Network Modeling of Epidemics

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The lesson plan for the week

Day	Content
1	Susceptible-Infected-Recovered/Susceptible models • Intuition and basic properties • Exploring simple SIR/S models in R
2	Cross-sectional network analysis • Exponential Random Graph Models (ERGMs) for networks
3	Dynamic network analysis • Separable Temporal ERGMs (STERGMs) for dynamic nets
4	Simulating disease transmission on dynamic networks • When network dynamics are independent of disease dynamics
5	Simulating disease transmission on dynamic networks • When network dynamics are dependent on disease dynamics
6	Discussion of projects

Intuition building: Poker chip simulation

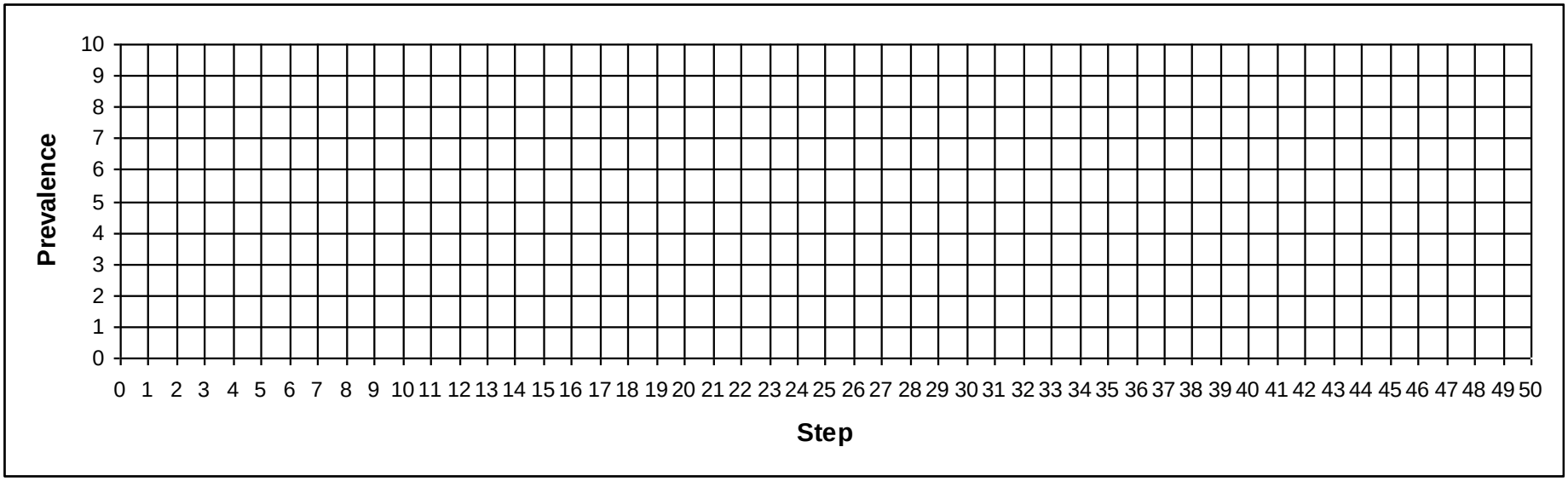
- **Blue chips** = susceptible 
- **Red chips** = infected 
  - White chips = recovered 

We will track the epidemic by hand using a prevalence chart grid.

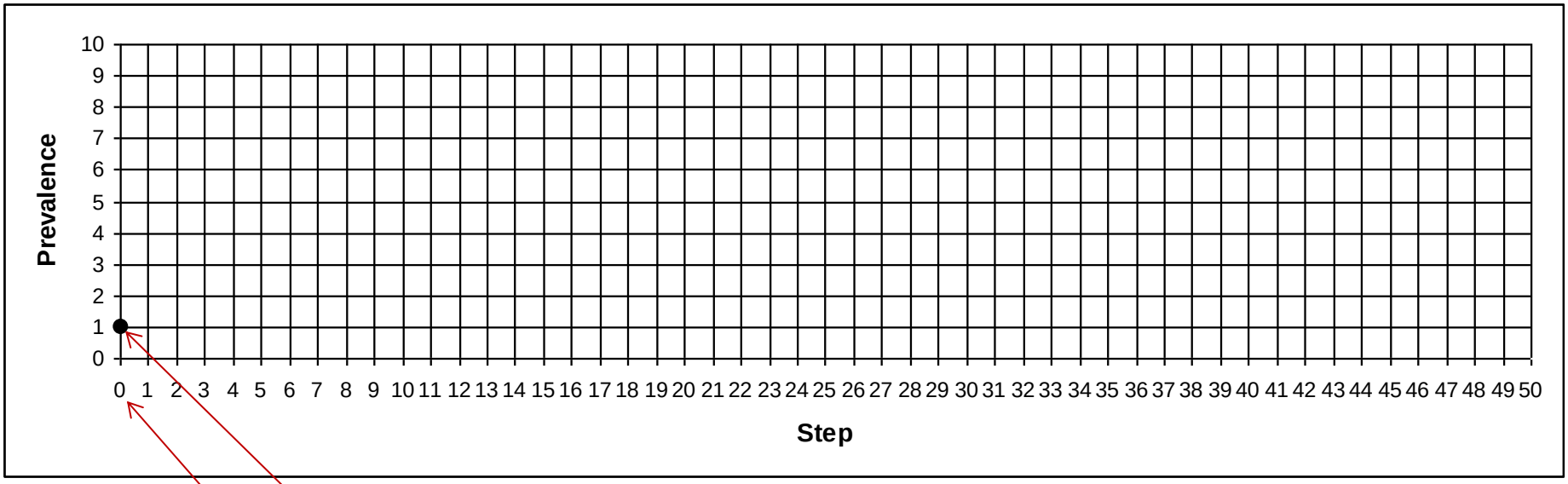
Note:

- 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
  - Some qualitative properties also

Prevalence Worksheet



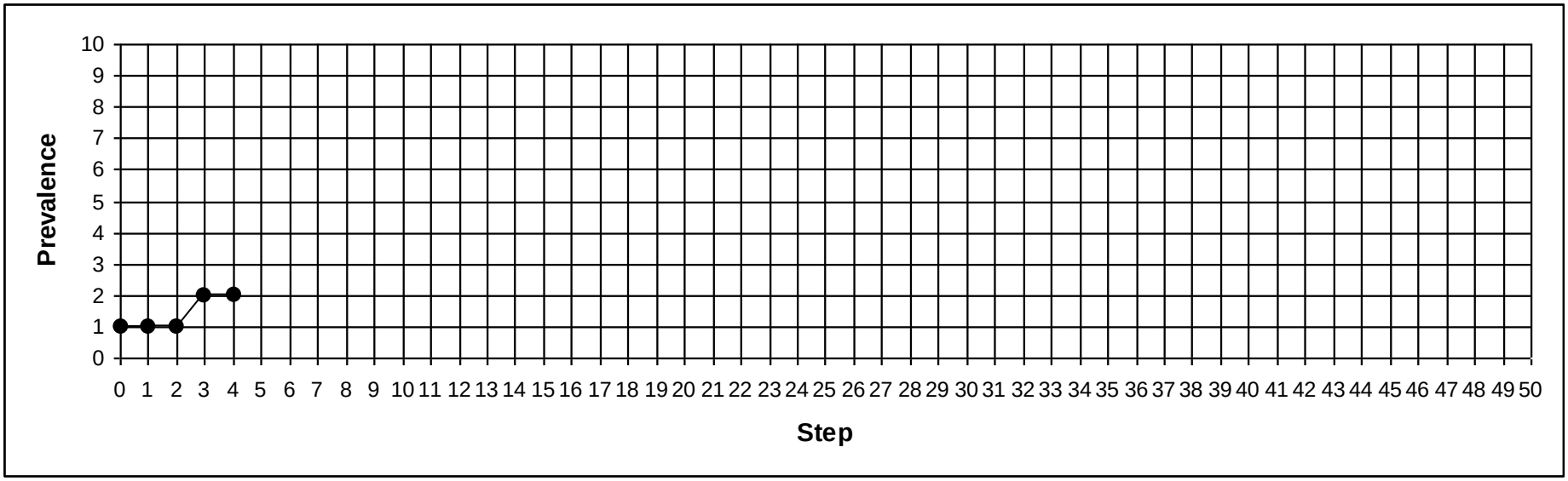
Prevalence Worksheet



We begin with one infected person

At time = 0, the start of the process

Prevalence Worksheet



At each subsequent time point we record the current number of infected persons

To the lab…

Constant growth model

INSTRUCTIONS: Start with 1 **red** chip (**red = I**)

For each round:

1. Add 1 more **red** chip
2. Mark outcome on prevalence tracking worksheet
3. Repeat

Constant growth: Implications

- What does the graph look like?
- What disease might this represent?
- What would change if 3 new people were infected every time step?

Insight 1: Always the same growth rate.

Insight 2: The slope of the line equals the number of new infections every day

Insight 3: The number of new infections does not depend on the number currently infected

Constant growth: Implications

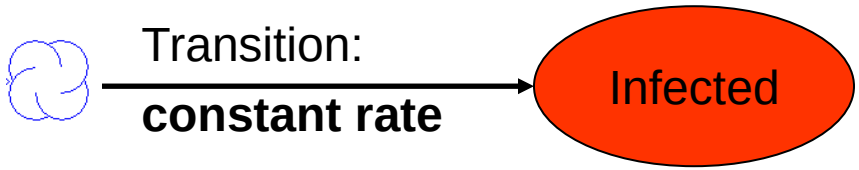
This example is not an infectious process – more like chronic disease

The model assumes there is an infinite susceptible population

(ie. Assume a “hidden” bag, with an infinite number of **blue** susceptibles becoming **red** infecteds)

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

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



I: Infected model (proportional growth)

INSTRUCTIONS: Start with 1 **red** chip

For each round:

1. Add 1 more **red** chip *for each red chip already on the table*
2. Mark outcome on prevalence tracking worksheet
3. Repeat

I model: Implications

- Each red chip infects 1 new case at each time step
- What does the graph look like?
- What disease might this represent?
- Is this realistic? What is missing?

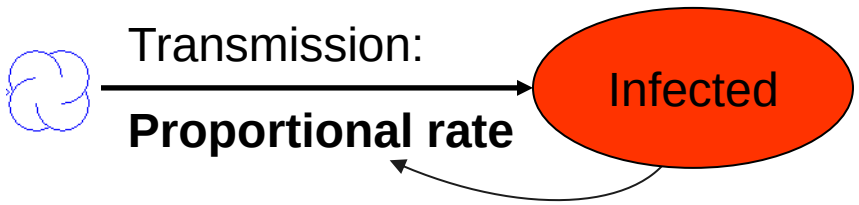
Insight 1: The number of infecteds grows exponentially.

Insight 2: The population size is infinite, so the number of infected is unbounded

I model: Implications

The simplest true infection process

- Still only one state (infected)
- An implicit state of **blue** susceptibles of infinite size
- Still only one transition,
  - but now the rate depends on the number currently infected



SI: Susceptible-Infected model

INSTRUCTIONS: Now we will use the bag (it represents 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. **Mark outcome on tracking sheet**

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

SI model: Implications

- What does the graph look like?
- Why do each of your graphs look different?
- What is the same and different across all of your runs?
- Will everyone eventually become infected?
- How long until everyone is infected?

SI model

Every draw has three possible outcomes:

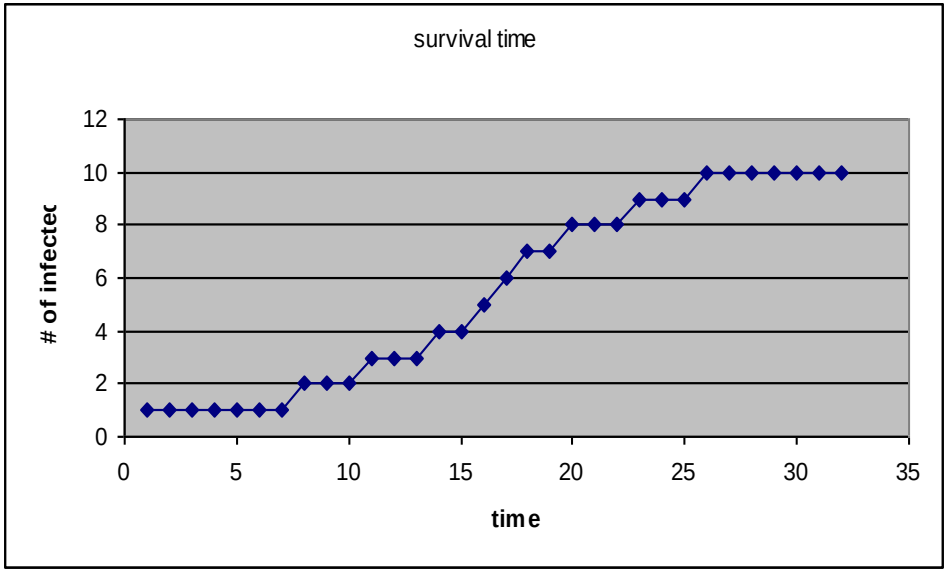
SS: concordant negative

SI: discordant

II: concordant positive

The probability of each outcome changes as the process evolves.

1. SS	9. SS	17. SI	25. II
2. SS	10. SS	18. SI	26. SI
3. SS	11. SI	19. II	27. II
4. SS	12. SS	20. SI	28. II
5. SS	13. SS	21. SS	29. II
6. SS	14. SI	22. II	30. II
7. SS	15. II	23. SI	31. II
8. SI	16. SI	24. II	32. II



SI model: Implications

- What does the graph look like?
- Why do each of your graphs look different?
- What is the same and different across all of your runs?
- Will everyone eventually become infected?
- How long until everyone is infected?

Insight 1: Everyone will eventually become infected

Insight 2: The rate of infection depends on the proportion of both infecteds and susceptibles. Therefore, the rate of infection starts low, reaches its max halfway through, then decreases again

Insight 3: The characteristic time signature for prevalence in a SI model is a logistic curve.

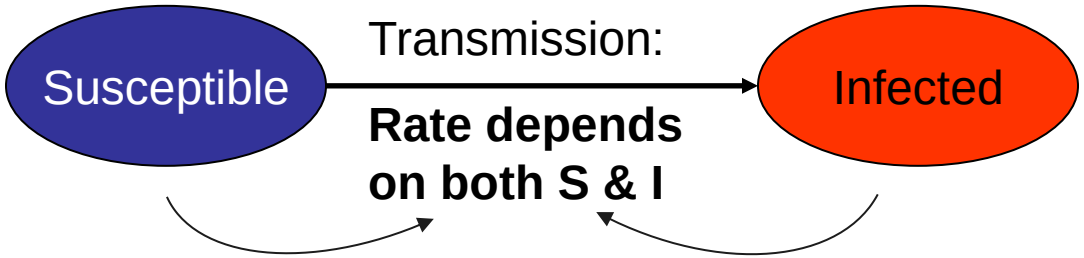
What does this model assume about the duration of infection?

SI model: Implications

Two states: **susceptible** and **infected**

One transition: transmission process

Now, we have **a finite population**, with total size **N** = **S** + **I**



Introductions

- Who we are
- Who are you?

Objectives for the 1 week course

- Gain intuition about population dynamics of infectious disease transmission, focusing on HIV
  - Strengths and limitations of the different modeling frameworks
- Understand the basic principles and methods of network analysis relevant to infectious disease epidemiology
  - Classical network analysis
  - Modern (statistical) network analysis with ERGMs
  - 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**

Objectives for today

Get an intuitive sense of epidemic modeling, including:

1. Elements of the transmission system
2. Signature dynamics of classic systems: the SIR/S family
3. The roles that chance can play
4. Key “qualitative properties” of a transmission system

Learn to explore simple SIR/S models in R using the EpiModel package, including:

1. Deterministic, compartmental models (ODEs)
2. Stochastic, individual-based models

Models have three basic components

- **Elements** – “actors” in the model
- **States** – attributes of system elements
- **Transitions** – rates of movement between states

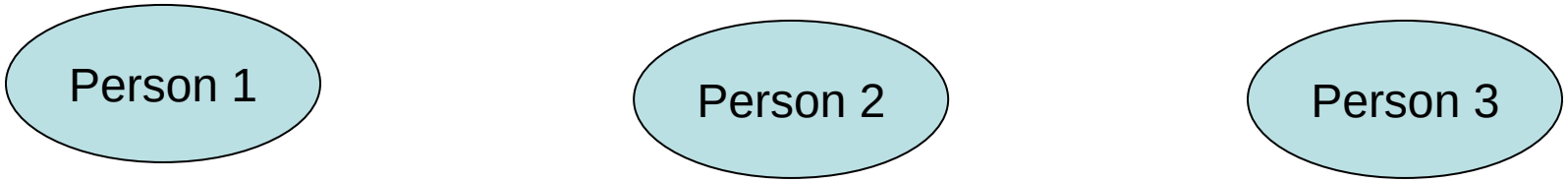
All models, simple and complex, are built on these same building blocks

Model component: Elements

- Elements can be:
  - Persons
  - Animals
  - Pathogens (microparasites, macroparasites)
  - Environmental reservoirs (water, soil)
  - Vectors (e.g., mosquitoes)

Example: Measles transmission requires people

We will not be tracking the measles virus elements explicitly – just the infection status of the persons



Model component: States

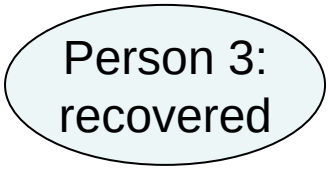
- States – attributes of elements. For example:
  - Person/animal states
    - Infection status (Susceptible, Infected, Recovered…)
    - Demographic characteristics (male, female, …)
  - Pathogen states
    - life cycle stage (e.g., larvae, reproducing adults, …)

Example: A simple measles model will have three person states:

susceptible (S)

infected (I)

recovered w/ immunity (R)



Model components: Transitions

- Transitions – movement between states
  - **Deterministic**: fixed *rate* of transition between states.
    - Uses a population mean rate to govern process of movement
  - **Stochastic**: random *probability* that an element transitions between states.
    - Uses a full probability distribution of rates to govern the process of movement.

Example: The simple measles model has two transitions:

becoming infected and recovering from infection

Transmission: the heart of system

Examples of transmission types:

STD/HIV: direct body fluid contact (sex, needles, MTC)

Measles, Influenza: respiratory, air-borne

Diarrheal diseases: fecal-oral

Malaria: vector-borne (mosquitoes)

Schistosomiasis: water and vector-borne, via snails and nematodes

Cholera: water and food-borne

Direct Transmission Parameters

Susceptible ⟶ **Infected**

A typical system requires:

I	**Infected person**
S	**Susceptible person**
α	**An act of potential transmission between them**
τ	**Transmission given act**

acts and transmission are sometimes combined into a single parameter

$\beta = \alpha\,\tau$ **"Force of infection"**

Direct Transmission Parameters

Why "act" and not "contact"? Why α and not c? Why τ and not β?

- "Contact" most often means the specific act that may cause transmission
- e.g. in HIV, a sexual act
- In this case: "contact rate" c means the frequency of sexual acts

  the "probability of transmission" parameter (often but not always called β) refers to prob. per act
- Such models implicitly assume that each act occurs with a different person
- usually a problematic assumption
- "Contact" is sometimes used to refer to the partnership in which acts occur
- In this case: c can be interpreted as "partner change rate",

  the "prob. of transmission" parameter (often but not always called β) refers to prob. per partnership

Direct Transmission Parameters

Why "act" and not "contact"? Why α and not c? Why τ and not β?

- The two uses have created a fair amount of confusion and ambiguity
- We wish to avoid this by being explicit about "partnerships" and "acts"
- We will use α for the "act rate"

  τ for the probability of transmission per act
- As we move into modeling partnerships, we will adopt a network approach
- There, we will discuss partnerships and acts, but use a larger set of terminology and notation to explore the broader array of relational configurations of interest

Preview of models for today:

States	Rate of change in I: $\frac{\Delta I}{\Delta t}$ =	Model
I	k *(Non-infectious process)*	Constant growth
I	βI	Proportional growth
SI	βSI	Susceptible-Infected
SIR	βSI – ρI	Susceptible-Infected-Recovered
SIS	βSI – ρI	Susceptible-Infected-Susceptible

β = "force of infection" for models with infinite population, $\beta = \tau\alpha$
for models with finite population $\beta = \tau\alpha/N$

These models have different states and rates, and therefore different properties.

Translating poker chips to epidemic modeling terminology

Poker chip component	Model component	Model Terminology
Poker chips	Elements	Individuals
Color	States	Individual disease status
Bag	Population	Population size (N, or infinite)
Draw out of bag	Transition process	Act (govered by α)
Draw blue and red *		Discordant act (SI)
Blue exchanged for red		Disease transmission given an act (goverened by τ)
* Blind draws out of bag	Model assumption	Random mixing
Red exchanged for white	Transition process	Recovery with immunity (governed by recovery rate ρ and/or disease duration D)

Recovery

Let us consider other possible *states* and *transitions* in the system

- **Recovery with immunity** (e.g. measles)

  This adds a new transition and a new state to the system: ***SIR***

- **Recovery with return to susceptibility** (e.g. common cold)

  This adds a new transition to the system: ***SIS***

Both models have a new transition rate

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

- Now, we need to keep track of time for I chips

DURATION TIMER

Day Case number	0	1	2	3	4	5	6	7	8	9	10 Change state to R
1	X	X	X	X	X	X	X	X	X	X	X
2	X	X	X	X	X	X	X	X			
3											
4											
5											
6											
7											
8											
9											
10											

SIR: Recovery with Immunity Example

INSTRUCTIONS: Prepare a bag with 1 red and 9 blue chips, put 10 white chips on the side.

For each round: 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
     - Mark duration sheet on new row for day 0

2. **Update duration worksheet for any 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. **Mark outcome on prevalence worksheet**

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

SIR: Implications (1)

Insight 1: With recovery w/ immunity in a closed finite population, infection always dies out.

final prevalence of ***I*** is always 0.

Insight 2: Time to extinction of ***I*** depends on N, α and D (qualitative property)

range of time to extinction = { D to D*N }

Insight 3: The time series signatures are characteristic of SIR models

I time series is bell-shaped

S & ***R*** time series are monotonic declining & increasing respectively.

Insight 4: Final prevalence of ***S*** and ***R*** (qualitative property)

depends on cumulative number of infections before extinction.

range(S,R) = { (0,N) to (N-1,1) }

SIR: Implications (2)

Insight 5: This is the first time a *threshold* for spread appears

The threshold is a **qualitative property** of the transmission system

If the first case does not transmit, there is no epidemic

R_0 = Expected number of secondary infections from the first case.

$$= \frac{\text{P(transmission)}}{\text{act}} \cdot \frac{\text{acts}}{\text{time}} \cdot \text{time}$$

$$= \tau \times \alpha \times D$$

$$= 1 \times 0.2 \times 10$$

in our poker chip example

so $R_0 = 2$

SIS: Recovery with Susceptibility (on your own)

INSTRUCTIONS: Prepare a bag with 9 blue and 1 red chips

For each round: S=blue, I=red

1. **Pick two chips**
   - If the chips are the same color, no infection occurs.
     - Go to (2)
   - If the chips are different colors, infection occurs
     - Replace blue chip with red chip and return to bag
     - Mark duration sheet on new row for day 0
2. **Mark outcome on prevalence worksheet**
3. **Update duration worksheet for any pre-existing infections**
   - Increment each active row by 1 day
   - If any durations are at {CHANGE STATE}, find a red chip and replace it with a blue chip
4. **Are there any more red chips in the bag?**
   - YES: Return to (1)
   - NO: Stop

SIS Recovery: Implications

- **Insight 1:** With recovery and a closed (finite) population, infection will always die out, given a long enough time.

  Final prevalence of ***I*** is always 0

  Final prevalence of ***S*** is always N.

- **Insight 2:** Time series signatures are characteristic of SIS models

  both ***S*** & ***I*** time series may be cyclical.

- **Insight 3:** Time to extinction of ***I***

  depends on α, D and N. Can be effectively infinite for large N

- **Insight 4**: This model also has a *threshold* for spread
  - $R_0 = \tau\alpha D$, as before

SUMMARY of MODELS

Transmission system	Rate of change in I * $\frac{\Delta I}{\Delta t}$	Prevalence time series signature	Assumptions
Non-infectious process for I	K	Constant linear growth	Infinite population of S, infinite D, no contact process
I	βI	Exponential growth	Infinite population of S, infinite D
SI	βSI	Logistic growth	Finite population, infinite D
SIR	βSI – ρI	Growth and decline	Finite population, finite D
SIS	βSI – ρI	Potentially cyclic growth and decline	Finite population, finite D

* For models with infinite population, $\beta = \tau\alpha$; for models with finite population $\beta = \tau\alpha/N$