SIR Model Review

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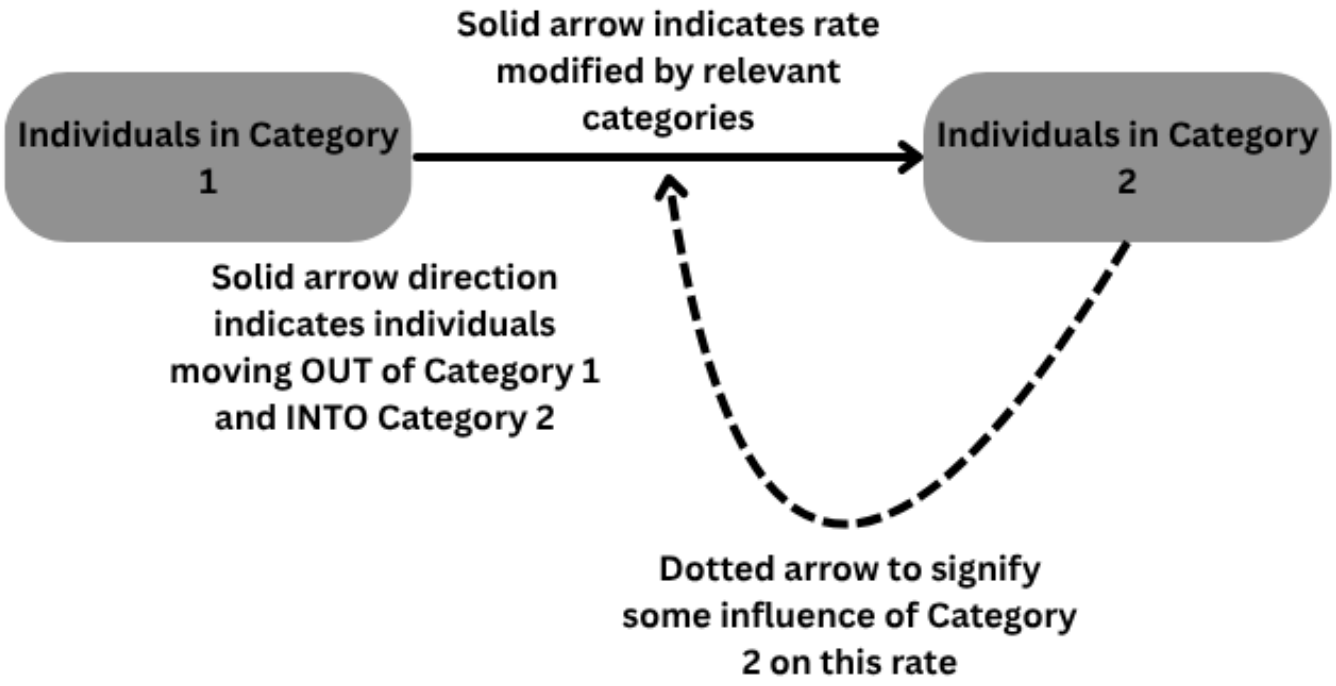
Compartmental Models: Generalized



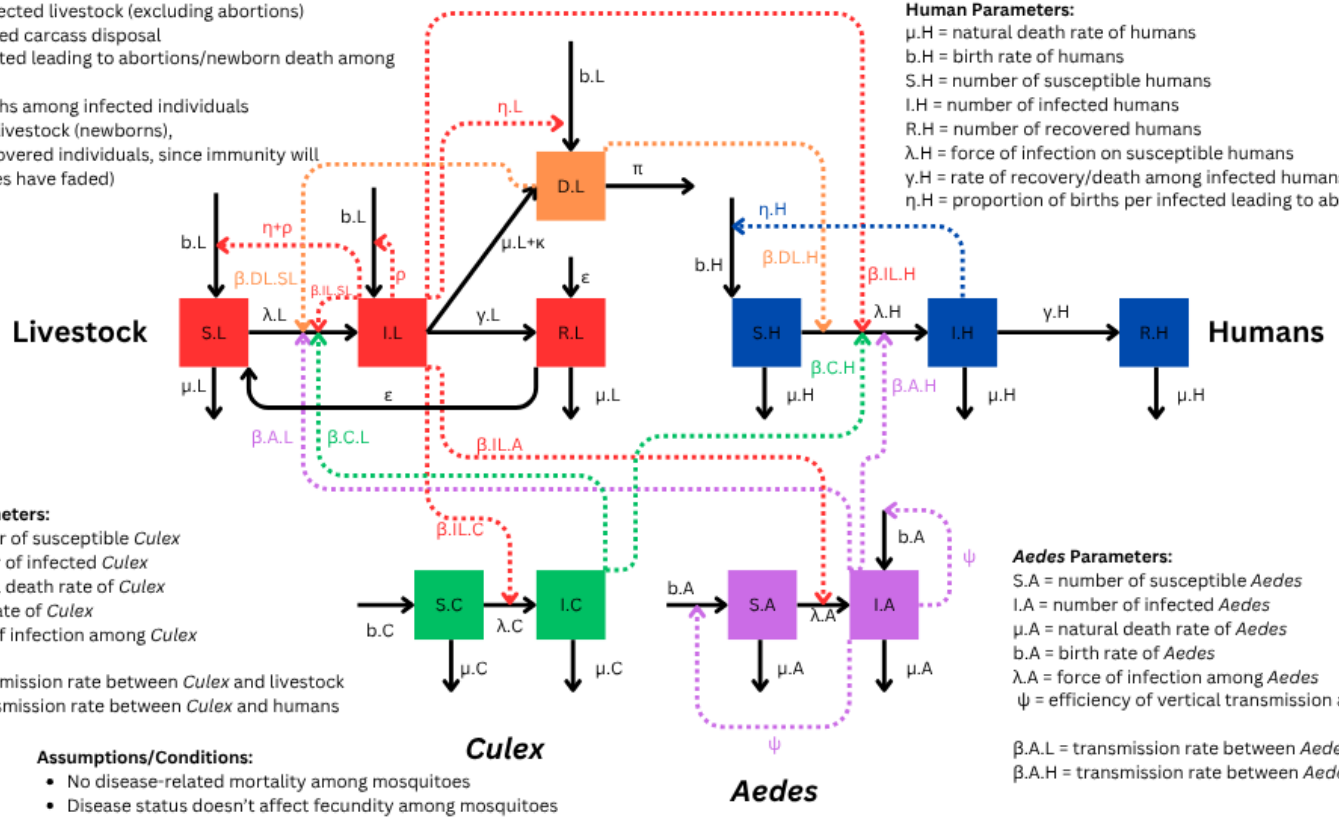
Diagrams created with Canva (www.canva.com)

Complex Example: Rift Valley Fever

Livestock Parameters:
S.L = number of susceptible livestock
I.L = number of infected livestock
R.L = number of recovered livestock
D.L = number of dead/infected livestock
μ.L = natural death rate of livestock
b.L = birth rate of livestock
λ.L = force of infection on susceptible livestock
γ.L = rate of recovery among infected livestock
κ = disease-related mortality of infected livestock (excluding abortions)
π = rate of virus inactivation/infected carcass disposal
η.L = proportion of births per infected leading to abortions/newborn death among infected livestock
ρ = proportion of live, infected births among infected individuals
ε = waning immunity of recovered livestock (newborns), (equal to the birth rate of recovered individuals, since immunity will fade after maternal antibodies have faded)

β.IL.H = transmission rate between living infectious livestock and humans
β.IL.A = transmission rate between infectious livestock and Aedes mosquitoes
β.IL.C = transmission rate between infectious livestock and Culex mosquitoes
β.IL.SL = transmission rate between infectious livestock and susceptible livestock (e.g. through contact with contaminated birthing fluids)
β.DL.H = transmission rate between dead/aborted infectious livestock and humans
β.DL.SL = transmission rate between dead livestock and susceptible livestock (e.g. through contact with contaminated fluids of dead individuals)

Human Parameters:
μ.H = natural death rate of humans
b.H = birth rate of humans
S.H = number of susceptible humans
I.H = number of infected humans
R.H = number of recovered humans
λ.H = force of infection on susceptible humans
γ.H = rate of recovery/death among infected humans
η.H = proportion of births per infected leading to abortions/newborn death among infected humans



***Culex* Parameters:**
S.C = number of susceptible *Culex*
I.C = number of infected *Culex*
μ.C = natural death rate of *Culex*
b.C = birth rate of *Culex*
λ.C = force of infection among *Culex*

β.C.L = transmission rate between *Culex* and livestock
β.C.H = transmission rate between *Culex* and humans

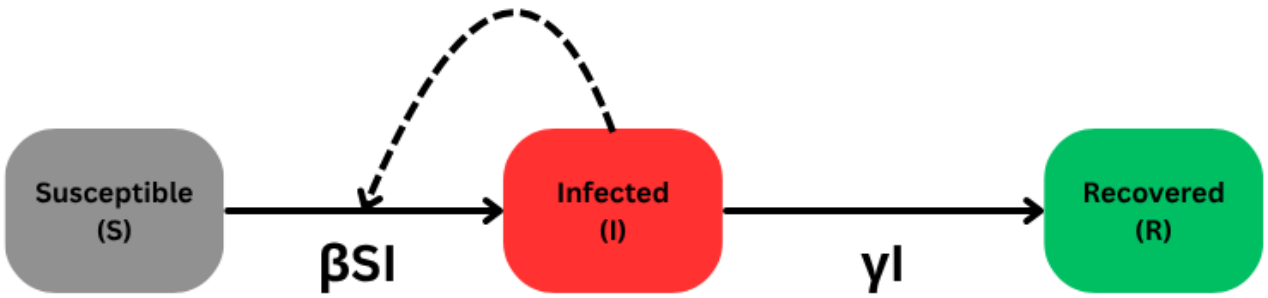
***Aedes* Parameters:**
S.A = number of susceptible *Aedes*
I.A = number of infected *Aedes*
μ.A = natural death rate of *Aedes*
b.A = birth rate of *Aedes*
λ.A = force of infection among *Aedes*
ψ = efficiency of vertical transmission among *Aedes* and offspring

β.A.L = transmission rate between *Aedes* and livestock
β.A.H = transmission rate between *Aedes* and humans

Assumptions/Conditions:
- No disease-related mortality among mosquitoes
- Disease status doesn't affect fecundity among mosquitoes
- Humans are dead-end hosts
- Only living livestock can transmit RFV to susceptible mosquitoes
- Transmission among wildlife isn't significant in maintenance of the intra-herd epidemic
- Intra-herd epidemic considered only
- Population of study is unvaccinated and vaccines aren't available for the farm
- Immunity is lifelong among animals post-infection, assumed to be similar to vaccine immunity
- (https://www.merckvetmanual.com/generalized-conditions/rift-valley-fever/rift-valley-fever-in-animals)
- Inherited immunity wanes with maternal antibodies and is thus a consistent rate among all newborns (ε in = ε out)
- Loss of immunity among humans is negligible (https://pmc.ncbi.nlm.nih.gov/articles/PMC10535968/)
- Birth rate of recovered individuals is different from susceptible individuals due to long-lasting reproductive tissue damage from infection
- Mosquito transmission is frequency-dependent
- Ignoring temporal and spatial variation in transmission
- Vertical transmission among humans is negligible (https://www.nature.com/articles/s41467-023-40187-z#)
- Assumed that pregnant animals/humans are equally as likely to get infected as non-pregnant individuals
- Assumed that recovered humans don't have long-term reductions in birth rate (lack of data/longitudinal studies, mostly)
- Assumed mosquitoes don't clear infection

SIR: Basic

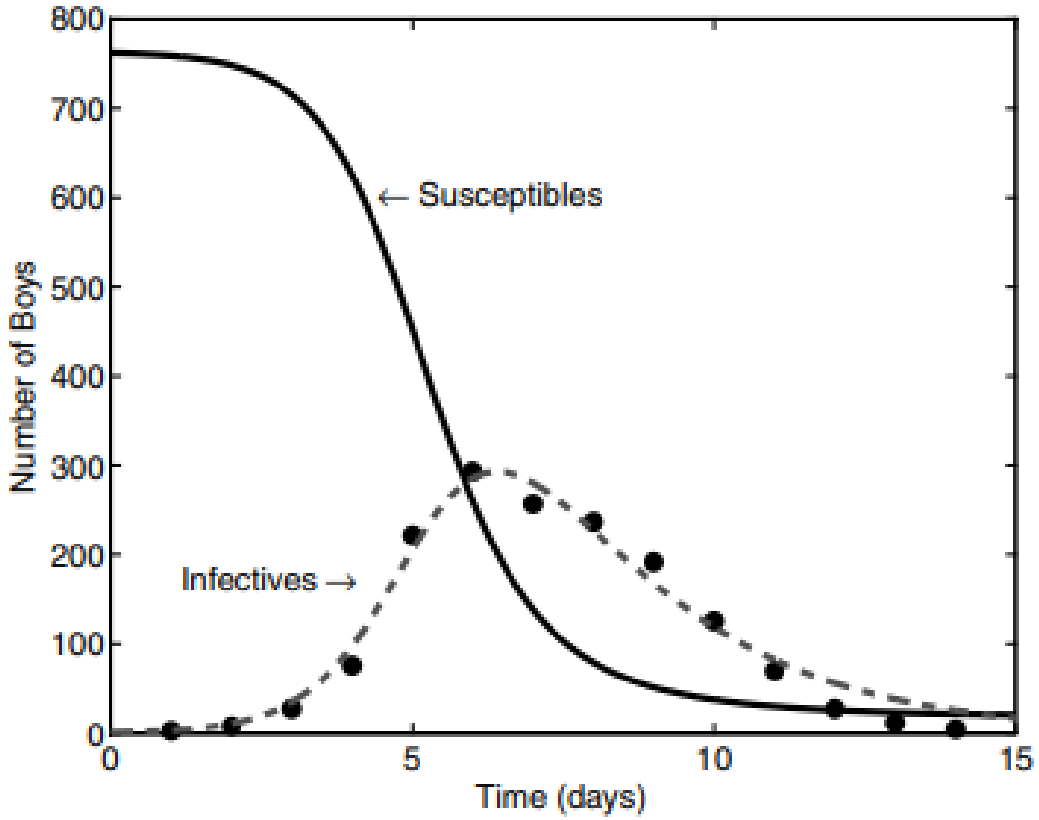
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t$
  - $I_{t+1} = I_t + \beta S_t I_t - \gamma I_t$
  - $R_{t+1} = R_t + \gamma I_t$



Where:

- S = # of Susceptibles
- I = # of Infected
- R = # of Recovered
- β = Infection Rate (rate of contact * P(infection | contact))
- γ = Recovery Rate

Graphical Example



Keeling, M. J., & Rohani, P. (2011). *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press. https://doi.org/10.1515/9781400841035

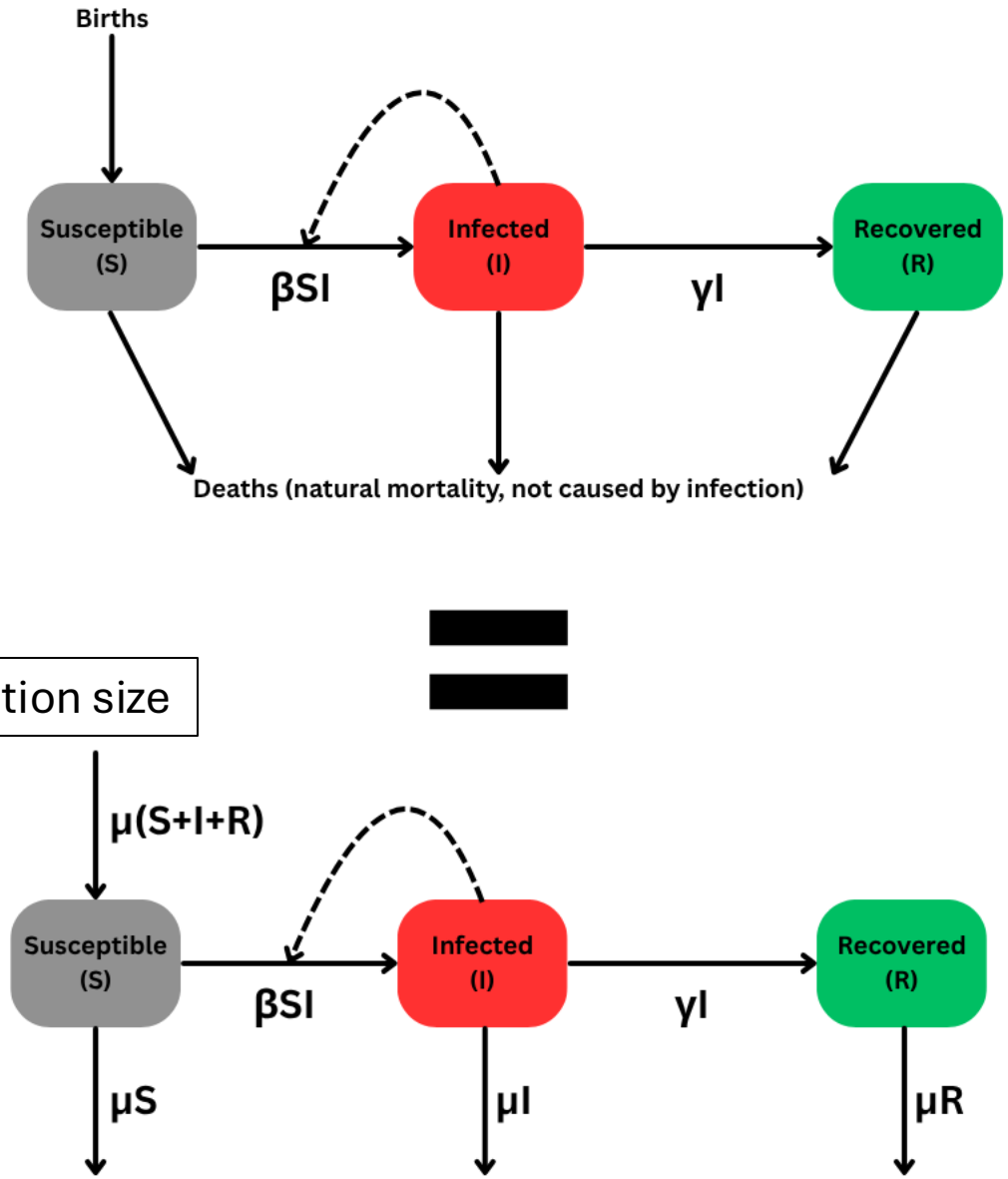
SIR with Demography

- Equations remain SAME except add birth/death rate
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t + (S_t + I_t + R_t)\mu - \mu S_t$
  - $I_{t+1} = I_t + \beta S_t I_t - \gamma I_t - \mu I_t$
  - $R_{t+1} = R_t + \gamma I_t - \mu R_t$

Where:

- S = # of Susceptibles
- I = # of Infected
- R = # of Recovered
- β = Infection Rate (rate of contact * P(infection | contact))
- γ = Recovery Rate
- μ = natural birth rate = natural death rate

Note: S+I+R = N, aka, population size



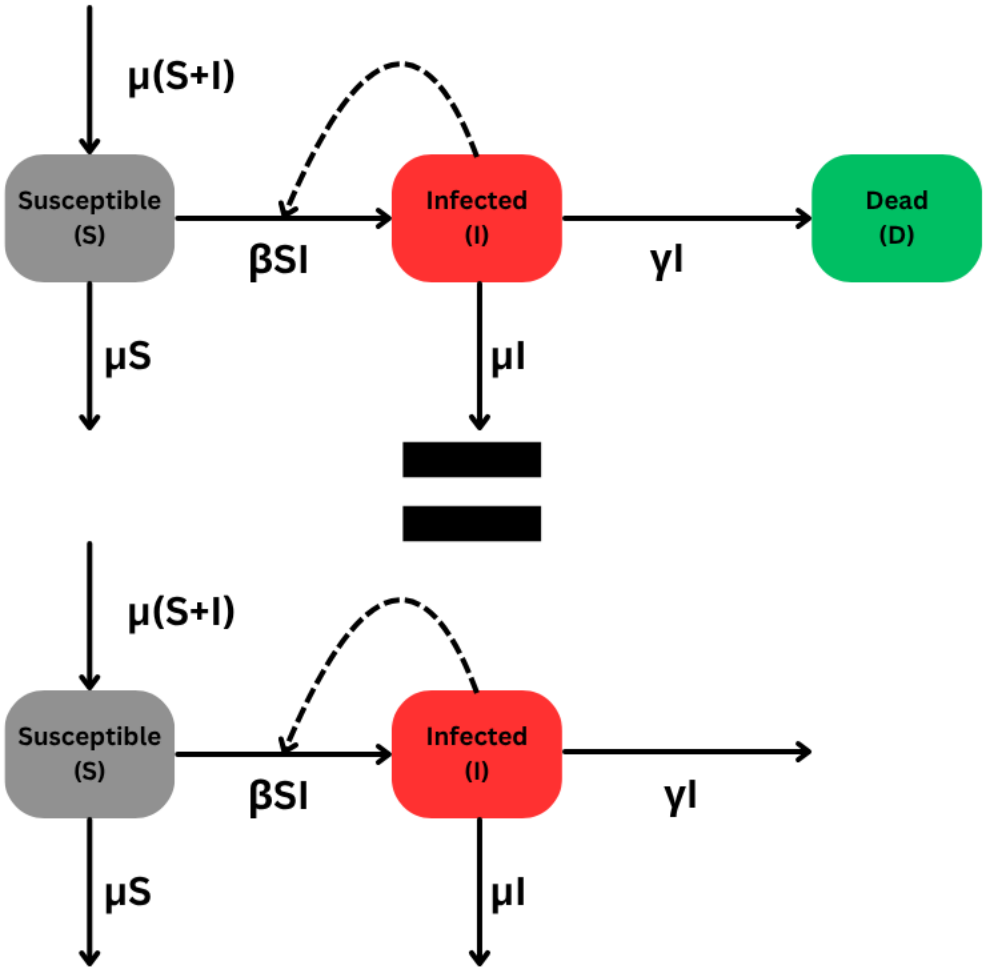
Note: Density vs. Frequency-Dependent

- Remember that:
  - β = Infection Rate (rate of contact * P(infection | contact))
- In density-dependent systems (e.g. flu):
  - # contacts is dependent on population size (N)
  - $\beta S_t I_t$ represents this…
    - β modified by **product** S * I, which increase with greater N
  - e.g. one individual infects all individuals within an average of 6 feet of them while infected with the flu
- In frequency-dependent systems (e.g. HIV)
  - # contacts is NOT dependent on population size (N)
  - $\beta S_t I_t / N$ represents this…
    - Dividing by N compensates for rate of contact remaining constant at higher N
  - e.g. one individual bites average of 3 other animals while infected with rabies

SI/SID: Fatal Infections

- Essentially same as SIR, but R replaced by D or omitted
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t + (S_t + I_t)\mu - \mu S_t$
  - $I_{t+1} = I_t + \beta S_t I_t - \gamma I_t - \mu I_t$
  - $D_{t+1} = D_t + \gamma I_t$ (or omit)

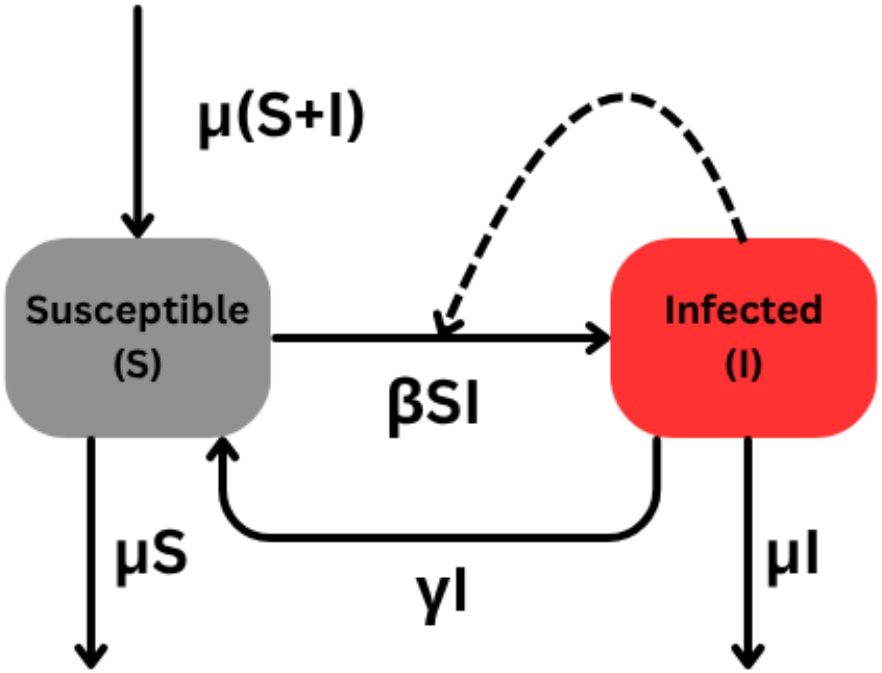
  Where:
  - S = # of Susceptibles
  - I = # of Infected
  - D = # of Dead due to infection
  - β = Infection Rate (rate of contact * P(infection | contact))
  - γ = death rate due to infection
  - μ = natural birth rate = natural death rate



SIS: No Recovery

- Infected individuals become susceptible again (no acquired immunity)
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t + (S_t + I_t)\mu - \mu S_t + \gamma I_t$
  - $I_{t+1} = I_t + \beta S_t I_t - \gamma I_t - \mu I_t$

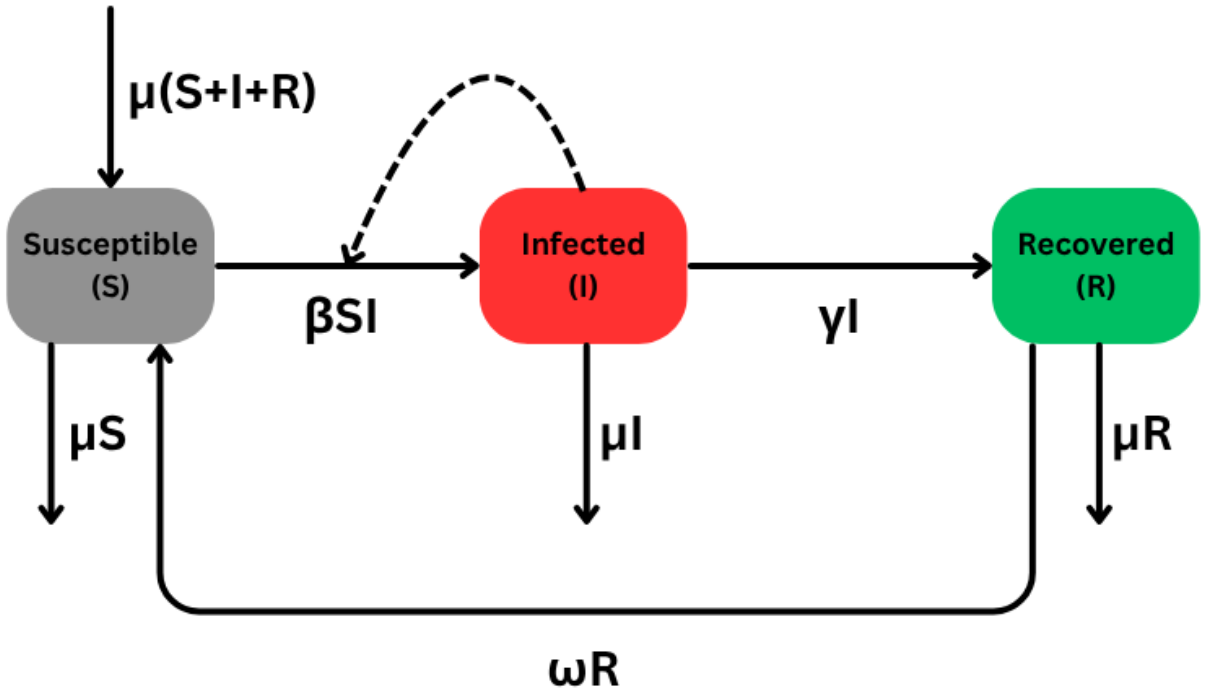
  Where:
  - S = # of Susceptibles
  - I = # of Infected
  - β = Infection Rate (rate of contact * P(infection | contact))
  - γ = Recovery Rate (but NO immunity)
  - μ = natural birth rate = natural death rate



SIRS: Waning Immunity

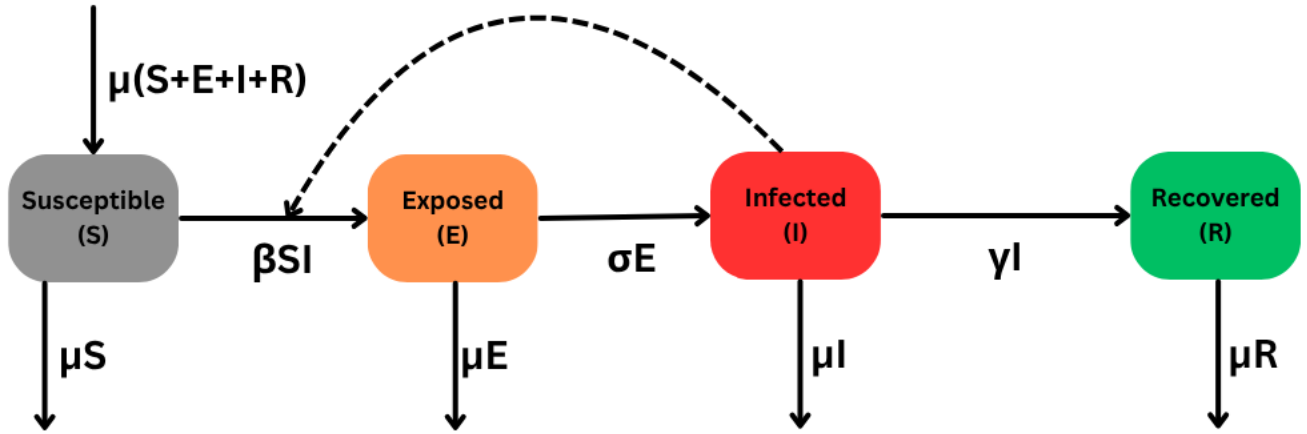
- Equations remain SAME except added waning immunity rate
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t + (S_t + I_t + R_t)\mu - \mu S_t$
  - $I_{t+1} = I_t + \beta S_t I_t - \gamma I_t - \mu I_t$
  - $R_{t+1} = R_t + \gamma I_t - \mu R_t - \omega R_t$

  Where:
  - S = # of Susceptibles
  - I = # of Infected
  - R = # of Recovered
  - β = Infection Rate (rate of contact * P(infection | contact))
  - γ = Recovery Rate
  - μ = natural birth rate = natural death rate
  - ω = rate of waning immunity



SEIR: Latent Infection

- Shedding of pathogen is latent; doesn't begin immediately
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t + (S_t + E_t + I_t + R_t)\mu - \mu S_t$
  - $E_{t+1} = E_t + \beta S_t I_t - \sigma E_t - \mu E_t$
  - $I_{t+1} = I_t - \gamma I_t - \mu I_t + \sigma E_t$
  - $R_{t+1} = R_t + \gamma I_t - \mu R_t$



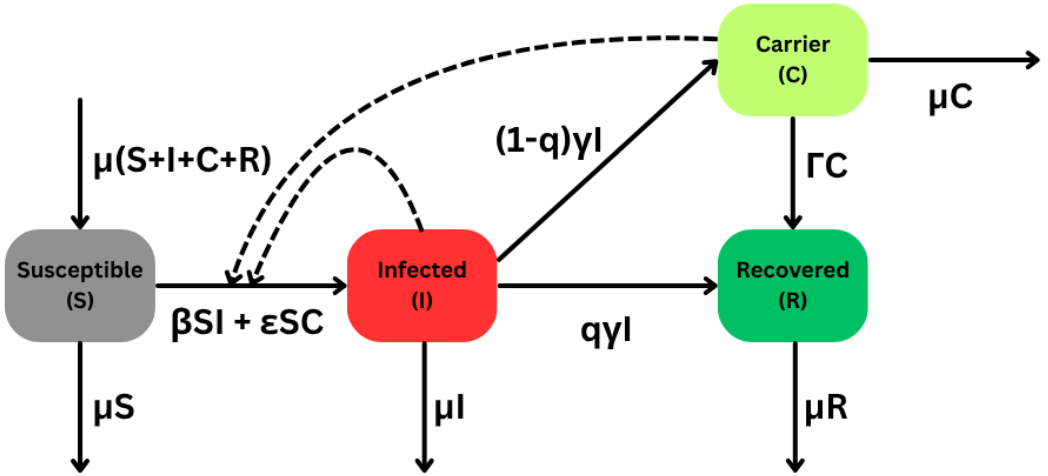
Where:

- S = # of Susceptibles
- I = # of Infected
- R = # of Recovered
- β = Infection Rate (rate of contact * P(infection | contact))
- γ = Recovery Rate
- σ = rate of shedding/symptom onset
- μ = natural birth rate = natural death rate

SIRC: Carrier State

- Added carrier state; hybrid of I and R states
- Equations:
  - $S_{t+1} = S_t - \beta S_t I_t - \varepsilon S_t C_t - (S_t + I_t + C_t + R_t)\mu - \mu S_t$
  - $I_{t+1} = I_t + \beta S_t I_t - \gamma I_t - \mu I_t + \varepsilon S_t C_t$
  - $C_{t+1} = C_t + (1 - q)\gamma I_t - \Gamma C - \mu C_t$
  - $R_{t+1} = R_t + q\gamma I_t - \mu R_t$

  Where:
  - S = # of Susceptibles
  - I = # of Infected
  - R = # of Recovered
  - C = # of Carriers
  - β = Infection Rate (rate of contact * P(infection | contact))
  - γ = Recovery Rate
  - ε = Infection rate of carriers on susceptibles
  - q = probability of recovering without becoming carrier
  - 1 – q = probability of becoming a carrier
  - Γ = rate of carrier recovery
  - μ = natural birth rate = natural death rate



SIR: Multiple Species (~Age Classes, too)

- Only difference is two SIR models, with infected contacting those from either population (ignoring demographics for now)
- May also have systems where **Group A moves to Group B** at some rate (e.g. age classes), or one group serves as a **dead-end host** and thus doesn't transmit back to the other group (e.g. some zoonoses)
- Equations:
  - $S.a_{t+1} = S.a_t - \beta.aa*S.a_tI.a_t - \beta.ba*S.a_tI.b_t$
  - $I.a_{t+1} = I.a_t + \beta.aa*S.a_tI.a_t + \beta.ba*S.a_tI.b_t - \gamma.a*I.a_t$
  - $R.a_{t+1} = R.a_t + \gamma.a*I.a_t$
  - $S.b_{t+1} = S.b_t - \beta.bb*S.b_tI.b_t - \beta.ab*S.b_tI.a_t$
  - $I.b_{t+1} = I.b_t + \beta.bb*S.b_tI.b_t + \beta.ab*S.b_tI.a_t - \gamma.b*I.b_t$
  - $R.b_{t+1} = R.b_t + \gamma.b*I.b_t$

  Where:
  - S.a = # of Susceptibles in Group A
  - S.b = # of Susceptibles in Group B
  - I.a = # of Infected in Group A
  - I.b = # of Infected in Group B
  - R.a = # of Recovered in Group A
  - R.b = # of Recovered in Group B
  - β.aa = Infection Rate of Group A on itself
  - β.bb = Infection Rate of Group B on itself
  - β.ab = Infection Rate of Group A on Group B
  - β.ba = Infection Rate of Group B on Group B
  - γ.a = Recovery Rate of Group A
  - γ.b = Recovery Rate of Group B