141 Census Tracts, RR=1.14).

Conclusions: Clusters from adjusted analyses indicate clustering that is not explained by selected covariates alone, many of which were social determinants of health. Mixed-methods approaches could help explain remaining clustering. The methods used here can be used to identify high-risk areas in which to implement interventions for both conditions, such as increasing mental health care utilization and supporting health literacy.

Contributed 08: Disease mapping and clustering

Geospatial clustering of auto-antibodies against apolipoprotein A-1, heavy metals and cardiovascular diseases in the city of Lausanne, Switzerland

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Abstract:

Objectives: Exposure to heavy metals (HM), byproducts of combustion, is linked to an increased risk of cardiovascular diseases (CVD) even at levels. Auto-antibodies against apolipoprotein A1 (AAA1) that are pro-atherogenic and pro-steatotic are prevalent in the general population for reasons that are not yet clear. This study examines the potential correlation between exposure to HM, AAA1, and risk factors for CVD using geospatial clustering techniques at the general population of the city of Lausanne, Switzerland.

Methods: Utilizing the CoLaus/PsyCoLaus cohort of 6361 participants, we conducted geospatial analyses using local Moran's I and geographically weighted regression (GWR) to examine the spatial correlations among serum AAA1 levels, urinary HM (cadmium, arsenic, lead) concentrations and SCORE2 CVD risk.

Results: Associations were identified between cadmium, lead and SCORE2. Independently of SCORE2, AAA1 levels were linked to higher levels of cadmium ($p<0.05$). Geospatial analysis revealed significant overlap between AAA1 hotspots and those of cadmium. GWR indicated that the correlation between cadmium and AAA1 was strongest near railway regions, with the association strength increasing up to ten times more than the overall analysis. AAA1 showed no significant correlation with other HMs.

Conclusions: The study uncovers distinct geospatial associations among cadmium exposure, AAA1, and CVD risk scores in the general populace. It suggests that environmental exposure to cadmium might play a role in the emergence of AAA1 in humans. Further experimental research is underway to determine any causal connections. The potential of AAA1 as an early indicator of cadmium exposure and related health risks warrants further exploration.

Contributed 09: Mathematical modeling of infectious diseases

Spatial modeling in support of measles control and elimination

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Abstract:

Measles is a highly infectious disease that can lead to severe outcomes and even death, especially in children. Despite the availability of a safe and effective vaccine, measles remains endemic in many parts of the world, where routine immunization coverage is low and heterogeneous. To achieve measles control and elimination, it is essential to understand the spatial dynamics of transmission and the impact of different vaccination strategies in heterogeneous settings. In this study, we apply a multi-resolution spatial model of measles transmission, calibrated to demographic and epidemiological country data. Our study focuses on establishing benchmarks that can inform policy and underscores the significance of capturing the spatial dynamics of this highly contagious disease.

Contributed 09: Mathematical modeling of infectious diseases

A Declarative Approach to Metapopulation Modelling

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Abstract:

Epidemiological models aim to capture the complex dynamics of infectious diseases. Creating a new infectious disease model typically requires writing computationally efficient, pathogen-specific code, which is hard to maintain and extend. We constructed DeclaraMID to facilitate building and solving structured compartmental metapopulation models (i.e., the population is subdivided into geographically separated subpopulations) in a declarative manner, separating the model specifications from the model evaluation, either deterministic or stochastic. We demonstrate the framework's model-building potential by reproducing existing models for COVID-19 and the Ebola virus.

Firstly, we investigated disease dynamics in the 2013-2016 West African Ebola Epidemic. DeclaraMID enabled us to systematically investigate the impact of model complexity to capture disease dynamics, starting from a basic SEIR model, focusing on core disease dynamics. We progressively added compartments, age structures, and mobility to analyze heterogeneities between patches. The analysis revealed how mobility and age impact transmission and demonstrated the framework's flexibility in building custom models.

Consequently, we reconstructed a metapopulation model for COVID-19 in Belgium containing 589 municipalities and two age groups. Our framework achieved performance comparable to the original implementation while reducing the model code significantly, improving code safety, minimizing development time, retaining computational efficiency and code maintainability, showing such a framework’s importance during pandemics where model changes are made ad hoc.

The framework separates the model description from evaluation, improving modularity, safety, and development time. We demonstrated this by constructing two metapopulation models of various complexities, proving it to be a valuable tool for researchers during pandemics.

Contributed 09: Mathematical modeling of infectious diseases

Uncertainty quantification in the predictions of a Ebola outbreak using Bayesian data assimilation

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Abstract:
We present a spatial variant of the common SVEIRD (Susceptible-Vaccinated-Exposed-Infectious-Recovered-Dead) model of epidemiology to capture the transmission dynamics of the spread of Ebola in the 2018-2020 outbreak in the Democratic Republic of the Congo (DRC). The challenge is that population mobility is low in this area of Africa, and distances are long, so spatial epidemics tend to burn out, or they expand only slowly. As such, predicting the transmission dynamics of Ebola is challenging and comes with a lot of uncertainty. The goal of this research is to minimize this uncertainty using Bayesian data assimilation methods and provide insight that would support public health officials towards informed, data-driven decision making.

Our simulations show good correspondences between the model and the available sparse empirical data. A comparison between the weekly incidence data set and our compartmental model coupled with Bayesian data assimilation highlights the role of a realization conditioned on all prior data and newly arrived data. In general, the compartmental model with data assimilation gives a better fit than the model without data assimilation for the same time period. We present spatio-temporal disease maps for the infectious variable for the progress of Ebola in the North-Kivu and Ituri provinces of DRC during 2018-2020. This case study was conducted using real-world data from the WHO and practical simulation exercises using free and open-source software.

Our analysis sheds light more broadly on how Ebola spreads in a large geographical area with places where no empirical data is recorded or observed.

Contributed 09: Mathematical modeling of infectious diseases

Forecasting the spatial spread of an Ebola epidemic in real-time: comparing predictions of mathematical models and experts

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Abstract:
Ebola virus disease outbreaks can often be controlled, but require rapid response efforts frequently with profound operational complexities. Mathematical models can be used to support response planning, but it is unclear if models improve the prior understanding of experts.

We performed repeated surveys of Ebola response experts during an outbreak. From each expert we elicited the probability of cases exceeding four thresholds between two and 20 cases in a set of small geographical areas in the following calendar month. We compared the predictive performance of these forecasts to those of two mathematical models with different spatial interaction components.

An ensemble combining the forecasts of all experts performed similarly to the two models. Experts showed stronger bias than models forecasting two-case threshold exceedance. Experts and models both performed better when predicting exceedance of higher thresholds. The models also tended to be better at risk-ranking areas than experts.

Our results support the use of models in outbreak contexts, offering a convenient and scalable route to a quantified situational awareness, which can provide confidence in or to call into question existing advice of experts. There could be value in combining expert opinion and modelled forecasts to support the response to future outbreaks.

Contributed 10: Spatial epidemiology in low and middle income countries

Identifying High-Risk areas for Untimely Administration of the Hepatitis B Birth Dose (HepB-BD) in low-income settings.

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Abstract:

Background: Viral hepatitis, notably Hepatitis B, poses a substantial public health challenge in Sub-Saharan Africa due to Mother-to-child transmission. Timely administration of HepB-BD within 24 hours post-delivery is crucial for preventing both vertical and horizontal transmission. This study, concentrating on non-facility deliveries as a proxy for untimely HepB-BD, aimed to identify high-risk areas for untimely administration in low-income settings.

Methods: Utilizing secondary data from the 2016 Uganda Demographic and Health Survey (UGDHS), a cross-sectional study was conducted. The sample included 10,263 reproductive-age women nested within 696 clusters. The spatial distribution of non-facility delivery was explored using thematic maps and hotspot analysis. Mixed-effect logistic regression models examined factors associated with non-facility delivery. Spatial interpolation was used to create a surface delineating high-risk and low-risk areas for untimely HepB-BD administration.

Results: Non-facility delivery prevalence was 31.8%, with significant spatial variation. Proximity to healthcare facilities, urban residence and higher wealth index were associated with reduced risk of non-facility delivery at the cluster level. At an Individual-level, media exposure and secondary-level education were associated decreased risk of non-facility delivery. High-risk areas for untimely HepB-BD were concentrated in the eastern, east-central, western, and southwest regions.

Discussion: The significant spatial variability in high-risk regions for untimely HepB-BD due to non-facility delivery underscores the influence of contextual and individual factors. Geographically targeted public health interventions are necessary to address untimely HepB-BD administration, particularly in resource-limited settings. Furthermore, adopting a spatial epidemiological paradigm is imperative for effectively eliminating viral hepatitis in low-income settings.

Contributed 10: Spatial epidemiology in low and middle income countries

Plasma selenium concentrations are associated with spatial variation in maize selenium concentrations in Malawi; implications for assessing dietary selenium adequacy

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Abstract:

Selenium deficiency is widespread in Malawi and affects antioxidant defence and immunity responses (1,2). With predominantly localised food systems, dietary selenium intakes and population status show large, spatially-dependent variation at sub-national scales (2, 3). This is largely driven by the selenium content of foods which depends primarily on selenium availability in agricultural soils, influenced by soil pH and other agro-environmental factors (4, 5). Despite this, food composition data used to estimate dietary selenium (and other micronutrient) intakes are typically reported as single data points, national aggregations or imputed values from other countries (6). This limits the ability to estimate intakes accurately and identify populations at risk of inadequacy.

This study aimed to identify the optimal spatial aggregation for geo-referenced maize grain selenium data for predicting selenium status in Malawi, where maize provides >60% of dietary energy. Geo-referenced biomarker and socio-economic data for women (n=732) were obtained from the DHS-Micronutrient survey (7) and combined with aggregated maize grain selenium concentration (4, 8) and confounders. Bayesian spatial models were compared using Integrated Nested Laplace Approximation (INLA).

Maize selenium concentration was the main explanatory variable, increasing plasma selenium con-centration, followed by age in Malawian women, irrespective of the maize aggregation level. The inclusion of the distance to main lakes, proxy for fish selenium supply, improved the overall predic-tive power of the model (DIC -40 vs -106). Hence, accurate estimates of selenium concentrations in maize grain, as well as other foods, at the subnational level are important for improving selenium inadequacy estimates in Malawi.

Contributed 10: Spatial epidemiology in low and middle income countries

Disparities in timely antenatal care initiation in Kenya: A geostatistical modelling approach using Demographic and Health Survey data.

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Abstract:
Globally, the maternal mortality ratio (MMR) in 2020 remains unacceptably high at 223 maternal deaths per 100,000 live births. In Kenya, the MMR was 530 deaths per 100,000 live births in 2020, emphasizing the significance of antenatal care (ANC) to mitigate this burden. Initiating ANC in the first trimester (timely) enhances the likelihood of achieving the recommended eight contacts. Notably, in Kenya, of the 98% who sought ANC, only 29% initiated ANC in the first trimester. However, estimates of timely ANC initiation needed to highlight hotspots of low coverage are lacking. We examine the spatial variation of timely ANC initiation among women of reproductive age in Kenya at high spatial resolution.

We used cross-sectional data from the 2022 Kenya Demographic and Health Survey. The survey used a stratified, two-stage sampling design. We included the ANC history for the pregnancy leading to the most recent live births of 7,638 women aged 15–49 years in the two years preceding the survey. We then fit a geostatistical model to predict estimates of timely ANC initiation at 3*3 km spatial resolution. Estimates were summarised into subnational units of decision-making (counties).

In Kenya, the coverage of timely initiation was highly heterogeneous at the county level, ranging from 6.2% (CI: 4.0–9.6) in Mandera to 54.1% (CI: 44.8–63.2) in Vihiga County. Within the counties, the geostatistical model showed further variation, unmasking different hotspots. There is a need for tailored and targeted interventions in the identified hotspots to improve the uptake of ANC in the first trimester.

Contributed 10: Spatial epidemiology in low and middle income countries

Estimating Subnational Under-Five Mortality Rates Using a Spatio-Temporal Age-Period-Cohort Model

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Abstract:
Subnational estimates of under-five mortality rates (U5MRs) are a vital statistic for the United Nations to reduce mortality inequalities between high-income and Low-and-Middle Income Countries (LMICs). Current methods of modelling U5MR in LMICs smooth across trends in age and year of death, but not birth-cohort, to reduce uncertainty in estimates caused by data-sparsity. Using survey data, we innovatively apply an Age-Period-Cohort model which accounts for spatial trends and the complex survey design of the data to estimate subnational U5MRs in LMICs. After validating our results against current methods, the inclusion of cohort can provide new insights into U5MRs in LMICs.

Contributed 11: Spatial heterogeneity in epidemiological studies

Bayesian Age Decomposition Modeling of Covid-19 Space-time Dynamics

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Abstract:

Age dependence of Covid19 infection potential is clearly important, but there is limited public access to age structure in the Covid19 pandemic progression. In this presentation I develop a space-time Bayesian model for disease spread with age stratification. Without knowledge of the breakdown of age structure we assume that the age groups have different relevant infection rates and we also condition on the observed case counts or deaths. We use imputation to infer the distribution of age-specific case and death counts. To test the relevance of the approach we have obtained age-stratified (anonymized) case and death counts for the counties of South Carolina during the main waves of the pandemic. This is used to evaluate the method but will also be used to consider whether nowcasting can be used to examine counterfactuals for different counties and hence policy evaluation.

Contributed 11: Spatial heterogeneity in epidemiological studies

The effect of spatial scale in agent-based model epidemiology

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Abstract:

Modelling the spread of epidemics in low-income countries is frequently complicated by a lack of high-quality data that captures how people move between areas. Understanding this mobility is a key part of designing and assessing the potential impacts of different interventions. To meet this need, Call Detail Records (CDR) are increasingly used as a proxy for estimating human movement. CDR access is often complicated by privacy and security concerns, however, requiring legal processes that can act as a barrier to progressing a research agenda. This can be an especially serious limitation in time-sensitive disease contexts, when operationally usable data must be gathered quickly or not at all. How, then, can we meet this need? Drawing upon a body of CDR data made available to the team in conjunction with the Covid-19 pandemic in Zimbabwe, this paper seeks to do three things: firstly, to see how effectively a CDR mobility matrix can be replicated using gravity, radiation and departure-diffusion models. Secondly, to see how the accuracy of the matrix holds when attempting to predict movement at lower levels of spatial aggregation (that is, moving from district to ward level). Thirdly and finally, it inputs each of these mobility matrices into an Agent Based Model for COVID-19, to demonstrate the differences in the rate and spatial distribution of the spread of this infectious disease associated with these varying patterns.

Contributed 11: Spatial heterogeneity in epidemiological studies

Quantifying the heterogeneous effect of mobile health code in containing COVID-19 in China during the pandemic

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Abstract:

Timely case and close contact tracing and quarantine are vital for containing severe infectious disease outbreaks. During the COVID-19 pandemic, big data-driven techniques, such as mobile device location-based health (mHealth) apps, have been widely adopted to augment conventional epidemiological investigations. However, to what extent these digital techniques aid traditional approaches still lacks quantitative evaluation. Using aggregated statistical data from mHealth QR code based on mobile signalling tower positioning in Jiangsu province, China from March 2020 to May 2022, we assessed the effect of 6.07 million mHealth-warned quarantines and 10.51 million cross-city movements of people at risk in zeroing out the COVID-19 transmission. We found that the mHealth code could not replace traditional investigations for rapidly and precisely identifying cases and close contacts at early outbreaks. However, it showed greater advantages in preventing residual spread in the latter stage and dominated the eventual elimination of transmission. Delayed implementation of the mHealth code could lead to wider spread, especially in the face of more contagious variants. Compared with the actual situation, delaying implementing the mHealth for 7 days would lead to 2.65 (95% CI: 2.50 - 2.86) times more infections in the Delta variant dominant period, which would be up to 5.50 (4.65 - 6.41) times during the Omicron period. The intercity mobility-integrated simulations further suggested that restricted implementation of the mHealth code would result in spillover of pathogens between cities. Our findings support more cost-effective integration strategies of traditional epidemiological investigations and digital approaches to tackle future severe infections with pandemic potentials.

Contributed 11: Spatial heterogeneity in epidemiological studies

An extended two-stage modelling framework for multi-location epidemiological studies

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Abstract:

Multi-location studies are increasingly used in environmental epidemiology to analyse health effects of environmental factors across large geographical areas. Their application is supported by designs and statistical techniques developed in the last decades, which however have known limitations. These pertain to the ability to model and pool complex exposure-response relationships involving non-linearities and lags, the need to account for between-location differences partly related to multiple correlated socio-economic and climatological factors, among others, and the presence of sparse data that prevents the full mapping across the whole geographical domain.

In this contribution, we propose an improved modelling framework that addresses these issues. Specifically, this flexible framework allows first the direct modelling of variations in risk across locations, linked to both demographic differences and heterogeneity due to various vulnerability factors. In addition, the framework can account for spatial clustering due to unobserved differences modelled through geostatistical methods, extrapolate the risks in areas not covered by the available data, and improve the assessment of uncertainty.

I will illustrate these new developments in an analysis of temperature-mortality associations in European cities, providing fully reproducible R code and data.

Contributed 12: Environmental impact on health

Exploring the effects of air pollution on chronic diseases using Intego-network data

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Abstract:
The adverse effects of air pollution on human health have been a prominent concern in recent decades particularly as the global agenda intensifies its focus on climate change. Significant increases in mortality and morbidity from respiratory diseases have been consistently reported as a consequence of exposure to air pollutants.

Generalized additive regression models were applied to understand the effects of air pollution on the odds of developing chronic obstructive pulmonary disease (COPD). This is based on data of 102057 patients from a sample of general practitioners in Flanders, for which annual exposure is available at the residential address level. To account for practice-specific heterogeneity the practice is considered as a random effect in the models.

The results show that males, smokers, those aged 55-85 years old, and socially vulnerable individuals have a higher risk of COPD. But also particulate matter PM2.5, PM10, Black Carbon, and Nitrogen dioxide are associated with increased risks. The results consistently point to Antwerp as a region with a strong effect of all air pollutants on the odds of developing COPD.

The impact of reducing exposure to air pollution on population health is investigated by estimating the attributable fraction using the generalized additive model for confounder adjustment. Two key strategies are considered: spatial local reduction of exposures and overall national reduction of the exposure. Assessing the impact of pollution thresholds on the population may help the implementation of strategies to reduce the burden of disease in areas with poor air quality.

Contributed 12: Environmental impact on health

Urban dengue hot- and coldspots in Lucknow, India: Unravelling the underlying environmental patterns.

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Abstract:

Dengue is one of the most important threats to public health in India. Its distribution is affected by factors like the climate change and sociodemographic. This work assessed the seasonality and clustering patterns of dengue cases reported in 2020, 2021, and 2022 in Lucknow, India by computing a weekly, ward-wise, Getis-Ord Gi*. Hot- and coldspots were then validated through the Fuzzy Kappa analysis. Additionally, univariate comparisons based on temperature, humidity, local climate zones, and population were conducted between hot- and coldspots. Our results indicate a constant seasonal pattern; cases start rising at the end of the monsoon, reach their maximum at the end of October, and finally decline in December. The weekly Getis-Ord Gi* showed a consistent trend: peripheral areas in eastern, southern, and northern wards were classified as hotspots. Contrary, wards situated in the city center were categorised as coldspots. This pattern was confirmed by the values (> 0.6) obtained from the Fuzzy Kappa statistic. Covariate comparison showed that hotspots have statistically lower temperatures, population density, and less densely built areas, but more trees and higher humidity. Even though our results are descriptive rather than predictive, they show a clear clustering pattern in which eastern and southern wards served as transmission foci. Furthermore, significant differences related to sociodemographic and environmental variables were found. These results suggest specific characteristics that make wards prone to become hot- or coldspots in cities such as Lucknow. This could be used to support dengue monitoring and management in the context of climate change.

Contributed 12: Environmental impact on health

Heat-related mortality in Flanders (Belgium): combining dose-effect relationships with climate and land use modelling.

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Abstract:
In Flanders, rising temperatures from more frequent and longer heat waves elevate the risk of heatstroke, cardiovascular or respiratory diseases, and premature mortality. Our study aims to identify the most vulnerable groups and areas to heat exposure to inform policy-makers by mapping heat-related mortality in Flanders, now and in the future. A Poisson regression with distributed lag non-linear models (DLNM) is applied to summer data from 2000-2019. This analysis indicates that older individuals face higher risks of heat-related mortality, particularly from respiratory diseases. Heat effects are most pronounced in those over 85 years old.

The study estimates heat-related mortality for three scenarios: the current situation, a high climate scenario for 2050, and a future scenario considering both temperature increase and population projections for 2050. Therefore, the use of the climate model UrbClim and the land use model GeodynamiX is combined with the relative risks of the dose-effect relationships. Expected deaths from heat could rise from 461 annually (2000-2019 average) to 1600 by 2050 only considering temperature rise, and up to 2904 by 2050, factoring in population aging and spatial distribution changes.

This map and data, along with an updated heat vulnerability map, are available through interactive online dashboards, providing valuable insights for targeted intervention and planning. The project was funded by the Flemish Department of Care to enable health professionals to take more targeted heat action plans.

Contributed 12: Environmental impact on health

Spatial Insights into potential Health Benefits from Urban Traffic Reduction: Case-study on Car-Free Initiatives in European Capitals and pediatric asthma

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M De Clercq, Eva (2)

Affiliations:
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2: Sciensano;
3: Hasselt University

Abstract:

Our study highlighted a considerable reduction in NO2 concentrations on car-free Sundays compared to regular Sundays, with a focus on cities like Brussels and Paris, where car-free initiatives have been notably impactful. We found that localized traffic management could decrease NO2 exposure by 63-83% in specific areas within Brussels and 27-56% in certain Parisian districts. A rigorous sensitivity analysis, incorporating methods such as direct calculations, meteorological condition adjustments, random forest modeling, and boosted regression tree modeling, underscored the robustness of our findings.

Delving into the public health sphere, we calculated the impact of air pollution on pediatric asthma. Utilising a Health Impact Assessment that simulated the car-free day setting, we assessed how traffic diminution strategies might lower pediatric asthma occurrences. Leveraging established Exposure Response Functions to gauge NO2 exposure's health impact, our research anticipated a decline in pediatric asthma incidences ranging from 14% to 29% in areas of Brussels with heavy traffic flow and between 14% to 17% in Paris. Importantly, our research revealed a clear spatial pattern within these cities: greater reductions in NO2 concentrations and potential reductions in asthma cases were most pronounced in areas burdened with high traffic volumes in both cities.

This study underscores the critical importance of policy interventions aimed at reducing urban traffic and emissions, which not only alleviate air pollution but also offer extensive health benefits, such as promoting physical activity, diminishing noise pollution, and augmenting urban greenery.

Contributed 13: Advancements in spatial statistics

Geostatistical and machine learning techniques for mapping vaccination coverage: A statistical comparison

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Abstract:
Over the past two decades, there has been a rapid increase in the production of spatially detailed estimates of health and development indicators (HDIs) such as childhood vaccination coverage. Boosted more recently by the launch of the Sustainable Development Goals (SDGs) in 2015 with the central goal of “leaving no one behind”, these estimates have been shown to be critical to uncovering the heterogeneities that exist in coverage and improving precise targeting of interventions to reach all missed communities and under-served populations. Different methodological approaches have been developed for producing gridded estimates of vaccination coverage using different geolocated input data sets, which are often integrated with geospatial covariate information to improve predictive performance. In this study, we undertake a statistical comparison of these modelling approaches, namely model-based geostatistics (MBG), machine-learning methods and a combination of MBG and machine learning methods, using a simulation study. In particular, we compare the predictive performances of these methods under varying spatial configuration of the sampling locations and different assumptions about the functional relationship between the outcome and the covariates included in the analyses. We also compare the performance of the models using a real-world application involving mapping the coverage of the first dose of the diphtheria-pertussis-tetanus (DTP1) vaccine using household survey data in Nigeria. The findings of our study provide guidance to users of these approaches, especially in the wider context of mapping SDG indicators or other HDIs.

Contributed 13: Advancements in spatial statistics

Integrating vulnerability and hazard in malaria risk mapping: the eradication context of Senegal

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Abstract:

Malaria still caused 608,000 deaths in 2022, with over 95% in sub-Saharan Africa. In this context, malaria risk maps are essential to help policymakers target control interventions. Yet, current maps usually rely on land cover and climatic factors that influence the suitability of the environment for vectors, referred to here as the hazard, and often overlook the vulnerability of society to this hazard. Senegal has a heterogeneous malaria endemic profile, with a gradient from high transmission in the southeast to low transmission in the north. With the goal of eliminating malaria by 2030, Senegal has seen a significant decrease in malaria prevalence in recent years due to increased control programs. However, malaria cases and deaths have stagnated since 2020 in the south-eastern regions, the most endemic areas of the country. In this eradication context, detailed malaria risk maps and a comprehensive understanding of all factors (both hazard and vulnerability) that perpetuate the disease in the country would allow better targeting of malaria control interventions and move closer to elimination. In this study, we model malaria risk in Senegal using a Bayesian geostatistical modelling framework, considering all potential malaria drivers, to identify the most important drivers. By combining different sets of variables, we show that including vulnerability variables alongside hazard variables in the models improves the accuracy of the predictive maps. These findings have important policy implications, highlighting the need to include both vulnerability and hazard in predictive maps to ensure that all factors contributing to disease persistence are considered.

Contributed 13: Advancements in spatial statistics

Specification of space-time interactions for prediction in Bayesian disease mapping

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Abstract:

The use of Bayesian disease mapping models has become very popular for data given not only by space but also by time. Commonly, structured, and unstructured random effects are incorporated in the linear predictor for both space and time together with a space-time interaction term. However, the use of intrinsic Gaussian Markov random fields implies a complex rank deficiency which requires the specification of numerous linear constraints to ensure identifiability of all model components. This is not only computationally expensive with increasing number of regions or timepoints, but makes the models hard to interpret. Recently, several approaches have been proposed for more efficient handling of the constraints. In this talk, we will focus on the question whether intrinsic models are the way to go. Using a simulation study, we use proper scoring rules to assess the predictive performance of the popular Knorr-Held interaction formulations compared to specifications based on proper models for time and space. Finally, we present a real data study.

Contributed 13: Advancements in spatial statistics

Investigating cross nearest neighbor methods in multitype overlapping point patterns as heterogeneity measures for hepatitis B infected liver sample cell phenotypes

Authors:
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Crabbe, Marjolein (2);
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Abstract:

Mass cytometry is a technique used on biological tissue samples to discover cell properties. Subsequent to using artificial intelligence to detect cells and their coordinates, spatial statistics can be utilized to infer spatial relations between cell phenotypes and possibly link them to patient-specific clinical features. This paper aims to investigate the effectiveness of pairwise cross nearest neighbor measures when applied to multitype point patterns where each point location can be assigned multiple types.

A total of 34 biopsies were taken from 19 chronic hepatitis B patients divided over two time points. Patients were divided into two panels according to clinical parameters. Imaging mass cytometry (Hyperion) was used to stain for 30 antigen types. Biopsies were subsequently scanned to an image, cell segmentation was performed and cell coordinates were calculated. Each cell was defined as positive for each type depending on signal intensity, resulting in a multitype point pattern with overlap. Multiple permutation-based pairwise cross nearest neighbor methods were used and compared to standard heterogeneity measures. All measures were tested as predictors for patient panel and time of biopsy. Simulation studies including data with random distribution of types, increased overlap or increased cross nearest neighbor proximity were constructed to validate the proposed methods.

Simulation studies showed that measures were almost universally influenced by the proportion of total cells of both types, and trends differed per setting. Despite this, the analyzed measures showed varying levels of predictive power for panel and time, with overall good accuracy using specific type pairs.

Contributed 14: Neglected Tropical Diseases

Geostatistical methods for efficient safety assessment of Ivermectin in Loa loa endemic areas.

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Johnson, Olatunji

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Abstract:

The elimination of onchocerciasis through community-based mass drug administration (MDA) of ivermectin (Mectizan) is hampered by co-endemicity of Loa loa, as individuals who are highly co-infected with Loa loa parasites can suffer serious and occasionally fatal neurological reactions from the drug. Testing all individuals participating in MDA is impractical due to cost and limited availability of diagnostic tools. Therefore, there is a need for a way to establish whether an area is safe for MDA using the prevalence of loiasis derived from multiple diagnostic tools. Existing statistical methods only focus on using data from one diagnostic tool and ignore the potential information that could be derived from other datasets. In this talk, I will discuss how we address this issue by developing a joint geostatistical model that combines data from multiple Loa loa diagnostic tools. We applied this model to Loa loa data from Gabon and propose a two-stage strategy to identify areas that are safe for MDA. Lastly, I will discuss how this work contributes to the global effort towards the elimination of onchocerciasis as a public health problem by potentially reducing the time and cost required to establish whether an area is safe for MDA.

Contributed 14: Neglected Tropical Diseases

Short-term effect of temperature and rainfall on the incidence of West Nile Neuroinvasive Disease in Europe: a multi-country case-crossover analysis.

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Abstract:

Background:

In recent years, Europe has experienced several West Nile Virus (WNV) outbreaks. WNV is transmitted to humans by Culex mosquitoes. Given the sensitivity of the disease vector and hosts to climate change, this study seeks to quantify the impact of meteorological factors in driving recent WNV outbreaks in Europe.

Methods:

This study, using a space-time-stratified case-crossover design, examined the short-term effects of average weekly temperature and cumulative weekly precipitation on all WNND incident cases reported in Europe from 2014 to 2022. WNND cases were obtained from ECDC, and meteorological data from ERA5-Land climate re-analysis. Distributed lag nonlinear models were implemented in conditional logistic regression models to assess temperature and precipitation effects on WNND risk. Heterogeneity of effects by country was tested by analyzing country specific coefficients with multivariate random effect meta-analytic model.

Results:

Between 2014 and 2022, Europe reported 3,437 WNND cases. A positive association was found between temperatures and WNND risk, with strongest effect at a lag of 2 weeks (OR: 1.15; 95% CI 1.12–1.19). Similarly, precipitation levels were positively associated with WNND risk, with strongest effect at a lag of 3 weeks (OR: 1.11; 95% CI 1.08–1.14). No evidence of strong heterogeneity of effects across countries was detected.

Conclusion:

These findings emphasize the significance of temperature and precipitation in driving WNND incidence in Europe. Addressing the impact of climate change on WNV transmission dynamics is crucial for adaptive strategies. Integrating environmental, meteorological and epidemiological data can aid in establishing early-warning systems for WNV infection.

Contributed 14: Neglected Tropical Diseases

Forecasting dengue incidence over space and time, in Thailand, 2013-2022

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Abstract:

Dengue is endemic in Thailand and is a high burden on the health system. Recognizing the need for local level forecasts to support interventions, we developed a district-level spatio-temporal statistical model to provide weekly forecasts.

We modelled dengue surveillance data from Ministry of Public Health, using a Bayesian hierarchical model with a zero-inflated Poisson likelihood. We used province-level weekly temporal random effects, and reparametrized Besag-York-Mollie (BYM2) district-level spatial random effects. Inference was conducted via integrated nested Laplace approximations in R-INLA. Forecasts were made for a time-horizon of 24 weeks, with an expanding window of 4 weeks. Forecast performance was assessed on the log-scale using the continuous ranked probability score (CRPS), weighted by district population, with lower CPRS indicative of better performance.

As expected, model performance decreased as prediction horizon increased indicated by high CRPS. Comparing regions, CRPS was highest in Bangkok. This difference is mainly driven by a large epidemic in 2015 in Bangkok. Predictions started in the second and third quarters of the year, corresponding to peaks of dengue epidemics, had higher CRPS than predictions that started in the first or fourth quarter, irrespective of the number of weeks predicted.

Our simple model is able to accurately reconstruct and predict local transmission dynamics of dengue in Thailand. Future work focusses on the specific circumstances when additional variables help improve forecasts, with special attention to improving >4 week ahead forecasts. This work provides a tool for local public health officials to mount an evidence-based response to increased dengue transmission.

Contributed 14: Neglected Tropical Diseases

Citizen science revolutionizing snail-borne diseases risk understanding in rural Uganda

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4: Ecosystem and Landscape Dynamics, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, The Netherlands

Abstract:

Schistosomiasis poses a significant global health challenge, affecting millions worldwide, with a particularly pronounced burden in sub-Saharan Africa. Its transmission dynamic, primarily mediated by intermediary snail vectors, is characterized by an interplay of behavioural patterns, notably engaging in high-risk water-related activities, and ecological factors. As a response to this public health issue, the Action Towards Reducing Aquatic snail-borne Parasitic diseases (ATRAP) project established a network of 25 citizen scientists dedicated to the systematic monitoring of snail populations and risky-water practices in the highly disease-endemic area of Southern Lake Albert in Uganda.

While ascertaining the presence of snail vectors is crucial for assessing the risk of schistosomiasis transmission, a comprehensive evaluation requires the integration of behavioural and ecological data. In our study, we bridge this gap by using the exposure-hazard-vulnerability framework including behavioural and ecological data to delineate disease risk. By analysing thousands of vector presence points collected over a span of more than two years on a weekly basis, and incorporating the latest remote sensing products, we estimated the probability of vector presence. This, coupled with the estimation of vector infection probability, provided insights about hazard. Moreover, the assessment of human presence through the analysis of risky-water practices, categorized based on the extent of skin exposure and duration, facilitated an understanding of exposure dynamics. Concurrently, vulnerability within the human population was assessed by delineating demographic factors, such as age groups, aligning with existing literature indicating higher vulnerability among children due to diminished acquired immunity.

This multidimensional approach facilitated the identification of potential transmission sites with a high level of accuracy, offering valuable insights for policymakers and public health

stakeholders. Our findings underscore the key role of community-driven methodologies, exemplified by citizen science, in enhancing our understanding of complex diseases such as schistosomiasis and providing detailed information for targeted intervention strategies.

Poster 1:

On the impact of report delays on dengue outbreaks via a temporal model with Bayesian framework

Authors:
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Abstract:

To achieve real-time scenario in a disease outbreak and precise estimation of parameters in a data-driven modeling technique, it is crucial that report of count outcomes be accurate. Yet, the inaccuracies or delays in the report of the actual count of dengue victims frequently hinder the timely acquisition of insights into outbreak dynamics.

This paper employs a Bayesian framework on a temporal model, as introduced by Bastos, et al. [1], to investigate the impact of report delays on weekly dengue data collected from Northern Mindanao, Philippines spanning from 2009 to 2010. The analysis extends beyond immediate nowcasting of dengue counts to include simulation studies assessing the impact of 2, 4, 6, and 8 weeks of report delays on the performance of the temporal model.

The results reveal that the model accurately captures eventual reported cases of dengue, even in the presence of significant report delays, thereby providing valuable insights to public health authorities to refine decision-making processes within dengue control efforts, accounting for potential discrepancies between reported and actual dengue counts.

Poster 2:

Uncovering socioeconomic disparities in modal age at death in Belgium since 2000

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3: Sciensano;
4: Montreal University

Abstract:

Many studies have investigated disparities in life expectancy at birth (e0) across socioeconomic strata in Belgium, but no studies have focused on disparities in modal age at death (M). Yet, as opposed to e0, M is solely influenced by old-age mortality and can reveal distinct patterns and differentials among the elderly. We aim to investigate M trends across the smallest Belgian geographical units, grouped by their deprivation levels into deciles. We show that in 2000, male M in most deprived areas was 79.91, i.e., 4 years lower than in the least deprived areas, whereas female M in those areas equaled to 86.60 years. Over time, male M in most and least deprived has increased at a similar pace, and the pace of female M differed significantly. In both sexes across all deciles, the standard deviation above the mode has decreased. We extend our study to cause-specific M to better understand these changes.

Poster 3:

Implementation and validation of a Bayesian geostatistical model to estimate spatio-temporal patterns of RMNCH in Mali, 2000 - 2018

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Abstract:

Background: Mali faces socio-political challenges that impede data collection efforts to inform its reproductive, maternal, newborn, and child health (RMNCH) programs and policies. New statistical approaches that leverage existing data to generate granular and precise estimates represent an important opportunity. This study aims to implement and validate a Bayesian geostatistical model to estimate the patterns of RMNCH service uptake at sub-regional levels from 2000 to 2018.

Methods: We use geo-located data from the Demographic and Health Surveys. Policy-relevant indicators of RMNCH are explored, namely the uptake of modern contraceptives, antenatal and postnatal care, assisted childbirth, and basic childhood immunization. Binomial generalized linear models identify geospatial covariates associated with the RMNCH indicators. Bayesian geostatistical models are being constructed using the significant geospatial covariates to estimate the probabilities of the RMNCH indicators at a 5 x 5 km resolution. Maps with the 5 x 5 km estimates of RMNCH service uptake and uncertainty maps depicting the standard deviation around the estimates are generated. We also build maps at the subregional decision-making scales by aggregating the probabilities of RMNCH service use.

Results: Data analyses are in progress. Preliminary results show the presence of heterogeneity over space and time for all RMNCH indicators. Spatial maps produced using Bayesian geostatistical modeling will allow us to estimate and study this spatio-temporal variability better.

Discussion: A better understanding of spatial variability in RMNCH service use and its evolution is essential for better capitalization of resources for health, particularly in a country facing competing priorities and socio-political challenges.

Poster 4:

Urban growth and intra-urban inequalities: A spatio-temporal analysis of the dynamics of mosquito-borne diseases in East Africa

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Abstract:

The East African (EA) region is rapidly urbanizing, resulting in heterogeneous urban landscapes marked by inequalities in socio-economic and environmental factors that significantly impact mosquito-borne diseases (MBDs). Moreover, the spread of invasive mosquito species adapted to urban environments in EA, such as the Anopheles Stephensi and Aedes Albopictus, highlights the importance of context-specific ecological assessments for informing effective health strategies. However, intricate socio-economic and environmental interactions are commonly overlooked in urban growth models used for public health surveillance. This potentially limits their utility in defining intra-urban heterogeneity and capacity to anticipate future disease outbreaks. An integrated spatial-temporal framework synthesizing the socio-environmental interactions in urban MBD dynamics can provide contextual insights into the intra-urban heterogeneities. To address these concerns, we propose an integrative approach to assess the intra-urban dynamics of MBDs in urban EA by combining entomological, socio-economic, and environmental data in a scenario-based spatial-temporal analytical framework. Specifically, we perform a literature review to identify the socio-ecological intricacies influencing mosquito species distributions and infectivity rates across different urban strata (urban and peri-urban settings) in EA. This information will form the basis to develop scenario-based models that aim to (i) predict MBD trajectories in the context of urban expansion in East Africa, particularly in Kenya, and (ii) evaluate the influence of urban growth on dengue in rapidly urbanising areas case studies. This integrative approach bridges gaps in scientific understanding and can provide nuanced insights to inform public health strategies amidst the challenges posed by urbanization in MBD dynamics in EA.

Poster 5:

Socioeconomic inequalities in excess mortality attributable to extreme heat during the summer of 2022 in Catalonia, Spain. A Bayesian spatio-temporal model

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4: Institut de Matemàtiques i Aplicacions, University Jaume I of Castelló, IMAC, Spain

Abstract:

Introduction: In 2022, excess mortality in Spain was the third highest, only surpassed by 2020 and 2015. However, a maximum of 25% of the excess has been directly attributed to extreme heat. The problem is that these estimates are based on models that could present biases and limitations.

Objectives: We first intended to estimate the excess mortality attributed to extreme heat in Catalonia in the summer of 2022, using much smaller units of analysis and temperature predictions obtained from a spatio-temporal Bayesian model. Second, we assessed the existence of socioeconomic inequalities in excess mortality attributed to extreme heat.

Methods: We used a longitudinal ecological design, from 2015 to 2022 with information on daily mortality and temperatures at the level of 288 health areas (ABS). We used a sample that includes covering 6.3 million people, 81.6% of the population of Catalonia.

Results: The excess mortality attributed to extreme heat during the summer months of 2022 was 49.41% using our model. This excess was 4 times greater than that attributed to extreme heat in the summers from 2015 to 2019. In rural areas and in the most socioeconomically deprived urban ABS, the excess of deaths was higher than in the rest.

Conclusions: The difference between our model and the standard one could be because this latter suffers from the modifiable areal unit problem and contains measurement errors in exposure to extreme temperatures. Socioeconomic inequalities could have existed, at the level of ABS, in the excess of mortality attributed to the extreme heat.

Poster 6:

Intra-city mobility and spatio-temporal heterogeneity of dengue cases

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2: Ministry of Health, Epidemiology and Vector Control team, Cienfuegos;
3: Instituto de Medicina Tropical Pedro Kouri

Abstract:
Introduction:

Dengue virus (DENV) fever outbreaks are causing significant mortality and morbidity in Cuba and other endemic countries each year. With an expanding Aedes vector, and the imminent threat of virus importation through global travel, more and more other regions become at risk of witnessing DENV epidemics as well.

Existing models, considering mobility only in terms of house-to-house movements, have failed to predict the low DENV incidences observed in most endemic settings during COVID-19 restrictions. We hypothesize that in addition to house-to-house movements, other forms of intra-city mobility and the use of public space also contribute to the spatio-temporal heterogeneity of DENV transmission.

Methods:

Within the SOFI 2023 DI-MOB project, fine-scaled weekly dengue case data of the Municipality of Cienfuegos, Cuba, at houseblock level (+/- 120 inhabitants), for the period 2012-2023, will be analyzed identifying temporal and spatial patterns using SaTScan. Case dispersion patterns will be compared between periods with different general human mobility (pre/during/post-COVID).

Work-related recurrent mobility patterns will be constructed based on Cuban mobile phone data and gravity models trained on census data of Belgium, France, Spain and Portugal.

A statistical model taking into account spatial dependency, will explore associations between mobility, epidemiological patterns, and district-level independent variables.

Results:

Case-data, spatial maps and phone data are already available, and analyses are currently ongoing.

Poster 7:

Boundary effects in the spatial modelling of cancer risk in the Flemish region of Belgium

Authors:
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Affiliations:
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Abstract:

Boundary effects are defined in the GIS dictionary as ‘problems caused by arbitrary boundaries being imposed on spatial data that represents unbounded spatial phenomena’ (Esri, 2024). Spatial models are thus inherently prone to the limitations imposed by the incorporation and availability of data across the border of the study area.

This study demonstrates how boundary effects influence the spatial modelling results of cancer risk (stomach, lung, mesothelioma and kidney) in the Flemish region in Belgium. The boundary effect was evaluated by comparing results obtained on the Flemish level with results obtained on the national level as well as Flanders including a small buffer area into the neighbouring regions of Wallonia and Brussels. A buffer of two communities deep was sufficient to counter the boundary effect for the spatial areas close to the regional border. Without this buffer area, the modelled relative cancer risk of most geographical entities will change by no more than 0.1 in absolute value. Entities near the edge of the study area displayed a larger difference in cancer risk and less frequently occurring cancer types will also lead to an increased difference in cancer risk .

The study also demonstrates how the choice of geographical scale influences the magnitude of the boundary effects by modelling on different administrative levels (municipality and submunicipality). Applications on a more detailed geographical level are based on lower incidence which imposes an increased uncertainty on the risk estimation. This results in more entities with increased cancer risk differences.

Poster 8:

Innovative use of wastewater microbiome as a spatio-temporal monitoring tool for community-level human gut health during pandemic and postpandemic

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3: Infectious Diseases Institute, The Ohio State University, Columbus, Ohio, USA

Abstract:

This study evaluates community-level gut microbiome health using innovative spatio-temporal wastewater-based epidemiology (WBE). Objectives are to, 1) characterize the core microbial community in human gut microbiome from municipal wastewater, 2) compare human gut microbiome health between two demographically different cities, and 3) examine longitudinal community gut health shifts throughout the COVID-19 pandemic and whether specific microbiota may be utilized as SARS-CoV-2 infection biomarkers.

Composite wastewater influent from wastewater treatment plants (WWTPs) were collected between August 2020 and June 2022 from 3 WWTPs in 2 central Ohio cities with contrasting sociodemographics. Bacterial DNA was concentrated and extracted for 16S rRNA gene sequencing to analyze the bacterial communities using QIIME2 pipeline. Human gut-associated microbiome reads were retained before examining differences by location (i.e., WWTP, city) and time (i.e., pandemic period based on vaccination rates [pandemic, transition, post-pandemic]) using various differential abundance and statistical analyses.

Core gut composition was relatively similar across locations, meanwhile WWTP beta diversity dissimilarity was greater than city dissimilarity. Alpha diversity significantly decreased following vaccine introduction; both alpha and beta diversity measures were significantly dissimilar over time by pandemic period. Four key differentially abundant taxa by pandemic period (Proteobacteria, Actinobacteriota, Collinsella, and Megasphaera) were further identified as potential SARS-CoV-2 infection biomarkers.

Notably, employing a WBE approach is a valuable, non-invasive tool to characterize community-level gut health. Both cities underwent significant gut microbiome shifts throughout the pandemic, highlighting that community gut microbiome surveillance can serve as an effective mechanism for understanding the spatio-temporal dynamics of public health beyond gut health.

Poster 9:

Identifying and generating spatial population structure archetypes for epidemiological analysis

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Abstract:

Modeling studies have shown that pathogen elimination tactics depend strongly on spatial scale. However, in the current state of model-based perspectives, there is a lack of understanding of the relationship between population structures, infectious disease transmission, and the efficacy of interventions. Population structures are complex and vary greatly across geographies of interest. Within this context, developing low-dimensional representations of population structures allows for the mapping of these structures onto transmission patterns, public health indicators, and ultimately, optimal interventions. This project advances existing work unsupervised population clustering into the global health and vaccine delivery contexts.

We embedded high resolution population data into a high-dimensional space through local growth curve calculations and utilized this feature space as an input for unsupervised clustering. This high-dimensional representation of population rasters represents information both about population density at various spatial scales as well as local fractal dimension, providing a rich feature set for clustering. We analyzed the results of a variety of dimensionality reduction and clustering techniques including PCA, k-means, and self-organizing maps to determine archetypical population structures in sub-Saharan Africa.

After classification of populations into their low-dimensional representations, we simulated the comparative transmission dynamics of the spread of infection by population archetype. Transmission simulations were run using the EMOD agent-based model. Additionally, we conducted covariate analysis between population structure archetypes and additional public health indicators related to mortality, nutrition, and access. This work provides a reproducible analytical methodology for understanding the effects of population structure in epidemiological analyses.

Poster 10:

Spatial patterns and characterization of early neonatal deaths in Brazil, by health macroregion from 2011 to 2021

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Abstract:

In Brazil, early neonatal mortality (deaths within 0-6 days of life) constitutes the primary component of infant mortality, accounting for 52.6% of deaths in 2021. An ecological study was conducted to discern spatial patterns and clusters of early neonatal deaths across health macroregions using exploratory spatial analysis spanning from 2011 to 2021. Clusters were characterized based on variables including sex, infant age, birth weight, maternal age group, pregnancy type, gestational age, and delivery method. Data from the Mortality Information Systems and Live Births were utilized. High-risk clusters were identified through the application of the spatial SCAN technique, employing SaTScan 10.1 software. Over the study period, Brazil recorded 211,664 early neonatal deaths, averaging 19,000 deaths annually before infants completed their first week of life. The highest mortality rates and high-risk clusters were observed in health macroregions situated in the North and Northeast. Deaths were predominantly male newborns, aged less than one day, and weighing <2,500g at birth. Elevated rates were associated with infants born to mothers aged 20-34 years, singleton pregnancies, preterm births, and vaginal deliveries. High-risk clusters predominantly manifested in regions characterized by the poorest social indicators in Brazil. Hence, enhancing access to comprehensive care, encompassing prenatal services, safe childbirth, early neonatal interventions, and breastfeeding support, stands imperative for mitigation infant mortality rates in Brazil

Poster 11:

Spatiotemporal Analysis of Suicide Mortality Trends and Associated Factors in Korea: Implications for Public Health Intervention

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Abstract:

Background: Despite the identification of disparities through spatial analyses, there exists a notable deficiency in the exploration of spatiotemporal dimensions of suicide mortality. The objective of this study is to examine the spatiotemporal trends of suicide in Korea, along with associated factors, while emphasizing the correlation with the availability of mental health facilities.

Methods: A spatiotemporal analysis of suicide mortality was undertaken covering the years 2010 to 2021 at the municipal level in Korea. Following the verification of spatial autocorrelation in suicide mortality utilizing Global Moran's I statistics, a Bayesian spatiotemporal regression analysis was performed to examine the determinants.

Results: An increasing trend was observed in suicide mortality for teenagers and adults, while a decreasing trend was observed in the elderly. Areas of heightened risk were identified in the northeastern and central regions, contrasting with regions of lower risk dispersed throughout the northwestern and southeastern areas. The presence of mental health promotion facilities (RR = 0·945, 95% CrI = 0·927–0·963), physician density (RR = 0·975, 95% CrI = 0·957–0·994), and mental health specialist density (RR = 0·975, 95% CrI = 0·957–0·994) emerged as protective factors against suicide mortality, even after accounting for various socioeconomic, health-related, behavioral, and environmental variables.

Conclusion: Suicide continues to pose a substantial public health challenge in Korea. The identification of localized areas of heightened risk underscores the necessity for tailored interventions. Public mental health centers have surfaced as a protective element, underscoring the importance for policymakers to prioritize their expansion and ensure sustained funding.

Poster 12:

Correlation between maternal mortality and distance to access obstetric care in Brazil, 2012-2022

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Abstract:

Brazilian population is distributed across a vast geographical area what sometimes implies travelling between distant cities. The Brazilian Public Health System is organized in 450 administrative health regions in order to reduce the commuting burden for people at all levels of healthcare, including maternal care. Despite the government efforts, some pregnant women still need to travel to a heath region different from their residence region, which can increase their maternal risk the more distant and long the journey. Therefore, in the present study we evaluate the correlation between maternal mortality and the distance traveled to access obstetric care in Brazil. We utilized official data on maternal deaths and live births from 2012 to 2022, categorized into three distinct periods: 2012-2015, 2016-2019, and 2020-2022. For each record, we calculated the Euclidean distance between the health regions of residence and occurrence, using the distgeo function from the Geosphere package, accessible in the R software. Based on their proximity, the participants were grouped into: individuals who remained in their respective locations and those who traveled within distances of 100, 500, and over 500 kilometers from one another. Finally, for each of these 12 period-distance combination, we calculated the maternal mortality ratio (MMR). We observed a direct correlation between MMR and the distance. There was an increase in MMR, ranging from 7 to 8 times at distances over 500 km. Furthermore, an increase was observed during the COVID-19 period, with a notable 30% rise in MMR in the group that travels greater distances.

Poster 13:

A Low-Rank Bayesian Approach for Geoadditive Modeling

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Abstract:

Kriging has been an established methodology for predicting spatial data in geostatistics. In recent years, big data has become increasingly prevalent, posing computational challenges to traditional methods. In this context, a low-rank approach to kriging proves to be helpful to handle large datasets. Moreover, while splines have shown promise in capturing nonlinear dependencies of covariates, their combination with kriging, especially in handling count data, remains underexplored.

We present a Bayesian approach to the low-rank representation of geoadditive models, which integrates splines and kriging to account for both spatial correlations and nonlinear dependencies of covariates. Our method accommodates Gaussian and count data inherent in many geospatial datasets. Additionally, Laplace approximations to selected posterior distributions enhances computational efficiency, resulting in faster computation times compared to Markov chain Monte Carlo (MCMC) techniques commonly used for Bayesian inference. Method performance was assessed through a simulation study, demonstrating the effectiveness of our proposed approach. Through this work, we provide a new flexible and computationally efficient framework for analyzing spatial data.

Poster 14:

Substantial but spatially heterogeneous progress in male circumcision for HIV prevention in South Africa

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Abstract:
Background: Voluntary medical male circumcision (VMMC) reduces the risk of male HIV acquisition by 60%. Programmes to provide VMMCs for HIV prevention have been introduced in sub-Saharan African countries with high HIV burden. Traditional circumcision is also a long-standing male coming-of-age ritual, but practices vary considerably across populations. Accurate estimates of circumcision coverage by age, type, and time at subnational levels are required for planning and delivering VMMCs to meet targets and evaluating their impacts on HIV incidence.

Methods: We developed a Bayesian competing risks time-to-event model to produce region-age-time-type specific probabilities and coverage of male circumcision with probabilistic uncertainty. The model jointly synthesises data from household surveys and health system data on the number of VMMCs conducted. We demonstrated the model to produce estimates of circumcision coverage for 52 districts in South Africa between 2008 and 2019.

Results: Nationally, in 2008, 24.1% (95% CI: 23.4–24.8%) of men aged 15–49 were traditionally circumcised and 19.4% (18.9–20.0%) were medically circumcised. Between 2010 and 2019, 4.25 million VMMCs were conducted. Circumcision coverage among men aged 15–49 increased to 64.0% (63.2–64.9%) and medical circumcision coverage to 42% (41.3–43.0%). Circumcision coverage varied widely across districts, ranging from 13.4 to 86.3%. The average age of traditional circumcision ranged between 13 and 19 years, depending on local cultural practices.

Conclusion: South Africa has made substantial, but heterogeneous, progress towards increasing medical circumcision coverage. Detailed subnational information on coverage and practices can guide programmes to identify unmet need to achieve national and international targets.

Poster 15:

Understanding how the COVID-19 pandemic impacted the prevalence of female genital mutilation among Nigerian women aged 15-49 years.

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Abstract:

Female genital mutilation (FGM) remains a significant human threat, affecting more than 3 million girls every year. Efforts have been made in recent decades by national and international organisations to stop the practice. However, progress may have been hampered by the COVID-19 pandemic. Several studies have suggested possible effects of the pandemic on FGM practice from interviews with programme implementers and the population, but there has been no clear evidence from statistical analysis and nationally representative data to confirm these effects. Therefore, in this study we use Bayesian regression models to assess the impact of the COVID-19 pandemic on the prevalence and likelihood of FGM among women aged 15-49 years in Nigeria in terms of individual (e.g. a woman's marital status, education) and community-level (e.g. the proportion of women in the community who have been cut) determinants of FGM practice and a woman's state of residence. We used data from the Demographic and Health Survey conducted in Nigeria in 2018, referred to as the pre-COVID-19 pandemic period, and the Multiple Indicator Cluster Survey of Nigeria in 2021, referred to as the post-pandemic period. Our results show that although there has been an overall decline in FGM prevalence nationally, FGM prevalence varies geographically within Nigeria and with respect to individual/community level determinants. These findings further suggest that FGM is still a social norm in Nigeria, which may have been exacerbated by the COVID-19 pandemic. Our findings call for persistence in FGM interventions to stop the practice.

Poster 16:

Forecasting dengue across settings: common drivers and trade-offs for Vietnam, Sri Lanka, and Malaysia

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Abstract:

Dengue is a climate-sensitive disease affecting many countries in Asia, the Americas, and parts of Africa. Anthropogenic climate change is expected to increase the spatial extent of the global disease distribution, and with increased intensity and frequency of extreme weather events the likelihood of large dengue outbreaks is also expected to increase. This work builds on the successful implementation of the Dengue forecasting MOdel Satellite-based System (D-MOSS) in Vietnam, Malaysia and Sri Lanka, which can provide lead-times of up to six months. In E4Warning we extend this work by further developing the modelling framework to produce dengue forecasts across different settings, able to accommodate for differences in spatial and temporal scales of reporting. A Bayesian modelling approach is taken and compared to standard practice for monitoring dengue outbreaks in each of the three countries. We explore the trade-offs between spatial and temporal prediction skill for different model formulations. Which will increase our understanding of which predictors of dengue are most consistent or unique across settings. This can inform the development of dengue early warning systems in other countries, given a live stream of remotely sensed data and dengue reporting. The online platform implementing the forecasting system is hosted by HR Wallingford. We will work closely with in-country partners to provide actionable data visualisations and summaries to facilitate a data-driven dengue control response.

Poster 17:

Impact of Environmental Stress on Mortality: A Spatial Analysis in Belgium

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Abstract:

Environmental factors significantly influence health, leading to a range of diseases, increased hospitalizations, and elevated mortality rates. This epidemiological study encompassed the entire Belgian population for the year 2016, with a focus on approximately 11.15 million out of 11.26 million individuals. Conducted across 19,794 geographical sectors, and honing in on 18,681 for in-depth spatial analysis, this research employed a multifaceted approach. By integrating diverse variables at the most granular geographical scale, we classified environmental stressors into three primary categories: degradation of air quality, noise pollution, and stress from specific land uses. Our spatial epidemiology analysis identified unique patterns in the distribution of these stressors. We explored the connection between environmental stress factors and age-adjusted mortality rates. The findings highlighted a marked association, especially in areas heavily affected by air pollution from vehicle emissions (with mortality rates increasing by 14.8%, 95% CI: 10.4 – 19.4%) and proximity to industrial sites (mortality rates up by 14.7%, 95% CI: 9.4 – 20.2%). Furthermore, our study found that exposure to a combination of detrimental environmental conditions—such as high air and noise pollution levels, closeness to industrial areas or main roads, and lack of green spaces—correlated with a significant increase in mortality rates (a 26.9% rise, 95% CI: 17.1 – 36.5%).

Poster 18:

Investigating high-risk areas of Liver Cancer through the Spatiotemporal Model-based Cancer Incidence Surveillance System in South Korea

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Abstract:

Objective: This study aimed to develop a cancer surveillance system that can identify and respond to high-risk areas using a spatiotemporal model before concerned citizens report cancer clusters through liver cancer examples.

Method: The Korea National Cancer Incidence Database was used from 1999 to 2018. The unit of analysis was the administrative municipal level (Si, Gun, and Gu) in 2018. To examine the possibility of clusters, Global Moran's I used. The study classified liver cancer, which has a high probability of cancer cluster, into hepatocellular carcinoma(HCC) and bile duct carcinoma(BDC) based on risk factors. Additionally, the Spatial scan statistics(SaTScan) and the Bayesian hierarchical model were applied to search for the space-time cancer clusters.

Result: The risk ratios(RRs) of HCC among men in Jindo-gun decreased from 2.33 in 1999-2003 to 1.77 in 2014-2018 but remained the highest compared with other areas. For HCC among women, Jindo-gun had the highest RR of 2.15 in 1999-2003, while Namhae-gun had an RR of 1.37 in 2014-2018. Miryang-si showed high and increased risk for both men(from 2.30 to 2.59) and women(from 1.31 to 1.79) in HBC. The candidate areas for the pre-investigation were selected based on the results of the SaTScan and the Bayesian hierarchical model.

Conclusion: A spatiotemporal model-based cancer incidence surveillance system was proposed to improve the existing epidemiological investigation system. This provides an opportunity for the Central Epidemiological Investigation Team to identify high areas before receiving civil complaints, and to assess the need for further investigations and responses.

Poster 19:

Long-term Urban Air Pollution and In Vitro Fertilization Outcomes

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Abstract:

Many studies have shown that traffic-related air pollution, the most common source of urban air pollution in North America, has a negative effect on both spontaneous and IVF pregnancy outcomes. This objective of this study was to explore urban air pollution exposure and IVF outcomes. The study was a single-center retrospective study of autologous IVF outcomes from fresh and frozen embryo transfer cycles between 2005-2021. Air pollution data for fine particulate matter (PM2.5) and nitrogen dioxide (NO2) were obtained from The Canadian Urban Environmental Health Research Consortium (CANUE). Clinical outcomes were regressed against air pollution exposure using logistic, Poisson, and negative binomial regression models. Clinical outcomes included 1) pregnancy outcome (logistic); 2) number of stimulation days (Poisson); 3) number of oocytes retrieved (negative binomial); 4) number of mature oocytes (negative binomial); 5) failure to reach egg retrieval (logistic); and 6) failure to reach embryo transfer (logistic). Analysis of the data includes 1,765 fresh embryo transfers (ET) and 1,535 frozen ETs. Long-term air pollution within patients' household area ranged from 4.8 to 12.6 µg/m3 for PM2.5 and 3.2 to 28 ppb for NO2. There was a negative association between pregnancy rate and NO2 exposure; odds ratio for a 10 ppb increase in NO2 was 0.76 (95% CI: 0.60-0.97). A suggestive positive association between increased failure to reach embryo transfer and NO2 exposure occurred; odds ratio for a 10 ppb increase in NO2 was 1.4 (95% CI: 0.97-2.01). No other associations were present.

Poster 20:

Uncovering the association and trends of health-related climate stress and negative sentiments on (X platform) across Europe

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Abstract:

This research focuses on utilizing the power of big data from social media (X platform) to gain insights into public expressed sentiments. Climate-sentiment studies associating data from social media to climate data has shown that weather can have significant impacts on expressed sentiments in social media. Through the text analysis of human expressions on (X), we are aiming to identify areas where there are alerts of potential negative sentiments in European countries. The ultimate goal beyond this data mining is to associate sentiments to various hazards and exposures such as climatic factors temperature, precipitation, relative humidity and wind. Extreme climatic events such as floods, heat waves, wildfires, and drought. climate-sensitive infectious diseases data related to the West Nile outbreaks. Allergens, and finally the heat related mortality: We are utilizing machine learning approach, natural language processing to preprocess the data. For initial text preprocessing we have incorporated NLTK, spacy, TextBlob and Regex libraries. Subsequently we leveraged the Linguistic inquiry word count LIWC for advanced sentiment analysis to determine the emotional tone in the text. The spatial analysis was conducted at the NUTS3 level that represents a regional classification system within the European Union. We employed Integrated Nested Laplace Approximation (INLA) Spatial-temporal Bayesian models to analyze the data. Within this comprehensive methodological approach, we are aiming to contribute to a better understanding of conveyed sentiments in relation to various environmental hazards, thereby enabling policymakers to formulate informed strategies for addressing emerging challenges and fostering resilience in the face of evolving climatic conditions.

Poster 21:

Socioeconomic inequities in the COVID-19 vaccination addressing spatial endogenous selection in Cali, Colombia

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Abstract:

The COVID-19 pandemic has accentuated the existing inequities among socioeconomically disadvantaged populations, reflected also in varying levels of vaccination coverage and mortality. Despite the global effort to combat the pandemic, disparities persist, particularly in regions with higher indices of deprivation. This study focuses on the urban area of Cali, Colombia, where substantial socioeconomic differences are prevalent, to investigate the spatiotemporal variability in COVID-19 vaccination coverage. We analysed 380,562 individual-level records obtained from the National Public Health Surveillance System (SIVIGILA), that contain demographic, health, and vaccination status information of COVID-19 patients from 2020 to 2022. For each vaccination outcome (single dose, full schedule, and booster dose) as well as death, a two-part Bayesian model was fitted based on the INLA framework. The first part of the model addresses the endogenous selection bias issue due to the lack of residential information on a proportion of patients, which shows signs of not being missing completely at random. The second part, which provides the odds of each outcome of interest, includes as covariates: demographics, comorbidities, socioeconomic indicators, and structured random effects for spatial and temporal dependence. Joined, both parts provide greater accuracy for parameter estimation. Smoothed odds maps were created to represent each outcome's spatial patterns, showing the strong association between vaccination progress and socioeconomic levels. Our findings highlight the interplay among socioeconomic factors, vaccination coverage, and mortality, in which vulnerable zones of the city have lower odds of vaccination schedule progress.

Poster 22:

Spatial Analysis of COVID-19 and Socioeconomic Factors in Toronto from January 2020 to December 2021

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Abstract:

Background

The COVID-19 pandemic in Toronto, Canada was unequal for its 2.7 million residents, varying over space and time. To assess the impact of socioeconomic status (SES) on risks of infection, we conducted a spatio-temporal analysis of COVID-19 that intends to highlight both the dynamic and variable experience of COVID-19 infections in Toronto during the first two years of the pandemic.

Methods

The study included four time periods, representing the first four major waves of COVID-19 from January 2020 to November 2021. For each wave, we assessed the relationship between SES on COVID-19 case rates across Forward Sortation Areas (FSA) using Poisson Geographically Weighted Regression (GWR) Models. SES factors included visible minorities, education, low-income status, and housing density captured from census data. The models were also adjusted for age, sex, 2-dose vaccination rates and testing rates per FSA.

Results

GWR coefficients highlight the diversity in the relationship between individual SES and COVID-19 and cases across FSA. Although the relationship between SES and covariates differs across FSA and waves, consistent patterns arose. Locations with a higher proportion of residents with at most a high school diploma, visible minorities or older residents (65 years +) were potentially correlated with more COVID-19 cases.

Implications

This analysis highlights persistent inequities in SARS-CoV-2 transmission in Toronto, as well as more dynamic effects that emerged in the face of more widespread immune experience, high vaccine uptake, and shifts in dominant viral variants. SES characteristics appear to have been important determinants of disproportionate risk during the pandemic.

Poster 23:

Heterogeneous changes in mobility in response to the SARS-CoV-2 Omicron BA.2 outbreak in Shanghai

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Abstract:

The coronavirus disease 2019 (COVID-19) pandemic and the measures taken by authorities to control its spread have altered human behavior and mobility patterns in an unprecedented way. However, it remains unclear whether the population response to a COVID-19 outbreak varies within a city or among demographic groups. Here, we utilized passively recorded cellular signaling data at a spatial resolution of 1km x 1km for over 5 million users and epidemiological surveillance data collected during the SARS-CoV-2 Omicron BA.2 outbreak from February to June 2022 in Shanghai, China, to investigate the heterogeneous response of different segments of the population at the within-city level and examine its relationship with the actual risk of infection. Changes in behavior were spatially heterogenous within the city and population groups, and associated with both the infection incidence and adopted interventions. We also found that males and individuals aged 30-59 years old traveled more frequently, traveled longer distances, and their communities were more connected; the same groups were also associated with the highest SARS-CoV-2 incidence. Our results highlight the heterogeneous behavioral change of the Shanghai population to the SARS-CoV-2 Omicron BA.2 outbreak and the effect of heterogenous behavior on the spread of COVID-19, both spatially and demographically. These findings could be instrumental for the design of targeted interventions for the control and mitigation of future outbreaks of COVID-19 and, more broadly, of respiratory pathogens.

Poster 24:

Spatio-temporal analysis of dengue epidemics in Argentina (2009-2023): The contribution of socio-economic factors

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Abstract:

Background

In recent decades, with more frequent and significant epidemics, dengue has become a major public health concern, especially in tropical and subtropical regions but also in non-endemic areas. Climate change seems to be an important driver in the spread of the disease and Argentina is not spared from this phenomenon. Although rising temperatures and precipitation are mainly pointed out, other lesser-studied variables could also influence the incidence and growing occurrence of dengue epidemics. Here we evaluate the contribution of socioeconomic and demographic factors alongside more common environmental variables.

Methods

Following the historical spread of dengue within the country, dengue cases were reported yearly and by department from 2009 to 2023. Environmental variables including elevation, mean temperature, mean precipitation and socioeconomic variables such as education, public water supply, population count and level of urbanization were implemented in different models for the epidemic peak years (2009, 2016, 2020, 2023). We first explored the multiple linear regression model and then the zero-inflated negative binomial approach to assess the contribution of socio-economic factors.

Results

As part of a systemic approach, this study aims to shed light on the contribution of variables commonly ignored or less considered in literature. We expect that our results will demonstrate the key role played by socioeconomic aspects as well as human behaviors in spatial variations of dengue incidence in Argentina.

Poster 25:

Spatial analysis of self-inflicted violence incidence in Brazil (2011-2022)

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Abstract:

Introduction: Self-inflicted violence is a serious public health problem and causes physical and psychological harm to victims, their families, and friends. The analysis of spatial patterns of self-inflicted violence is innovative and can provide updated evidence on the topic. Objective: Analyze the spatial patterns of the incidence of self-inflicted violence in Brazil, in the period between 2011 and 2022. Methods: Ecological study through exploratory and spatial analyzes of the age specific and age-standardized incidence rates of self-inflicted violence present in the Information System of Notifiable Diseases (SINAN), between 2011 and 2022, in the Immediate Geographic Region (RGI) of Brazil, according to life cycles: adolescents (10 to 19 years old), young people (20 to 24 years old), adults (25 to 59 years) and elderly people (60 years and over). Results: There were 695.002 cases of self-inflicted violence, among them 29.2 were adolescents (n=203,146); 16.6% young people (n=115,483); 50.7% adults (n=352,330) and 3.5% elders (n=24,043). The spatial patterns of self-inflicted violence were similar across all the age groups, with spatial clusters of high incidence along the south coast and in the capital, Brasília. Conclusion: This study generated important information that could support future public policies, seeking to promote health and prevent self-inflicted violence.

Poster 26:

Spatiotemporal risk modeling for Highly Pathogenic Avian Influenza transmission based on seasonal wild bird distribution

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Abstract:

Since 2003, highly pathogenic avian influenza (HPAI) viruses have caused global economic and public health crises. From 2020 to 2024, H5, H7, and H9 viruses have spread, evolving to infect a range of hosts, including humans, with migratory wild birds playing a critical role in their transmission.

The goal of this study is to build a dynamic prediction model for the risk of HPAI introduction in Africa, Asia and Europe.

We used ecological niche models (ENMs), based on Wetland International's wild bird sightings and a wide array of environmental predictors, to map seasonal ecological suitability for wild birds at a 10 km resolution. The maps of 80 anatidae species form the basis of our AIV risk factor maps.

The AIV risk factor maps are derived from the cumulative seasonal probability of wild bird species presence, as generated by the ENMs. To account for seasonal and species-specific variations in virus transmission, we conducted an extensive review to quantify the prevalence of AIV in wild birds. A database compiled from 201 studies allowed us to use the prevalence rate as a weighting factor to enhance the accuracy of the risk factor maps.

The risk factor maps effectively predict AIV occurrences (EMPRES-i database). Surprisingly, the introduction of species prevalence rates or population densities only marginally improved the predictive power of the model. These results highlight the importance of species richness mapping and the need for extensive knowledge of the distribution and movements of wild birds to refine HPAI risk modeling.

Poster 27:

Prototype Development of a Light-Agent Spatial modeling tool for Eradication planning (LASER)

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Abstract:

Understanding the dynamics of disease spread across different areas is key to planning effective elimination and eradication strategies. The uneven coverage of routine vaccinations and the interconnectedness of populations significantly impact the frequency of outbreaks, as seen in diseases like measles. The spread of diseases such as polio is also influenced by variations in vaccination rates and the occurrence of undetected case chains, highlighting the importance of understanding how people move and interact in efforts to design supplemental immunization efforts. Additionally, tracking the movement of mosquitoes is crucial for managing insecticide and drug resistance and evaluating the effectiveness of genetically modified mosquitoes against mosquito-borne diseases.

To address these issues, we present an innovative, Python-based, agent-based modeling tool designed to simulate the actions of 10^7 to 10^8 agents across hundreds of locations quickly, even on a standard laptop. This tool utilizes data layout optimizations and GPU computing to enhance processing speed and efficiency, allowing for the rapid exploration of various disease control strategies.

Our model's ability to quickly simulate detailed scenarios on a broad scale offers valuable insights for researchers and policymakers, facilitating the development of targeted interventions. By providing a powerful platform for detailed analysis and strategic planning, this tool represents a significant advancement in the global fight against infectious diseases, supporting efforts to optimize responses and improve public health outcomes.

Poster 28:

Modelling inequalities in the different phases of COVID19 in the Netherlands

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Abstract:

Background: The COVID-19 pandemic has brought to the fore long-standing inequities that resulted in already-vulnerable groups bearing a disproportionate burden of the disease. People with low socio-economic status (SES) and several ethnic groups have been particularly affected by the COVID-19 pandemic in the Netherlands.

Methodology: We assess COVID-19 related inequalities in the cascade of care, from reported infections (positive tests) to hospitalizations. We fit a hierarchical Bayesian model estimating the time-varying association between COVID-19 outcomes and areal level SES, education level, and ethnicity from June 2020 to the end of 2021 in the Netherlands. We consider different spatial resolutions (i.e., neighborhood level, zip-code level) and adjust for confounders and spatio-temporal correlation structure.

Results: Areas with low SES, low education levels and a higher proportion of people with a migration background are associated with a higher number of reported cases and hospitalizations. The strength of association varies in the different phases of the pandemic, characterized by different control measures and different variants. Highest COVID19 inequalities are observed in the period following more stringent measures, where national contact surveys also showed a differential exposure of vulnerable groups.

Conclusions: The consistency of results across reported cases and hospitalizations suggests that the inequalities are due to differences in exposure and/or susceptibility. The development of these models can support and guide the identification of vulnerable areas during an epidemic.

Poster 29:

Understanding Dengue Dynamics in Brazil: Spatio-Temporal Patterns and Future Projections

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Abstract:

Dengue is a neglected tropical disease that has rapidly expanded globally in recent decades, possibly due to climatic factors. In Brazil, 2024 has seen a historic surge, with over 5 million probable cases reported by the Ministry of Health. Our study focused on dengue incidence in Brazil, a country with continental dimensions, encompassing 557 microregions. We used monthly data from 2000-2021 as the historical training set and projected incidence trends for 2021-2040 and 2041-2060, considering different greenhouse gas emission scenarios. Climatic and population variables varied under these scenarios for the projections, while socioeconomic, climatic, and environmental variables were used for model fitting and assessment. Using the R language with the Integrated Nested Laplace Approximation – INLA approach, we assessed the rates of dengue incidence associated with the covariates of interest and forecasted future trends by building hierarchical models within a Bayesian framework, while accounting for latent Gaussian spatio-temporal patterns. We also performed cross-validation to assess the robustness and predictive performance of our models. Our analyses show an association between dengue dynamics and precipitation, minimum temperature, urban infrastructure, Normalized Difference Water Index - NDWI, deprivation index, seasons, and elevation. Regarding the forecast, we observed an interesting pattern: despite the projected temperature increase, the rise in dengue incidence is not uniform across the Brazilian regions. Some non-endemic regions are expected to experience a significant increase, while some previously endemic regions may maintain or even witness a decrease. Understanding these spatial and temporal patterns, alongside future projections, is essential for effective surveillance and control.

Poster 30:

Factors influencing chikungunya incidence in Brazil: Insights from Spatiotemporal Modeling

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Abstract:

Chikungunya, transmitted by Aedes aegypti and Ae. albopictus mosquitoes, has seen a notable increase in Brazil, particularly evident during the 2024 summer compared to the previous year, with Brazil now representing 98% of all cases in the Americas. This study focuses on modeling the spatiotemporal distribution of chikungunya across 5,569 Brazilian municipalities from 2015 to 2023 on a seasonal basis. Utilizing Bayesian statistics with the Integrated Nested Laplace Approximation (INLA) approach, the research examines climatic and environmental conditions (such as precipitation, temperature, ENSO, biome, and vegetation), mobility, sociodemographic and socioeconomic variables (sewage systems, piped water, and garbage collection services). Out of the 1,757,169 reported cases by the Brazilian Ministry of Health, 883,853 were analyzed, following the exclusion of cases with inconclusive classification, under investigation, or falling outside the area and study period, including imported cases. Preliminary findings suggest that higher chikungunya incidence is associated with higher minimum temperatures, increased precipitation, smaller temperature ranges, lower altimetry, and the presence of the Caatinga biome. Interestingly, mobility patterns correlate with socioeconomic factors, indicating a nuanced interplay between human behavior and disease transmission dynamics. Additionally, we observed a potential interaction effect between socioeconomic factors and biomes. These findings aid in predicting high-risk areas for chikungunya outbreaks,facilitating targeted interventions to mitigate its spread, and safeguarding public health in Brazil. This interdisciplinary approach underscores the importance of considering multifaceted factors in combating vector-borne diseases, especially in regions prone to rapid disease transmission like Brazil.

Poster 31:

A timeseries analysis of salmonella cases in a UK climate and the impact of public health interventions

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Abstract:

The impacts of climate change on health have been extensively analysed for heat

mortality, impacts of air pollution linked to burning of fossil fuels and to some extent risk of flooding.

The linkage between climate and health is however less studied in a UK context for other health risks, such as infectious diseases, as highlighted in the latest 'Health Effects of Climate Change in the

UK' report. Previous studies on the effect of temperature on salmonella cases were published over a decade ago, prior to some of the latest public health interventions were introduced and not

including data from the hot summers experienced during the 2010s. In this study we have used the distributed lag non-linear model to study the impact of high temperatures on salmonella cases in

England at a regional scale for the time period 1989-2020. The DLNM has been widely used in heat-attribution studies, particularly for mortality studies, but so far not widely applied in infectious disease studies. Our results demonstrate the substantial reduction in risk thanks to widespread vaccination by estimating the expected disease burden in a counterfactual world had the interventions not been introduced.

Poster 32:

Spatial and Temporal trends in COVID-19 Mortality at the county-level in US

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Abstract:

COVID-19 is a nationally notifiable disease. Although many studies and reports have reported large-scale geographic patterns in COVID-19 mortality, spatial patterns at the county-level have not been much explored because of the potential instability in mortality rates at smaller geographical scales such as counties. Hierarchical Bayes models have been used in disease mapping to examine small scale geographic variation. The objectives of this analysis are to implement Bayesian space-time models with space–time interaction terms, correlated and uncorrelated time effects and spatially structured and unstructured random effects to produce stable county-level mortality estimates by time, allowing for examination of spatio-temporal patterns and trends in COVID-19 mortality rates at the county level. This study will also examine whether COVID-19 mortality rates show evidence of clustering for identifying groups of counties with extremely high or low rates. Describing how counties with high or low COVID-19 rates cluster geographically may aid efforts to further reduce COVID-19 disease burden rates in specific areas of the U.S.

Poster 33:

Water and Wastewater Infrastructure Inequities in Unincorporated Communities: Evidence from the United States.

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Abstract:

A substantial number of United States households lack adequate access to water and wastewater infrastructure - a disparity linked to the community's local governance structure. In the U.S., nearly 37% of the population lives outside of city boundaries, in unincorporated areas that lack centralized government at a level more local than the county. Our analysis focuses on the relationship between a locality's incorporation status and its lack of centralized infrastructure. We first compiled a novel dataset of 31,685 U.S. Census Block-groups, located across 9 States and representing over 25% of the national population. This includes infrastructure coverage information (obtained via digitized service area maps), incorporation status (using Microsoft building foot-print data and U.S. Census Tiger data), and census demographic variables. We then fit a negative binomial generalized linear model, with county-level random effects, to describe the relationship between area of a block-group not served and governance status. Our regression analysis reveals that, when comparing two block-groups in the same county and with similar socio-demographic fabric, one classified as unincorporated and the other as incorporated, the former is on average 89% more likely to not be served by drinking water infrastructure, and on average 50% more likely to not be served by wastewater infrastructure. When looking at specific types of unincorporated communities, results do not translate equally. In particular, so-called "islands", that is unincorporated communities embedded within incorporated city bounds exhibit even higher incidence rates highlighting that governance type is associated with access even in communities that are urban and densely populated.

Poster 34:

School absence data for acute infectious disease surveillance in the Netherlands

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Abstract:

School-aged children, although at lower risk of severe illness from acute respiratory infections (ARI), can significantly contribute to transmission due to their close interactions in educational settings. We evaluated the potential of school absenteeism data as a tool for ARI surveillance by comparing national and regional absenteeism rates from Dutch high schools (± 50% coverage) across three school years (2017/18, 2018/19, 2022/23) with trends in general practitioners (GP) visits for ARI among school-aged and general populations. Using cross-correlation, we found a strong correlation between national patterns in absenteeism rates and GP visit rates, with absenteeism peaks typically preceding GP visit peaks by 1-3 weeks. While regional differences in the timing of peaks were observed in both absenteeism and GP visit rates, these variations were more pronounced in the GP visit data. Overall, these results suggest that absenteeism data could serve as an early indicator of upcoming epidemic waves.

Poster 35:

Spatial Variation of Anaemia Prevalence among School-Aged Children in Western Kenya: Implications for Targeted Interventions.

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Abstract:

Anaemia poses a significant public health challenge among school-aged children (SAC), yet surveillance efforts have predominantly targeted other demographic groups, leaving SAC relatively underrepresented. This study delves into the prevalence of anaemia among SAC (5-14 years) in western Kenya, a region characterized by dense population and high malaria infection rates compounded by limited access to basic sanitation. Our investigation involved the examination of 8051 SAC from 82 schools, with haemoglobin concentrations assessed at school and village levels. We found that anaemia prevalence was 27.8%, exhibiting a discernible non-random spatial pattern (Moran's I 0.2; p-value < 0.002). Moreover, significant local clusters of anaemia were identified, indicating spatial heterogeneity in prevalence rates. Notably, anaemia rates at both school and village levels were influenced by contextual residential characteristics, with no statistically significant difference in median prevalence, suggesting that the prevalence observed at schools mirrors the surrounding community. Our analysis suggests that factors such as age, malaria prevalence, and sanitation play pivotal roles in driving anaemia rates in this region, with nutrition and gender less likely to be significant contributors. These findings underscore the importance of targeted interventions, pinpointing geographical areas with elevated anaemia prevalence, to effectively alleviate the burden of anaemia among SAC in Western Kenya.