Individual-based modelling of COVID-19 on the Acadia University campus with a realistic contact structure

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August 12, 2020

AARMS COVID-19 Seminar

Introduction

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- etc. pp.

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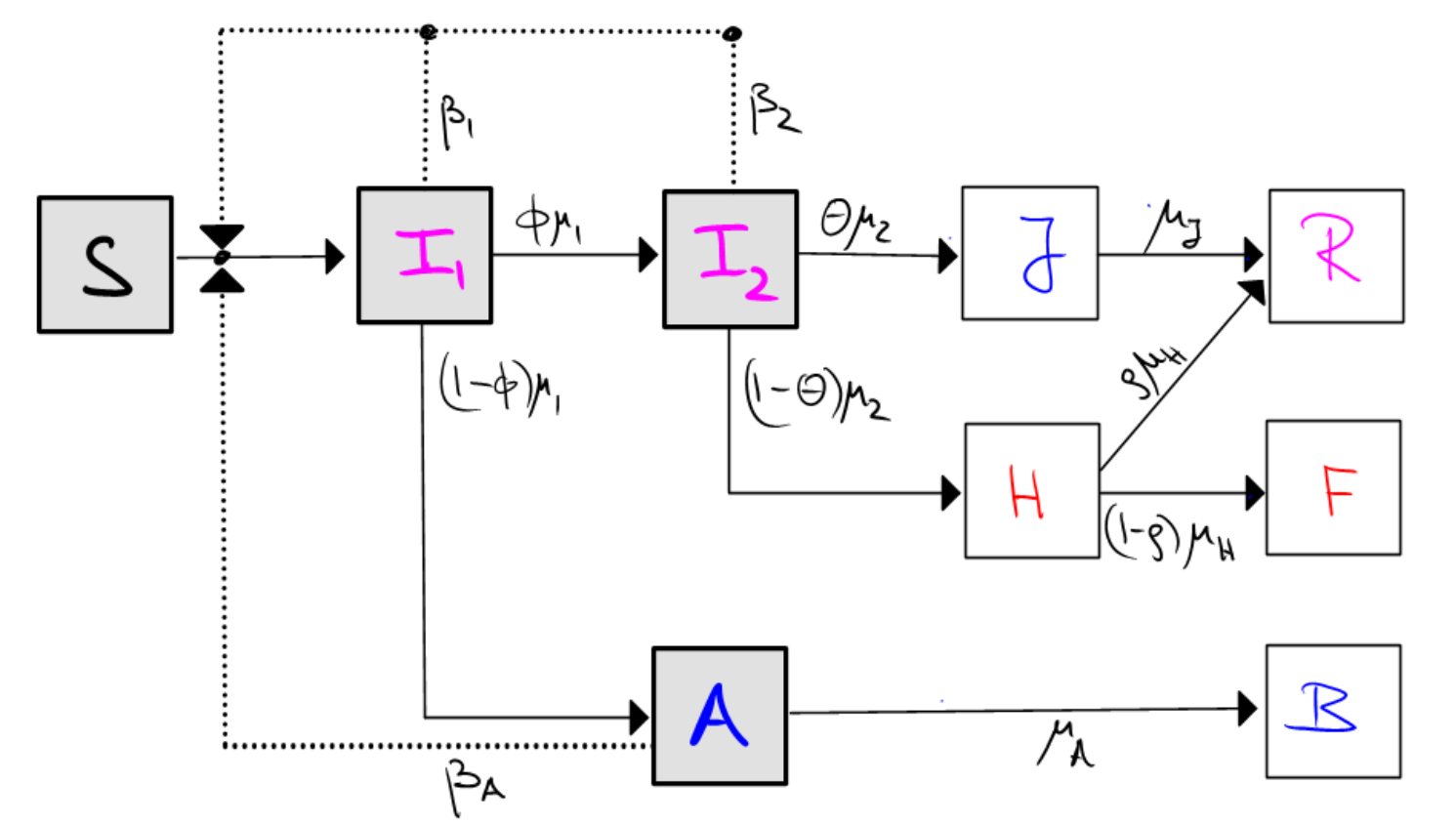

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stochastic. in each time step $t \to t+1$ the state vector transitions stochastically between states according to the transition matrix

	S	$E+I_1$	I_2	A	J	H	R	F	B
S	$1-b$	b	0	0	0	0	0	0	0
$E+I_1$	0	$1-\mu_1$	$\phi\mu_1$	$(1-\phi)\mu_1$	0	0	0	0	0
I_2	0	0	$1-\mu_2$	0	$\theta\mu_2$	$(1-\theta)\mu_2$	0	0	0
A	0	0	0	$1-\mu_A$	0	0	0	0	μ_A
J	0	0	0	0	$1-\mu_J$	0	μ_J	0	0
H	0	0	0	0	0	$1-\mu_H$	$\rho\mu_H$	$(1-\rho)\mu_H$	0
R	0	0	0	0	0	0	1	0	0
F	0	0	0	0	0	0	0	1	0
B	0	0	0	0	0	0	0	0	1

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R	0	0	0	0	0	0	1	0	0
F	0	0	0	0	0	0	0	1	0
B	0	0	0	0	0	0	0	0	1

where

$$b = 1 - \prod_{j'=1}^{N_{pop}} \Big(1 - \beta(x_{j'}(t), y_{j'}(t))\Big)^{C_{j,j'}} \qquad \text{(probability that individual } j \text{ gets infected)}$$

$C_{j,j'}$ = contact matrix (average number of infectious contacts between individuals j and j' per day)

$$\beta(x,y) = \begin{cases} \beta_1(x), & \text{if } y = 1 \\ \beta_2(x), & \text{if } y = 2 \\ \beta_A(x), & \text{if } y = 3 \\ 0, & \text{otherwise} \end{cases} \qquad \text{(probability of infection per contact)}$$

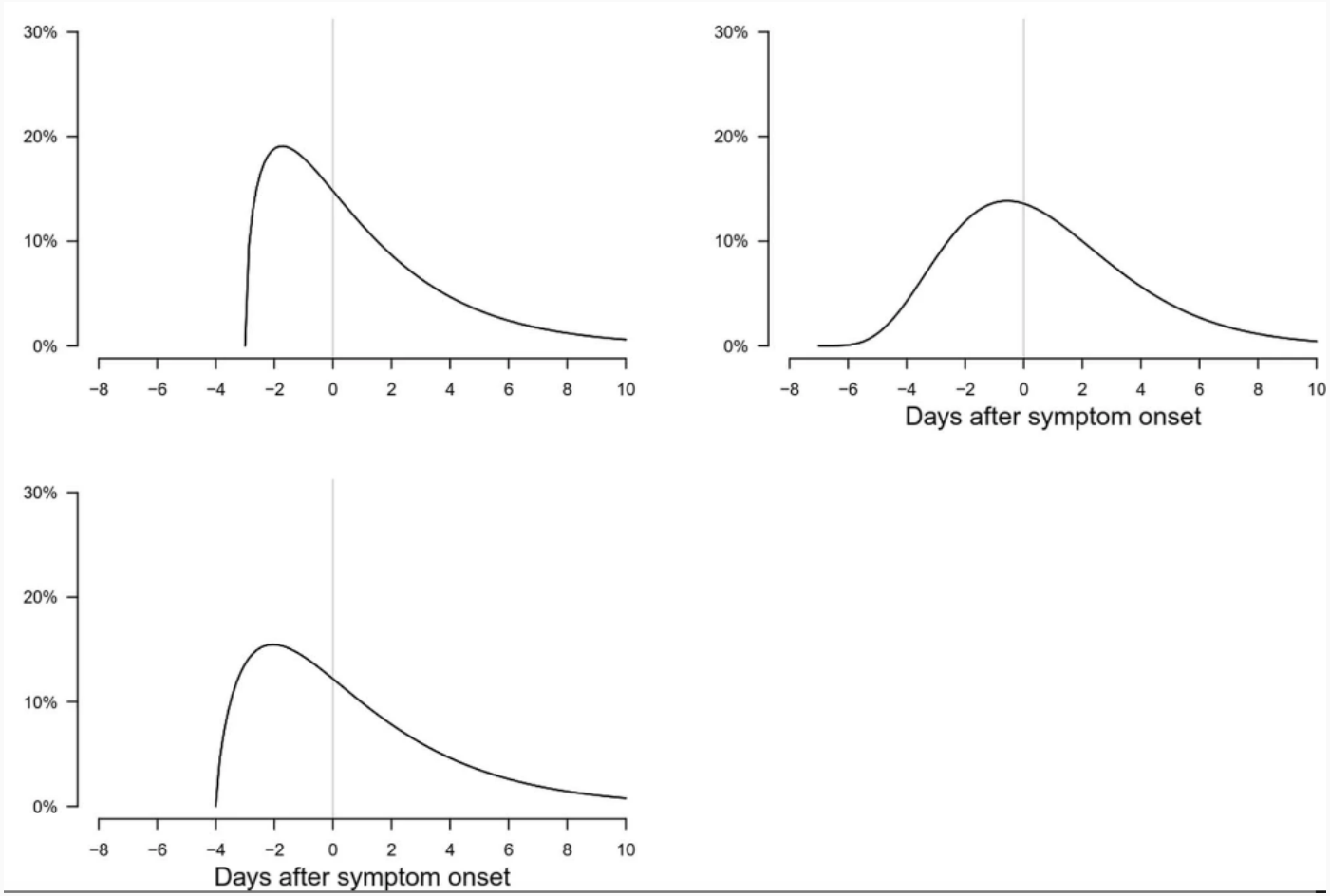
$x_j(t)$ = infection age (time since individual j got infected)

μ_* = $\mu_*(x_j(t))$ (probability of advancing to next stage of disease)

ϕ, θ, ρ = probabilities of branching.

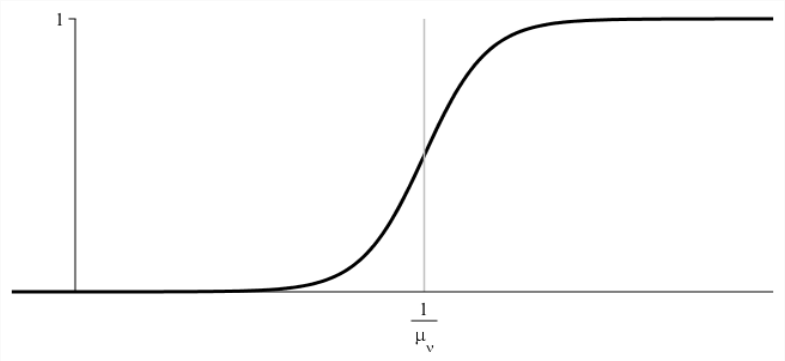
Model description: Parameters

- We choose $\beta_1(x) \equiv \beta_2(x) \equiv \beta_A(x) \equiv \beta b(x)$, where the function $b(x)$ is expected to follow the temporal shape of "viral shedding" [6, 1, 9]:



Model description: Parameters

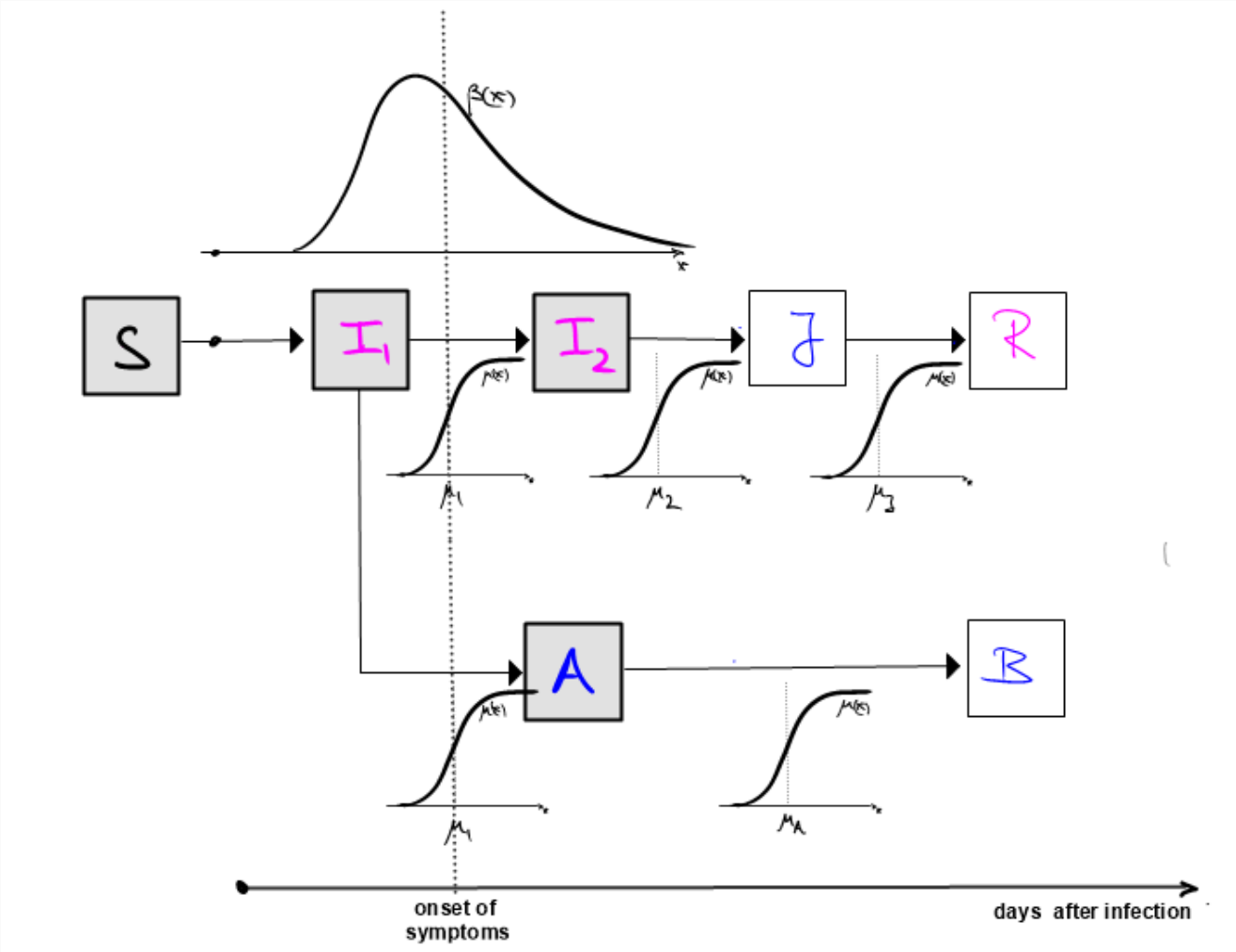
- Similarly, the functions $\mu_\nu(x)$ have a general shape like this:



- The probability of infection per contact β is chosen such that $\mathcal{R}_0 \approx 3.8$ (value chosen in [5]). Here "contact" is interpreted as "being in the same room for 15 mins."
- The (median) times $\frac{1}{\mu_\nu}$ in the various stages are typical values found in the literature; see e.g. [3, 4, 2, 8, 7], https://gabgoh.github.io/COVID/index.html

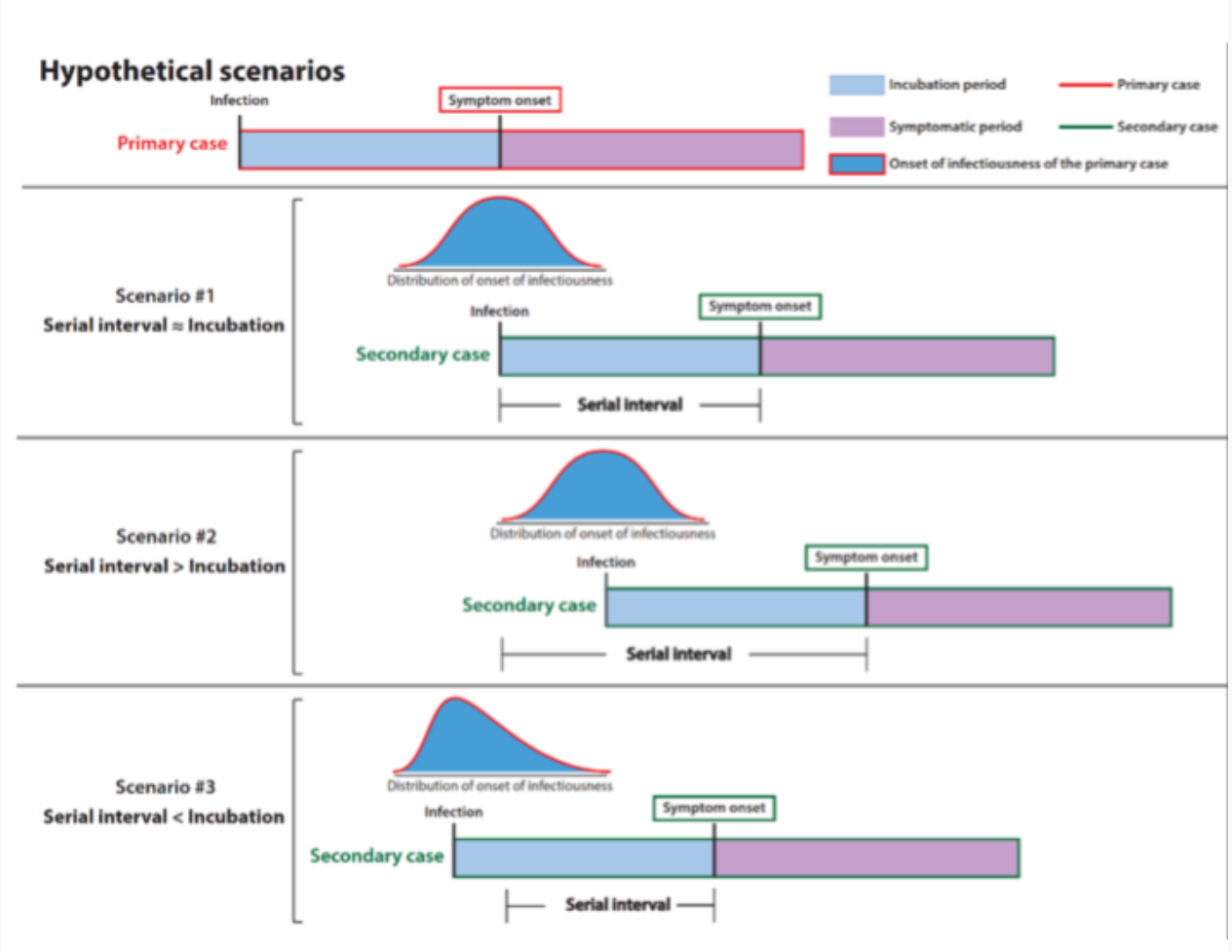
Model description: Parameters

- Summary (ignoring hospitalizations and deaths for now):



Model description: reproduction number and serial interval

- [6] has this pedagogical diagram:



Contact structure

Contact structure: Classes

Contact structure: Residences

Contact structure: Off-campus living

Contact structure: Social life

Simulation results

Results: baseline (regular semester, no intervention)

Results: quarantining index cases and contacts

Results: add campus lockdown ...

Results: testing protocol 1

Results: testing protocol 2

Results: “onboarding”

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