Individual-based modeling of day care centers can predict optimal surveillance strategies against SARS-CoV-2

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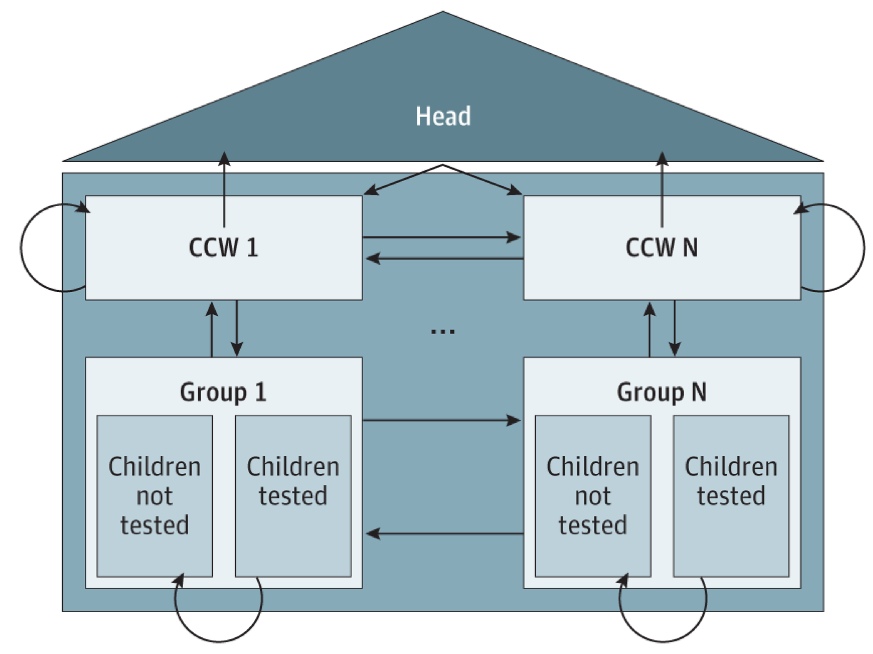
Background

- global closure of day care centers to prevent viral spread
- results include negative effects on children's well being
- viral spread through interactions inside day care centers [1]
- temporal viral load governs transmission dynamics [2]

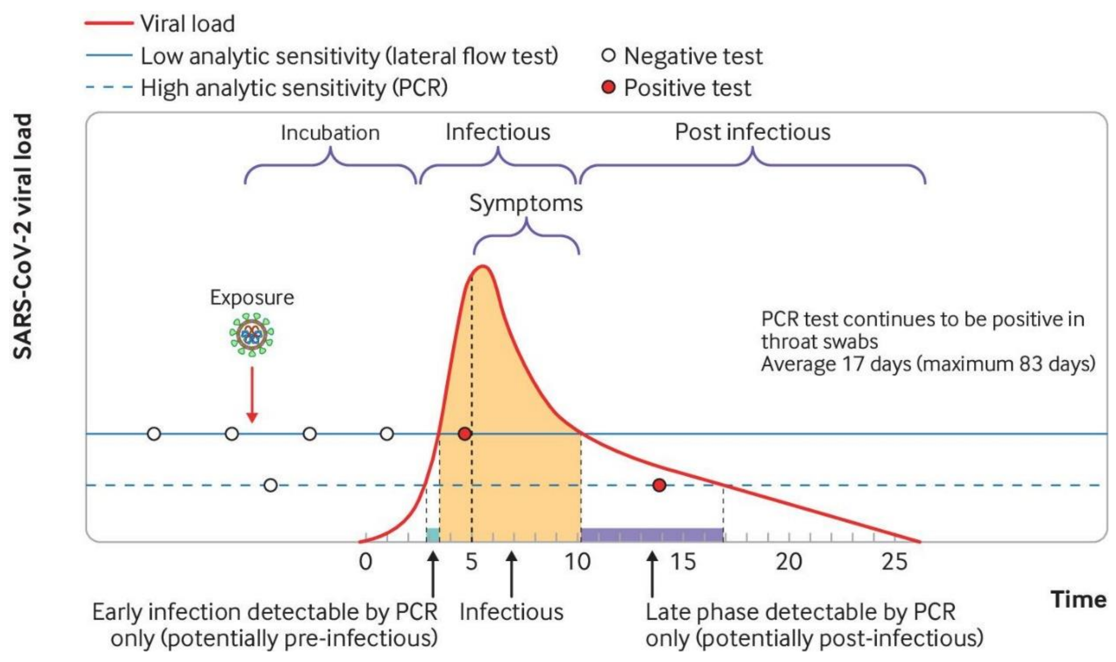
Objective:

computational modeling can aid in predicting surveillance strategies to prevent viral spread while keeping day care centers open

Day care center (DCC) structure

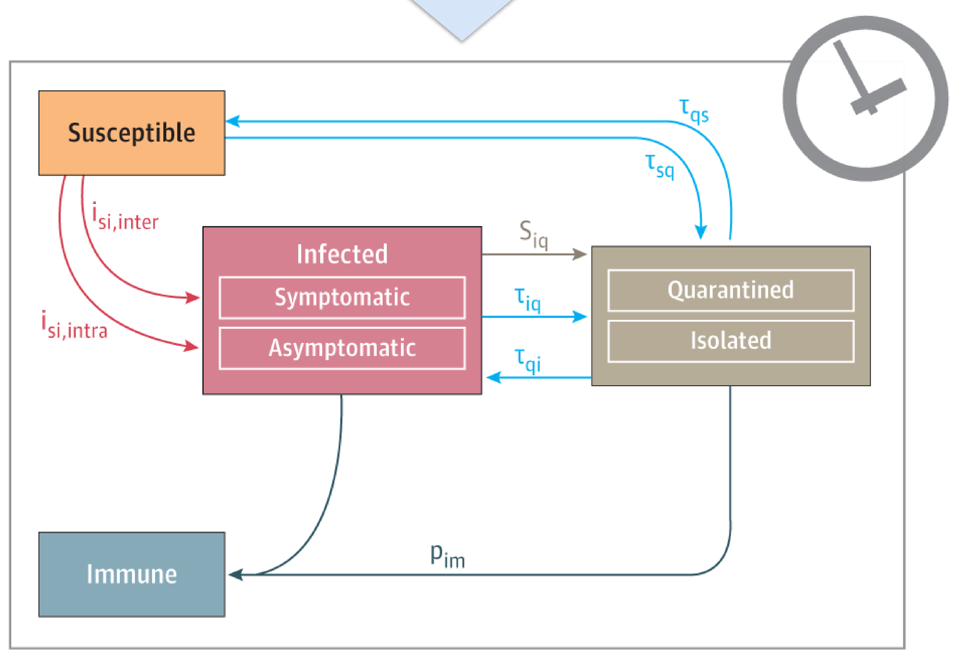


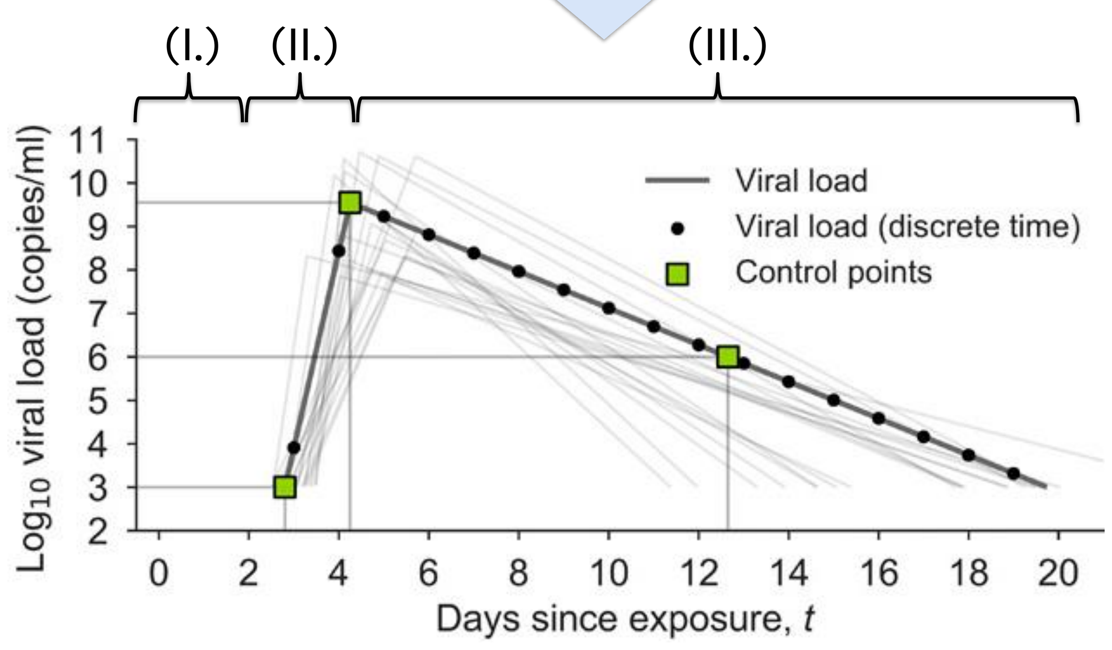
Viral load dynamics



Individual-based model

- day care centers are described by a modified **stochastic individual-based model** [3] based on a SIR model [4]
- through repeated simulations we can capture
  1. **random events** of a small population size
  2. effects of **surveillance strategies**
- the probability of a state transition depends on viral load
- the **viral load kinetic model** [5] is designed through a piecewise linear function with a
  I. variable **latent** phase
  II. rapid **growth** phase
  III. slow **decay** phase





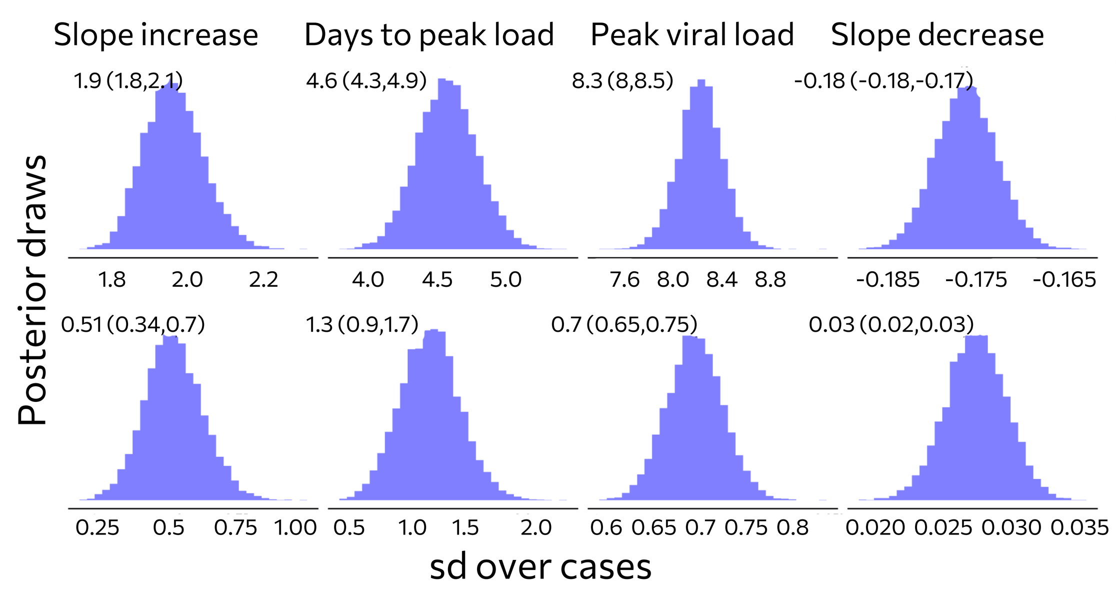
Experimental data

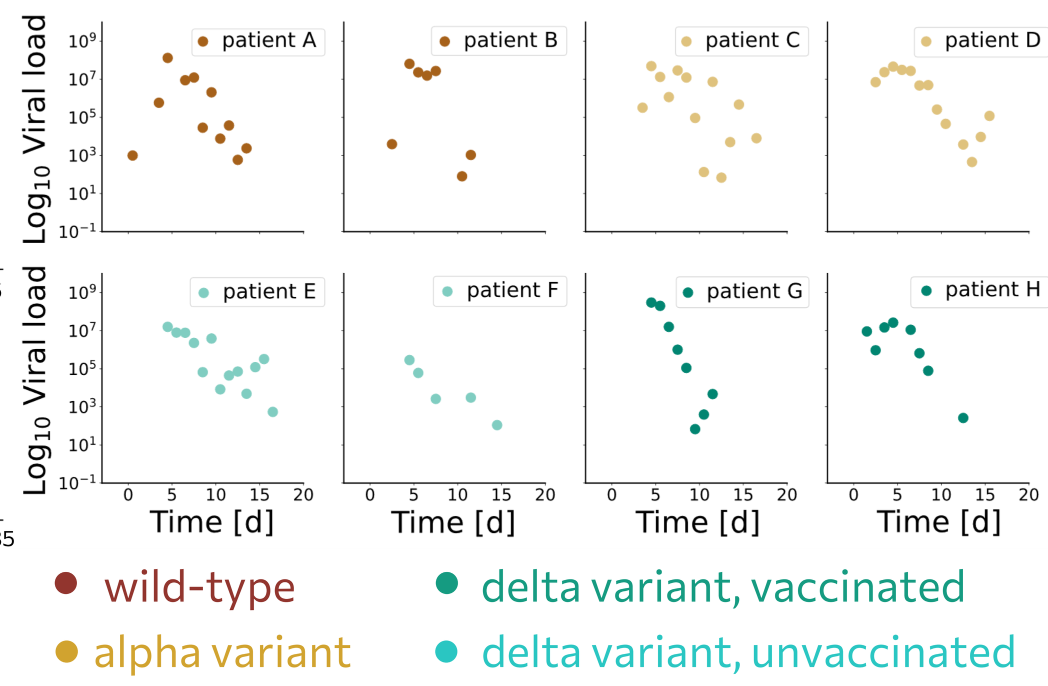
- **viral load** depicts the amount of alive and dead viral cells

1) piecewise linear functions are generated by sampling from a **posterior distribution** for key parameters [6]
2) continuous viral load curves are generated using parameter estimation of **temporal viral load data** [7]

- **challenges** regarding viral load data
  1. few number of data points per individual
  2. sparse growth phase
  3. viral peak not precisely recognizable

Group-level parameters

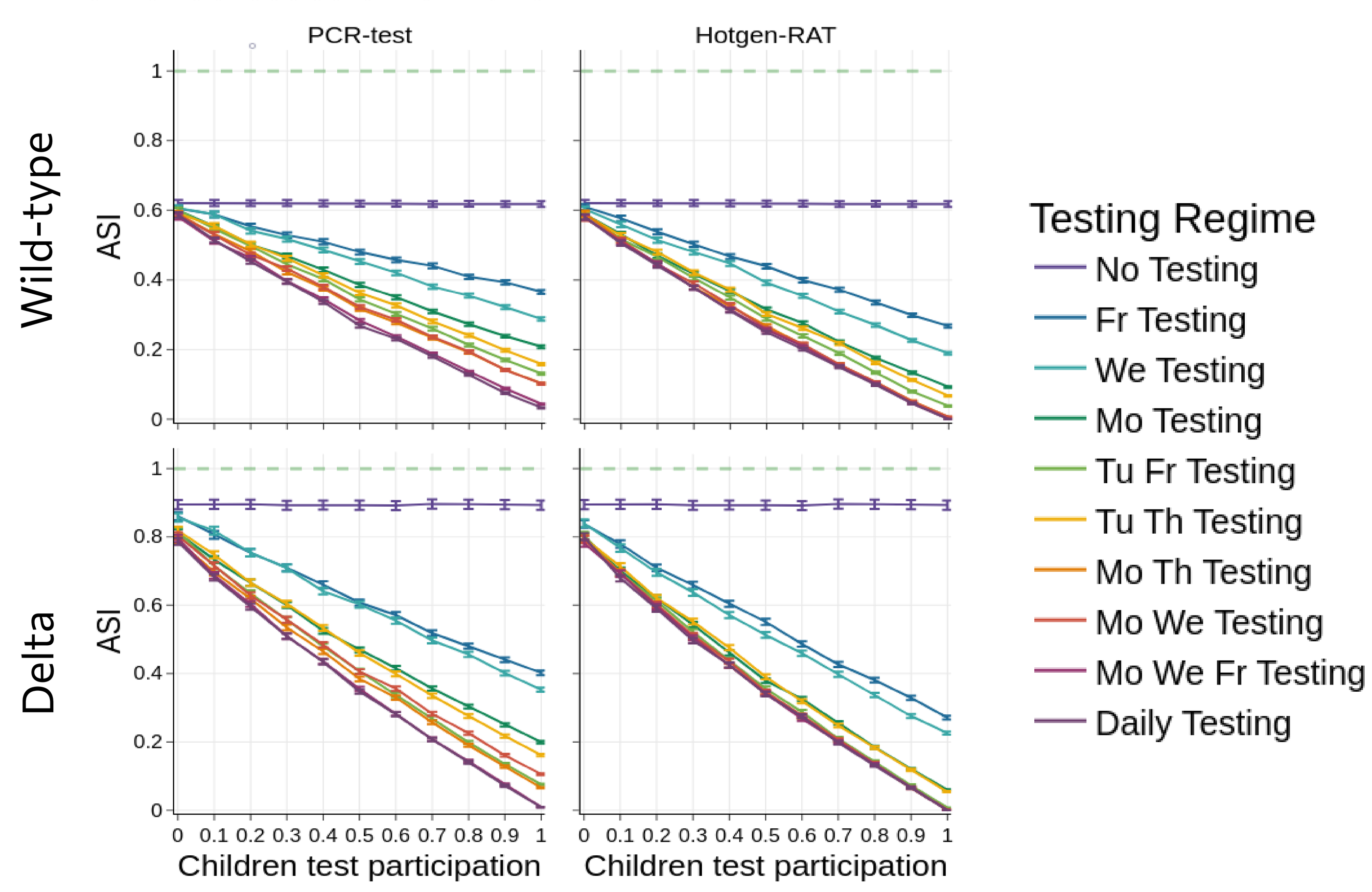




* we thank Prof. Ajit Lalvani from the National Institute for Health and Care Research, London, for providing the temporal viral load data

Results

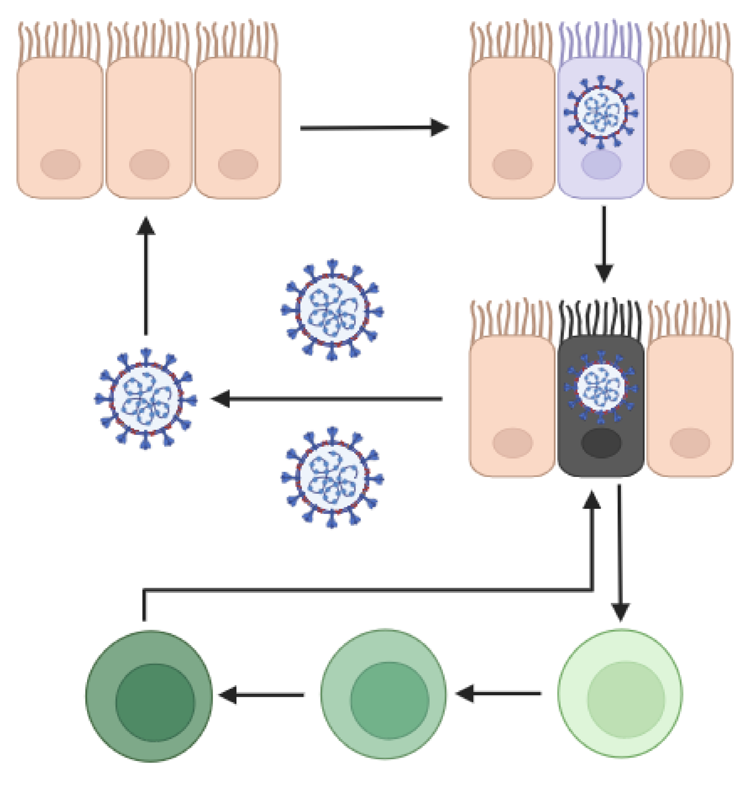
- **monday** is an important testing day
- **rapid antigen test** is less sensitive than PCR but has a lower waiting time
- testing **twice a week** balances a lower average secondary infection rate with fewer stresses on children



Outlook

- we can model the **mechanisms** behind viral load dynamics by using an ODE model
- it covers the interplay between **epithelial** cells, **virus** and the **adaptive immune system**

Component	ODE	Initial condition
Virus particles	$\dot{V} = r_V I_2 - \delta_S V S - \mu_V V$	$V(0) = V_0$
Susceptible epithelial cells	$\dot{S} = \lambda_S - \delta_S V S - \mu_S S$	$S(0) = S_0$
Infected epithelial cells	$\dot{I}_1 = \delta_S V S - k_I I_1$ $\dot{I}_2 = k_I I_1 - \delta_I T_3 I_2 - \mu_I I_2$	$I_1(0) = I_0$ $I_2(0) = 0$
Adaptive immune response	$\dot{T}_1 = \lambda_T + r_T T_1 \frac{I_2}{I_2 + C} - k_T T_1$ $\dot{T}_2 = k_T T_1 - k_T T_2$ $\dot{T}_3 = k_T T_2 - k_T T_3$	$T_1(0) = T_0$ $T_2(0) = 0$ $T_3(0) = 0$



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References

[1] Forster *et al.* 2022 *JAMA Network Open* 13
[2] Crozier *et al.* 2021 *bmj* 7
[3] Timme *et al.* 2018 *Front Immunol.* 9
[4] Groendyke *et al.* 2021 *Epidemiol Met.* 10:1
[5] Larremore *et al.* 2021 *Science Advances* 11
[6] Jones *et al.* 2021 *Science.* 373
[7] Hakki *et al.* 2022 *Lancet Respiratory Medicine* 13

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