Disease Transmission Models

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Old Dominion University, Norfolk, Virginia

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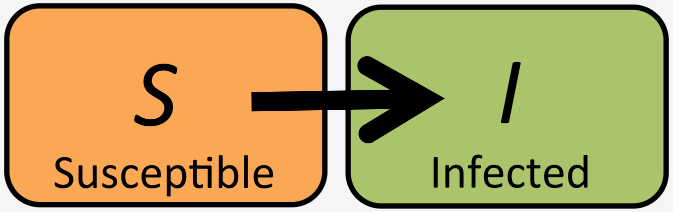
Outline of topics covered

- What is, how to build
    - a **simple compartmental disease model (**transmission)
- Mortality and Reproduction
- Common disease transmission ways
- Host heterogeneity
- Latency period, exposure
- Seasonality associated to processes
- Basic reproduction number , ‘disease risk’

Compartmental models

SI model

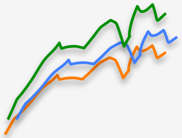


S
Susceptible

I
Infected

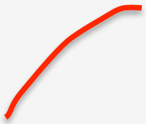
How many and how fast individuals move between compartments?

STOCHASTIC MODELS

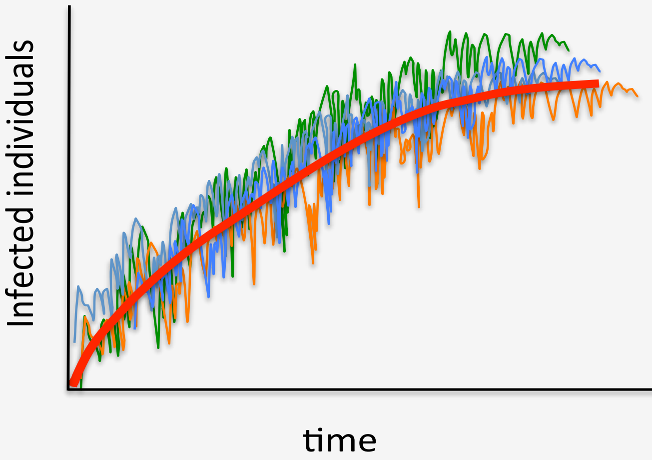


- **More realistic in general**
- All diseases are subjected to stochasticity in terms of chance of disease transmission.

DETERMINISTIC MODELS

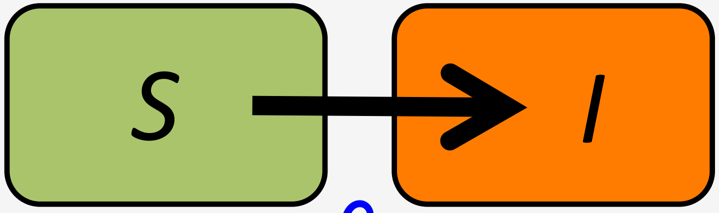


- Describe what happens ‘on average’ in a population.
- Parameters are fixed.
- The model predictions are ‘predetermined’.
- **A good approximation in large populations and high disease incidence** (stochastic fluctuations are small).



Discrete time models

… to understand continuous time models



β Transmission rate

Contact rate X **transmission probability**

Proportion of contacts over all possible contacts (t step)

Proportion of contacts that develop the disease

1/10= 0.1 X *infected/contact 1.0 (100%)*

All contacts develop the disease

$$\beta = 0.1$$

All possible contacts between *S* and *I*

S x I =10 contacts

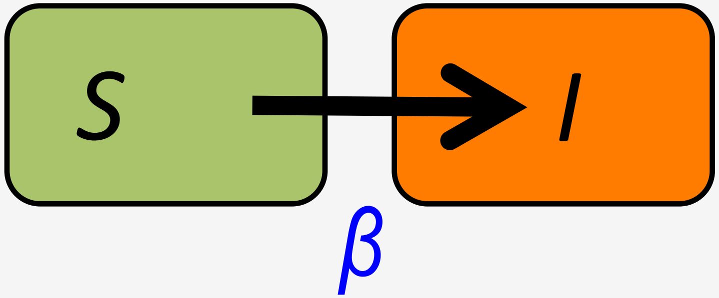
$$S_{t=0} = 10$$

$$I_{t=0} = 1$$

$$S_{t+1} = S_t - \beta \overbrace{S_t\ I_t} = 10 - 0.1\ x\ 10 = 9$$

$$I_{t+1} = I_t + \beta\ S_t I_t = 1 + 0.1\ x\ 10 = 2$$

Discrete time models



S

I

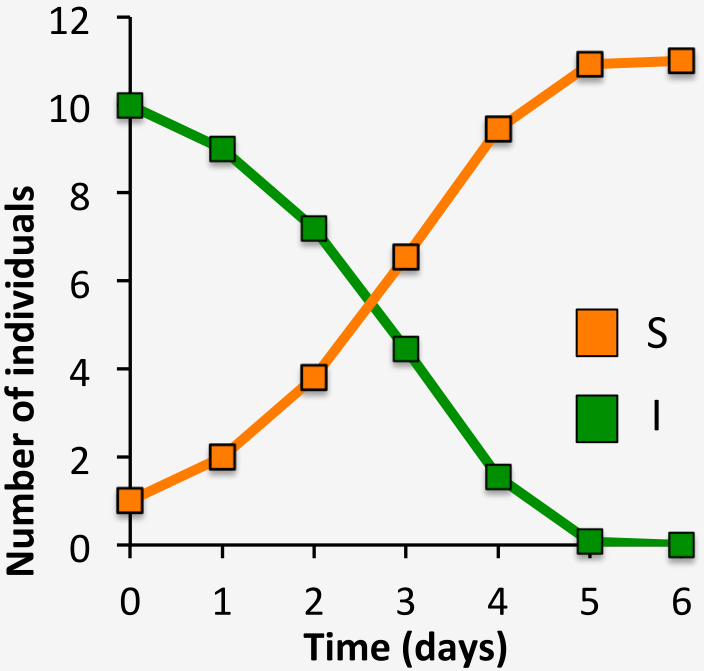
β

$$S_{t+1} = 9 \; ; I_{t+1} = 2$$

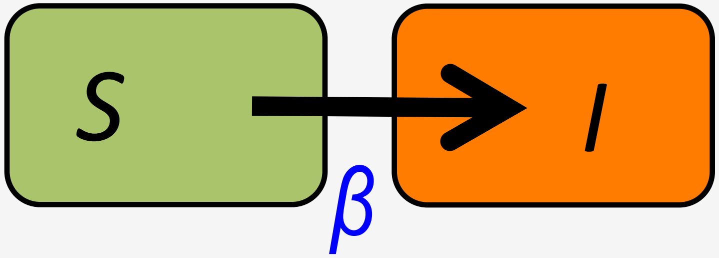
Next time step t+2

$$S_{t+2} = S_{t+1} - \beta \; S_t \, I_t \; = 9 - 0.1 \; x \overbrace{9 \; x \; 2}^{S \; x \; I = 18} = 7.2$$

$$I_{t+2} = I_{t+1} + \beta \, S_t I_t = 2 + 0.1 \; x \; 9 \; x \; 2 = 3.8$$



Continuous time models

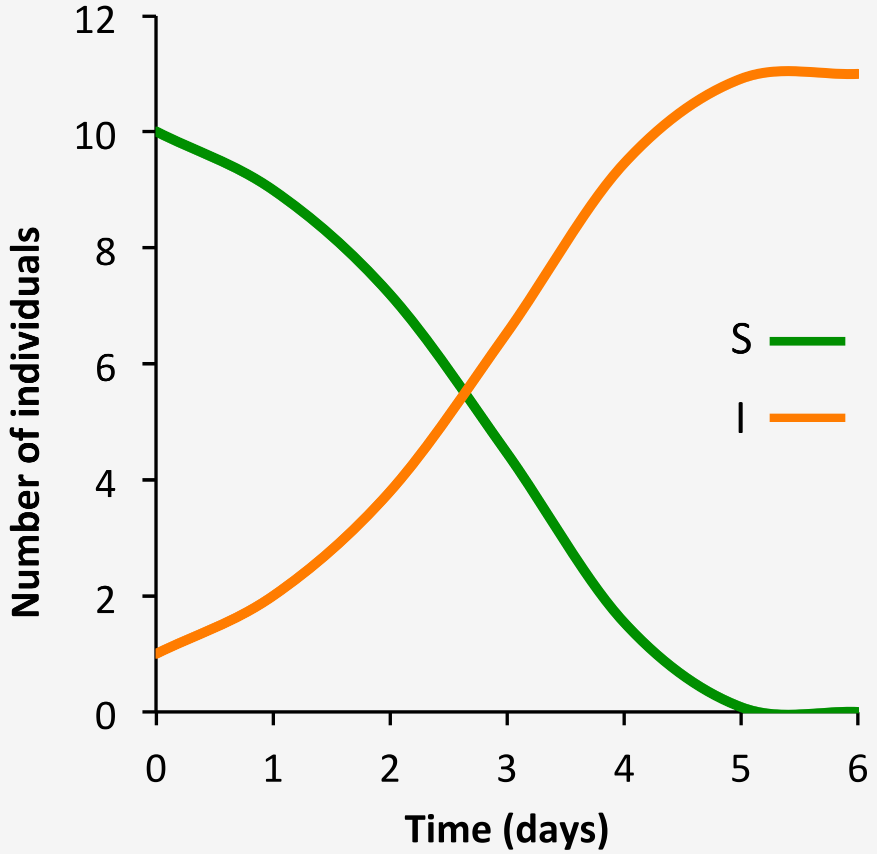


- Describe events occurring continuously (rather than at discrete time intervals)
- Imply to solve Differential Equation systems
- Each derivative function → rate of change of each subpopulation

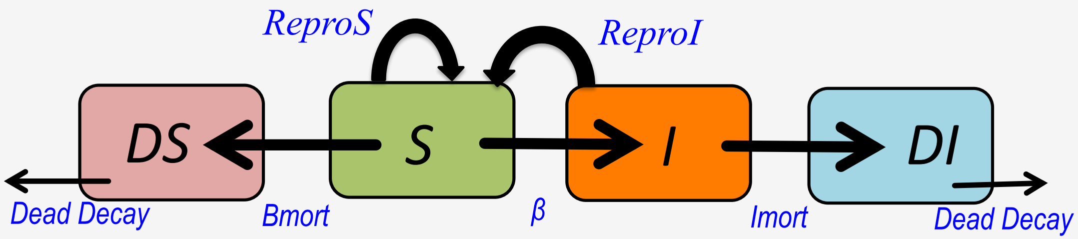
$$\frac{dS}{dt} = -\,\beta\; S(t)\; I(t)$$

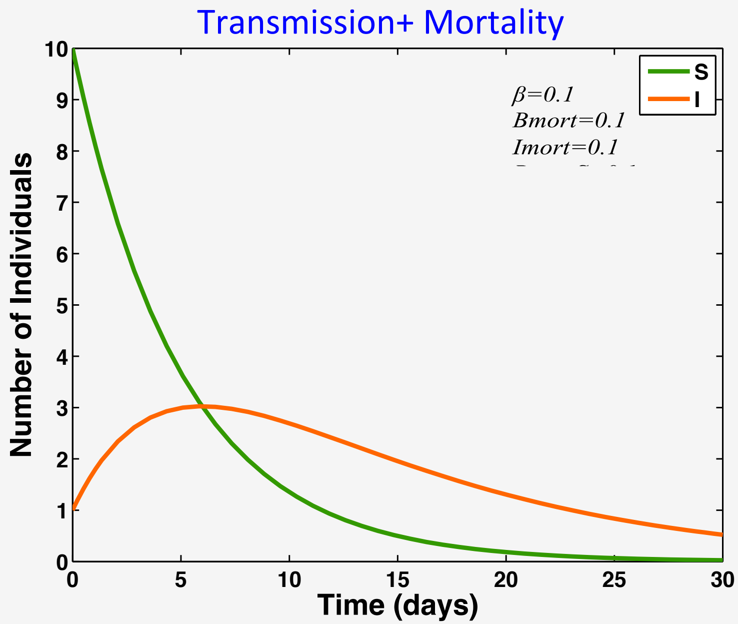
$$\frac{dI}{dt} = +\,\beta\; S(t)\; I(t)$$

$$\text{Initial conditions} \begin{cases} S(t=0) = S_0 = 10 \\ I(t=0) = I_0 = 1 \end{cases}$$



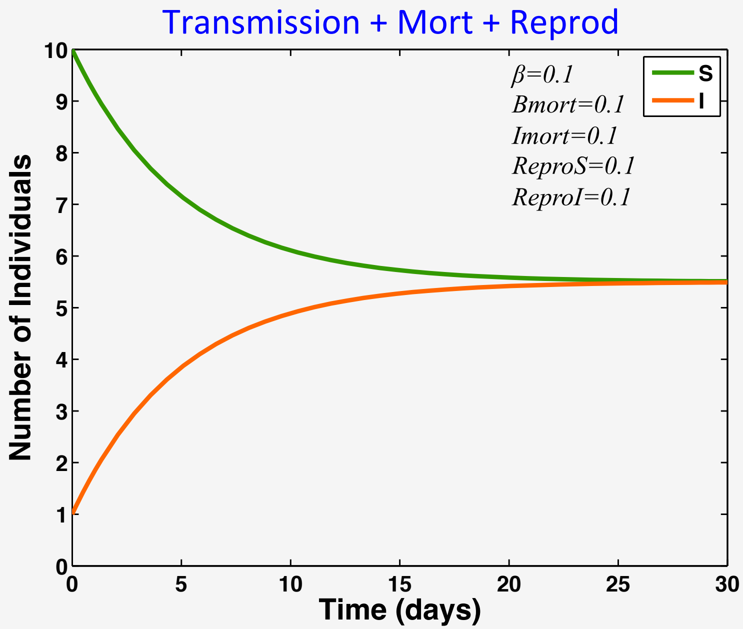
Mortality, Reproduction





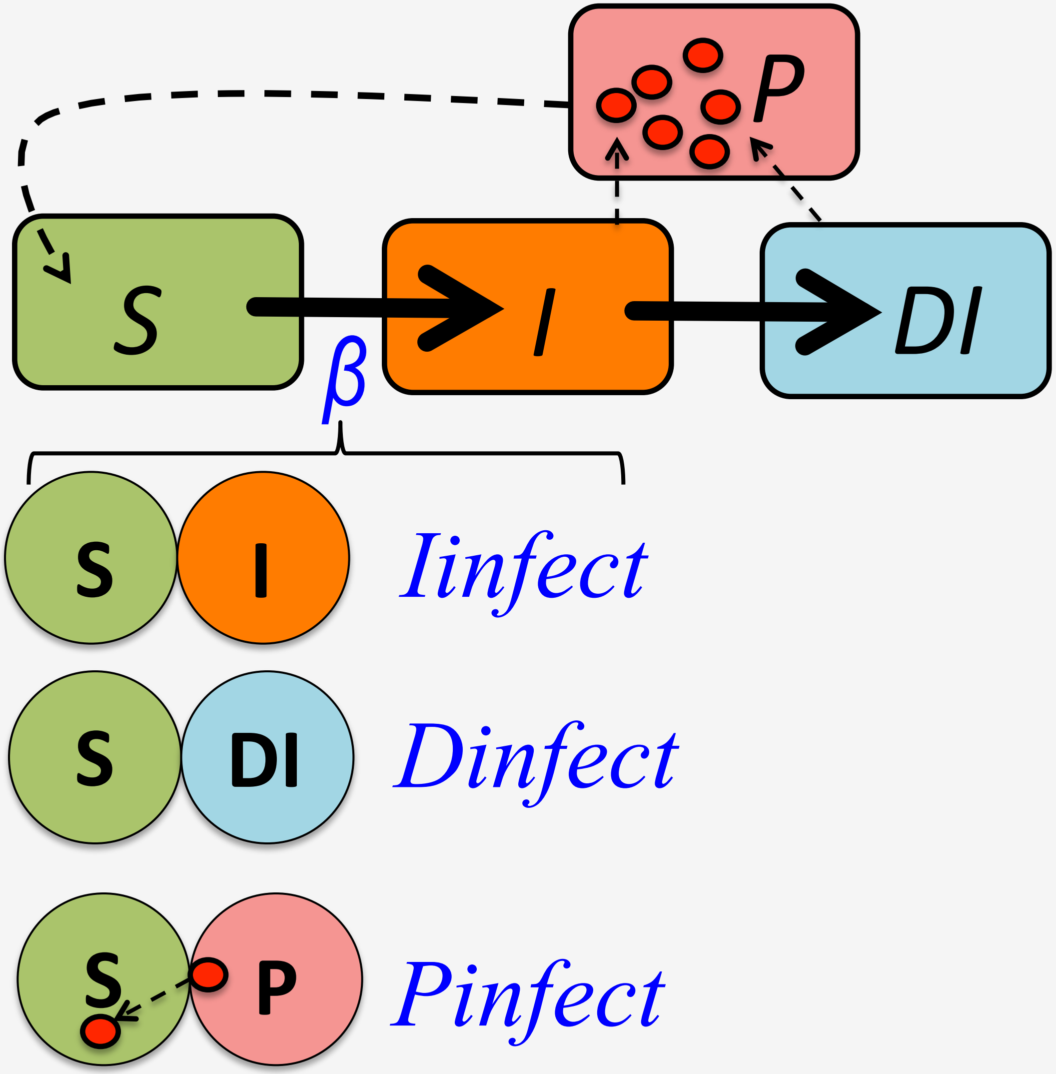
$$\frac{dS}{dt} = -\ \beta\ S\ I - Bmort\ \ S + ReproS\ S + ReproI\ I$$

$$\frac{dI}{dt} = +\ \beta\ \ S\ \ I - Imort\ \ I$$



Disease transmission

Infected, Dead infected and particles



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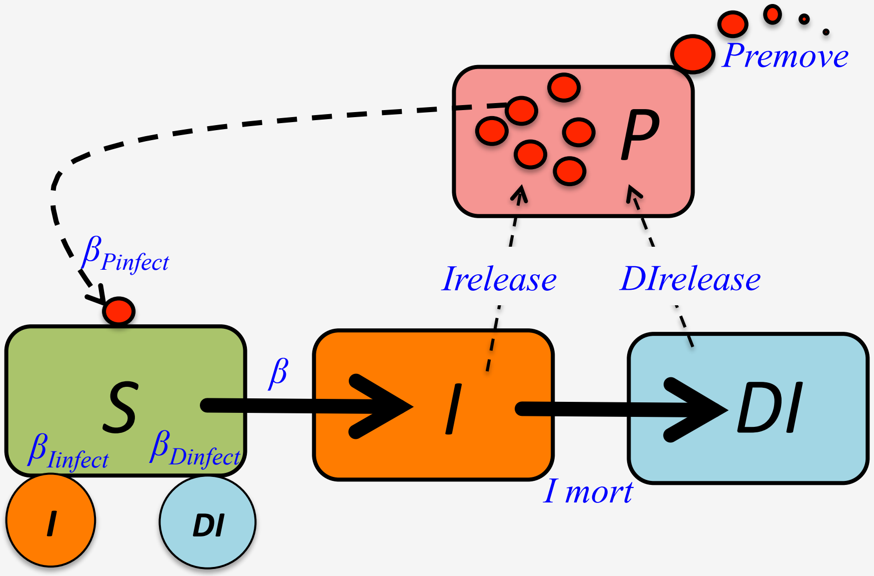


$$\frac{dS}{dt} = -\overbrace{(\beta_{Iinfect}\, S\, I + \beta_{Dinfect}\, S\, \underline{DI} + \beta_{Pinfect}\, S\, \underline{P})}^{\text{Transmission terms}} + \mathit{ReproS}\, S + \mathit{ReproI}\, I$$

$$\frac{dI}{dt} = +\ (\beta_{Iinfect}\, S\, I + \beta_{Dinfect}\, S\, DI + \beta_{Pinfect}\, S\, P) - \mathit{Imort}\ I$$

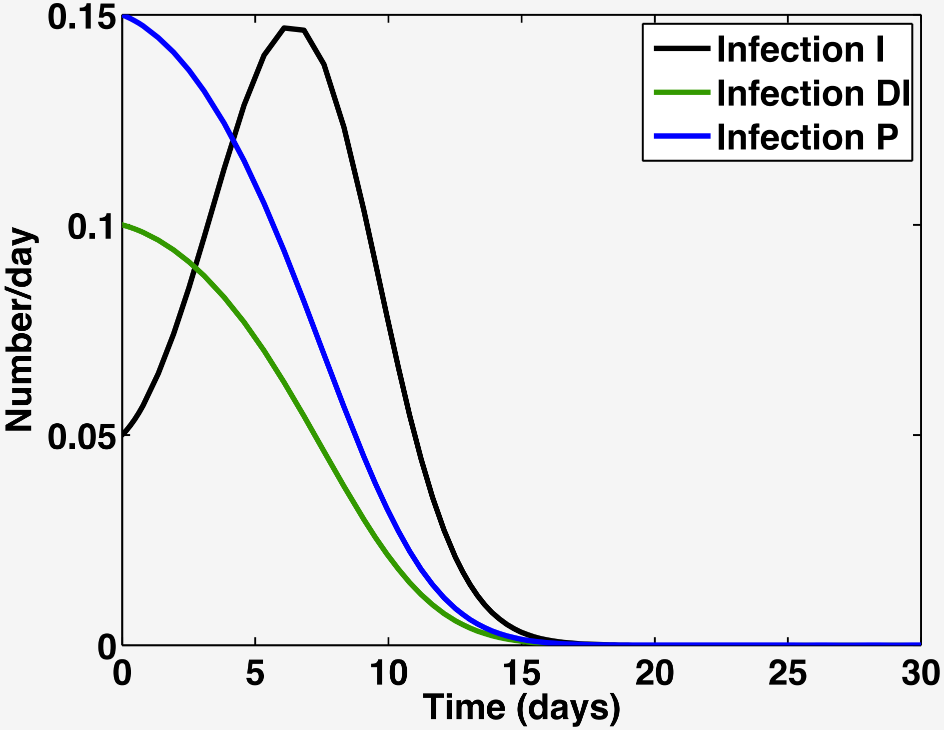
$$\frac{d\underline{DI}}{dt} = +\ \mathit{Imort}\ I - \mathit{DeadDecay}\, DI$$

$$\frac{d\underline{P}}{dt} = +\ \overbrace{\mathit{Irelease}\, I + \mathit{DIrelease}\, DI}^{\text{Particle release}} - \mathit{Premove}\, P$$

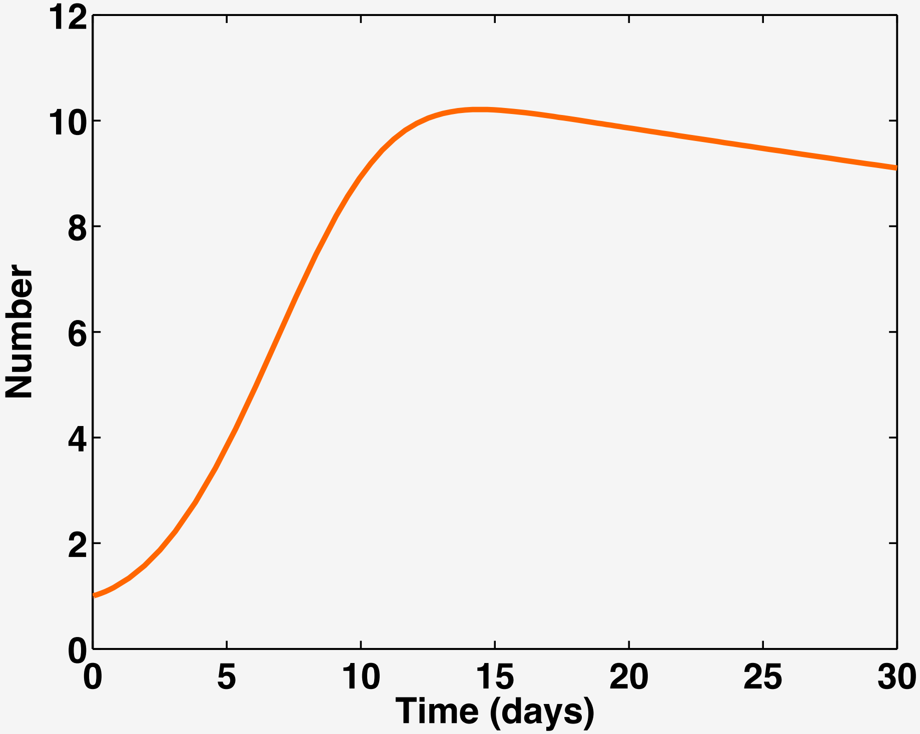
Disease transmission

Infected, Dead infected and Particles

Infection Rate



Infected



S(0)= 10, I(0)= 1, DI(0)= 1, P(0)= 1, Iinfect=0.005, DIinfect=0.01, Pinfect=0.015

Imort=0.008, DIdecay-=0.5, Irelease=0.5, DIrelease=0.5, Premove=0.3

Disease transmission

Host heterogeneity (age dependent transmission)

S1 Class 1 (juveniles) $\beta 1 = 0.01$

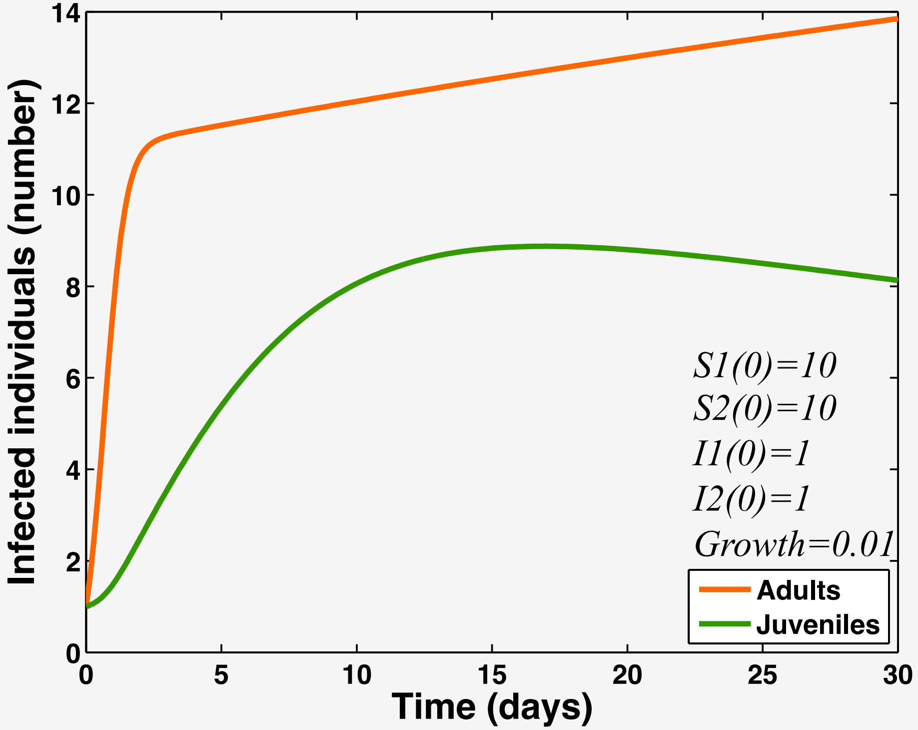
S2 Class 2 (adults) $\beta 2 = 0.2$

$$\frac{dS1}{dt} = -\beta 1\, S_1\,(I_1 + I_2) - growth\, S_1$$

$$\frac{dS2}{dt} = -\beta 2\, S_2\,(I_1 + I_2) + growth\, S_1$$

$$\frac{dI1}{dt} = +\beta 1\, S_1\,(I_1 + I_2) - growth\, I_1$$

$$\frac{dI2}{dt} = +\beta 2\, S_2\,(I_1 + I_2) + growth\, I_1$$



Disease transmission

With a latency period (New class → Exposed)

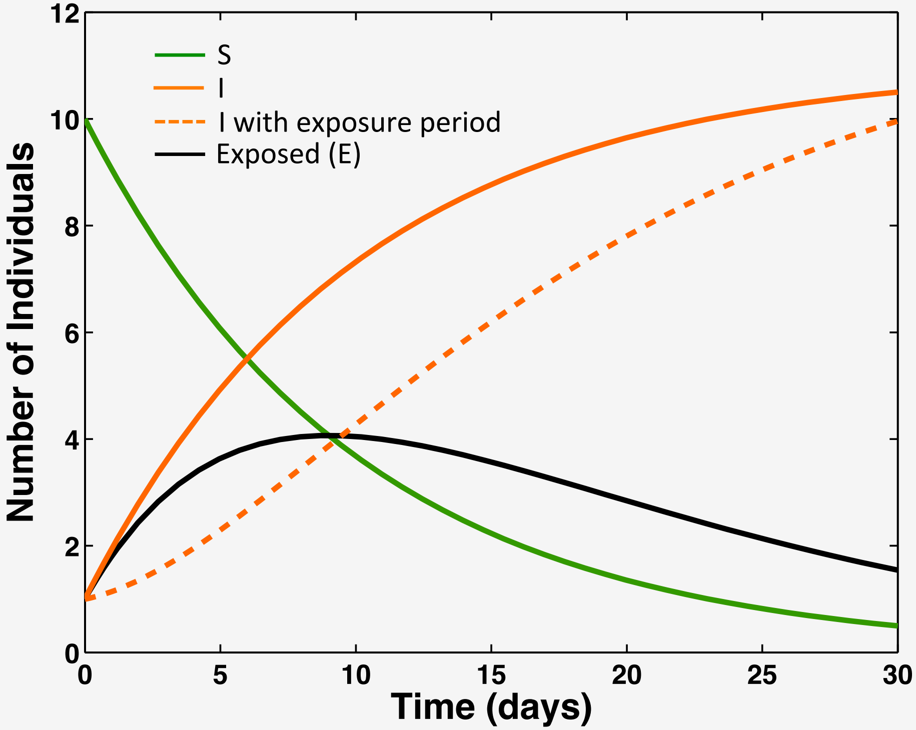
Duration of the latent period ~ $1/\sigma$

$$\frac{dS}{dt} = -\beta S I$$

$$\frac{dE}{dt} = +\beta S I - \sigma E$$

$$\frac{dI}{dt} = \sigma E$$

$\beta = 0.1 \quad \sigma = 0.1$ (10 days)

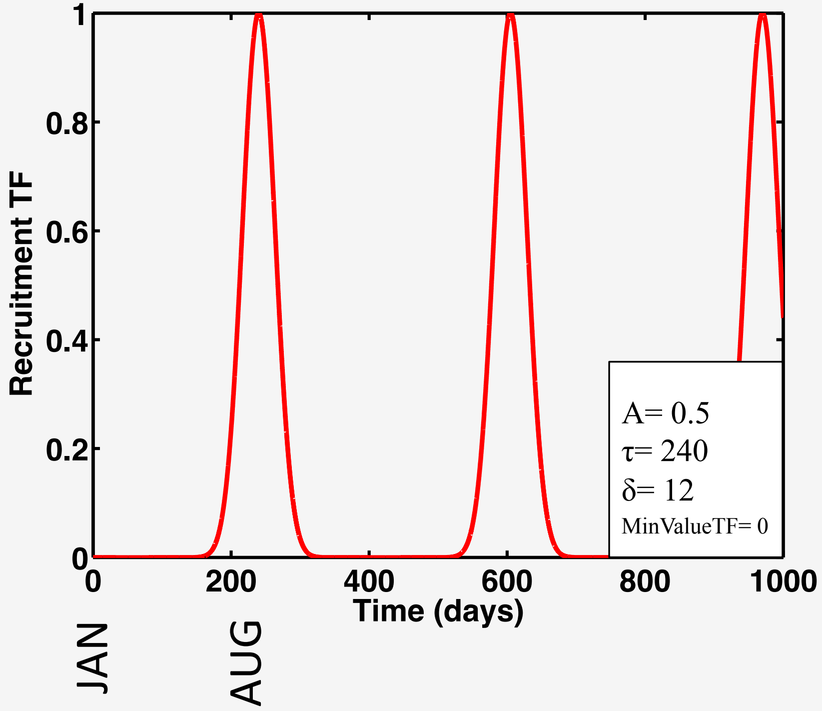


Disease transmission

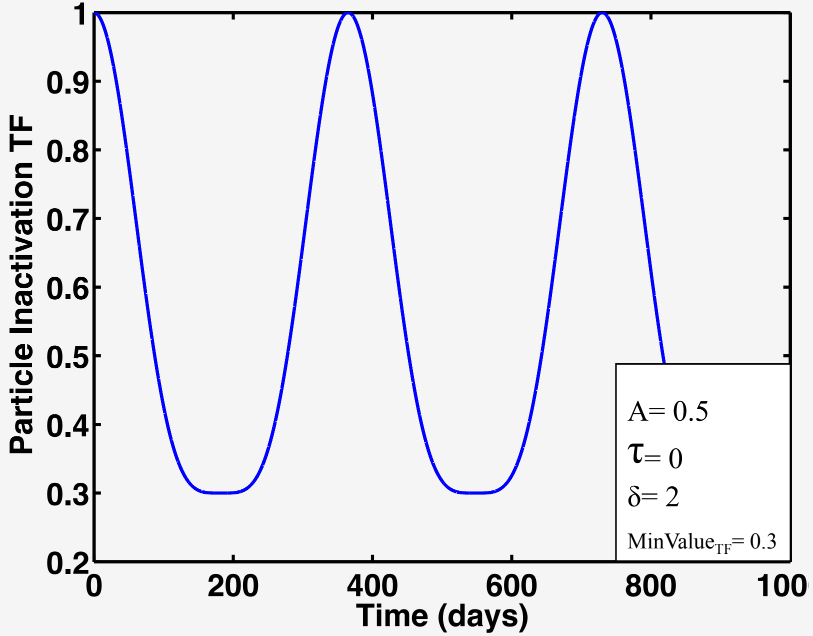
Seasonality; Time Factors (TF)

$$\mathrm{TF}= (1-\mathrm{MinValue}_{\mathrm{TF}})\ \overset{\text{Amplitude}}{\overset{\swarrow}{A}} \cos\left(1- 2\pi\,(t-\overset{\text{Time lag}}{\overset{\swarrow}{\tau}}) / 365\right)^{\overset{\text{Skewedness}}{\overset{\swarrow}{\delta}}} + \mathrm{MinValue}_{\mathrm{TF}}$$

Recruitment



Inactivation of particles



Seasonality

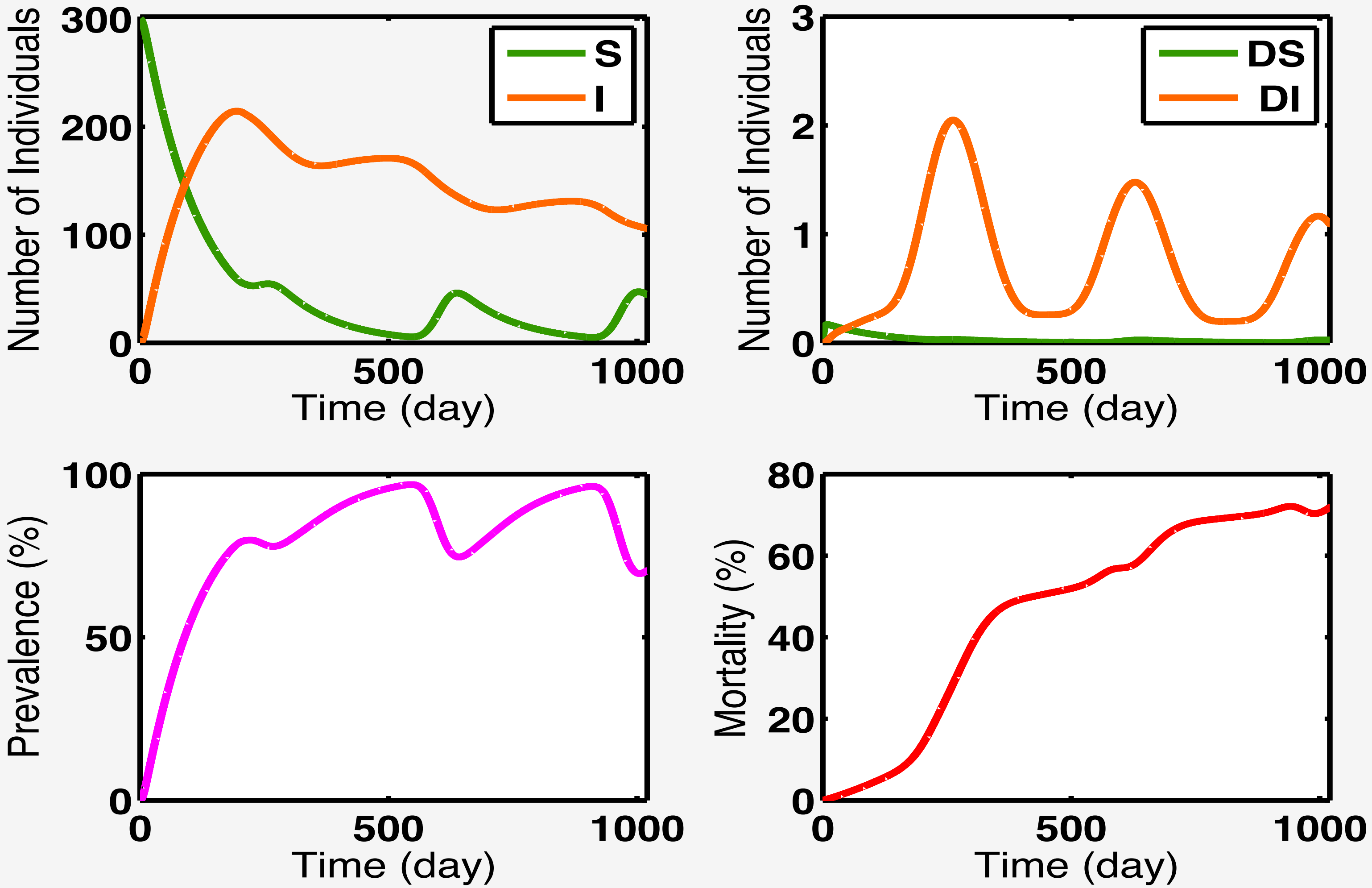
$$\frac{dS}{dt} = -\beta_{Pinfect}\, S\, P + TF_{recruitment}\, (ReproS\ \ S + ReproI\ I) - TF_{mortality}\, Bmort\ S$$

$$\frac{dI}{dt} = +\ \beta_{Pinfect}\, S\, P\ - TF_{mortality}\, Imort\ I$$

$$\frac{dDI}{dt} = +\ TF_{mortality}\, Imort\ \ I - TF_{decay}\, DeadDecay\ DI$$

$$\frac{dP}{dt} = \ Irelease\ I + Direlease\ DI)\ - \ TF_{inactivation}\, Premove_{Inact.}\ P\ \ \text{-}\ Premove_{others}\ P$$

Seasonality in the model S–I–P



Basic reproduction number, R_0 - *for model S-I-P*

$R_0 > 1$ Epizootic $R_0 < 1$ Disease extinction

Next Generation Matrix

Diekmann et al . 2010

$$\left\{\begin{aligned} \frac{dS}{dt} &= -\beta_{Pinfect}\, P\, S \\ \frac{dI}{dt} &= +\beta_{Pinfect}\, P\, S - Imort\, I \\ \frac{dP}{dt} &= +Irelease\, I - Premove\, P \end{aligned}\right.$$

1. **Find the steady state for a disease free population→** I=P=0

$$\frac{dS}{dt} = 0$$ the population is constant at the initial population level $S_0=N$

2. **Linearize the equations that are involved in the infectious processes**
   Around **N** and for **I and P << N**

$$\frac{dI}{dt} = +\beta_{Pinfect}\, P\, N - Imort\, I$$

$$\frac{dP}{dt} = +Irelease\, I - Premove\, P$$

Basic reproduction number, R_0

Next Generation Matrix (NGM)

$$\frac{dI}{dt} = + \beta_{Pinfect}\, P\, N - Imort\, I \qquad \text{Eq. } I$$

$$\frac{dP}{dt} = + Irelease\, I - Premove\, P \qquad \text{Eq. } P$$

3. Descompose the Jacobian matrix, used to describe the ODE, in two matrix:

T (transmission, gain terms +)

Σ (transition, loss terms -)

$$\mathbf{T} = \begin{array}{cc} +\mathrm{I} & +\mathrm{P} \\ \left(\begin{array}{c} 0 \\ Irelease \end{array}\right. & \left.\begin{array}{c} \beta_{Pinfect}\, N \\ 0 \end{array}\right) \end{array} \begin{array}{l} \\ \text{Eq. } I \\ \text{Eq. } P \end{array} \qquad \mathbf{\Sigma} = \begin{array}{cc} -\mathrm{I} & -\mathrm{P} \\ \left(\begin{array}{c} -Imort \\ 0 \end{array}\right. & \left.\begin{array}{c} 0 \\ -Premove \end{array}\right) \end{array} \begin{array}{l} \\ \text{Eq. } I \\ \text{Eq. } P \end{array}$$

$$\mathbf{\Sigma}^{-1} = \begin{pmatrix} \frac{-1}{Imort} & 0 \\ 0 & \frac{-1}{Premove} \end{pmatrix}$$

4. Construct the NGM for the large domain (K_L = - T·Σ^{-1})

$$\mathbf{K_L} = -\mathbf{T} \cdot \mathbf{\Sigma}^{-1} = \begin{pmatrix} 0 & \frac{\beta_{Pinfect}\, N}{Premove} \\ \frac{Irelease}{Imort} & \end{pmatrix}$$

Basic reproduction number, R_0

5. **Calculate the eigenvalues for K_L. The dominant eigenvalue is R_0.**

$$\begin{vmatrix} -\lambda & \frac{\beta_{Pinfect} N}{Premove} \\ \frac{Irelease}{Imort} & -\lambda \end{vmatrix} = 0$$

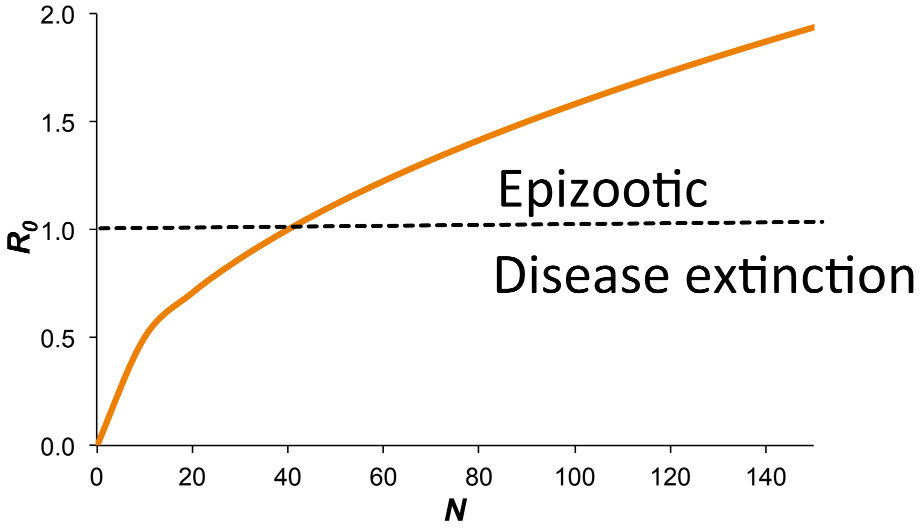
$$\lambda^2 - \frac{\beta_{Pinfect} N \, Irelease}{Imort \cdot Premove} = 0$$

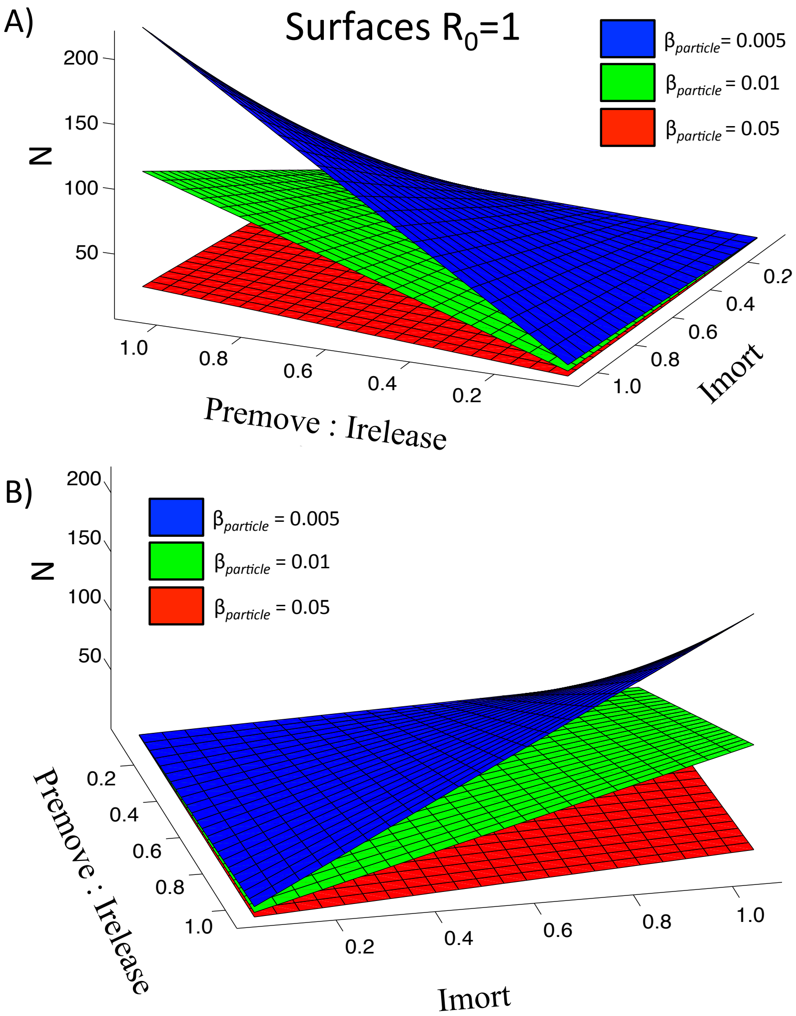
with solution

$$\lambda = \sqrt{\frac{\beta_{Pinfect} N}{Imort} \frac{Irelease}{Premove}} = \boldsymbol{R_0}$$

Basic reproduction number, R_0

$$R_0=\sqrt{\frac{\beta_{Pinfect}\,N}{Imort}\,\frac{Irelease}{Premove}}$$





Summary

1) Compartmental deterministic models are particularly suitable for large populations and high infection incidence diseases

2) Transmission models can contemplate…

   - Both host and pathogen associated biological factors.
   - Host heterogeneity in terms of transmission (e.g. age)
   - Exposure period (latency)
   - Seasonality
   - Formulation/calculation of basic reproduction number, *R0*

3) Next…

   - **Model parameterization with available data**
   - Numerical solving of differential equations in these 1-pop models
   - Metapopulation models
   - Multispecies models

Some Abalone Data and an Intro To Parameter Estimation

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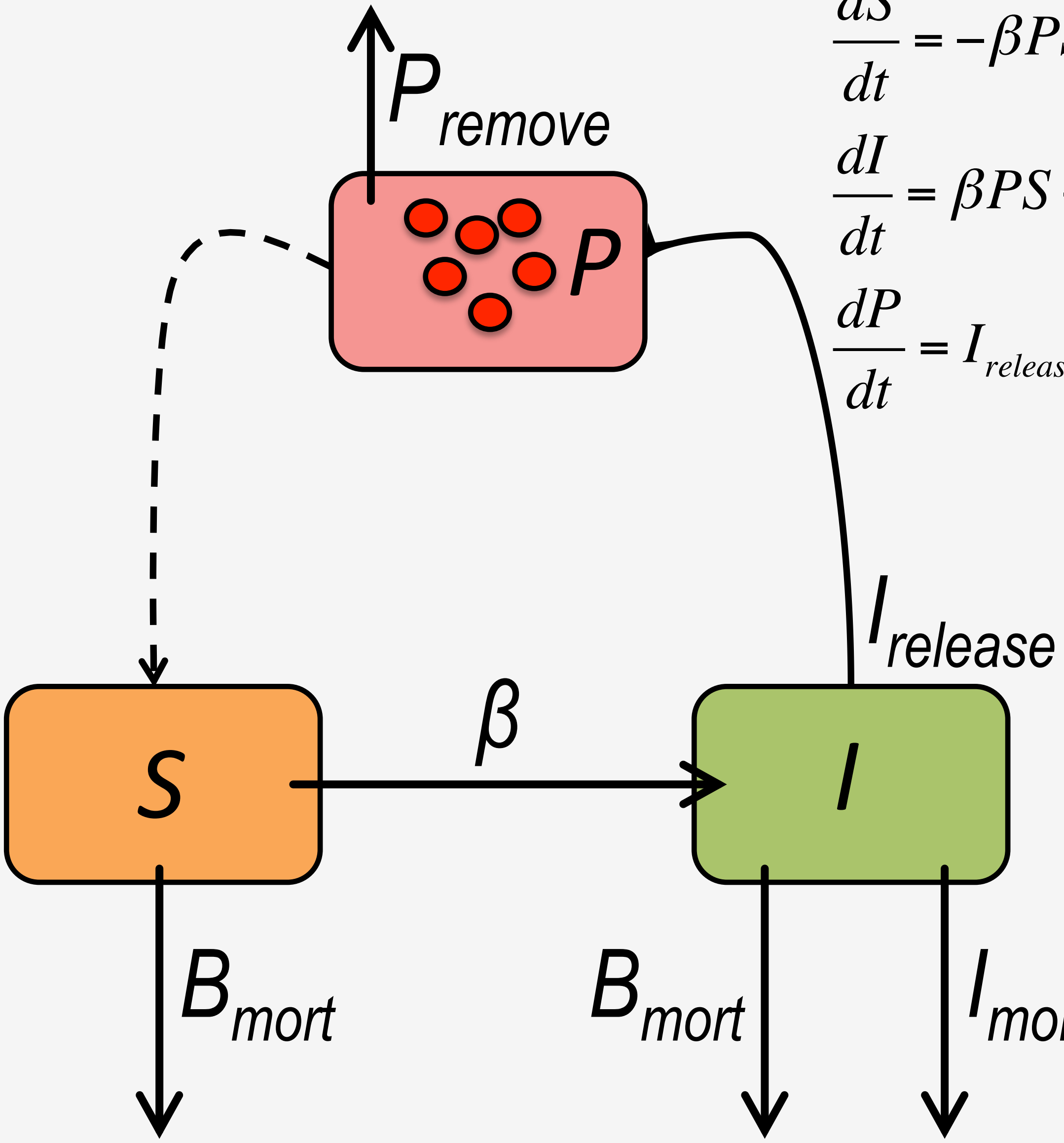
Recap: a simplified particle contact model

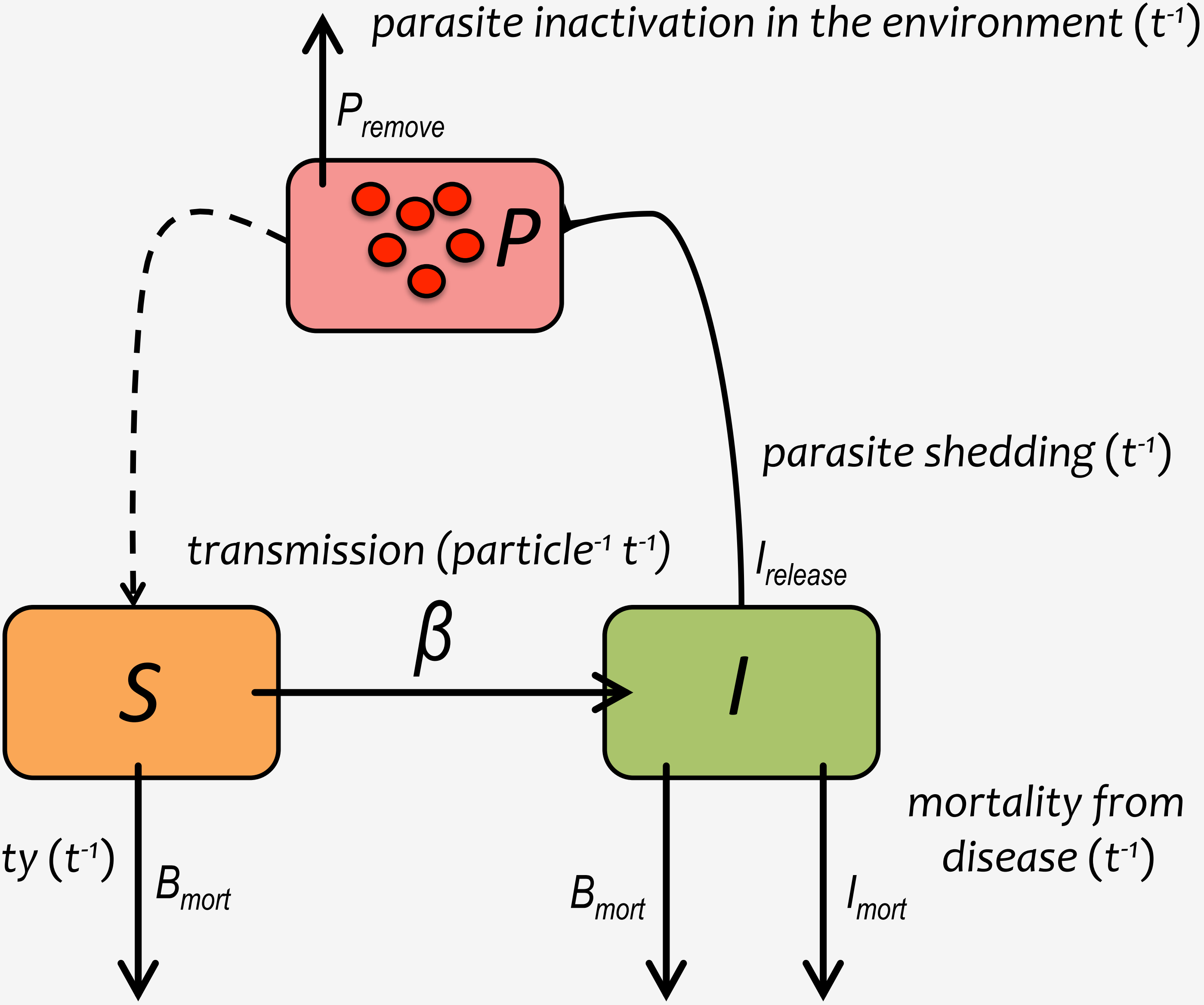


$$\frac{dS}{dt} = -\beta PS - B_{mort}S$$

$$\frac{dI}{dt} = \beta PS - (B_{mort} + I_{mort})I$$

$$\frac{dP}{dt} = I_{release}I - P_{remove}P$$

Common ecological rate parameters



parasite inactivation in the environment (t^{-1})

P_{remove}

parasite shedding (t^{-1})

$I_{release}$

transmission ($particle^{-1}\ t^{-1}$)

β

natural mortality (t^{-1})

B_{mort}

mortality from disease (t^{-1})

I_{mort}

Transmission (β) and the force of infection (λ)

$$\lambda = \frac{\text{\# of new infections}}{\text{\# exposed} * \text{duration of exposure}}$$

Transmission (β) and the force of infection (λ)

$$\lambda = \frac{\text{\# of new infections}}{\text{\# exposed * } \cancel{\text{duration of exposure}}}$$

If λ is a *per capita* instantaneous incidence of infection, under density dependent transmission $\lambda = \beta P$

$$\beta = \frac{\lambda}{P}$$

Observations of the abalone WS-RLO system

Parameter	Definition	Value	Reference
B_{mort}	Natural mortality rate	0.15 yr^{-1}	Tegner et al (1989)
I_{mort}	WS mortality rate	0.05 – 0.90 yr^{-1}	Moore et al (2011)
β	Coefficient of transmission	?	
$I_{release}$	Production of infectious stages	?	
P_{remove}	Parasite inactivation in the environment	52.14 – 365 yr^{-1}	C. Friedman *pers. comm.*

Parameter estimation – mortality

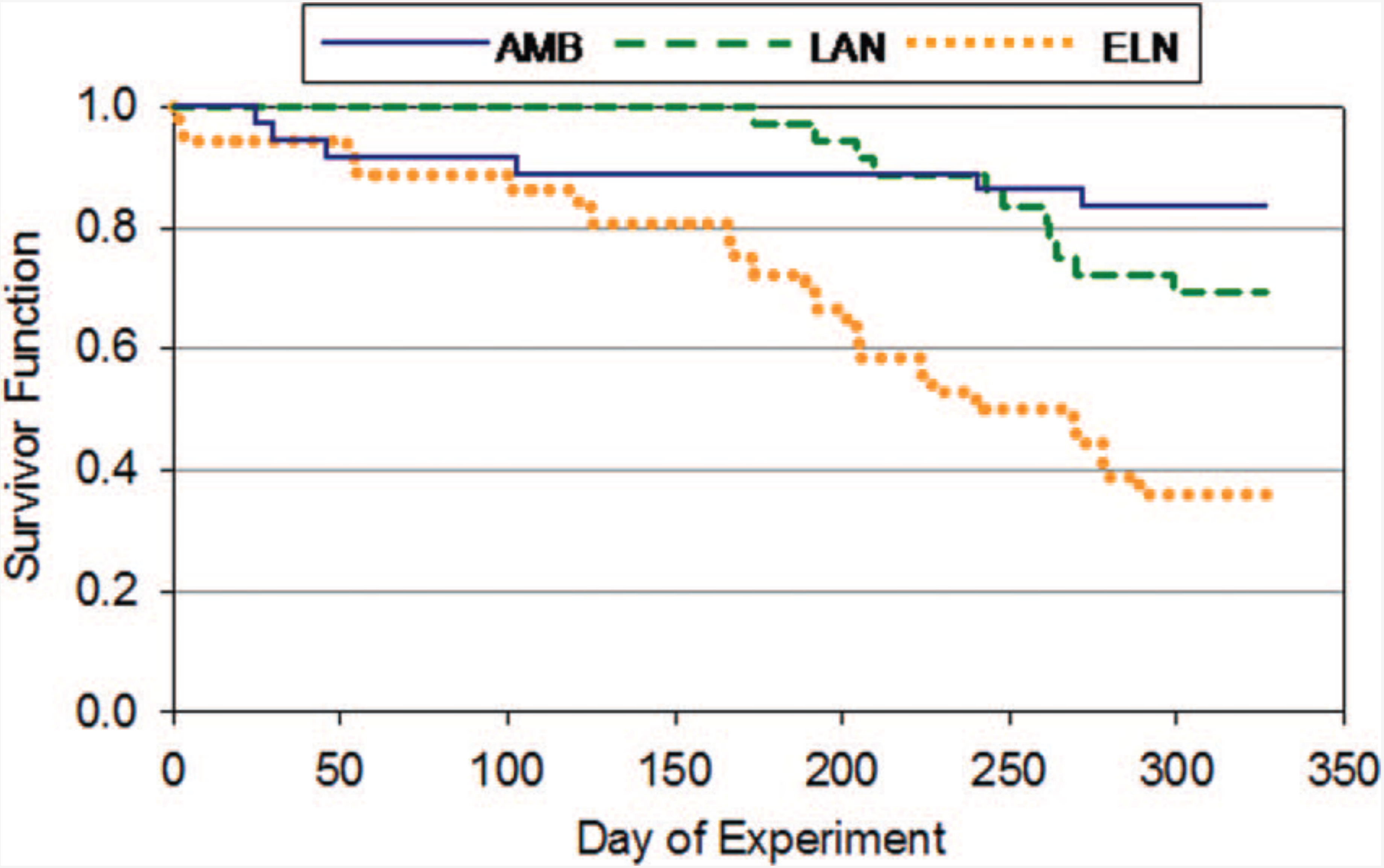
Estimating survival or mortality is a problem of estimating the proportion of individuals that survive or die from one time period to the next

Parameter estimation – mortality

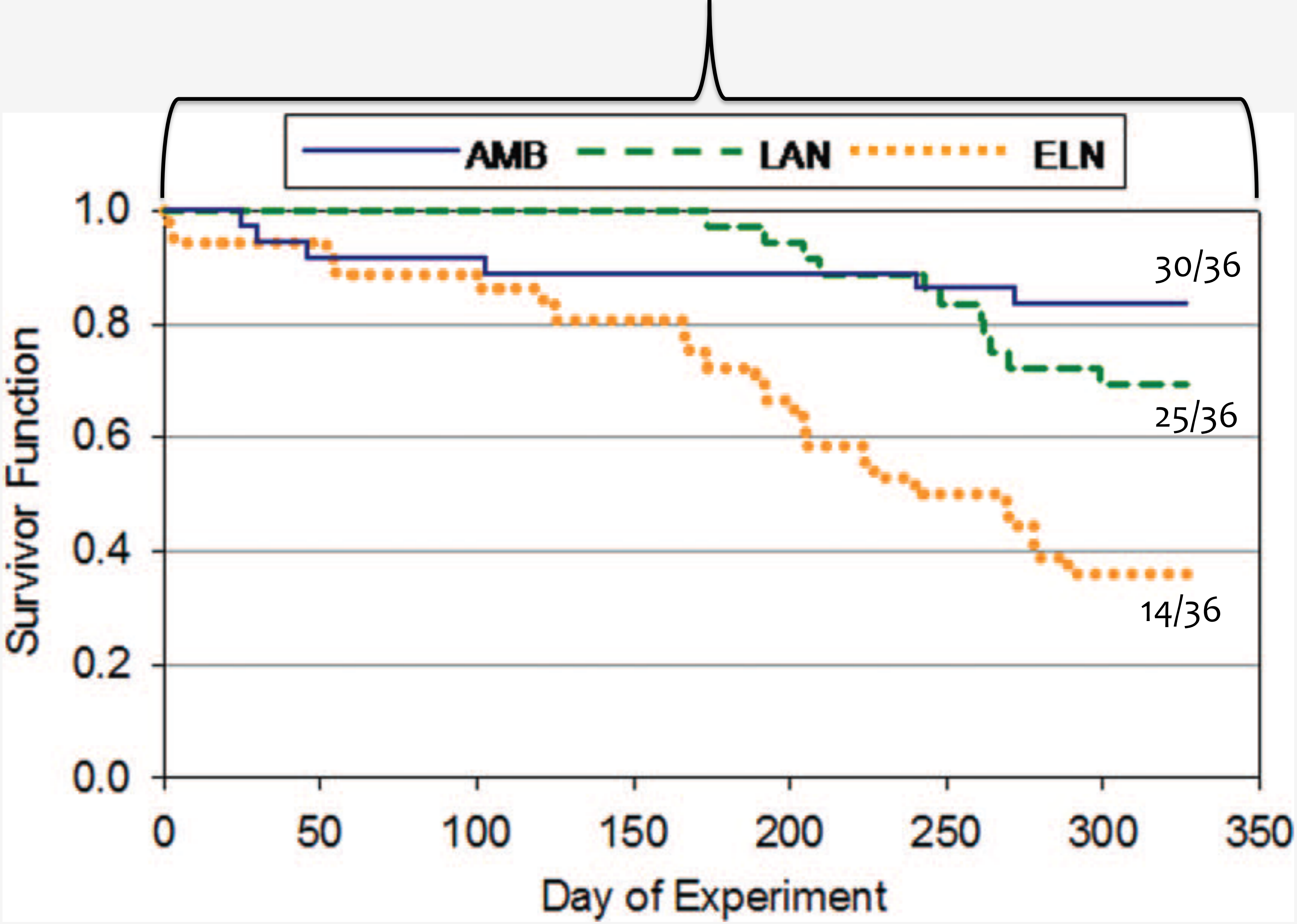
Estimating survival or mortality is a problem of estimating the proportion of individuals that survive or die from one time period to the next

If the rate of an event happening to any one individual is ***p***, and there are ***n*** independent individuals, the number of individuals ***y*** to which the event happens follows a **binomial** distribution

$$LogL(p \mid n, y) = y\log(p) + (n - y)\log(1 - p)$$



Moore et al (2011)



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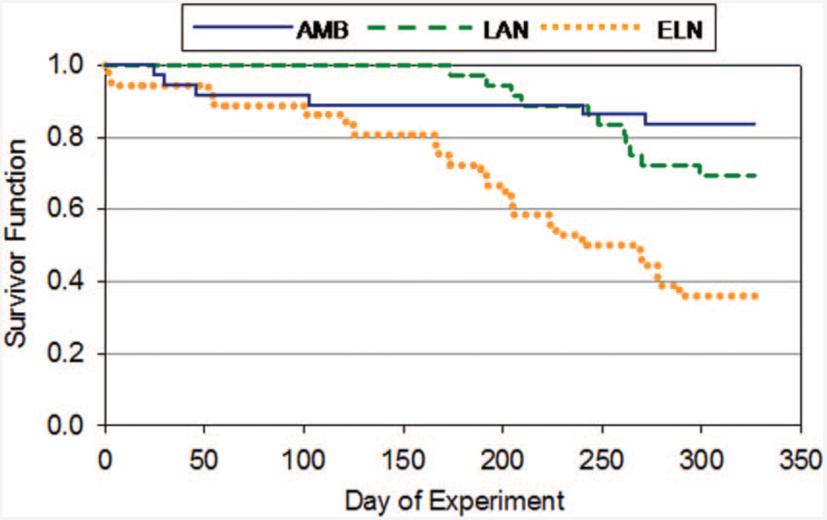
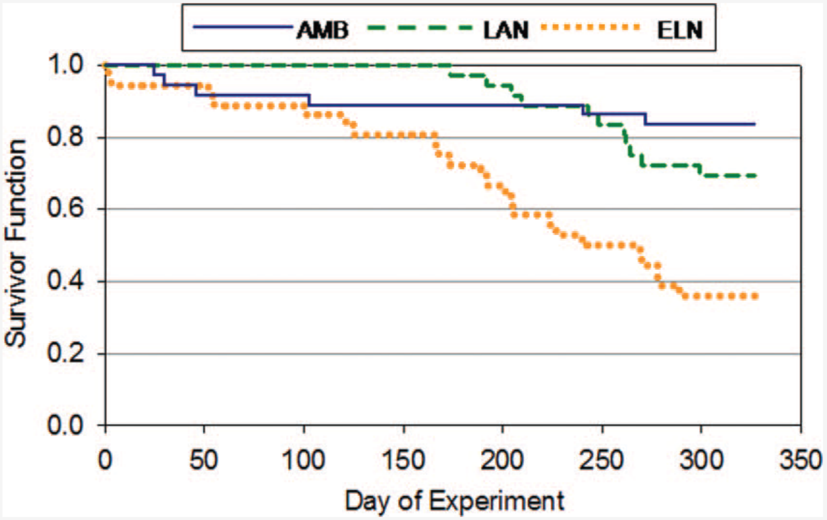


$$p = e^{(B_{mort} + I_{mort})t}$$

$$LogL(p \mid n, y) = y\log(p) + (n - y)\log(1 - p)$$



$$p = e^{(B_{mort} + I_{mort})t}$$

$$LogL(p \mid n, y) = y\log(p) + (n - y)\log(1 - p)$$

$$LogL(I_{mort} \mid n, y) = y(0.15 + I_{mort})t + (n - y)\log[1 - e^{(0.15 + I_{mort})t}]$$

Lets try it!

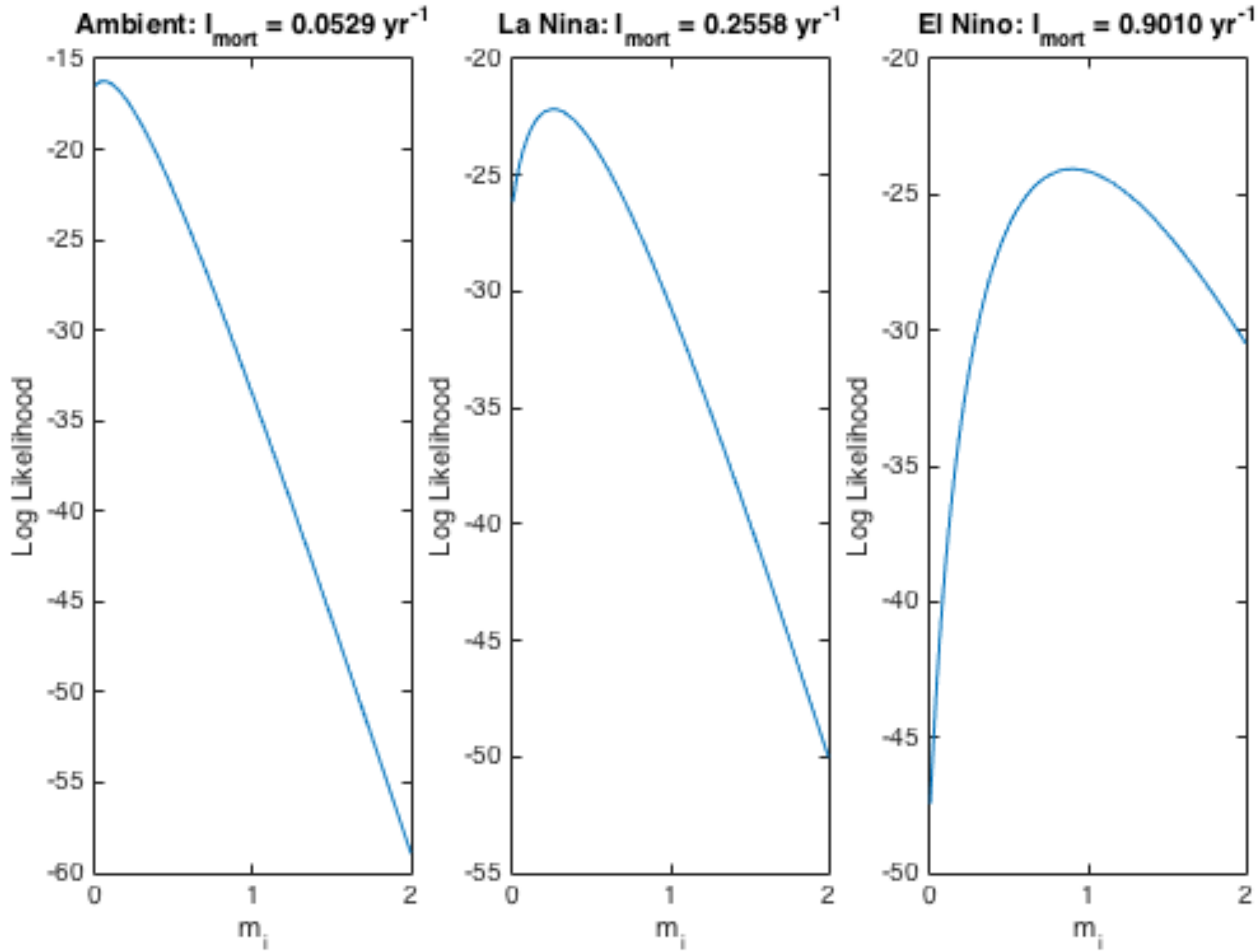
$$LogL(I_{mort} \mid n, y) = y(0.15 + I_{mort})t + (n - y)\log[1 - e^{(0.15+I_{mort})t}]$$

Function files

- binoLogLike.m
- binoNLogLike.m

Scripts

- fit_mortality.m


Ambient: l_{mort} = 0.0529 yr^{-1}
La Nina: l_{mort} = 0.2558 yr^{-1}
El Nino: l_{mort} = 0.9010 yr^{-1}
Log Likelihood
m_i
-15
-20
-25
-30
-35
-40
-45
-50
-55
-60
0
1
2