Modeling daily flow patterns individuals to characterize disease spread

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MODELLING DAILY FLOW PATTERNS OF INDIVIDUALS TO CHARACTERIZE DISEASE SPREAD

Abstract: The effect of an individual's travels throughout a day on the spread of disease is examined using a deterministic SIR model. We determine which spatial and demographic characteristics most contribute to the disease spread and whether the progression of the disease can be slowed by appropriate vaccination of people belonging to a specific location-type.
Modelling daily flow patterns of individuals to characterize disease spread

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Outline

• Determining Core Groups for a population

• Calculation of $R_0$ for individuals and demographic subgroups

• Overview of TRANSIMS data

• SIR model discussion

• Conclusions and Future Work
Core Subgroups

- Want to find which demographic subgroups are active spreaders of the disease

- Want to find if any spatial characteristics are associated with active spreaders

- First use simulation data from TRANSIMS to answer these questions
**TRANSIMS data format**

TRANSIMS data is in the following form:

<table>
<thead>
<tr>
<th>ID</th>
<th>Loc</th>
<th>Arrival Time</th>
<th>Departure Time</th>
<th>Reason for Being</th>
</tr>
</thead>
<tbody>
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<td>4225</td>
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<td>6.6667</td>
<td>0</td>
</tr>
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<td>4</td>
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<tr>
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<td>0</td>
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<td>0</td>
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<td>0</td>
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<tr>
<td>3</td>
<td>5867</td>
<td>15.5833</td>
<td>24</td>
<td>4</td>
</tr>
</tbody>
</table>

0: Home  3: Visit  6: Serve Passenger  
1: Work   4: Social/Rec  7: School  
2: Shop   5: Other       8: College
Finding Core Subgroups

One or more subgroups may be highly active as spreaders in the disease to the population as a whole. These subgroups are called core groups.

To determine which groups are core groups, we first calculate an $R_0$ value for each demographic subgroup.

$R_0 \equiv$ the expected number of secondary cases produced in a completely susceptible population, by a typical infected individual during its entire period of infectiousness.

If $R_0 > 1$ the disease will spread, if $R_0 < 1$, the disease will die out.
Calculation of $R_0$ for demographic subgroups

In general, 

$$R_0 = r\beta\tau$$

where

$r = $ Number of contacts per person

$\beta = $ Probability of transmission

$\tau = $ Mean duration of the infectious period

Define

$R_{0ij} \equiv$ the basic reproduction number for the group $i$ contacts of an infected in group $j$

$R_{0j} \equiv$ the basic reproduction number for all the contacts of a group $j$ infected
A subgroup $i$ is in the core for the spread of the disease if both

$$R_0 > 1 \text{ (the disease persists), and}$$

$$R_{0i} > 1$$

$R_0$ for the overall disease will be the largest eigenvalue from the matrix of $R_{0ij}$ values.
Calculating $R_0$ values for Individuals from a 1% sample

For each interaction between individuals, we calculated an $R_{0ij}$ value.

$$R_{0ij} \equiv \frac{r_{ij} \beta_{ij}}{\gamma}$$

where

$r_{ij} = \text{Fraction of Person } i\text{'s contacts that are with Person } j$

$\beta_{ij} = \text{Probability of transmission between an infected } j \text{ and susceptible } i$

$1/\gamma = \text{Mean duration of the infectious period}$
Calculating $R_0$ values for Individuals

Cont’d

Using TRANSIMS data, we let

$$\beta_{ij} = \frac{\text{length of contact}_{(i,j)}}{24}$$  \hspace{1cm} \text{(fraction of the day spent together)}

$$r_{ij} = \frac{\text{length of contact}_{(i,j)}}{\sum_i \text{length of contact}_{(i,j)}}$$  \hspace{1cm} \text{(fraction of i's contacts that are with j)}

We then calculated the $R_{0j}$ values for each individual:

$$R_{0j} = \sum_i \frac{r_{ji} \beta_{ij}}{\gamma}$$
For the 1% sample: $\gamma = .5 \Rightarrow R_0 = 2$

Age Distribution for Individual $R_0 > 1$ values

$R_0$ 1.0-1.2

$R_0$ 1.8-2.0
Distribution of Population vs. $R_{0j} > 1$ subset

**Age Distributions**

**Number of Contact Distributions**
Distribution of Population vs. $R_{0j} > 1$ subset

Length of Activity Log Distribution
Conclusions and Future Work

- Calculated $R_0$ values for a population and for each individual in the population under different parameter scenarios.

- Beginning to identify which types of individuals might be classified as "super-spreaders" by determining which types of individuals belong to the core group for different disease parameters.

- Begin calculating $R_0$ values for demographic subgroups.

- Identify subgroups that contribute to the disease spread.

- Single the core groups out for vaccination to see how infection changes in the population as a whole.