WELCOME!

NETWORK MODELING FOR EPIDEMICS

Martina Morris, Ph.D.
Steven M. Goodreau, Ph.D.
Samuel M. Jenness, Ph.D.
Objectives for the 1 week course

Gain intuition about epidemic dynamics
  ▪ Strengths and limitations of the different modeling frameworks

Understand the principles and methods of network analysis relevant to infectious disease epidemiology
  ▪ Descriptive network analysis
  ▪ Statistical network analysis with ERGMs and TERGMs
  ▪ Empirical study designs for networks

Develop the knowledge and software skills to run your own simple network transmission models.
  ▪ Using R, statnet and the EpiModel package

Learn how to extend EpiModel code for your own research applications
The lesson plan for the week

<table>
<thead>
<tr>
<th>Day</th>
<th>Content</th>
</tr>
</thead>
</table>
| 1   | Epidemic models – overview of the range of methods available  
  • Deterministic vs. Stochastic; Compartmental vs. Individual vs. Network  
  Network analysis basics |
| 2   | Statistical models for networks  
  • Simple null models  
  • Exponential Random Graph Models (ERGMs) for static networks  
  • Separable Temporal ERGMs (STERGMs) for dynamic networks |
| 3   | Simple disease transmission on dynamic networks  
  • When network dynamics are independent of disease dynamics |
| 4   | Disease transmission on dynamic networks with feedback  
  • When network and disease dynamics interact |
| 5   | Extending EpiModel  
  • Exploring your research questions |
Software: based on R

Core statnet packages
(network, sna, ergm; networkDynamic, tsna, tergm)

static nets dynamic (temporal) nets

For a broad range of descriptive and statistical network analysis

statnetWeb
User-friendly GUI to access main statnet functionality
Days 1-2

EpiModel
Package to conduct network-based epidemic modeling
Both GUI and command-line versions
Days 1-5
Objectives for today

Get an intuitive sense of epidemic modeling, including:

- Elements of an infectious disease transmission system
- Signature dynamics of classic systems: the SIR/S family
- The range of modeling frameworks, and differences between them
  - Deterministic compartmental models (DCMs)
  - Stochastic individual-based (or “agent-based”) models
  - Stochastic network models

Learn to explore simple individual-based SIR/S models using the **EpiModel** web interface

Develop a basic familiarity with network concepts and analysis, using **statnetWeb**
Starting with intuition:

Poker chip simulation

- **Blue chips** = susceptible
- **Red chips** = infected
- **White chips** = recovered

We will simulate and track the epidemic by hand

*old school, analog style*
Note:

- We will simulate an individual-level process
  - Poker chips represent persons
    - Drawing poker chips from the bag represents the contact process
    - Replacing blue chips with red represents transmission
    - Replacing red chips with white represents recovery
  - And record population-level outcomes
    - Prevalence: number of infecteds
    - Qualitative properties: extinction, persistence, equilibrium
Prevalence Worksheet

We will use this to track the prevalence over time
We begin with one infected person

At time = 0, the start of the process
At each subsequent time point we record the current number of infected persons (prevalence)
To the lab...

Record your outcomes on the

Constant Growth Model
Constant growth model

INSTRUCTIONS: Start with 1 red chip (red = 1) on the table

For each round:

1. Add 1 more red chip

2. Update the current prevalence on the tracking worksheet

3. Repeat
## Constant growth: Summary

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Population size</strong></td>
<td>Infinite</td>
</tr>
<tr>
<td><strong>Final epidemic size</strong></td>
<td>Infinite</td>
</tr>
<tr>
<td><strong>Prevalence curve</strong></td>
<td>Flat: does not depend on prevalence</td>
</tr>
<tr>
<td><strong>Incidence curve</strong></td>
<td>Linear: slope = incidence</td>
</tr>
</tbody>
</table>

**Was this process stochastic or deterministic?**
Constant growth: Implications

Not like an infectious process, more like chronic disease

Each step is some unit of time (i.e. minute, hour, day, etc.)

- Only one state (infected)
- Only one transition (the infection process)

Infinite population of susceptibles → Infection: constant rate → Infected
I: Infected model (proportional growth)

INSTRUCTIONS: Start with 1 red chip on the table

For each round:

1. Add 1 more red chip for each red chip already on the table

2. Update the prevalence on the tracking worksheet to the current number of red chips on the table

3. Repeat
# I Model: Summary

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Population size</strong></td>
<td>Infinite</td>
</tr>
<tr>
<td><strong>Final epidemic size</strong></td>
<td>Infinite</td>
</tr>
<tr>
<td><strong>Prevalence curve</strong></td>
<td>Exponential (slope = incidence)</td>
</tr>
<tr>
<td><strong>Incidence curve</strong></td>
<td>Exponential: Depends on prevalence at t</td>
</tr>
</tbody>
</table>

*Was this process stochastic or deterministic?*

We'll get more specific this afternoon.
The simplest true infection process

- Still only one state (infected)
- Still only one transition,

but now the incidence is determined by the prevalence

But … what if the population of susceptibles is \textit{not} infinite?
**SI: Susceptible-Infected model**

**INSTRUCTIONS:** Now we will use the bag to represent the “population”

Prepare a bag with **1 red** chip and **9 blue** chips (10 total)

For each round: **S=blue, I=red**

1. **Pick two chips**
   - If the chips are the same color, no infection occurs.
   - **Return both chips to bag, go to step (2)**
   - If the chips are different colors, infection occurs
     - **Replace blue chip with red chip and return to bag**

2. **Update the prevalence on tracking sheet to # of red chips now in the bag**

3. **Are there any more blue chips in the bag?**
   - **YES:** Return to (1)
   - **NO:** Stop
### SI model

Every draw has three possible outcomes:

<p>| | | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
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</thead>
<tbody>
<tr>
<td>1.</td>
<td>SS</td>
<td>9.</td>
<td>SS</td>
<td>17.</td>
<td>SI</td>
<td>25.</td>
</tr>
<tr>
<td>2.</td>
<td>SS</td>
<td>10.</td>
<td>SS</td>
<td>18.</td>
<td>SI</td>
<td>26.</td>
</tr>
<tr>
<td>3.</td>
<td>SS</td>
<td>11.</td>
<td>SI</td>
<td>19.</td>
<td>II</td>
<td>27.</td>
</tr>
<tr>
<td>4.</td>
<td>SS</td>
<td>12.</td>
<td>SS</td>
<td>20.</td>
<td>SI</td>
<td>28.</td>
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<tr>
<td>5.</td>
<td>SS</td>
<td>13.</td>
<td>SS</td>
<td>21.</td>
<td>SS</td>
<td>29.</td>
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<tr>
<td>6.</td>
<td>SS</td>
<td>14.</td>
<td>SI</td>
<td>22.</td>
<td>II</td>
<td>30.</td>
</tr>
<tr>
<td>7.</td>
<td>SS</td>
<td>15.</td>
<td>II</td>
<td>23.</td>
<td>SI</td>
<td>31.</td>
</tr>
<tr>
<td>8.</td>
<td>SI</td>
<td>16.</td>
<td>SI</td>
<td>24.</td>
<td>II</td>
<td>32.</td>
</tr>
</tbody>
</table>

**SS**: concordant negative  
**SI**: discordant  
**II**: concordant positive

Only SI can create incidence

The probability of each outcome changes as the process evolves.

- P(SI) low at the start
- reaches its max when S=I,
- decreases again as S get depleted.

![Prevalence Curve](image-url)
## SI Model: Summary

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td><strong>Population size</strong></td>
<td>FINITE: ( N = S + I )</td>
</tr>
<tr>
<td><strong>Final epidemic size</strong></td>
<td>( N ) (everyone)</td>
</tr>
<tr>
<td><strong>Prevalence curve</strong></td>
<td>Logistic ( (\text{slope} = \text{incidence}) )</td>
</tr>
<tr>
<td><strong>Incidence curve</strong></td>
<td>Bell shaped: Depends on ( S ) and ( I )</td>
</tr>
</tbody>
</table>

*Was this process stochastic or deterministic?*
Model: New concepts

1: Stochasticity (of some model aspects, but not others)

- The contact process is stochastic
- The infection process is deterministic (why?)

2: Equilibrium outcome

- Final prevalence at equilibrium: is *deterministic*, always = N
- Time to equilibrium: is *stochastic*, because of the contact process
  - Range is open ended: \([N-1, \infty]\)
  - If the infection rate/probability \(\tau < 1\), it would depend on that too
SI model: Components

Two states, but still only one transition: infection

So ... what does this model assume about the duration of infection?
Consider other possible *states* and *transitions* in the system

- **Recovery with return to susceptibility** (e.g. common cold)
  
  *This adds a new transition to the system: SIS*

- **Recovery with immunity** (e.g. measles)
  
  *This adds a new transition and a new state to the system: SIR*
Both models have a new transition

- What does the transition from $I \rightarrow R$ or $I \rightarrow S$ represent?
  - Not an infectious process
  - More like the constant rate we had before
  - Defined by the “duration of infection” $D$

- Let’s see how this changes the process, with a final poker chip example of an SIR process
  - Now, we will need a new time tracker for $I$ chips
## DURATION TIMER

<table>
<thead>
<tr>
<th>Days infected</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
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<tbody>
<tr>
<td>Case</td>
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<td>1</td>
<td>X</td>
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<td>X</td>
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</tbody>
</table>

Change state to R

Take a **red** chip (any one is fine) and replace it with a **white** chip.
INSTRUCTIONS:
Prepare a bag with 1 red and 9 blue chips; put 10 white chips on the side.

S=blue, I=red, R=white

1. **Pick two chips**
   - If the chips are not red and blue, no infection occurs.
     - Replace both chips in bag, go to step (2)
   - If the chips are red and blue, infection occurs
     - Replace blue chip with red chip and return to bag

2. **Update duration worksheet for BOTH new and pre-existing infections**
   - Increment each active row by 1 day
   - If any durations are at {CHANGE STATE}, take a red chip from the bag and replace it with a white chip

3. **Update prevalence worksheet with the # red chips now in the bag**

4. **Are there any more red chips in the bag?**
   - YES: Return to (1)
   - NO: Stop
# SIR Model: Summary

<table>
<thead>
<tr>
<th>Population size</th>
<th>FINITE: $N = S + I + R$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Final epidemic size</td>
<td>0: These infections always die out</td>
</tr>
<tr>
<td>Prevalence curve</td>
<td>Bell shaped: $(\text{slope} = f(\text{incidence and } R))$</td>
</tr>
<tr>
<td>Incidence curve</td>
<td>Bell shaped: Depends on $S$, $I$ and $R$</td>
</tr>
</tbody>
</table>

**Was this process stochastic or deterministic?**
SIR: New concepts

1: Extinction

Time to extinction of $I$: stochastic (why?)

Range is $\{ D \text{ to } D*N \}$ (for our poker chips, 10 to 100)

If the infection rate/probability $\tau < 1$, it would depend on that too

2: Final prevalence of $S$ and $R$

Stochastic, but has a range $\{ (0,N) \text{ to } (N-1,1) \}$

Depends on cumulative number of infections before extinction.
INSTRUCTIONS: Prepare a bag with 9 blue and 1 red chips (S=blue, I=red)

1. **Pick two chips**
   - If the chips are not red and blue, no infection occurs.
     - Replace both chips in the bag, go to step (2)
   - If the chips are red and blue, infection occurs
     - Replace blue chip with red chip and return to bag

2. **Update duration worksheet for any new and pre-existing infections**
   - Increment each active row by 1 day
   - If any durations are at {CHANGE STATE}, take a red chip from the bag and replace it with a blue chip

3. **Update prevalence worksheet with the number of red chips currently in the bag**

4. **Are there any more red chips in the bag?**
   - YES: Return to (1)
   - NO: Stop
1: Equilibrium prevalence in a closed (finite) population

*In a deterministic model*, equilibrium prevalence can range from \([0, N]\).

*If there is stochasticity*, infection will always eventually die out. Final prevalence of \(I\) is always 0, and \(S\) is always \(N\). But it can take ... forever to get there. And the probability of extinction at any time may be vanishingly small.

2: Both \(S\) & \(I\) prevalence may be cyclical.
Model parameters

- These have been implicit in most of the discussion above, but we will foreground them in the next session.

- Examples:
  - Contact: a rate of acts per capita per time step ($\alpha$)
  - Infection: the probability of transmission per act ($\tau$)
  - Recovery: a rate or probability of recovery per time step ($\rho$)

- And these are sometimes combined to simplify equations:
  - e.g.: $\beta = \tau \alpha$ to represent the overall infection rate
## SUMMARY of MODELS

<table>
<thead>
<tr>
<th>Transmission system</th>
<th>Rate of change in I = $\frac{\Delta I}{\Delta t}$</th>
<th>Prevalence signature</th>
<th>Assumptions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-infectious process for I</td>
<td>$k$</td>
<td>Constant linear growth</td>
<td>Infinite population of S, infinite D, no contact process</td>
</tr>
<tr>
<td>$I$</td>
<td>$\beta I$</td>
<td>Exponential growth</td>
<td>Infinite population of S, infinite D</td>
</tr>
<tr>
<td>$SI$</td>
<td>$\beta SI$</td>
<td>Logistic growth</td>
<td>Finite population, infinite D</td>
</tr>
<tr>
<td>$SIR$</td>
<td>$(\beta S - \rho)I$</td>
<td>Bell shaped</td>
<td>Finite population, finite D</td>
</tr>
<tr>
<td>$SIS$</td>
<td>$(\beta S - \rho)I$</td>
<td>Potentially cyclic</td>
<td>Finite population, finite D</td>
</tr>
</tbody>
</table>

For “density dependent” transmission, $\beta = \tau \alpha$; for “frequency dependent” transmission $\beta = \tau \alpha / N$

https://parasiteecology.wordpress.com/2013/10/17/density-dependent-vs-frequency-dependent-disease-transmission/
## Poker chips to epidemic modeling terminology

<table>
<thead>
<tr>
<th>Poker chip component</th>
<th>Model component</th>
<th>Model Terminology</th>
</tr>
</thead>
<tbody>
<tr>
<td>Poker chips</td>
<td>Elements</td>
<td>Individuals</td>
</tr>
<tr>
<td>Color</td>
<td>States</td>
<td>Individual disease status</td>
</tr>
<tr>
<td>Bag</td>
<td>Population</td>
<td>Population size (N, or infinite)</td>
</tr>
<tr>
<td>Draw out of bag</td>
<td>Transition</td>
<td>Act (governed by $\alpha$)</td>
</tr>
<tr>
<td>Draw blue and red *</td>
<td>Transition</td>
<td>Discordant partnership (SI)</td>
</tr>
<tr>
<td>Blue exchanged for red</td>
<td></td>
<td>Transmission (governed by $\tau$)</td>
</tr>
<tr>
<td>* Blind draws out of bag</td>
<td>Model assumption</td>
<td>Random mixing</td>
</tr>
<tr>
<td>Red exchanged for white</td>
<td>Transition</td>
<td>Recovery with immunity (governed by recovery rate $\rho$ via disease duration $D$)</td>
</tr>
</tbody>
</table>
Introductions

- Who are we?
- Who are you?
Course Website

http://statnet.github.io/nme/