Predicting Optimal Surveillance Strategies against SARS-CoV-2 in Virtual Day Care Centers using Individual-based Modeling

Philipp Städter[1,2], Paul Rudolph[1,2], Sandra Timme[1], Johannes Forster[3], Oliver Kurzai[3], Marc Thilo Figge[1,4]

[1] Applied Systems Biology, Leibniz Institute for Natural Product Research and Infection Biology – Hans Knöll Institute, Jena, Germany

[2] Faculty of Biological Sciences, Friedrich Schiller University Jena, Jena, Germany

[3] Institute for Hygiene and Microbiology, University of Würzburg, Würzburg, Germany

[4] Institute of Microbiology, Faculty of Biological Sciences, Friedrich Schiller University Jena, Jena, Germany

Background

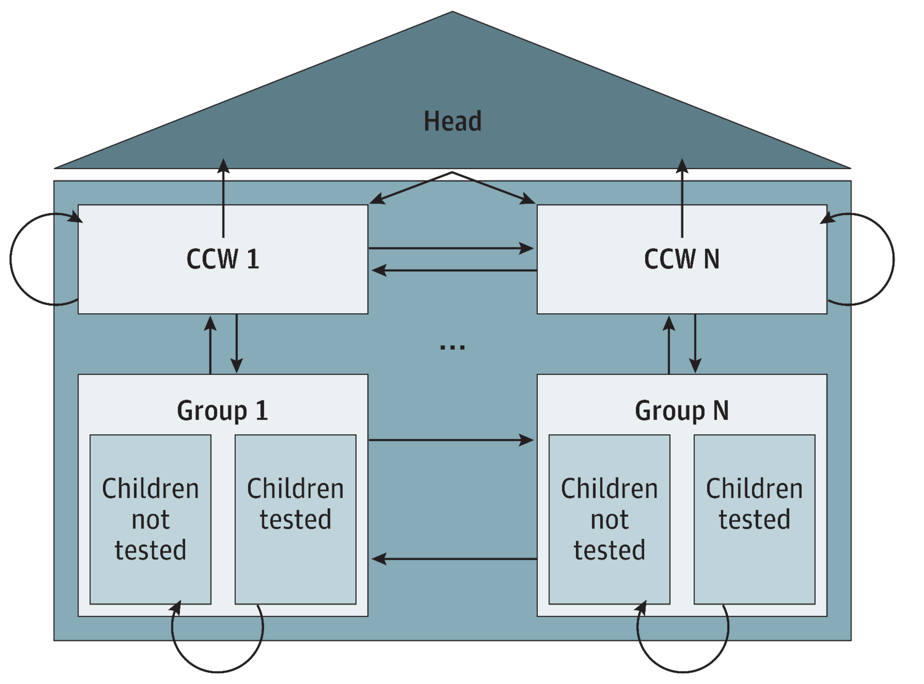
- global closure of day care centers to prevent viral spread
- results include negative effects on children's well being

- viral spread through interactions inside day care centers [1]
- temporal viral load governs transmission dynamics [2]

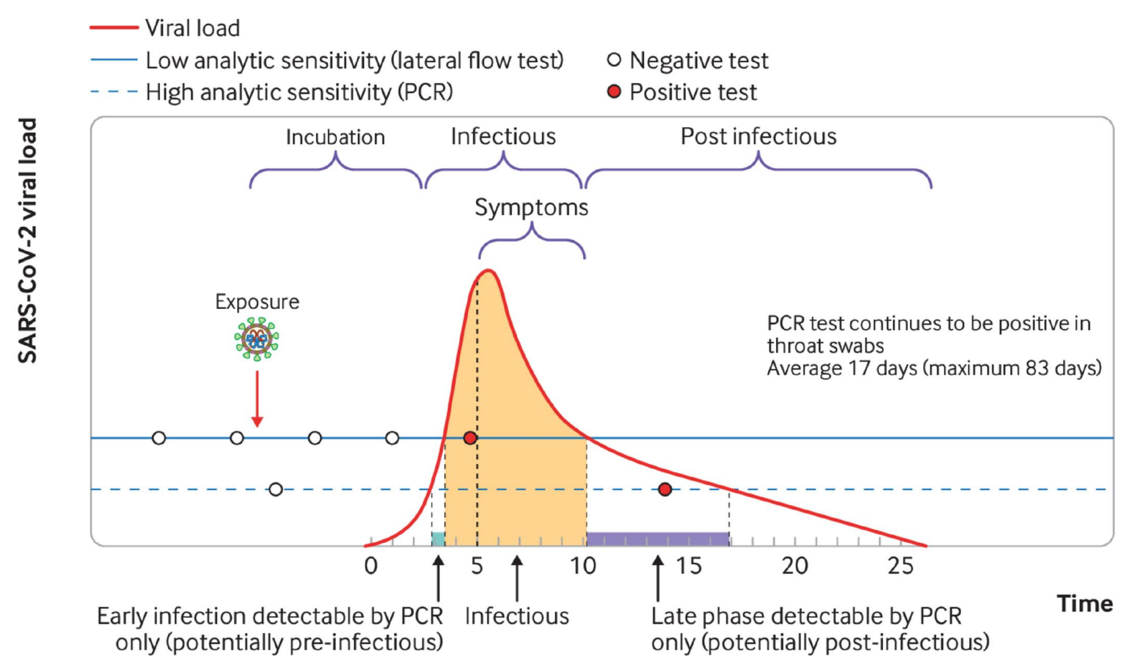
Objective:

Prediction of optimal surveillance strategies to prevent viral spread while keeping day care centers open by computational modeling

Day care center structure

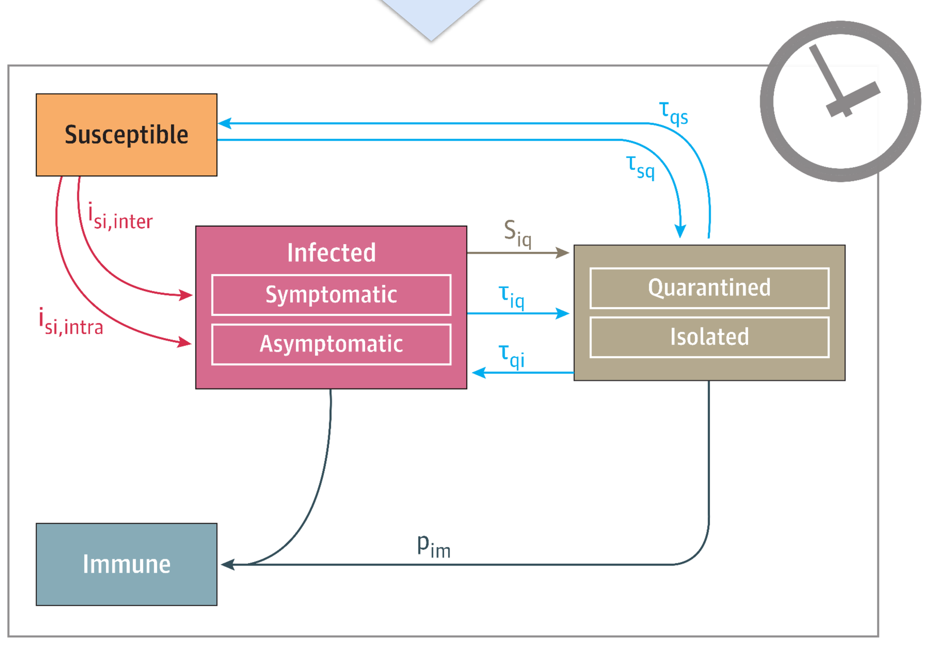


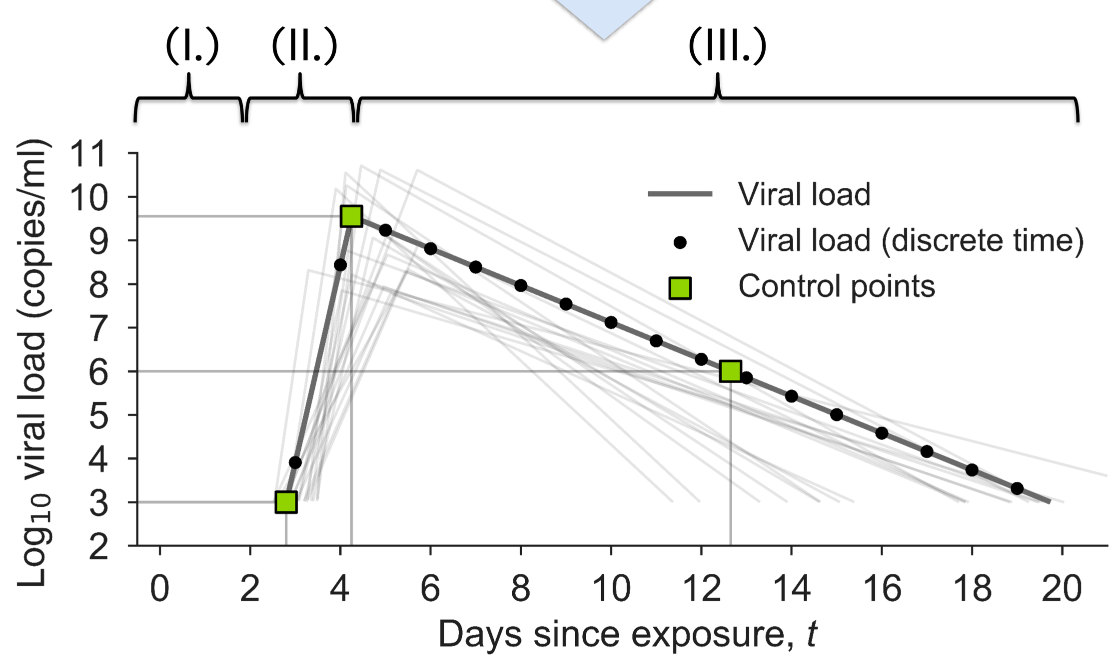
Viral load dynamics



Individual-based model

- day care centers are described by a modified **stochastic individual-based model** [3] based on an 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



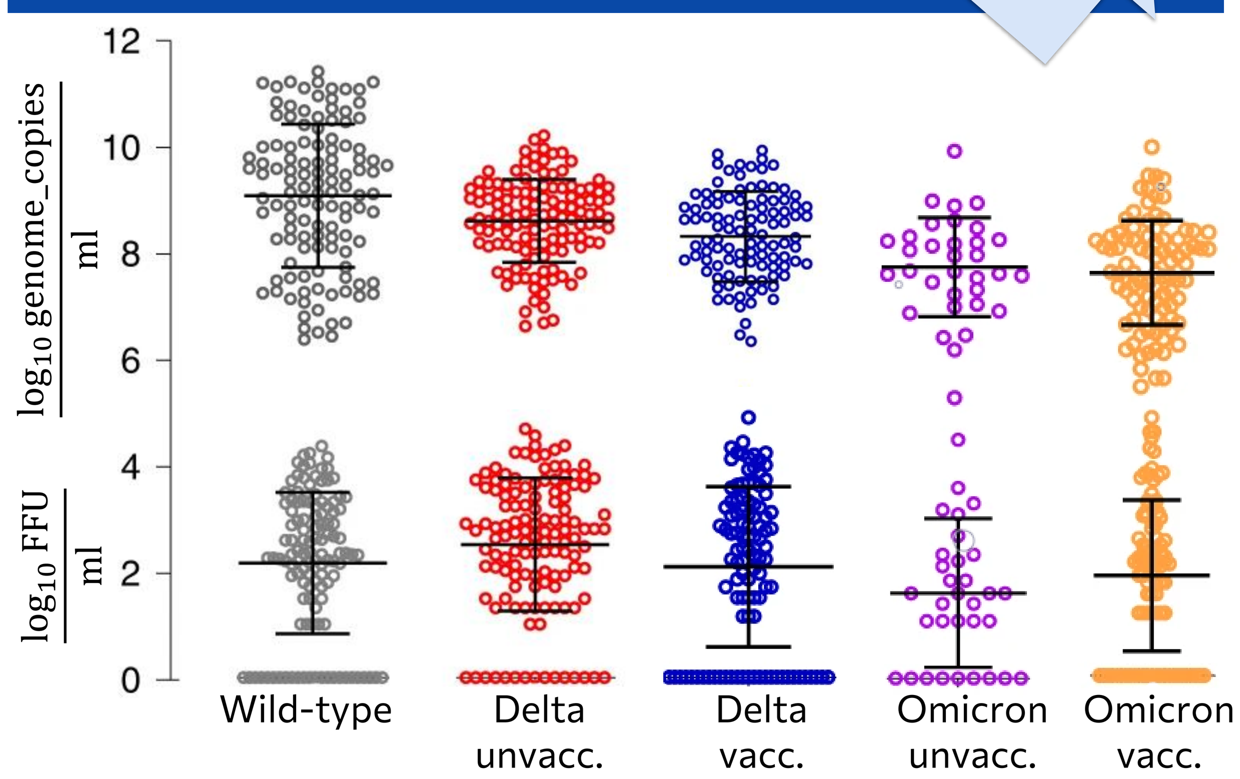


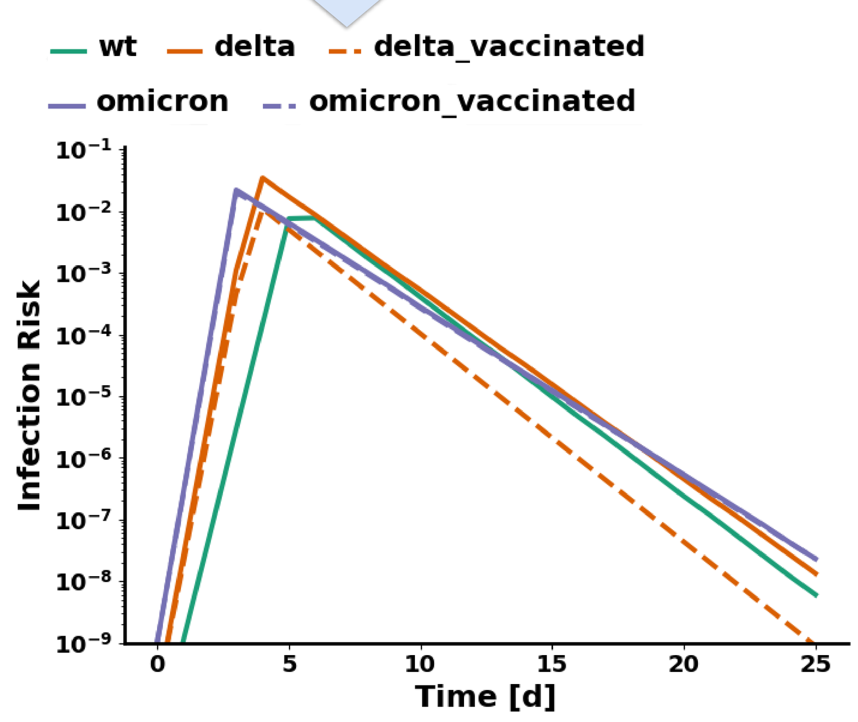
Experimental data & Infection risk

- **viral load** represents the **total** amount of viral particles
- **viral titre** represents the amount of **infectious** viral particles

1) piecewise linear functions are generated by sampling from **viral load posterior distributions** for key parameters [6]
2) the infectivity is described by the D50 value that is inferred from the **viral titre posterior distributions**
3) the infection risk probability is calculated using the **infection risk calculator** [7]

$$P_{infection\_risk} = 1 - \left(\frac{1}{10^{D_{50}}}\right)^{genome\_copies}$$

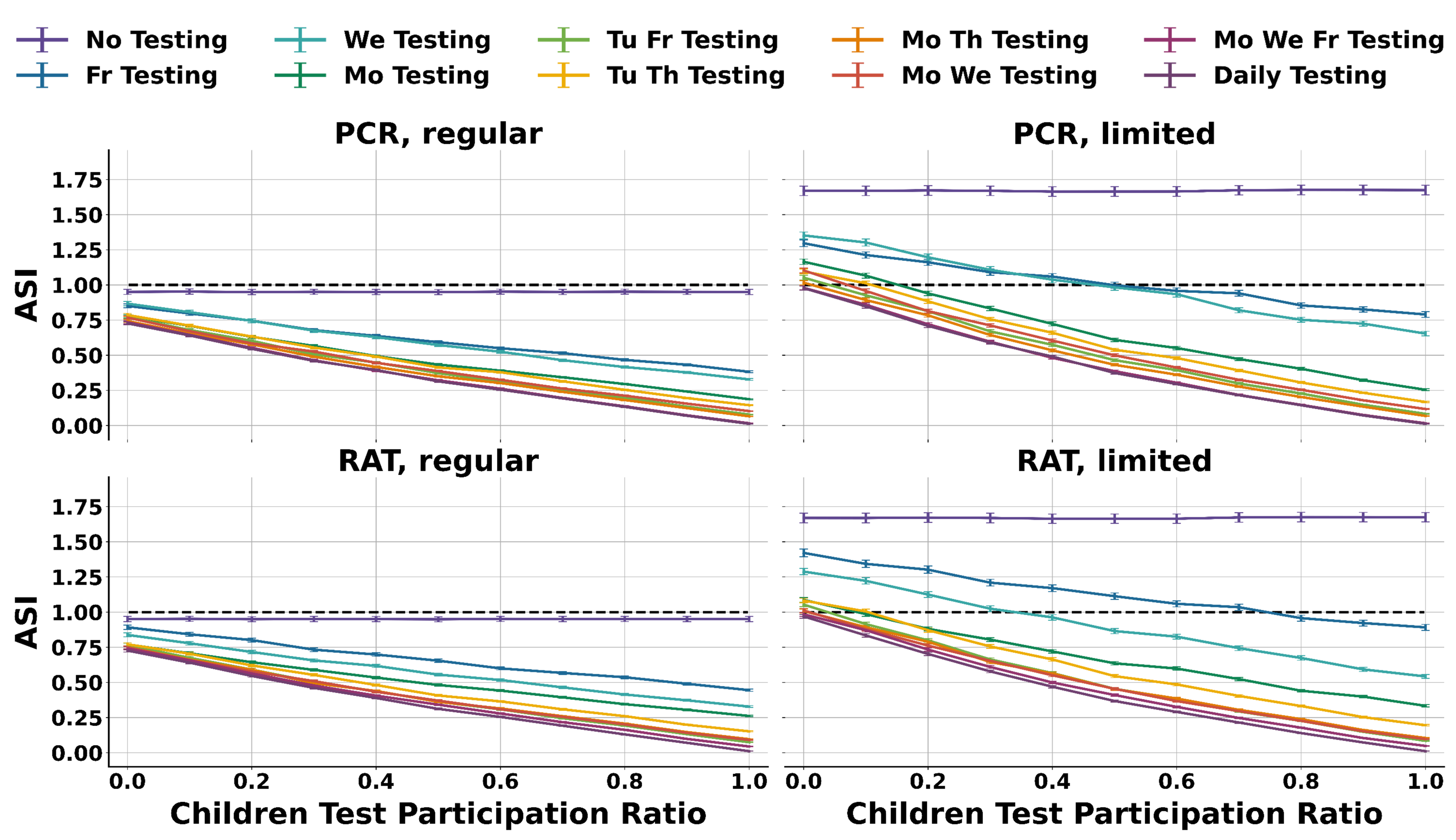


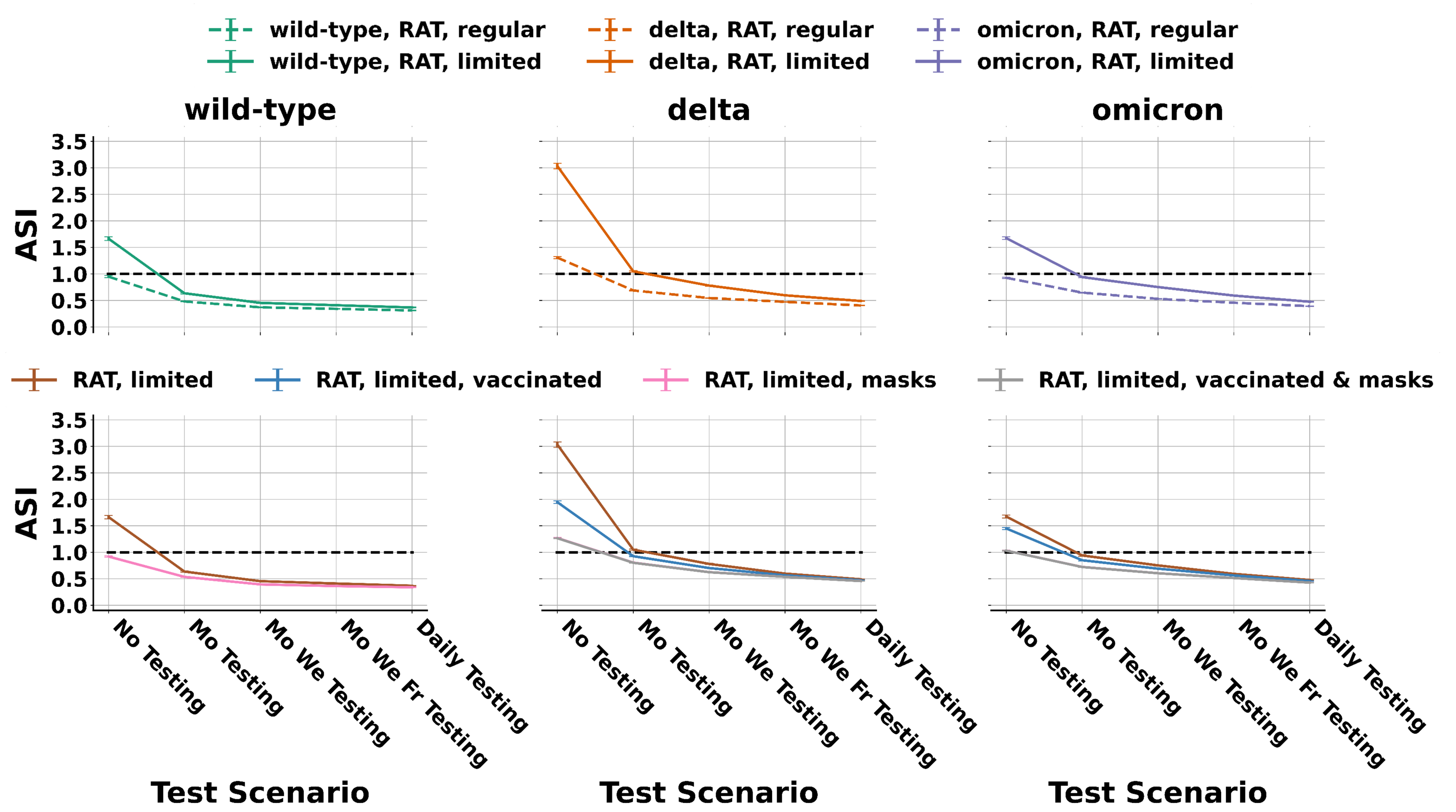


Results

- **rapid antigen test** outperforms PCR test due to receiving **test result fast**
- **limited** policy **as efficient** as regular policy with at least **1x/week** testing
- **monday** is the best **1x/week** test scenario

- **delta** and **omicron** variants lead to an **increase** in **average secondary infections (ASI)**
- **masks** are the most **efficient** infection prevention measure





Philipp.Staedter@leibniz-hki.de

www.leibniz-hki.de

References

[1] Forster *et al.* 2022 *JAMA Network Open* 5(1)

[2] Crozier *et al.* 2021 *BMJ* 372

[3] Timme *et al.* 2018 *Front Immunol.* 9

[4] Groendyke *et al.* 2021 *Epidemiol Met.* 10(1)

[5] Larremore *et al.* 2021 *Science Advances* 7(1)

[6] Puhach *et al.* 2022 *Nature Medicine* 28(7)

[7] Lelieveld *et al.* 2020 *Int. J. Environ. Res. Public Health* 17(21)