Modelling problem

We are interested in modelling the 1918 influenza pandemic, specifically what its impact may have been on Greater London at the time. It is estimated that the average person infected will have been infectious from 2 days after exposure, until 6 days after exposure. The basic reproduction number, R_0, was estimated at around 2.4. Individuals who recover have long-lasting immunity.

What is an appropriate model structure?

SEIR

Draw the model structure?

What are the key parameters (by name/symbol)?

What are the key parameters (by value)?

Initial conditions?

δ = 0.5 days^{-1}

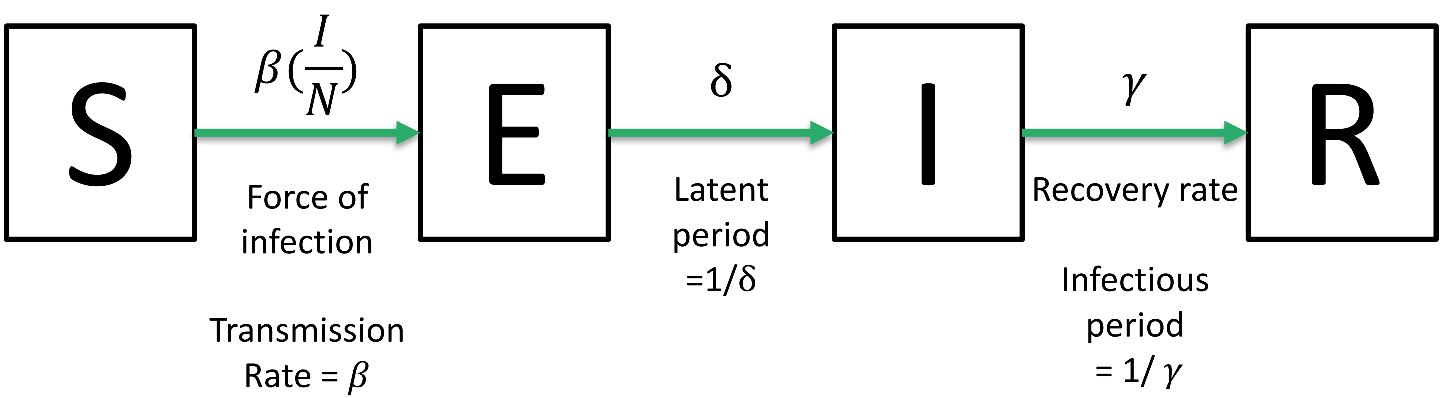
γ = 0.25 days^{-1}

$R_0 = \beta(1/\gamma)$

$\beta = R_0\gamma = 2.4 \times 0.25$ days^{-1}

$\beta = 0.6$ days^{-1}

$N = 7.3$ million



Metapopulations with ODEs

Modern Techniques in Modelling

LONDON SCHOOL of HYGIENE & TROPICAL MEDICINE

Recap

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Previously: ODE models in R

- We defined a set of ODEs
- Then used `deSolve` to simulate the model output

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta S I / N$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta S I / N - \gamma I$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I$$

Example code

```
SIR_model <- function(times, state, parms){
  ## Define variables
  S <- state["S"]
  I <- state["I"]
  R <- state["R"]
  N <- S + I + R
  # Extract parameters
  beta <- parms["beta"]
  gamma <- parms["gamma"]
  # Define differential equations
  dS <- - (beta * S * I) / N
  dI <- (beta * S * I) / N - gamma * I
  dR <- gamma * I
  res <- list(c(dS, dI, dR))
  return(res)
}
```

Metapopulations

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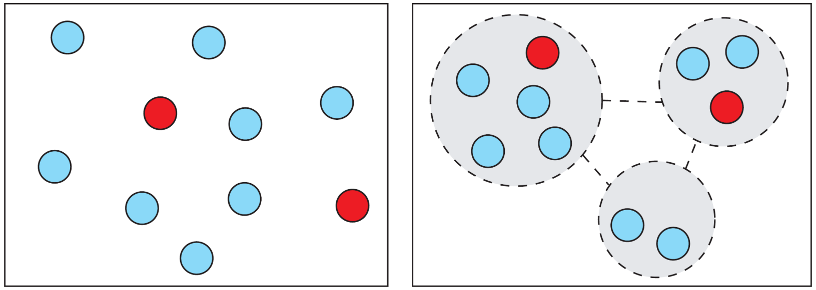
Non-random mixing

- So far we've assumed everyone mixes together randomly
- In reality, people may group together in different locations / settings / groups
- If we're interested in heterogeneity, we need to model multiple populations ('metapopulations')



Random mixing vs metapopulations

Metapopulation model

- Let's consider two linked populations.
- This means expanding our SIR model:

$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = -\beta S_1 I_1/N_1$$

$$\frac{\mathrm{d}I_1}{\mathrm{d}t} = \beta S_1 I_1/N_1 - \gamma I_1$$

$$\frac{\mathrm{d}R_1}{\mathrm{d}t} = \gamma I_1$$

$$\frac{\mathrm{d}S_2}{\mathrm{d}t} = -\beta S_2 I_2/N_2$$

$$\frac{\mathrm{d}I_2}{\mathrm{d}t} = \beta S_2 I_2/N_2 - \gamma I_2$$

$$\frac{\mathrm{d}R_2}{\mathrm{d}t} = \gamma I_2$$

Connecting the populations

- Susceptibles in population 1 can have contact with infectives in population 1 and population 2.
- But may contact population 2 at a different (lower?) rate:

$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = -S_1\left[\overbrace{\beta I_1/N_1}^{\text{from pop 1}} + \overbrace{\alpha\beta I_2/N_2}^{\text{from pop 2}}\right]$$

Connecting the populations

– And same logic for infectious compartment and population 2:

$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = -S_1[\beta I_1/N_1 + \alpha\beta I_2/N_2]$$

$$\frac{\mathrm{d}I_1}{\mathrm{d}t} = S_1[\beta I_1/N_1 + \alpha\beta I_2/N_2] - \gamma I_1$$

$$\frac{\mathrm{d}S_2}{\mathrm{d}t} = -S_2[\beta I_2/N_2 + \alpha\beta I_1/N_1]$$

$$\frac{\mathrm{d}I_2}{\mathrm{d}t} = S_2[\beta I_2/N_2 + \alpha\beta I_1/N_1] - \gamma I_2$$

Practical

– Objective: implement SIR metapopulation model with two populations
– Answer questions A-D
– Question E is optional
– Book by Keeling & Rohani (Princeton, 2007) has more details about metapopulations.

General approach

Contact matrices – e.g. by age

	0-4	5-9	10-14
0-4	4.1	1.8	0.7
5-9	1.2	5.6	1.2
10-14	0.8	0.9	7.8

C_{ij} = daily number of age-j individuals contacted by an age-i individual

$$\frac{dS_i}{dt} = -\left(\sum_j c_{ij}\frac{I_j}{N_j}\right)pS_i$$

$$\frac{dI_i}{dt} = \left(\sum_j c_{ij}\frac{I_j}{N_j}\right)pS_i - \gamma I_i$$

…

General approach

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10-14	0.8	0.9	7.8

A question that often comes up… why isn't this matrix symmetrical about the diagonal? Is it supposed to be?

To see why it doesn't need to be, consider contact rates among a group of friends with these ages:

(20-29) (20-29) (30-39)