

Epidemiology Section: POSTER SESSION: *Epidemiologic Methods and Data Science - II*

APHA 2025 Annual Meeting and Expo

Abstract

Robust Bayesian parameter estimation for stochastic modeling of healthcare-associated infection transmission dynamics

Zinabu Melese Sr.

Amstelveen, North Holland, Netherlands

APHA 2025 Annual Meeting and Expo

Accurate parameter estimation in epidemiological models is essential for understanding disease dynamics and guiding public health interventions. Stochastic differential equations (SDEs) are commonly used to model complex systems, but their application is limited by the lack of explicit transition probability densities, especially with discrete-time observations. This study develops a robust framework for estimating unknown parameters in stochastic dynamical systems to improve epidemiological predictions. We employed a Bayesian Naive maximum likelihood estimation approach, using approximation methods due to the absence of closed-form transitional density solutions. Extensive numerical simulations were conducted to validate the method, evaluating performance through bias and root mean squared error (RMSE) metrics across varying sample sizes and initial parameter values. Graphical analyses were also performed to assess parameter convergence and robustness. Results demonstrated accurate and reliable parameter estimates, with low bias and RMSE across sample sizes, and confirmed convergence, highlighting the method's consistency. These findings indicate the framework's effectiveness for parameter estimation in complex epidemiological models, even without explicit transitional densities. The ability to estimate parameters from discrete-time observations has significant implications for improving disease modeling and public health decision-making. Healthcare experts and policymakers can use this framework to enhance epidemiological predictions and design more effective interventions. Future research should apply this approach to real-world data and extend it to more complex models, such as those with multiple interacting populations or time-varying parameters.

Biostatistics, economics Chronic disease management and prevention Epidemiology Public health biology
Public health or related public policy Public health or related research

Abstract

Collaboration with CIPHER: Breaking Down Siloes with a Phenotype Library

Francesca Fontin, MPH, Jacqueline Honerlaw, RN, MPH, Yuk-Lam Ho, MPH, Tiffany Sim, MPH, Michael Murray, MS and Kelly Cho, MPH, PhD
VA Boston Healthcare System, Boston, MA

APHA 2025 Annual Meeting and Expo

Background: Electronic health records (EHR) are frequently leveraged to create computable phenotype algorithms to define health conditions for use in research and clinical operations. The U.S. Department of Veterans Affairs (VA) developed the Centralized Interactive Phenomics Resource (CIPHER), a phenotype library cataloging over 6,500 definitions to facilitate algorithm reuse and development (available at <https://phenomics.va.ornl.gov/web/>).

Objectives: We aimed to design a new feature which captures algorithm implementation information from the CIPHER user community. The goal of this feature is to promote sharing of validation and performance metrics, as well as provide context on how a phenotype has been implemented to inform researchers on the

quality and utility of the definition before they apply it to their cohort.

Methods: We conducted usability studies and focus groups with analysts and investigators from the VA and other healthcare systems. Attendees responded to open-ended questions on their needs, proposed elements to capture, and reviewed examples of a user interface. This feedback was compiled and integrated into website requirements.

Results: This algorithm reuse feature will allow users to contribute implementation metrics for existing phenotypes on CIPHER. This includes whether they used it for their own work, citation of an associated publication, description of the cohort to which they applied the algorithm, and validation metrics such as sensitivity and specificity. This feature will be available in summer 2025.

Conclusion: CIPHER allows for direct feedback to authors on their work, enables collaborative evaluation of phenotype quality, and captures algorithm feedback by the user community.

Conduct evaluation related to programs, research, and other areas of practice Epidemiology Public health or related research

Abstract

The Kansas City Health Department's School-Based Syndromic Surveillance for Early Disease Detection.

Caylin Henry, Bachelor of Health Sciences (BHS)
Kansas City, MO Health Department, Kansas City, MO

APHA 2025 Annual Meeting and Expo

Background: The Kansas City Health Department (KCHD) School Syndromic Surveillance (SSS) Dashboard pilot was modeled after neighboring jurisdiction Clay County Public Health Center, which they developed in 2013. The KCHD SSS program was launched in the 2023-2024 school year in a collaborative effort with the Kansas City Public Schools (KCPS).

Objective: To implement a dashboard to identify disease symptoms and enable early detection of illness trends among Kansas City's school-age children and support timely public health interventions.

Methods: The dashboard was created with input from KCHD's Population Health and presented to KCPS nurses for training and feedback. The SSS Dashboard monitored eight symptoms (cough, sore throat, diarrhea, vomiting, stomachache, fever, headaches, rashes), and nurses were required to submit weekly symptom reports for their school. The weekly submitted data was uploaded into the Dashboard to display symptom counts and case rates. A weekly summary of identified trends was sent to KCPS, along with educational information about seasonal health conditions.

Results: The dashboard identified trends and outbreaks within each school and demonstrated the district's case rate per 1,000 students. The goal of an 80% compliance rate was achieved for the 2023-2024 school year. No outbreaks were detected during the school year.

Conclusion: The Dashboard was successful in analyzing data reported by the nurses. The program strengthened relationships with schools, which improved communication with reporting other infectious diseases and possible outbreaks. KCHD intends to expand the program to include additional KCMO school districts and compare trends with state/national syndromic data.

Epidemiology Planning of health education strategies, interventions, and programs Public health or related research

Abstract

The Power of Artificial Intelligence to Examine Multi-drug-resistant Community-onset *Staphylococcus aureus* from Children Living in the Southeastern United States

Samuel Owusu, BS¹, Peter Baltrus, PhD¹, Chaohua Li, MPH¹, Traci Leong, PhD², Abdolreza Mosaddegh, PhD³, Declan Quinn, BS⁴, Xiting Lin¹, Casey Cazer⁵, Robert Jerris, PhD, D(ABMM)⁶ and Lilly Immergluck, MD, MS, FAAP⁴

(1)Morehouse School of Medicine, Atlanta, GA, (2)Emory University, Atlanta, GA, (3)Northeastern University College of Engineering, Oakland, CA, (4)University of Chicago, Chicago, IL, (5)Cornell University, Ithaca, NY, (6)Children's Healthcare of Atlanta and Emory University School of Medicine, ATLANTA, GA

APHA 2025 Annual Meeting and Expo

Background

Community-onset *Staphylococcus aureus* (CSA) remains a leading cause of skin and soft tissue infections (SSTIs) with increasing rates due to multi-drug-resistant (MDR) *S. aureus*. Since the late 1990s, CSA has increasingly included not only methicillin-resistant CSA but MDR methicillin-sensitive *S. aureus*. Artificial intelligence (AI) using association rule mining has been shown to effectively analyze phenotypes of MDR in healthcare settings.

Objectives

(1) Characterize trends in MDR *S. aureus* phenotypes over time and geographic location.

(2) Apply AI-association rule mining to assess MDR *S. aureus* causing SSTIs and conduct hierarchal clustering related to clinically significant MDR *S. aureus* phenotypes.

Methods

A retrospective analysis of CSA isolates from children (<19 years) living in Atlanta, Georgia, 2002–2019 will be conducted, whereby association rule mining is applied. Group-based trajectory modeling will assess temporal trends, and spatial statistical methods will map geographic shifts related to hierarchal clusters of specific priority MDR phenotypes.

Results

A total of 21,228 unique records of *S. aureus* SSTI (2002-2019) were collected from 2 pediatric hospitals in Atlanta, Georgia. We identified more than 60 unique phenotypes using association rule mining. We anticipate identifying distinct MDR *S. aureus* phenotypes, particularly involving resistance to clindamycin and β -lactam antibiotics. Hierarchal clusters for MDR phenotypes will be determined and we anticipate specific MDR phenotypes to vary over time.

Conclusion

Understanding the spatial and temporal distribution of clinically relevant MDR *S. aureus* phenotypes that cause SSTI in the community setting will guide antibiotic stewardship and impact real-world prevention strategies.

Communication and informatics

Abstract

Barriers and opportunities of wastewater surveillance for transmissible infectious diseases in the emergency department: a qualitative analysis

Zachary Renfro¹, Abigail Tapper², Alessandro Zulli¹, Julie Parsonnet¹, Alexandria Boehm¹ and Christopher Bennett, MD, MSc, MA¹

(1)Stanford University, Stanford, CA, (2)Boston, MA

APHA 2025 Annual Meeting and Expo

Background

Wastewater surveillance (WS) is a promising method to monitor community-level infectious disease burden. However, most WS is conducted at wastewater treatment plants that serve multiple communities, limiting data granularity. Implementing WS within emergency department (ED) settings could yield higher resolution information about community infectious disease burden, allow for correlation of wastewater data with clinical indices, and guide public health efforts.

Objective(s)

In parallel to a pilot study from our group implementing WS in two California EDs, our objective was to explore stakeholder perceptions of and to identify barriers and facilitators to ED-based WS implementation.

Methods

We completed 16 semi-structured interviews with a diverse stakeholder group including physicians, infection control personnel, and public health officials recruited from both facilities and surrounding county/state health departments. Interviews were audio-recorded, transcribed verbatim, and then analyzed using thematic analysis.

Results

16 individuals participated in our study. Our analysis revealed several addressable barriers – including concerns about actionability, data representativeness, operationalization, public perceptions of data from WS, and confidentiality – while also noting leverageable facilitators such as the potential for WS to complement traditional approaches, guide resource allocation, serve as an early warning system, and inform public health outbreak response efforts.

Conclusion

Through engaging our stakeholder group, we find that ED-based WS shows promise as a tool for enhancing infectious disease surveillance by serving as an early warning system and providing more granular data on community infectious disease burden. However, key barriers must be addressed to ensure not only operationalization but also sustainability and scaling.

Epidemiology Protection of the public in relation to communicable diseases including prevention or control

Abstract

Development and Psychometric Validation of a Multidimensional HIV-Specific Social and Structural Determinants of Health Index

Chen Zhang¹, Yu Liu, PhD, MPH², Yao Tang³ and Wonkyung Chang³

(1)University of Rochester, Penfield, NY, (2)University of Rochester School of Medicine and Dentistry, Rochester, NY, (3)University of Rochester, Rochester, NY

APHA 2025 Annual Meeting and Expo

Background: Structural inequities are key drivers of disparities across the HIV care continuum, yet public health research lacks a standardized, validated tool to quantify HIV-specific structural vulnerability across geographic regions.

Objective: We developed and rigorously validated a novel HIV-Specific Social and Structural Determinants of Health Index (HIV-SSDI) to assess place-based structural barriers to HIV prevention and care at the state level.

Methods: The HIV-SSDI was constructed using 29 theoretically grounded indicators spanning nine domains: economic inequality, education, healthcare access, HIV service availability, criminalization, segregation, environment, demographics, and policy context. Indicators were sourced from publicly available state-level

datasets. Scale validity was assessed through comprehensive psychometric analysis. Exploratory Factor Analysis (EFA) using three extraction methods revealed a stable and interpretable three-factor structure (Kaiser-Meyer-Olkin = 0.64; Bartlett's test of sphericity $p < 0.001$), supporting underlying latent domains of structural HIV risk.

Results: The robustness of the index was evaluated by comparing multiple weighting strategies (e.g., EFA-derived, equal weighting). Construct validity was established through multi-year regression models linking HIV-SSDI scores to longitudinal HIV outcomes, including diagnosis rates, PrEP use, and PrEP-to-Need Ratios (PnR). Higher HIV-SSDI scores were significantly associated with increased HIV diagnoses ($p < 0.05$), with coefficients declining over time. Associations with PrEP use and PnR became stronger in recent years, demonstrating the index's growing predictive relevance.

Conclusion: The HIV-SSDI demonstrates strong conceptual coherence, empirical reliability, and construct validity. It offers researchers and policymakers a scalable, data-driven tool to monitor structural disadvantage and inform targeted, equity-focused HIV prevention and care strategies.

Epidemiology Public health or related public policy Public health or related research Social and behavioral sciences

Abstract

Carbapenem-Resistant Enterobacterales Reporting Completeness among New York City Acute Care Hospitals, 2021–2023

Thomas Portier, MPH, Katelynn Devinney, MPH, Celina Santiago, MPH, Addie Crawley, MPH, Tristan McPherson, MD and Nicole Burton, PhD, MPH
New York City Department of Health and Mental Hygiene, New York City, NY

APHA 2025 Annual Meeting and Expo

BACKGROUND: Carbapenem-resistant Enterobacterales (CRE) may cause healthcare-associated infections. The New York City (NYC) Health Department requires laboratories to report CRE among residents to the New York State Electronic Clinical Laboratory Reporting System (ECLRS). NYC hospitals also report CRE to the National Healthcare Safety Network (NHSN).

OBJECTIVE: CRE reporting concordance between ECLRS and NHSN by NYC hospitals was assessed.

METHODS: ECLRS and NHSN data were limited to CRE collected among NYC residents between 2021–2023 and reported by hospitals that submitted ≥ 1 CRE to NHSN. CRE was defined as *Enterobacter* species, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, or *Escherichia coli* resistant to ≥ 1 carbapenem or producing a carbapenemase. The earliest ECLRS CRE report per patient and facility were matched to NHSN based on facility, specimen collection date, organism, and patient identifiers.

RESULTS: Forty-nine hospitals reported 3,771 CRE to NHSN and 4,844 to ECLRS. Of these, 2,634 (70% of NHSN, 54% of ECLRS) were reported to both surveillance systems. NHSN-reported CRE that were reported to ECLRS increased over time (58% in 2021 to 77% in 2023). Among 43 hospitals that submitted ≥ 10 CRE to both surveillance systems, the percentage of NHSN-reported CRE that was reported to ECLRS ranged from 2% to 97% (median: 73%).

CONCLUSIONS: Most CRE reported to NHSN were also reported to ECLRS and vice versa. ECLRS-reporting allows for rapid assessment of local dynamics while NHSN-reporting provides information on nationwide trends. Concurrent reporting allows assessment of disease transmission at different scales. The NYC Health Department will outreach to hospitals with low reporting concordance.

Communication and informatics Conduct evaluation related to programs, research, and other areas of practice Epidemiology Protection of the public in relation to communicable diseases including prevention or control Public health or related laws, regulations, standards, or guidelines Public health or related research

Abstract

Factor analysis of the Metabolic Syndrome in a multi-ethnic community in rural Hawai'i.

Vanessa Cunanan, PhD, MPH

Thompson School of Social Work and Public Health, University of Hawaii at Manoa, Honolulu, HI

APHA 2025 Annual Meeting and Expo

Background

Metabolic syndrome (MetS) is a constellation of risk factors increasing the risk for cardiovascular disease and type 2 diabetes, affecting 20-25% of the global adult population. It is defined by the presence of three or more of five risk factors: increased waist circumference, elevated triglycerides, reduced HDL cholesterol, elevated blood pressure, and increased fasting glucose.

Objective

The aim of this study was to apply factor analysis of the MetS in a multi-ethnic rural community in Hawai'i.

Methods

The study analyzed data from 1,456 participants of the Kōhala Health Research Project, a cross-sectional study conducted in North Kōhala, Hawai'i. Factor analysis was employed to identify components of MetS. This included reviewing the literature, testing data normality, and performing confirmatory factor analysis (CFA) with competing models. A multi-group CFA assessed measurement invariance across ethnic groups, examining how MetS variables clustered by ethnicity.

Results

The results supported a 4-factor model of MetS: obesity, lipids, insulin resistance, and hypertension, consistent with established diagnostic guidelines. BMI and waist circumference were the most significant risk factors across all ethnic groups. The strongest correlations in the 4-factor model were between the insulin resistance and lipid factors and obesity and insulin resistance factors.

Conclusion

The 4-factor model demonstrated an acceptable fit across ethnic groups, high factor loadings for the obesity and hypertension factors emphasized the importance of preventing and/or mitigating the effects of these MetS components across all ethnic groups. Identifying ethnic differences in MetS clustering is crucial for developing effective prevention and intervention strategies.

Chronic disease management and prevention Epidemiology Public health or related research

Abstract

Comparing Respondent-Driven Sampling and Starfish Sampling: A Natural Experiment in Recruiting People Who Inject Drugs in San Francisco

Bow Suprasert, MPH¹, Raul Ruiz, MPH¹, Paavani Lella¹, Iris R. O'neal¹, Gueslyn Velasquez¹, Glenda Baguso, PhD, RN¹, Eileen F. Dunne, MD², Erin C. Wilson, DrPH, MPH¹ and Willi McFarland, MD, PhD, MPH&TM¹

(1)San Francisco Department of Public Health, San Francisco, CA, (2)Alameda County Public Health Department, Oakland, CA

Background: Respondent-driven sampling (RDS) is considered a state-of-the-art method to recruit representative samples from hard-to-reach populations. However, RDS relies on challenging assumptions about recruitment from social networks. Starfish sampling combines the peer-referral approach of RDS with outreach recruitment at venues as with time-location sampling (TLS) to increase efficiency and reduce overrepresentation from certain networks. We conducted a natural experiment to compare RDS and starfish sampling in recruiting people who inject drugs (PWID) from two contemporaneous studies in San Francisco in 2024.

Methods: Data were from National HIV Behavioral Surveillance (NHBS) using RDS and Brief Longitudinal Incidence Sentinel Surveillance (BLISS) study recruiting via starfish sampling.

Results: NHBS (N=512) and BLISS (N=300) samples were comparable on key demographics including age (average of 43.2 years, SD=10.9 vs. 44.3 years, SD=10.4, $p=0.170$), household income (57.7% vs. 62.3% earning \leq \$1000/month, $p=0.197$), education (51.0% vs. 56.0% with education level at or below high school, $p=0.166$). In both samples, the three most commonly injected drugs were methamphetamine, heroin, followed by fentanyl. HIV prevalence was comparable at 6.5% in NHBS and 6.7% in BLISS ($p=0.902$) as was HCV prevalence (38.7% and 41.7%, respectively, $p=0.400$). Among PWID not living with HIV, PrEP awareness was 66.4% vs. 69.9%, $p=0.310$ and PrEP use was 3.5% vs. 2.8%, $p=0.582$.

Conclusions: We found that RDS and starfish sampling produced comparable samples of PWID. While no gold standard sampling frame exists for community-based surveys of PWID and other vulnerable populations, starfish sampling may offer a more flexible approach that can adapt outreach- and peer-based approaches.

Epidemiology Protection of the public in relation to communicable diseases including prevention or control
Public health or related research

