

# Modelling the COVID-19 pandemic in Australia: a tipping point in social distancing

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Large-scale computational modelling of epidemics in  
Australia (ARC DP160102742)

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GMT Workshop on Nonlinear Dynamics and Statistics  
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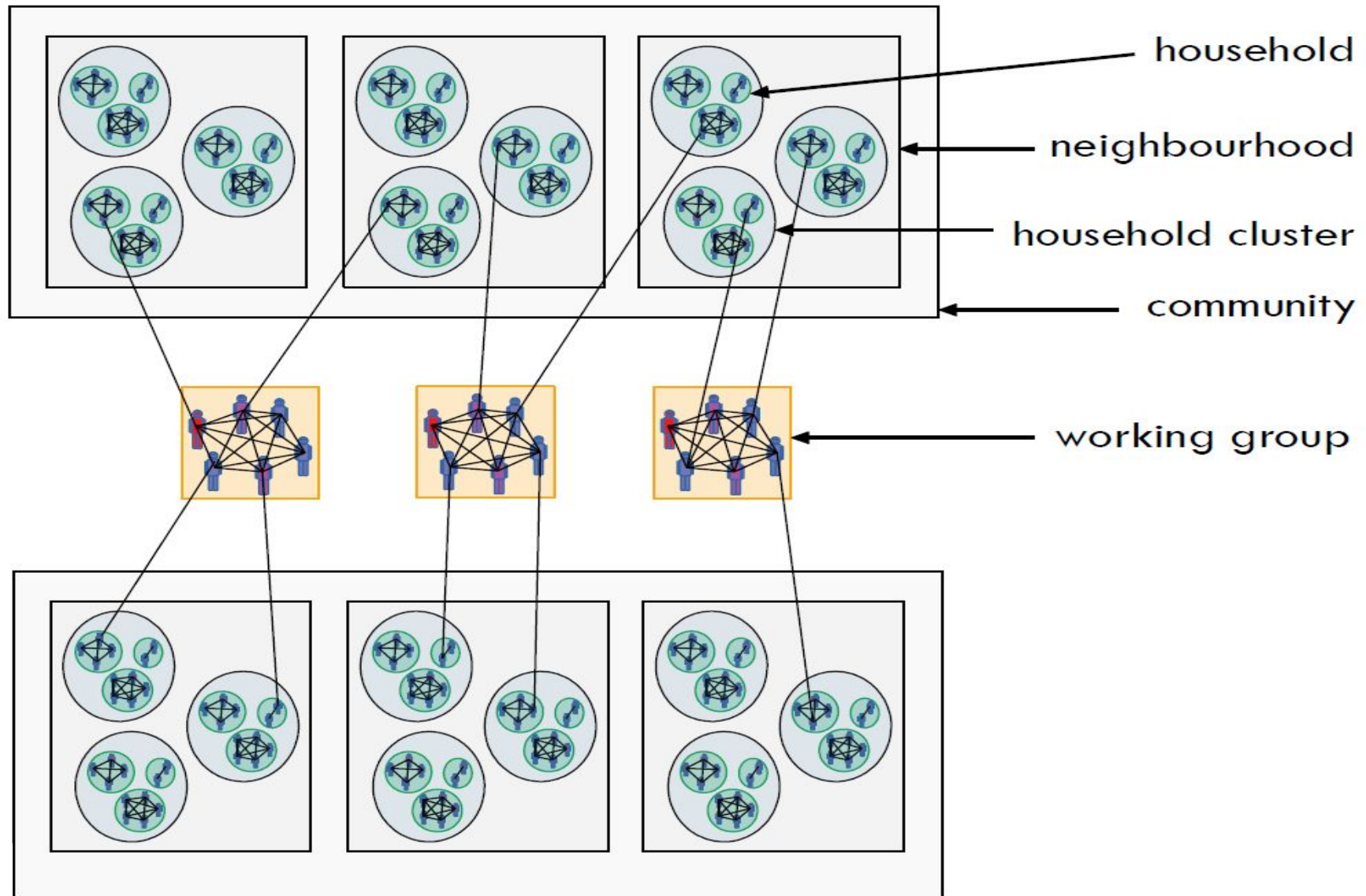
- Modelling pandemics with large-scale high-resolution agent-based models
  - *demographics*: from census based data to agents
  - *mobility*: travel patterns including long-distance
  - *infection*: disease transmission and natural history models
  - AMTraC-19 – Agent-based Model of Transmission and Control of the COVID-19 pandemic in Australia
  
- COVID-19 pandemic
  - age-dependent epidemiological characteristics
  - pandemic trends (peaks, resurgence), and model validation
  - strategies for mitigation, suppression (or elimination)
  - tipping points (e.g., in social distancing)

# Agent-based Modelling (ABM) of epidemics

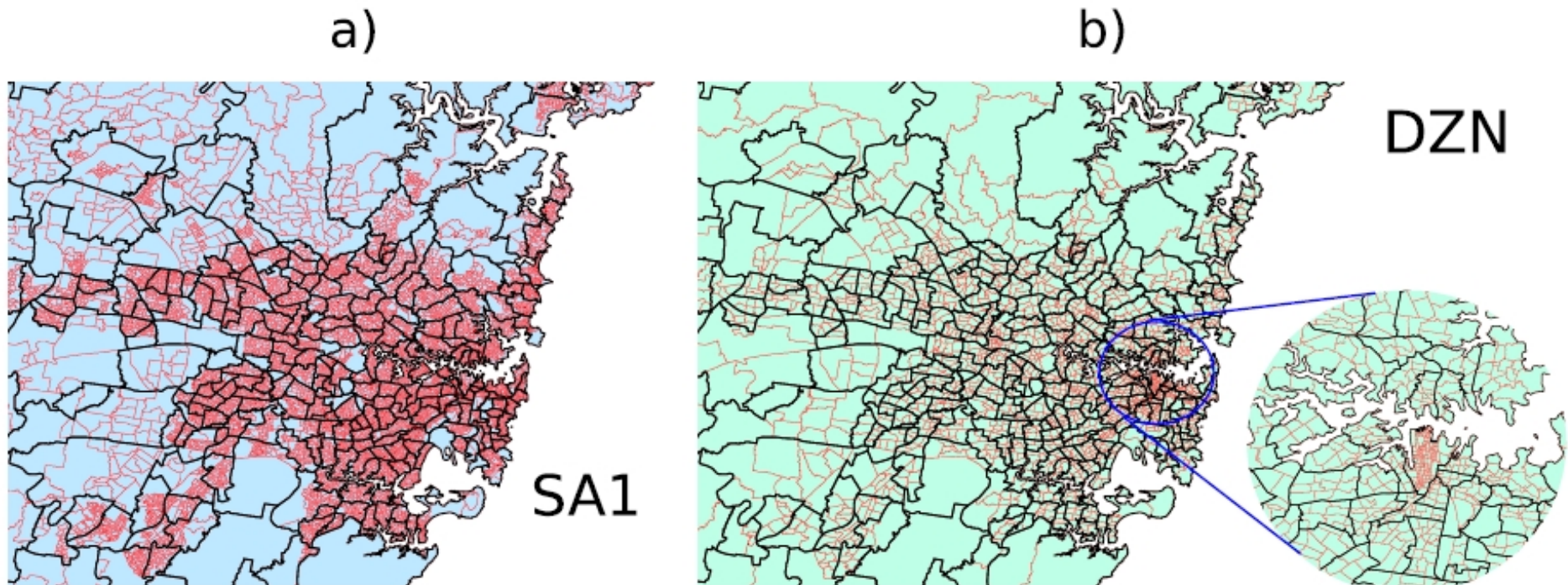
- anonymous individuals (census based) → agents with attributes (e.g., age, gender, occupation, susceptibility and immunity to diseases)
- agent interactions: contacts and disease transmission over about 24M agents, grouped in social “contexts” (households, neighbourhoods, communities, workplaces, schools, classrooms, etc.)
- specific virus (transmission rates, natural history of the disease)
- outbreak modelling of pandemic scenarios (international air traffic)
- varying sources and intensity of infection, as well as population sets
- calibration to known data on reproductive ratio  $R_0$ , attack rates (across “contexts”), growth rates, generation period, other parameters



# “Same storm, different boats”: ABM mixing contexts



# Population partitions: residential areas and destination zones



**Fig. 1** Maps of the Greater Sydney region illustrating the distribution of population partitions. (a) A map of the Greater Sydney region showing SA2 (black) and SA1 (red) population partitions. (b) A map of the same area showing SA2 (black) and DZN (red) partitions. The inset in (b) zooms in on the Sydney central business district to illustrate the much denser packing of DZN partitions in that area.



Airport code	State	City	Passengers
SYD	NSW	Sydney	40884
MEL	VIC	Melbourne	25859
BNE	QLD	Brisbane	14250
PER	WA	Perth	11449
OOL	QLD	Gold Coast	3022
ADL	SA	Adelaide	2214
CNS	QLD	Cairns	1874
DRW	NT	Darwin	597
TSV	QLD	Townsville	105

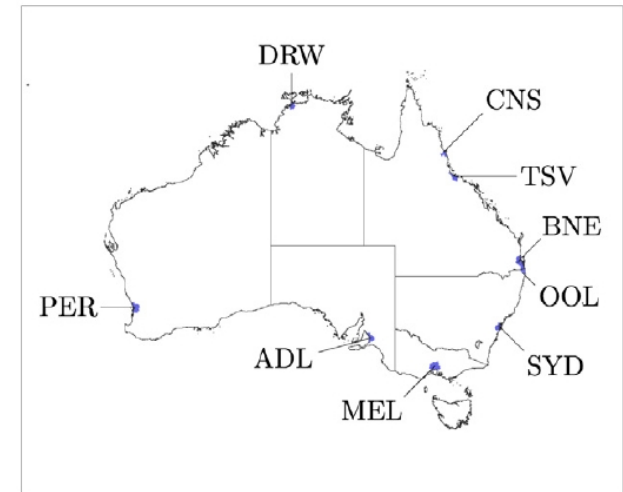
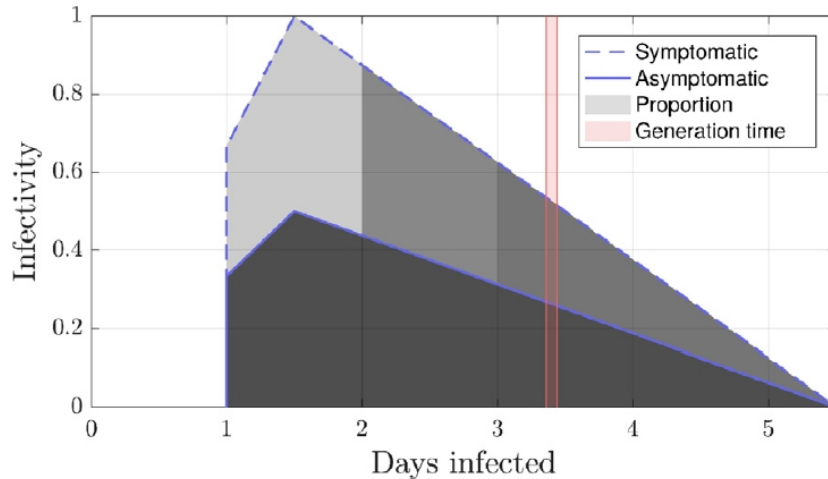
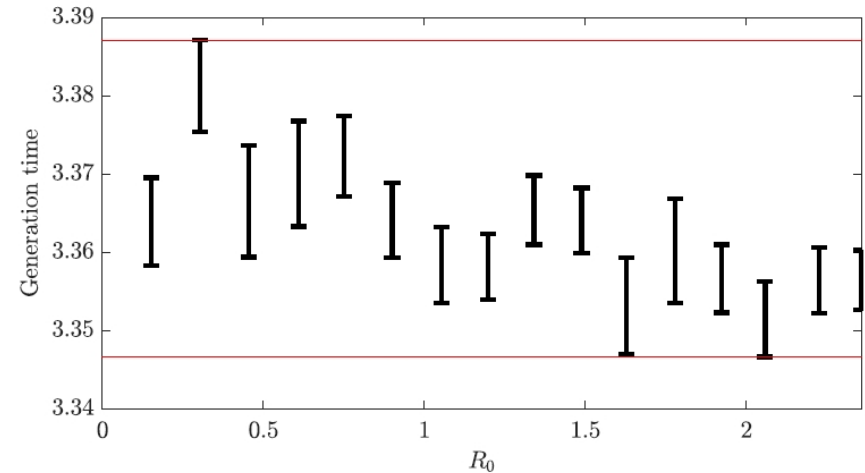


Fig. 3. Daily incoming passengers per Australian international airport obtained from BITRE [30] along with a map detailing the airport locations.

# Epidemic modelling: natural history of the disease



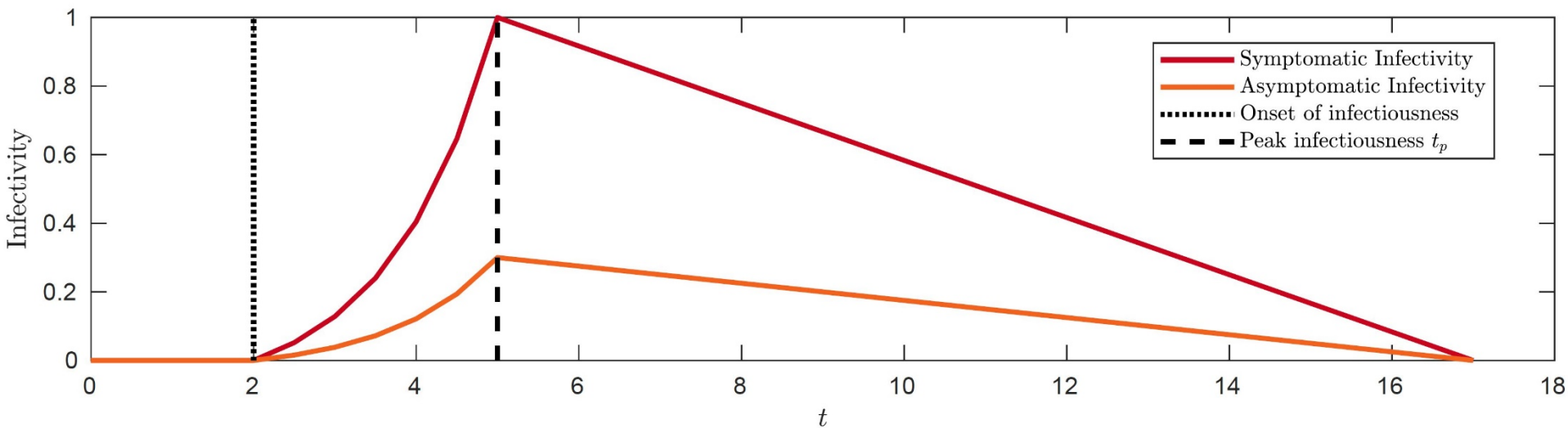
(a) Natural history of the disease.



(b) Simulated generation time.

**Fig. 2.** Natural history of the disease and corresponding simulated generation time. The disease dynamics are modelled as having a linear increase followed by a linear decrease, as illustrated in Fig. 2 (a). In the figure, the area under the curve is shaded according to the proportion of people *at least* that infectious after disease onset (darker representing a higher proportion). If an agent becomes symptomatic, their infectiousness doubles (dashed blue line) from that day onward. Moreover, 67% of agents become symptomatic; of these agents, 30% start showing symptoms on day 1, 50% on day 2, and the remaining 20% on day 3. We obtain empirical generation times from simulations resulting from this model, shown in 2(b) for a number of  $R_0$  values. The confidence intervals range from 3.35 to 3.39 days (also shown on Fig. 2(a)), depending on  $R_0$  and, in general, the generation time has a slight downward trend as a function of disease severity.

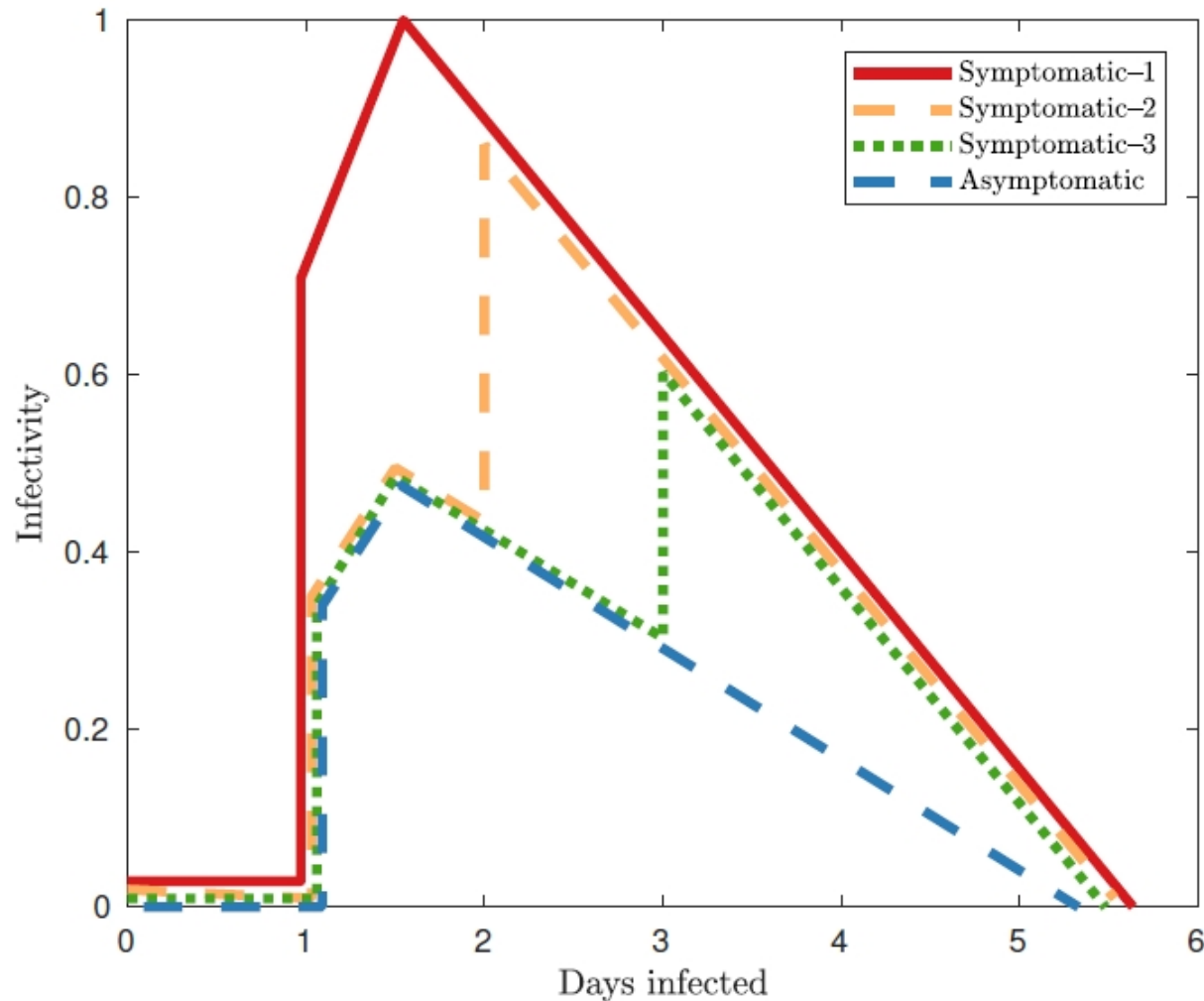
# Epidemic modelling: natural history of the disease







# Epidemic modelling: natural history of the disease



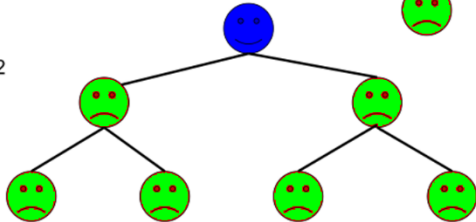


# Epidemic modelling: reproductive ratio $R_0$

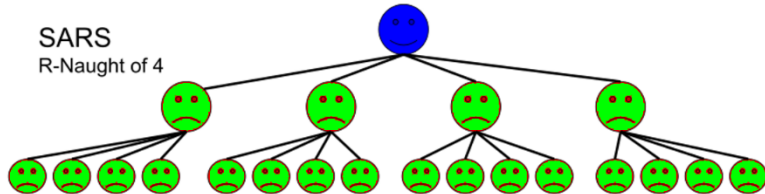
Patient Zero

Infected

Ebola:  
R-Naught of 2



SARS  
R-Naught of 4



$$\frac{dS}{dt} = \gamma I - \beta IS$$

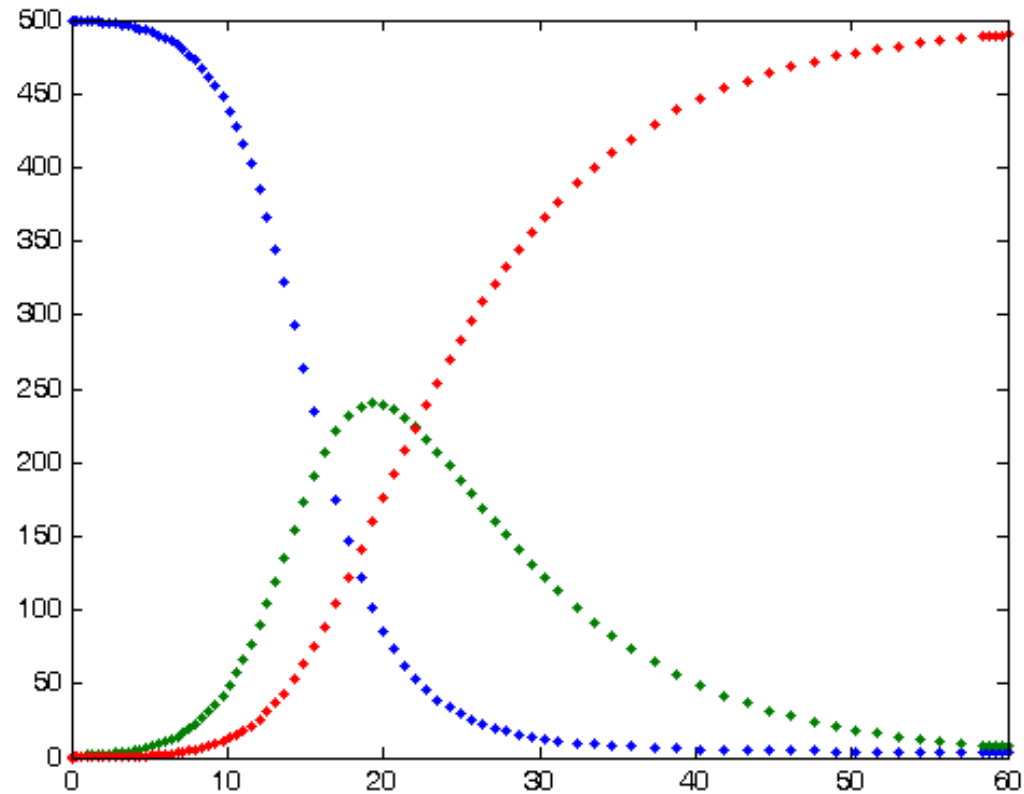
$$\beta / \gamma = R_0$$

$$\frac{dI}{dt} = \beta IS - \gamma I,$$

Susceptible

Infectious

Recovered



# Epidemic modelling: transmission probabilities

**Table C2**

Daily transmission probabilities  $q_{j \rightarrow i}^g$  for different contact groups  $g$ , obtained by Eq. (4) where  $\beta_{j \rightarrow i}^g$  are reported by [10].

Contact Group $g$	Infected Individual $j$	Susceptible Individual $i$	Transmission Probability $q_{j \rightarrow i}^g$
Household size 2	Any	Child (< 19)	0.0933
	Any	Adult (> 18)	0.0393
Household size 3	Any	Child (< 19)	0.0586
	Any	Adult (> 18)	0.0244
Household size 4	Any	Child (< 19)	0.0417
	Any	Adult (> 18)	0.0173
Household size 5	Any	Child (< 19)	0.0321
	Any	Adult (> 18)	0.0133
Household size 6	Any	Child (< 19)	0.0259
	Any	Adult (> 18)	0.0107
School	Child (< 19)	Child (< 19)	0.000292
Grade	Child (< 19)	Child (< 19)	0.00158
Class	Child (< 19)	Child (< 19)	0.035

$$p_{j \rightarrow i}^g(n) = \kappa f(n - n_j \mid j) q_{j \rightarrow i}^g$$

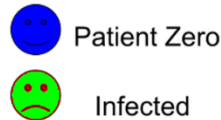
$$p_i(n) = 1 - \prod_{g \in G_i(n)} \left[ \prod_{j \in \mathcal{A}_g \setminus i} (1 - p_{j \rightarrow i}^g(n)) \right]$$

global scalar

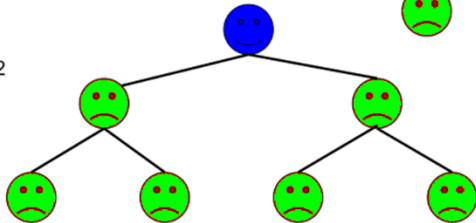


# Epidemic modelling: reproductive ratio $R_0$

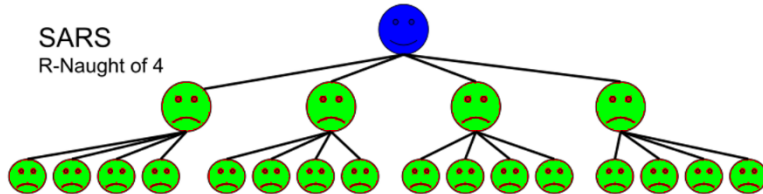
$$\beta / \gamma = R_0$$



Ebola:  
R-Naught of 2

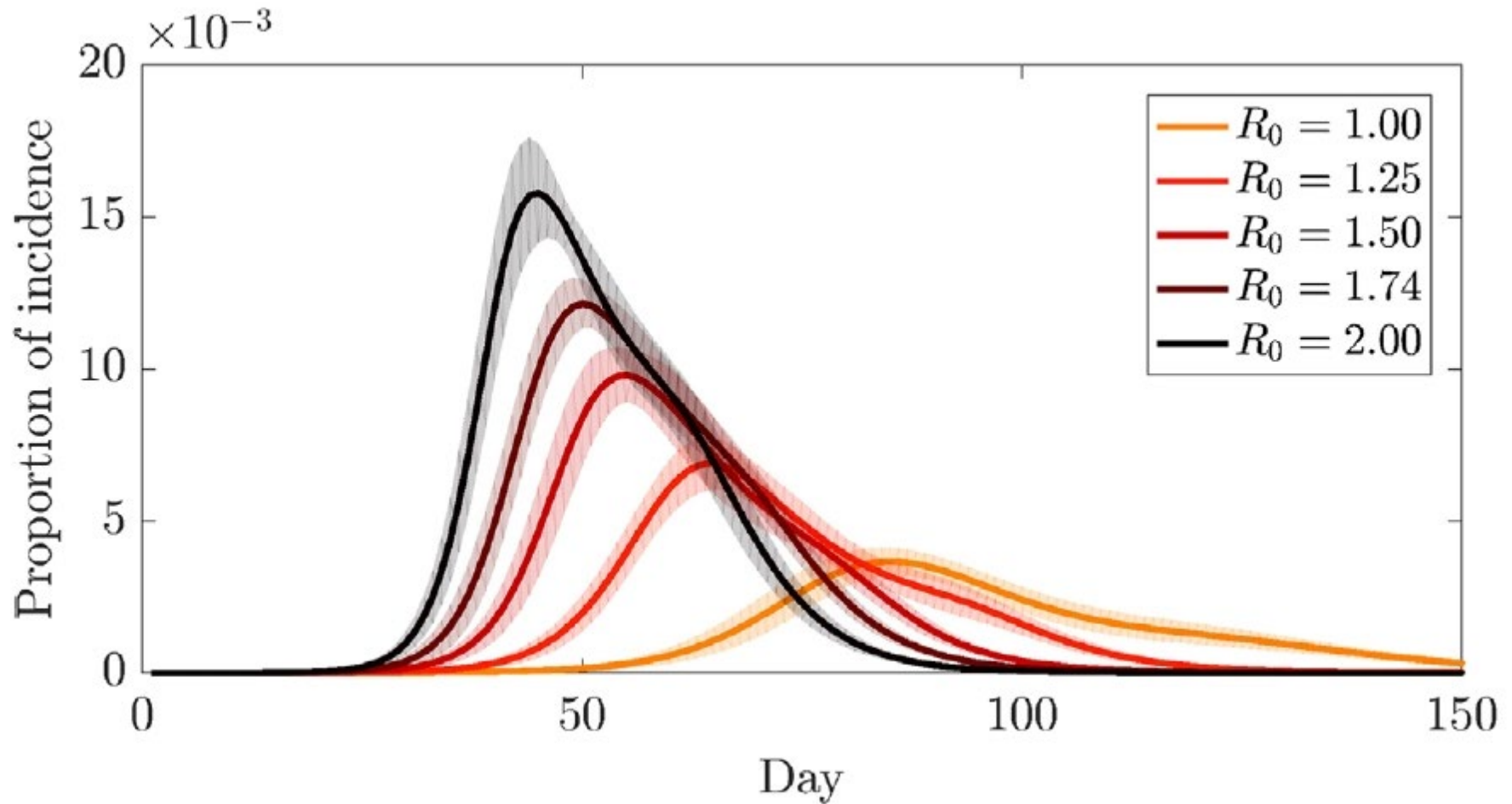


SARS  
R-Naught of 4



$$\begin{aligned}
 R_0 &= \mathbf{E} \left( \sum_i X_i(N) = \text{SYMPTOMATIC} \middle| X_J(0) = \text{SYMPTOMATIC} \right) \\
 &= \mathbf{E} \left( \mathbf{E} \left( \prod_n p_I(n) \middle| X_J(0) = \text{SYMPTOMATIC} \right) \right) \\
 &= \sum_j \sum_i \prod_n \left( 1 - \prod_{g \in \mathcal{G}_j(n)} \left( 1 - p_{j \rightarrow i}^g(n) \right) \right),
 \end{aligned}$$

# Epidemic modelling: reproductive ratio $R_0$

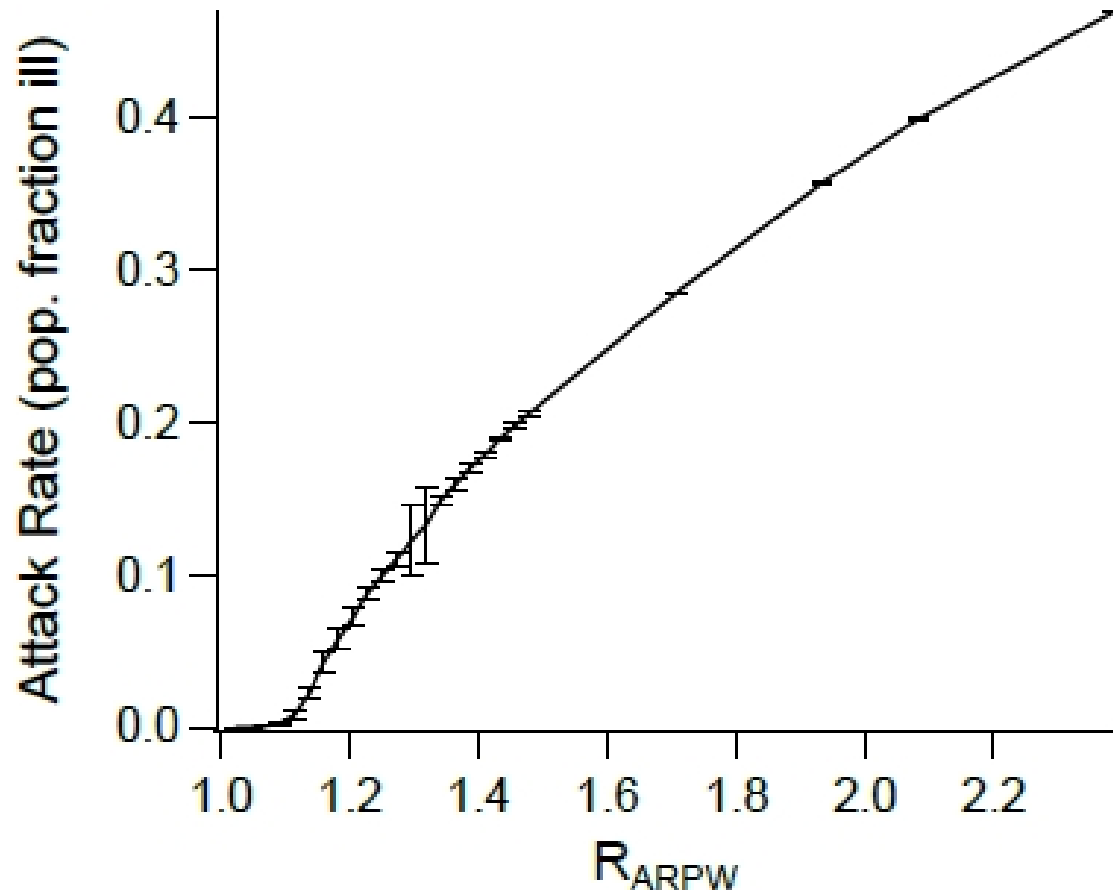


O. M. Cliff, N. Harding, M. Piraveenan, E. Y. Erten, M. Gambhir, M. Prokopenko, Investigating Spatiotemporal Dynamics and Synchrony of Influenza Epidemics in Australia: An Agent-Based Modelling Approach, *Simulation Modelling Practice and Theory*, 87, 412–431, 2018.





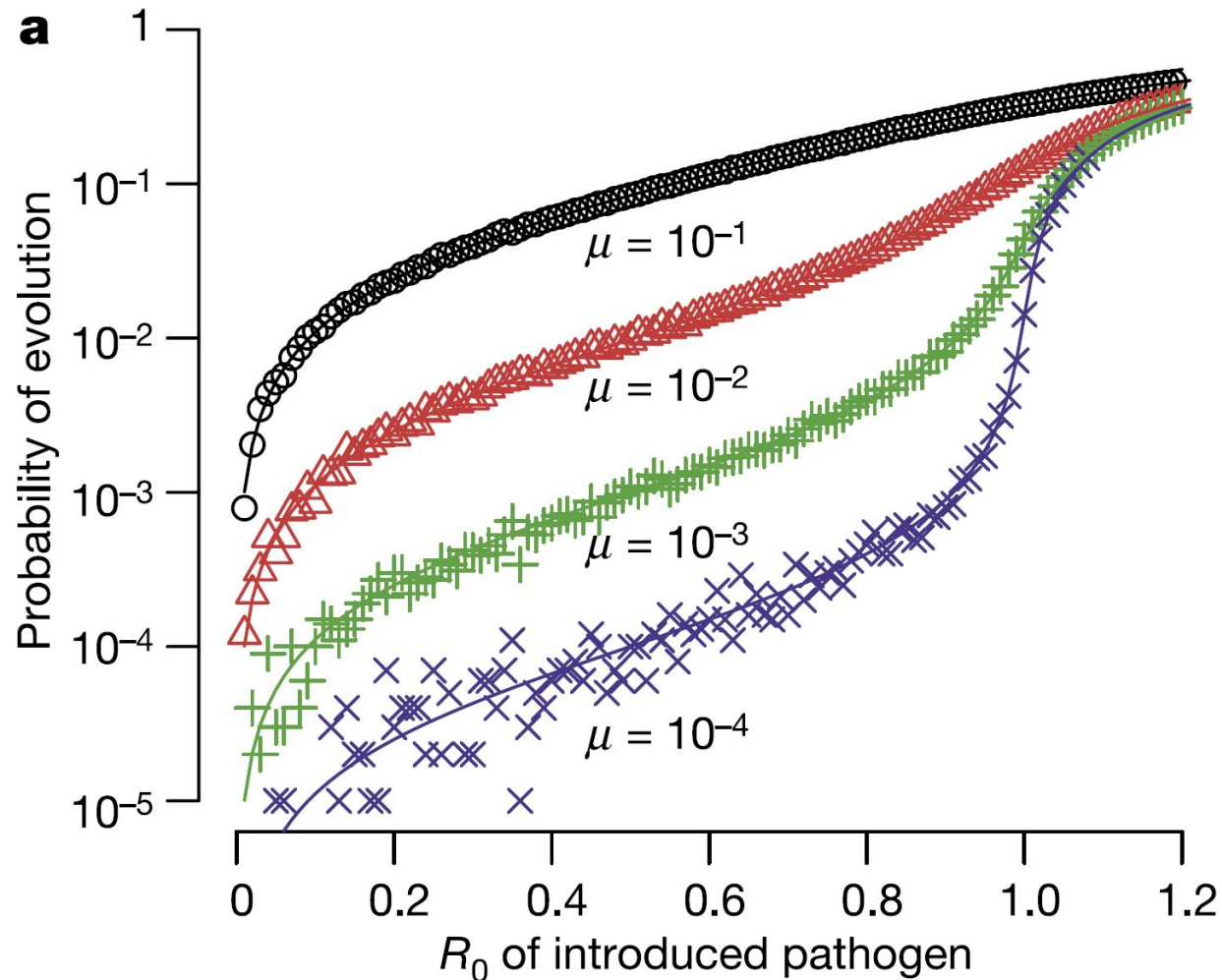
# Epidemic modelling: reproductive ratio $R_0$



C. Zachreson, K. M. Fair, N. Harding, M. Prokopenko, Interfering with influenza: nonlinear coupling of reactive and static mitigation strategies, *J. Royal Society Interface*, 17(165), 20190728, 2020.



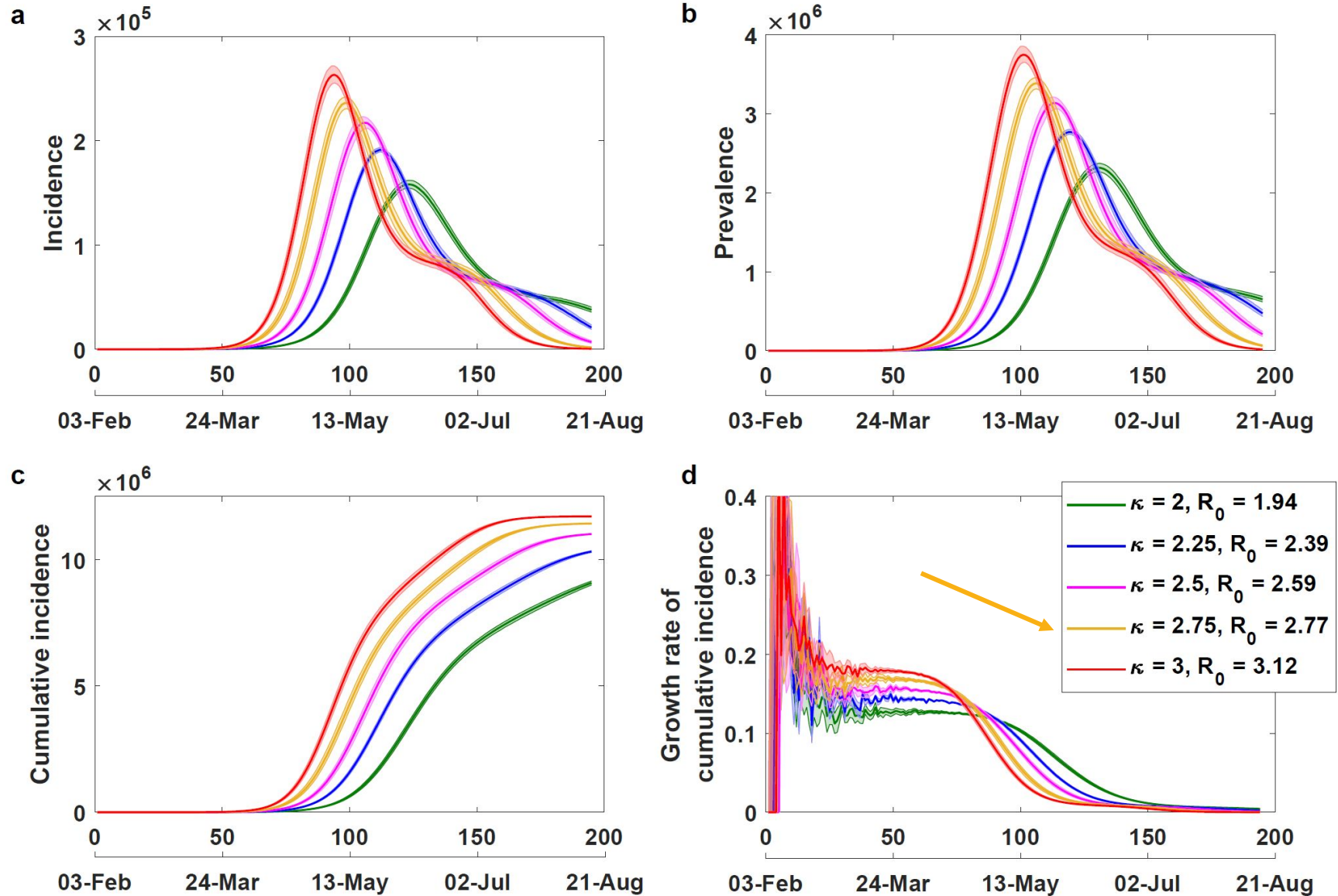
# Evolution and emergence: reproductive ratio $R_0$



R. Antia, R. R. Regoes, J. C. Koella, C. T. Bergstrom. The role of evolution in the emergence of infectious diseases. *Nature*, 426, 658, 2003.

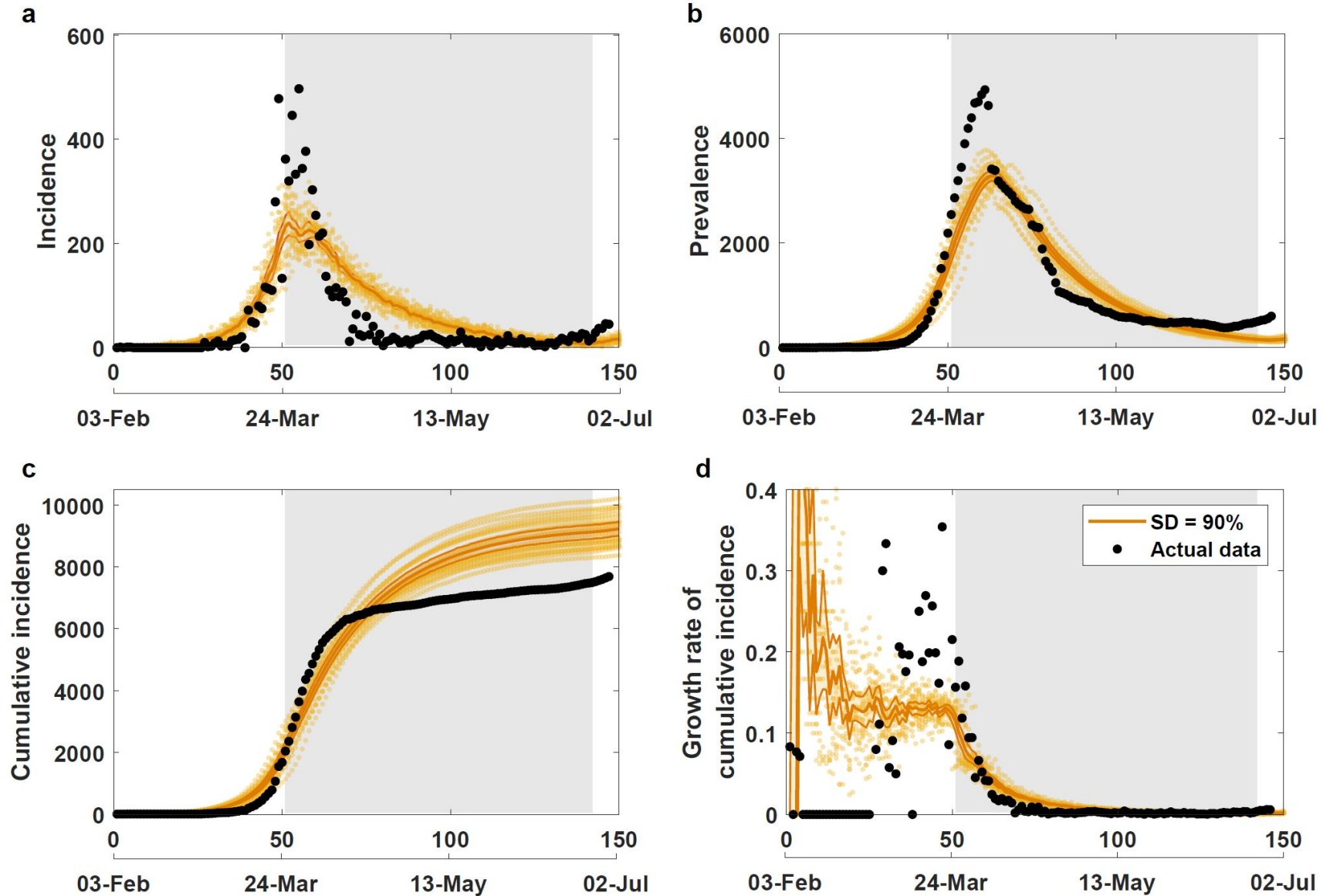


# Calibration ( $R_0$ ): COVID-19



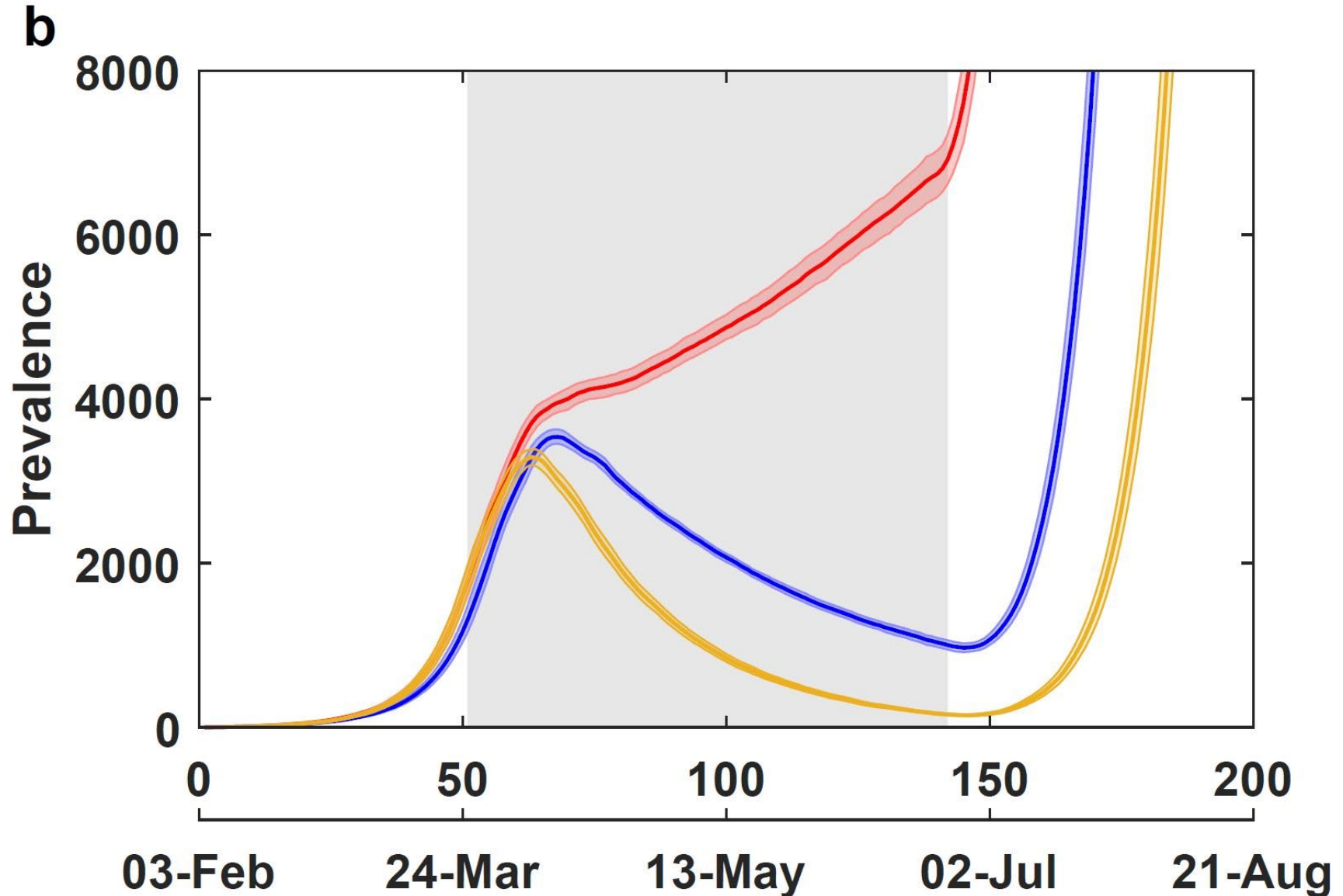


# Model validation





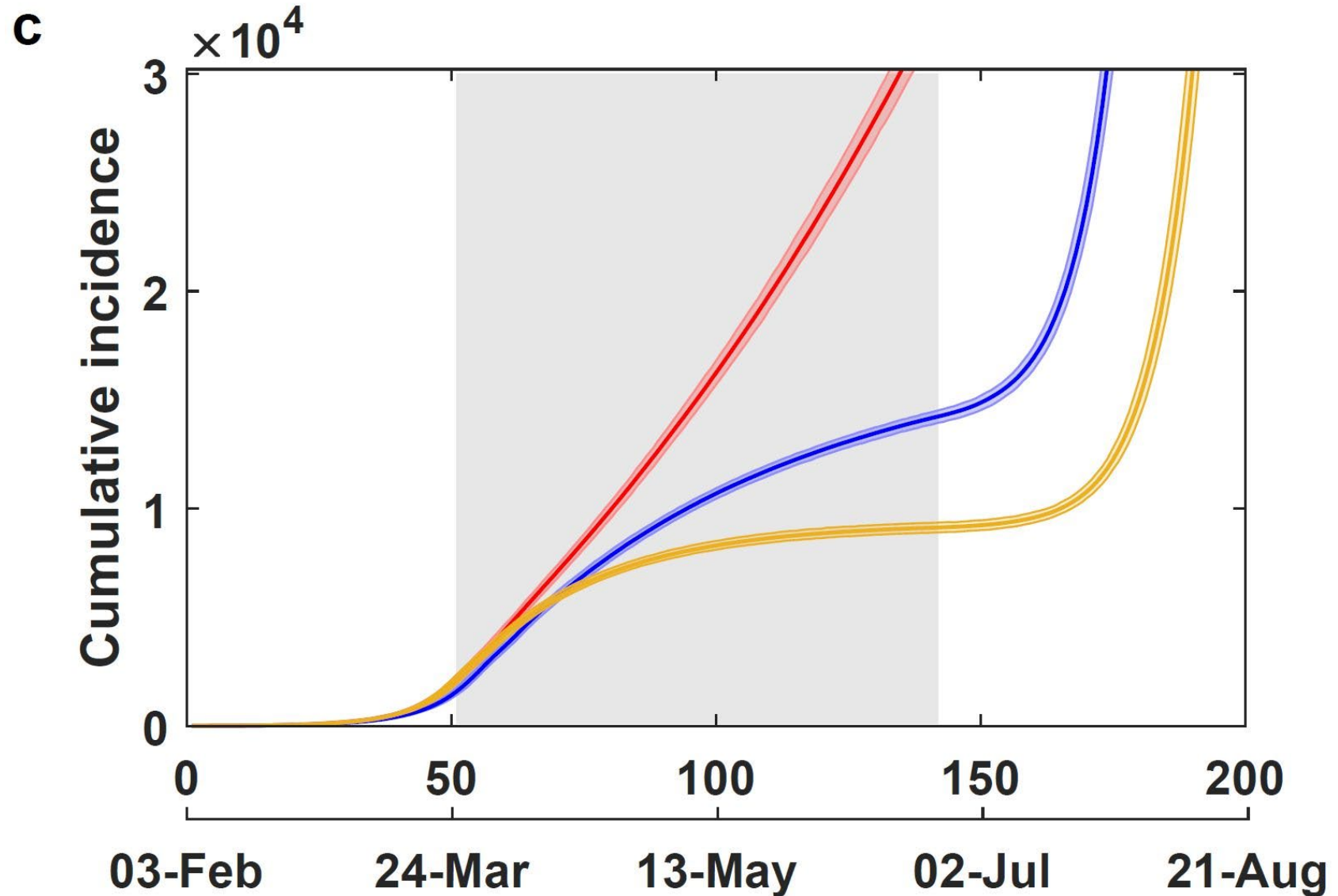
# Suppression (Social Distancing, SD): COVID-19







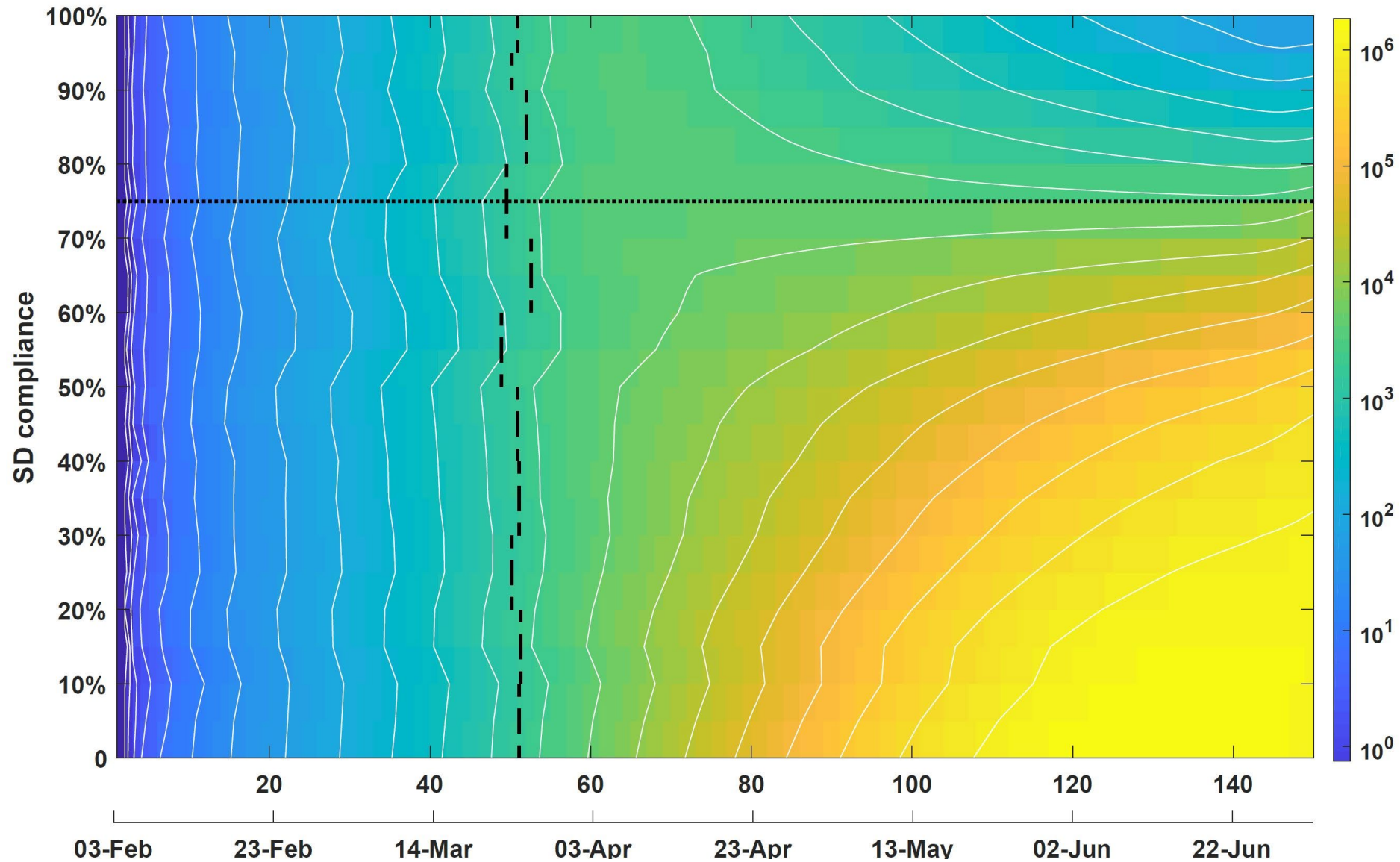
# Suppression (Social Distancing, SD): COVID-19



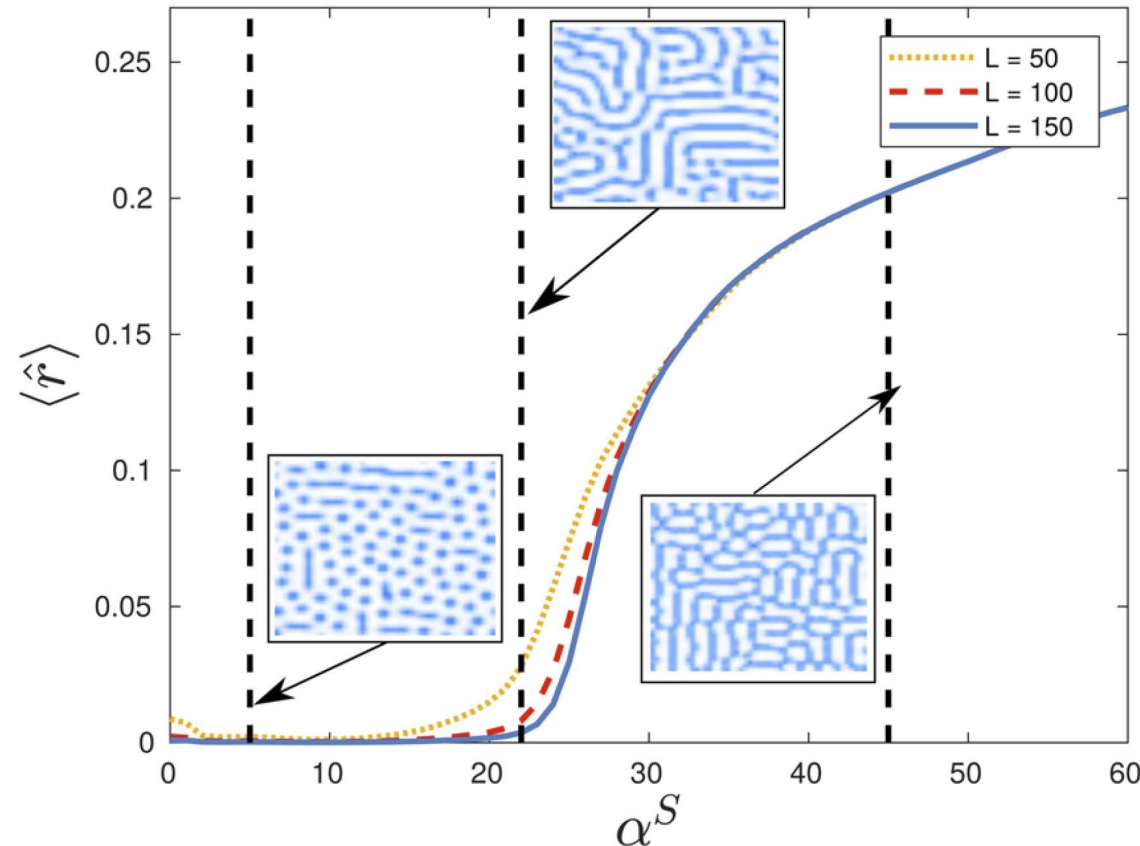


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# Critical regime (phase transition): COVID-19



# Spatial morphology: population mobility and degree of rationality



$$\frac{dI_i}{dt} = -\gamma I_i + \beta \sum_{j,k} \phi_{ij}^S(\mathbf{I}, \mathbf{C}) \phi_{kj}^I(\mathbf{I}, \mathbf{C}) \frac{S_i I_k}{\hat{N}_j(\mathbf{I}, \mathbf{C})},$$

$$\hat{N}_j(\mathbf{I}, \mathbf{C}) = \sum_k S_k \phi_{kj}^S(\mathbf{I}, \mathbf{C}) + I_k \phi_{kj}^I(\mathbf{I}, \mathbf{C}),$$

$$\phi_{ij}^x(\mathbf{I}, \mathbf{C} | \alpha^x, \omega) = Z_{x,i}^{-1} \exp(\alpha^x b_j - \omega c_{ij})$$

➤ Nonlinearity:

- natural history of the disease
- transmission across mixing social contexts
- feedbacks (positive and negative)
- effects of social distancing

➤ Tipping points:

- emergence of strains ( $R_0 \geq 1.0$ )
- minimal required social distancing
- spatial morphology vs rationality

- R. Antia, R. R. Regoes, J. C. Koella, C. T. Bergstrom, The role of evolution in the emergence of infectious diseases. *Nature*, 426, 658, 2003.
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- K. M. Fair, C. Zachreson, M. Prokopenko, Creating a surrogate commuter network from Australian Bureau of Statistics census data, *Scientific data*, 6, 150, 2019.
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- C. Zachreson, K. M. Fair, N. Harding, M. Prokopenko, Interfering with influenza: nonlinear coupling of reactive and static mitigation strategies, *Journal of Royal Society Interface*, 17(165), 20190728, 2020.





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# AMTraC-19 team

