

Workshop on R and movement ecology:

Hong Kong University, Jan 2018



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Lecture 7

Epidemiological models



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College of
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Continuous time deterministic SEIR disease state model

S: susceptible

E: exposed
(infected but not infectious)

I: infectious

R=V+D:
(V: immune, D: dead)

λ : recruitment

μ : natural mortality

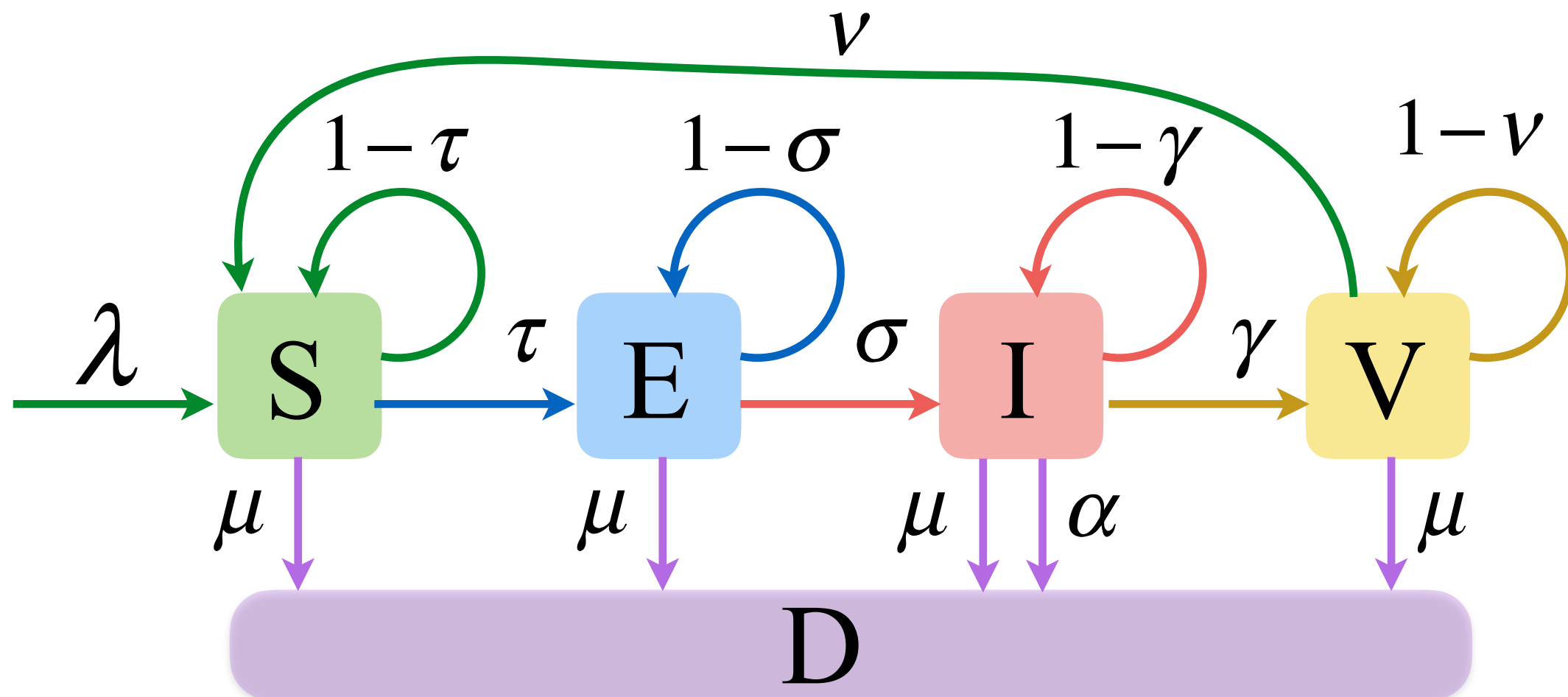
α : disease-induced mortality

τ : per-capita S transmission rate

$1/\sigma$: latent-period

$1/\gamma$: infectious-period

$1/\nu$: immune-period



Continuous time deterministic SEIR disease state model

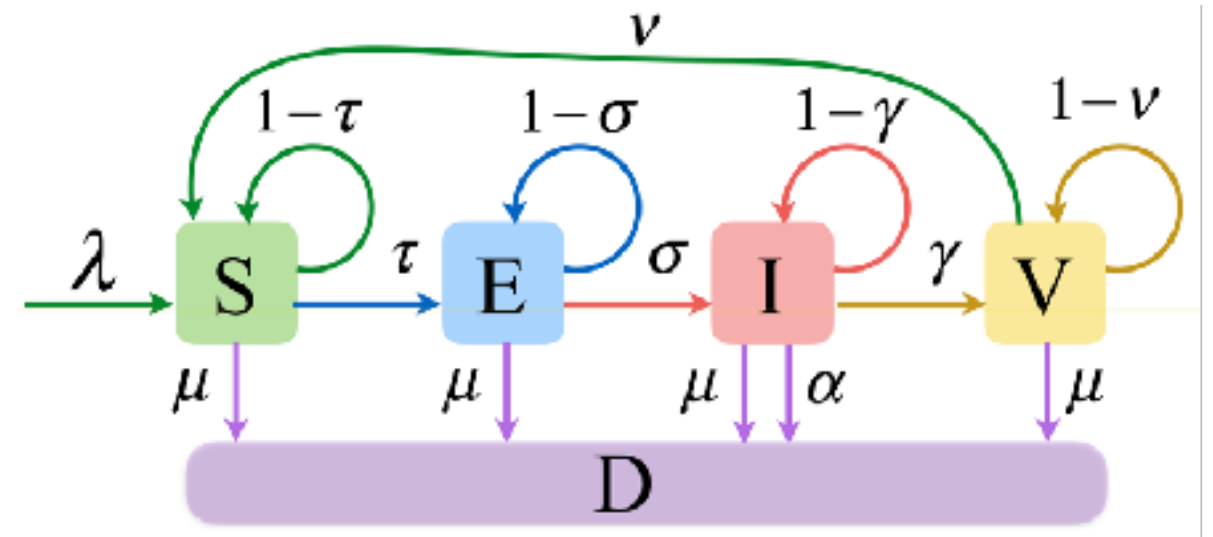
$$\frac{dS}{dt} = \lambda(t) + \nu V - (\tau(I, N) + \mu)S$$

$$\frac{dE}{dt} = \tau(I, N)S - (\sigma + \mu)E$$

$$\frac{dI}{dt} = \sigma E - (\gamma + \alpha + \mu)I$$

$$\frac{dV}{dt} = \gamma I - (\nu + \mu)V$$

$$\tau(I, N) = \frac{\beta I}{N}, \quad \text{where } N = S + E + I + V$$



Expected number of new infections from index case

$$R_0 = \frac{\beta \sigma}{(\sigma + \mu)(\gamma + \mu + \alpha)}$$

Outbreak threshold

$$\beta > \frac{(\sigma + \mu)(\gamma + \mu + \alpha)}{\sigma}$$

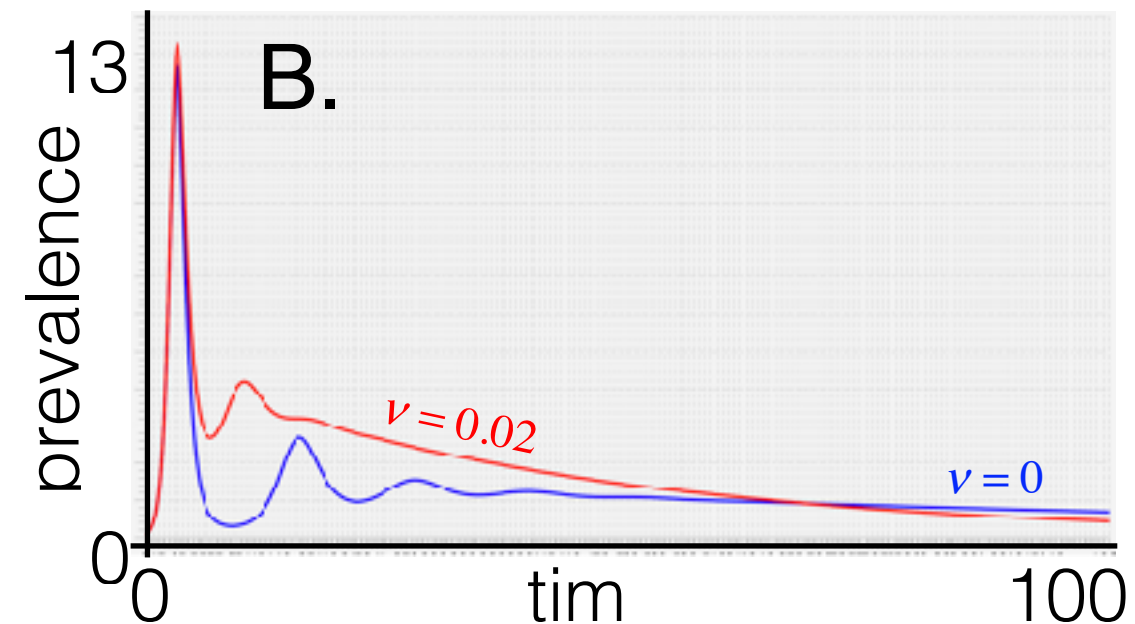
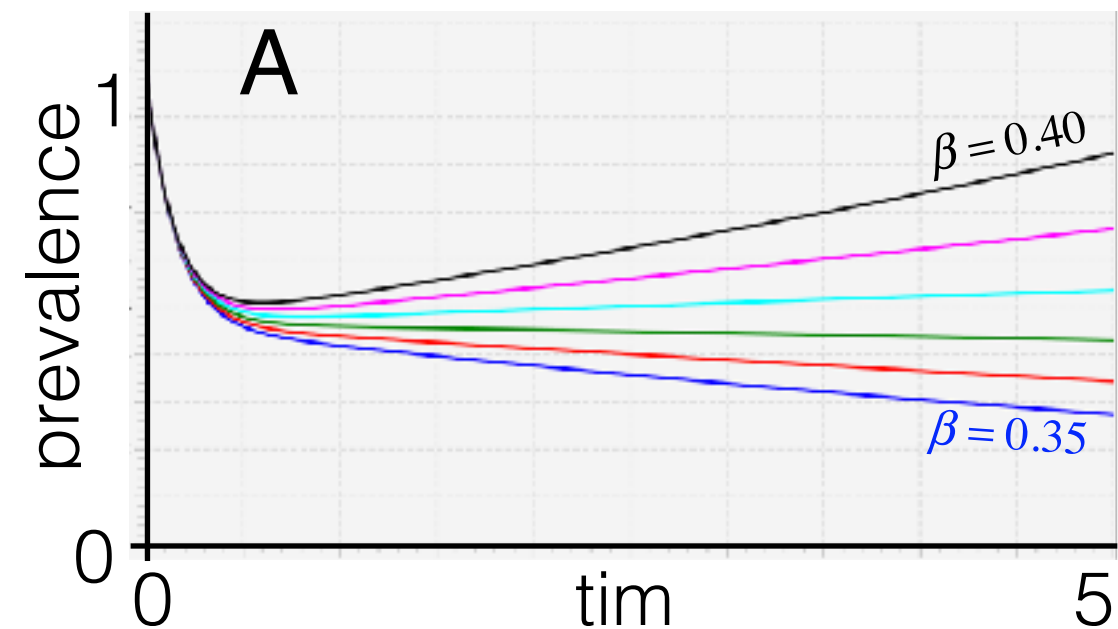
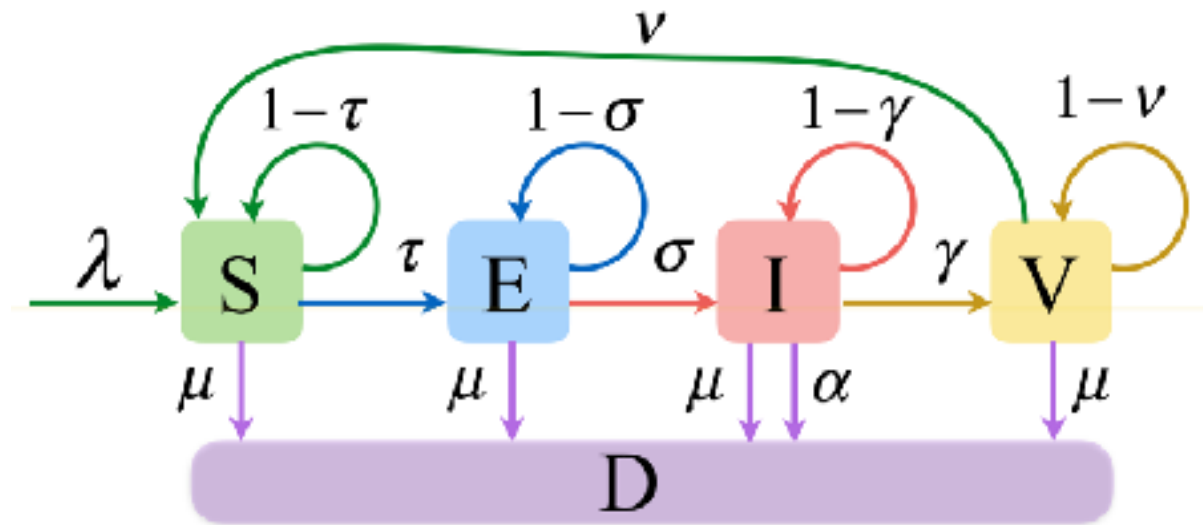
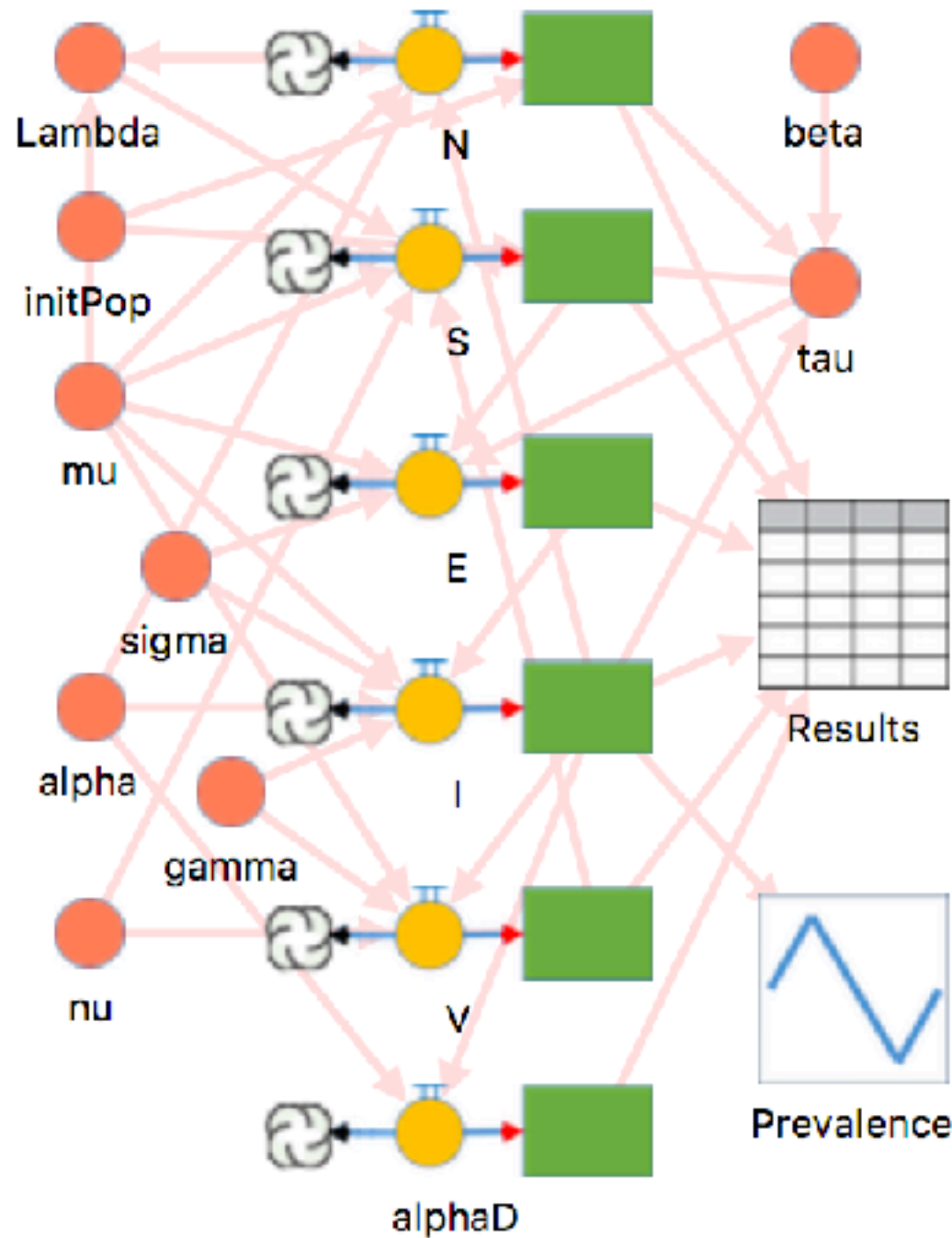
Deaths: natural & disease

$$D^\mu(t) = \int_0^t \mu N(z) dz$$

$$D^\alpha(t) = \int_0^t \alpha I(z) dz$$

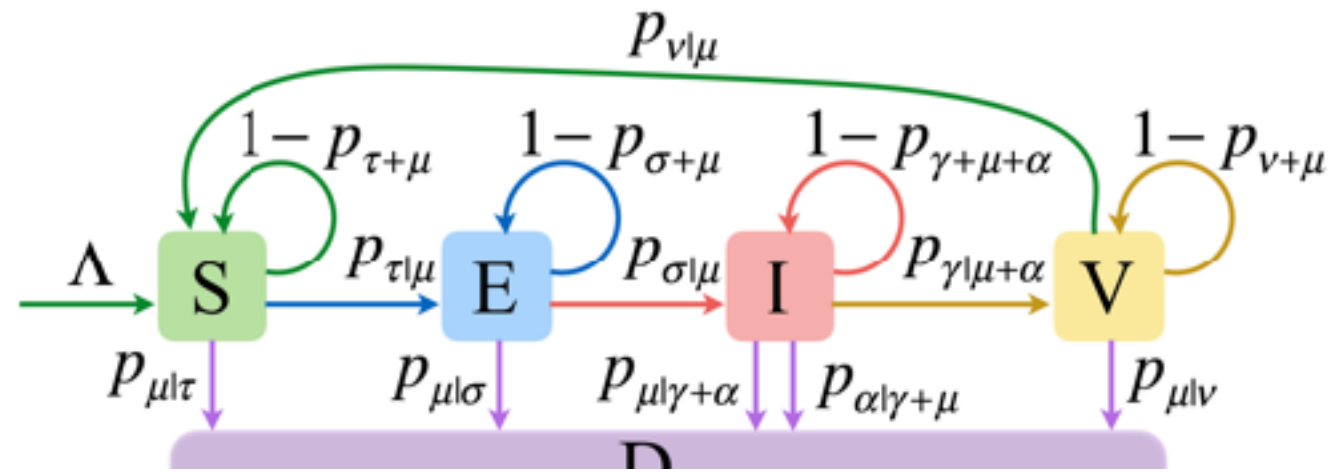
Continuous time deterministic SEIR disease state model

Numerus Model Builder Implementation

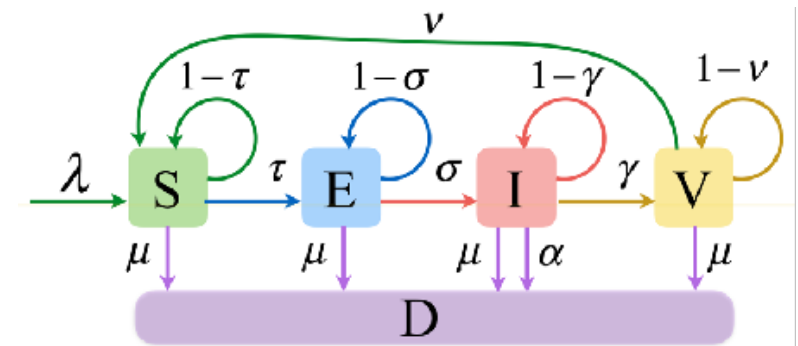


$S(0) = 999$,
 $E(0) = 0$, $I(0) = 1$, and $V = 0$ for the case $\mu = 0.01$,
 $\alpha = 0.05$, $\sigma = \gamma = 0.3$, under the assumption that
 $\lambda(t) = \mu N(t)$. In addition: in A. $\nu = 0$ and β varies
 from 0.35 to 0.40 (in steps of 0.01); and in B. $\beta = 1$
 and $\nu = 0.02$ (red) and $\nu = 0$ (blue).

Discrete time deterministic SEIR disease state model



Recall the continuous



$$\Lambda_t = \int_t^{t+1} \lambda(s) ds \quad \text{and} \quad \tau_t = \tau(I(t), N(t))$$

$$S(t+1) = \Lambda_t + p_{\nu|\mu} V(t) + S(t)(1 - p_{\tau_t+\mu})$$

$$E(t+1) = p_{\tau_t|\mu} S(t) + E(t)(1 - p_{\sigma+\mu})$$

$$I(t+1) = p_{\sigma|\mu} E(t) + I(t)(1 - p_{\gamma+\alpha+\mu})$$

$$V(t+1) = p_{\gamma|\mu+\alpha} I(t) + V(t)(1 - p_{\nu+\mu})$$

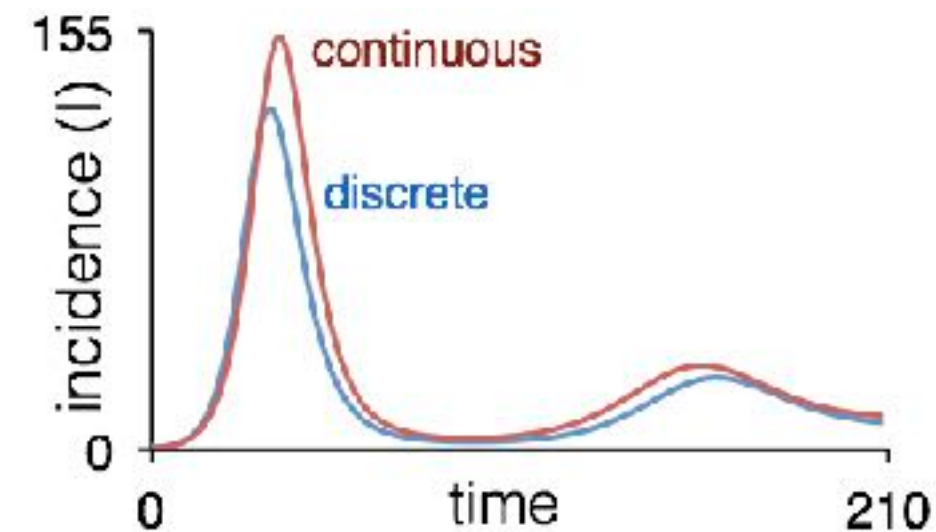
$$p_{\gamma|\alpha+\mu} = \frac{\gamma (1 - e^{-(\gamma+\alpha+\mu)})}{\gamma + \alpha + \mu}$$

$$p_{\alpha|\gamma+\mu} = \frac{\alpha (1 - e^{-(\gamma+\alpha+\mu)})}{\gamma + \alpha + \mu}$$

$$p_{\mu|\gamma+\alpha} = \frac{\mu (1 - e^{-(\gamma+\alpha+\mu)})}{\gamma + \alpha + \mu}$$

Competing rates
formulation and so on
for rest of p 's

$$p_{\gamma|\alpha+\mu} + p_{\alpha|\gamma+\mu} + p_{\mu|\gamma+\alpha} = p_{\gamma+\alpha+\mu}$$



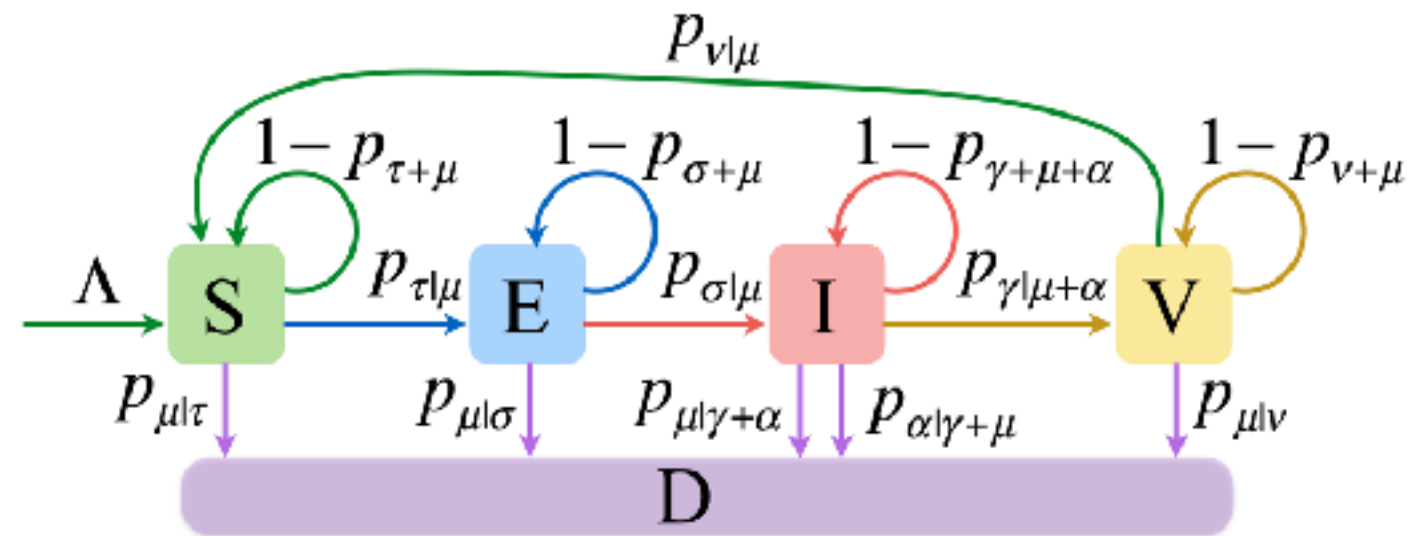
Discrete time stochastic SEIR disease state model

$$S(t+1) = S(t) + \hat{\Lambda}_t + \hat{U}^V(t) - (\hat{T}(t) + \hat{M}^S(t))$$

$$E(t+1) = E(t) + \hat{T}(t) - (\hat{U}^E(t) + \hat{M}^E(t))$$

$$I(t+1) = I(t) + \hat{U}^E(t) - (\hat{U}^I(t) + \hat{M}^I(t) + \hat{D}(t))$$

$$V(t+1) = V(t) + \hat{U}^I(t) - (\hat{U}^V(t) + \hat{M}^V(t))$$



$$(\hat{S}(t), \hat{T}(t), \hat{M}^S(t)) := \text{MULTINOMIAL}[S(t); 1 - p_{\tau_t+\mu}, p_{\tau_t|\mu}, p_{\mu|\tau_t}]$$

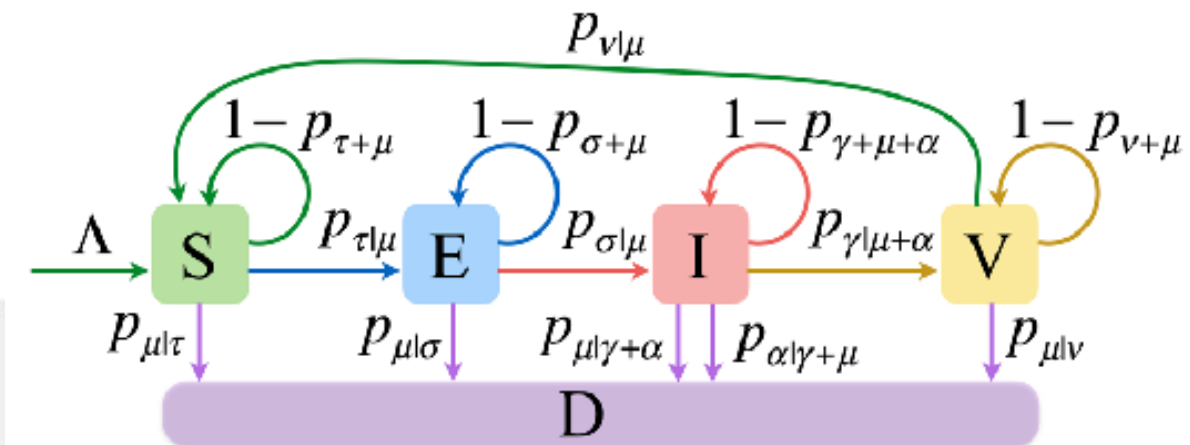
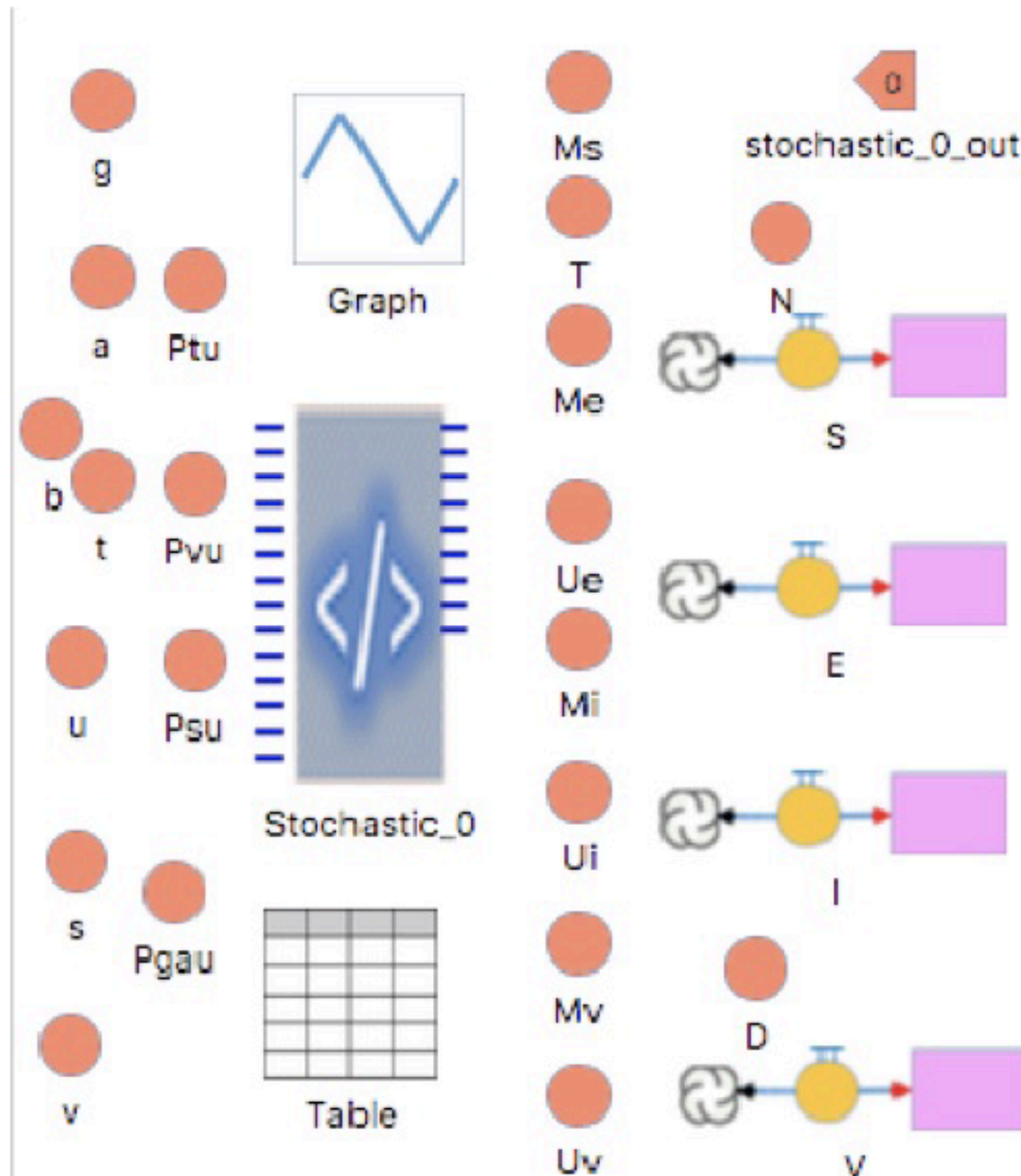
$$(\hat{E}(t), \hat{U}^E(t), \hat{M}^E(t)) := \text{MULTINOMIAL}[E(t); 1 - p_{\sigma+\mu}, p_{\sigma|\mu}, p_{\mu|\sigma}]$$

$$(\hat{I}(t), \hat{U}^I(t), \hat{M}^I(t), \hat{D}(t)) := \text{MULTINOMIAL}[I(t); 1 - p_{\gamma+\alpha+\mu}, p_{\mu|\alpha+\mu}, p_{\gamma|\alpha+\mu}, p_{\alpha|\gamma+\mu}]$$

$$(\hat{V}(t), \hat{U}^V(t), \hat{M}^V(t)) := \text{MULTINOMIAL}[V(t); 1 - p_{\nu+\mu}, p_{\mu|\nu}, p_{\nu|\mu}]$$

Discrete time stochastic SEIR disease state model

Numerus Model Builder Implementation



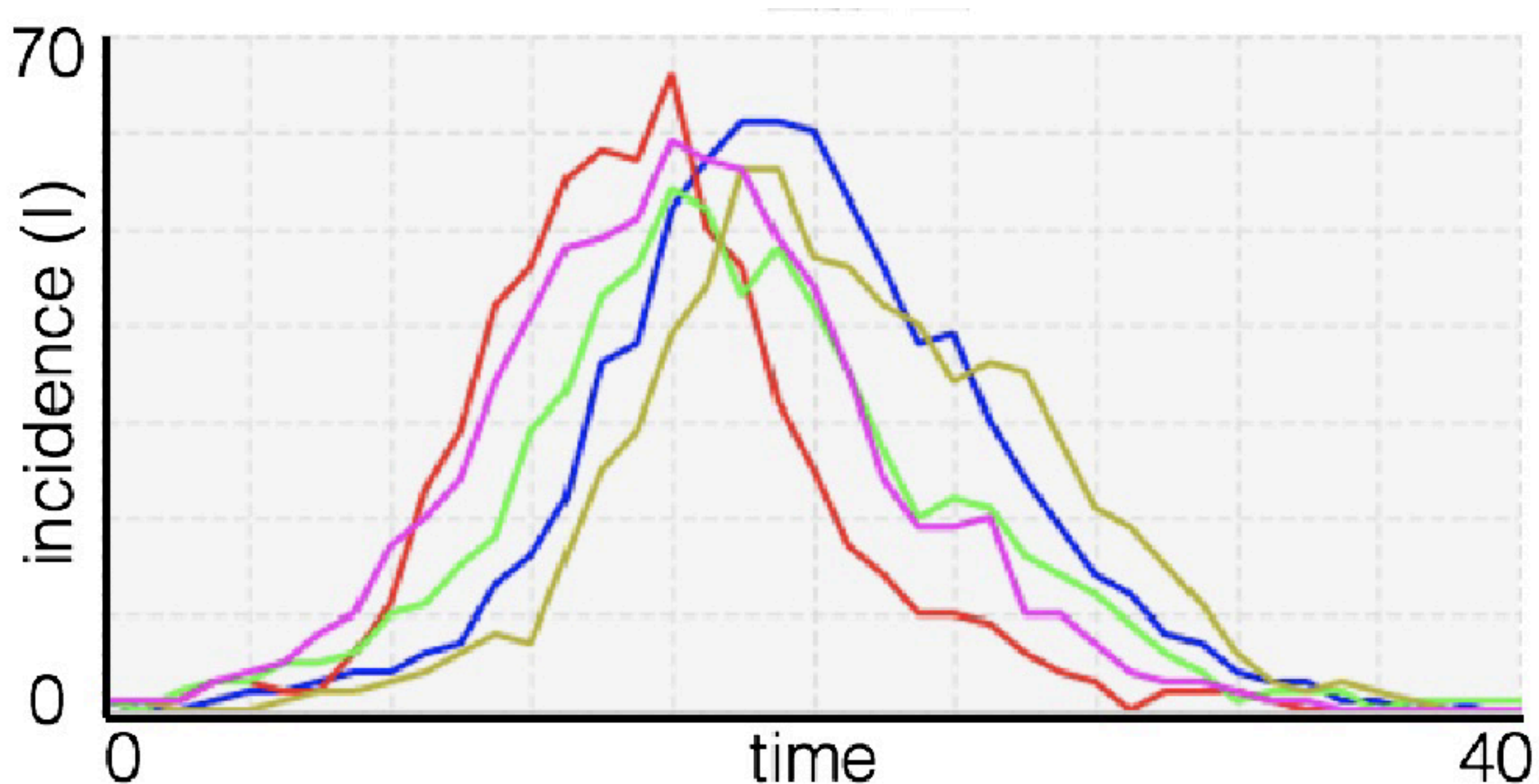
```

1 Sset = MULTINOMIAL(S, [(1-Ptu),
2   (t/(t+u))*Ptu, (u/(t+u))*Ptu])
3 T = Sset[1]
4 Ms = Sset[2]
5
6 Eset = MULTINOMIAL(E, [(1-Psu),
7   (s/(s+u))*Psu, (u/(s+u))*Psu])
8 Ue = Eset[1]
9 Me = Eset[2]
10
11 Iset = MULTINOMIAL(I, [(1-Pgau),
12   (g/(g+a+u))*Pgau, (u/(g+a+u))*Pgau,
13   (a/(g+a+u))*Pgau])
14 Ui = Iset[1]
15 Mi = Iset[2]
16 D = Iset[3]
17
18 Vset = MULTINOMIAL(V, [(1-Pvu),
19   (v/(v+u))*Pvu, (u/(v+u))*Pvu])
20 Uv = Vset[1]
21 Mv = Vset[2]
22

```

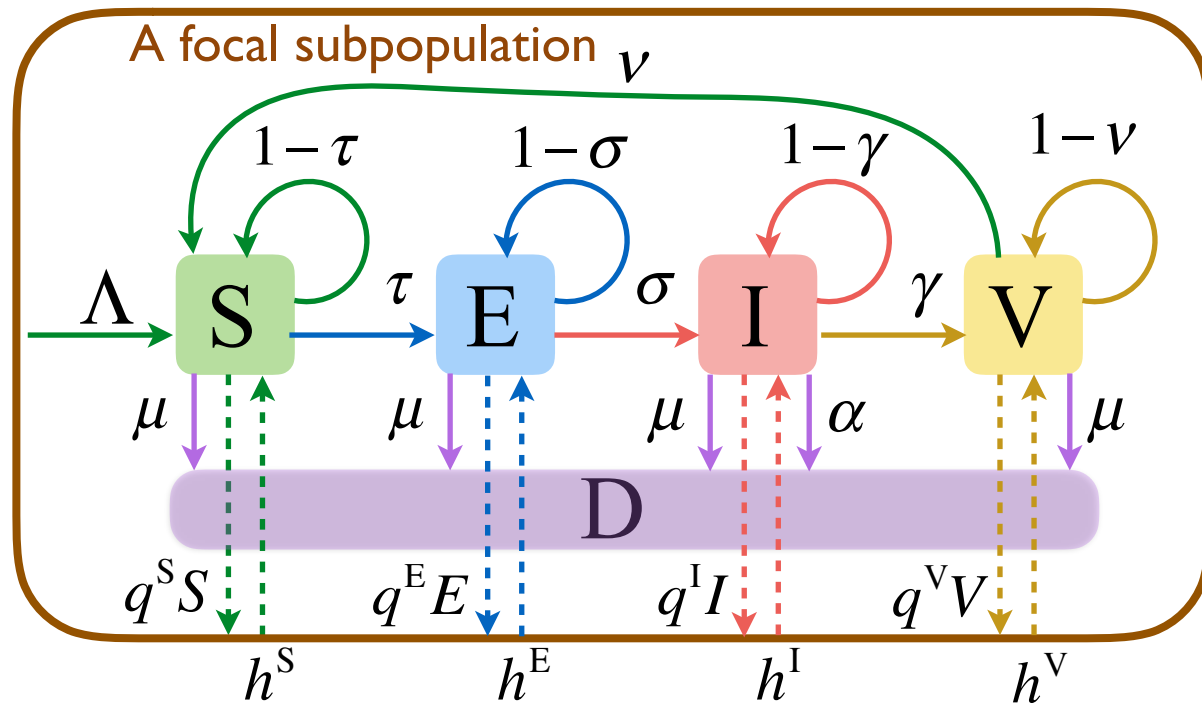

Discrete time stochastic SEIR disease state model

Stochastic solutions highly variable for small populations:
expectation very close to deterministic solution

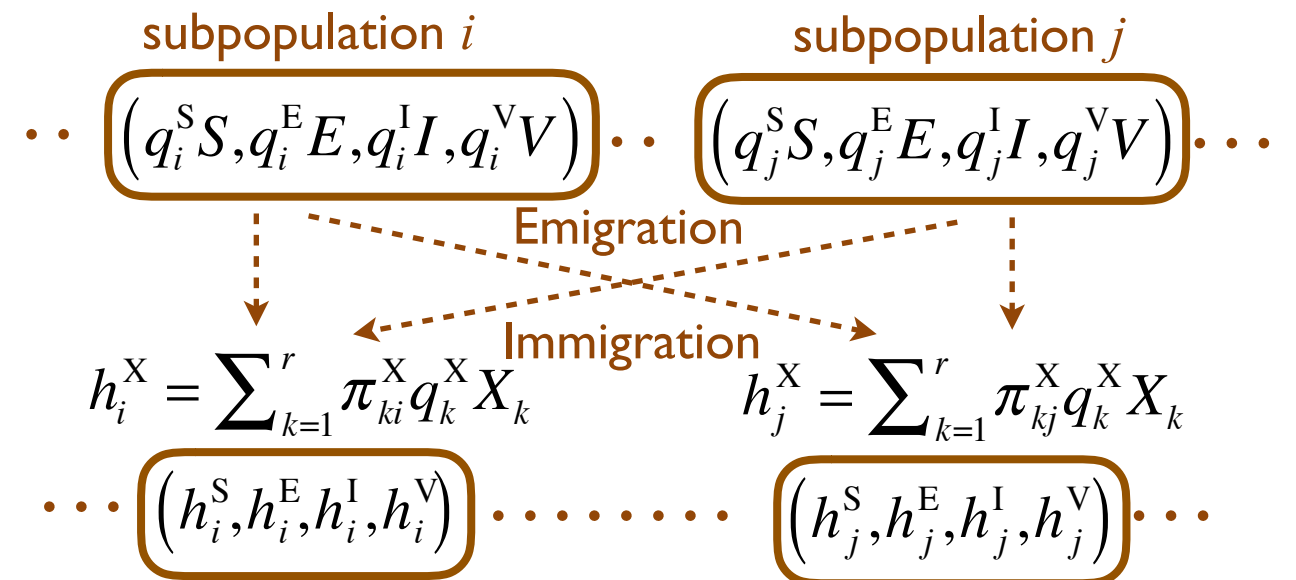


Metapopulation Formulation

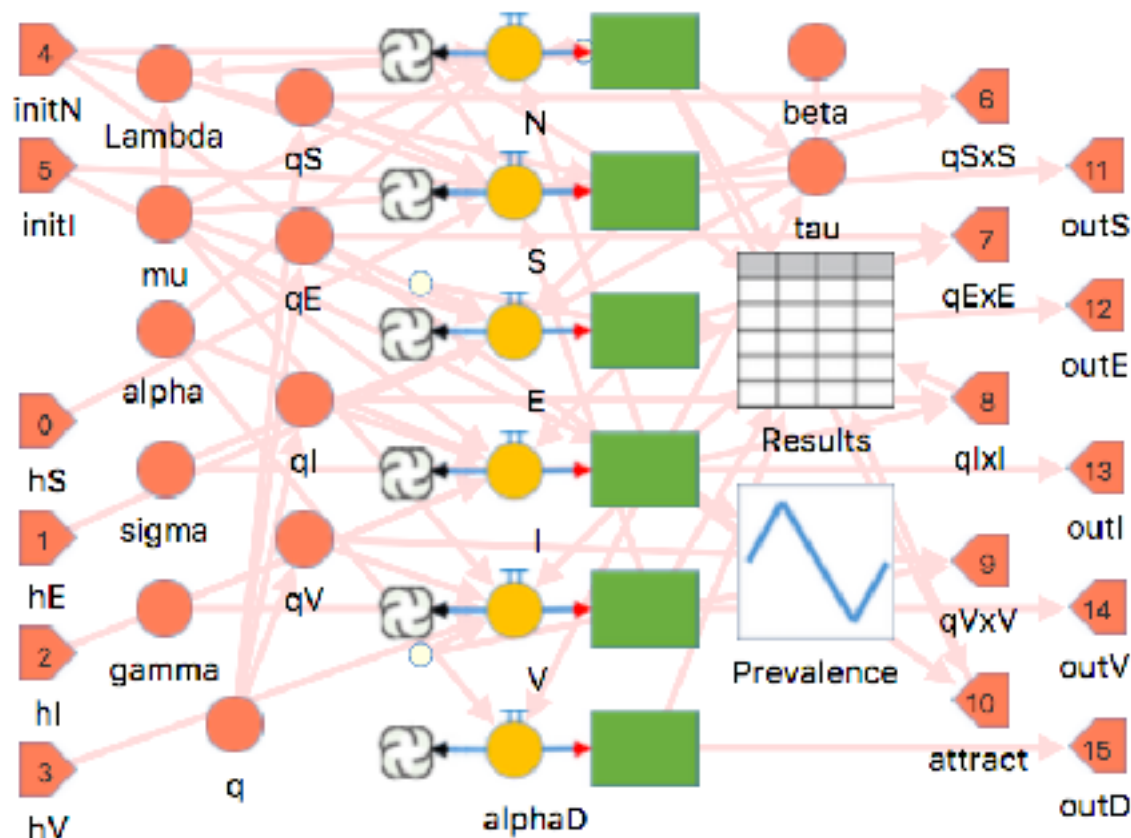
A. Continuous SEIR in a metapopulation setting



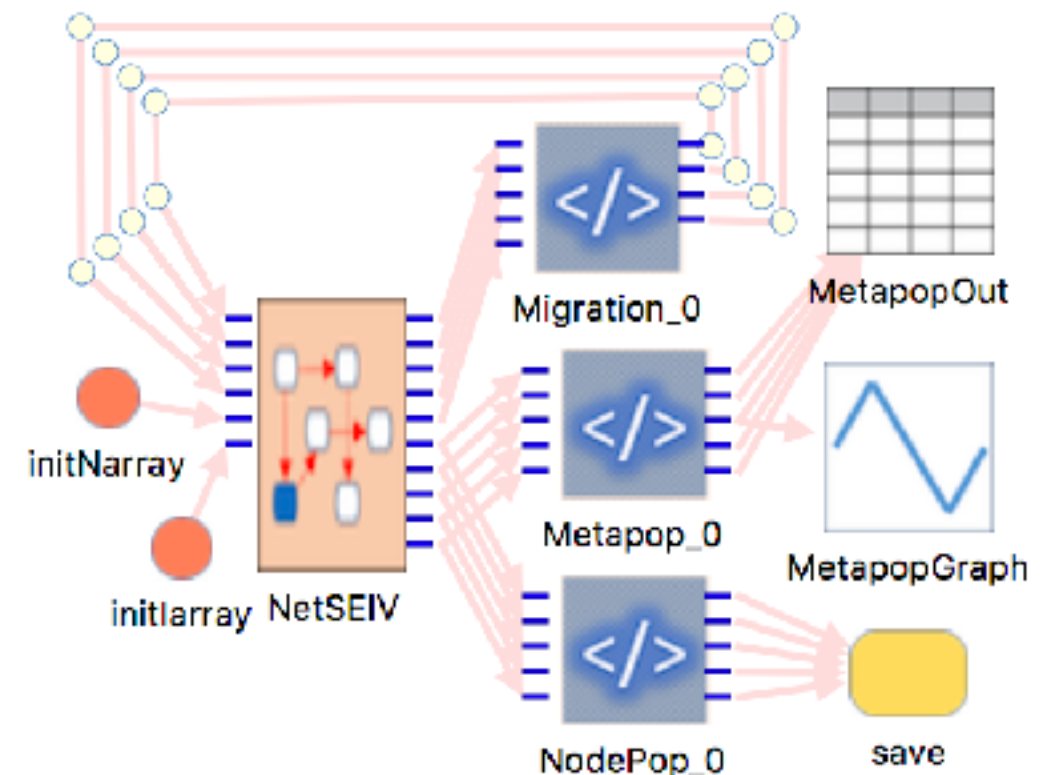
B. Metapopulation network



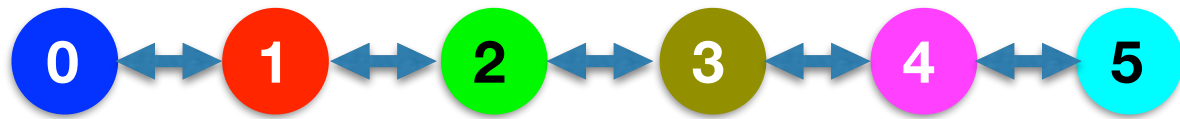
C. Nova Homogeneous SEIR Model with pins



D. Nova Metapopulation Implementation



Metapopulation simulation

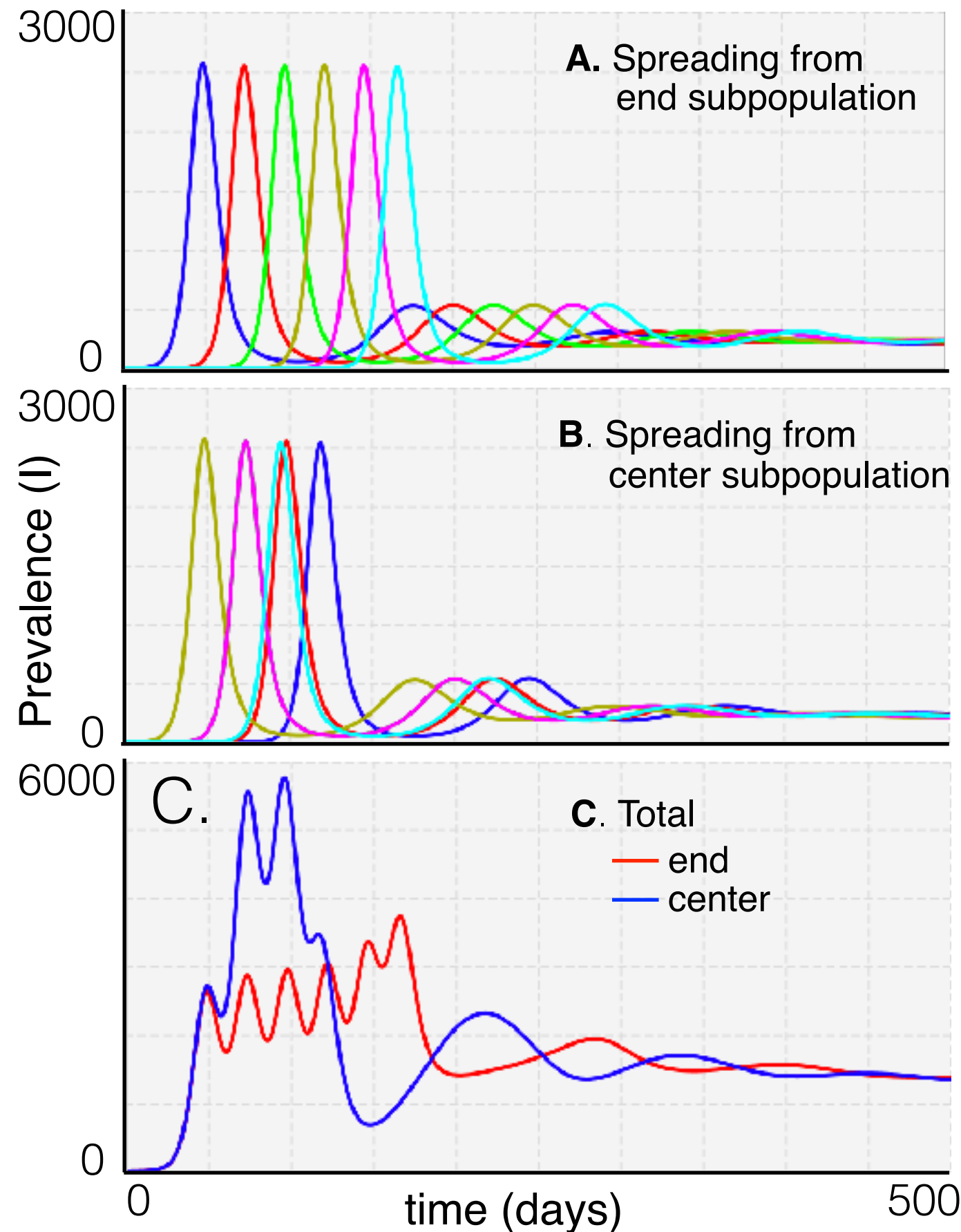


Prevalence plots (SEIV process at each node with migration: individuals flow only to subpopulations that are immediate neighbors.)

A. (index case in subpopulation 0)

B. (index case in subpopulation 2)

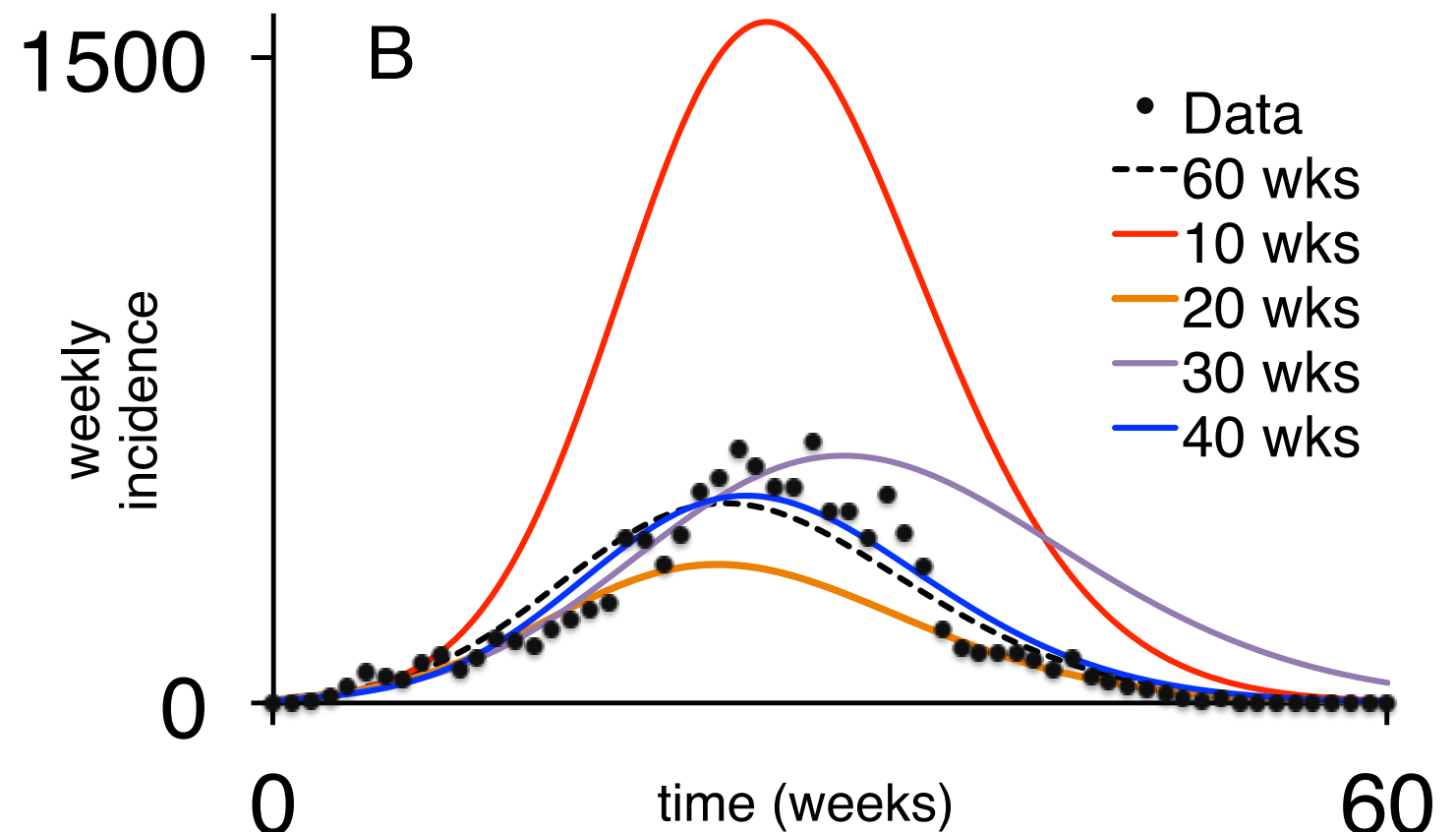
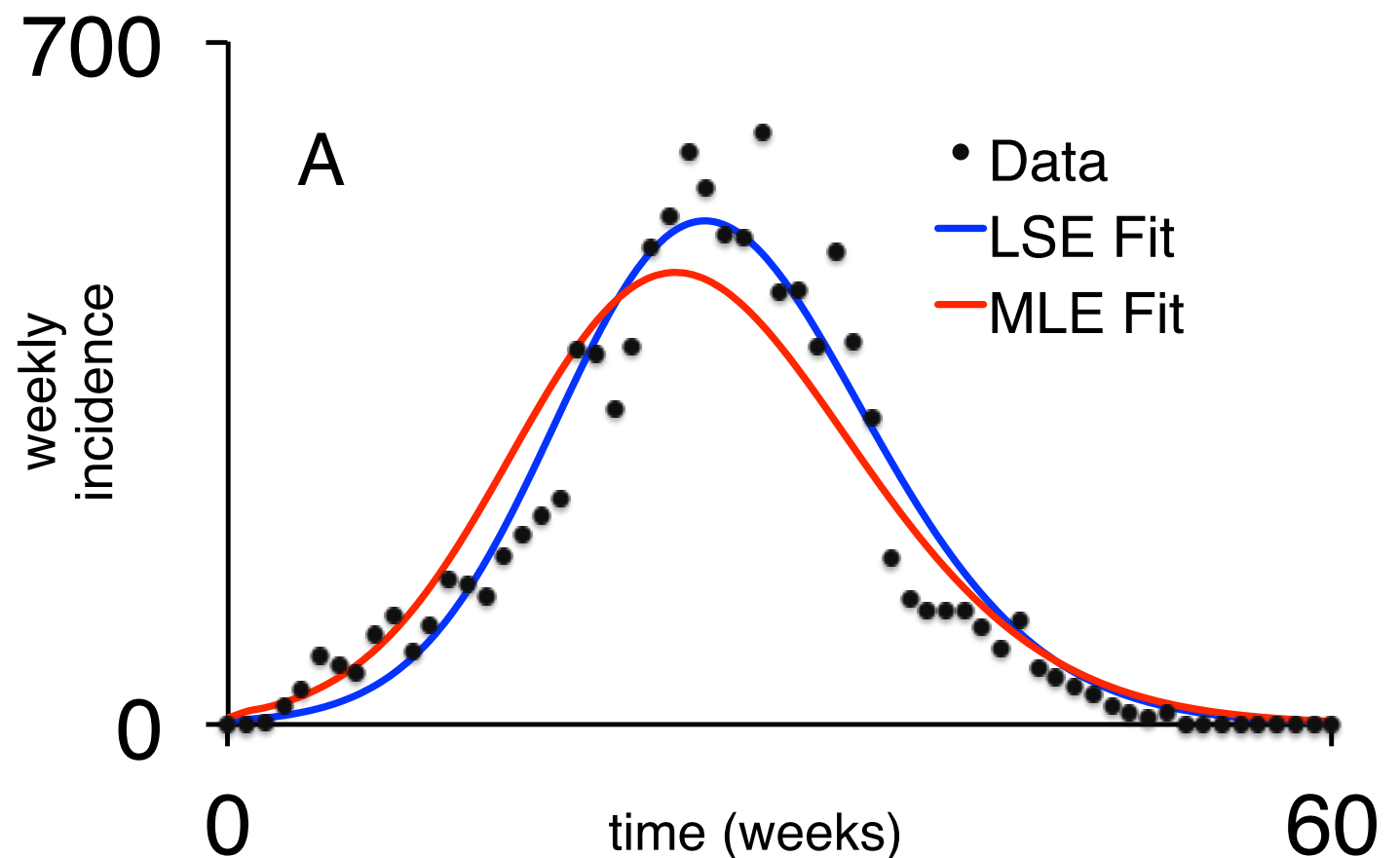
C. Total prevalence for two index cases that are either the end two (red plot, index cases on 0 and 5) or center two (blue plot, index cases in 2 and 3) subpopulations.



Fitting the SEIV model to Ebola data

A. The blue and red curves are the best fit least-square and maximum-likelihood estimate fits of the discrete-time SEIV model to Ebola incidence data from the Sierra Leone 2014

B. The black dotted line is the MLE fit, as in Panel A, with the red, orange, purple and blue plots, being simulations obtained after obtaining the best ML fits to the first 10, 20, 30 and 40 weeks of incidence respectively.



Access Models and Videos

Models available at: https://www.dropbox.com/home/NumerusMB_Epi_Models

Videos: search on **Youtube** using terms: **GetzEtAl SEIR**



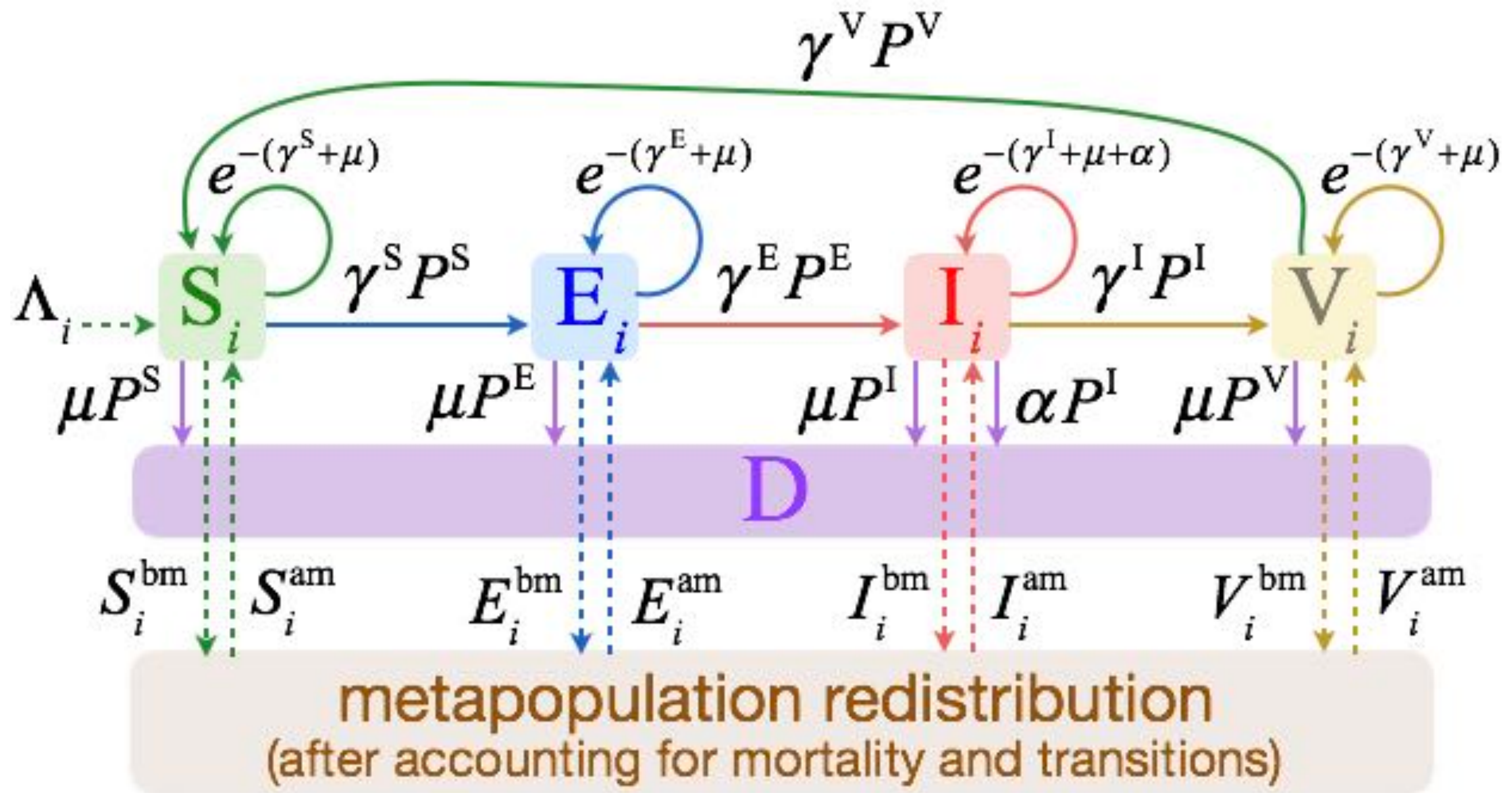
SEIR Model Tutorial

2. Continuous SEIR Model
Hyun Seok Yoon

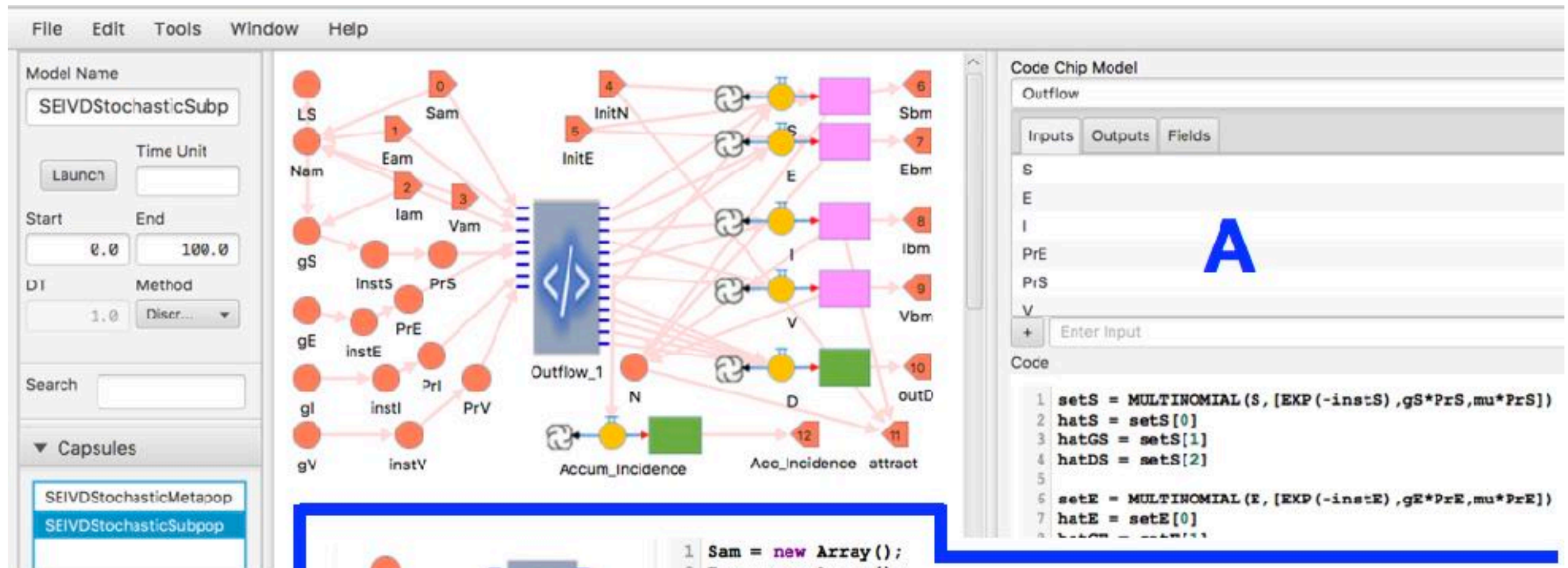
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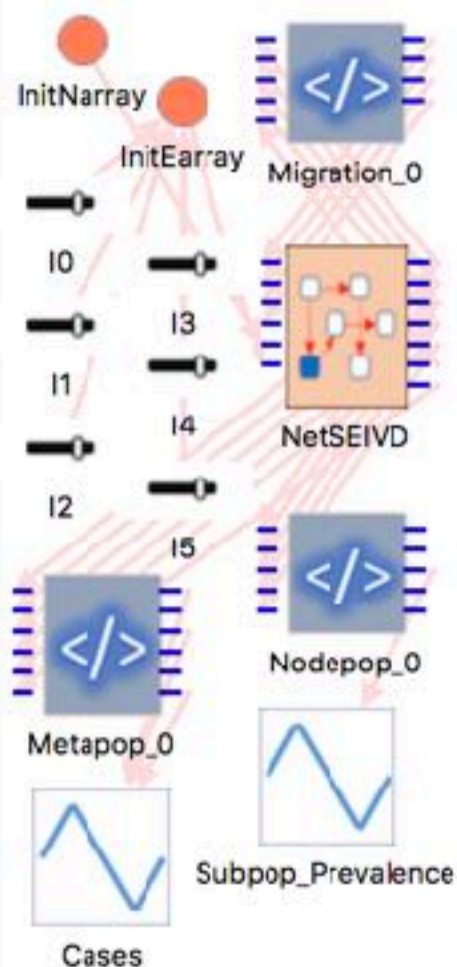
Discrete time stochastic SEIR metapopulation model



Discrete time stochastic SEIR metapopulation model



B

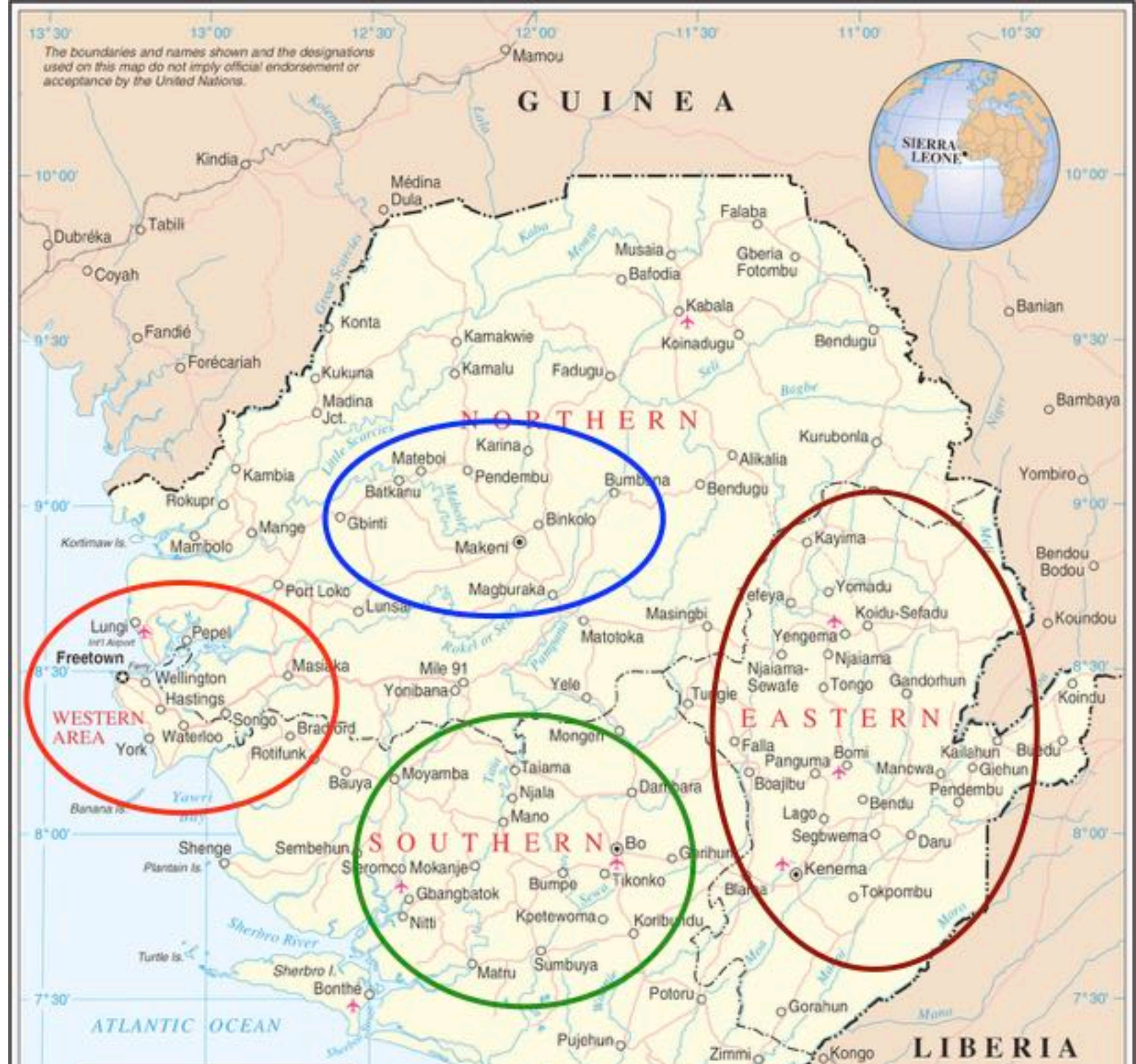
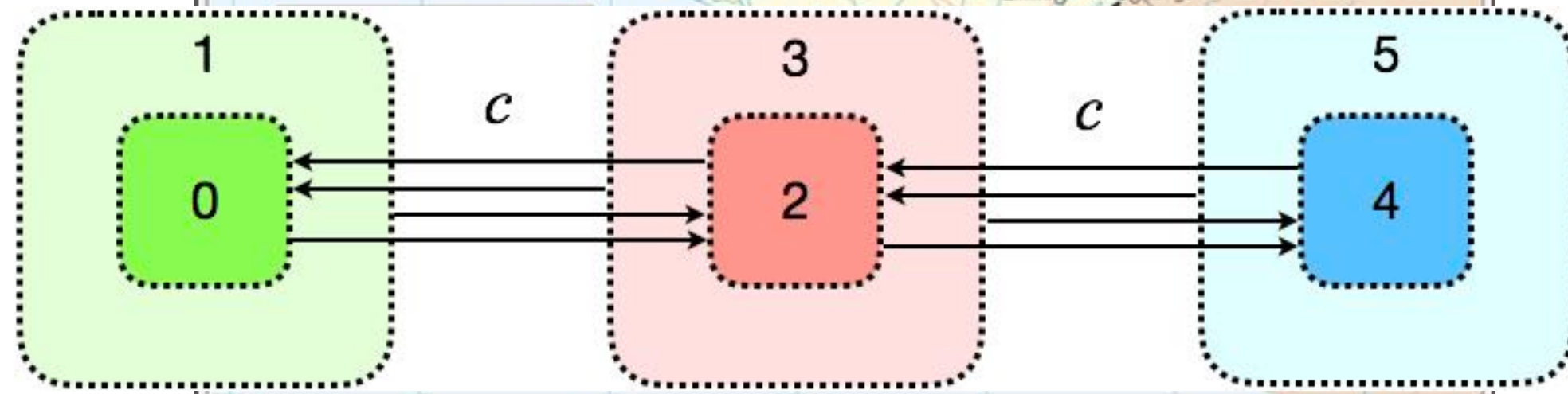


```
1 Sam = new Array();
2 Eam = new Array();
3 Iam = new Array();
4 Vam = new Array();
5 fSam = function(i){return (TIME()==0) ? 0 : Sam[i]}
6 fEam = function(i){return (TIME()==0) ? 0 : Eam[i]}
7 fIam = function(i){return (TIME()==0) ? 0 : Iam[i]}
8 fVam = function(i){return (TIME()==0) ? 0 : Vam[i]}
9 for (var i = 0; i < NetSEIVD.NODECOUNT(); i++) {
10   Sam[i] = Eam[i] = Iam[i] = Vam[i] = 0;
11 }
12 for (var i = 0; i < NetSEIVD.NODECOUNT(); i++) {
13   var connects = NetSEIVD.nodes[i].CONNECTIONS_OUT();
14   var p = new Array();
15   for (j = 0; j < NetSEIVD.NODECOUNT(); j++) p[j] = 0;
16   for (var idx in connects) {
17     var j = connects[idx].target;
18     p[j] = connects[idx].strength*attract(j);
19   }
20   var tot = ARRAYSUM(p);
21   p = _.map(p, function(x){return x/tot;});
22   disperseS = MULTINOMIAL(Sbm, [p[0], p[1], p[2], p[3], p[4], p[5]]);
23   disperseE = MULTINOMIAL(Ebm, [p[0], p[1], p[2], p[3], p[4], p[5]]);
24   disperseI = MULTINOMIAL(Ibm, [p[0], p[1], p[2], p[3], p[4], p[5]]);
25   disperseV = MULTINOMIAL(Vbm, [p[0], p[1], p[2], p[3], p[4], p[5]]);
26   fSam[i] = ARRAYSUM(disperseS);
27   fEam[i] = ARRAYSUM(disperseE);
28   fIam[i] = ARRAYSUM(disperseI);
29   fVam[i] = ARRAYSUM(disperseV);
30 }
```


Discrete time stochastic SEIR metapopulation model

$$C = \begin{pmatrix} 1 & 1/4 & c & c & 0 & 0 \\ 1/4 & 1 & 0 & 0 & 0 & 0 \\ c & c & 1 & 1/4 & c & c \\ 0 & 0 & 1/4 & 1 & 0 & 0 \\ 0 & 0 & c & c & 1 & 1/4 \\ 0 & 0 & 0 & 0 & 1/4 & 1 \end{pmatrix}$$

Set up core plus
periphery node
structure (e.g., for
three regions)



Discrete time stochastic SEIR metapopulation model

$$C = \begin{pmatrix} 1 & 1/4 & c & c & 0 & 0 \\ 1/4 & 1 & 0 & 0 & 0 & 0 \\ c & c & 1 & 1/4 & c & c \\ 0 & 0 & 1/4 & 1 & 0 & 0 \\ 0 & 0 & c & c & 1 & 1/4 \\ 0 & 0 & 0 & 0 & 1/4 & 1 \end{pmatrix}$$

Set up core plus
periphery node
structure (e.g., for
three regions)

