DAY 1:
INDIVIDUAL MODELS

NME WORKSHOP

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Model frameworks

In the epidemic modeling literature, we often see two poles:

- Deterministic compartmental models
- Stochastic network models

But there a continuum between these two poles.

Let us tease these apart by considering

- Deterministic compartmental models (done)
- Stochastic compartmental models (brief discussion)
- Stochastic individual-based models (poker-chips, what you just saw, this session)
- Stochastic network models (rest of the week)

Deterministic vs. stochastic models

- To begin: how does stochasticity change a compartmental model?
  - Always via the transitions rate parameters or "flows" in the model

- Consider a simple proportional growth model
  - States: only I is tracked; population has an infinite number of susceptibles
  - Transition rate parameters: only β, the average growth rate of infection

- As a compartmental model, this would be:

$$i(t+1) = i(t) + \beta i(t)$$

which we can also write as:

$$incidence(t) = \beta i(t) \qquad \text{where: } incidence(t) = i(t+1) - i(t)$$

Deterministic vs. stochastic models

	Deterministic	Stochastic
Incidence	$incidence(t) = \beta i(t)$	$P(incidence(t) = k \mid \beta, i(t))$
Incidence is	determined by a rate β	drawn from a probability distribution that depends on β

Deterministic vs. stochastic models

- What does $P(incidence(t) = k \mid \beta, i(t))$ equal?
  - Depends on the model you choose for P(●)
  - P(●) is a probability distribution
  - Probability of what? That the count of new infections = k at time *t*
- So what kind of distributions are appropriate?
  - proper probability distributions (sum across *k* must equal 1)
  - that are discrete
  - on non-negative integers only
- Can you think of an appropriate distribution here?

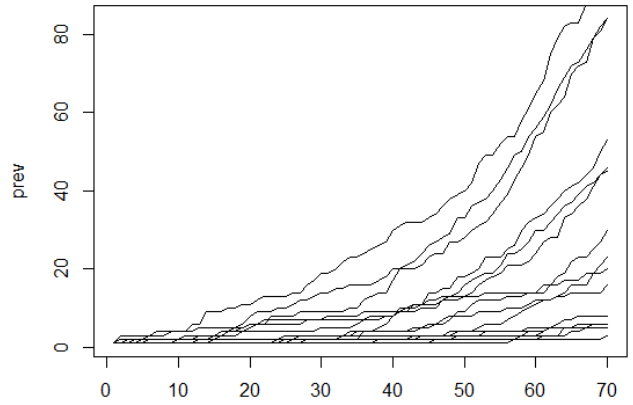
Deterministic vs. stochastic models

- the Poisson distribution
  - Used to model the number of events per time unit (or spatial unit)
  - Arises when the events occur independently with equal probability
  - Defined by one parameter, λ , which is both the mean and variance
  - Range: 0, 1, 2, … (the non-negative integers)
  - The *probability mass function* (PMF) is given by:

$$P(X = k) = \frac{\lambda\, e^{-\lambda}}{k!} \qquad \text{denoted: } Poisson(\lambda)$$

  - What would it look like if we drew the incident infections at each time step from a Poisson distribution with mean $\lambda = \beta i(t)$?

Deterministic vs. stochastic models



Each line represents the epidemic trajectory under a different value of β,

with $incidence(t)$ a stochastic draw from a Poisson($\lambda = \beta i(t)$) distribution

- This approach of drawing the incidence from a distribution at each time step is one way to add stochasticity to a compartmental model
  - Provides a means to quantify the potential variation in outcomes
- But note that we are still only counting aggregates – there are no explicitly represented individuals
  - This limits our ability to represent the relevant aspects of individual heterogeneity

Individual models

- Individual elements are represented explicitly in this model
  - poker chips, EpiModel lab
- Mechanics are different from the very outset
  - While the two approaches may look similar for a simple SI model, the divergence quickly grows as more as more complexity is added
  - Individual models allow for much more fine-grained heterogeneity, and many more forms of it, in a tractable way

Individual SIR model: basic structure

```
# create individuals
# assign status

for (at=1:num.timesteps) {
     # infection
         # calculate number of acts
         # determine who has an act with whom (ie construct "edgelist")
         # limit edgelist to discordant pairs
         # determine infections
         # do bookkeeping for infections
     # recovery
         # identify infecteds
         # determine recoveries
         # do bookkeeping for recoveries
}

# process output
```

Individual models: setup

- create individuals

```
ids <- 1:num                          # num = the initial # of individuals
```

- assign status

```
status <- rep("s", num)               # init.inum = the initial # of infecteds
status[sample(ids,
          size = init.inum)] <- "i"
```

```
> status
[1] "s" "s" "s" "i" "s" "s" "s" "i" "i" "i" "i" "s" "s" "i" "s" "s" "s"
```

Individual models: Infection process

- Step 1: calculate number of acts

```
# n Acts per Time Step = fixed act rate * n/2
acts <- round(act.rate * num[at - 1] / 2)
```

Individual models : Infection process

- Step 2: determine who has an act with whom

```
# Make edgelist of partnerships by ID number
el <- t(replicate(acts, sample(1:num, 2)))
```

```
     [,1] [,2]
[1,]   80    9
[2,]    9   59
[3,]    5   66
[4,]    4   84
```

Individual models: Infection process

- Step 3: limit edge list to discordant pairs

```
# look up the status of each member of the pair
discordant <- (status[el[, 1]] == "i" & status[el[, 2]] == "s") |
         (status[el[, 1]] == "s" & status[el[, 2]] == "i")
[1]  TRUE  TRUE  TRUE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE

# create a "discordant edgelist"
del <- el[discordant == TRUE, ]
     [,1] [,2]
[1,]   80    9
[2,]    9   59
[3,]    5   66
[4,]   29   38
```

Individual models: Infection process

- Step 4: determine infections

```
# Infection is a Bernoulli draw for each discordant pair
infections <- rbinom(nrow(del), 1, tprob)

> infections
[1] 1 0 0 1
```

Individual models: Infection process

- Step 5: bookkeeping for infections

```
# Limit discordant edge list to pairs with incident infection
del <- del[infections == TRUE, ]

# Look up newly infected ID in each pair
susIds <- ifelse(status[del[, 1]] == "s", del[, 1], del[, 2])
newInfIds <- susIds[infections == 1]

# Update individual-level status attribute
status[newInfIds] <- "i"
```

Individual models: Recovery process

```
# Identify infected (persons eligible to recover)
idsElig <- which(active == 1 & status == "i")
nElig <- length(idsElig)

# Draw random numbers to determine recoveries
vecRecov <- which(rbinom(nElig, 1, rec.rate) == 1)

# Do bookkeeping
if (length(vecRecov) > 0) {
    idsRecov <- idsElig[vecRecov]
    nRecov <- length(idsRecov)
    status[idsRecov] <- "r"
}
```

Individual models

- Process output

```
# Calculate summary statistics
prevalence <- sum(status == "i")
incidence <- length(newInfIds)
```

Individual SIR model: basic structure

```
# create individuals
# assign status

for (at=1:num.timesteps) {
     # infection
         # calculate number of acts
         # determine who has an act with whom (ie construct "edgelist")
         # limit edgelist to discordant pairs
         # determine infections
         # do bookkeeping for infections
     # recovery
         # identify infecteds
         # determine recoveries
         # do bookkeeping for recoveries
}

# process output
```

Code summary

```
ids <- 1:num                                                    # initial # of individuals
status <- rep("s", num)
status[sample(ids,  size = init.inum)] <- "i"                   # initial # of infecteds

acts <- round(act.rate * num[at - 1] / 2)                       # n Acts per Time Step
el <- t(replicate(acts, sample(1:num, 2)))                     # Edgelist of partnerships by ID
discordant <- (status[el[, 1]] == "i" & status[el[, 2]] == "s") |
         (status[el[, 1]] == "s" & status[el[, 2]] == "i")      # Status lookup
del <- el[discordant == TRUE, ]                                 # Find "discordant edgelist"
infections <- rbinom(nrow(del), 1, tprob)                       # Infection is a Bernoulli draw
del <- del[infections == TRUE, ]                                # Incident pairs
susIds <- ifelse(status[del[, 1]] == "s", del[, 1], del[, 2])   # Inci ID lookup
newInfIds <- susIds[infections == 1]                            # Update individual infection status
status[newInfIds] <- "i"
idsElig <- which(active == 1 & status == "i")
nElig <- length(idsElig)

vecRecov <- which(rbinom(nElig, 1, rec.rate) == 1)              # Recovery is a Bernoulli draw
if (length(vecRecov) > 0) {                                     # Update individual recovery status
    idsRecov <- idsElig[vecRecov]
    nRecov <- length(idsRecov)
    status[idsRecov] <- "r"
}
prevalence <- sum(status == "i")                                # Calculate summary statistics
incidence <- length(newInfIds)
```

Individual models: *Revisiting partnerships*

- Step 2: determine who has an act with whom

```
# Make edgelist of partnerships by ID number
el <- t(replicate(acts, sample(1:num, 2)))
```

```
     [,1] [,2]
[1,]   80    9
[2,]    9   59
[3,]    5   66
[4,]    4   84
```

Individual models

- Was there relational persistence (multiple acts with the same person)?
  - No. How would you add this?
- Were there an constraints on the # of partners per person per time step?
  - No. How would you add this?
- How did we decide who had an act with whom?
  - Purely randomly.
- What if you wanted to add more structure to that process here, in a way that matched observed data. E.g.:
  - Assortative mixing
  - Differential partnership formation rates by attribute or by individual
  - A monogamy bias
  - A tendency to form triangles
  - ***All of these at the same time*** ***NETWORK MODELS!***

Session summary

- One can add stochastic transitions to compartmental models
  - This buys you some quantification of the uncertainty in outcome for that model, but not much else
- Individual models allow one to better represent heterogeneities among elements/actors in the model
  - But control over their relational structure is quite limited
- Network models are needed to explicitly represent systematic patterns in pair formation and dissolution
  - And it is important that these tools be data driven, hence statistical.