



GEOMED 2022
UCI, October 12-14, 2022

Abstract book - Oral presentations

Plenary sessions

Speaker: Katie Hampson

Affiliation: University of Glasgow, School of Biodiversity, One Health & Veterinary Medicine

Title: The importance of the spatial scale of transmission for infectious disease dynamics

Abstract:

Fundamental questions remain about the regulation of acute pathogens in the absence of acquired immunity, both how they persist and what curtails epidemic growth. This is especially true for rabies, a universally fatal zoonosis that circulates endemically at low prevalence in domestic dog populations in low- and middle-income countries. From tracing rabies transmission in a population of 50,000 dogs in northwest Tanzania over a twenty-year period we unravel the processes through which rabies persists and is regulated. Using Approximate Bayesian Computation we fit individual-based models to spatially resolved data to investigate the mechanisms modulating transmission and the scale over which they operate. We find that while prevalence never exceeds 0.15%, we detect significant susceptible depletion at local scales commensurate with rabid dog movement, reducing transmission through clustering of rabies deaths and individuals incubating infection. Individual variation in rabid dog behaviour facilitates virus dispersal and co-circulation of lineages, enabling metapopulation persistence. These mechanisms likely operate in many pathogens circulating in spatially structured populations, with important implications for prediction and control, yet are difficult to observe unless the scale of host interactions is identified.

Co-authors: Rebecca Mancy, Elaine A. Ferguson, Malavika Rajeev, Ahmed Lugelo, Matthias Magoto, Daniel T. Haydon.

Speaker: Sudipto Banerjee

Affiliation: UCLA Department of Biostatistics

Title: Detecting spatial difference boundaries using Bayesian disease mapping

Abstract:

Regional aggregates of health outcomes over delineated administrative units (e.g., states, counties, and zip codes), or areal units, are widely used by epidemiologists to map mortality or incidence rates and capture geographic variation. To capture health disparities over regions, we seek “difference boundaries” that separate neighboring regions with significantly different spatial effects. Matters are more challenging with multiple outcomes over each unit, where we capture dependence among diseases as well as across the areal units. Here, we address multivariate difference boundary detection for correlated diseases. We formulate the problem in terms of Bayesian pairwise multiple comparisons and seek the posterior probabilities of neighboring spatial effects being different. To achieve this, we endow the spatial random effects with a discrete probability law using a class of multivariate areally referenced Dirichlet process models that accommodate spatial and interdisease dependence. We evaluate our method through simulation studies and detect difference boundaries for multiple cancers using data from the Surveillance, Epidemiology, and End Results Program of the National Cancer Institute.

Co-authors: Leiwen Gao and Beate Ritz of UCLA Fielding School of Public Health.

Speaker: Becky P.Y. Loo

Affiliation: HKU Department of Geography

Title: Human mobility, facilities and location agglomeration: Are there regularities that inform the creation of a superspreading environment?

Abstract:

Thinking about space is key to the geographical mind. From a public health perspective, identifying and isolating superspreaders in a timely manner can be critical in stopping the spread of an epidemic. This was one of the major lessons learned from the SARS outbreak. Beyond individuals, a superspreading environment exists across space and time. While research on superspreaders focuses on people, a superspreading environment incorporates the space dimension. Theoretically, an individual's reproductive number can be seen as a random variable representing the expected number of cases caused by a particular infected individual. The spatial risk factor is more complex and needs to be calculated based on the number and characteristics of visitors, as well as features of a place, notably its functions and conditions. Are there regularities that can inform the risk of the formation of a superspreading environment? This study focuses on six common types of facilities (bars, cinemas, gym and fitness centers, places of worship, public libraries and shopping malls) and analyzes detailed human mobility data in six global cities across four continents (Chicago, Hong Kong, London, Sao Paulo, Seoul and Zurich) to test whether visitors' mobility characteristics vary for different facility types and for different locations based on facility agglomeration. Then, based on the nature of activities in relation to the risk of the spread COVID-19, a kernel density function is employed to derive the spatial risk surface in each city. Based on the geographical analysis, a more differentiated and location-sensitive policy of disease control and exit strategies that balances the control of the pandemic and people's daily life can be formulated.

Co-authors: Ka Ho Tsoi, Yongsung Lee and Keumseok Peter Koh from HKU Department of Geography, Kay W. Axhausen from ETH Zurich Department of Civil, Environment and Geomatic Engineering and Mengqiu Cao from University of Westminster School of Architecture and Cities.

Oral presentations

Session 1 “*Geospatial perspective on environmental influences on mental health*”

Presenter (First Name, Last Name): Kai Chen

Affiliation: Yale University

Title: Back extrapolating historical air pollution based on long-term in-situ measurements: an example from the United Kingdom

Abstract:

Background: Historical PM_{2.5} data are important for assessing the health effects of air pollution exposure across the life course or early life. Satellite-based aerosol optical depth (AOD) has been widely used as a major predictor in high-resolution PM_{2.5} exposure models. However, the lack of satellite-based AOD products with high precision and resolution before the 2000s constrains the development of back extrapolation PM_{2.5} exposure models.

Aim: To construct a back extrapolation daily PM_{2.5} exposure model at a spatial resolution of 1 km in the United Kingdom.

Method: We utilize the Extreme Gradient Boosting (XGBoost) model to capture reliable spatiotemporal associations between daily PM_{2.5} concentrations and multi-source geographical predictors, including meteorological factors, land cover types, and anthropogenic emissions. Monitoring data from 2010 to 2019 are used to train and validate the models, and observations from 2000 to 2009 are used to test the models' extrapolation capability. Then the associations could be used to back-extrapolate historical PM_{2.5} concentrations.

Results: The ranges of coefficients of determination (R²) and root mean square errors (RMSE) for the by-year cross-validation (CV) are 0.64-0.78 and 3.57-5.33 $\mu\text{g}/\text{m}^3$ respectively from 2010 to 2019, which shows comparable agreement with in-situ measurements when compared with previous studies. The ranges of R² and RMSE for the external testing are 0.68-0.71 and 4.65-7.42 $\mu\text{g}/\text{m}^3$ respectively from 2000 to 2009, demonstrating that our datasets are reliable over time.

Conclusion: This study demonstrates the feasibility of constructing back extrapolation models based on long-term in-situ observations, which is critical for further epidemiological studies.

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Presenter (First Name, Last Name): Eunhye Yoo

Affiliation: University at Buffalo, State University of New York (SUNY)

Title: Community level comorbidity between mental disorders and respiratory disease: multivariate spatio-temporal disease mapping

Abstract:

Growing evidence shows substantial comorbidity between mental disorders and physical illnesses, such as asthma. However, most existing studies focus only on individual level and thus little is known about community level comorbidities. While the former refers to the joint occurrence of two disorders within an individual, we define the latter as the joint occurrence of disorders within a specific areal unit. To investigate community level comorbidity, we examined emergency room (ER) visits involving comorbid mental disorders and respiratory disease in Erie/Niagara counties in

New York, US, between 2005 and 2016. We used the outpatient ER visit data, which were further aggregated at census tracts annually for subsequent analyses. We quantified and mapped bivariate local indicators of spatial association between ER visits for mental disorders and respiratory disease to examine their spatial patterns. We also developed a Bayesian hierarchical spatio-temporal model for the joint analysis of comorbidities of mental disorders and respiratory disease. We explicitly accounted for both spatial dependence and correlation between mental disorder and respiratory disease using a joint spatio-temporal model for multiple diseases with R-INLA. Lastly, we assessed the effects of risk factors on community level comorbidities (i.e., shared spatial effect estimates). We found that two communities in the study region were at higher risk in terms of their shared spatial effect (comorbidity) during the study period. We also found that community level comorbidity was associated with lower socio-economic conditions, higher crime rates, and less greenspace. In summary, we identified communities at higher risks of comorbidity between mental disorders and respiratory disease using multivariate spatiotemporal disease mapping, although longitudinal studies are needed to investigate possible shared causative mechanisms between mental disorders and respiratory disease.

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Presenter (First Name, Last Name): Xiaojiang Li

Affiliation: Temple University

Title: The discrepancies of the urban heat metrics generated from different geospatial datasets

Abstract:

Extreme heat events are increasing in frequency and intensity in US cities and are responsible for a greater annual number of climate-related fatalities, on average, than any other form of extreme weather. The urban heat island effect is believed to further exacerbate the mortality increase caused by heat stress in cities. The land surface temperature (LST) derived from remotely sensed thermal imageries has been widely used to map the spatial distributions of the urban heat at large scales and study the heat-related morbidity and mortality. The LST usually indicates the surface temperature building roofs and the tops of tree canopies, which are not the places that human activities happen. Compared with the LST, the air temperature is more reasonable to represent human heat stress level. However, the air temperature is usually measured at a limited number of fixed weather stations, which cannot represent the spatial and temporal variations of the air temperature within cities. The climate modeling like the Weather Research and Forecasting (WRF) model provides a new option to examine the urban heat at the mesoscale. However, the WRF is too coarse for examine the urban microclimate, which varies spatially significantly street by street and neighborhood by neighborhood. Fine level urban microclimate modeling based on high-resolution three-dimensional urban models and local meteorological data provides a more comprehensive way to model the dynamically changing urban thermal environment. This study will conduct the microclimate modeling in Philadelphia and compare the discrepancies of different urban heat metrics in Philadelphia.

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Presenter (First Name, Last Name): Timothy Collins

Affiliation: University of Utah

Title: Cascading disasters and mental health inequities: Winter storm Uri, COVID-19 and post-traumatic stress in Texas

Abstract:

Previous research on health effects of extreme weather has focused more on hot than cold events, even though cold-attributable mortality exceeds heat-attributable mortality worldwide. The small literature on cold weather events emphasizes physical health rather than mental health, leaving an important knowledge gap in context of climate change. We take a novel “cascading disaster health inequities” approach to examine winter storm-associated post-traumatic stress (PTS) using primary survey data collected in eight metro areas in Texas following Winter Storm Uri in 2021, which occurred against the backdrop of COVID-19 (n=896). The overall incidence of storm-related PTS among householders was 18%. Being Hispanic and non-Hispanic Black increased odds of PTS by 2.9 and 6.1 times respectively vs. being non-Hispanic White, which highlights racially inequitable impacts. Having a household member with a disability increased odds by 2.4 times (all $p < 0.05$). Having a piped water outage during Uri and having high COVID-19 impacts increased odds of householder PTS by 1.7 and 2.7 times, respectively (both $p < 0.05$). When modelling how COVID-19 and Uri-induced power and water outages cascaded, we compared to households with no outages and low COVID-19 impacts. Householders were more likely to have high PTS ($p < 0.05$) if they had one outage (water or power) and high COVID-19 impacts (4.9 times), if they had two outages (water and power) with low COVID-19 impacts (2.9 times), and if they had two outages and high COVID-19 impacts (8.2 times). In sum, the paper contributes new knowledge about health inequities and cascading impacts of extreme weather events.

Session 2 “*Spatial models to infer upon cancer incidence and prognosis*”

Presenter (First Name, Last Name): Annelies Agten

Affiliation: Hasselt University

Title: Measures of spatial heterogeneity in the liver tissue micro-environment as prognostic factors for fibrosis score.

Abstract:

Liver diseases are caused by a complex interaction between hepatocytes and other hepatic non-parenchymal cells. Although spatial heterogeneity within the tumor micro-environment has been proven to be a fundamental feature in cancer progression, the role of the liver tissue micro-environment in the context of liver damage has not been widely studied yet. We obtained 110 core needle biopsies from a cohort of chronic hepatitis B patients with different fibrosis stages. The tissue sections were imaged using immunofluorescence microscopy to determine the locations of immune cells, HBsAg-positive and HBsAg-negative hepatocytes. We applied several descriptive techniques adopted from ecology, including Getis-Ord, the Shannon and the Morisita-Horn Index, to quantify the extent of liver cell co-localization. Additionally, we modelled the spatial distribution

of the different cell types using a joint log-Gaussian Cox process and proposed several features to quantify spatial heterogeneity. We relate these measures to the patient fibrosis stage by using a linear discriminant analysis approach. Our analysis revealed that the co-localization of HBsAg-positive hepatocytes with immune cells and the co-localization of HBsAg-negative hepatocytes with immune cells are important prognostic factors for fibrosis score in chronic hepatitis B patients. Moreover, we found that if we allow for an error of 1 on the METAVIR score, we are able to reach an accuracy of around 80%. With this study we demonstrate how methods adopted from ecology and applied to the liver tissue micro-environment can be used to quantify heterogeneity and how these approaches can be valuable in biomarker analyses for liver diseases.

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Presenter (First Name, Last Name): Oana Petrof

Affiliation: Hasselt University

Title: Disease mapping method comparing the spatial distribution of a disease with a control disease

Abstract:

Small-area methods are being used in spatial epidemiology to understand the effect of location on health and detect areas where the risk of a disease is significantly elevated. Disease mapping models relate the observed number of cases to an expected number of cases per area. Expected numbers are often calculated by internal standardization, which requires both accurate population numbers and disease rates per gender and/or age group. However, confidentiality issues or the absence of high-quality information about the characteristics of a population-at-risk can hamper those calculations.

Based on methods in point process analysis for situations without accurate population data, we propose the use of a case-control approach in the context of lattice data, in which an unrelated, spatially unstructured disease is used as a control disease. We correct for the uncertainty in the estimation of the expected values, which arises by using the control disease's observed number of cases as a representation of a fraction of the total population. We apply our methods to a Belgian study of mesothelioma risk, where pancreatic cancer serves as the control disease.

The analysis results are in close agreement with those coming from traditional disease mapping models based on internally standardized expected counts. The simulation study results confirm our findings for different spatial structures. We show that the proposed method can adequately address the problem of inaccurate or unavailable population data in disease mapping analysis.

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Presenter (First Name, Last Name): Garazi Retegui

Affiliation: Public University of Navarre (UPNA)

Title: Evaluating multivariate models for predicting cancer incidence using mortality data

Abstract:

For a correct allocation of health resources in cancer, different indicators such as incidence and mortality are considered. In most countries, Statistical Offices routinely record cancer mortality figures. In contrast, incidence is recorded by national or regional population-based cancer registries (PBCRs). However, in most southern European countries, the local PBCRs cover only a fraction of the country. Therefore, national cancer incidence numbers can only be obtained through estimation methods. Moreover, due to the complexity of data collection, classification, validation and processing, cancer incidence figures provided by the PBCRs are usually available with a delay and therefore, methods that provide short-term predictions are very useful. In this work, we have two objectives: the first is to provide cancer incidence projections in areas not covered by a PBCR to subsequently obtain national cancer incidence estimates and, the second one is to predict short-term estimates.

In a first spatial study, we evaluate the suitability of different multivariate models to project cancer incidence in areas not covered by PBCRs, by joint modelling mortality and available incidence data. Due to the good predictive performance of the multivariate models, in a second step, we extend the multivariate models to a spatio-temporal context. The short-term predictive ability of the models is evaluated in an in-depth simulation study. The results are illustrated using regional data on cancer incidence and mortality in Germany in the period 2001-2015.

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Presenter (First Name, Last Name): Giorgia Stoppa

Affiliation: University of Padua

Title: Spatial distribution of mortality risk for ovarian cancer and asbestos exposure in Lombardy

Abstract:

There is sufficient evidence for a causal association between exposure to asbestos and ovarian cancer. We propose a shared trivariate Bayesian model to assess the presence and geographic distribution of the risk of ovarian cancer mortality related to asbestos exposure at municipality level in the Lombardy Region (Italy) in the period 2000-2018. Deaths from ovarian, pleural, and breast cancer were extracted from the National Institute of Statistics archives. Expected cases were calculated by indirect internal standardization. We specify a series of spatially structured trivariate models with shared and disease-specific components. We show the correspondence of our framework with Graphical modelling, where models are represented as graphs. These graphs display the structure of dependencies, both spatially structured or unstructured, among the diseases as shared components of the trivariate Bayesian models. We found shared dependencies between ovarian and pleural cancer which capture risk factors common to the two diseases (interpretable as asbestos exposure); and a spatially structured clustering component shared between ovarian and breast cancer capturing risk factors that are not related to asbestos. Our results are consistent with known heavy asbestos pollution in selected municipalities and show the contribution of asbestos exposure in mortality for ovarian cancer. Bayesian modelling provides helpful information to tailor

epidemiological surveillance. The introduction of a third disease, or in general a multivariate framework, helps to mitigate the identifiability problems in such shared-component modelling and better control for the effect of any other risk factors that might explain the geographic distribution of the disease of interest.

Co-authors: Dolores Catelan and Annibale Biggeri from University of Padua, Carolina Mensi, Lucia Fazzo, Giada Minelli and Valerio Manno from Superior Institute of Health, Dario Consonni from Hospital Polyclinic of Milan.

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Session 3 “*Cross-border health, one neglected global health challenge*”

Presenter (First Name, Last Name): Christovam Barcellos

Affiliation: Oswaldo Cruz Foundation (Fiocruz)

Title: Cross-border sentinel sites of the Climate and Health Observatory

Abstract:

Sentinel sites can be defined as a place where diseases and environmental changes can be monitored in order to inform local and regional stakeholders about long term tendencies, extreme events and outbreaks. In this sense, international borders are strategic sites where social, political and environmental processes are exacerbated, including some regional expressions of climate change. Our project aims to build a cross-border surveillance system that can provide and make available comparable and qualified data to all parties involved in malaria control between French Guiana and Brazil. Data reconciliation rules based on expert knowledge were defined and applied to the heterogeneous data provided by the existing malaria surveillance systems of both countries. Visualization dashboards were designed to facilitate progressive data exploration, analysis, and interpretation. This cross-border monitoring tool could help produce new scientific evidence on cross-border malaria dynamics, implementing cross-border cooperation for malaria control and elimination, and can be quickly adapted to other cross-border contexts. This experience was initiated to monitor malaria incidence and more recently expanded to other diseases, such as dengue and Covid-19, and other international cross-border zones, such as Brazil-Colombia-Peru.

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Presenter (First Name, Last Name): Paulo Peiter

Affiliation: Oswaldo Cruz Foundation (Fiocruz)

Title: Access to health care between system margins: drifting populations on the border between Brazil and French Guiana

Abstract:

Brazil and France share a 730 km border on the Oiapoque river basin where the cities of Oiapoque (15 thousand inhabitants), Vila Brasil and Ilha Bela - in Brazil; Saint Georges de

l'Oyapock (2 thousand inhabitants) and Camopi - in French Guyana - are located. A place with intense movement of miners and indigenous people. Its informal character gives its own characteristics to the relationships with other sectors of the local society, with implications for access to health. The municipality of Oiapoque, distant from the capital Macapá, has a lack of health professionals and equipment, especially in rural and distant areas, such as Vila Brasil and Ilha Bela, at a distance of 5 hours by boat from the urban core of Oiapoque. The question is: How do the populations of these border localities solve their health needs? Our objective is to understand the health access strategies of the populations of Ilha Bela and Vila Brasil. This is an exploratory quali-quantitative study, involving the characterization of health in the border region; survey of secondary data and interviews with the population, health professionals and local managers. The results point to the overlapping vulnerabilities of populations living on the margins of society in international borders and between the legal and illegal developing strategies that involve the establishment of cross-border networks for access to health. These results will contribute to rethink cooperation actions in border health, and strategies for health care for vulnerable populations living in border regions of the Amazon.

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Presenter (First Name, Last Name): Esmeralda Iniguez-Stevens

Affiliation: CA Department of Public Health , Office of Binational Border Health

Title: Building public health partnerships in the U.S.-Mexico border region

Abstract:

Strong binational cross-border partnerships are fundamental to fighting infectious diseases in geographic areas spanning two countries. Recognizing this need the California Department of Public Health Office of Binational Border Health (CDPH-OBBH) has worked jointly with local, state and federal partners in the U.S. and Mexico to enhance the regions' ability to detect and respond to infectious disease threats. The formation of strong cross-border networks and partnerships has been instrumental in strengthening infectious disease surveillance and communication capabilities in the border region. Efforts have focused on establishing binational surveillance and monitoring systems, working with border health partners to develop and maintain routine and emergency communication protocols, facilitating cross-border exchange of information, and establishing mechanism to facilitate public health action when binational cases and outbreaks are detected. CDPH OBBH has been an active participant and contributor to numerous cross-border, multi-disciplinary, multi-agency initiatives that have successfully built capacity for effective public health response. This presentation will provide a historical perspective on CDPH OBBH's role as a partner in building public health partnerships in the U.S.-Mexico Border Region.

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Presenter: Tatiana Marrufo, MD MPH

Affiliation: National Institute of Health (Instituto Nacional de Saúde) of Mozambique

Title: International boundaries and internal limits of public health systems in southern Africa: sharing the experience of Mozambique

Abstract:

Health systems that function properly must rely on multiple factors such as financial, socioeconomic, environmental, workforce resources, and a leadership that is committed, with a vision focusing primarily on people, particularly the poor, the sick and the disabled, and, through various initiatives that encourages change in individual unhealthy behaviors. In Africa, those factors are challenging because it should include a more balanced, horizontal approach to disease prevention, education, and awareness of the mode of transmission or exposure to both infectious and chronic diseases. Apart from challenges derived from the COVID-19 pandemic, in southern Africa, particularly in Mozambique in the recent years, international boundaries encouraged to reinforce measures and strategies to cope with imposed challenges on internal limits of public health systems. Experiences to be shared are related to people displacement from Mozambique to Malawi due to the impacts of the cyclones; cholera outbreak at the central region of the country affecting the border districts with the impacts to nearest countries, and the response and control of the wild poliovirus outbreak in southern Africa. Those emergencies called for an integrated approach to health, involving sectors of government, such as the ministries of health and of education; transportation and infrastructure; water and sanitation; food security and housing; aiming at sharing information to meet the same health goals and strategies for disease management, as well as more attention to the real needs of the people through proper retooling of the health personnel, accurate diagnosis of disease and systematic increase of children's immunization against preventable diseases.

Session 4 “*On challenges posed by uncertainty in geospatial health research*”

Presenter (First Name, Last Name): Michael R. Desjardins

Affiliation: Johns Hopkins University

Title: Uncertainty in geospatial health: challenges and opportunities ahead

Abstract:

Uncertainty is not always well captured, understood, or modeled properly, and can bias the robustness of complex relationships, such as the association between the environment and public health through exposure, estimates of geographic accessibility and cluster detection, to name a few. We review current challenges and future opportunities as geospatial data and analyses are applied to the field of public health. We are particularly interested in the sources of uncertainty in geospatial data and how this uncertainty may propagate in spatial analysis. We present opportunities to reduce the magnitude and impact of uncertainty. Specifically, we focus on (1) the use of multiple reference data sources to reduce geocoding errors, (2) the validity of online geocoders and how confidentiality (e.g., HIPAA) may be breached, (3) use of multiple reference

data sources to reduce geocoding errors, (4) the impact of geoinputation techniques on travel estimates, (5) residential mobility and how it affects accessibility metrics and clustering, and (6) modeling errors in the American Community Survey. Our paper discusses how to communicate spatial and spatiotemporal uncertainty, and high-performance computing to conduct large amounts of simulations to ultimately increase statistical robustness for studies in public health. Our paper contributes to recent efforts to fill in knowledge gaps at the intersection of spatial uncertainty and public health.

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Presenter (First Name, Last Name): Lingzhi Chu

Affiliation: Yale University, School of Public Health

Title: Associations between short-term ambient temperature exposure and kidney-related diseases in New York State: The influence of exposure spatial resolution, temperature scale, and temperature metric

Abstract:

Introduction: Evidence on the associations between short-term temperature exposure and kidney diseases is inconclusive. We aimed to evaluate the influence of spatial resolution, temperature scale, and temperature metric on such associations.

Methods: We estimated daily mean temperature at 1-km resolution in New York State, and obtained health data from the SPARCS dataset (2007-2016). We used a symmetric case-crossover design analyzed by conditional logistic regression with distributed lag non-linear models, and evaluated five spatial resolutions from 1-km to 35-km. We compared one-stage and two-stage models using temperature on the absolute or relative scales. We also compared the performance of different temperature metrics incorporating humidity, wind speed, and/or solar radiation.

Results: This study included 1,209,934 non-elective adult kidney-related cases. We observed similar estimates when using different spatial resolutions. We found that one-stage models using daytime mean outdoor WBGT on the absolute scale performed the best. For the 95th percentile compared to the minimum morbidity temperature at lag 0-6 days, we found odds ratios of 1.36 for acute kidney failure (95% confidence interval [CI]: 1.09, 1.69), 1.41 for urolithiasis (95% CI: 1.16, 1.70), 1.26 for dysnatremia (95% CI: 1.01, 1.59), and 1.88 for volume depletion (95% CI: 1.41, 2.51), but no significant associations for chronic kidney disease, renal tubulo-interstitial diseases, or glomerular diseases.

Conclusions: Short-term exposure to high temperature was associated with elevated risk for acute kidney failure, urolithiasis, dysnatremia, and volume depletion. The influence of exposure spatial resolution was negligible and of temperature scale and temperature metric was modest.

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Presenter (First Name, Last Name): Hui Luan

Affiliation: University of Oregon

Title: The association between geographical accessibility of pre-exposure prophylaxis (PrEP) and social determinants of health: does the choice of accessibility measure matter?

Abstract:

Pre-exposure prophylaxis (PrEP) is one effective biomedical technology of HIV prevention. Improving PrEP accessibility is one of the priorities of the Ending the HIV Epidemic initiative. In ecological studies, quantifying geographical accessibility of PrEP has become a critical first step for identifying areas with low accessibility. Further investigations are conducted to examine whether PrEP accessibility is associated with social determinants of health (SDH) including socioeconomic deprivation and income inequality. Inconsistent findings, however, have been identified in previous studies, with inconsistent PrEP accessibility measurements as a potential reason. Using zip codes in New York City as a case study, this research examines whether the choice of accessibility measures impacts the findings on the association between PrEP accessibility and SDH. Ten indicators of geographical PrEP accessibility that belong to three categories were compared (i.e., density, proximity, and gravity-based measures with different parameter specifications). Bayesian spatial regression models were used to analyze the associations. Results indicate that the correlation among these different indicators can be as low as 0.39. Using density to measure PrEP accessibility for small areas such as a zip code poses challenges to statistical modeling since the measured accessibility values are highly skewed with excess zeros, leading to the necessity of using complex models such as the two-part mixture model. Compared with other measures, the two-step gravity-based measures are less sensitive to parameter modifications. This research adds to the nascent research on PrEP accessibility measurement and sheds lights on selecting an appropriate indicator to assess spatial disparities in PrEP accessibility.

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Presenter (First Name, Last Name): Shupeng Zhu

Affiliation: University of California Irvine

Title: The inequality of air pollution-associated mortality burdens increased despite significant air quality improvement between 2002 and 2018 in the US

Abstract:

In the US, the exposure to hazardous air pollutants such as fine particulate matter (PM_{2.5}) has decreased significantly in the last two decades, as well as the associated premature death. Such improvement is largely due to the strengthening of air quality regulations. However, the equality for the distribution of the mortality burdens among different racial and social-economical groups has not been well targeted in past regulations. In this study, we quantify the annual mortality burdens from PM_{2.5} in the US from 2002 to 2018, based on detailed daily air pollutant concentrations at the census tract level, together with racial and ethnicity specified health impact functions and incidence rates, to quantify the trends and inter-annual variability of mortality burden and its distribution equality. A Lorenz curve-based statistical method (Inequality Index) is designed to measure the inequalities of mortality burden associated with the Social Vulnerability Index

published by the Centers for Disease Control and Prevention. Our results show that for the all-age group (age 30-99), the mortality burden decreased by 46% from 100007 death per year (95% confidence interval, 67545-131236) in 2002 to 54133 death per year (36396-71304) in 2018. However, for the aged group (age 65-99), the decrease is only 25% from 2002 to 2018, a 21% less decrease compared to the all-age group. Among the aged group, the shared mortality burden decreased by 8% for White non-Hispanic (WNH) while it increased by 287% for Asians, 194% for Hispanics, and 3% for Black. Black's risk of premature death is more than three times higher than the WNH and has not been improved since 2002. For other racial groups, such a gap with the WNH has continued to increase throughout the years. The Inequality Index shows a steady increase in mortality burden distribution inequality from 2002 to 2018. For the all-age group, the Inequality Index increased from 1.29 to 5; for the aged group, the index increased from 0.82 to 7.07.

Session 5 “*Inferring upon epidemics spread, clusters and mutations: novel data sources and methods*”

Presenter (First Name, Last Name): Devan Becker

Affiliation: Public Health Agency of Canada

Title: Proportions of variants of concern in space and time

Abstract:

There has been great interest in detecting the spread of variants of concern (VOCs) of SARS-CoV-2 (e.g., Delta or Omicron/BA.1/BA.2 etc.). Clinical sequencing can be expensive and rarely represents a simple random sample. Wastewater sampling has been proposed as a solution, but wastewater samples can capture at most 400 nucleotides per read out of a nearly 30,000 nucleotide genome. From these data, I have developed a model that estimates the proportions of VOCs present that incorporates spatial and temporal similarity.

I fit a binomial model to the number of observed mutations (successes) and the number of times its position on the genome was observed (trials) in the sequencing. The mutation frequency in the data is modelled as the sum of the proportions of each variant (a latent variable that is estimated) that contain that particular mutation (determining a mutation list is a challenging task unto itself). These proportions are constrained to be less than or equal to 1, allowing for unknown variants to be present. Inspection of the residuals may reveal missing mutations or variants in the mutation lists.

The proportions are expected to be similar in wastewater treatment plants that are close in space and time. This similarity is modelled with an AR(1) model in time and as joint truncated normal distributions with covariance between spatial locations, with all parameters estimated via Bayesian methods. This model can track VOCs across space and time and will also be useful for other pathogens such as influenza and rhinovirus.

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Presenter (First Name, Last Name): Nelson Walker

Affiliation: U.S. Air Force Materiel Command

Title: Predicting the risk of novel pathogen introductions from disease surveillance data

Abstract:

In the course of an infectious disease outbreak, researchers often must estimate or infer the source of the causative pathogen, the risk factors associated the spread and growth of the pathogen, and risk factors that may be associated with new outbreaks. Because the exact time and location of introduction for the pathogen is usually unobserved, these questions must be addressed using incomplete or indirect data, such as spatio-temporal disease surveillance data. We introduce a Bayesian hierarchical mixture model for spatio-temporal, binary disease surveillance data that accounts for the dynamic process of the pathogen diffusing and multiplying through a population from multiple sources. Our framework provides approximate posterior estimates for the number, locations, and times of introduction of the pathogen in a population, as well posterior inference on parameters associated with pathogen growth and diffusion. We also obtain posterior inference on the generative spatial process that produced the pathogen introductions. We demonstrate this framework using disease surveillance data for chronic wasting disease in white tailed deer from Wisconsin and Illinois in the United States.

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Presenter (First Name, Last Name): Marta Blangiardo

Affiliation: Imperial College

Title: A spatio-temporal framework for modelling wastewater concentration during the COVID-19 pandemic

Abstract:

Wastewater based epidemiology has been used during the COVID-19 pandemic as a tool for early warnings. Extensive work has been done to evaluate the relationship between viral concentration and COVID-19 case numbers at the catchment areas of sewage treatment works (STWs) over time. Nevertheless, no attempt has previously been made to develop a spatially explicit model to predict wastewater concentration at fine spatio-temporal resolution covering the entire country, a necessary step towards using wastewater as an early detection tool. We specify a geostatistical model that quantifies the relationship between weekly viral concentration at the STW catchment area level and a collection of covariates (Genomic sequencing, Index of Multiple Deprivation, percentage of Black, Asian and Minority Ethnic, land use, population density and age structure of the population in the catchment area), while accounting for spatial and temporal correlation. We use the weekly average of flow-normalised viral concentration, reported as the number of SARS-CoV-2 N1 gene copies per litre of wastewater, at 302 STWs between 1-6-2021 and 7-3-2022. In addition to creating maps of weekly viral concentration at any required level of spatial resolution, we can use the model outputs to quantify the probability of local increases in viral concentration over short periods (e.g. 2 consecutive weeks), which can be employed as an early warning tool for public health surveillance.

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Presenter (First Name, Last Name): Joanne Kim

Affiliation: Medical University of South Carolina

Title: A novel Bayesian metric to predict emerging high risk clusters in infectious disease outbreaks.

Abstract:

Identifying the ‘hotspot’ areas is the important first step for public health intervention in the infectious disease outbreak. Detection of the high-risk disease cluster has been the main research area for spatial disease mapping researchers and numerous clustering methods have been developed to map the high-risk areas of the disease of interest. However, previous spatial disease mapping research focused on identifying the current “hotspot” of the elevated risk area but it did not provide information about where the next high-risk cluster is likely to occur given the existing hotspot. In this presentation, we will introduce a novel Bayesian metric to predict the occurrence of new clusters of the elevated risk areas for the infectious disease outbreak. Our novel metric is based on the Bayesian spatio-temporal hierarchical model and extends the posterior exceedance probability which is commonly used for hotspot clustering. Specifically, we predict the next high-risk neighboring area given the existing hotspot by (i) using both exceedance probability and exceedance level and (ii) integrating the information about the area’s own risk with its risk trend over time and its neighborhood risk. We evaluate the performance of our metric with a simulation study based on different infectious disease outbreak situations and the real data of the COVID-19 outbreak in South Carolina. We expect our novel metric would contribute to the public health surveillance of infectious disease outbreaks by providing a novel perspective on high-risk area cluster prediction.

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Session 6 “*Modeling spatial misaligned or multivariate disease data*”

Presenter (First Name, Last Name): Duncan Lee

Affiliation: University of Glasgow

Title: Identifying boundaries in spatially continuous disease risk surfaces from spatially aggregated disease count data

Abstract:

Health is an irreplaceable good for humanity. In order to acquire, maintain or improving health, and in a global context of weakening of state institutions, many people is searching health services beyond borders. Borders are spaces that offer a broad empirical possibility to address aspects that coexist in so-called spaces of exception, and when the main theme is health services, borders have various simultaneous processes, such as migration due to humanitarian crises, purchase of trip

packages to obtain medical services and cross-border search of medical care. But even these phenomena are unequal for North and Global South.

This work reviews the diversity of health mobilities in two Latin American border regions, Northern Mexico and Northern Brazil. A systematic bibliographic review was used to understand the multiple dynamics related to health services occurring in these regions. Results show that in Northern Mexico prevails the commodification of health, as it is offered for Americans and Canadians, which have a higher payment capability; but, in contrast, health prevails mostly as a public good that is searched even by citizens of other countries in Northern Brazil. Among the conclusions of the research, the need to build a theoretical and methodological basis to study these mobilities related to health is argued.

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Presenter (First Name, Last Name): Umut Altay

Affiliation: The Norwegian University of Science and Technology (NTNU)

Title: Accounting for jittering in raster- and distance-based geostatistical analysis of DHS data

Abstract:

The Demographic and Health Surveys (DHS) Program provides data from household surveys where GPS coordinates are available for visited clusters. Fine-scale rasters are routinely applied with geostatistical models to map demographic and health indicators based on such data. However, the GPS coordinates are jittered to preserve anonymity, and the rasters can be highly variable within typical jittering distances. If observed coordinates are treated as true, this leads to attenuation of the association between response and covariates, and reduced predictive power when the covariate is important to describe spatial variability in the response. We propose a computationally efficient Bayesian approach to account for jittering both in raster- and distance-based covariates, and in the spatial effect. We use this approach to estimate the completion of secondary education amongst 15-39 years old women based on the DHS survey in Nigeria 2018. The approach is fast and we find that accounting for jittering on average decreases the coefficients of variation by 12% compared to not accounting for jittering. By simulating data that mimics the original data, we see that root mean square errors of predictions are improved by accounting for jittering.

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Presenter (First Name, Last Name): Marco Gramatica

Affiliation: Queen Mary University of London

Title: Structure induced by a multiple membership transformation on the Conditional Autoregressive model

Abstract:

The usual context for disease mapping is to model data aggregated at the areal level. In some contexts, however, (e.g. residential histories, general practitioner catchment areas) the data are not recorded on a particular spatial framework, but it is possible to specify spatial random effects, or

covariate effects, at the areal level, by using a multiple membership principle (MM). In fact, both Petrof (2020) and Gramatica (2021) use a weighted average of conditional autoregressive (CAR) spatial random effects to embed spatial information for a spatially-misaligned outcome and estimate relative risk for both frameworks (areas and memberships). In this talk we investigate the application of the MM principle to the CAR prior in terms of its parameterisation, properness and identifiability. We carry out simulations involving different numbers of memberships as compared to number of areas and assess impact of this on estimating of CAR parameters and relative risks. Results show under which conditions overall posterior samples are well calibrated for both frameworks across each simulation scenario. Finally, we present the results of an application of the MM modelling strategy to diabetes prevalence data in South London.

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Presenter (First Name, Last Name): Jonathan Bradley

Affiliation: Florida State University

Title: Exact Bayesian inference for a class of spatial Generalized Linear Mixed effects Models

Abstract:

Markov chain Monte Carlo (MCMC) has become a standard in Bayesian statistics that allows one to generate dependent replicates from a posterior distribution for general Bayesian hierarchical models. However, convergence issues, tuning, and the effective sample size of the MCMC are nontrivial considerations that are often overlooked or can be difficult to assess. This motivates us to consider finding expressions of the posterior distribution that are computationally straightforward to sample from directly. We focus on a broad class of Bayesian generalized linear mixed-effects models (GLMM) that allows one to jointly model data of different types. We derive a class of distributions that allows one to specify the prior on fixed and random effects to be any conjugate multivariate distribution. The expression of the posterior distribution is given, and direct simulations have an efficient projection form. An analysis of a spatial dataset is presented.

Session 7 “*Advances in environmental and social epidemiology*”

Presenter (First Name, Last Name): Ulf Strömberg

Affiliation: University of Gothenburg, Sweden

Title: The Swedish geomapping system for surveillance of equity in early cancer detection

Abstract:

Background: Equity in cancer care can hardly be achieved unless population-level inequities in 1) participation proportions in organized screening programs and 2) proportions of tumors detected at an early stage are counteracted. Our aim is to demonstrate a spatial analytic approach for addressing such inequities.

Materials & Methods: We obtained data from 3 national quality registers for: cervical cancer screening (NKCx), colorectal cancer screening (SCREESCO [Screening of Swedish Colons]) and colorectal cancer patients (SCRCR). Specifically, we obtained individual-level data on age, sex, calendar year for each invitation to the organized screening program at issue along with attendance (yes/no; from NKCx and SCREESCO), calendar year at diagnosis along with tumor stage (I, II, III or IV; from SCRCR) and postal address. Based on registered postal addresses, we geocoded each individual to a residential neighborhood, defined by the DeSO division (Sweden consists of 5,984 DeSO:s with population sizes between 650-4,500). We analyzed aggregated outcome data in each DeSO, together with DeSO-level characteristics on economic standard, ethnic diversity, grade of urbanization and distance to screening center (when applicable), by employing Bayesian logit/Poisson models with spatially structured random effects (software package R-INLA).

Results: We geocoded 1,843,548 women aged 33-62 years (in 2020) from NKCx, 90,513 men and women aged 60 years (period: 2014-2020) from SCREESCO, and 19,044 colorectal cancer cases aged 60-79 years (period: 2015-2019) from SCRCR. Each analysis revealed both sociodemographic and spatial disparities in screening attendance/early detection.

Conclusions: The Swedish geomapping system can provide useful information about inequities in early cancer detection.

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Presenter (First Name, Last Name): Monica Pirani

Affiliation: Imperial College

Title: Impact of climate and local environment on Dengue and Zika virus diseases in Brazil: A joint spatio-temporal model

Abstract:

Human dengue and Zika viral infections are Aedes mosquito-borne diseases, caused by viruses which are members of the Flaviviridae family. Despite a substantial body of research, a few studies have attempted to probabilistically model the two diseases simultaneously. In this study, we present their joint analysis across Brazil, from January 2015 to June 2019. We take advantage of multiple data sources, including satellite-derived information on the local vegetation, re-analysis data on climate, census-based data, and population characteristics, and we use spatio-temporal canonical correlation analysis to investigate their multivariate relationships. Then, by relying on a hierarchical approach grounded in a Bayesian framework, we build a multi-likelihood model for monthly disease counts, using as spatial unit of analysis the 5570 Brazilian municipalities, and we quantify the risks associated with climate, local environmental and socioeconomic conditions, while accounting for latent spatio-temporal patterns. Preliminary analyses show that the risk of disease is unequally distributed, both geographically and socioeconomically (e.g., areas with poor water supply and most deprived municipalities have the highest rates of infections) and present different temporal patterns across the Brazilian regions. This underlines the presence of regional needs and local coordinated actions to support early warning systems.

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Presenter (First Name, Last Name): Aina Roca-Barcelo

Affiliation: Imperial College

Title: Development of spatiotemporal high-resolution temperature data for Sao Paulo, Brazil; a valuable resource for epidemiologists

Abstract:

Background and aim: Most studies investigating the temperature-mortality association in cities, overlook the spatial variability of temperature, using a few meteorological stations or models with coarse spatial resolution. This may lead to biased epidemiological findings and limit our ability to identify areas of high risk. We aim to develop an open-access dataset of daily ambient temperature at 500 meters resolution for São Paulo (2015-2020).

Methods: We obtained daily mean temperature from 50 ground meteorological stations and auxiliary data from remote sensing products, including built environment, atmospheric processes, and topography information. To predict temperature at unmeasured locations, we used random forest, a supervised, tree-building machine learning algorithm which operates using decision trees trained in parallel. The final prediction and accuracy are the average prediction and accuracy of all decision trees. Here, we split the dataset in to 70 % training (tuning) and 30 % testing (validation). We validated the model using a leave-one-out and 5-fold spatial cross-validation, using R-squared, Mean Absolute Error, and Root Mean Squared Error as metrics.

Results: Of the 50 monitoring stations, 36 had data >75% valid data. Temperature records showed some spatial heterogeneity (interstation standard deviation: 1.4°C), supporting the need for spatially resolved temperature data. Of all covariates explored, remotely sensed land surface temperature was the best predictor. Validation is currently underway.

Conclusions: This dataset provides epidemiologists with a unique opportunity to investigate exposure patterns of daily mean temperature over the São Paulo at high spatial resolution, and to identify areas of high risk.

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Presenter (First Name, Last Name): Katie Wilson

Affiliation: University of Washington

Title: Modeling under-five mortality using multiple birth history data sources

Abstract:

There is a demand for high quality subnational estimates of under-five mortality. In regions where the burden of under-five mortality is often highest, household surveys, which provide full birth history data, are typically the most reliable source. Unfortunately, these data are spatially sparse and so data are pulled from other sources to increase the available information. Summary birth histories represent a large fraction of the available data, and provide numbers of births and deaths aggregated over time. Specialized methods are needed to leverage both sources of information. We describe a computationally efficient model-based approach based on fertility and mortality models that allow for smoothing over time and space and the inclusion of relevant socio-demographic covariates. We apply the model to household survey and census data from Malawi.

Session 8 “*Advances in spatial statistical methods for clustered and disease data*”

Presenter (First Name, Last Name): Yu Lan

Affiliation: University of North Carolina at Charlotte

Title: A Web-based Geographic Framework to Detect and Visualize Space-time Clusters of Infectious Diseases

Abstract:

Infectious diseases pose a significant threat to public health worldwide as evidenced by the COVID-19 pandemic. Despite significant human losses, the advent of web-accessed, map-based “data dashboards” that monitored disease outbreaks, proved essential in managing public health responses. In many cases, the backend of these dashboards employed basic mapping functionality, displaying counts or rates. As the pandemic advanced, the identification of elevated rates was increasingly important in the geographical allocation of public health resources. However, such maps miss the opportunity to provide accurate information to policy decision-makers such as the rate of disease spread, cyclicity, direction, intensity, and the risk of diffusion to new regions. Space-time analytics, when coupled with rich visualizations, can address these shortcomings. Moreover, when implemented over the web, such space-time functionality can be accessed from virtually anywhere. This study presents a tightly-coupled web-based geographic framework for detecting and visualizing explicit space-time clusters of infectious diseases, using interactive and animated 3D visualizations to aid epidemiologists in readily and adequately uncovering the characteristics of space-time clusters. As a proof of concept, we populate the framework with COVID-19 county-level data in the US and demonstrate data retrieval and storage, space-time cluster detection analysis, and 3D visualization within an open-source WebGIS environment. This tightly coupled approach will facilitate the detection of space-time clusters of diseases in a computationally acceptable timeframe. We anticipate that the characteristics of this framework (generic, open-source, highly accurate, modifiable) will enable low-cost monitoring of the spatial and temporal trends of diseases causing high risks of infection.

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Presenter (First Name, Last Name): Renato Assunção

Affiliation: ESRI Inc. and Universidad Federale Minas Gerais, Brazil

Title: Bias Correction in Clustered Underreported Data

Abstract:

Data quality from poor and socially deprived regions have given rise to many statistical challenges. One of them is the underreporting of vital events leading to biased estimates for the associated risks. To deal with underreported count data, models based on compound Poisson distributions have been commonly assumed. To be identifiable, such models usually require extra and strong information about the probability of reporting the event in all areas of interest, which is not always available. We introduce a novel approach for the compound Poisson model assuming

that the areas are clustered according to their data quality. We leverage these clusters to create a hierarchical structure in which the reporting probabilities decrease as we move from the best group to the worst ones. We obtain constraints for model identifiability and prove that only prior information about the reporting probability in areas experiencing the best data quality is required. Several approaches to model the uncertainty about the reporting probabilities are presented, including reference priors. Different features regarding the proposed methodology are studied through simulation. We apply our model to map the early neonatal mortality risks in Minas Gerais, a Brazilian state that presents heterogeneous characteristics and a relevant socio-economical inequality.

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Presenter (First Name, Last Name): Andrew Lawson

Affiliation: Medical University of South Carolina & University of Edinburgh

Title: Space-Time Infectious Disease Modeling, Nowcasting and counterfactuals

Abstract:

The Covid-19 pandemic has played out in different ways depending on local public health policies. Non pharmaceutical interventions (NPIs) such as lockdown and movement restriction have played different roles in different places. In the talk I will outline an approach to assessing the impact of these interventions by resorting to nowcasting from past case counts to provide counterfactual evidence. This is based on the application of a Bayesian spatio-temporal model for the spread of Covid-19. The model is a SIR-type model with spatial structuring in the propagation of disease risk. Neighborhood effects are directly modeled. An application to the comparison of two US states is shown: South Carolina and New Jersey. The results show that NPIs produced different case load outcomes and hence policy implications.

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Presenter (First Name, Last Name): Chris Jewell

Affiliation: Lancaster University

Title: Non-centred proposals for MCMC in epidemic inference: SARS-CoV-2 a case study

Abstract:

Bayesian epidemic models can be highly effective at supporting policy decisions during outbreaks such as the recent SARS-CoV-2 pandemic. The detail required of such models, particularly with respect to space, represents a severe challenge for existing inference methods. Epidemic models are a special case of state transition models, which require observations of state transition events and time-evolving states in order to compute a likelihood function. However, many of these data may be censored and direct computation of the likelihood is not possible. Whilst forward-simulation-based methods such as particle filtering and ABC are popular for circumventing this limitation, they fail rapidly as the population granularity of the model increases. Moreover, current MCMC-based data augmentation methods,

which are successful for highly detailed models in small populations, are slow to converge for national population sizes and long epidemic timeseries.

Addressing this, we propose a new MCMC algorithm, “Rippler”, designed for detailed discrete-time stochastic epidemic models incorporating space and population characteristics. By using the epidemic model geometry within a non-centering framework, the Rippler is able to improve on previous single-site MCMC updates by making large model-consistent moves in the censored transition event space. We apply this algorithm to testing data from the UK SARS-CoV-2 epidemic using a discrete-space, discrete-time SEIR epidemic model, to provide a method for rapid, reliable, and unbiased parameter inference suitable for real-time analysis of outbreak data. Code modules implementing our algorithm are publicly available as part of the `gemlib` library for Bayesian epidemic computation ([https://urldefense.com/v3/_https://gitlab.com/gem-epidemics/gemlib_!!CzAuKJ42GuquVTTmVmPViYEvSg!PLAYvs8UIQwiWmF2WXDtvnsGzYvb4aQQPL7bJBowILM98YiqzUQc8QcdITZ1mk53eNjNGUIZ09aMvNODP69BVNg\\$](https://urldefense.com/v3/_https://gitlab.com/gem-epidemics/gemlib_!!CzAuKJ42GuquVTTmVmPViYEvSg!PLAYvs8UIQwiWmF2WXDtvnsGzYvb4aQQPL7bJBowILM98YiqzUQc8QcdITZ1mk53eNjNGUIZ09aMvNODP69BVNg$)).

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Session 9 “*Spatial modeling of opioid, drug abuse and HIV data*”

Presenter (First Name, Last Name): Susan Cassels

Affiliation: University of California Santa Barbara

Title: HIV risk hotspots for sexual minority men in Los Angeles, CA

Abstract:

One of the key strategies to ending the HIV epidemic in the U.S. is to increase investments in geographic hotspots, or areas of elevated disease burden. Even though the term hotspot is increasingly used in policy, a few key challenges limit the ability for hotspot mapping to inform effective HIV interventions. First, hotspot mapping typically uses residential address of an individual with an incident infection. Yet for many individuals, potential risky sex and drug-use behaviors do not occur at home. Identifying the places in which risk occurs, as opposed to where an individual with an incident infection lives, will help target and increase exposure to place-based interventions. Second, individual behavior is often constrained or dictated by larger socio-ecological factors, and these can work together to create or maintain health disparities. The objective of our research is to identify and describe HIV transmission and acquisition risk hotspots for non-White sexual minority men within Los Angeles. We use individual activity space data on sexual risk and drug use locations (n=250), neighborhood characteristics of the hotspots, and sociodemographic characteristics and behaviors of individuals at risk in the hotspots. We estimate the spatial-temporal distribution of HIV risk hotspots to identify clusters, and assess individual and neighborhood characteristics of hotspot clusters with spatial logistic regression. We hypothesize that clusters of risk hotspots will have distinct socio-demographic, behavioral, place-based, and socio-ecological characteristics. Our findings will inform which combination of interventions will be most successful, by characterizing the context and composition of the hotspot.

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Presenter (First Name, Last Name): Staci Hepler

Affiliation: Wake Forest University

Title: An Integrated Abundance Model for Estimating County-Level Prevalence of Opioid Misuse in Ohio

Abstract:

Opioid misuse is a national epidemic and a significant drug related threat to the United States. While the scale of the problem is undeniable, estimates of the local prevalence of opioid misuse are lacking, despite their importance to policy-making and resource allocation. This is due, in part, to the challenge of directly measuring opioid misuse at a local level. In this paper, we develop a Bayesian hierarchical spatio-temporal abundance model that integrates indirect county-level data on opioid-related outcomes with state-level survey estimates on prevalence of opioid misuse to estimate the latent county-level prevalence and counts of people who misuse opioids. A simulation study shows that our integrated model accurately recovers the latent counts and prevalence. We apply our model to county-level surveillance data on opioid overdose deaths and treatment admissions from the state of Ohio.

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Presenter (First Name, Last Name): David Kline

Affiliation: Wake Forest University

Title: A spatio-temporal factor model to describe the opioid syndemic in Ohio

Abstract:

The opioid epidemic has been an ongoing public health problem for over 20 years in the United States. As opioid misuse has shifted over time towards injection of illicit opioids, the overlapping epidemics of opioid use disorder, overdose, HIV, and HCV have formed a syndemic. Syndemic theory recognizes that these epidemics occur and interact within specific social, temporal, and geographic contexts. In Ohio, the opioid syndemic is particularly severe. We will model the syndemic at the county-level in Ohio from 2014-2019 using surveillance data on treatment admissions, overdose deaths, and cases of HCV and HIV. To describe these complex relationships, we use a spatio-temporal factor model where we assume dynamic spatial factors describe the common hidden processes that drive the syndemic. After fitting the model, we estimate factors that reflect the overall burden, disproportionate harms, and the infectious disease burden. These factors highlight spatio-temporal variability in the syndemic and provide clues about where to direct future epidemiologic and public health investigations and interventions. Spatio-temporal factor models provide an excellent foundation for future syndemic modeling given their ability to capture complex multivariate dependence structures.

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Presenter (First Name, Last Name): Jeremy Mennis

Affiliation: Temple University

Title: Integrated Peer Network and Activity Space Characteristics of 1,100 Young Adults Enrolled in a Randomized Controlled Trial of an mHealth Cannabis Use Disorder Intervention

Abstract:

The growth of recreational cannabis legalization across the US and attendant increases in the prevalence and frequency of cannabis use warrant a greater focus on cannabis use disorder (CUD) prevention and treatment, particularly for young adults, among whom CUD is rising. This presentation reports descriptive statistics and associations among key demographic, activity space, peer network, substance use, and mental health variables collected at baseline for a randomized controlled trial of a mobile phone-delivered CUD intervention. The intervention, called Peer Network Counseling-text (PNC-txt), leverages peer and neighborhood social/built environment influences on substance use in a motivational interviewing framework. The sample consists of 1,100 young adults (age 18-25) with indicated CUD recruited via social media, posted advertisements, and other methods from Tennessee and Colorado, facilitating comparison by recreational cannabis legalization status. Among 510 subjects enrolled as of December 2021, the average age is 21.6 years, 57% identify as female, and 74% identify as white. Preliminary statistics indicate that 79% of subjects used marijuana 25 days or more in the last 30 days, 84% used marijuana to help depression or anxiety, and 46% typically used alcohol, tobacco, or other substances when using marijuana. Among activity spaces outside the home, friends' houses were the most common (17.3%), followed by outdoor spaces or places of physical activity (16.8%), and then stores or shopping malls (10.5%). Twenty-nine percent said marijuana was available within walking distance of their home. Analytical results describing characteristics of the complete sample will be reported at the presentation.

Session 10 “*Geospatial perspective in studies of environmental health*”

Presenter (First Name, Last Name): Xiangyu Jiang

Affiliation: Georgia Environmental Protection Division

Title: The impact of wildland fire-related PM_{2.5} calibration on health effect analysis

Abstract:

The Community Multiscale Air Quality (CMAQ) model can directly quantify PM_{2.5} concentrations stemming from wildland fire emissions. However, the CMAQ model is subject to biases originated from uncertainties in its parameter settings and input data. To reduce the biases of CMAQ-based outputs, we proposed a two-stage calibration strategy that improves the accuracy of wildland fire-specific PM_{2.5} predictions. First, we calibrated CMAQ-based non-fire PM_{2.5} to ground PM_{2.5} observations retrieved during non-fire days using a random forest method. In the second stage, we quantified fire-specific PM_{2.5} concentrations based on calibrated non-fire PM_{2.5} obtained from the first stage and CMAQ-derived fire and non-fire conversion ratios. In a case study of Washington state during the wildland fire season in 2016, we evaluated the performance

of the proposed PM_{2.5} calibration approach by comparing the associations between cardio-respiratory hospitalizations and CMAQ-based fire PM_{2.5} with and without calibration. Our results showed that the cross-validated R² was improved from 0.12 to 0.74 once the calibration strategy was applied. In the health risk analysis of fire-specific PM_{2.5}, we found a 1 $\mu\text{g}/\text{m}^3$ increase in calibrated fire PM_{2.5} was associated with both respiratory disease (relative risk (RR):1.07, 95% confidence interval (CI):1.01-1.14 in October; RR: 1.05, 95%CI: 1.05-1.26 in November) and cardiovascular hospitalizations (RR: 1.07, 95%CI: 1.02-1.11 in October; RR: 1.14, 95%CI: 1.05-1.23 in November). In contrast, no significant link shown for cardio-respiratory hospitalizations when we used the raw CMAQ-based fire PM_{2.5} concentrations. We concluded that it is important to calibrate CMAQ-based fire-specific predictions before conducting health effect analysis.

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Presenter (First Name, Last Name): Kristen Hansen

Affiliation: University of California San Diego

Title: Spatially varying estimates of mediation effects in the presence of spatial confounding and autocorrelation

Abstract:

The use of mediation analysis is common in epidemiology applications to decompose an exposure-outcome total effect into direct and indirect effects via a given set of mediators. The counterfactual framework in causal inference methodology allowed for great improvements in mediation analysis to define identification assumptions and address for sources of bias in different settings. There are methods for decomposition of effect in the presence of confounders of various types, however there is a particular confounding factor that the current research has not extended to: spatial confounding as well as spatial structure of the data. Furthermore, in some settings we may reasonably expect a need for heterogeneous spatial estimates of both natural direct and indirect effects. In various problems, especially in environmental and social epidemiology, we would expect there to be dependence on spatial location and certainly a spatial relationship that could be leveraged. In this presentation, we describe and compare a set of approaches to conduct spatial mediation analyses and present an extensive set of simulations to quantify the performance of these approaches. We also present a case study about the mediating role of PM_{2.5} in the association between income and cardiovascular diseases. We find that using a framework combining geographically weighted regression (GWR) and other spatially varying coefficient (SVC) models and the product method of mediation analysis is accurate and precise at estimating spatially heterogeneous effects and handling spatial confounding in a grid setting that could be extended to other spatial scales like zip codes.

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Presenter (First Name, Last Name): Youngseob Eum

Affiliation: University at Buffalo, State University of New York (SUNY)

Title: Evaluating mobility changes associated with influenza-like symptoms using mobile phone-based GPS Data

Abstract:

An improved understanding of human behavioral response to influenza-like symptoms (ILS) has implications for influenza surveillance and modeling the spread of the disease. However, little is known about individuals' specific mobility patterns change in response to ILS. The present study examined the association between the changes in routine mobility and ILS using mobile phone-based GPS locations and self-reported ILS survey data. We collected the data from 1,155 participants in Buffalo metropolitan area, New York, during the 2016-2017 influenza season. Each individual's routine mobility patterns were captured by a set of mobility metrics that were matched with their weekly ILS survey reports. A time-stratified case cross-over analysis was conducted to evaluate their associations. We also performed a stratified analysis to examine if such associations are moderated by demographic and socioeconomic factors, such as age, gender, occupational status, neighborhood poverty and education levels, and work type. Results indicated that routine mobility significantly decreased in association with the experience of ILS. Furthermore, we found that the changes in mobility patterns are particularly significant for individuals with high socioeconomic status, indicating potential disparity in the ability to change mobility in response to illness. These research findings advance our understanding of the impact of ILS on mobility changes at the individual level, implying the potential for using individual mobility information as a complementary means of public health surveillance.

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Session 11 “*Spatio and spatio-temporal models for global health*”

Presenter (First Name, Last Name): Silvia Liverani

Affiliation: Queen Mary University of London

Title: Bayesian modelling for spatially misaligned health areal data: A multiple membership approach

Abstract:

Diabetes prevalence is on the rise in the United Kingdom, and for public health strategy, estimation of relative disease risk and subsequent mapping is important. We consider an application to London data on diabetes prevalence and mortality. In order to improve the estimation of relative risks, we analyse jointly prevalence and mortality data to ensure borrowing strength over the two outcomes. The available data involve two spatial frameworks, areas (Middle Layer Super Output Areas, MSOAs) and general practices (GPs) recruiting patients from several areas. This raises a spatial misalignment issue that we deal with by employing the multiple membership principle. Specifically, we translate areal spatial effects to explain GP practice prevalence according to proportions of GP populations resident in different areas. A sparse implementation in RStan of both the multivariate conditional autoregressive (MCAR) and

generalised MCAR (GMCAR) with multiple membership allows the comparison of these bivariate priors as well as exploring the different implications for the mapping patterns for both outcomes. The necessary causal precedence of diabetes prevalence over mortality allows a specific conditionality assumption in the GMCAR, not always present in the context of disease mapping. Additionally, an area-locality comparison is considered to locate high versus low relative risk clusters.

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Presenter (First Name, Last Name): Gianluca Baio

Affiliation: University College London

Title: One year of Covid-19 in 5 major European countries: a comparative analysis of excess mortality

Abstract:

In this talk, I'll discuss a Bayesian spatio-temporal model of excess mortality due to the Covid 19 pandemic over 2020-21 in five European countries. The modelling is used to account for small-area level correlation and based on mortality data from the previous 5 years, at the local geographical level, to estimate the expected rates of mortality. These are compared with the observed data in the observation period, affected by the pandemic, and the posterior predictive distributions from the model are used to determine an estimate of the excess mortality.

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Presenter (First Name, Last Name): Xiang Wang

Affiliation: Lawrence Berkeley National Laboratory

Title: Using geospatial models and socioeconomic features to predict mortality rates in the United States

Abstract:

Recent studies have argued that the socioeconomic and environmental factors in a community might contribute more to health outcomes than access to medical care.

Our work focuses on social determinants of health (SDoH) and their relationship with Suicide Mortality Rate (SMR). Suicide is the top 10 leading cause of death in the US, the second among 10-34 year old individuals and fourth among 35-54 year old individuals. Suicide rates increased 33% between 1999 and 2019. In 2019, 12 million American adults seriously thought about suicide, 3.5 million planned a suicide attempt, 1.4 million attempted suicide, and 47,500 people died by suicide.

We build a predictive model for SMR by using aggregate measures of more than 300 SDoH covariates. Our response variable is a 5 year time series (2016-2020) obtained from CDC Wonder Data, and our predictor variables come from multiple sources, such as demographic distribution (Hispanic/language/age), economic distress (housing cost burdened, food insecurity), socioeconomics (education/employment rate), and environment (temperature, air quality). Given the high-dimensionality of our predictor variables, we first apply feature reduction methods to reduce

complexity. We fit geo-spatial models to take into account the spatial correlation of our variables of interest, and use these to predict yearly SMR. We hold out the 2021 time series as a testing set for our predictive model.

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Presenter (First Name, Last Name): Guowen Huang

Affiliation: Shantou University

Title: Urban/rural differences in air pollution impacts on deaths in Scotland: a comparison study on different pollution data sources

Abstract:

The long-term air pollution health effects can be estimated by utilizing geographical and temporal contrasts in air pollution and disease risk across contiguous small areas, where one main challenge lies in the assessment of the exposure of air pollution for each small area. In this paper, we study the air pollution health effects in Scotland, by using either the gridded concentrations from a dispersion model or the predictions from the proposed fusion model which combines both monitoring observations and gridded concentrations to obtain a better estimation. In addition, we consider using the population-weighted air pollution exposure and also investigate the potential different effects for urban and rural areas. The results show that both the particulate matter with a diameter of 10 microns or less (PM10) and nitrogen dioxide (NO₂) were significantly associated with all-cause deaths in Scotland, based on gridded concentrations or those produced from the fusion model. Furthermore, the adverse effects of pollutants in rural areas seem to be more harmful to human health than those in urban areas, and this difference of air pollution effects was disappeared while considering the population-weighted air pollution exposure.

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Session 12 “*Advances in urban health*”

Presenter (First Name, Last Name): Niloofar Shoari

Affiliation: Imperial College

Title: Spatial and temporal analysis of child pedestrian crashes in England

Abstract:

Pedestrian-motorised vehicle injuries are a major public health concern, especially for children who are developmentally vulnerable. Despite its importance, understanding spatial and temporal variations of child pedestrian safety at a national level remains relatively unexplored. We used a Bayesian space-time model to explain crashes involving child pedestrians at local authority level in England from 2011 to 2020, using a host of socio-economic, transport-related, and built-environment factors. The national time trend of child pedestrian crashes has been gradually decreasing over the 10-year study period. However, the socio-economic inequality gap in the number of child crashes has slightly improved. We examine local authority-specific temporal trends and study whether the road safety conditions for children improved/deteriorated over the

study period. In terms of policy, we pinpoint high-crash local authorities and discuss how our results can be used for implementing targeted safety interventions.

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Presenter (First Name, Last Name): Brisa Sánchez

Affiliation: Drexel University

Title: Heterogeneous effects of the built environment

Abstract:

An approach is presented to estimate distance-dependent heterogeneous associations between point-referenced exposures to built environment characteristics and health outcomes. By estimating associations that depend non-linearly on the distance between subjects and point-referenced exposures, this method addresses the modifiable area-unit problem that is pervasive in the built environment literature. Additionally, by estimating heterogeneous effects, the method also addresses the uncertain geographic context problem. The key innovation of our method is to combine ideas from the non-parametric function estimation literature and the Bayesian Dirichlet process literature. The former is used to estimate nonlinear associations between the subject's outcomes and proximate built environment features, and the latter identifies clusters within the population that have different effects. We study this method in simulations and apply our model to study heterogeneity in the association between fast-food restaurant availability and weight status of children attending schools in Los Angeles, California.

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Presenter (First Name, Last Name): Yi Sun

Affiliation: University of California, Irvine

Title: Associations between urban green space and postpartum depression, and the role of physical activity

Abstract:

Background: Relationships between green space and postpartum depression (PPD), and the role of physical activity (PA) have not been studied.

Objectives: This study aimed to investigate the relationships between PPD and green space exposure and vegetation types using multiple green space indicators, and the mediation effect of PA.

Methods: Clinical data were obtained for 415,020 pregnancies in southern California (2008-2018) from Kaiser Permanente Southern California electronic health records. Multiple green space indicators were used to characterize maternal residential green space exposure at delivery, including street view-based green space and vegetation types (i.e., street tree, low-lying vegetation, and grass), satellite-based measures [i.e., Normalized Difference Vegetation Index (NDVI), land-cover green space, and tree canopy cover], and proximity to the nearest park. Multilevel logistic regression was applied to estimate the association between green space and PPD. A causal

mediation analysis was performed to estimate the proportion mediated by PA during pregnancy in the total effects of green space on PPD.

Results: We observed a reduced risk for PPD associated with street green space (500m buffer, OR=0.980, 95% CI: 0.966-0.994), but not NDVI, land-cover greenness, or proximity to a park. Tree coverage showed stronger protective associations with PPD among different types of green space. The proportions of mediation effects attributable to PA during pregnancy ranged from 4.2% to 6.3% across green space indicators.

Conclusion: Street view green space and tree coverage were associated with a decreased risk of PPD. Protection and restoration of trees may translate into a more pronounced reduction of PPD.

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Presenter (First Name, Last Name): Arrianna Marie Planey

Affiliation: University of North Carolina, Chapel Hill

Title: Spaces of segregation and health: Complex associations for Black immigrant and U.S.-born mothers in New York City

Abstract:

Black immigrants are a growing proportion of the Black population in the U.S., and despite the fact that they now comprise nearly a quarter of Black urban residents, few studies address the relationships between racial segregation and maternal and birth outcomes among Black immigrants. In this study of birth outcomes among U.S.-born and immigrant Black mothers in New York City between 2010-2014, we applied multilevel models, assessing the association between segregation (measured through a novel kernel-based measure of local segregation) and adverse birth outcomes (preterm birth (PTB) and low birthweight (LBW; <2500 grams) among African-born, Caribbean-born, and U.S.-born Black mothers. We found that African-born and Caribbean/Latin American-born Black mothers had significantly lower incidence of PTB and compared with U.S.-born Black mothers (7.0 and 10.1 respectively, compared with 11.2 for U.S.-born mothers). We also found disparities in the incidence of infant LBW by nativity, with the highest incidence among infants born to U.S.-born mothers (10.9), compared with African-born (6.9) and Caribbean-born mothers (9.0). After adjusting for maternal (maternal age; higher rates of reported drug use and smoking) and contextual characteristics (neighborhood SES; green space access), we found that maternal residence in an area with high Black segregation increases the likelihood of PTB and LBW among U.S.-born and Caribbean-born Black mothers. In contrast, the association between segregation and birth outcomes was insignificant for African-born mothers. Associations between tract-level socioeconomic disadvantage and birth outcomes also varied across groups, with only U.S.-born Black mothers showing the expected positive association with risk of PTB and LBW.

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Session 13 “*Vaccination and infectious diseases transmission*”

Presenter (First Name, Last Name): Alexandra Schmidt

Affiliation: McGill University

Title: A Poisson-multinomial spatial model for simultaneous outbreaks with application to arboviral diseases

Abstract:

Dengue, Zika, and chikungunya are arboviral diseases (AVD) transmitted mainly by *Aedes aegypti*. Rio de Janeiro city, Brazil, has been endemic for dengue for over 30 years, and experienced the first joint epidemic of the three diseases between 2015-2016. They present similar symptoms and only a small proportion of cases are laboratory-confirmed. These facts lead to potential misdiagnosis and, consequently, uncertainty in the registration of the cases. We have available the number of cases of each disease for the $n=160$ neighborhoods of Rio de Janeiro. We propose a Poisson model for the total number of cases of *Aedes*-borne diseases and, conditioned on the total, we assume a multinomial model for the allocation of the number of cases of each of the diseases across the neighborhoods. This provides simultaneously the estimation of the associations of the relative risk of the total cases of AVD with environmental and socioeconomic variables; and the estimation of the probability of presence of each disease as a function of available covariates. Our findings suggest that a one standard deviation increase in the social development index decreases the relative risk of the total cases of AVD by 28%. Neighborhoods with smaller proportion of green area had greater odds of having chikungunya in comparison to dengue and Zika. A one standard deviation increase in population density decreases the odds of a neighborhood having Zika instead of dengue by 18% but increases the odds of chikungunya in comparison to dengue by 18% and by 43% in comparison to Zika.

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Presenter (First Name, Last Name): Kyunghee Rhyu

Affiliation: The University of Texas at Dallas

Title: A Spatio-temporal Ecological Model of COVID-19 Vaccination Rate Disparities in Texas

Abstract:

Although being fully vaccinated is one of the most effective means to prevent the spread of COVID-19, vaccination coverage lags behind the goal of developing herd immunity with noticeable spatial and temporal inequalities. The propensity to become fully vaccinated may be caused by locally and temporally variations of vaccine hesitancy and acceptance and, to a less degree, accessibility issues. Relevant risk and protective factors were drawn from the cultural, political, public health interventions, demographic, perception of risk, urban-rural disparities, and socio-economic domains in each county of Texas. Also, several relevant control variables are employed for specific demographic groups. The temporal disparities are placed in relation to factors such as matching supply and demand for vaccines, eligibility age, and waves of COVID-19 variants.

The main objective of this study is to evaluate the underlying determinants of the space-

time disparities and to explain the weekly county rates of being fully vaccinated. An additional objective is to identify any shifts in the relevance of the risk factors over time. An ecological Bayesian mixed-effects model is built, which accounts for any interaction among the temporal and spatial dimensions. The target variable is the cumulative weekly county rates of being fully vaccinated (at least two jabs) over time for the eligible populations living in the 254 counties of Texas starting in February 2021 and ending in July 2022. The results of our model indicate that [a] a simultaneous spatial autoregressive component of the model for each week is highly relevant, as is the serial autocorrelation due to the cumulative nature of the target variable. Furthermore, [b] Texas is inherently spatially heterogeneous with respect to vaccine acceptance, and [c] the relevant factors are influential with a shifting trajectory over time.

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Presenter (First Name, Last Name): Georges Bucyibaruta

Affiliation: Imperial College London

Title: Community-level characteristics of COVID-19 vaccine hesitancy in England: A nationwide cross-sectional study

Abstract:

One year after the start of the COVID-19 vaccination programme in England, more than 43 million people older than 12 years old had received at least a first dose. Nevertheless, geographical differences persist, and vaccine hesitancy is still a major public health concern; understanding its determinants is crucial to managing the COVID-19 pandemic and preparing for future ones. In this cross-sectional population-based study we used cumulative data on the first dose of vaccine received by 01-01-2022 at Middle Super Output Area level in England. We used Bayesian hierarchical spatial models and investigated if the geographical differences in vaccination uptake can be explained by a range of community-level characteristics covering socio-demographics, political view, COVID-19 health risk awareness and targeting of high risk groups and accessibility. Deprivation is the covariate most strongly associated with vaccine uptake (Odds Ratio 0.55, 95% CI 0.54-0.57; most versus least deprived areas). The most ethnically diverse areas have a 38% (95% CI: 36-40%) lower odds of vaccine uptake compared with those least diverse. Areas with the highest proportion of population between 12 and 24 years old had lower odds of vaccination (0.87, 95% CI: 0.85-0.89). Finally increase in vaccine accessibility is associated with higher COVID-19 uptake (OR: 1.07, 95% CI: 1.03-1.12). Our results suggest that one year after the start of the vaccination programme, there is still evidence of inequalities in uptake, affecting particularly minorities and marginalised groups. Strategies including prioritising active outreach across communities and removing practical barriers and factors that make vaccines less accessible are needed to level up the differences.

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Presenter (First Name, Last Name): Christel Faes

Affiliation: Hasselt University

Title: The impact of national and international travel on spatio-temporal transmission of SARS-CoV-2 in Belgium

Abstract:

The rapid worldwide emergence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) has impacted global health enormously. In Belgium, over 1.2 million confirmed cases of coronavirus disease (COVID-19) were reported in 2021 alone with substantial spatial heterogeneity across municipalities. Being located central in Europe, the Belgian disease situation even becomes more complex given the relatively large influx of individuals, potentially infected with SARS-CoV-2, traveling to the country, at least in periods in which no travel restrictions are imposed. In addition, the country is densely populated, and people are commuting a lot within the country. The endemic-epidemic framework as proposed by Held et al (2005) is a very flexible tool to model the spatio-temporal spread of infectious disease. This framework was adapted to investigate the impact of both national and international travel on the spatio-temporal transmission of SARS-CoV-2 in Belgium.

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Session 14 “*Advancing research on neighborhood effects using geospatial technologies and multilevel (hierarchical) models*”

Presenter (First Name, Last Name): Sue C. Grady

Affiliation: Michigan State University

Title: Maternal exposures to sulfur dioxide airborne concentrations and adverse birth outcomes: Detroit Metropolitan Area

Abstract:

Sulfur dioxide (SO₂) is a gaseous air pollutant emitted by industry during fossil fuel combustion and other industrial processes. High concentrations of SO₂ are harmful to human health and the environment. The Environmental Protection Agency (EPA) regulatory 1-hour SO₂ standard is 75 parts per billion (ppb). Short-term exposure to SO₂ (range, 5 minutes to 24 hours) can irritate the human respiratory system causing bronchoconstriction. There is also evidence that exposure to SO₂ during pregnancy is associated with adverse birth outcomes, including low-birth weight and preterm birth. This study utilizes AERMOD the EPA’s advance plume modeling program to measure airborne SO₂ in the Detroit Metropolitan Area (DMA). Maternal exposures to monthly average concentrations are assigned to women giving birth 2008-2015. The DMA is also highly segregated by race and household income; thus the moderating effects of concentrated poverty in the SO₂ exposure and birth outcome relationship is examined. The results further explain the large racial disparities in adverse birth outcomes in this metropolitan area of Michigan.

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Presenter (First Name, Last Name): Ana Rivera

Affiliation: Michigan State University

Title: Environmental injustice among Hispanics in Santa Clara, California: A human-environment heat vulnerability assessment

Abstract:

This study spatially identifies heat-vulnerable neighborhoods, evaluates the relationship between race/ethnicity and temperature exposure, and emphasizes differences among Hispanics by origin to capture environmental injustices in Santa Clara County (SCC), CA. The current methodology assesses the physical environment using the calculation of Land Surface Temperature (LST) and Normalized Difference Vegetation Index (NDVI). The human environment is evaluated using the Darden-Kamel Composite Socioeconomic Index to determine the spatial variability of socioeconomic status (SES) and the Index of Dissimilarity to determine the level of segregation between non-Hispanic Whites and among Hispanics/Latinos. The combination of these assessments comprises a comprehensive human-environment approach for health exposure evaluation by which to define environmental injustice. Results reveal socioeconomic inequalities and an uneven residential distribution between Hispanics and non-Hispanic Whites and thus imply that the racial composition of a neighborhood is strongly linked to LST values. Low NDVI and high LST values were found in Mexican neighborhoods, implying possible environmental racism. Almost half the Mexican population lives in highly segregated neighborhoods with low and very low SES, mainly located in East San Jose, where historically they have been ghettoized. Mexicans, in general, could be at a higher risk of heat stress and heat mortality during heatwaves. Future work should examine additional variables (e.g., housing characteristics, crime, social cohesion, and collective behaviors) to provide a more comprehensive evaluation of the at-risk population in urban areas, where heat stress is expected to intensify.

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Presenter (First Name, Last Name): Eric Delmelle

Affiliation: University of Eastern Finland; University of North Carolina at Charlotte

Title: Modeling the role of geography in survival analysis: an application to children with birth defects

Abstract:

Background: One out of 33 infants born in the United States has a birth defect (BD). Children with BDs are more likely to have chronic development, physical, emotional or behavioral conditions. They also tend to use more health services, have greater costs, and face more barriers to accessing care than children without special needs. BDs are the leading cause of infant mortality. Survival rates vary by the type of defects but are also influenced by several factors including gestational age at birth, size at birth, type of defect and other socio-demographic factors, such as maternal race and ethnicity. Less known however is the role of place of residence (e.g. urban, rural) and geographic barriers to health services (i.e. proximity) on elevated mortality risks. **Objective:** We examine the association of geographic factors (urban versus rural residence) and proximity to care (as measured in distance) with varying levels of mortality risks for children with BDs.

Methods: We use a retrospective cohort study of children born with BDs in Florida, pooled from the Florida Birth Defects Registry (FBDR) and Agency for Health Care Administration (AHCA) for 1998 to 2007. We include children born with Spina Bifida. We use the Kaplan-Meier methods to calculate cumulative survival probabilities and a Cox proportional hazard model with time-varying variables to estimate mortality risks. This includes accumulated time spent in a particular geographic residence. We also examine the effects of selected maternal, child and system characteristics on survival.

Study Benefits: Results will improve our understanding on the role of place on survival for children with birth defects. Ultimately, improved service delivery and coordination of care for children with BDs may reduce infant mortality and improve health outcomes.

Session 15 “*Accounting for spatial variation in environmental risk factors, disease prevalence and mortality*”

Presenter (First Name, Last Name): Guofeng Cao

Affiliation: University of Colorado Boulder

Title: Revisiting the estimations of PM2.5-attributable mortality with advancements in PM2.5 mapping and mortality statistics

Abstract:

With the advancements of geospatial technologies, geospatial datasets of fine particulate matter (PM2.5) and mortality statistics are increasingly used to examine the health effects of PM2.5. Choices of these datasets with different geographic characteristics (e.g., accuracy, scales, and variations) in disease burden studies can significantly impact the results. The objective of this study is to revisit the estimations of PM2.5-attributable mortality by taking advantage of recent advancements in high resolution mapping of PM2.5 concentrations and fine scale of mortality statistics and to explore the impacts of new data sources, geographic scales, and spatial variations of input datasets on mortality estimations. We estimated the PM2.5-mortality for the years of 2000, 2005, 2010 and 2015 using three PM2.5 concentration datasets [Chemical Transport Model (CTM), random forests-based regression kriging (RFRK), and geographically weighted regression (GWR)] at two resolutions (i.e., 10km and 1km) and mortality rates at two geographic scales (i.e., regional-level and county-level). The results showed that the estimated PM2.5-mortality from the 10km CTM-derived PM2.5 dataset tended to be smaller than the estimations from the 1km RFRK- and GWR-derived PM2.5 datasets. The estimated PM2.5-mortalities from regional-level mortality rates are similar to the estimations from those at county level, while large deviations exist when zoomed into small geographic regions (e.g., county). In a scenario analysis to explore the possible benefits of PM2.5 concentration reduction, the uses of the two newly developed 1km resolution PM2.5 datasets (RFRK and GWR) led to discrepant results. Furthermore, we found that the change in PM2.5 concentration is the primary factor that leads to the PM2.5-attributable mortality decrease from 2000 to 2015. The above results highlight the impact of the adoption of input datasets from new sources with varied geographic characteristics on the PM2.5-attributable

mortality estimations and demonstrate the necessity to account for these impacts in future disease burden studies.

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Presenter (First Name, Last Name): Laís Picinini Freitas

Affiliation: Université de Montréal

Title: Zika emergence in Colombia and related environmental and sociodemographic factors

Abstract:

The first Zika cases in Colombia were recorded in August 2015. To advance the knowledge of Zika emergence in Colombia, we fitted a zero-state Markov-switching Poisson spatiotemporal model to the weekly case counts of 167 municipalities of four Colombian departments (Cauca, Valle del Cauca, Huila and Tolima). We explored whether environmental and sociodemographic factors were related to the emergence, transmission intensity, and/or persistence of the disease. There were 26931 Zika cases in the study area between epidemiological weeks 26/2015 and 39/2016. Zika emerged earlier in areas with higher weekly maximum temperatures (OR 1.57, 95%CI 1.28;1.92, lagged one week) and smaller percentages of people with unsatisfied basic needs (OR 0.74, 95%CI 0.55;0.99). A one standard deviation increase in the maximum temperature was associated with a 95% increase in Zika transmission (RR 1.95, 95%CI 1.79;2.11, lagged one week); while a one standard deviation increase in the average Normalized Difference Vegetation Index for the study period was associated with a 44% reduction in Zika transmission (RR 0.56, 95%CI 0.40;0.77). Zika transmission also showed a direct association, although weak, with the weekly accumulated precipitation of four weeks before (RR 1.04, 95%CI 1.02;1.06). Zika persisted for longer in areas with high population density (OR 1.80, 95%CI 1.24;2.62), however, Zika did not emerge sooner in the same areas. Our results indicate that environmental factors were more related to the transmission intensity and the emergence of Zika in selected municipalities of Colombia, while the population density was the only factor associated with the disease persistence.

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Presenter (First Name, Last Name): Jussara Rafael Angelo

Affiliation: National School of Public Health, Oswaldo Cruz Foundation (Fiocruz)

Title: Monitoring COVID-19 in Rio's favelas: territorial-based surveillance and shared production of knowledge

Abstract:

This work aimed to elaborate a critical analysis on COVID-19 in suburban areas in Rio de Janeiro through a documental analysis of the three socio-epidemiological bulletins COVID-19 in the favelas, published in FIOCRUZ COVID-19 Observatory. We described the results of these bulletins and discussed them grounded on critical epidemiology and the social determination of the health-disease process, discussing the magnitude of the disease in the favelas. Areas classified as "no favelas" showed the highest incidence per coronavirus in Rio de Janeiro municipality. First bulletin, the incidence rate in these areas was 116 per 10.000 population, while in the

neighbourhoods classified as "high" and "very high) areas covered per favelas, the incidence rate varied from 24 to 33 cases per 10.000 population. These results showed that the covid-19 test access was unequal and insufficient in favelas, reflecting the historical inequalities that became more evident with the current pandemic. We also analysed the work process to prepare the bulletins and the methodological challenges of monitoring diseases in the suburbs.

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Presenter (First Name, Last Name): Robin Muegge

Affiliation: University of Glasgow

Title: National lockdowns in England: The same restrictions for all, but do the impacts on COVID-19 mortality risks vary geographically?

Abstract:

Quantifying the impact of lockdowns on COVID-19 mortality risks is an important priority in the public health fight against the virus, but almost all of the existing research has only conducted macro country-wide assessments or limited multi-country comparisons. In contrast, the extent of within-country variation in the impacts of a nationwide lockdown is yet to be thoroughly investigated, which is the gap in the knowledge base that this paper fills. Our study focuses on England, which endured 3 national lockdowns between March 2020 and March 2021. We model weekly COVID-19 mortality counts for the 312 Local Authority Districts in mainland England, and our aim is to understand the impact that lockdowns had at both a national and a regional level. Specifically, we aim to quantify how long after the implementation of a lockdown do mortality risks reduce at a national level, the extent to which these impacts vary regionally within a country, and which parts of England exhibit similar impacts. As the spatially aggregated weekly COVID-19 mortality counts are small in size we estimate the spatio-temporal trends in mortality risks with a Poisson log-linear smoothing model that borrows strength in the estimation between neighbouring data points. Inference is based in a Bayesian paradigm, using Markov chain Monte Carlo simulation. Our main findings are that mortality risks typically begin to reduce between 3 and 4 weeks after lockdown, and that there appears to be an urban-rural divide in lockdown impacts.

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Session 16 “*Infectious disease and surveillance*”

Presenter (First Name, Last Name): Rob Deardon

Affiliation: University of Calgary

Title: Variable screening for spatial epidemic models

Abstract:

Information obtained from statistical infectious disease transmission models can be used to inform the development of containment strategies. Inference procedures such as Markov chain Monte

Carlo in a Bayesian framework are typically used to estimate parameters of such models. However, these analyses are often computationally expensive, especially the epidemic model is spatial in nature. This computational complexity obviously increases as the number of potential covariates we wish to include in the model increase. This can be due to the increased difficulty of estimating parameters in higher dimensional epidemic models (e.g. due to posterior correlation) and/or the size and structure of the model space to be explored. Here, we present and contrast a number of methods of screening potential covariates in the context of spatial infectious disease modelling. We consider methods based on the spike in slab priors, a Bayesian LASSO, stepwise inclusion and bagging to choose the covariates in our final model.

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Presenter (First Name, Last Name): Cindy Feng

Affiliation: Dalhousie University

Title: Spatial-temporal generalized additive model for modeling COVID-19 mortality risk in Toronto, Canada

Abstract:

This talk will present a spatial-temporal model for modeling geo-referenced COVID -19 mortality data in Toronto, Canada. A range of factors and spatial-temporal terms are incorporated into the model. The non-linear and interactive effects of the neighborhood-level factors, i.e., population density and the average of income, are modeled as a two-dimensional spline smoother. Tensor product smoother is used for modeling the space-time interaction. By fitting this model, the residual spatial terms can provide insight into detecting high-risk areas not explained by the covariates. The predictive accuracy of the proposed model is evaluated based on out of sample predictive checking, and the findings showed that the model has high predictive power (10-fold cross-validation AUC =0.963) for predicting mortality risk among positive COVID -19 cases.

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Presenter (First Name, Last Name): Caitlin Ward

Affiliation: University of Calgary

Title: Capturing dynamic behavioral change in Bayesian spatial epidemic models

Abstract:

For many infectious disease outbreaks, the at-risk population changes their behavior in response to the outbreak severity, changing the transmission dynamics to change in real-time. In addition, both transmission and the population response may vary across regions. We propose a spatially stratified behavioral change epidemic model formulation where spatio-temporal transmission is captured by the level of “alarm” in the population and specified as a function of past epidemic. By

incorporating spatial heterogeneity in the model, we can measure the relative importance of local vs. global epidemic trajectory in informing the population alarm. The model is set in a data-augmented Bayesian framework as epidemic data are often only partially observed, and we can utilize prior information to help with parameter identifiability. The benefit and utility of the proposed approach is illustrated through an application to county-level COVID-19 data from the United States.

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Presenter (First Name, Last Name): Dirk Douwes-Schultz

Affiliation: McGill University

Title: Coupled Markov switching count models for the detection and forecasting of COVID-19 outbreaks in Quebec hospitals

Abstract:

COVID-19 has greatly strained the hospital system in Quebec since the first cases emerged in February 2020. We develop a novel Bayesian Markov switching model to better understand the emergence and persistence of COVID-19 outbreaks in the 30 largest hospitals in Quebec, and to detect/forecast the outbreaks within each hospital. We assume each hospital switches between outbreak and non-outbreak periods through a series of coupled nonhomogeneous hidden Markov chains. We allow the probability of an outbreak emerging, or persisting, in a hospital to depend on space-time covariates, such as lagged COVID-19 test positivity rates and lagged mobility data. We also allow the probability of an outbreak emerging to depend on the outbreak status of other hospitals previously, which allows the outbreaks to spread between hospitals. We assume the effects of outbreak spread can change over space and time to account for differing levels of connectivity in the hospital network. In contrast, previous spatio-temporal Markov switching models that switch between outbreak and non-outbreak periods have only assumed homogenous effects of outbreak spread and have not allowed covariates to affect the probabilities of outbreak emergence or persistence. We assume incidence in the endemic period is stable and predictable overtime, following a log-linear negative binomial model with simple seasonal and time trends. During the epidemic period we assume incidence follows a log-linear autoregressive negative binomial model to allow the cases to rise or fall rapidly.

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Session 17 “*Spatial modeling of climate and health*”

Presenter (First Name, Last Name): Garyfallos Konstantinoudis

Affiliation: Imperial College London

Title: The interplay between excess mortality and laboratory-confirmed COVID-19-related deaths in Switzerland

Abstract:

There are two main approaches to quantify the impact of COVID-19 mortality at the population level. The first approach relies upon the reporting of laboratory-confirmed deaths, i.e. deaths with a recent positive COVID-19 test, whereas the second approach on excess mortality, and relies upon all-cause mortality data and counter-factual reasoning. In this nationwide study in Switzerland in 2020 and 2021, we aimed to characterize the similarities and discrepancies between laboratory-confirmed COVID-19-related deaths and excess mortality by time, location, and age group. We used Bayesian hierarchical models to predict expected number of all-cause deaths in 2020 and 2021 by week, age group and location using historical data from 2011-2019, accounting for the effect of temperature and population. We then developed a statistical method to decompose all-cause deaths into death excesses directly attributable to SARS-CoV-2 infections and deaths excesses or deficits indirectly attributable to the pandemic. We reported 155,924 all-cause deaths and 13,130 laboratory-confirmed COVID-19 from 24 February 2020 to 3 April 2022 in Switzerland. We found that there were on average 39% (95%CrI: 21 to 58) more deaths directly attributable to SARS-CoV-2 than laboratory-confirmed deaths, suggesting an underreport of COVID-19 related deaths. Outside of large epidemic waves, we found 8% (95%CrI: -1 to 14) fewer all-cause deaths than expected had the pandemic not occurred. The observed mortality deficit could be attributed to a harvesting effect but also to indirect effects of the pandemic, including non-pharmaceutical interventions and a large array of social and environmental changes.

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Presenter (First Name, Last Name): Robbie M. Parks

Affiliation: Columbia University

Title: New frontiers in climate and health

Abstract:

My research focuses on quantifying the health impacts of climate-related hazards and modelling population dynamics using detailed and large datasets, on scales ranging from small-area to multi-country. In this seminar, I will highlight some of my major research efforts so far covering hurricanes and other tropical cyclones, wildfires, anomalous temperatures, air pollution, and compound events.

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Presenter (First Name, Last Name): Yuzi Zhang

Affiliation: Emory University

Title: A scaler-on-quantile function approach for estimating short-term health effects of environmental exposures

Abstract:

Time-series analysis is a widely used population-based study design for estimating short-term health effects of ambient temperature and air pollution by linking aggregated health outcomes to exposure. With advances in satellite imagery, low-cost sensor technology and numerical modeling, environmental exposures are being estimated at increasingly fine-spatial resolutions. However, when linked to aggregated health outcomes, areal averages are typically used to derive population-level exposure, which may not fully capture the spatial variation and individual heterogeneity in exposures. We describe a general modeling approach to incorporate population-level exposure heterogeneity via exposure quantile functions. Furthermore, by viewing exposure as a functional covariate, our approach provides additional flexibility in characterizing associations at different exposure quantile levels. Simulation studies are conducted to demonstrate the potential benefits of utilizing information from the entire exposure distribution compared to the conventional population-average. Finally, we apply the proposed approach to a time-series analysis of air pollution and emergency department visits in the Atlanta metropolitan area over a 4-year period. The analysis utilizes personal exposure to air pollutants simulated from Stochastic Human Exposure and Dose Simulator to investigate associations between the population-level exposure distribution and emergency department visits.

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Presenter (First Name, Last Name): Chigozie Edson Utazi

Affiliation: University of Southampton

Title: Conditional probability and ratio-based approaches for mapping the coverage of multi-dose vaccines

Abstract:

Many vaccines are often administered in multiple doses to boost their effectiveness. In the case of childhood vaccines, the coverage maps of the doses and the differences between these often constitute an evidence base to guide investments in improving access to vaccination services and health system performance in low and middle-income countries. A major problem often encountered when mapping the coverage of multi-dose vaccines is the need to ensure that the coverage maps decrease monotonically with successive doses. That is, for doses i and j , $i < j$ implies $p_i(s) \geq p_j(s)$, where $p_i(s)$ is the coverage of dose i at spatial location s . To model $p_i(s)$, we investigate conditional probability (CP) and ratio-based (RB) approaches, embedded within a binomial geostatistical modelling framework, to address this problem. The fully Bayesian model is implemented using the INLA and SPDE approaches. Using a simulation study, we find that both approaches perform equally well for out-of-sample point estimation under varying point-level sample size distributions. We apply the methodology to map the coverage of the three doses of diphtheria-tetanus-pertussis vaccine using data from the 2018 Nigeria Demographic and Health Survey. The coverage maps produced using both approaches are almost indistinguishable,

although the CP approach yielded more precise estimates on average in this application. The methodology is straightforward to implement and can be applied to other vaccines and geographical contexts.

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Session 18 “*Association between urban built environment and public health*”

Presenter (First Name, Last Name): Yanjia Cao

Affiliation: City of Hope Comprehensive Cancer Center; The University of Hong Kong

Title: Comparing and validating food environment using multi-source geospatial datasets

Abstract:

Background: Access and exposure to the built food environment may be an important component for human health, however diverging data sets and methods for measuring food environment result in lack of consistency of associations with health. In this research, we conducted a hierarchical point of interest (POI) matching strategy to compare and merge food outlets represented by government, commercial, and crowdsourced data for a case study in San Diego County.

Methods: Two matching parameters were used: distance with latitude and longitude, and POI name match with Levenshtein distance (LD) and Double Metaphone (DM). Sensitivity analysis to determine thresholds of matching parameters was conducted. After the first data matching round, we applied a weighted multi-attribute model on the unmatched records using relaxed matching parameters and accounting for spatial distance, LD, and DM at the same time. We selected the top ranked match and combined results from first round matches. We assessed trends of matched and unmatched records to determine unique dataset characteristics.

Results: We selected 100-meter distance threshold, LD ≤ 4 and DM ≤ 2 match parameters for round one matching resulting in 21% matched records. The weighted ranking model returned 31% matched records. In total, 52% of food outlets were matched. Unmatched outlets consisted of beer gardens, personal chefs and food trucks.

Conclusions: The hierarchical POI matching strategy found several reliable food POIs across datasets and identified unique food POIs to specific data sources. Triangulation of food environment data may increase reliability and precision of estimating relationships between food environment and health outcomes.

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Presenter (First Name, Last Name): Ryan Zhenqi Zhou

Affiliation: University at Buffalo, State University of New York (SUNY)

Title: Deriving neighborhood-level diet and physical activity measurements from anonymized mobile phone location data for enhancing obesity estimation

Abstract:

Obesity is a serious public health problem. Existing research has shown a strong association

between obesity and an individual's diet and physical activity. If we extend such an association to the neighborhood level, information about the diet and physical activity of the residents of a neighborhood may improve the estimate of neighborhood-level obesity rate and help identify the neighborhoods that are more likely to suffer from obesity. However, it is challenging and costly to measure neighborhood-level diet and physical activity through surveys and interviews, especially for a large geographic area. In this study, we propose to leverage anonymized mobile phone location data to derive neighborhood-level diet and physical activity measurements, and examine the extent to which the derived measurements can enhance obesity estimation, in addition to the socioeconomic and demographic variables typically used in the literature. We conduct case studies in three different US cities (New York City, Los Angeles, and Buffalo) using the anonymized mobile phone location data from the company SafeGraph and employing five different statistical and machine learning models to test the potential enhancement brought by the derived measurements for obesity estimation. We find that it is feasible to derive neighborhood-level diet and physical activity measurements from anonymized mobile phone location data. However, these derived measurements provide only small enhancement for obesity estimation across the studied cities and tested models, compared with using neighborhood-level socioeconomic and demographic variables alone. We further investigate the potential reasons for such results and discuss their implications.

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Presenter (First Name, Last Name): Avipsa Roy

Affiliation: University of California, Irvine

Title: Predicting COVID 19 risk from movement patterns and sociodemographic factors

Abstract:

Mobility is an indicator of human movement through space and time. With the increasing availability of geolocated data (from GPS, accelerometers, etc.), it is now possible to examine individual as well as group human mobility patterns. Human mobility is influenced by both intrinsic (i.e. personal motivations) and extrinsic (i.e., events like natural hazards or a pandemic like the COVID-19) factors. However, the intricate relationships between human mobility patterns and sociodemographic characteristics in the context of a pandemic are yet to be fully explored. Our goal is to overcome this gap by using human mobility data at the census block group level from mobile phones and combining those with social vulnerability indicators to examine the overall spread of COVID-19 at local spatial scales. We used 585,878 weekly visits to 37,871 points of interests (POIs) from Safegraph to quantify mobility indices and social distancing metrics in 2,820 census block groups in the city of Los Angeles (LA) - before and during lockdown as well as during the phase1 and phase 2 reopening. Finally, using supervised machine learning algorithms, we classified the census block groups in LA into High, Medium and Low categories that represented the vulnerability of these block groups based on the cumulative number of occurrences of COVID-19 cases till July 24, 2020. Our results indicate that the tree-based classifiers performed well in comparison to the Support Vector Machines and Multinomial Logit

models. Gradient Boosting had the highest classification accuracy of 97.4% COVID-19 with an AUC score of 0.987. The block groups with high COVID-19 cases also had a high concentration of socially vulnerable populations, high human mobility index and a low social distancing index.

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Presenter (First Name, Last Name): Maria de Fátima De Pina

Affiliation: Oswaldo Cruz Foundation - Fiocruz, Brazil

Title: Mapping urban parks in Latin America, through the classification of satellite images using collaborative web data

Abstract:

Rationale: Reliable park variables are scarce and the use of widely different park metrics in different studies, may contribute to mixed evidence on parks and health outcomes.

Objectives: The main objective was to develop a tool to map urban parks (greenspaces that combine vegetation with built infrastructure) and validate the tool using official datasets.

Methodology: Study area: 77 municipalities from four countries (Argentina, Brazil, Chile and Peru) of the SALURBAL (Salud Urbana in America Latina) study, from which there were official vector maps of urban parks (n=9116).

We used Sentinel-2 satellite images (European Space Agency) for delineating urban park boundaries. We selected the more recent satellite images (from April 2017 to May 2020) considering the cloud cover of the image area < 10% and no clouds in the urban perimeter. The extraction, transformation and automation routines were implemented in R language. The data administration and data loading was developed in Postgresql + Postgis.

We used a mixed supervised and non-supervised classification of satellite images through collaborative data from Google Cloud to classify the parks areas.

Results: Overall, we identified 77% of the parks from the official datasets, being 97% of the Argentinean parks (n=2071), 94.8% of the Chilean parks (n=274), 88.3% of the Brazilian parks (n=700) and 70.6% of Peruvian parks (n= 6071).

Discussion: Our tool showed to be efficient to automatically map urban parks. This tool is especially important and pertinent to overcome the deficit of updated data of urban parks in several Latin American cities.