

Multistrain models



Model types are fuzzy

Statistical

Mechanistic (mathematical v. agent-based)



Advantages and disadvantages of each?

History-based models

Track individuals' histories of infection, $\mathcal{S}_{(0)}, \mathcal{S}_{(1)}, \mathcal{S}_{(1,2)}, \dots$

Cross-immunity reduces probability of infection or infectiousness

Numerically unwieldy: 2^n histories for n strains

Dimensional reduction

Requires cross-immunity through reduced transmission (only)

Cross-immunity must be in context of antigenic "neighborhoods"

(with n strains in m neighborhoods, system is $n \times (m + 1)$)

Impossible to calculate immunity to new strains

Kucharski et al. 2015

Status-based models

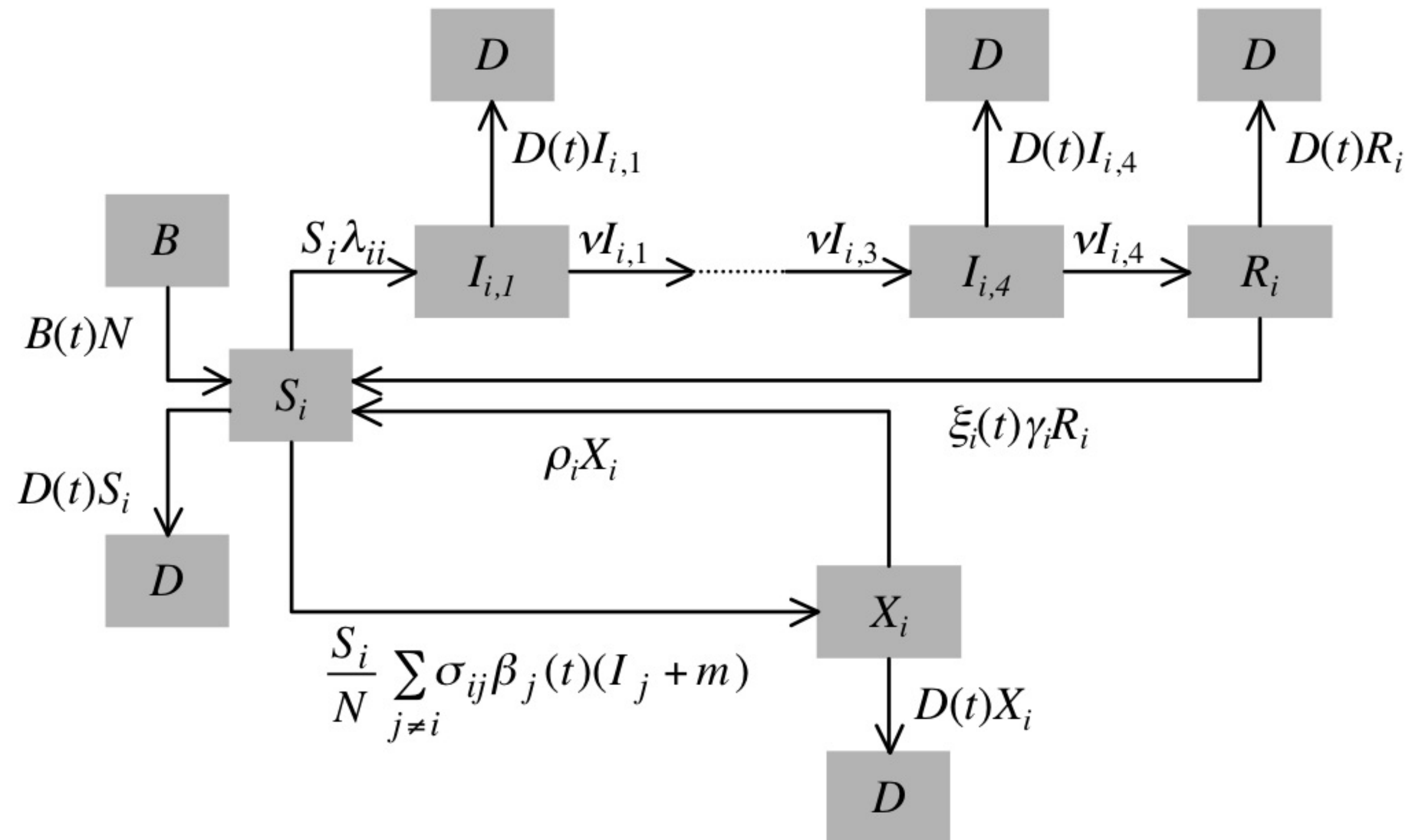
Track individuals S, I, or R to each strain

$O(n)$ equations possible

"Polarized" immunity: If i and j cross-react, infection with j leads to perfect immunity to i in some fraction of hosts

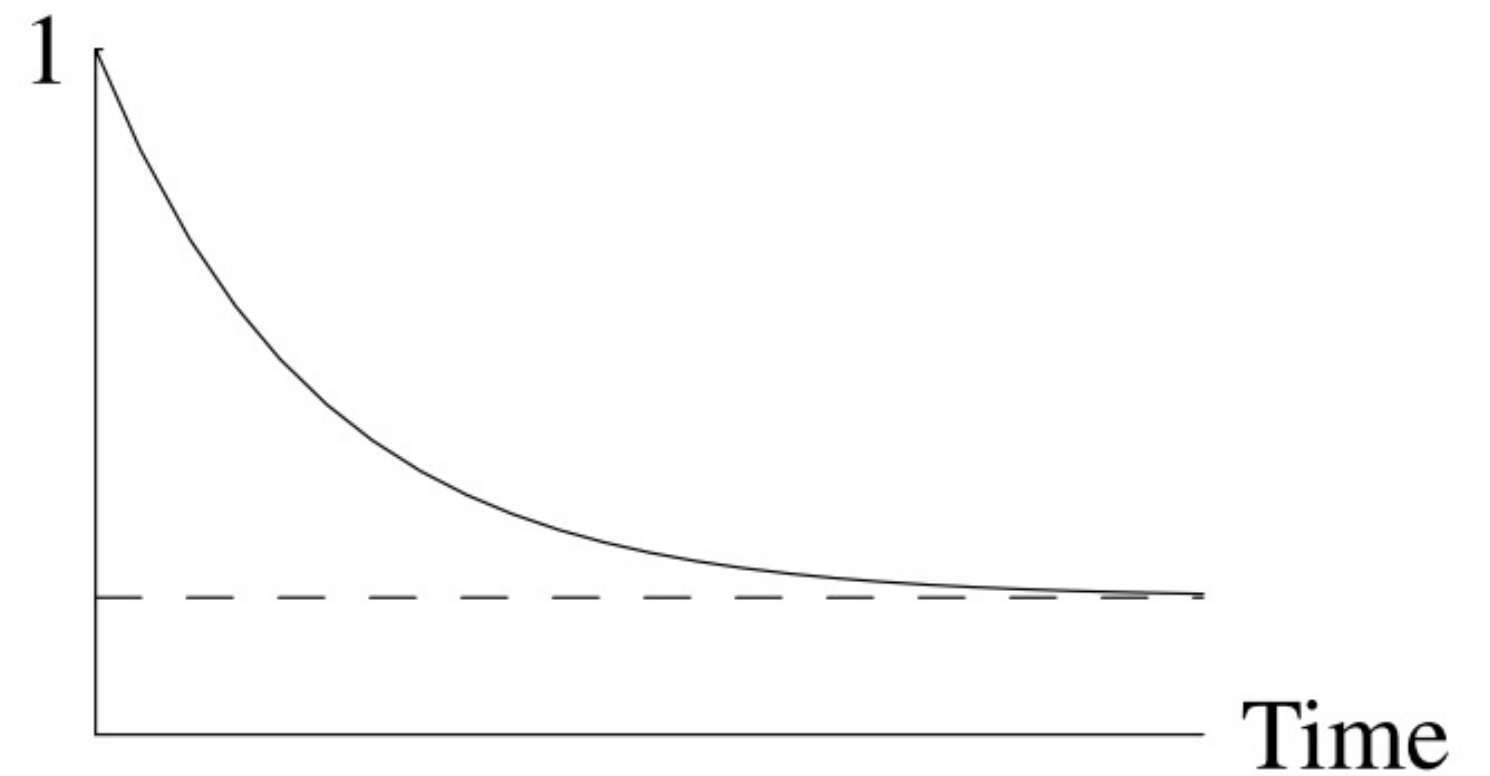
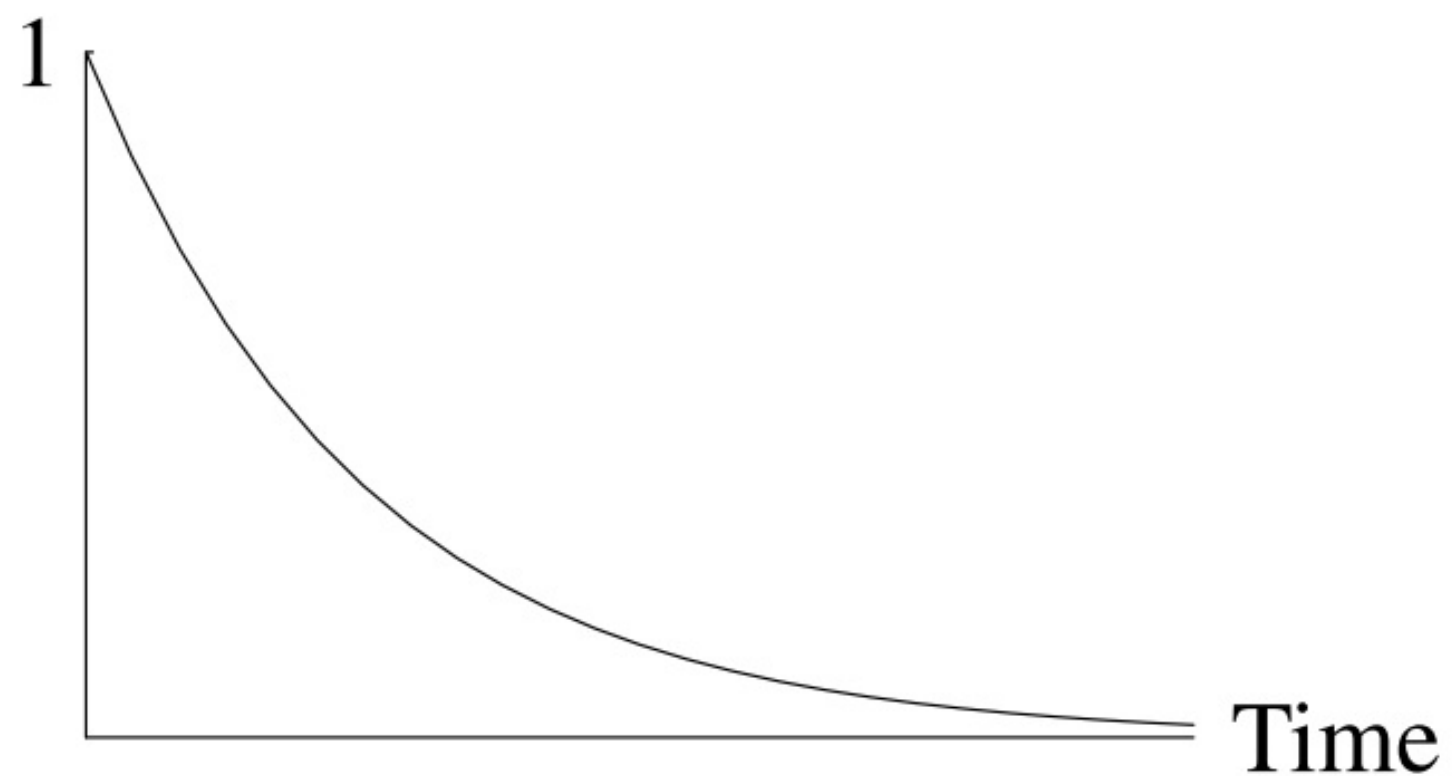
Gog and Swinton, 2002

A "simple" status-based model



Implicit assumption

Proportion of population not infected by second strain



Gog and Swinton, 2002

Some options for multistrain models

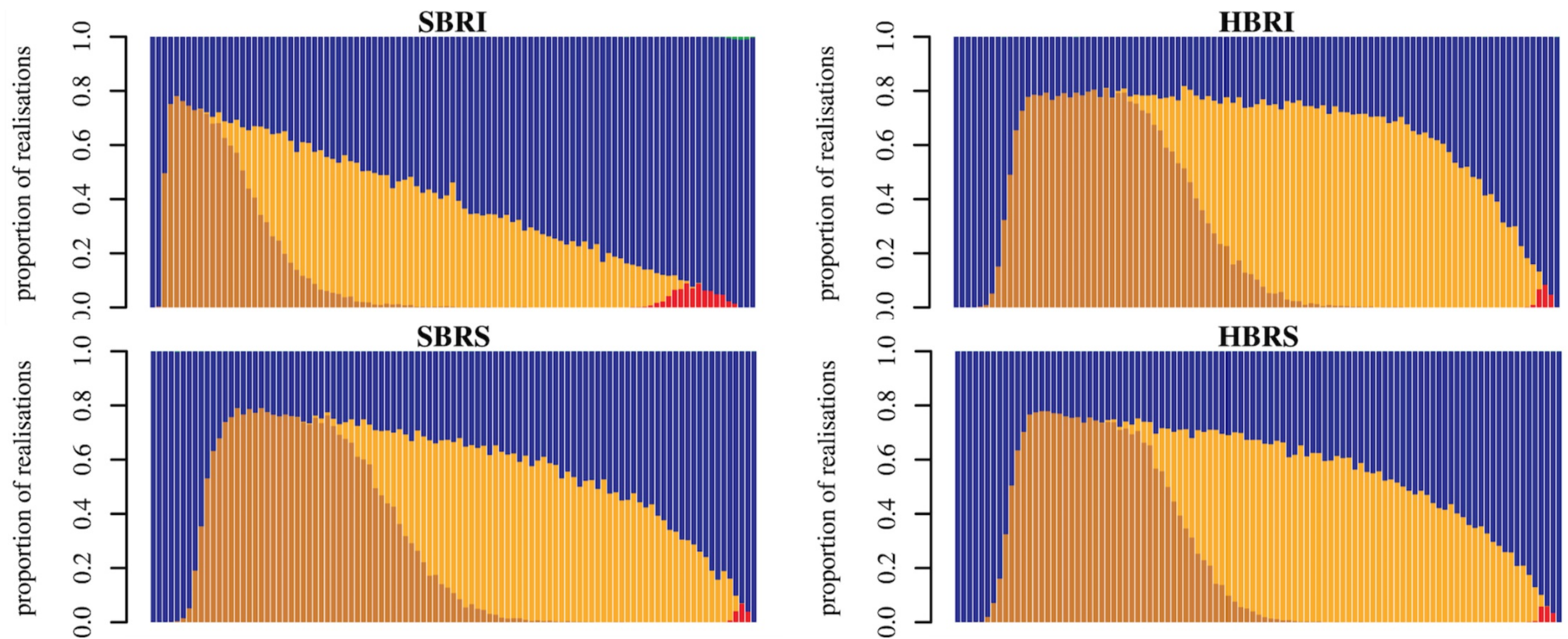
Model	Type	Variables	New strains	Immunity reduces
Individual-based model	–	Many	Yes	Susceptibility/transmission
Andreasen et al. (1997)	HB	$\mathcal{O}(2^n)$	Yes	Susceptibility/transmission
Gupta et al. (1998)*	HB	$\mathcal{O}(n)$	No	Transmission
Kucharski and Gog (2012a)	HB	$\mathcal{O}(n)$	Yes	Transmission
Gog and Swinton (2002)	SB	$\mathcal{O}(2^n)$	No	Susceptibility
Gog and Grenfell (2002)	SB	$\mathcal{O}(n)$	No	Transmission
Kryazhimskiy et al. (2007)	SB	$\mathcal{O}(n^2)$	No	Susceptibility/transmission

Only two models store enough information to permit the introduction of new strains

HB history-based, *SB* status-based

* Generalised by [Ferguson and Andreasen \(2002\)](#)

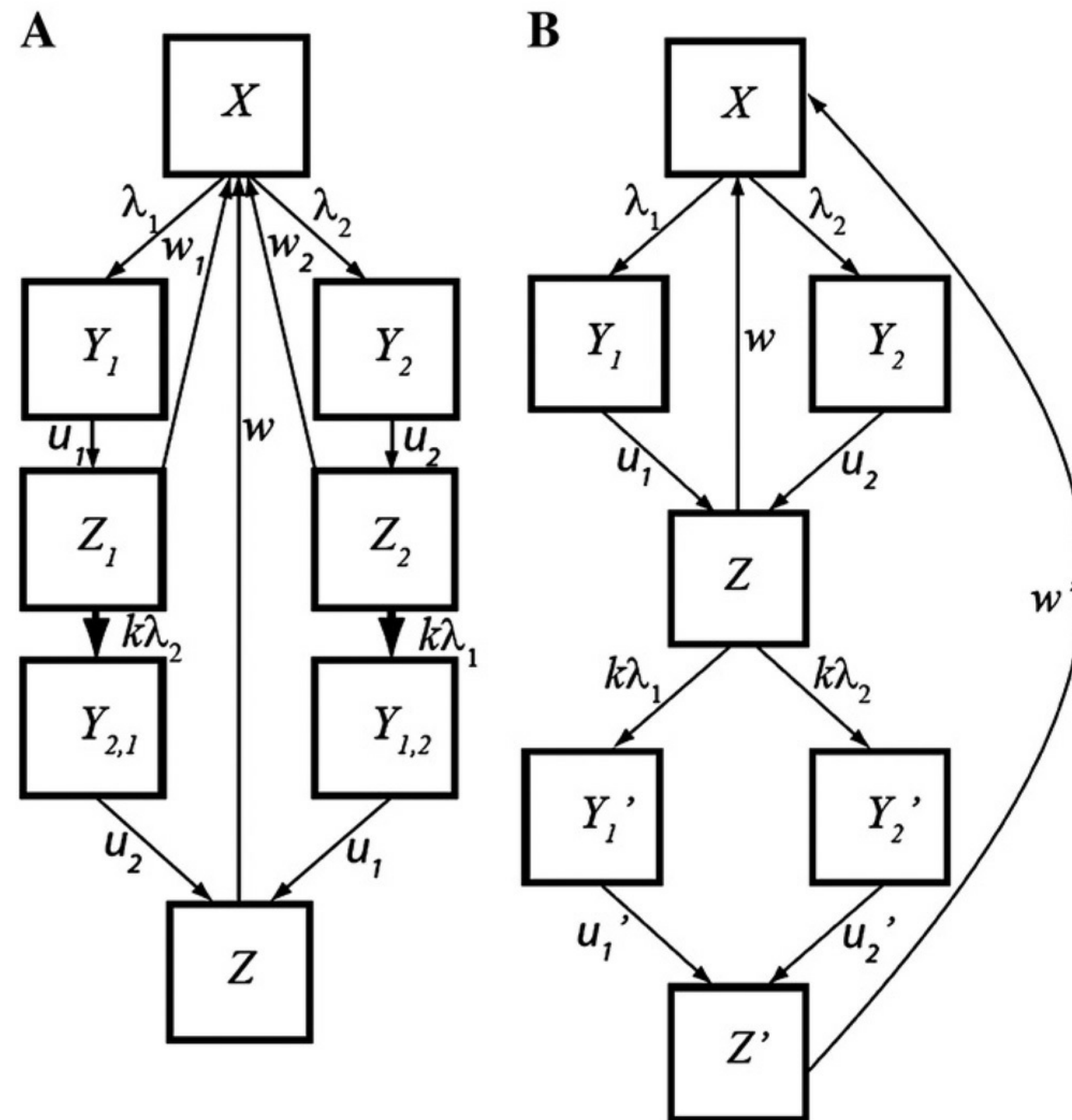
Subtle differences change dynamics



Cross-immunity

Know your assumptions

Which model promotes coexistence?



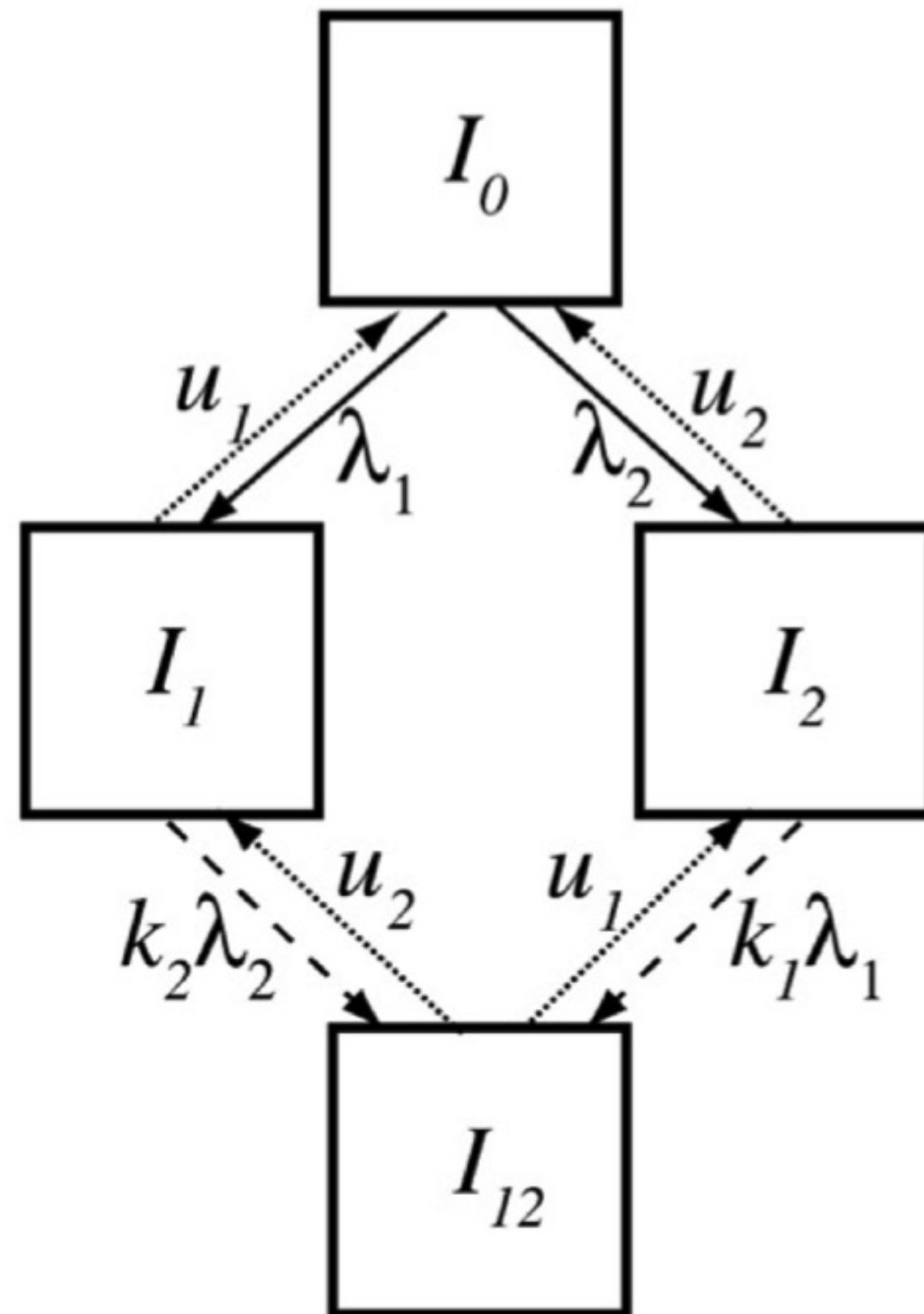
Model A

$$\begin{aligned}\frac{dX}{dt} &= -(\lambda_1 + \lambda_2)X + w_1Z_1 + w_2Z_2 + wZ \\ \frac{dY_1}{dt} &= \lambda_1X - u_1Y_1 \\ \frac{dY_2}{dt} &= \lambda_2X - u_2Y_2 \\ \frac{dZ_1}{dt} &= u_1Y_1 - k\lambda_2Z_1 - w_1Z_1 \\ \frac{dZ_2}{dt} &= u_2Y_2 - k\lambda_1Z_2 - w_2Z_2 \\ \frac{dY_{1,2}}{dt} &= k\lambda_1Z_2 - u_1Y_{1,2} \\ \frac{dY_{2,1}}{dt} &= k\lambda_2Z_1 - u_2Y_{2,1} \\ \frac{dZ}{dt} &= u_1Y_{1,2} + u_2Y_{2,1} - wZ \\ \lambda_i &= \beta_i(Y_i + qY_{i,\sim i}), i = 1, 2\end{aligned}$$

Model B

$$\begin{aligned}\frac{dX}{dt} &= -(\lambda_1 + \lambda_2)X + w'Z' + wZ \\ \frac{dY_1}{dt} &= \lambda_1 X - u_1 Y_1 \\ \frac{dY_2}{dt} &= \lambda_2 X - u_2 Y_2 \\ \frac{dZ}{dt} &= u_1 Y_1 + u_2 Y_2 - k(\lambda_1 + \lambda_2)Z - wZ \\ \frac{dY'_1}{dt} &= k\lambda_1 Z - u'_1 Y'_1 \\ \frac{dY'_2}{dt} &= k\lambda_2 Z - u'_2 Y'_2 \\ \frac{dZ'}{dt} &= u'_1 Y'_1 + u'_2 Y'_2 - w'Z' \\ \lambda_i &= \beta_i(Y_i + qY'_i), i = 1, 2\end{aligned}$$

Does this model bias for coexistence?



Equations

$$\frac{dI_0}{dt} = -(\lambda_1 + \lambda_2)I_0 + u_1I_1 + u_2I_2$$

$$\frac{dI_1}{dt} = \lambda_1I_0 - u_1I_1 - k_2\lambda_2I_1 + u_2I_{12}$$

$$\frac{dI_2}{dt} = \lambda_2I_0 - u_2I_2 - k_1\lambda_1I_2 + u_1I_{12}$$

$$\frac{dI_{12}}{dt} = k_2\lambda_2I_1 + k_1\lambda_1I_2 - (u_1 + u_2)I_{12}$$

$$\lambda_1 = \beta_1(I_1 + qI_{12})$$

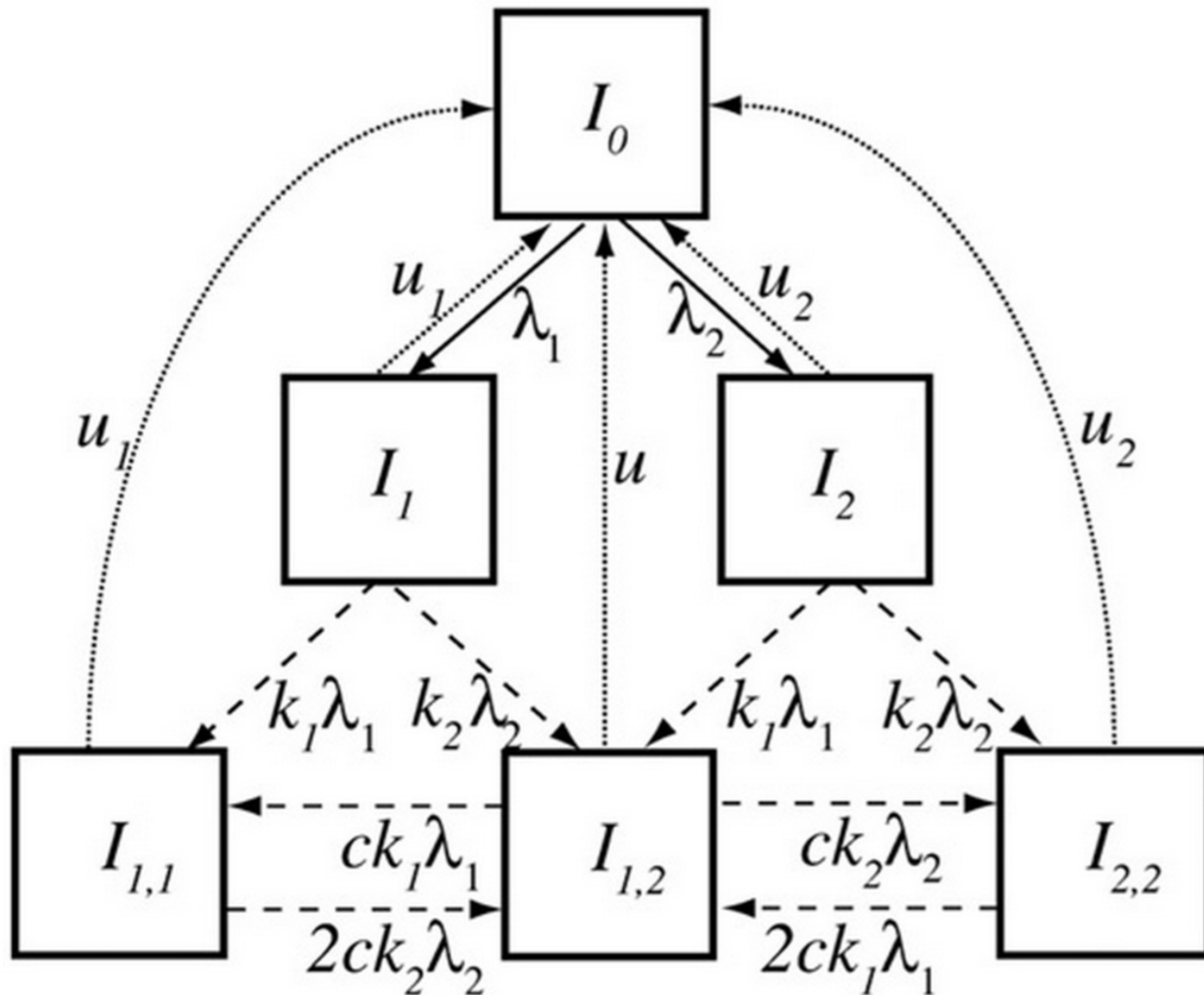
$$\lambda_2 = \beta_2(I_2 + qI_{12})$$

Equations

Ecological dynamics depend on strain composition

$$\begin{aligned}\frac{dN_0}{dt} &= -\beta(N_1 + qN_2)N_0 + uN_1 \\ \frac{dN_1}{dt} &= \beta(N_1 + qN_2)N_0 - uN_1 - 2k\beta[I_1I_2 + qN_2N_1] \\ \frac{dN_2}{dt} &= -2uN_2 + 2k\beta[I_1I_2 + qN_2N_1]\end{aligned}$$

Multiplicity of infection



ODEs

$$\frac{dI_0}{dt} = -(\lambda_1 + \lambda_2)I_0 + u_1I_1 + u_2I_2 + uI_{11} + uI_{12} + uI_{22}$$

$$\frac{dI_1}{dt} = \lambda_1I_0 - k_1\lambda_1I_1 - k_2\lambda_2I_1 - u_1I_1$$

$$\frac{dI_2}{dt} = \lambda_2I_0 - k_1\lambda_1I_2 - k_2\lambda_2I_2 - u_2I_2$$

$$\frac{dI_{11}}{dt} = k_1\lambda_1I_1 - uI_{11} - 2ck_2\lambda_2I_{11} + ck_1\lambda_1I_{12}$$

$$\frac{dI_{12}}{dt} = k_1\lambda_1I_2 + k_2\lambda_2I_1 - uI_{12} + 2ck_2\lambda_2I_{11} + 2ck_1\lambda_1I_{22} - ck_1\lambda_1I_{12} - ck_2\lambda_2I_{12}$$

$$\frac{dI_{22}}{dt} = k_2\lambda_2I_2 - uI_{22} - 2ck_1\lambda_1I_{22} + ck_2\lambda_2I_{12}$$

$$\lambda_1 = \beta_1(I_1 + qI_{12} + 2qI_{11})$$

$$\lambda_2 = \beta_2(I_2 + qI_{12} + 2qI_{22})$$

Ecological dynamics

$$\begin{aligned}\frac{dN_0}{dt} &= -\beta(N_1 + 2qN_2)N_0 + u(N_1 + N_2) \\ \frac{dN_1}{dt} &= \beta(N_1 + 2qN_2)N_0 - k\beta(N_1 + 2qN_2)N_1 - uN_1 \\ \frac{dN_2}{dt} &= k\beta(N_1 + 2qN_2)N_1 - uN_2\end{aligned}$$

Ancestor tracing

$$\dot{M}_{11} = \beta(M_{11} + qM_{21})N_0 - uM_{11} - k\lambda_{\text{total}}M_{11}$$

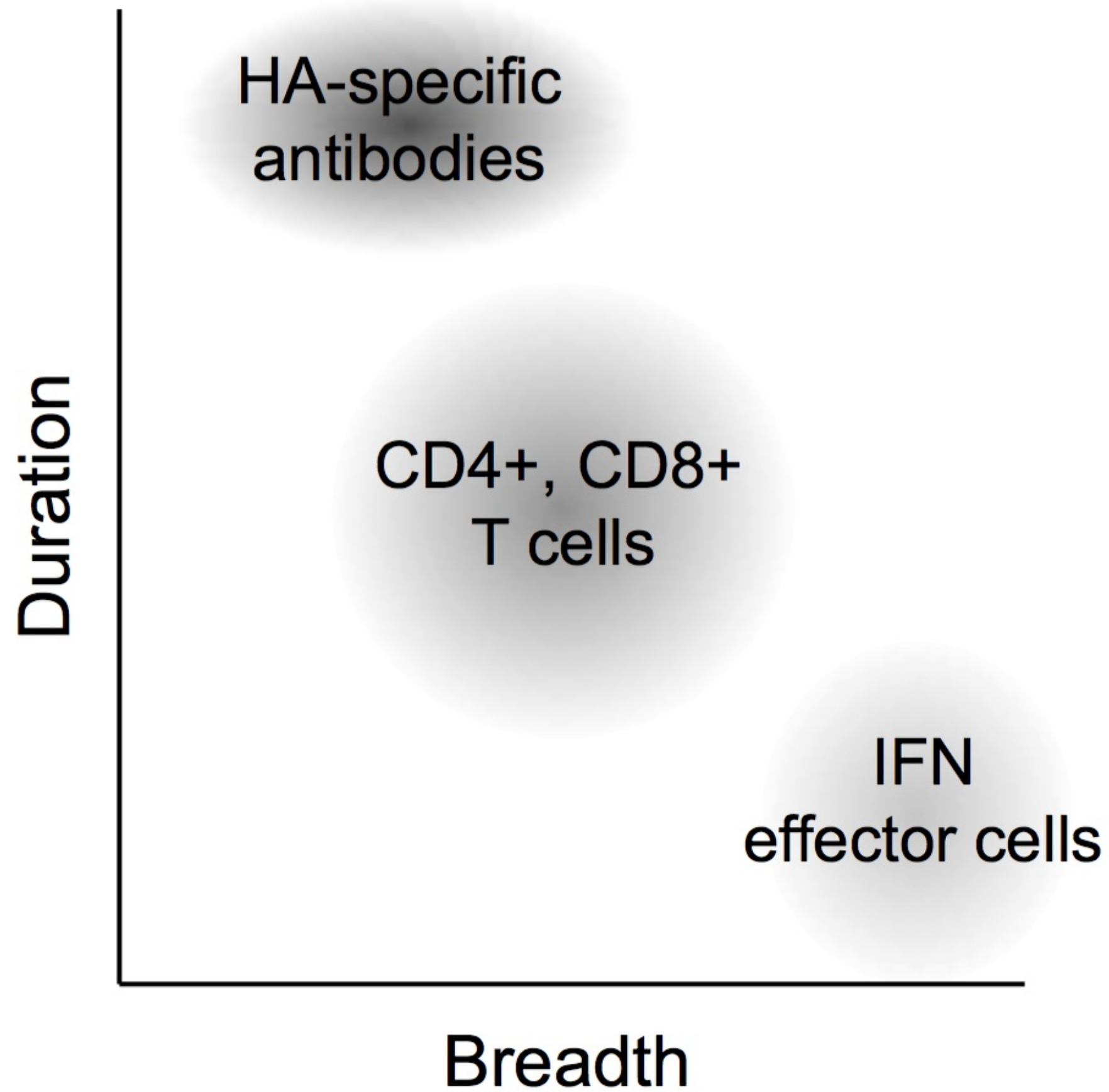
$$\dot{M}_{12} = \beta(M_{12} + qM_{22})N_0 - uM_{12} - k\lambda_{\text{total}}M_{12}$$

$$\begin{aligned}\dot{M}_{21} = & \beta k(M_{11} + qM_{21})N_1 + k\lambda_{\text{total}}M_{11} - uM_{12} \\ & - c\beta k(M_{12} + qM_{22})M_{21} + c\beta k(M_{11} + qM_{21})M_{22}\end{aligned}$$

$$\begin{aligned}\dot{M}_{22} = & \beta k(M_{12} + qM_{22})N_1 + k\lambda_{\text{total}}M_{12} - uM_{22} \\ & + c\beta k(M_{12} + qM_{22})M_{21} - c\beta k(M_{11} + qM_{21})M_{22}\end{aligned}$$

$$\lambda_{\text{total}} = \beta(M_{11} + M_{12} + qM_{21} + qM_{22}) = \beta(N_1 + 2qN_2)$$

Immune response to flu



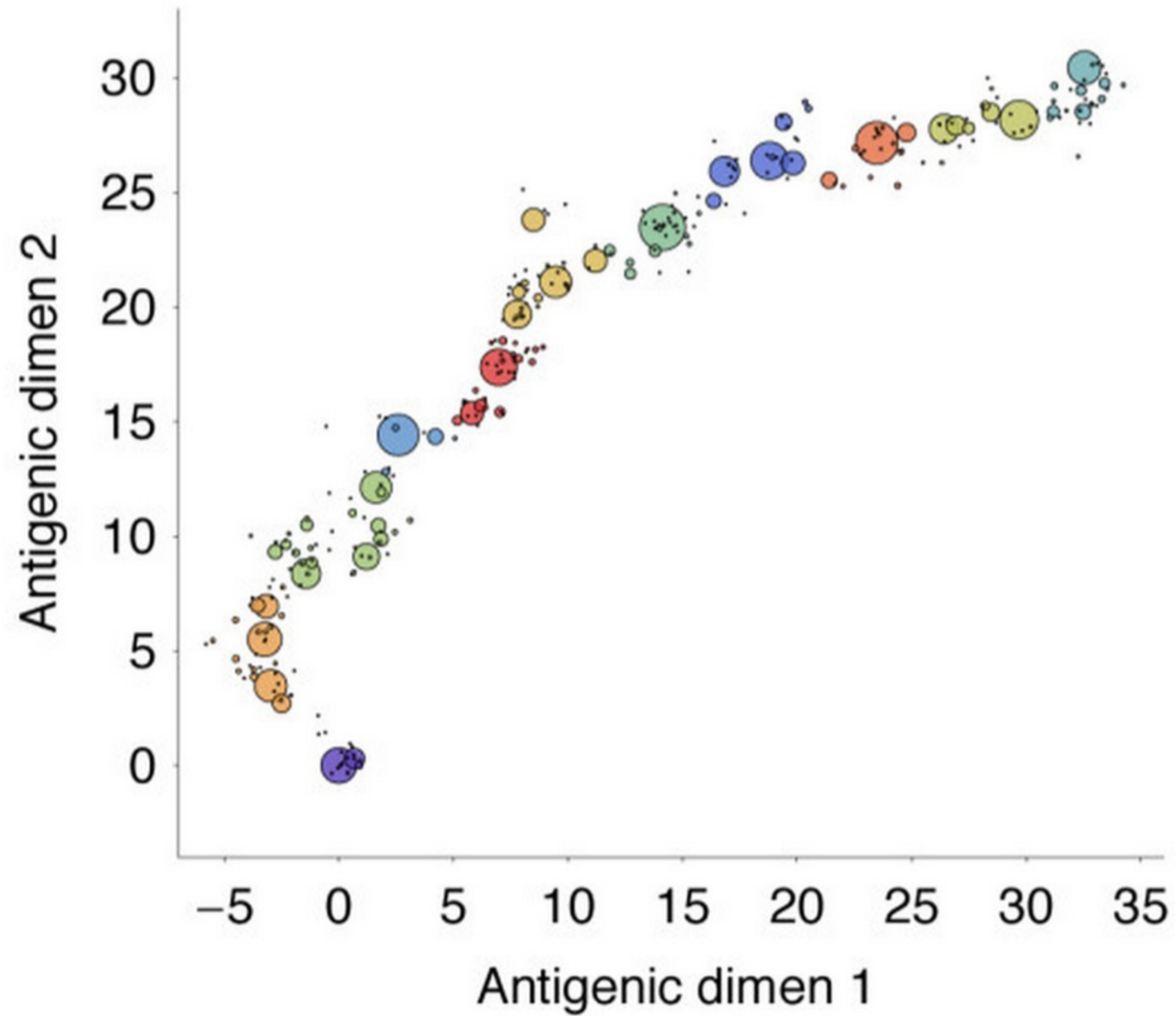


The question of strain space

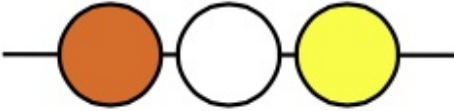
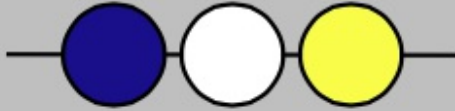
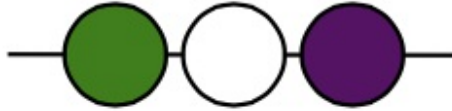



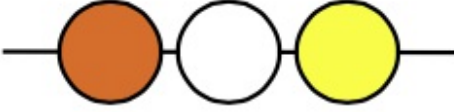
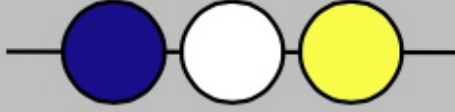
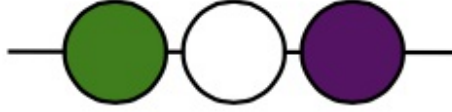



Continuous or discrete?

How many dimensions?

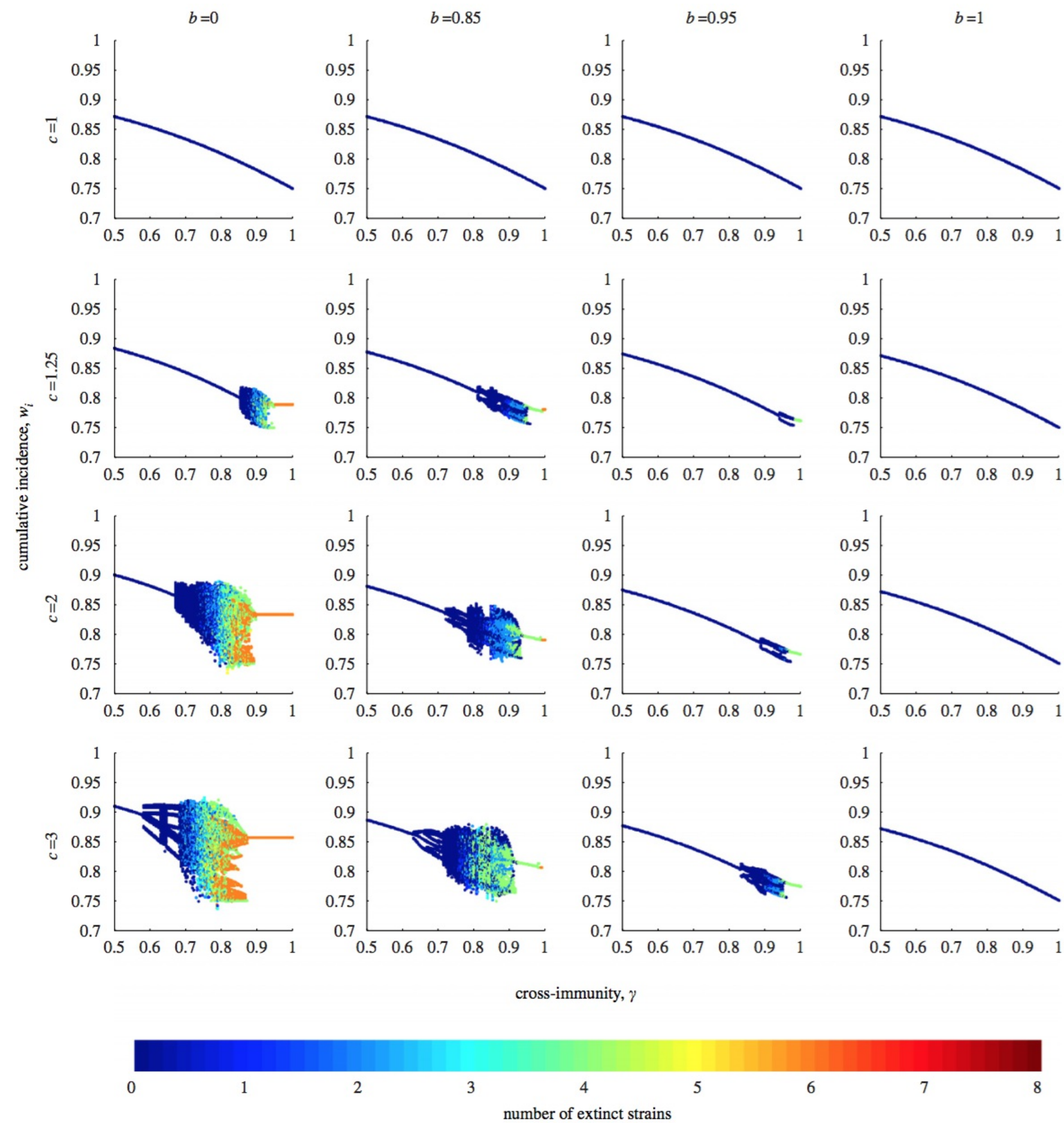
Continuous space



Discrete space

		first challenge	second challenge	third challenge
Host A	strain			
	outcome	infection	infection	protection
	response			
Host B	strain			
	outcome	infection	protection	infection
	response			

Immunodominance and breadth affect diversity





Agent-based models

Potentially most efficient with many strains

Support complex interactions

Naturally incorporate demographic stochasticity

Analytic approaches

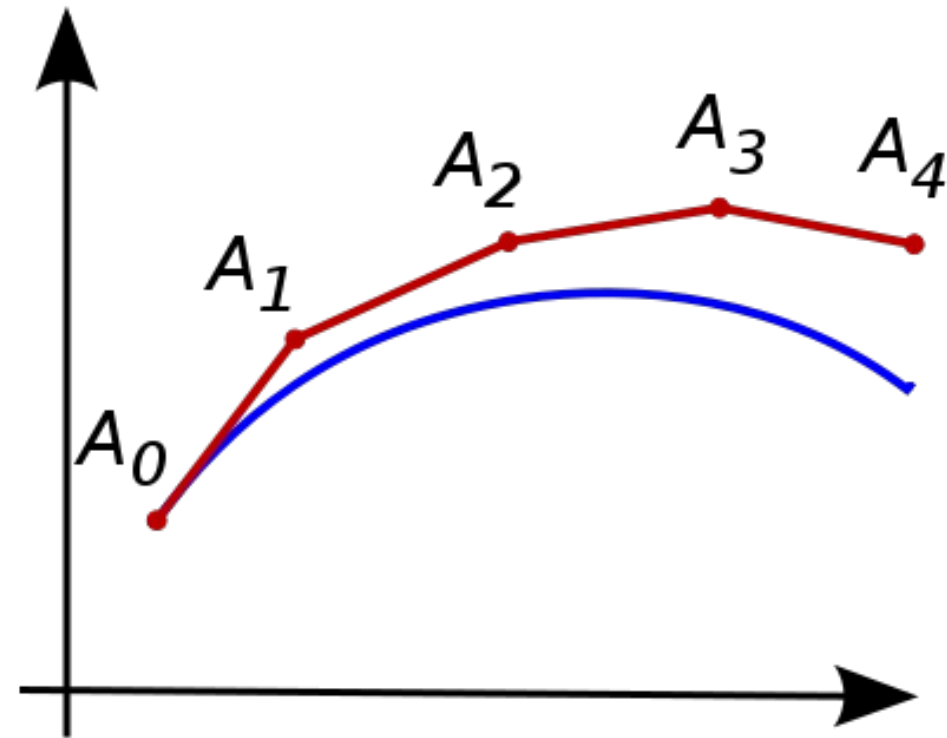
Equilibria: Solve for $\mathbf{S}'_i = \mathbf{I}'_i = \dots = \mathbf{0}$

Stability analysis: Linearize at equilibria

Invasion analysis: Is $\mathbf{I}'_2 > \mathbf{0}$ at \mathbf{I}_1^* ?

Integration: Calculate $\mathbf{I}_1(t), \mathbf{I}_2(t), \dots$

Numerical integration




Approximate solution to $N' = f(N)$:

$$N(t_0 + \Delta t) \approx N_0 + f(N_0)\Delta t = N_1$$

Re-iterating, we get

$$N_{z+1} \approx N_z + f(N_z)\Delta t$$


$$N_{z+1} \approx N_z + f(N_z)\Delta t$$

We could assume $f(x)$ is constant for Δt (Euler's method)

Even better, average over multiple points!

A second-order method

$$N_{z+1} \approx N_z + f(N_z) \Delta t$$

$$M_{z+1} = N_z + f(N_z) \Delta t$$

$$N_{z+1} = N_z + \frac{1}{2} [f(N_z) + f(M_{z+1})] \Delta t$$

4th-order Runge-Kutta

$$k_1 = f(N_z) \Delta t$$

$$k_2 = f \left(N_z + \frac{1}{2} k_1 \right) \Delta t$$

$$k_3 = f \left(N_z + \frac{1}{2} k_2 \right) \Delta t$$

$$k_4 = f(N_z + k_3) \Delta t$$

$$N_{z+1} = N_z + \frac{1}{6} (k_1 + 2k_2 + 2k_3 + k_4)$$

Why not just pick an extremely small Δt ?



Considerations for multistrain models

Form of immunity (duration, strength, polarity)

Effect of immunity (susceptibility, infectiousness, clearance)

Coinfections and timing of interactions

Accuracy for individuals v. populations

Dimensionality and discretization of strain space

Analytic and numeric approaches, including stochasticity