# Outline: Expanding Models

The first SIP model can be expanded in a number of ways:

- Local recruits (model 2)
- Immigrants from remote (uninfected) population (model 2)
- Multiple subpopulations (model 3a)
- Particle exchange between subpopulations (model 3a)
- Multiple species (model 3b)
- Multiple species, multiple subpopulations (model 4)

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#### Model 2 - local recruits

For simulations longer than a few months, recruitment and mortality need to be included:

Recruitment control by carrying capacity (k)

$$\frac{dS}{dt} = -\beta_p h P S - \beta_i I S - \beta_d D S - m_b S + max(0, [1 - (S + I)/k]) (a_s S + a_i I)$$

Recruitment control by fecundity and density dependent mortality

$$\frac{dS}{dt} = -\beta_p h P S - \beta_i I S - \beta_d D S$$
  
+F(S+I) - (m<sub>b</sub> + m<sub>c</sub>(S+I)) S  
$$\frac{dI}{dt} = \beta_p h P S + \beta_i I S + \beta_d D S$$
  
-(m<sub>i</sub> + b + c(S + I)) I

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2 / 7

### Model 2- remote recruits

A remote susceptible population (S2) exchanges with the infected population.

Exchange can be at a continuous rate or proportional to the density difference (diffusive).

$$\frac{dS}{dt} = -\beta_p h P S - \beta_i I S - \beta_d D S - m_b S + b_d max[0, (S2 - S)] + b_i S2 \frac{dS2}{dt} = a_2 max[0, (1 - S2/k2)] S2 - b_d max[0, (S2 - S)] - b_i S2$$

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#### Model 3a - Multiple Subpopulations

Rectangular array of subpopulations with different characteristics:

$$\frac{d S(y,x)}{dt} = -\beta_p h P(y,x) S(y,x) - \beta_i I(y,x) S(y,x) -\beta_d D(y,x) S(y,x) - m_b S(y,x) \frac{d I(y,x)}{dt} = \beta_p h P(y,x) S(y,x) + \beta_i I(y,x) S(y,x) +\beta_d D(y,x) S(y,x) - m_i I(y,x) \frac{d D(y,x)}{dt} = m_i I(y,x) - e D(y,x) \frac{d P(y,x)}{dt} = c_i I(y,x) + c_d D(y,x) - r P(y,x)$$

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4 / 7

## Model 3a - Particle exchange

Particles can exchange between subpopulations based on an advection-like process. *Uex* is east/west exchange between boxes; *Vex* is north/south exchange.

Calculate the direction of exchange with the following:

NUex = .5 \* (abs(Uex) - Uex) and PUex = .5 \* (abs(Uex) + Uex). Only one of these is non-zero.

$$\frac{d P(y,x)}{dt} = -PUex(y,x) P(y,x) + NUex(y,x) P(y,x+1)$$
  
+PUex(y,x-1) P(y,x-1) - NUex(y,x-1) P(y,x)  
-PVex(y,x) P(y,x) + NVex(y,x) P(y+1,x)  
+PVex(y-1,x) P(y-1,x) - NVex(y-1,x) P(y,x)  
+other terms

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### Multiple Species - model 3b

Each population count can be associated with different species (s). Parameters are different for different species.

 $\Sigma_i$  is a sum of the index *i*.

$$\frac{d S(s)}{dt} = -\sum_{i} \beta_{p}(i,s) h P(i) S(s) - \sum_{i} \beta_{i}(i,s) I(i) S(s) 
-\sum_{i} \beta_{d}(i,s) D(i) S(s) 
+max(0, [1 - (S(s) + I(s))/K)] (a_{s} S(s) + a_{i} I(s)) - m_{b} S(s) 
\frac{d I(s)}{dt} = +\sum_{i} \beta_{p}(i,s) h P(i) S(s) + \sum_{i} \beta_{i}(i,s) I(i) S(s) 
+\sum_{i} \beta_{d}(i,s) D(i) S(s) - m_{i} I$$

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## Multiple Species infection

Each of the transmission parameters ( $\beta$ ) are arrays (Nspecies X Nspecies). The order is that the first index indicates the species doing the infecting and the second index indicates the species being infected. A diagonal matrix means that species only infect themselves.

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