## Lessons learned from modelling COVID-19 transmission and control in Australia

Funding: Australian Research Council project Large-scale computational modelling of epidemics in Australia (ARC DP160102742)

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Centre for Complex Systems, Faculty of Engineering

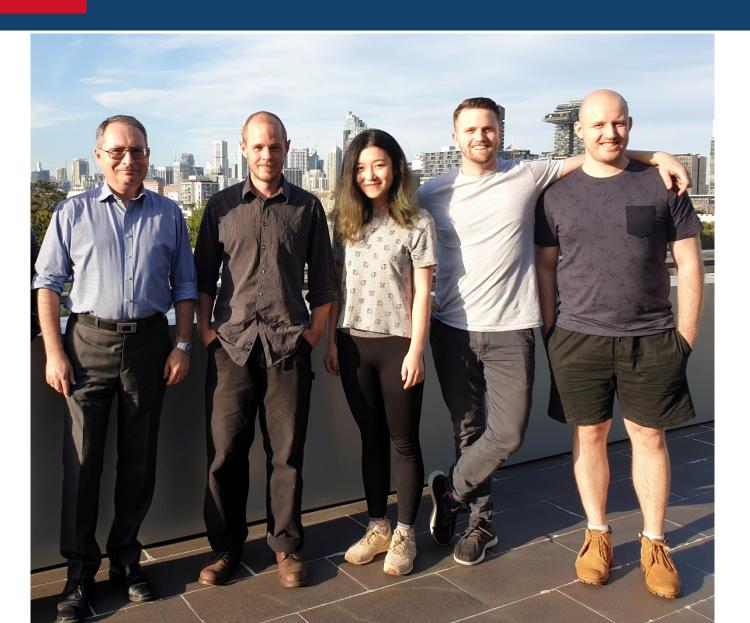
Marie Bashir Institute for Infectious Diseases and Biosecurity



Beyond COVID-19: modeling sustainable exit strategies
Virtual Workshop hosted by the Beyond Center for Fundamental
Concepts in Science in collaboration with Moogsoft
May 28th, 2020



### AMTraC-19 team





### 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<sub>0</sub>, attack rates (across "contexts"), growth rates, generation period, other parameters



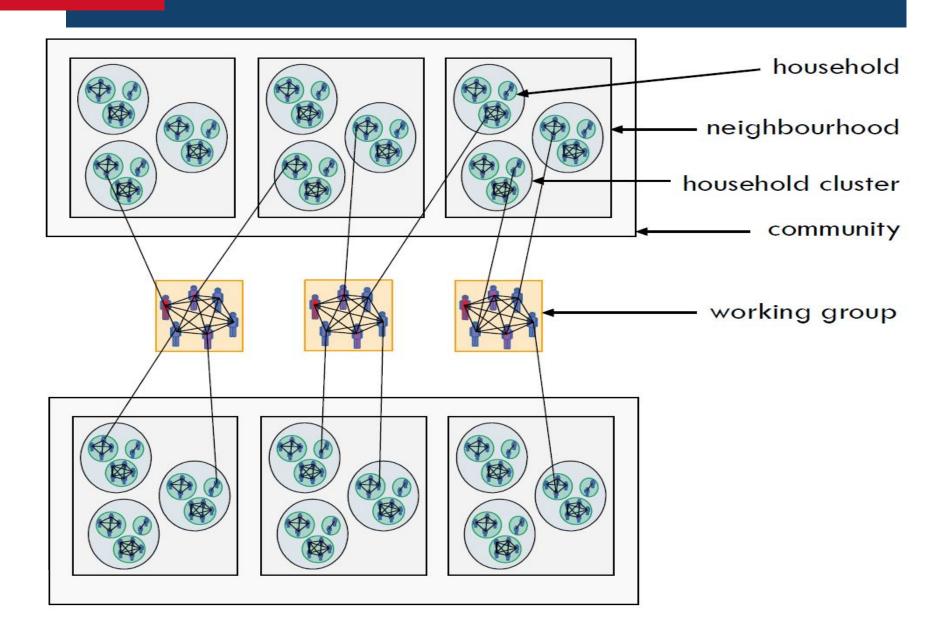
### Our pandemic modelling research (since 2016)

- 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
  - ACEMod Australian Census-based Epidemic Model

- Influenza pandemics (H1N1):
  - pandemic trends (peaks, synchrony, bimodality, critical regimes)
  - effects of urbanisation
  - counter-factual analysis
  - efficiency of interventions: geographically-targeted anti-prophylaxis (GTAP), contact-targeted anti-prophylaxis (TAP), vaccination



### "Same storm, different boats": ABM mixing contexts





### Population partitions: residential areas and destination zones

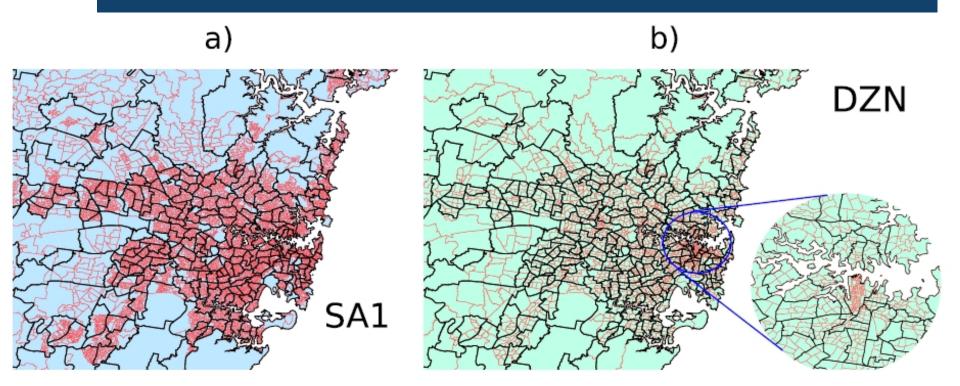


Fig. 1 Maps of the Greater Sydney region illustrating the distribution of population partitions. (a) A map of the Greater Sydney region showing SA2 (black) and SA1 (red) population partitions. (b) A map of the same area showing SA2 (black) and DZN (red) partitions. The inset in (b) zooms in on the Sydney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

K. M. Fair, C. Zachreson, M. Prokopenko, Creating a surrogate commuter network from Australian Bureau of Statistics census data, *Scientific Data*, 6, 150, 2019.



### International air traffic

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

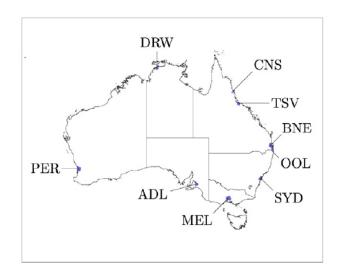
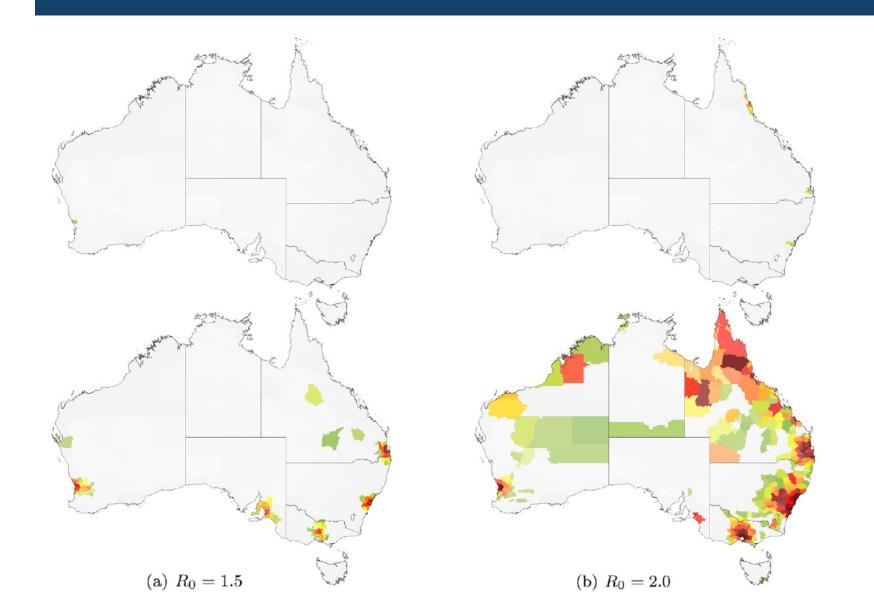


Fig. 3. Daily incoming passengers per Australian international airport obtained from BITRE [30] along with a map detailing the airport locations.

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.

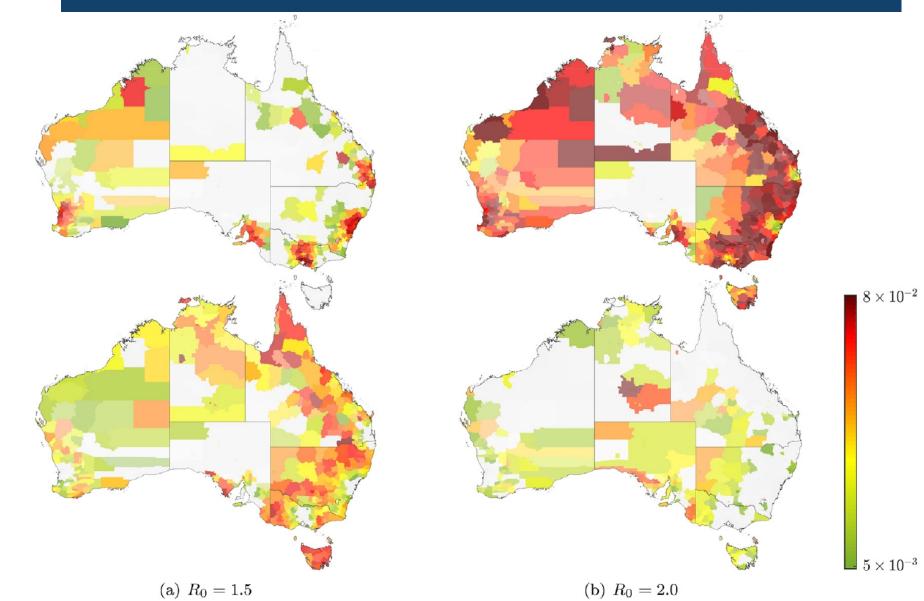


### Australian Census based Epidemic Modelling: ACEMod



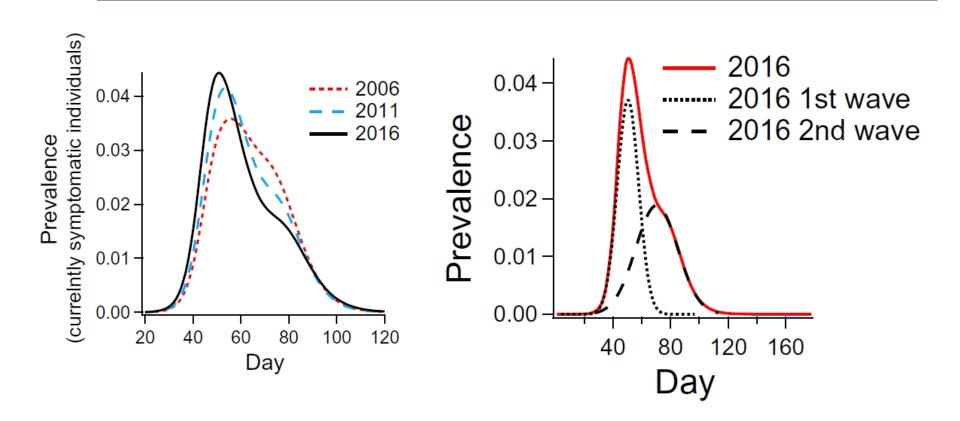


### Spatiotemporal synchrony



(b)  $R_0 = 2.0$ 

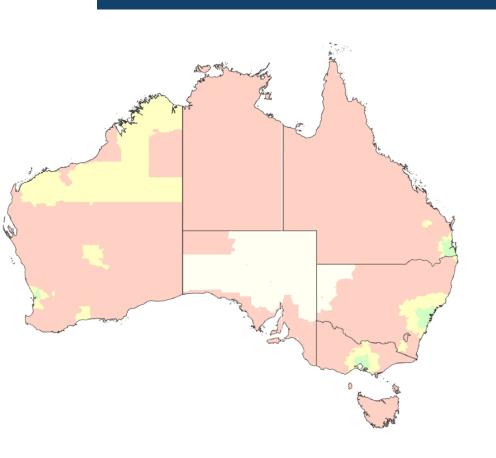
### Prevalence and epidemic peaks: H1N1

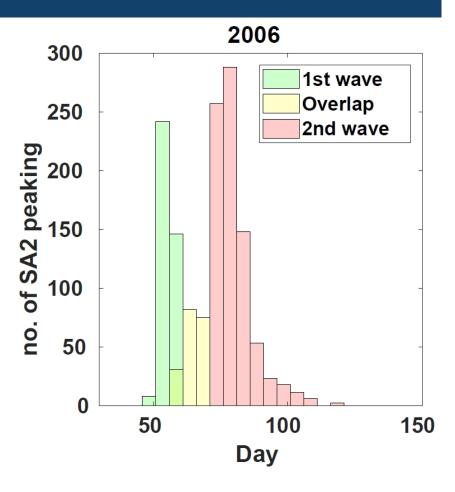


C. Zachreson, K. M. Fair, O. M. Cliff, N. Harding, M. Piraveenan, M. Prokopenko, Urbanization affects peak timing, prevalence, and bimodality of influenza pandemics in Australia: Results of a census-calibrated model, *Science Advances*, 4(12), eaau5294, 2018.



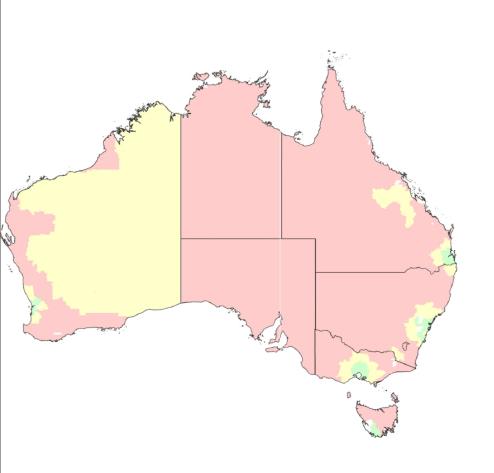
### Bimodality: H1N1

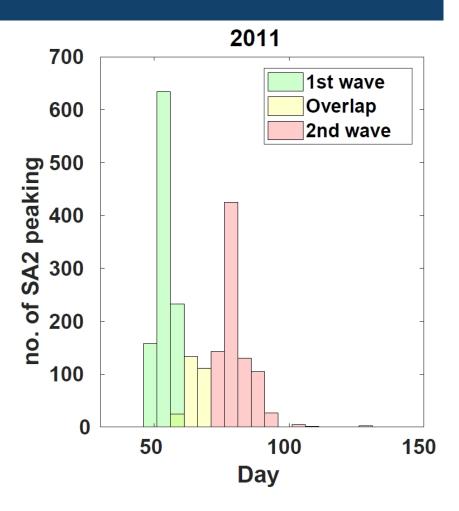






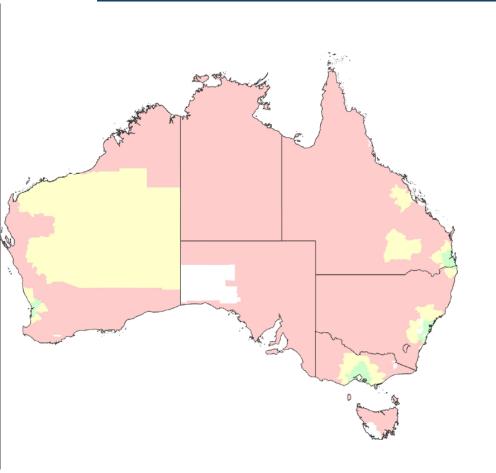
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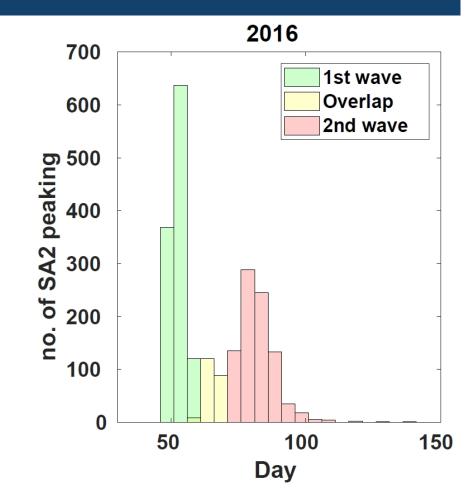






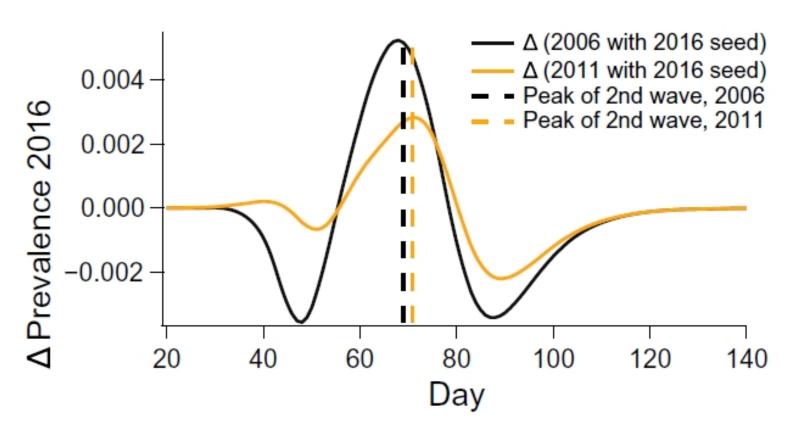
### Bimodality: H1N1







### Higher urbanisation or more air traffic?



- seeding conditions have a larger impact on the first wave than on the second
- seeding does not account for the decrease in the intensity of the second pandemic wave from year to year, a trend that we ascribe to increased urbanisation



### Our COVID-19 pandemic modelling research (2020)

- 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, and calibration
  - pandemic trends (peaks, resurgence), and model validation
  - strategies for mitigation, suppression (or elimination)
  - critical regimes (phase transition)

### Modelling transmission and control of the COVID-19 pandemic in Australia

Sheryl L. Chang<sup>1</sup>, Nathan Harding<sup>1</sup>, Cameron Zachreson<sup>1</sup>, Oliver M. Cliff<sup>1</sup>, and Mikhail Prokopenko<sup>1,2,\*</sup>

#### **Submission history**

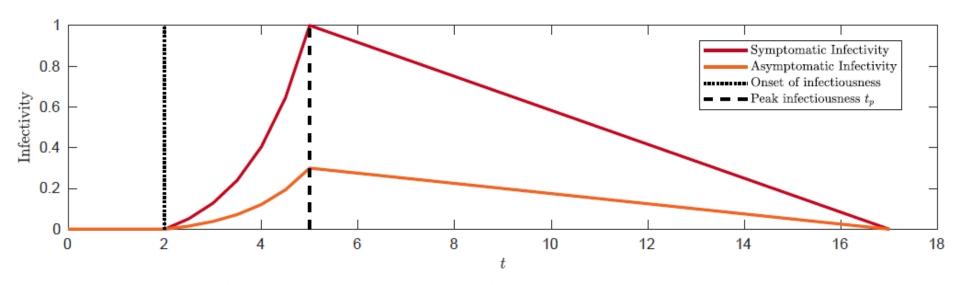
From: Mikhail Prokopenko [view email]

[v1] Mon, 23 Mar 2020 12:31:56 UTC (1,515 KB)

[v2] Thu, 2 Apr 2020 03:20:00 UTC (1,543 KB)

[v3] Sun, 3 May 2020 18:11:15 UTC (2,815 KB)



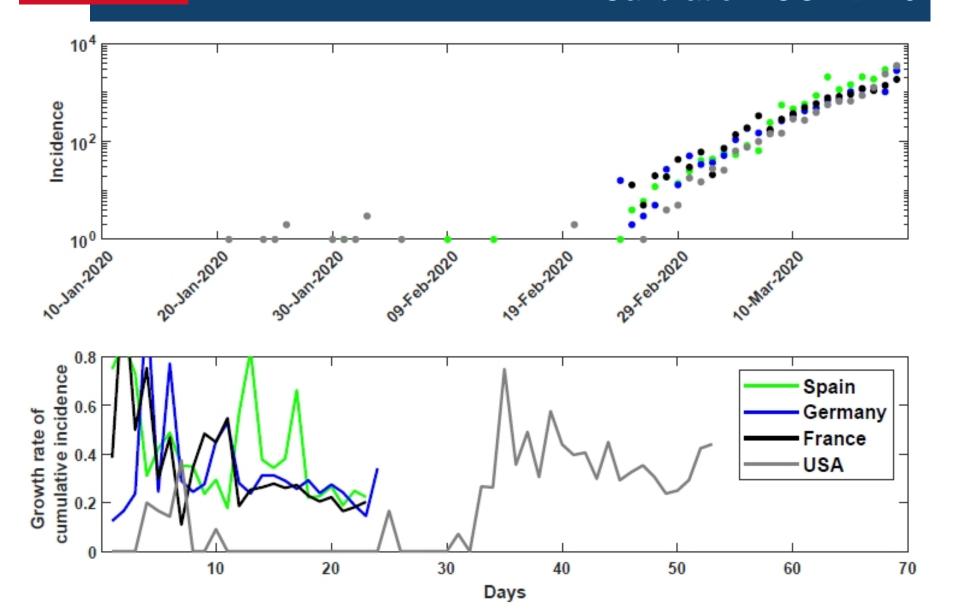


S. L. Chang, N. Harding, C. Zachreson, O. M. Cliff, M. Prokopenko, Modelling transmission and control of the COVID-19 pandemic in Australia, *arXiv*: 2003.10218, 2020.

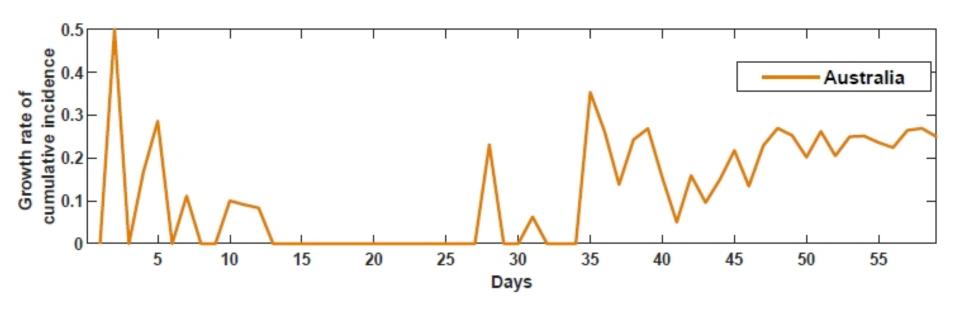
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 \* Corresponding author: mikhail.prokopenko@sydney.edu.au



### Calibration: COVID-19

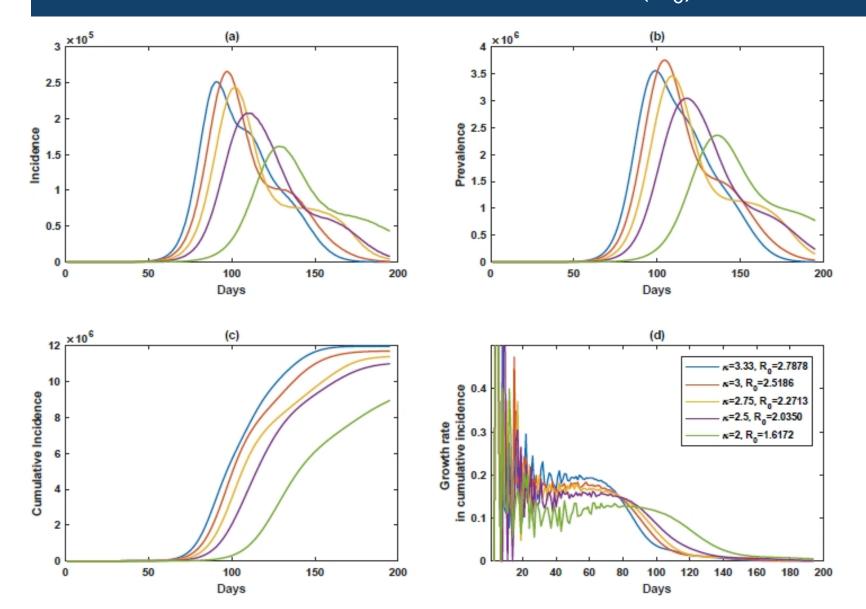


### Calibration: COVID-19

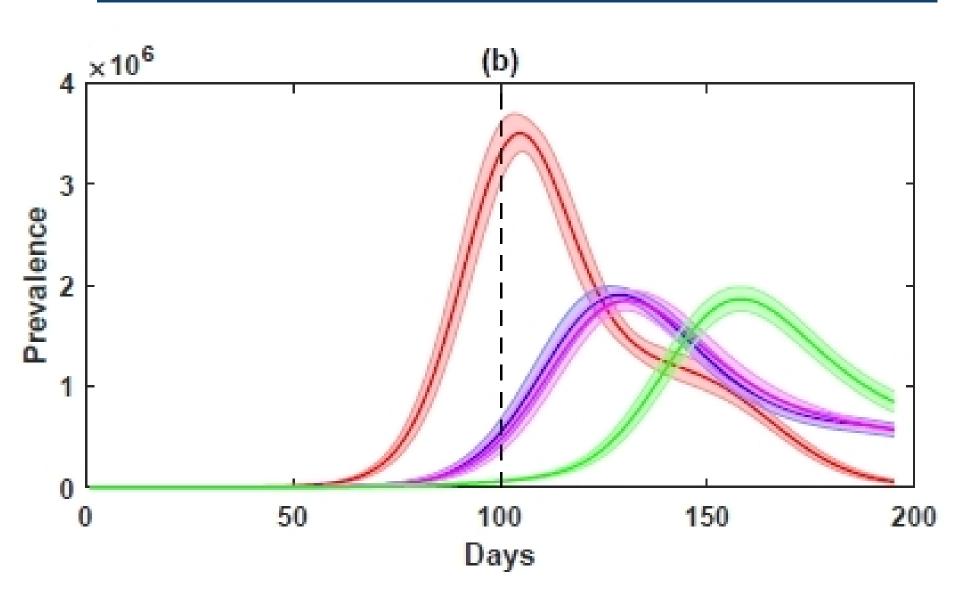




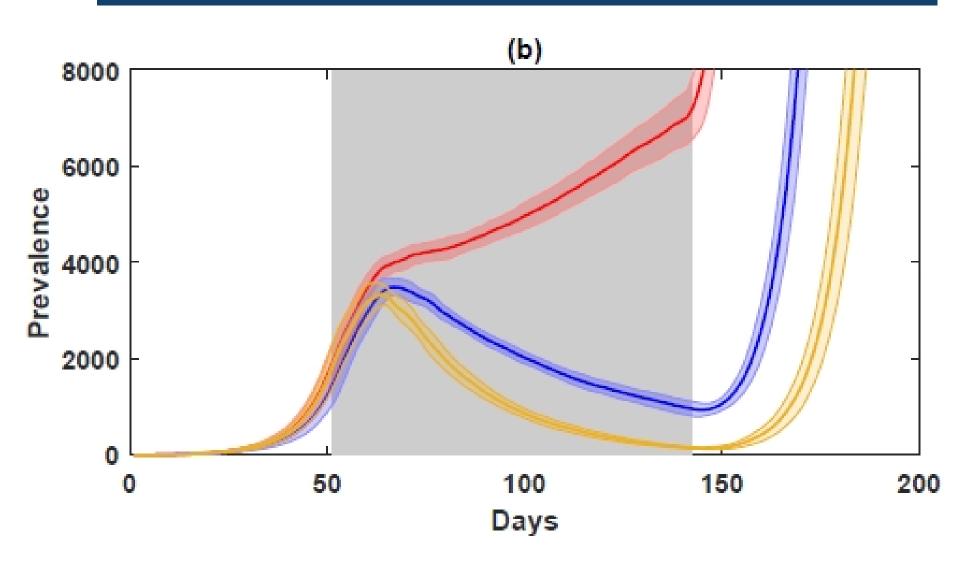
### Calibration (R<sub>0</sub>): COVID-19



### Mitigation (CI, HQ, SC): COVID-19

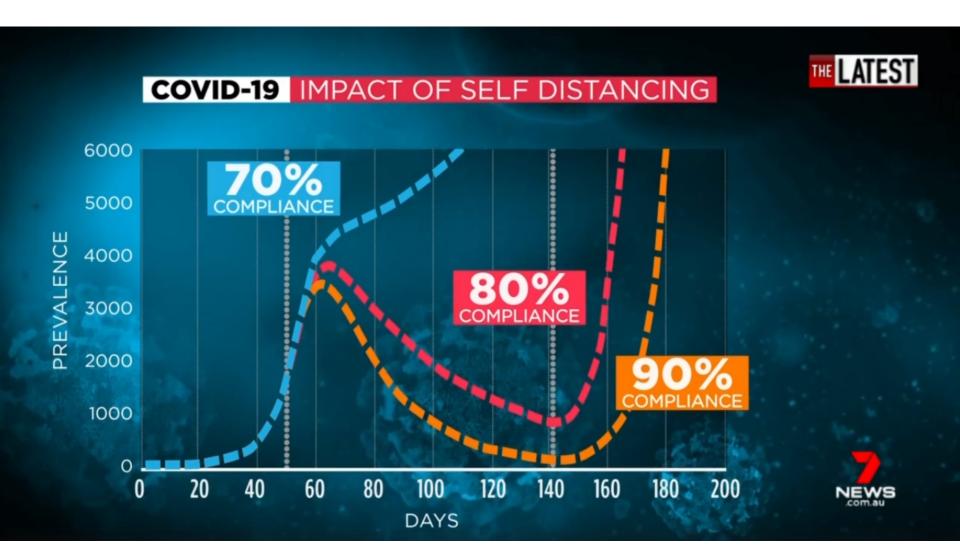


### Suppression (Social Distancing, SD): COVID-19











### Report to Federal Government



The updated model of Chang et al. (2020) suggests that the social distancing compliance levels in Australia have approached 90% between 24 March and mid-April 2020, providing evidence of high community engagement with the measures.

# COVID-19 Roadmap to Recovery

A Report for the Nation



### WHO: Western Pacific Region

# Calibrating long-term non-pharmaceutical interventions for COVID-19

Principles and facilitation tools

15 May 2020



#### SARS-CoV-2

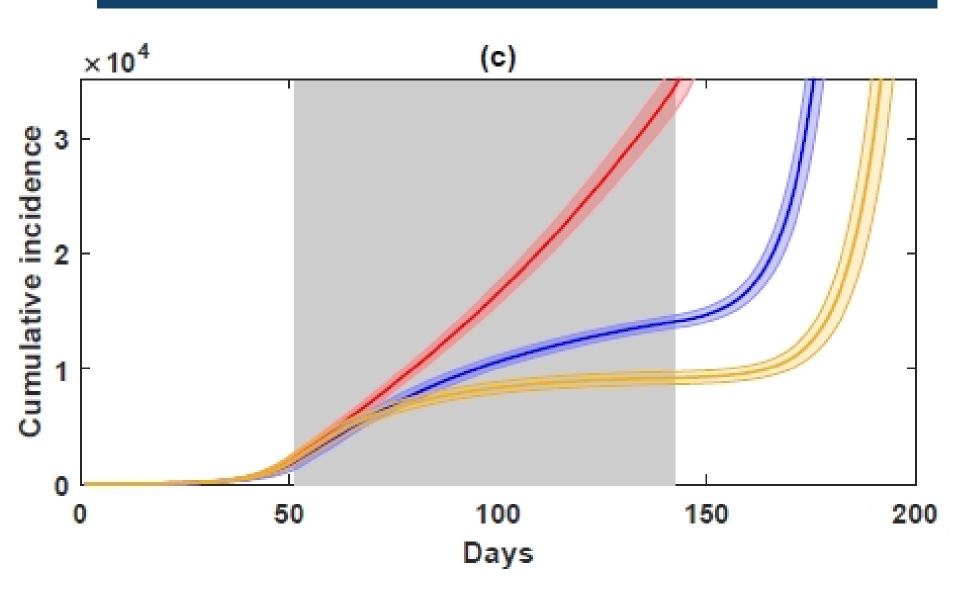
An Australian modelling study suggests that 80–90% compliance with physical distancing measures for 13 weeks will be required to control the spread of COVID-19.<sup>22</sup>

One study estimates that 13% of transmission events occurred prior to symptom onset,<sup>13</sup> highlighting the importance of physical distancing measures.

The effect of cancelling mass gatherings is yet to be determined. Although they have previously been implicated in infectious disease spread globally, the social and economic impacts of cancellation must also be considered, with context-specific risk assessments.<sup>24</sup>

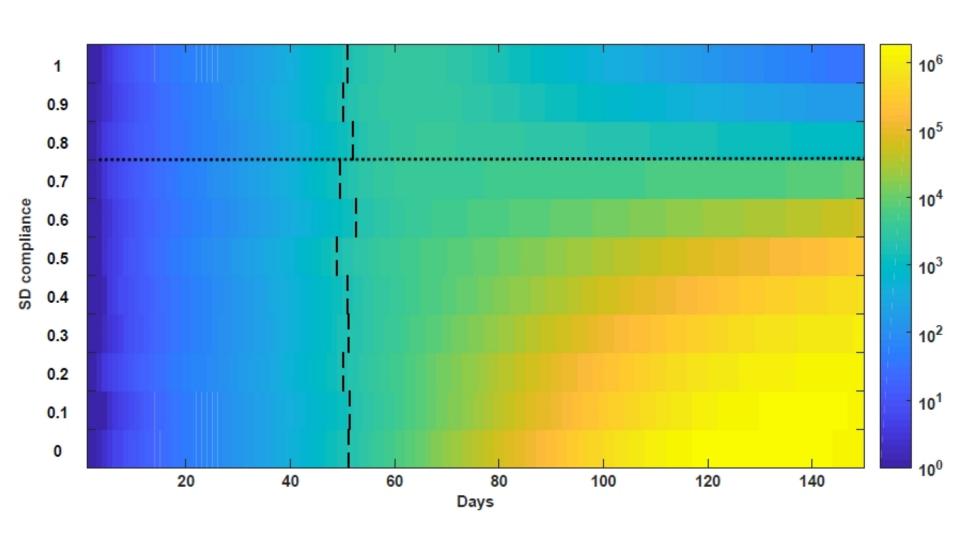


### Suppression (Social Distancing, SD): COVID-19



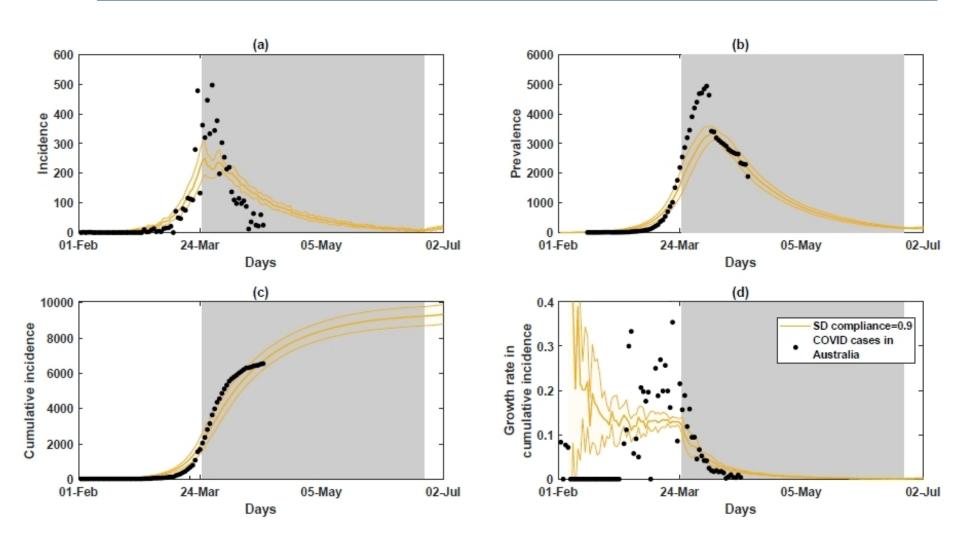


### Critical regime (phase transition): COVID-19



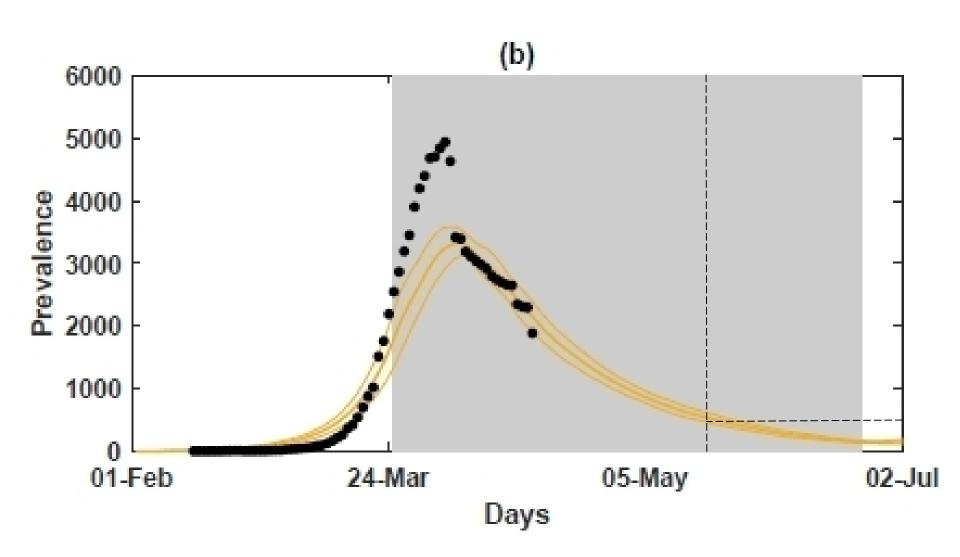


### AMTraC-19 validation



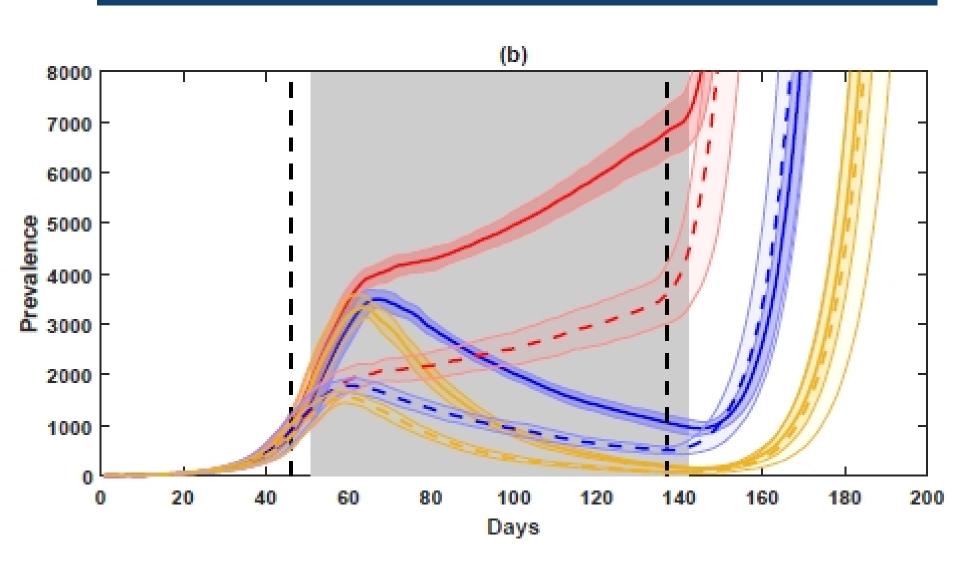


### "All models are wrong, but some are useful"



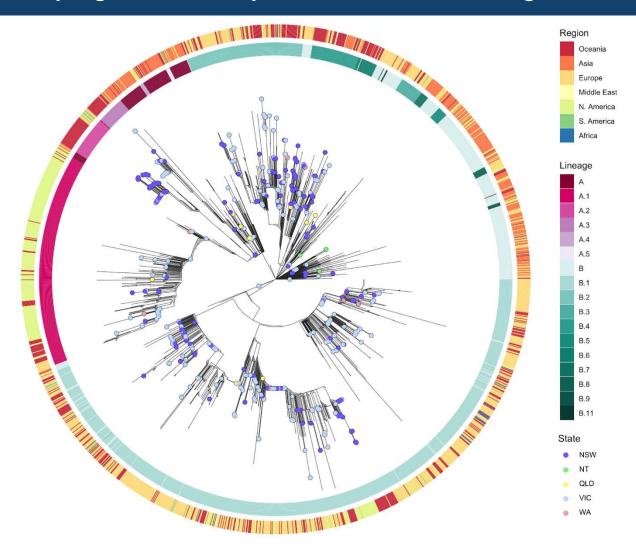


### Delays (counter-factual analysis): "provide actionable intelligence..."





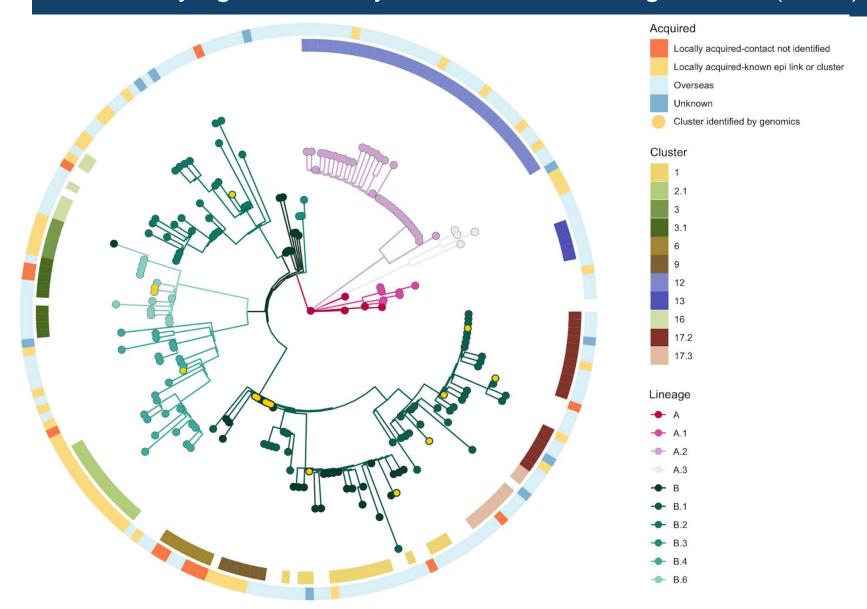
### Phylogenetic analysis of SARS-CoV-2 genomes (NSW)



R. J. Rockett, et al. Revealing COVID-19 transmission by SARS-CoV-2 genome sequencing and agent based modelling, *bioRxiv*: 2020.04.19.048751, 2020.

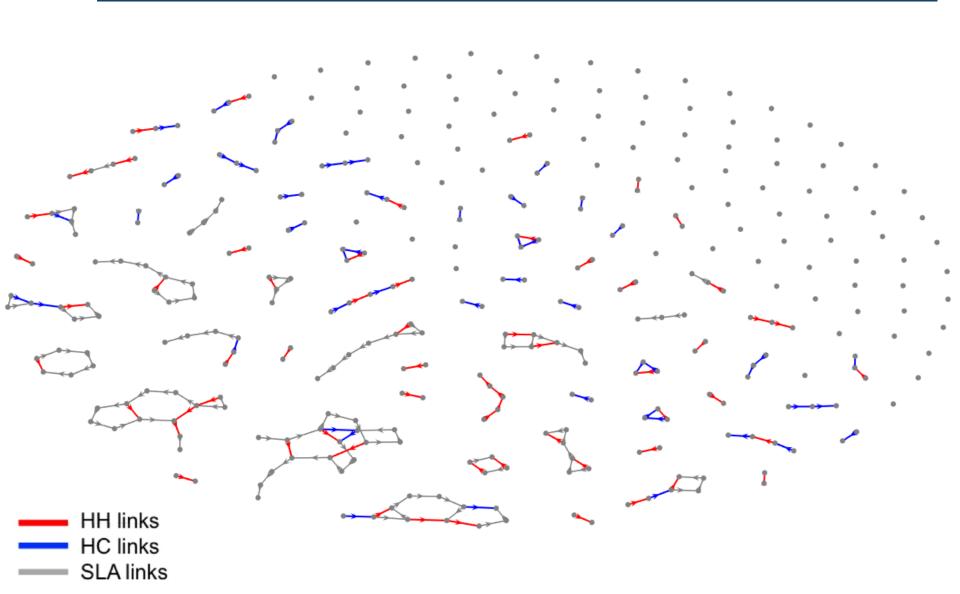


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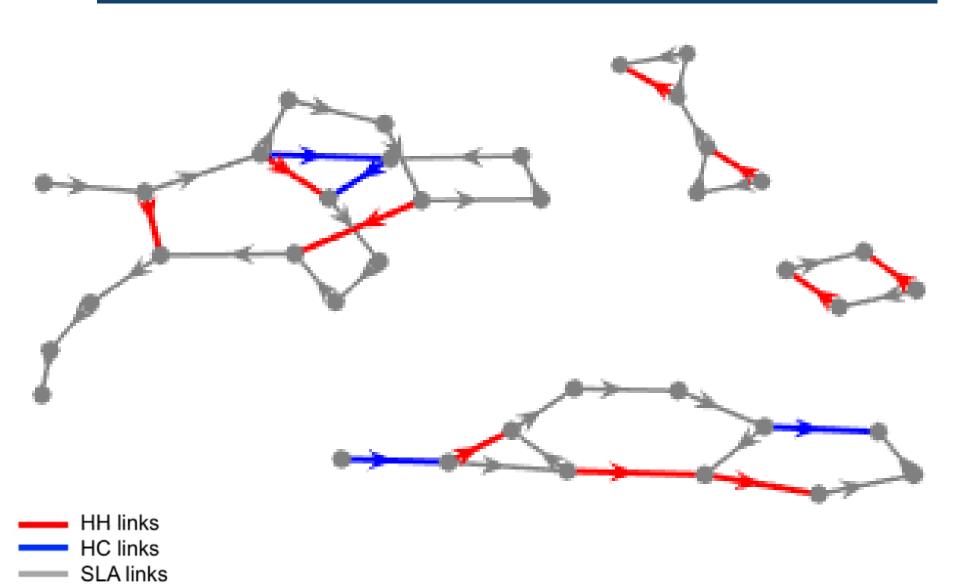


### Community transmission: ABM inferred network



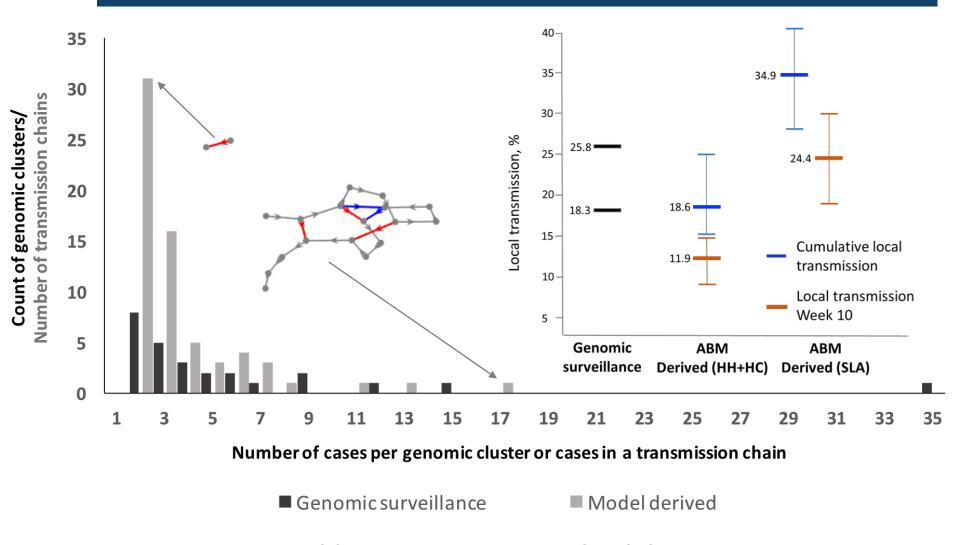


### Community transmission: friendship networks



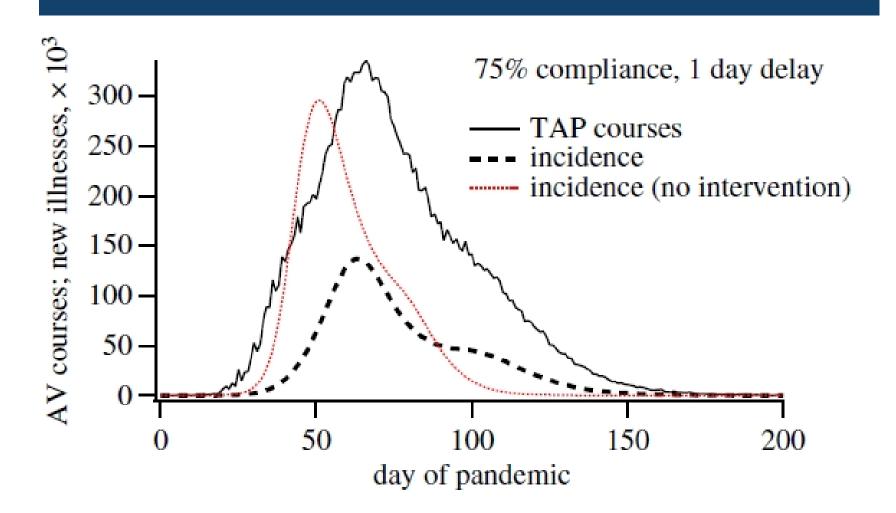


### Community transmission: comparison



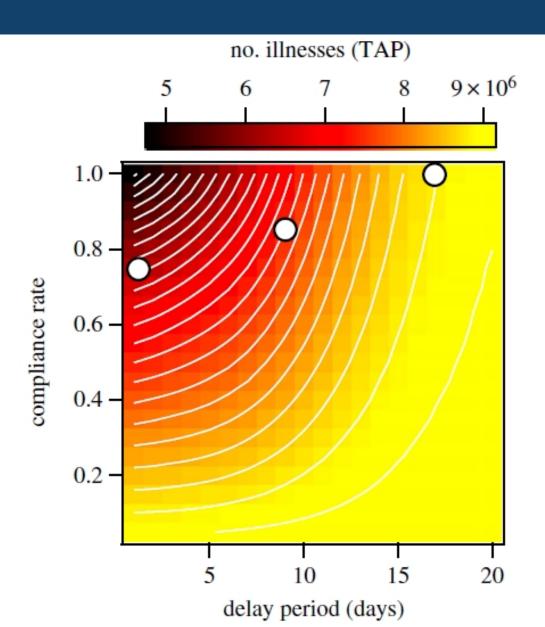
R. J. Rockett, et al. Revealing COVID-19 transmission by SARS-CoV-2 genome sequencing and agent based modelling, *bioRxiv*: 2020.04.19.048751, 2020.

### Pharmaceutical interventions: H1N1

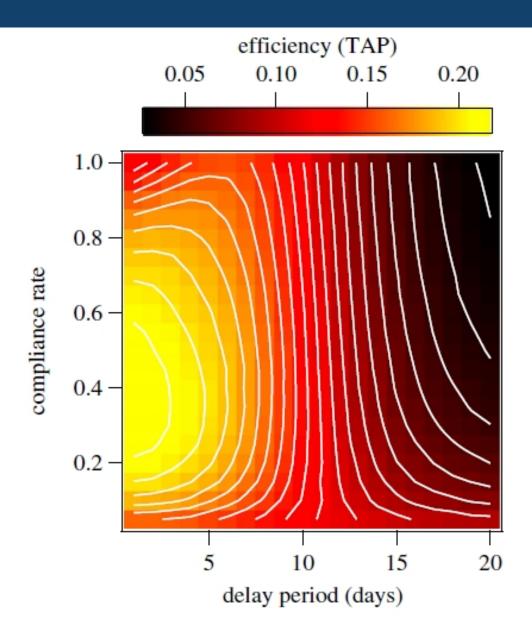


C. Zachreson, K. M. Fair, N. Harding, M. Prokopenko, Interfering with influenza: nonlinear coupling of reactive and static mitigation strategies, *J. Royal Society Interface*, 17(165): 20190728, 2020.

### Phase space of intervention parameters: H1N1



### Efficiency of interventions: H1N1





### ABM: a fine-grained approach

### Strengths:

- sensitivity analysis is embedded in heterogeneous agents
- individual-based rather than aggregate focus
- age-dependent epidemic characteristics
- spatial / geographic accuracy
- cross-jurisdictional impact
- time-dependent and context-dependent interventions
- counter-factual analysis ("what-if" scenarios: delays, scale, scope)
- critical phenomena analysis

### Weaknesses:

- need to calibrate multiple parameters
- reliance on high-performance computing



### Lessons: modelling wish-list

- in-hospital transmissions
- holidays, school terms, annual leaves, etc.
- maritime traffic (cruise ships)
- friendship networks
- contact tracing and large-scale testing capacity
- feedback from genomics
- in-hotel quarantine
- occupation-based (sector-based) analysis → refined exit strategies
- seasonal effects
- GTAP, TAP and vaccination (COVID-19 specific)
- local "lockdowns" (area quarantine)
- secondary waves, endemic transmission
- adaptive recommendations for public health policy





- O. M. Cliff, N. Harding, M. Piraveenan, E. Erten, M. Gambhir, M. Prokopenko, Investigating spatiotemporal dynamics and synchrony of infuenza epidemics in Australia: An agent-based modelling approach, Simulation Modelling Practice and Theory, 87, 412-431, 2018.
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- N. Harding, R. E. Spinney, M. Prokopenko, Phase transitions in spatial connectivity during influenza pandemics, *Entropy*, 22(2), 133, 2020.
- N. Harding, R. E. Spinney, M. Prokopenko, Population mobility induced phase separation in SIS epidemic and social dynamics, *Scientific Reports*, 10: 7646, 2020.
- S. L. Chang, N. Harding, C. Zachreson, O. M. Cliff, M. Prokopenko, Modelling transmission and control of the COVID-19 pandemic in Australia, *arXiv*: 2003.10218, 2020.
- R. J. Rockett, et al. Revealing COVID-19 transmission by SARS-CoV-2 genome sequencing and agent based modelling, *bioRxiv*: 2020.04.19.048751, 2020.



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