Modelling epidemics

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What are models?

- A useful summary provided by (Louz et al. 2010)
- All models are wrong: Some are useful
- Not all models of epidemics are useful for policy formation
- Critical approach to modelling essential
- To critique a model you must understand it, at least intuitively.

How many types of models are there?

- Reviewed for flu by (Dorjee et al. 2013)
- Deterministic models
- Stochastic models
- Compartmental models
- Agent based models
- Network models
- Metapopulation models
- Gravity models

How are models used?

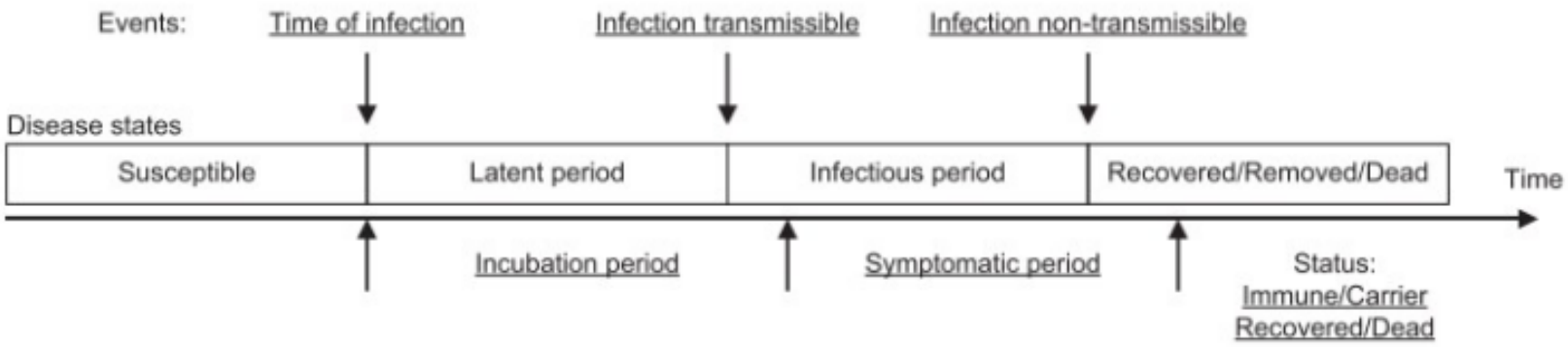
- "Mathematical models are powerful tools for exploring this complex landscape of intervention strategies and quantifying the potential costs and benefits of different options." Ferguson et al. (2006)
- Proposed non-pharmaceutical measures
- Case isolation,
- Household quarantine
- School or workplace closure
- Restrictions on travel

What is the SIR model?

- The SIR model Kermack and McKendrick: Mathematics shown in detail by Hethcote (2000)
- Compartment/flow model
- Set of differential equations representing rates
- Susceptible (S)
- Infected (I)
- Removed (R)

How can we represent the changes between states)

- Draw up a simple diagram



How is the SIR model used?

- An SIR is not suitable for predicting the future precisely
- If any of the assumptions are not met the model will not predict
- However, the model helps analyse possible scenarios
- Also allows criticism of the models assumptions
- We can us it for *heuristics*. This means learning about reality from using the model

What are the assumptions used in the SIR model?

- Population at risk is known
- Complete mixing (panmixia)
- No stratification of risk
- Homogeneity within compartments
- No change in properties of the agent being transmitted
- No change in host behaviour

When are the assumptions most closely approximated?

- SIR approximates the situation in small, local **outbreaks** very well
- It is not well suited for modelling larger epidemics
- Certainly not suitable for modelling global pandemics
- It cannot be paramaterised before an outbreak
- It cannot model changes in host behaviour during outbreak

How do we interpret the SIR model?

- Used for "What if" scenario building
- Improves understanding of the differences between model and real world system
- Can be looked at using post hoc i.e. after the event model fitting
- It is useful for learning from the past
- It is useful as a basis for more sophisticated models
- It can help in estimating parameters for more sophisticated models

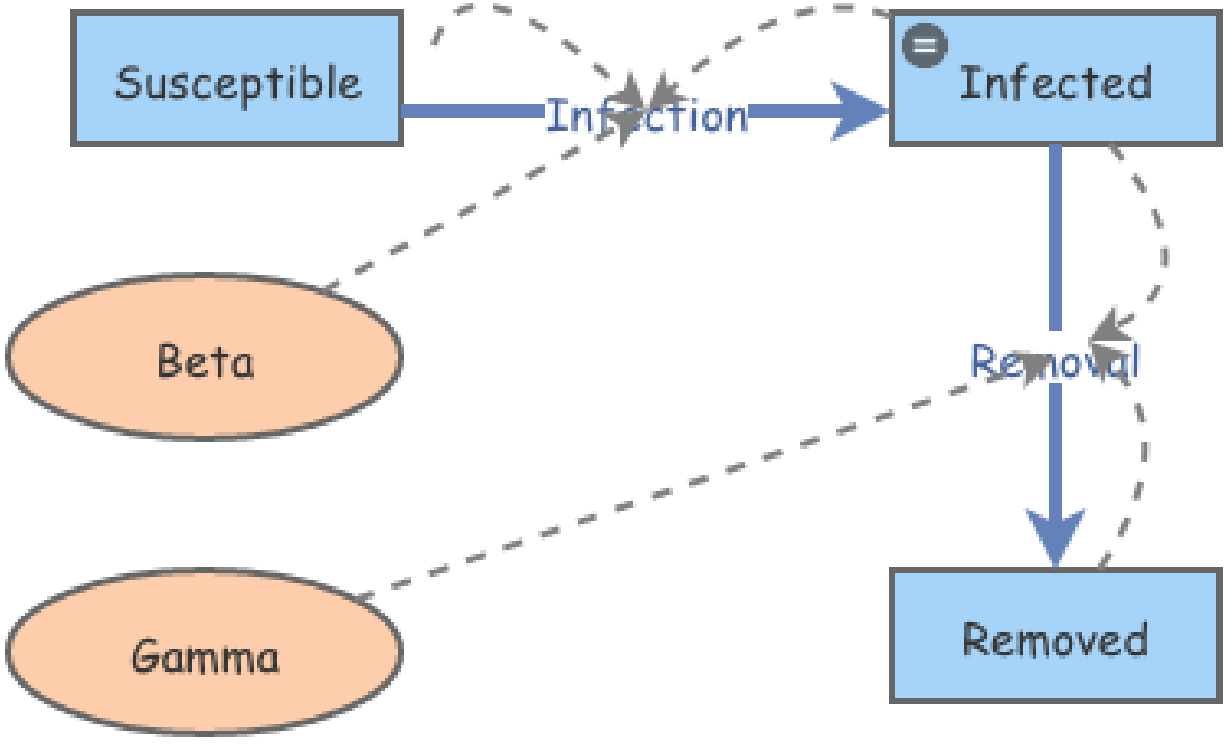
Why use an SIR?

- The model is **tractable**: mathematics can be well understood.
- The model is **understandable**: simple enough to be used intuitively
- The model is **adequate**: Captures enough aspects of complex system dynamics
- The model provides **insight**: When the SIR does not match reality we learn more than when it does

How do we build an SIR?

- Steps shown as storyline here

https://insightmaker.com/insight/189276/SIR

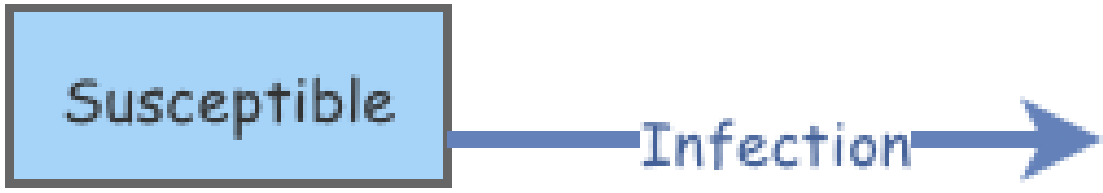


How do we start the model?

- The starting point for the model is the susceptible compartment. This contains the proportion of the total population at risk that is susceptible to infection.
- As this is a proportion its value varies between 0 i.e. no one at risk because all are either infected or removed and 1 i.e the whole population is at risk
- To start a model run the compartment is set at 1 minus the infected proportion.
- In this case if we seed the model with 1% infected the value for the proportion will be 0.99

How is infection represented?

- Infection is represented as an outflow from the susceptible compartment.



What is the situation at the start of an outbreak?

- Susceptibles become infected through the process of infection.
- In this model it is assumed that a person who is infected is also infectious.
- Infection takes place when infected (i.e. infectious) people come into contact with susceptibles. So the flow is influenced by both the proportion infected and the proportion susceptible.
- At the start of an outbreak the number of contacts that result in transmssion is low, as most contacts are between susceptible and susceptible individuals.

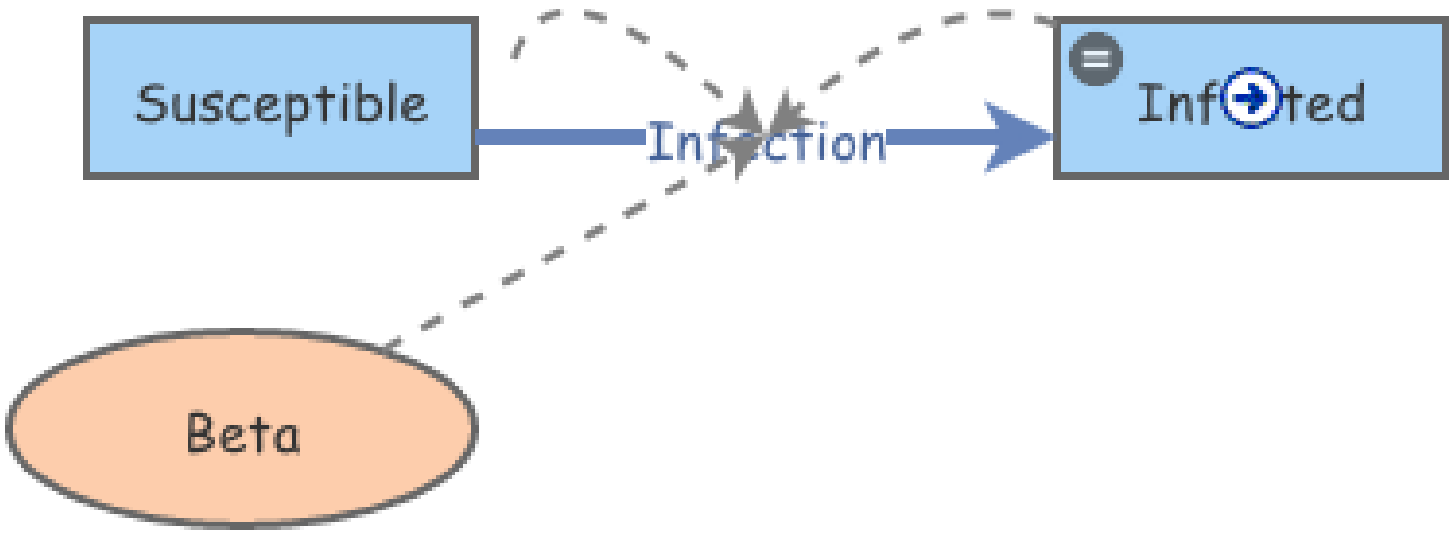
What happens to the susceptibles in the model?

- Outflow from the susceptibles adds to the number of infected
- The process of infection occurs when the susceptibles meet the infected
- So, the proportion of both infected and susceptibles influence the process.
- Represented as influence arrows (both S and I influence the rate of infection)

What controls the rate of spread?

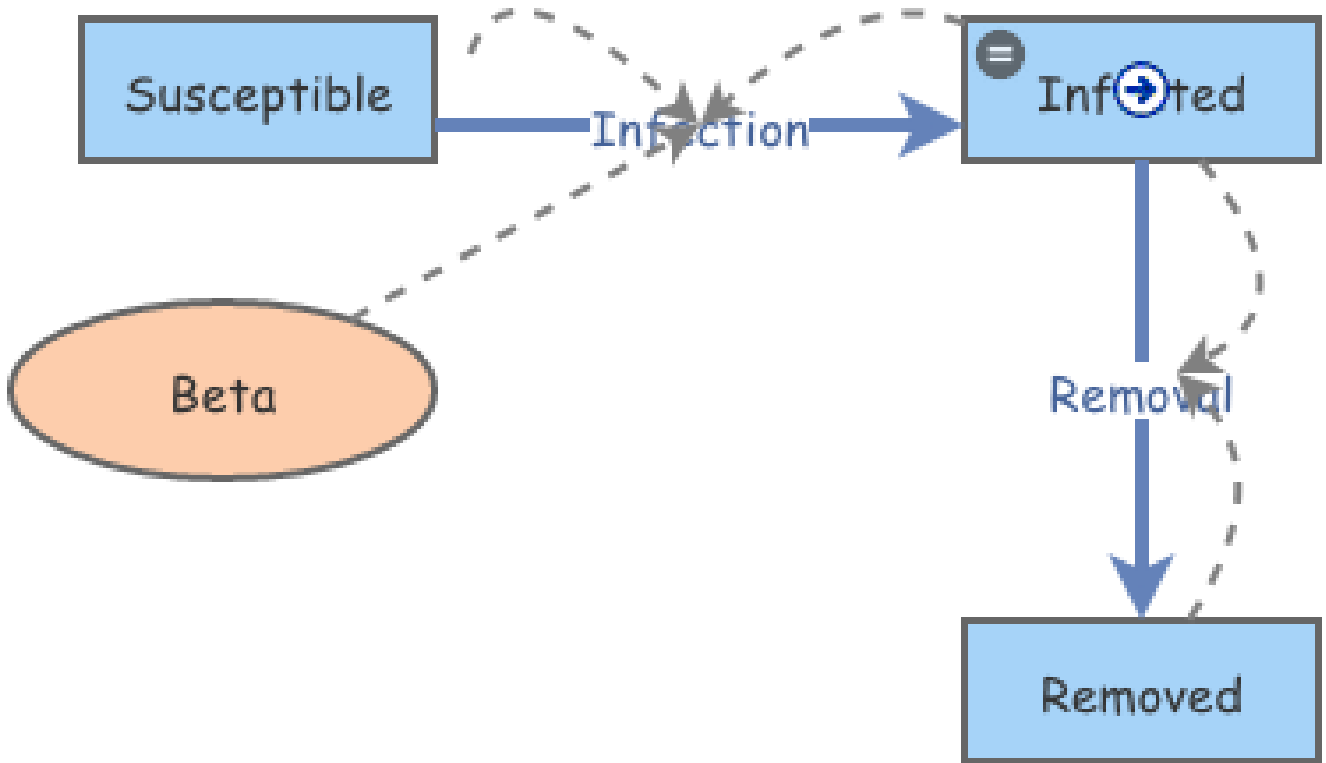
- The model parameter β (beta) controls the rate of spread.
- The transfer between the susceptibles and the infected is mediated by the beta parameter β
- We multiply the proportion of susceptibles and the proportion of infected by beta β
- This is a **positive** flow into I and a **negative** flow from S

$$\frac{dI}{dt} = \beta SI$$
$$\frac{dS}{dt} = -\beta SI$$



What happens to the infected?

- The infected are then "removed" from the I compartment
- A flow occurs from the infected compartment to the removed compartment
- Removal can occur through either **recovery** or **death**.
- The model behaves in the same way regardless of the way removals occur.



How is removal modelled?

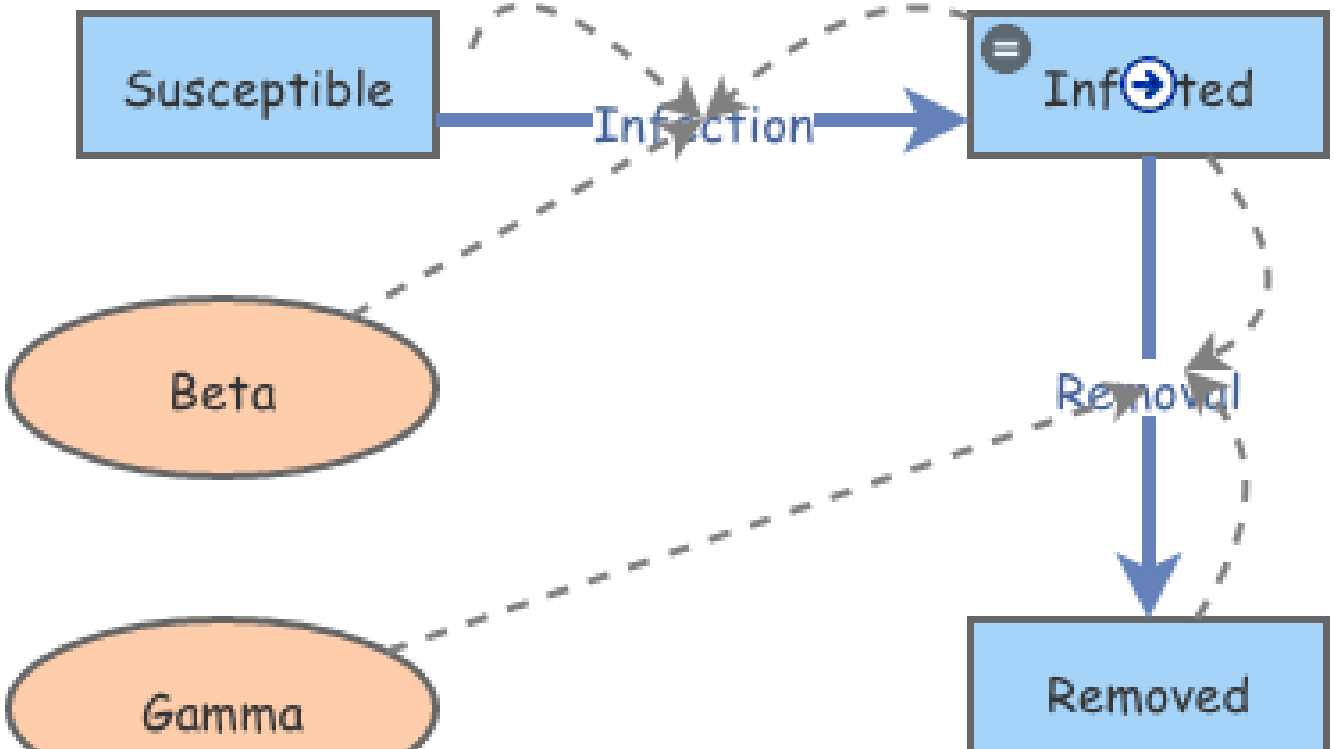
- The γ (gamma) parameter controls the rate of removal.
- If the time step is one day and gamma is 0.1 then 10% of the cases are removed each day.
- This can be through either **death** or recovery with **immunity**

How is removal modelled?

- We can multiply I by gamma γ
- This leads to a negative flow from I
- It leads to a positive flow into R

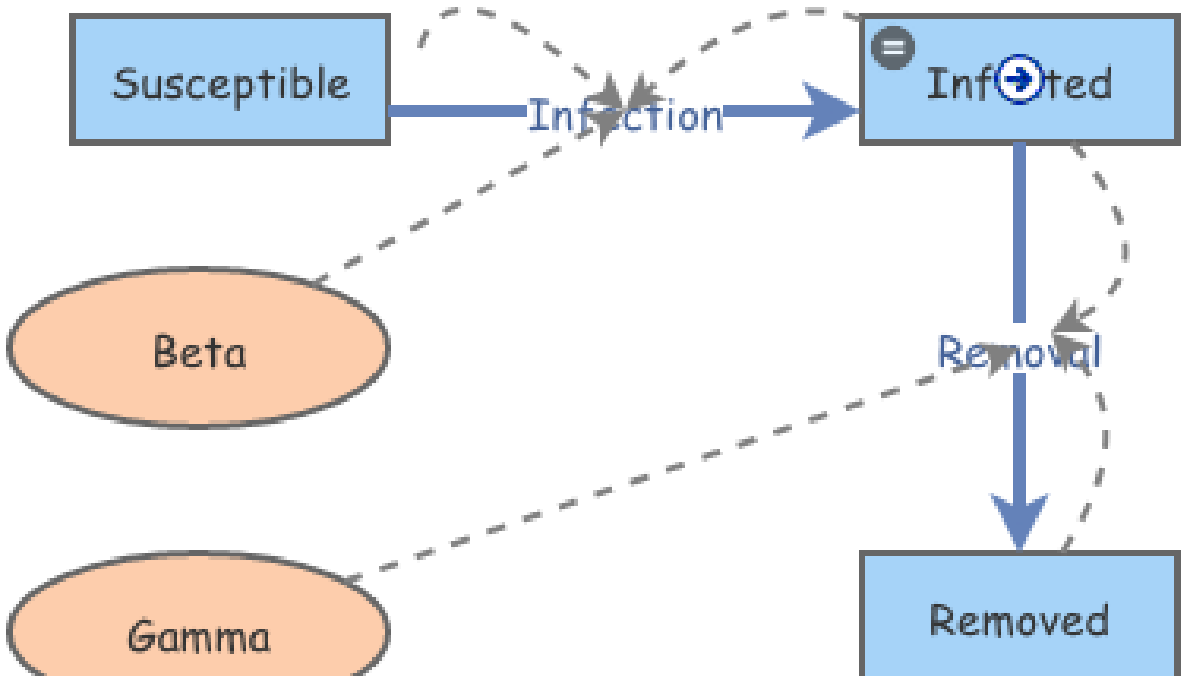
$$\frac{dI}{dt} = \beta SI - \gamma I$$

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



How can we make the gamma (γ) parameter more intuitive?

- The gamma parameter is a proportion of infected removed each day
- An easier way to think about it is that $\frac{1}{\gamma}$ is the number of days infectious
- We can add that to the model diagram
- So if *gamma* equal 0.1 then $\frac{1}{\gamma}$ equals 10 (days)



What is R_0?

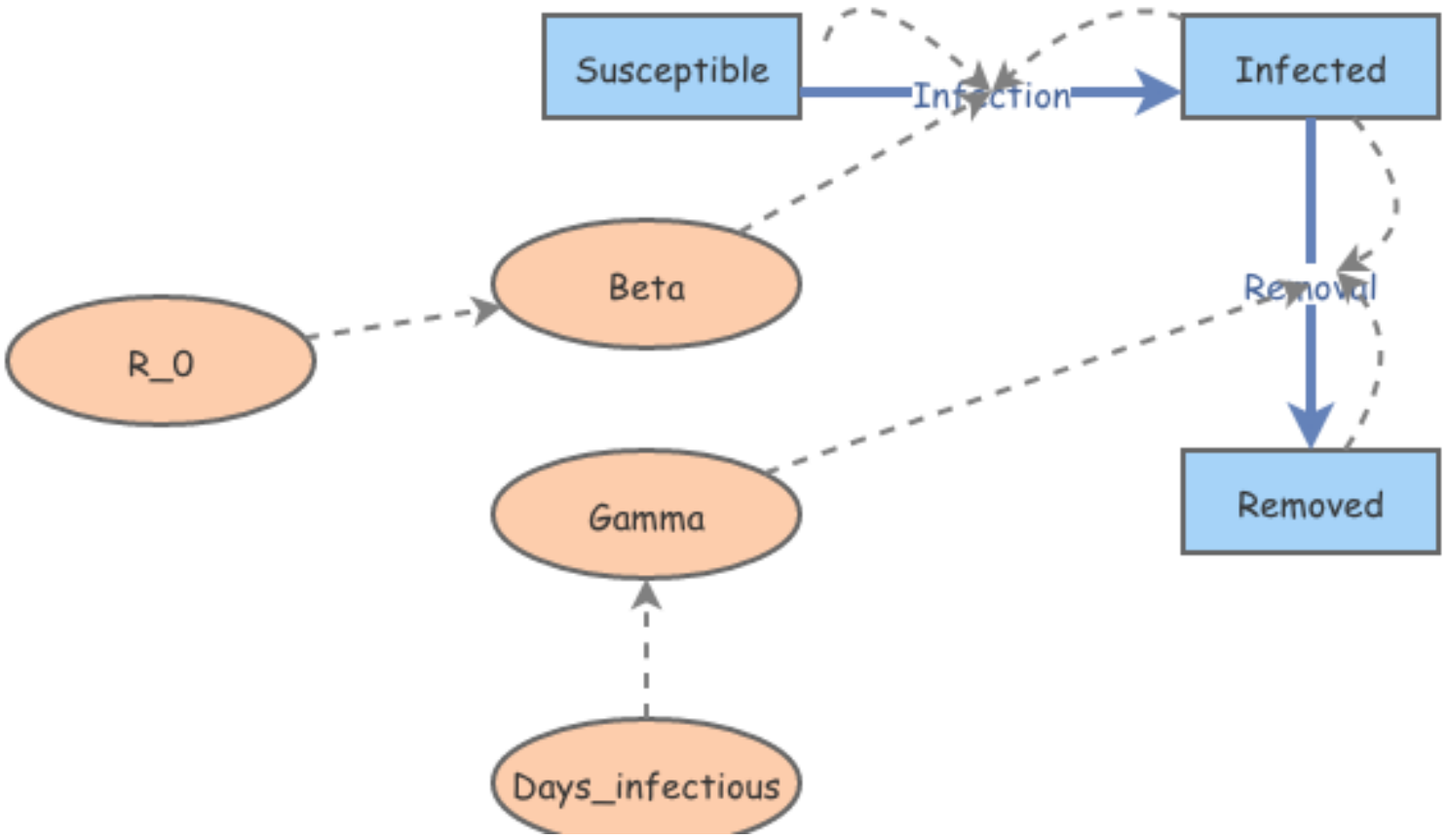
- The basic reproductive number is a key parameter when considering any epidemic
- R_0 is the average number of individuals infected by a single individual when all the population is susceptible
- If R_0 is below 1 then an epidemic cannot spread
- Understanding the SIR model will help In understanding R_0

How do we find R_0 from β?

- R_0 depends on both β (number of new infections per day per infectious person) and length of time infectious $\frac{1}{\gamma}$

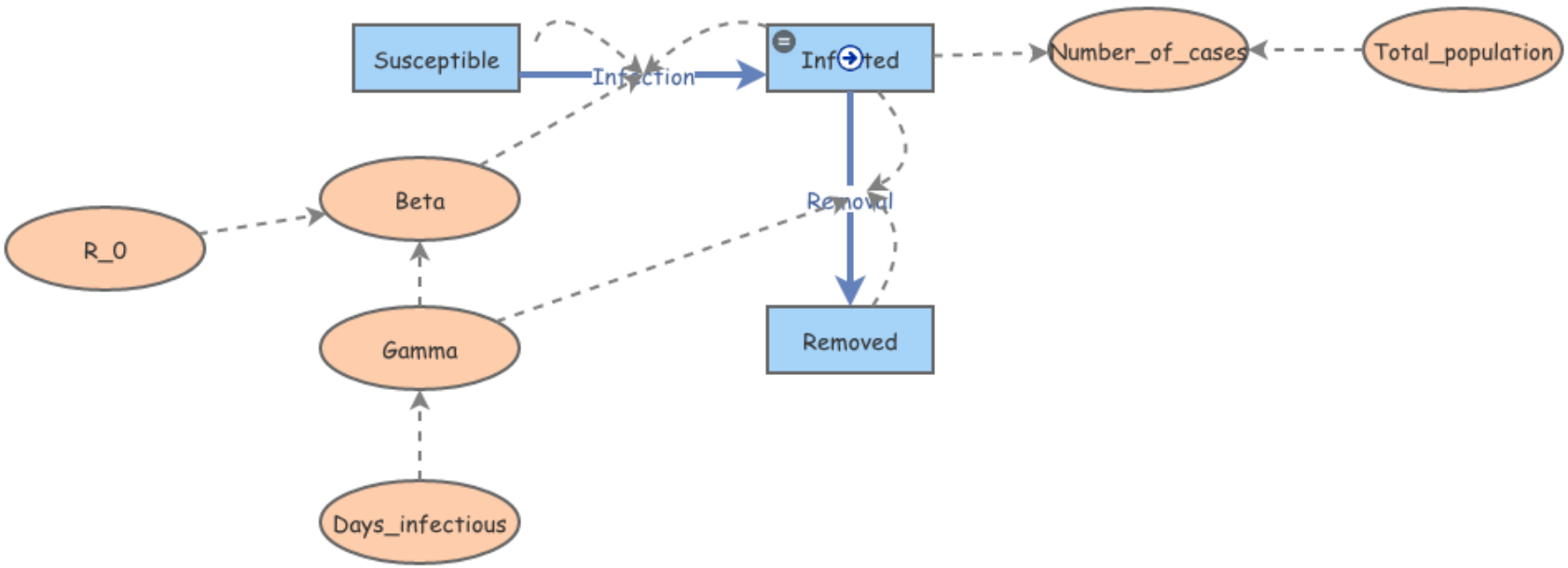
$$R_0 = \frac{\beta}{\gamma}$$

$$\beta = R_0\gamma$$



How do we find the absolute numbers?

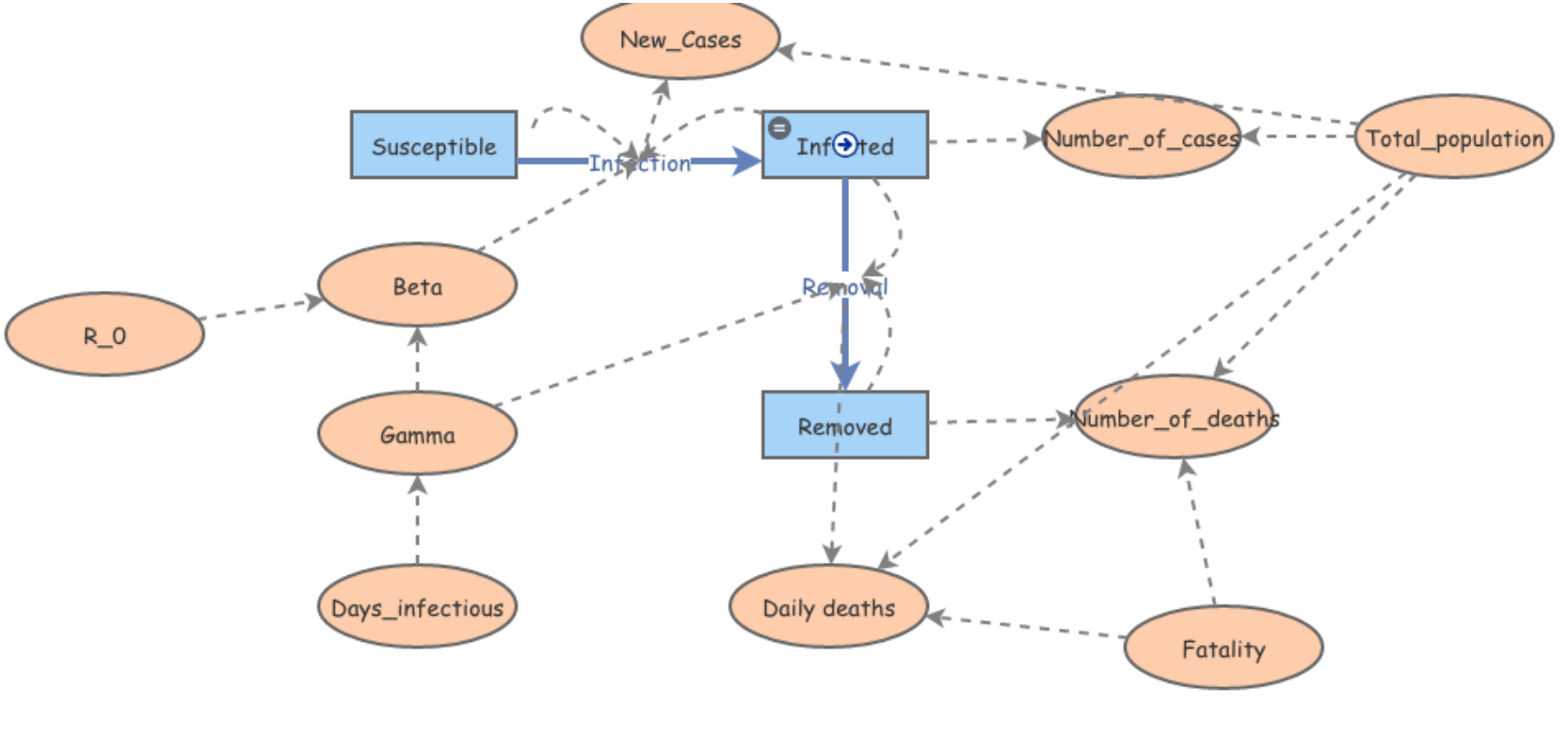
- If we know the size of the population we can multiply all the proportions by this ammount
- This gives us the total numbers of susceptibles, infected and removed.



How is the complete model shown as a compartment flow model?

- To complete the model we need to take into account that some removed die and others recover
- This can be added in to the structure.
- A full model looks rather more complex

How is the complete model shown as a compartment flow model?



What do the complete maths look like?

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$
$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma \frac{I}{N}$$
$$\frac{dR}{dt} = \gamma \frac{I}{N}$$

How do we summarise the characteristics of the model?

A simple SIR mode represents the dynamics of a generic epidemic. The SIR model assumes panmixia, in other words there is a uniform probability of transmssion between any infected(infectious) individual and any susceptible individual. This assumption is in fact rarely completely met. However it is often approximately met. Under panmixia there is no requirement for all the possible contacts between individuals to take place directly in any single model time step. Transmission just needs to be possible through a chain of contacts. A dense network of well connected individuals will approximate panmixia at a national to global scale.

What is the herd immunity threshold?

- A simple relationship can be derived from the SIR model that relates R_0 with the proportion of immune (or recovered) needed for the epidemic to spread.
- The critical portion of the population that needs to be immue in order to prevent the spread of an epidemic is

$$P_i = 1 - \frac{1}{R_0}$$

Fine, Eames, and Heymann (2011)

What if I didn't understand any of this?

- To understand a model takes a lot of time and practice
- We will go through all this again in the practical
- You do not need to understand all the mathematics to use the model
- All modelling will be done by software.

References

Dorjee, S., Z. Poljak, C. W. Revie, J. Bridgland, B. Mcnab, E. Leger, and J. Sanchez. 2013. "A review of simulation modelling approaches used for the spread of zoonotic influenza viruses in animal and human populations." *Zoonoses and Public Health* 60 (6): 383–411. https://doi.org/10.1111/zph.12010.

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