

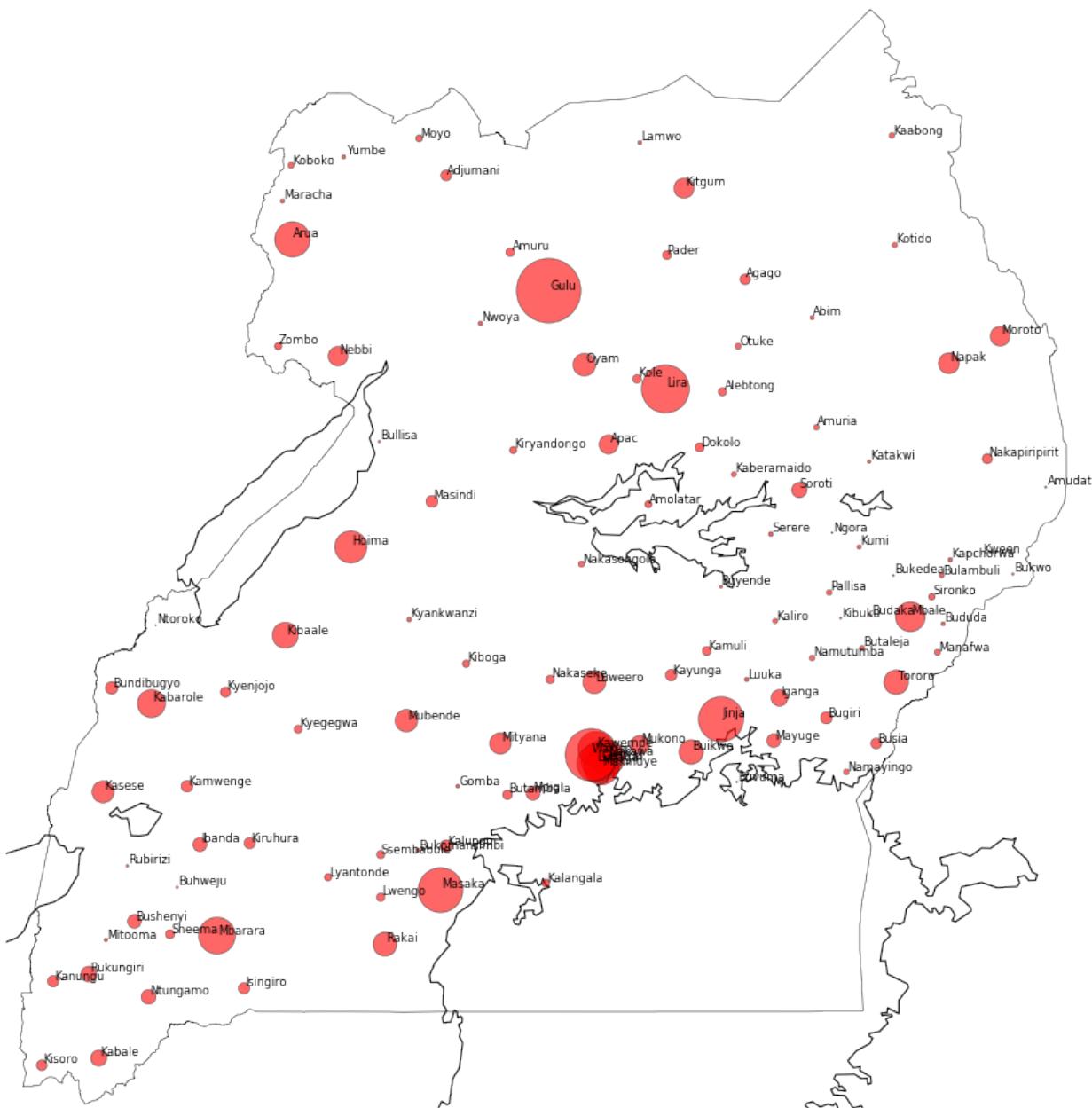


Using spatial features of human settlement to predict epidemic properties

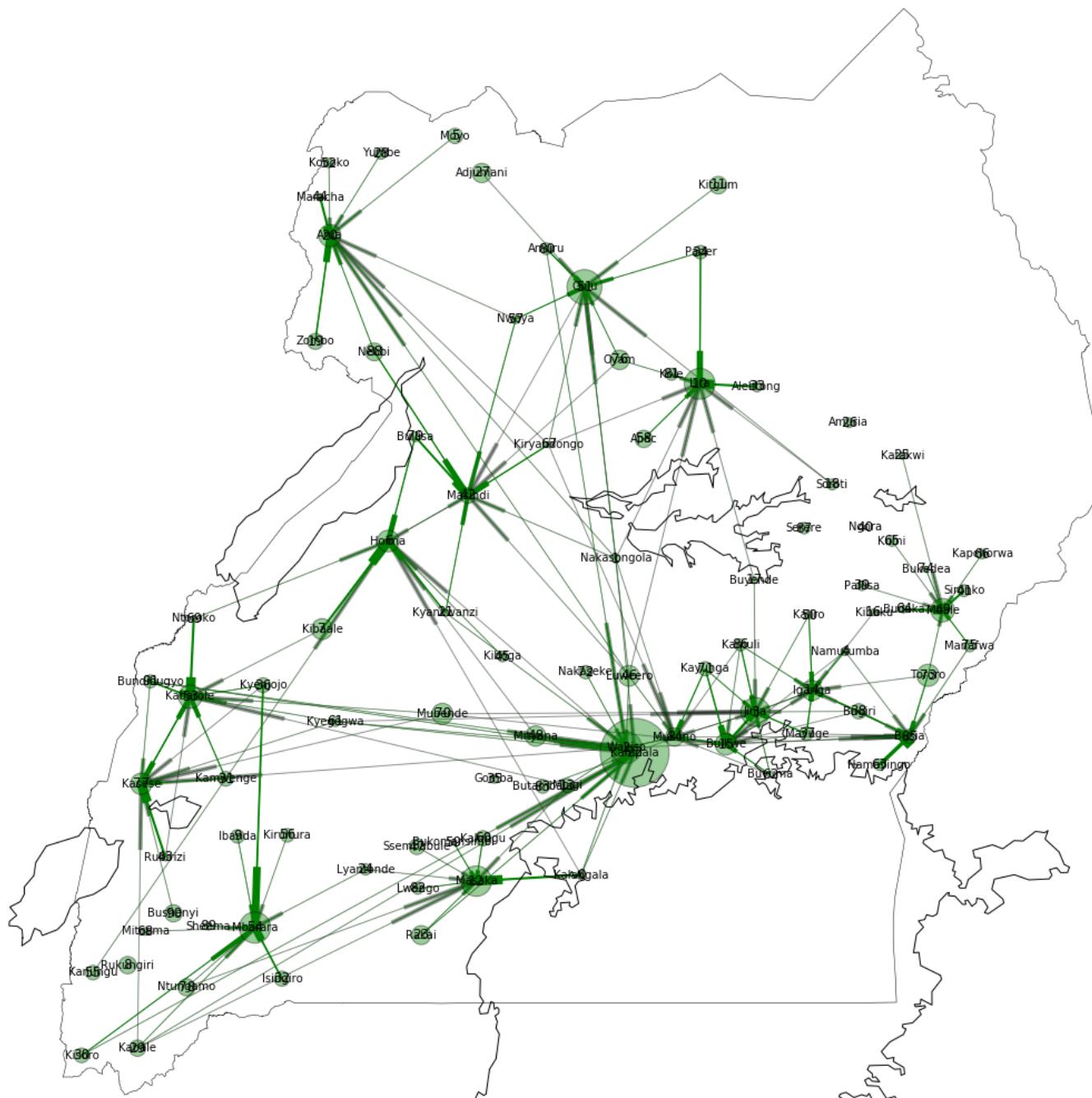
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Data Science Africa 2017 Workshop, Jul 20th – 21st, 2017 NM-AIST Arusha Tanzania

the problem



2-tier hierarchical population mobility in Uganda in 2013



the goal

Understand how settlement characteristics implicate observed spatial epidemic pattern

Features we want to explore

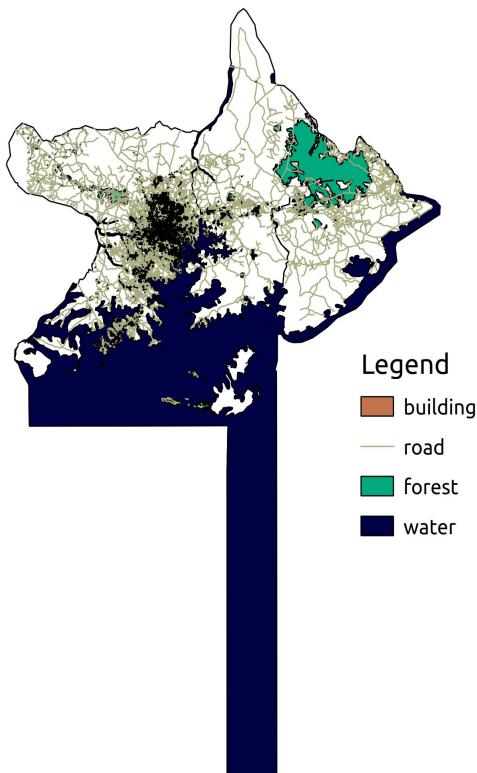
- urbanization, accessibility, mobility flux, connectivity, and population density

In this talk: urbanization

- Look for relationship between urban density & spatial epidemic dynamic
- How best to investigate potential relationship



study area



- Four contiguous LAU 4's
- Pop size 4,524,073
- Area size 5,114.3 km²
- 58.95 % urban
- Built-up, bare soil, vegetation, water

data sources

Satellite imagery (Landsat 8) from USGS

- 11 bands, cloud < 10%, 30m spatial res

Geospatial dataset (OSM) from Geofabrik

- road network, building blocks

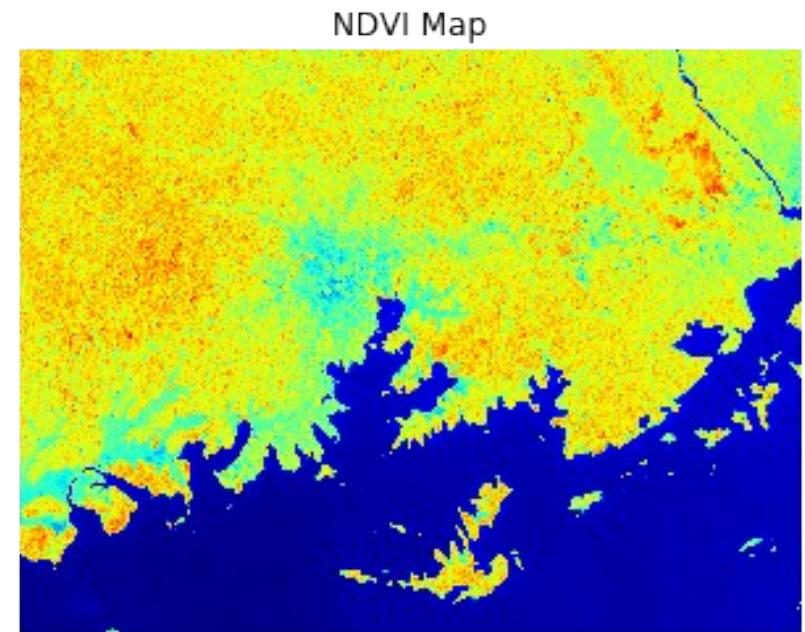
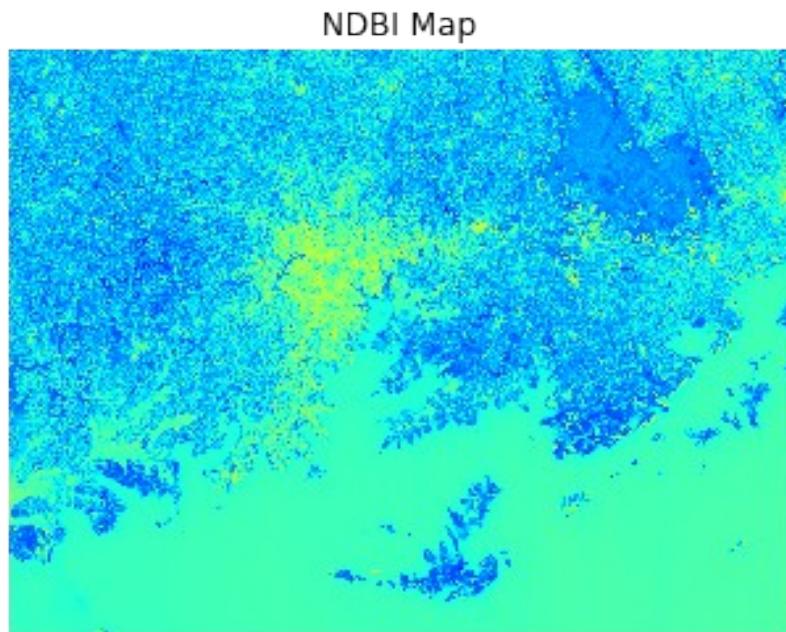
Disease case (DHMIS2)

- TB, HIV/AIDS

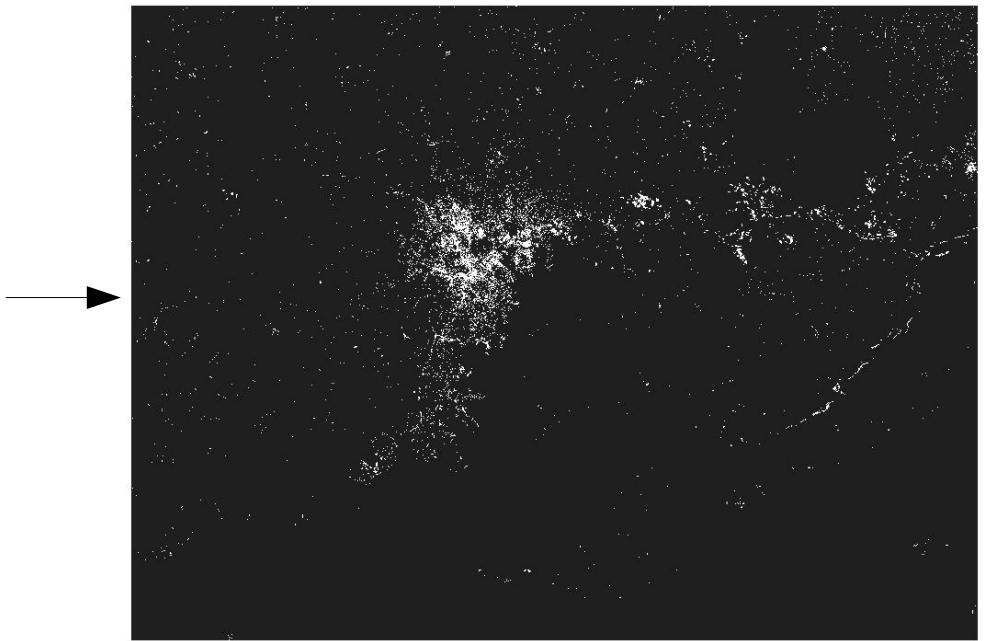
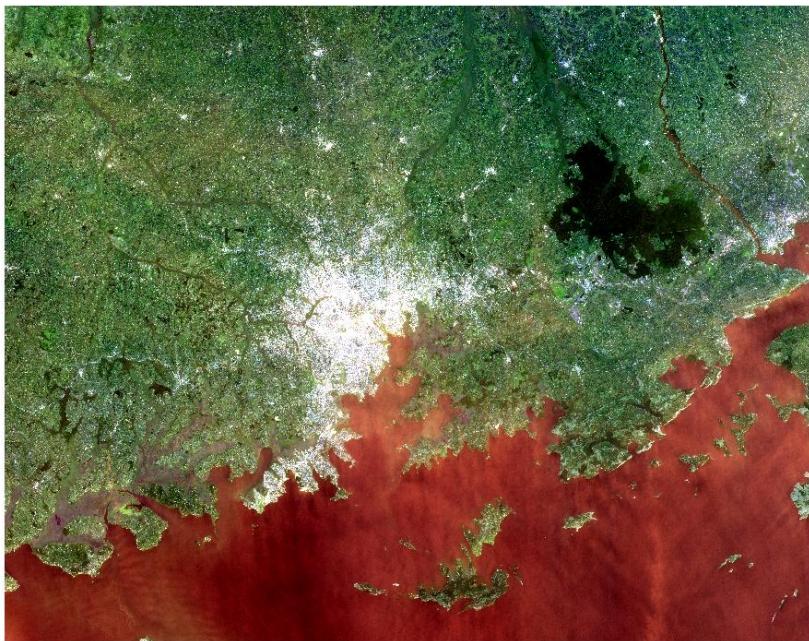
general approach

- Map settlements, quantify urban
- Classify settlements into rural or urban
 - urban is 'a place dominated by built environment'
- Model relationship between urban concentration and disease dynamics

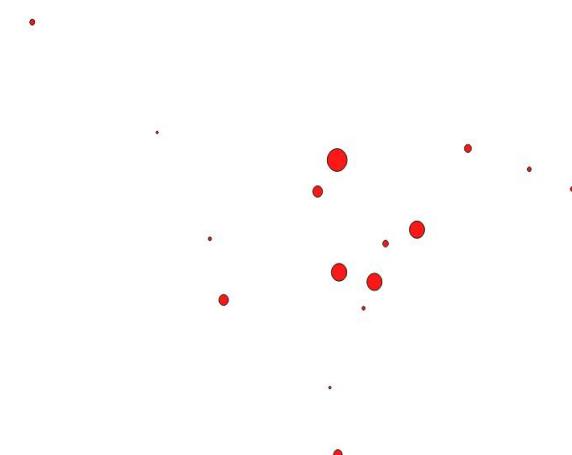
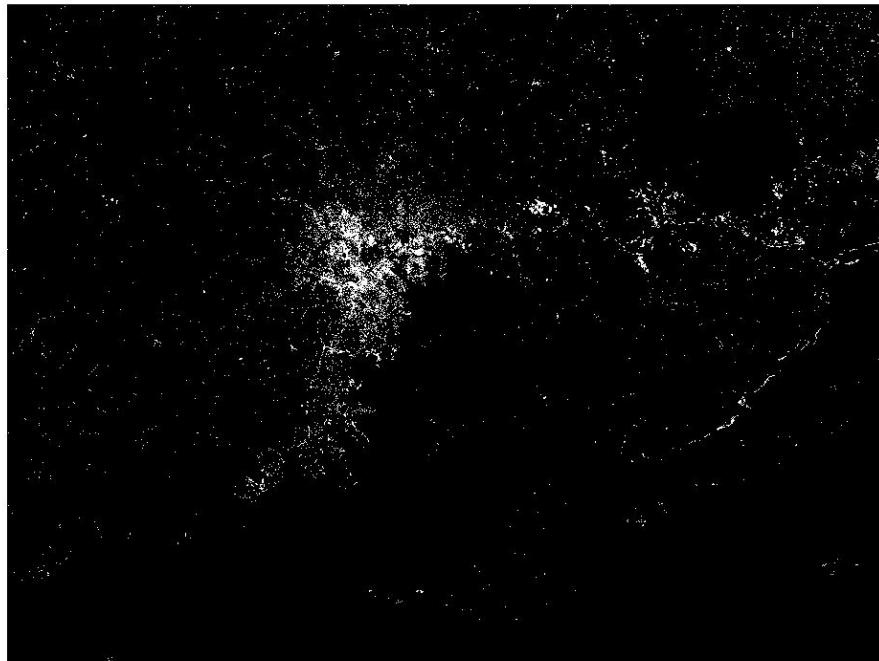
Extract built-up footprint



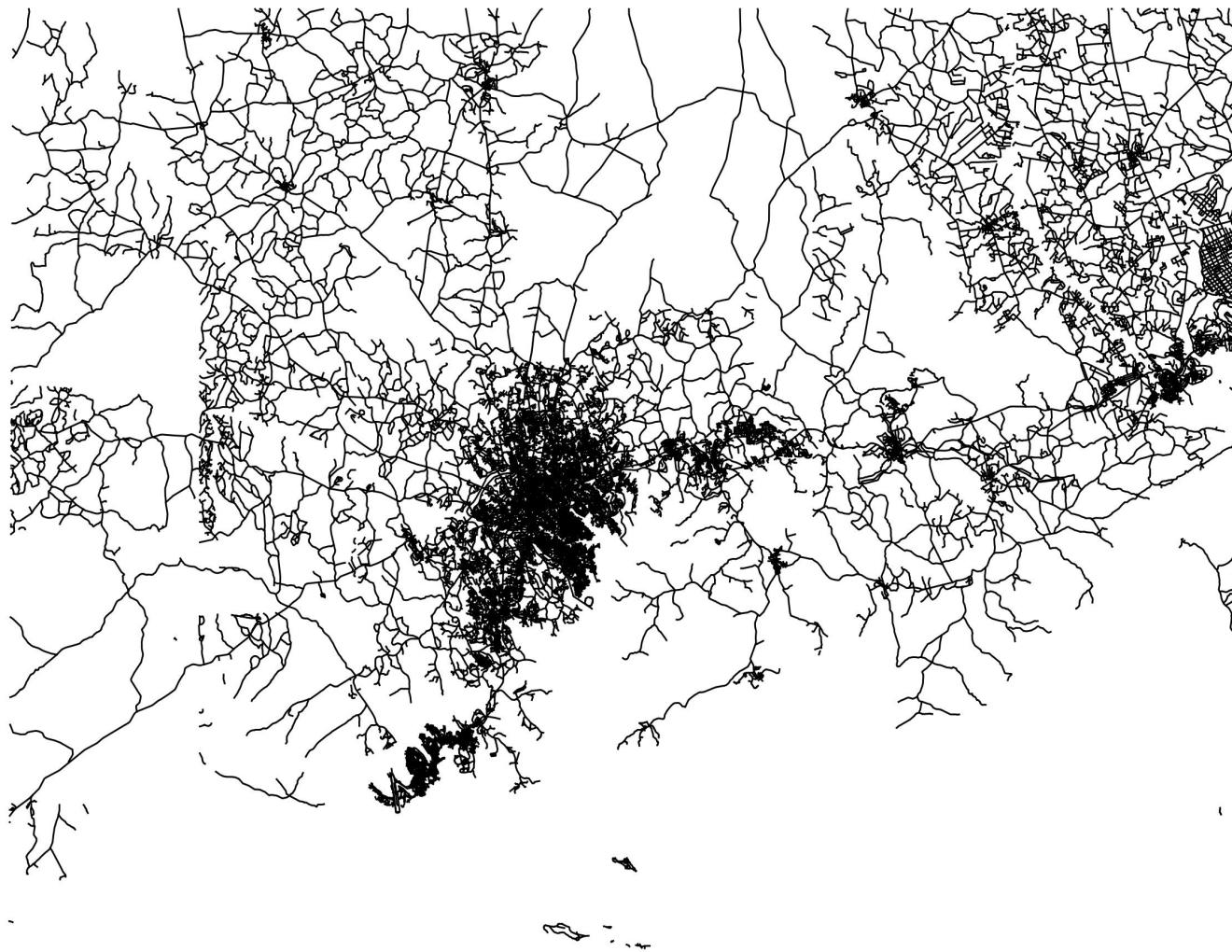
built-up footprint



urban density vs. case distribution



road density



we want to...

relate features to epidemic properties

Using mutual information I ,

$$I(X;Y) = H(X) + H(Y) - H(X,Y)$$

where

$$H(t) = \frac{-1}{\log V} \sum_j \gamma_j(t) \log \gamma_j(t)$$

extract communities

Using agglomerative hierarchical clustering

$$\chi_{mn}^o = \frac{J_{(mn)}}{\min(k_m, k_n) + 1 - \Theta(A_{mn})}$$

where

- X^o is topological overlap matrix
- $J_{(mn)}$ is no. of shared neighbors of nodes m, n
- k is node degree
- $\Theta(A_{mn})$ is Heaviside step function

relate pattern across nodes

Node pairs expected to have similar epidemic properties if they

- share neighbors
- have direct link between them
- have comparable spatial features

relate pattern across nodes

Epidemic similarity between nodes m, n

$$\phi_{mn} = \frac{\rho_m}{\rho_n} = \frac{\rho_n}{\rho_m} \quad \rho_m \approx \rho_n; \vartheta_m \approx \vartheta_n$$

$$\rho = \frac{i_m}{\sum_n i_n} \quad \text{and} \quad i(t) = \frac{I(t)}{N}$$

$\phi = 1$ if nodes m, n have similar epidemic properties

$\phi > 1; \phi < 1$ otherwise

conclusion

- Its early days to conclude
- However, our goal is to explore predictive potential of five spatial settlement features for epidemic modeling in coupled human population systems