Developing a complex agent network model to predict HIV and HCV incidence in Canada

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Overview

- Part 1 - Agent-Based Model Introduction
- Part 2 - Network Models (Interaction Networks)
- Part 3 - Results
Part 1
Agent-Based Model Introduction
Traditional Models

- Markov model vs. micro-simulation model
- Dynamic model (SIR model) vs. agent-based model

\[
\begin{align*}
\frac{dS}{dt} &= -\beta SI + f R + \mu S - \delta S \\
\frac{dI}{dt} &= \beta SI - \gamma I - \delta I \\
\frac{dR}{dt} &= \gamma I - f R - \delta R
\end{align*}
\]
Agent-based model Overview

- Three hierarchical levels
  - Environment
  - Individual / Agent
  - Behaviors / Health status

- Relationships
  - Individuals live in the environment
  - Each individual has his/her own behaviors and health status
  - Individuals can interact with each other
Individual / Agent

- Individuals are characterized by:
  - Age
  - Sex
  - Sexual orientation
    - heterosexual, homosexual, bisexual
  - Immigrant status
  - Body mass index (BMI)
  - Each individual has their own
    - injection behavior
    - sexual behavior
    - health status
Diseases: HCV
Diseases: HIV

- Primary Infection
  - Undetected
  - Detected

- Chronic Infection
  - Undetected
  - Detected
  - On-treatment

- AIDS-mild
  - Detected
  - On-treatment

- AIDS-severe
  - Detected
  - On-treatment
Part 2
The Interaction Networks
The Networks

- The model contains three networks
  - Heterosexual network
  - MSM (men who have sex with men) network
  - Drug injection network
- All three networks are
  - Scale free network
    - Property: number of links originating from a given node exhibits a power law distribution \( P(k) \sim k^{-\eta} \)
    - Assumption in our model: The chance of forming a relationship is dependent on number of partners both agents have.
General Networks Algorithm

- **Forming relationship**
  - Choose two agents \((x, y)\), forming relationship with probability \(p\)
    \[
    p = (1 - r) + \frac{r \cdot \text{partner}(x) \cdot \text{partner}(y)}{m^2}
    \]
  - \(r\): preference parameter
  - \(\text{partner}(x \text{ or } y)\): number of partners that \(x \text{ or } y\) has
  - \(m\): total number of partners allowed in the network

- **Separate relationship**
  - All existing relationships have \(\sigma\) probability of separation at each time step.

- **Transmitting diseases**
  - For every relationship between an uninfected and an infected person, the disease is transmitted with a probability \(\lambda\).
Heterosexual Network Example

- Forming heterosexual relationship algorithm:
  1. Randomly choose one male agent and one female agent.
  2. Determine whether both are looking for a sexual partner and satisfy the distance constraint?
     - If so, form relationship with probability $p$.
  3. Determine whether this is a casual relationship?
  4. Determine the duration of the relationship.
  5. Determine the rate of sexual intercourse and probability of condom use.
Injection Network

- Transition into/out IDU (Injected Drug User)

- Only share injection is at risk

- Transmitting diseases algorithm:
  1. Queue are formed daily for share IDUs
  2. Determine the sharing group size, form group within the distance constraint
  3. Determine whether IDUs clean syringe before reuse
  4. Transmit disease with probability $\lambda$ if someone in group was infected.
How it works?

- **Initialization**
  - Geographical Information System (GIS) created.
  - Agents created in GIS according to demographic and epidemiological data.
  - We simulated the entire Canadian population, stratified by age groups, sex, sexual orientation, and immigrant status.
  - Heterosexual network, MSM network and injection network initialized.

- **At each time step (daily)**
  - Update sexual network, MSM network and injection network.
  - Random formation, separation, and transmit diseases.
  - Record disease status if changes occur.
  - Update behavior and background data.
The model was run for 5 years, to stabilize the partnership dynamics.

Model then run to establish a steady state for HIV and HCV prevalence.

Calibration against historically detected HIV and HCV between 1999 to 2007.

- Adjust network parameters.
Main Data Sources

- Canadian Census
- Canadian Community Health Survey
- Canadian Alcohol and Drug Use Monitoring Survey
- Public Health Agency of Canada:
  - I-Track Report (Enhanced Surveillance of Risk Behaviors Among Injecting Drug Users in Canada)
  - M-Track Report (second generation sentinel surveillance across Canada)
  - HIV and AIDS in Canada: Surveillance Reports
  - Notifiable Diseases On-Line
## Selected Calibrated Parameters

### Heterosexual network

<table>
<thead>
<tr>
<th>Selected Parameters</th>
<th>Calibrated Value (married, under 25, others)</th>
<th>Calibrate Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Probability of agent seeking for a partner</td>
<td>(92%, 84%, 78%)</td>
<td>50% - 99%</td>
</tr>
<tr>
<td>Probability of casual relationship</td>
<td>(6%, 45%, 23%)</td>
<td>1% - 60%</td>
</tr>
<tr>
<td>Probability of condom use</td>
<td>(13%, 58%, 62%)</td>
<td>13% - 70%</td>
</tr>
<tr>
<td>Rate of sexual intercourse</td>
<td>(10, 17, 15) times/month</td>
<td>1 - 24 times/month</td>
</tr>
<tr>
<td>Duration of the relationship</td>
<td>(11, 9, 20) months</td>
<td>0.5 - 23 months</td>
</tr>
<tr>
<td>Distance constraint of the relationship</td>
<td>130 km</td>
<td>50 - 500 km</td>
</tr>
</tbody>
</table>

### Injection Network

<table>
<thead>
<tr>
<th>Selected Parameters</th>
<th>Calibrated Value</th>
<th>Calibrate Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proportion of persons who share syringes</td>
<td>16%</td>
<td>15% - 20%</td>
</tr>
<tr>
<td>Proportion of injections that are shared</td>
<td>15%</td>
<td>13% - 17%</td>
</tr>
<tr>
<td>Size of the sharing group</td>
<td>3</td>
<td>2 - 4</td>
</tr>
<tr>
<td>Distance constraint of the relationship</td>
<td>400 km</td>
<td>50 - 500 km</td>
</tr>
</tbody>
</table>
Part 3
Results
Calibration Results

- Comparing with historical Canadian HIV and HCV detection data
  - HIV and AIDS in Canada: Surveillance Reports
  - Notifiable Diseases On-Line
Projection Results

Number of diagnosed HIV cases

Number of diagnosed HCV cases

Cdn History HIV

Cdn Predicted HIV
Advantages and Limitations

- **Advantages**
  - Captures heterogeneous populations
  - Provides a natural environment for the study
  - Highly flexible

- **Limitations**
  - Complex development process
  - Computationally intensive
  - Data intensive
Conclusion

- Our network model showed good calibration between historical Canadian HIV and HCV data and the simulation results.

- This complex network model reflects dynamics of HIV and HCV transmission, which enables forecasting of the epidemiology of HIV and HCV for policy-level decision making in Canada.

- Future works include:
  - Predicting the epidemiological impact of hepatitis C treatment strategies on the burden of HIV/HCV co-infection
  - Cost-effectiveness of hepatitis C treatment strategies related to HIV and HCV co-infected population
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