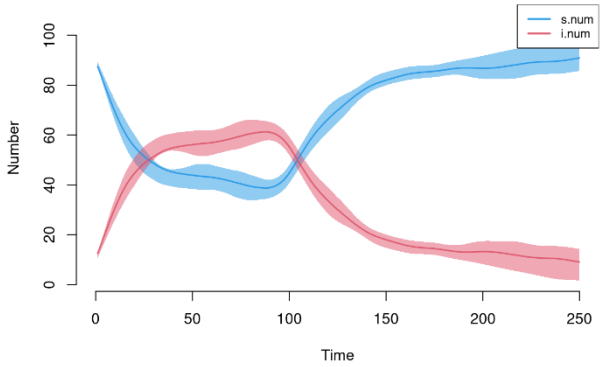

WELCOME!

NETWORK MODELING FOR EPIDEMICS

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Objectives for the course

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

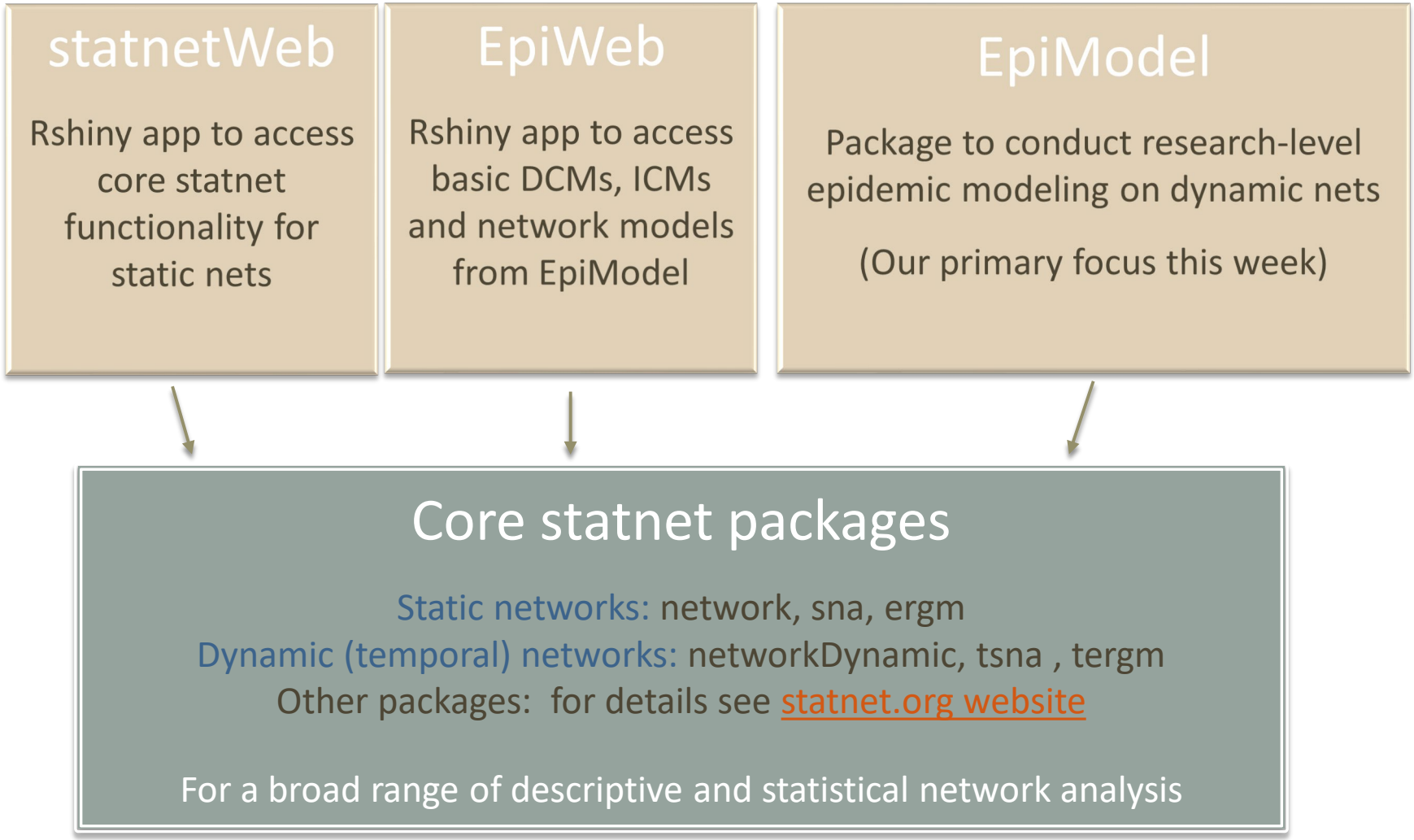
Develop the knowledge and software skills to run your own simple network transmission models, using R and the EpiModel package

Begin to learn how to extend EpiModel code for your own research applications

Lesson plan

Day	Module	Content
W	1	Intro, terms & concepts
	2	Statistical models for networks: theory
T	3	Statistical models for networks: practice
	4	Basic EpiModel in closed populations
	5	EpiModel: working with nodal attributes
	6	Data and network model parameterization
F	7	EpiModel in open populations (demography) pt. 1
	8	EpiModel in open populations (demography) pt. 2; visualization
	9	Extending EpiModel
	10	Discussion of projects; next steps; future resources

Software (all based in R)



Show of hands - who has experience:

- With epidemic modeling?
  - Using compartmental models? *
  - Using stochastic agent-based models? *
  - Using (full-fledged) network models? *
  - Using EpiModel?

What do we mean by these terms? We'll elaborate in a bit. For now just give your best answer.

Show of hands - who has experience:

- With R?

- With social network analysis?
  - Using descriptive methods?
  - Using statistical inference methods?
  - For static networks?
  - For dynamic networks?
  - Using the statnet suite of packages?

Whose research interests relate to:

- Human pathogens?
  - HIV?
  - Other sexually transmitted infection(s)?
  - Respiratory /airborne pathogen(s)?
  - Vector-borne pathogen(s)? (mosquitos, etc.)
  - Some other human pathogen?
- Animal pathogens?
- Diffusion of an intervention/behavior/information?
- Diffusion of something else entirely?

Background to epidemic modeling (1)

A lightning- fast overview

All* models, regardless of type, will contain the following ideas:

1. Time as a dimension over which the model unfolds
2. At least one type of element (aka agent; e.g. human beings)…
   - … of which there is a population…
   - … whose members are capable of being "infected"…
   - … and also capable of infecting others
3. At least one entity capable of doing the "infecting" (e.g. SARS-CoV2)
4. Some type of contact process by which the infection occurs
5. A record of whether and when the elements are infected

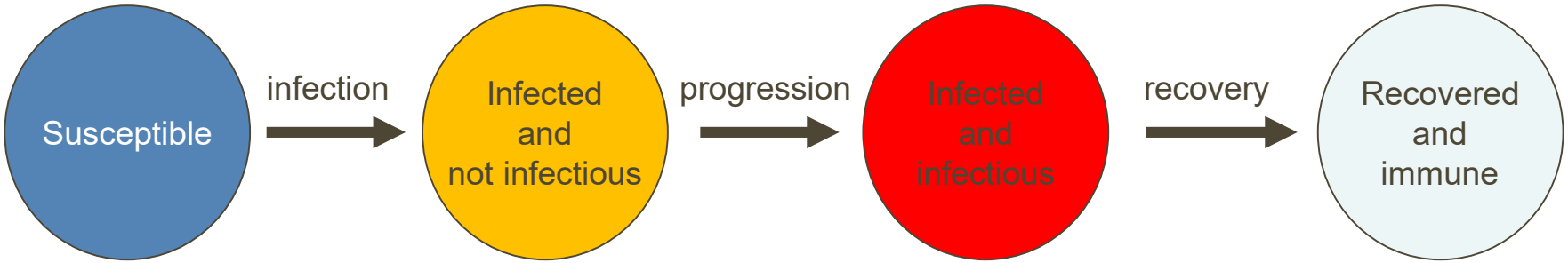
** pretty much; there are always weird exceptions to every rule*

Background to epidemic modeling (2)

A lightning- fast overview

Some models have additional infection statuses, e.g.

- recovered and immune
- infected but not yet infectious
- perhaps stages with different levels of infectiousness



Background to epidemic modeling (3)

A lightning- fast overview

Most but the very simplest of toy models will have:

1. Attributes of the elements (other than infection status), e.g.
   - demographic (sex, age….)
   - behavioral (level of sociality; occupation….)
   - clinical (tested or not; on treatment or not…)
   - geospatial (community; coordinates….)
2. Processes by which at least some of those attributes can change

Many consider attributes for the infectious agent as well, e.g.

- strain
- presence of specific mutations

Background to epidemic modeling (4)

A lightning- fast overview

Fundamental summary measure: R_0

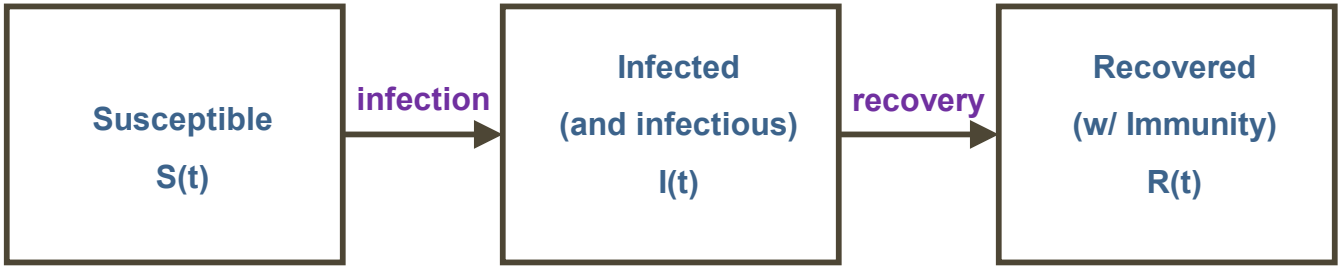
Captures the epidemic "persistence threshold" and velocity of transmission

Definition: The expected number of secondary infections generated by the first infected case in a population of susceptibles

Value of R_0	Implication
< 1	The first infected individual will on average infect < 1 person total. Transmission is too low for epidemic persistence
> 1	The first infected individual will on average infect >1 person total. Epidemic will typically grow and persist
= 1	Right on the threshold between persistence and extinction. Epidemic will typically just putter along

Deterministic compartmental modeling (DCMs)

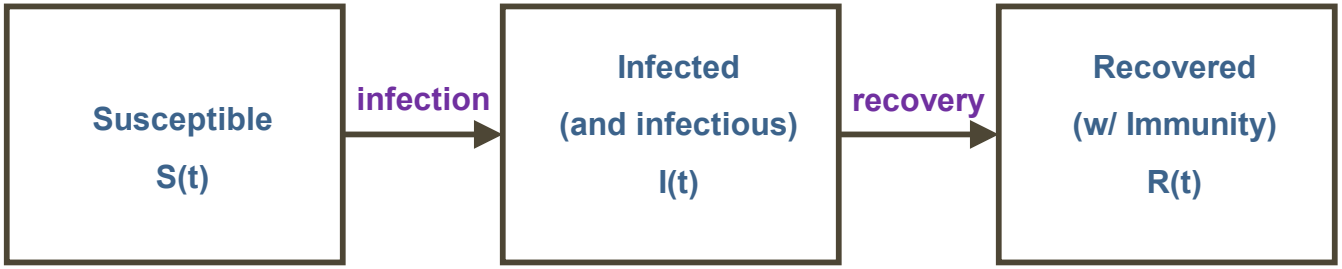
A lightning- fast overview



- Only the aggregate count in each state ("compartment") is represented, not individual persons
  - S(t) = # susceptible, etc.
  - Within each compartment, units are homogeneous
- Transitions ("flows") represent the aggregate count that moves from one compartment to another at any time point
  - Flows are represented by differential equations (or difference equations if in discrete time)

Deterministic compartmental modeling (DCMs)

A lightning- fast overview



Change in # of susceptible persons per time unit

$$\frac{dS}{dt} = -\beta\, SI/N$$

Infection flow

Change in # of infected persons per time unit

$$\frac{dI}{dt} = \beta\, SI/N - \rho I$$

Recovery flow

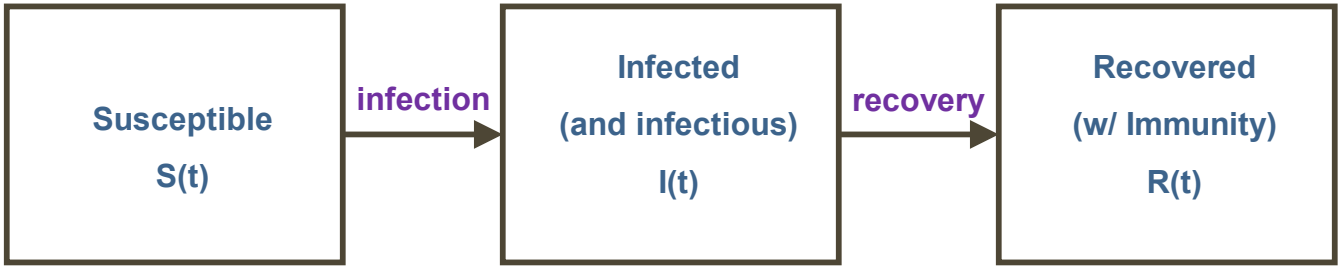
Change in # of recovered persons per time unit

$$\frac{dR}{dt} = \rho I$$

- β and ρ are model parameters
- Q: Where are the contact events?
- A: embedded in the infection flow

Deterministic compartmental modeling (DCMs)

A lightning- fast overview



Common notation for infections $\beta SI/N$ where β is called the "force of infection"

Can be disaggregated as: $\tau c SI/N$ where c = "contact rate"
τ = "transm. prob"

So: S susceptibles each have c contacts per unit time
I/N of the contacts are with infected
each susceptible-infected contact has probability τ of transmitting

Deterministic compartmental models

- Compartmental models are usually deterministic – each run gives the same result
- Measures = predicted counts (and represent the means of an equivalent stochastic process over an infinite number of runs)
- Compartments and flows can represent fractional persons

DCM strengths

- Familiar to many (and familiarity breeds comfort)
- Have a long body of literature identifying properties of different classes of models
- Simple models have simple closed form expressions for R_0
  - Intuitively, the number of secondary infections for the first case is:

    Contact rate/timestep * duration infected * transmission prob/contact

    c D τ
  - So for a simple SIR DCM: $R_0 = cD\tau$

DCM weaknesses

- Do not show the stochastic variation in a system
  - Stochastic CMs do exist, but only solve this one weakness
- Adding heterogeneity blows up quickly
  - Requires new compartments
    - e.g. adding 2 sexes means going from 3 compartments to 6: SF, IF, RF, SM, IM, RM
    - What if we wanted to add in 4 racial/ethnic groups? 5 ages? 5 categories of viral load? Testing? Treatment? Circumcision? Etc.
  - And if heterogeneity isn't in discrete categories?

DCM weaknesses

- Representing complex partnership network patterns is hard (or impossible, depending who you ask)
  - Non-random mixing on an attribute can be added into the incidence term easily enough
    - Raises additional questions in open populations where group sizes can change
  - But other partnership patterns are harder
    - Like a tendency to only have one partner at a time?
    - To be more (or less) less likely to have contact with your partner's partner?
    - Remember that compartments only considered people in the aggregate; individuals are not uniquely identified
- And there is no general method for jointly estimating the parameters of a system of partnerships like this

Individual-based models

- Represent each individual member of the population explicitly
- This might take the form of a data frame (in R speak)
  - Each row is an individual
  - Each column is an attribute
- Use code instead of equations to represent the relevant dynamic processes

IBM pseudocode

```
# Initial conditions
    # create a data.frame (nrow = # of agents, ncols = # of attributes)
    # assign infection status (S, I, R) as one attribute
    # assign all other attributes
# Simulate epidemic
for (at = 1:num.timesteps) {
     # infection
         # draw the number of contacts for that step
         # draw 1 pair of agents for each contact
         # filter to just the discordant SI pairs
         # flip coin for each pair to determine if transmission
         # do bookkeeping for new infections
     # recovery
         # identify infected elements
         # flip coin for each case to determine recovery
         # do bookkeeping for recoveries
      # update other attributes
         # exact code depends on the nature of the attribute
}
# process output
```

these can be made to depend on the attributes of the agents

IBM strengths

- Show the stochastic variability in these systems
- Can handle multiple forms of heterogeneity with relative ease
  - With individuals identified, they just get labeled
- Simple models have some simple closed form solutions for R_0
  - For examples, see this article

IBM weaknesses

- Representing heterogeneity *in the contact process* that creates the partnership network is still hard
  - Some example include queuing processes and "stub matching"
  - But these are not very realistic representations

- And here, too, there is no general method for jointly estimating the parameters of this complex process from data.

Final note on terminology

- Contacts vs. acts: a key distinction
  - E.g. think of sexual activity - when we say "# of contacts per year"
    - Does it mean number of sex acts?
    - Or numbers of different partners?

- From here on out, we will use the terms "acts" and "partners"
- This distinction matters for disease dynamics when there are repeated acts with the same person