



UNIVERSITY OF COPENHAGEN



Inferring Drivers of Cholera Transmission from Historical Data

Matthew Phelps



Rationale

- Uncertainty of cholera transmission pathways still exists and is difficult to infer
- High quality data from 1853 Copenhagen outbreak can potentially provide information on transmission pathways

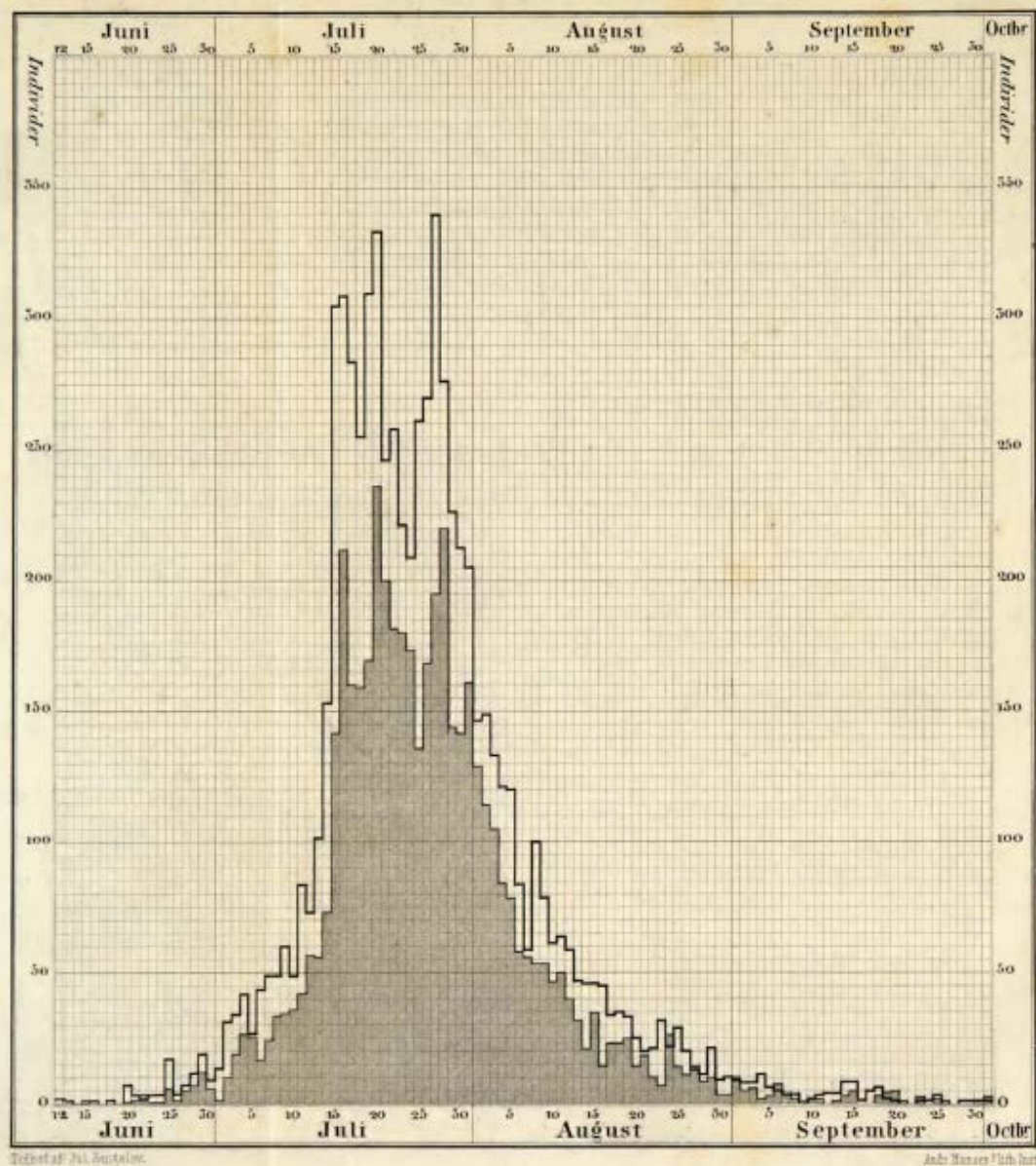
Objectives

- Evaluate the degree to which water-borne transmission routes drove the Copenhagen cholera outbreak of 1853, relative to non-water-borne transmission routes

Methodology

- Construct spatially-explicit discrete-time models of Copenhagen outbreak
- Select most appropriate model using Deviance-Information Criteria

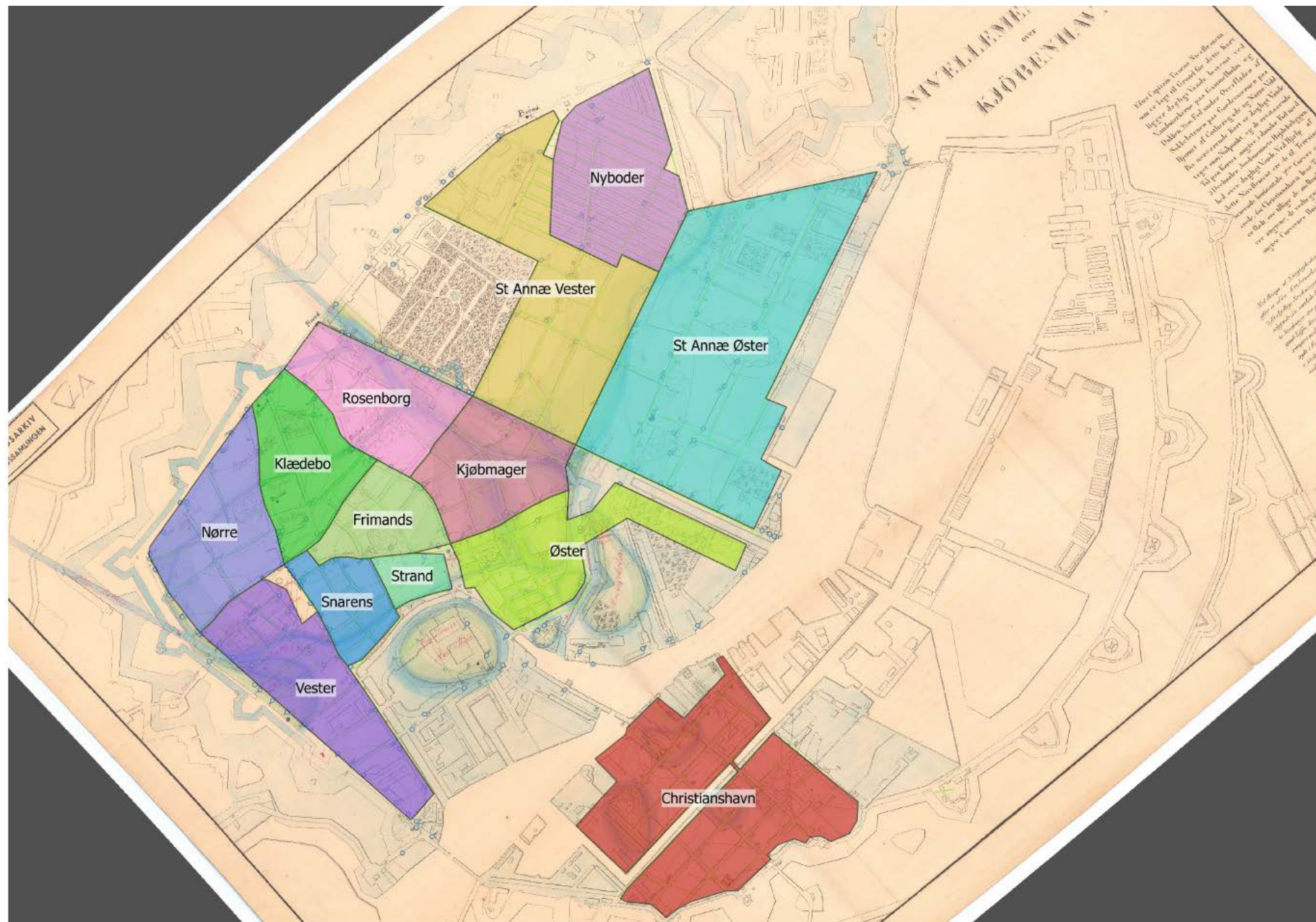
DIAGRAM OVER UDBREDELSEN AF SYGDOM OG DÖD
I CHOLERA - EPIDEMIEN I KJÖBENHAVN 1853.

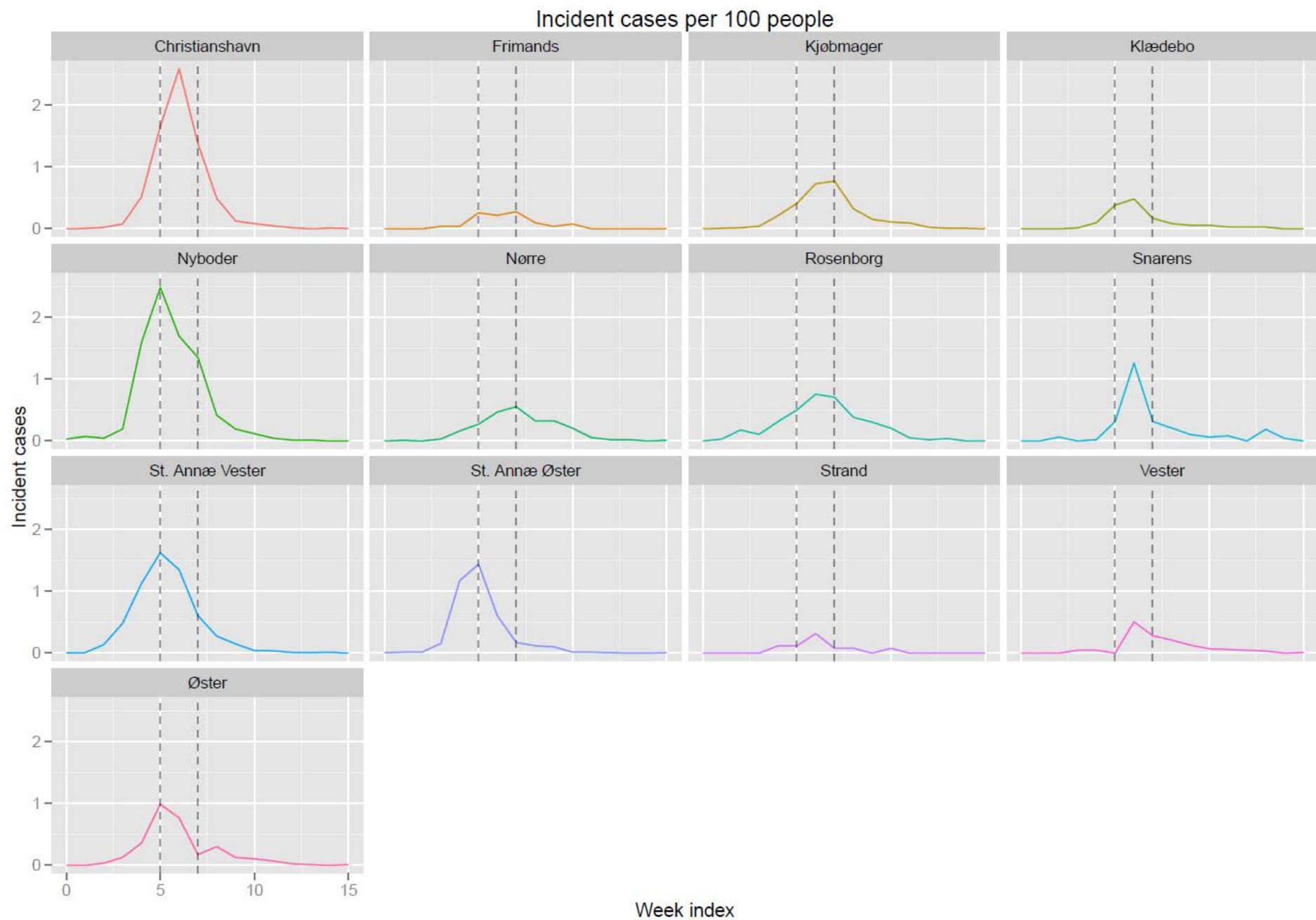


Tegnet af J. A. Aagaard.

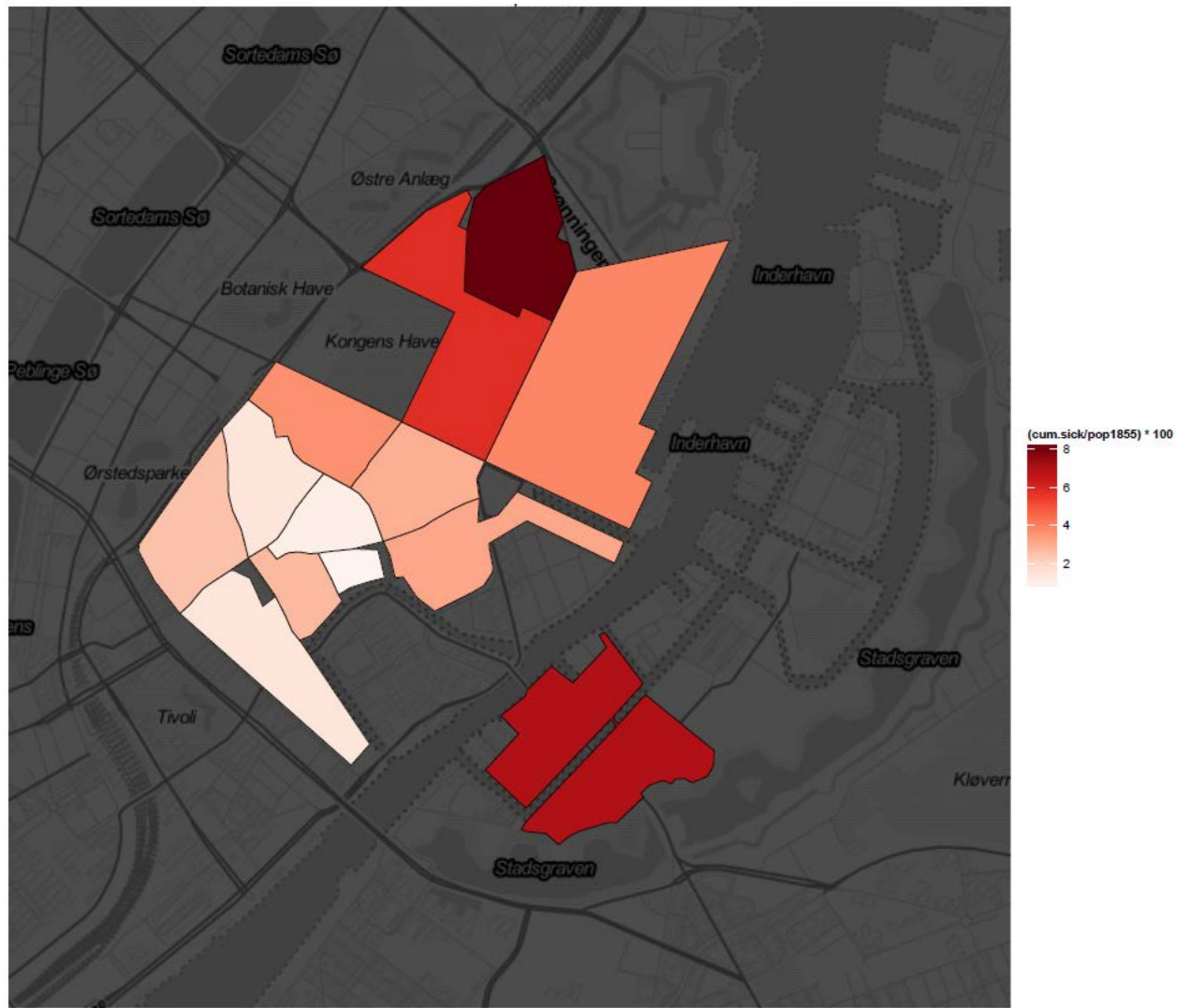
A. H. Hansen's Arkiv.

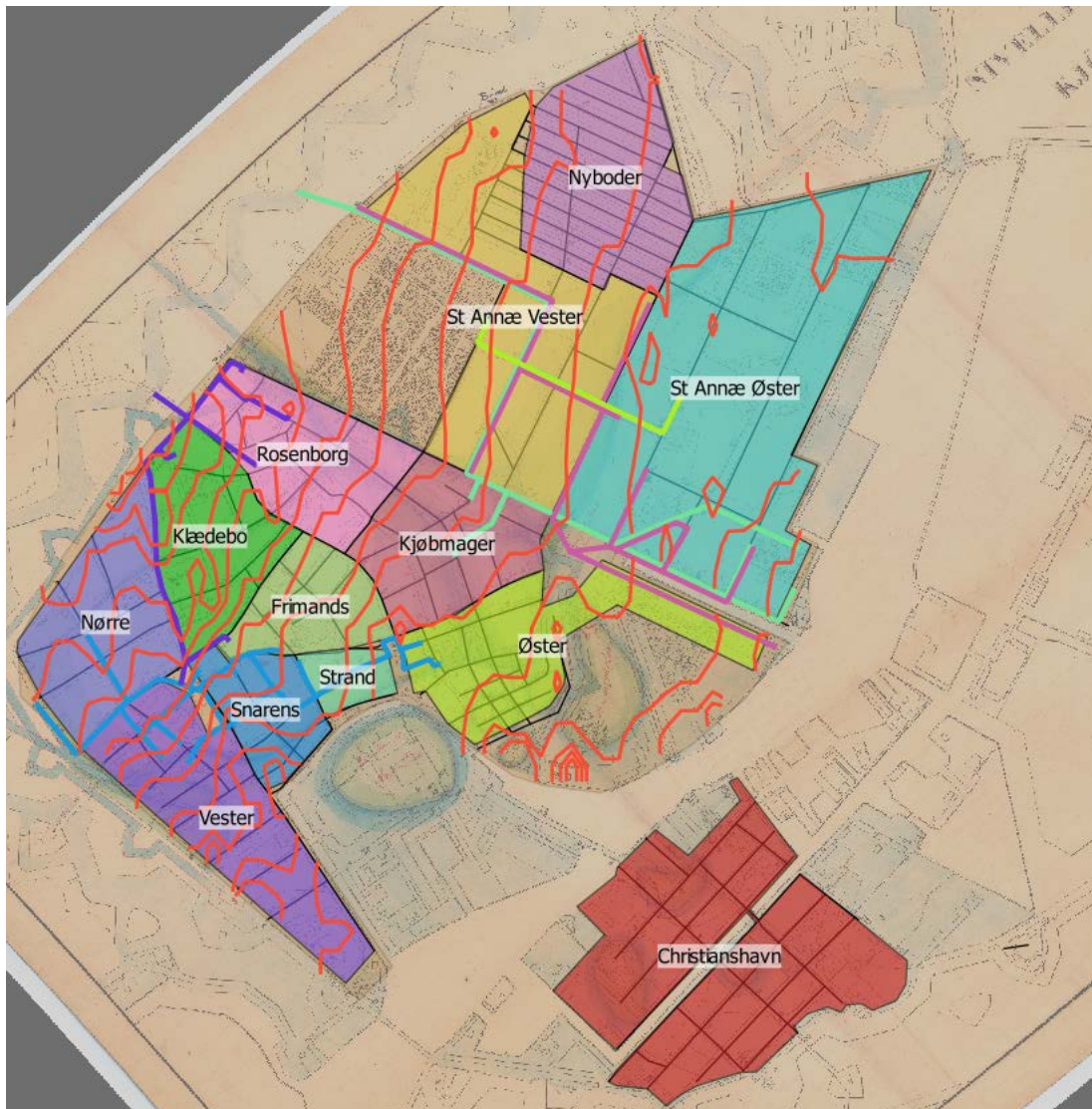






Cumulative infections





$$I_{i,t+1} \sim \text{Poisson} \left(\frac{S_{i,t}}{N_i} \left(\beta_i I_{i,t} + \sum_j I_{j,t} \alpha_{j,i} \right) + \Omega_{\text{water}} \right)$$

Funding

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Collaborators

- Lone Simonsen – University of Copenhagen Global Health Section
- Ginny Pitzer – Yale University
- Viggo Andreassen – Roskilde University
- Thomas Alexander Gerds – University of Copenhagen Biostatistics Section



Dynamic Compartmental Model of Yaws Elimination among Baka Communities in DRC

- Currently >65,000 incident cases worldwide
- One-time dose of oral antibiotic sufficient treatment (2012)
- WHO Targeted yaws for eradication by 2020 via MDA programs
- MDA programs for eradication never been modeled
- Our model tests 510 treatment scenarios
- Results indicate WHO guidelines too optimistic



