Meta-Regression Case Studies in Infectious Disease Epidemiology

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- Study of how and why infectious diseases emerge and spread among different populations¹
- Investigating what strategies prevent or contain the spread of disease at the population level¹
- Data gathered/collected from multiple sources to answer questions of interest
- Various modeling strategies used (e.g., statistical and mathematical/mechanistic/transmission modeling)

- Studies can be time-consuming and resource intensive, while only focusing on a very specific setting (e.g., spatial location, disease outbreak, population)
- Meta-analyses/-regressions are important tools for generalizing study findings; results potentially useful for policy makers
- An opportunity for statisticians to get involved to ensure appropriate models are being used, and to develop new methodology for unique/emerging data sources

- Spatial and spatiotemporal correlation
- Multivariate outcomes
- Hierarchical modeling
- Survival data
- Causal inference
- Changepoint methods

- Global, regional, and national estimates of tuberculosis incidence and case detection among incarcerated persons: A systematic analysis
 - Collaborators: Leonardo Martinez, Ted Cohen, Jason Andrews, many others
- An analytical framework to extrapolate results across multiple sites: Real-world examples from rotavirus clinical trials
 - Collaborators: Virginia Pitzer, Ottavia Prunas, Elizabeth Sajewski, Ernest Asare, many others

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Studies of TB in prisons often report incidence and/or prevalence estimates (and uncertainty) for a given location/population and point in time

- Separately, many countries collect TB notifications across time, and also monitor the prisoner population size
- Study Goals:
 - Quantify the global TB burden among incarcerated persons across time
 - Develop an interpretable meta-regression model to jointly model all data sources, correctly characterize their uncertainty, and interpolate in countries/years with sparse/no data

Systematic literature review:

- January 1980 August 2020
- Studies must have estimated/reported TB incidence and/or prevalence among incarcerated populations
- 48 countries with incidence estimates, 92 with prevalence estimates
- Received TB notification data from 152 of 199 countries
- Incarceration data from 193 countries

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Data Availability



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Proposed Statistical Model Summary

- Use all observed data/estimates (i.e., incidence, prevalence, notifications) within a single meta-regression framework (i.e., no multi-stage approximation)
- Leverage the completeness in space and time of the notification data, and its strong (hypothesized) association with incidence, to interpolate incidence estimates in unobserved countries/years
- Similarly, use the more complete prevalence estimates to provide additional predictive information for incidence
- Work in hierarchical Bayesian setting to allow for more natural uncertainty quantification and prediction

$$\widehat{\theta}_{ijtkl} \stackrel{\text{ind}}{\sim} \mathbb{N} \left(\theta_{ijtkl}, \widehat{\sigma}_{itjkl}^2 \right);$$

$$i = 1, \dots, r; \ j = 1, \dots, c_i; \ t = 1, \dots, s_{ij};$$

$$k = 1, \dots, n_{ijt}; \ l = 1, \dots, m_{ijtk}$$

θ_{ijtkl}: Estimated log incidence rate from cohort *I*, within study
 k, within year *t*, within country *j*, within region *i*

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$$\hat{\sigma}_{itjkl}^2$$
: Standard error

• θ_{ijtkl} : True but unobserved log incidence rate

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$$\widehat{\psi}_{ijtkl} \stackrel{\mathsf{ind}}{\sim} \mathsf{N}\left(\psi_{ijtkl}, \widehat{ au}_{itjkl}^2
ight)$$

• $\hat{\psi}_{ijtkl}$: Estimated log prevalence rate

▶ $\hat{\tau}^2_{itjkl}$: Standard error

• ψ_{ijtkl} : True but unobserved log prevalence rate

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Notification Rates (Observed Data)

 $Z_{ijt} \stackrel{\text{ind}}{\sim} \text{Negative Binomial}(p_{ijt}, r),$

$$p_{ijt} = \frac{r}{r + \lambda_{ijt}},$$
$$\ln(\lambda_{ijt}) = O_{ijt} + \mathbf{x}_{ijt}^{\mathsf{T}} \boldsymbol{\beta}_z + \alpha_z + \mu_{zi} + \kappa_{zij}$$

- Z_{ijt}: Number of notifications
- O_{ijt}: Log of the estimated prison population
- x_{ijt}: Vector of covariates
- α_z : Global intercept
- μ_{zi}: Region-specific intercept
- κ_{zij}: Country-specific intercept

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$$\theta_{ijtkl} \stackrel{\text{ind}}{\sim} \mathsf{N}\left(\theta_{ijt} + \pi_{\theta g(i,j,t,k)}, \sigma_{\theta}^{2}\right),$$

$$\begin{aligned} \theta_{ijt} &= \max\left[\ln\left(\frac{Z_{ijt}}{\exp\left\{\mathsf{O}_{ijt}\right\}} + c\right)\gamma_{\theta} + \mathbf{x}_{ijt}^{\mathsf{T}}\boldsymbol{\beta}_{\theta} + \alpha_{\theta} + \mu_{\theta i} + \kappa_{\theta ij} + \eta_{\theta ijt}, \\ \ln\left(\frac{Z_{ijt}}{\exp\left\{\mathsf{O}_{ijt}\right\}} + c\right)\right] \end{aligned}$$

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- α_{θ} : Global intercept
- $\mu_{\theta i}$: Region-specific intercept
- κ_{θij}: Country-specific intercept
- $\eta_{\theta ijt}$: Year-specific intercept
- $\pi_{\theta g(i,j,t,k)}$: Study-specific intercept
- σ_{θ}^2 : Describes variability across cohorts within a study

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$$\psi_{ijtkl} \stackrel{\text{ind}}{\sim} \mathsf{N}\left(\mathsf{ln}\left(D\right) + \mathsf{ln}\left(\exp\left\{\theta_{ijt}\right\} - \frac{Z_{ijt}}{\exp\left\{\mathsf{O}_{ijt}\right\}}\right) + \pi_{\psi g(i,j,t,k)}, \sigma_{\psi}^{2}\right)$$

Mean structure comes from literature

- D: Duration of disease
- exp { θ_{ijt} }: Incidence rate
- $\frac{Z_{ijt}}{\exp\{O_{ijt}\}}$: Notification rate
- $\pi_{\psi g(i,j,t,k)}$: Study-specific intercept
- σ_{ψ}^2 : Describes variability across cohorts within a study

$$\mu_{zi} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\mu z}^{2}\right), \ \mu_{\theta i} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\mu \theta}^{2}\right)$$

$$\kappa_{zij} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\kappa z}^{2}\right), \ \kappa_{\theta ij} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\kappa \theta}^{2}\right)$$

$$\eta_{\theta ijt} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\eta \theta}^{2}\right)$$

$$\pi_{\theta g(i,j,t,k)} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\pi \theta}^{2}\right), \ \pi_{\psi g(i,j,t,k)} \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\pi \psi}^{2}\right)$$

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- Weakly informative prior distributions used throughout
- Markov chain Monte Carlo (MCMC) posterior sampling algorithm used for making posterior inference
- Main quantities of posterior interest: $\exp \{\theta_{ijt}\}$ for all *i*, *j*, *t*
- Bayesian framework makes posterior inference and interpolation straightforward

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Estimated TB Incidence, 2019



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Estimated TB Incidence in WHO Regions



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10-Fold Cross Validation Results



95% prediction intervals included the true values 94.1% of the time

- Extraordinarily high TB incidence rate among incarcerated persons globally
- Incarcerated populations must be addressed with interventions specifically tailored to improve diagnoses and prevent transmission as a part of the broader global TB control effort
- Need for more comprehensive and standardized country-level data collection/reporting effort to improve estimates moving forward

- Efficacy: Impact under ideal conditions (randomized controlled trial)
- Effectiveness: Impact under real world conditions (case-control study)
- Can differ by setting and depend on many underlying factors
- Study Goal:
 - Extrapolate results of studies conducted in multiple countries/settings for use by decision-makers in low-and middle-income countries

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 Literature review for rotavirus vaccine efficacy and effectiveness estimates

 Identified 74 studies including 33 vaccine efficacy and 54 vaccine effectiveness estimates

 Collected country-specific predictors that may explain variability in efficacy and effectiveness

- Diarrhea prevalence among children
- Population density
- GDP per capita
- Safe sanitation %
- Safe drinking water %
- Poverty %

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Data Availability



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Rotavirus Vaccine Efficacy



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- Joint meta-regression modeling framework for vaccine efficacy and effectiveness
- Accounts for the fact that study-specific estimates may include individuals from different countries (i.e., mixture effect)
- Country-specific predictors used to explain variability in estimates, and predict unobserved countries
- Efficacy estimates used to predict effectiveness

$$z_i; \ \widehat{\theta}_i \stackrel{\text{ind}}{\sim} \mathsf{N}\left(\theta_i, \widehat{\sigma}_i^2\right), \ i = 1, \dots, n;$$

θ̂_i, *σ̂_i²*: Log estimate and variance, respectively,
 z_i = 0: Vaccine efficacy

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$$z_i = 1$$
: Vaccine effectiveness

- θ_i : True value (unobserved latent process)
- n: Total number of studies

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Latent Process Model

$$\theta_i \stackrel{\text{ind}}{\sim} \mathsf{N}\left(\sum_{j=1}^{n_c} \mathsf{w}_{ij} \eta_{z_i j}, \sigma_{\theta z_i}^2\right)$$

η_{z_ij}: True log estimate of vaccine efficacy (η_{0j}) or vaccine effectiveness (η_{1i}) from country j

n_c total countries

w_{ij}: Proportion of total people in study *i* that are from country *j*

• $\sum_{j=1}^{n_c} w_{ij} \eta_{z_i j}$: Weighted average of country-specific log estimates

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$$\sigma_{\theta z_i}^2$$
: Describes study-level variability

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Latent Process Model: Vaccine Efficacy

$$\eta_{0j} \stackrel{\text{ind}}{\sim} \mathsf{N}\left(\mu + \mathbf{x}_{j}^{\mathsf{T}}\boldsymbol{\beta} + \phi_{\mathfrak{s}(j)}, \sigma_{\eta_{0}}^{2}\right), \ j = 1, \dots, n_{c}$$

x_j: Vector of country j-specific predictors (excludes intercept)

$$\blacktriangleright \phi_k \stackrel{\text{iid}}{\sim} \mathsf{N}\left(0, \sigma_{\phi}^2\right), \ k = 1, \dots, n_s$$

•
$$\sigma_{\eta_0}^2$$
: Describes the country-level variability

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$$\eta_{1j} \stackrel{\mathsf{ind}}{\sim} \mathsf{N}\left(\gamma_0 + \gamma_1 \eta_{0j}, \sigma_{\eta_1}^2\right)$$

- Vaccine efficacy from the same country used to predict the corresponding vaccine effectiveness
- γ₀, γ₁: Intercept and slope terms that connect vaccine effectiveness with vaccine efficacy
- $\sigma_{\eta_1}^2$: Describes country-level variability in this relationship

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- Weakly informative prior distributions used throughout
- MCMC posterior sampling algorithm used for making posterior inference
- Main quantities of posterior interest: η_{0i} and η_{1i} for all j
- Bayesian framework makes posterior inference and interpolation straightforward

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Vaccine Efficacy Estimation



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Vaccine Effectiveness Estimation



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Leave-One-Country-Out Cross Validation Results



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- A limited number of widely available predictors can successfully predict vaccine efficacy in countries without study-based estimates
- Vaccine efficacy can be used to predict vaccine effectiveness
- In both projects, close communication with subject-matter experts helps to guide model development and results in methods that are effective and interpretable for a more general audience

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1 Cornell University Public Health Infectious Disease Epidemiology, Website

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