



ABSTRACT

Public health planners need an understanding of how disease outbreaks propagate in different populations to formulate effective control strategies. To this end, a framework to simulate and visualize infectious disease epidemics in a population was created. Contacts between individuals drive the spread of infectious disease outbreaks. Since actual behavior patterns of the population are unknown, the likelihood of a simulated contact between two individuals is determined by demographic similarities and geographic proximity. Geographic spread of the outbreak is visualized using a color coded map to represent proportions of populations affected. Geographic and demographic data from the U.S. Census Bureau are used in the simulation to facilitate exploration of outbreak propagation in real populations.

MOTIVATION

Why do we need epidemic simulation?

- Planning the response to an epidemic outbreak in advance can help minimize human and monetary costs.
- Lack of reliable historical data and under-reporting of diseases complicate planning public health planning.

What factors do we need to account for when building an epidemic spread model?

- Non-uniform distribution of population over a geographic region.
- Differences in daily habits and social interactions of different demographic groups.
- Computational overhead - if it takes too long to get results, the model is impractical.

Visualization

A color-coded map of the region is used to show the disease dynamics. At every time-step of the epidemic, intensity of the infection in each census block is displayed on the geographic map using a color code. Intensity of infection is measured on the basis of proportion of infected individuals in that block at a given time.



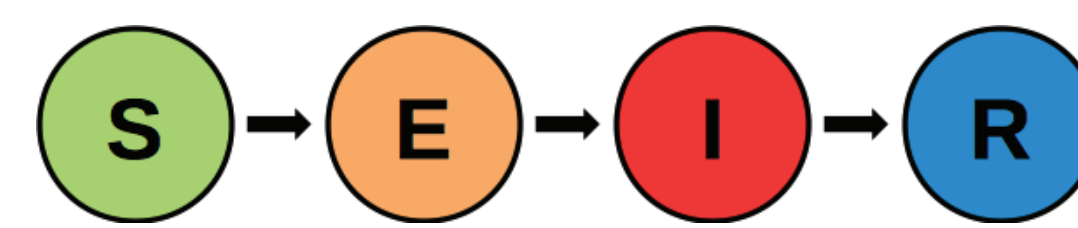
Dallas County Census Block Populations 0 - 54 55 - 224 225 - 597 598 - 1356 1357 - 6362

Population distribution in Dallas County, Texas. Above is the color code used for the heat-map.

METHODOLOGY

SEIR Model

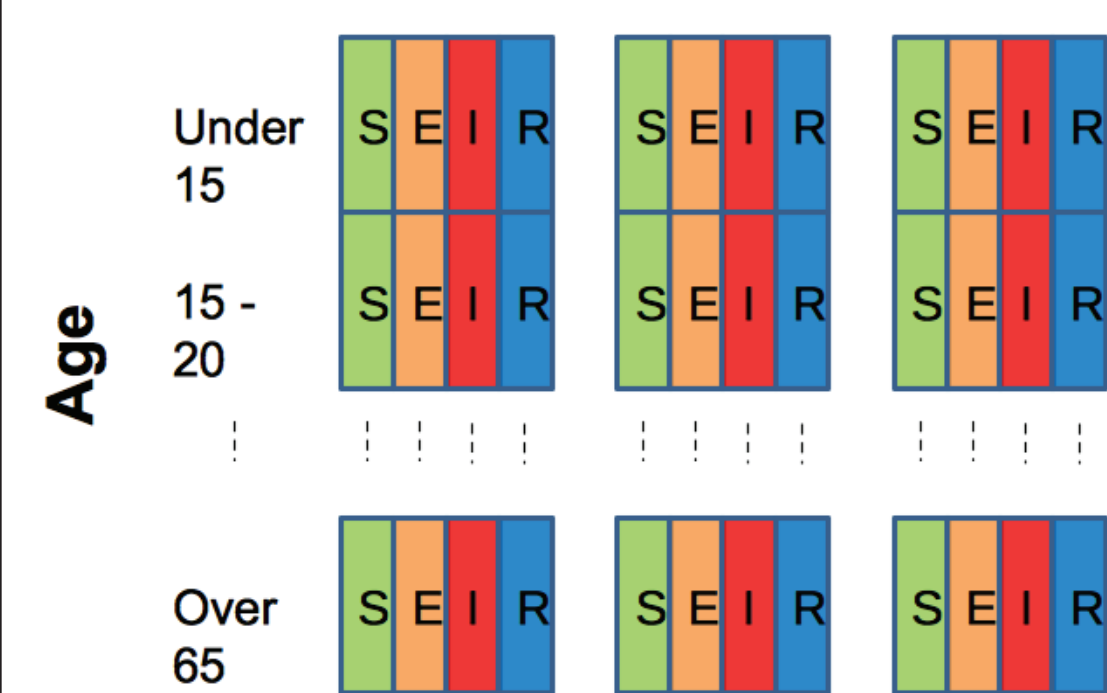
Progression of the disease within each individual is modeled by moving each individual between the disease states Susceptible (S), Exposed (E), Infected (I) or Recovered (R) as shown in the diagram below.



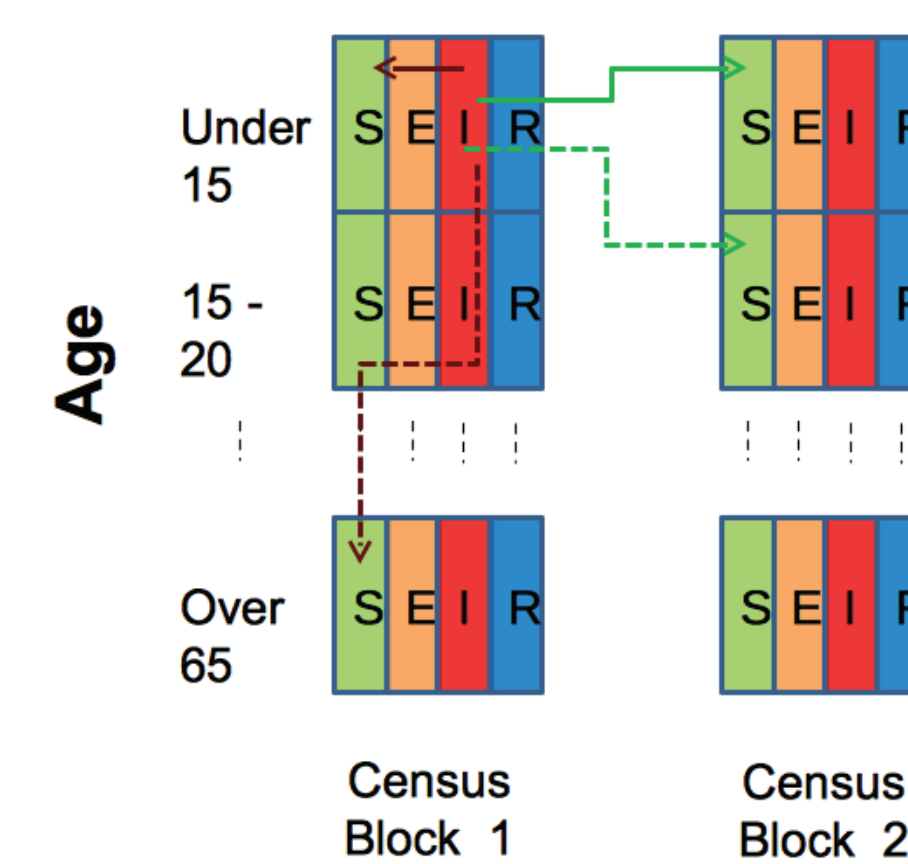
Population Distribution

The region is partitioned into census blocks with different population densities. Within a census block, individuals are stratified into **demographic groups**. Individuals belonging to each group are classified into one of the disease states S, E, I, or R.

Population Distribution Model



Contact Generation Model



Census Blocks

- Global within age group
- Local within age group
- - - Global outside age group
- - - Local outside age group

Spread of disease is modeled by means of **infectious contacts** between demographic groups in the different census blocks.

Infectious contacts can either be **local** (within a single block) or **global** (between different blocks).

Contacts are generated between population groups on the basis of:

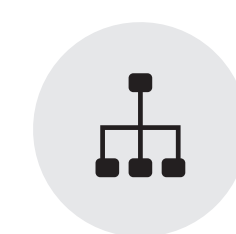
- Interaction Coefficients** between census blocks
- Social-behavioral Characteristics** of demographic groups

The Interaction Coefficient between any two census blocks is a measure of the strength of interaction between them. It is directly proportional to the populations of the participating blocks and inversely proportional to the distance between them. Thus, pairs of census blocks that are more populous and are closer to each other are likely to have a larger number of contacts between them.

Social-behavioral Characteristics are used to determine the likelihood of contacts between different demographic groups. The following parameters are used to capture the social-behavioral characteristics:



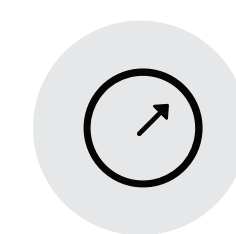
Contact Rate: The total number of contacts an individual makes with all other individuals in the population per time unit.



Mobility: Likelihood of a contact made by an individual with an individual in an external block.



Affinity: Likelihood of a demographic group contacting a group in an external block.



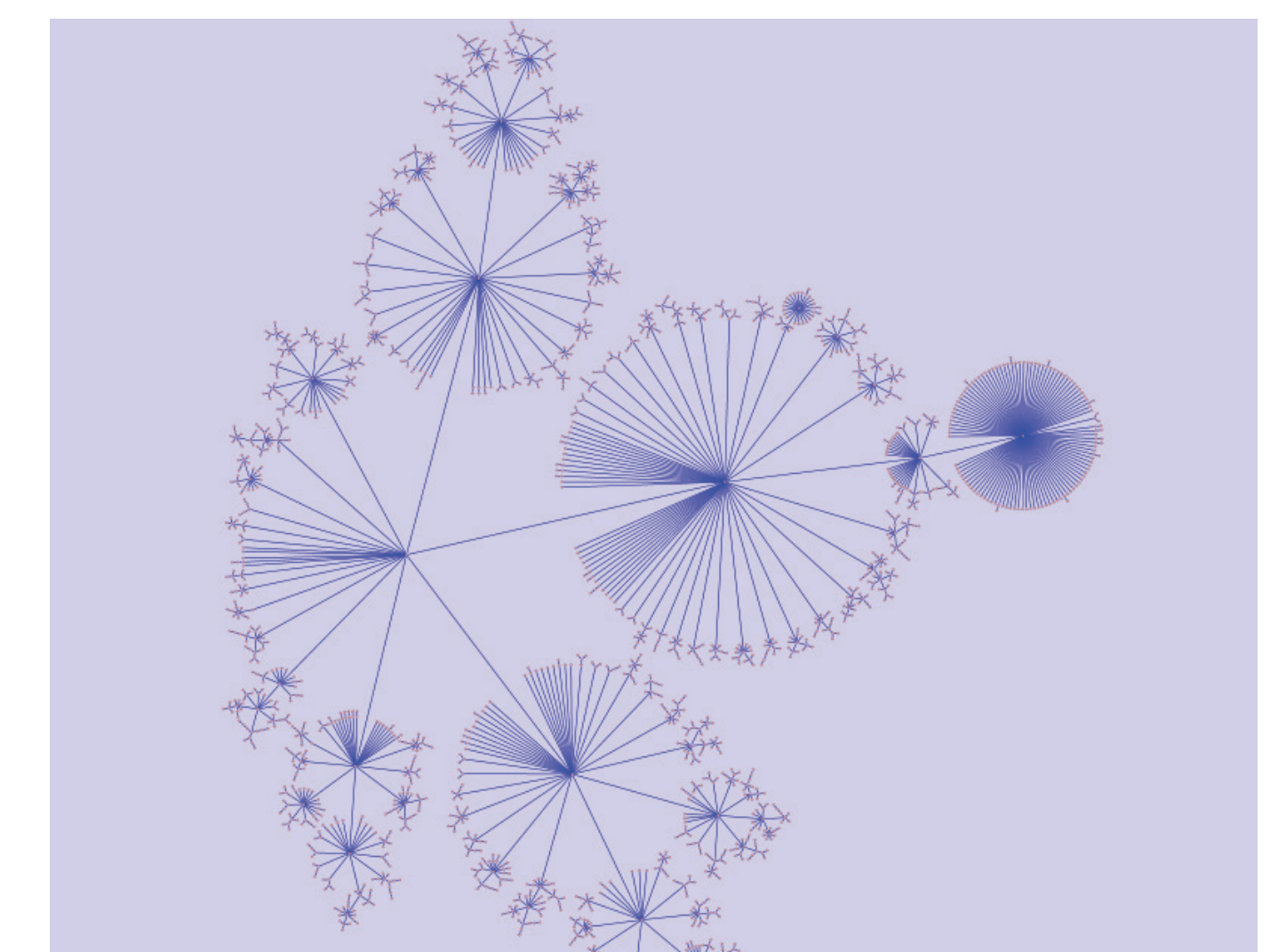
Reach: A measure of maximum contact distance.

EPIDEMIC SPREAD PATTERN

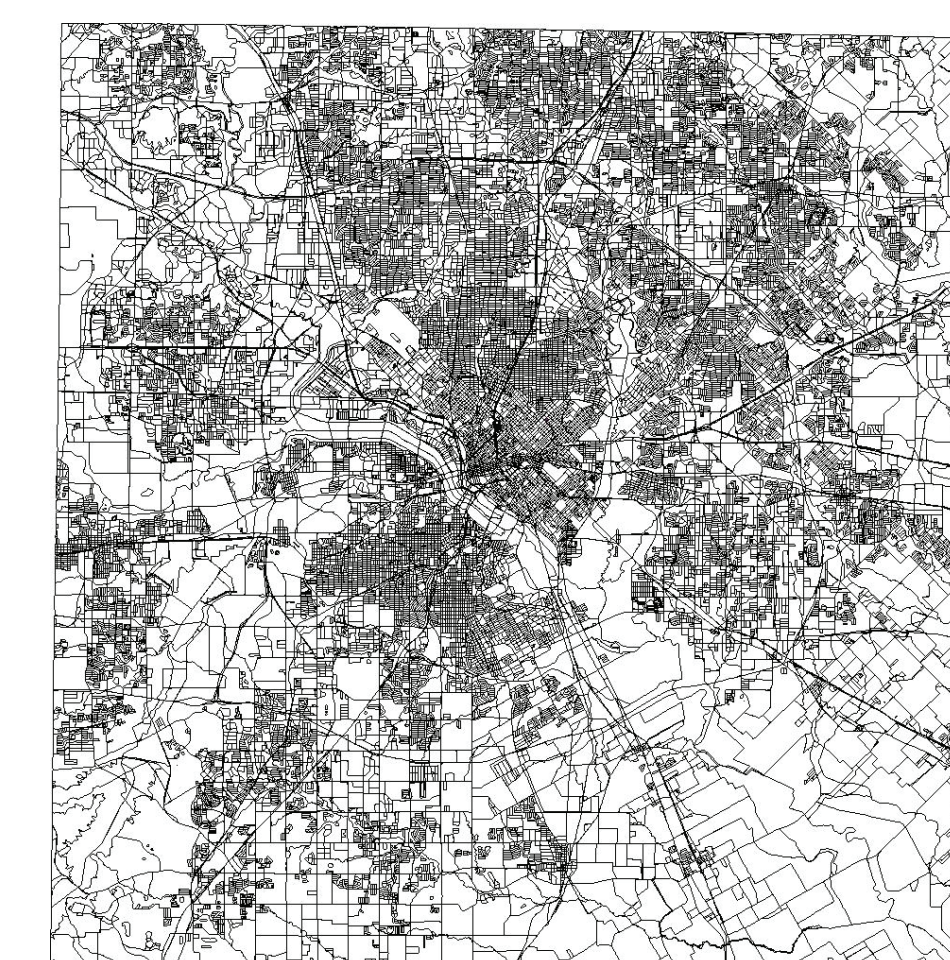
The heat-maps below show the propagation of a simulated epidemic in Dallas County, Texas. The population in one of the census blocks is initially infected to trigger the disease outbreak. The outbreak spreads through the population, reaches a peak, and then subsides.

Parameter	Value
Infectious Period	5
Exposed Period	3
Infectivity	0.05
Contact Rate	50
Mobility	0.995
Reach	1.0

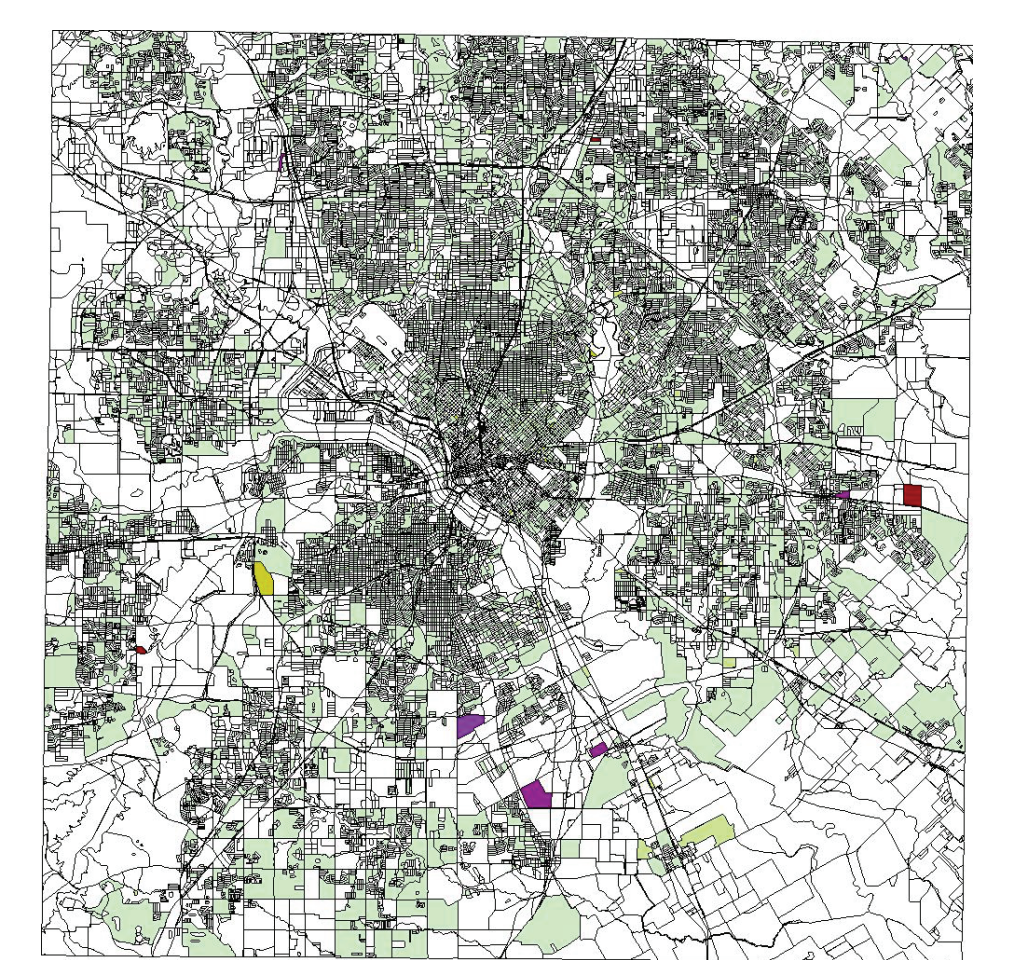
Parameters used for the simulation



Chronological order of disease spread starting from index block



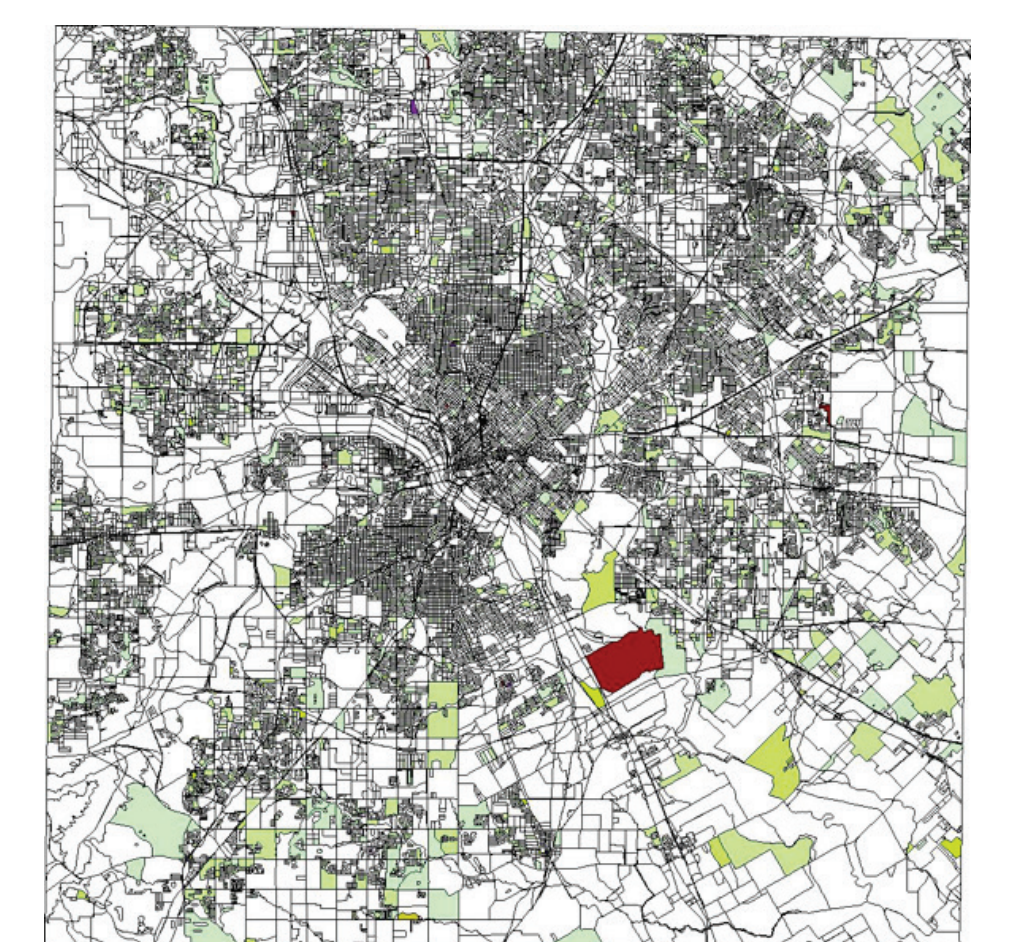
Outbreak Begins



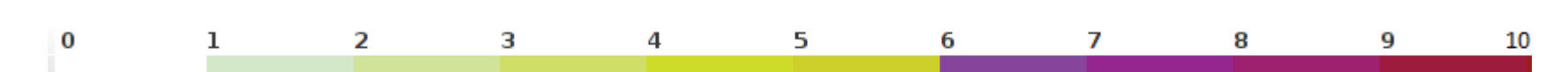
Outbreak Progresses



Outbreak Peaks



Outbreak Subsides



Heat-maps displaying the infection state in the county during the course of the epidemic. (Each integer on the scale represents a tenth of the population infected.)