Spreading dynamics in neural networks - and of COVID-19

Viola Priesemann

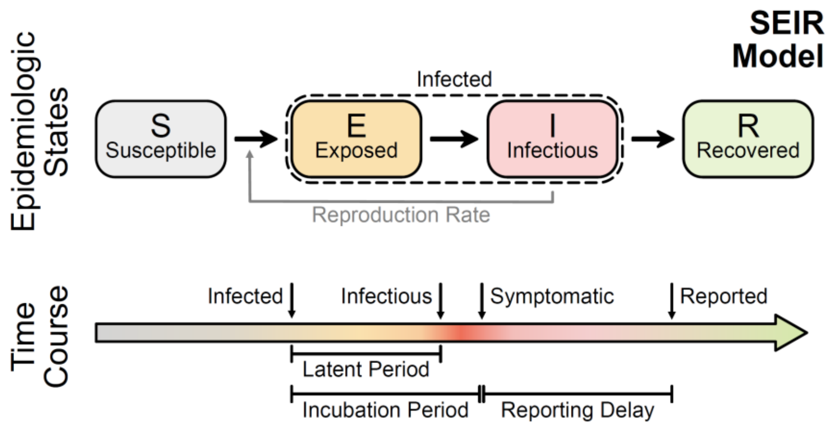
Max-Planck-Institut für Dynamik und Selbstorganisation Göttingen

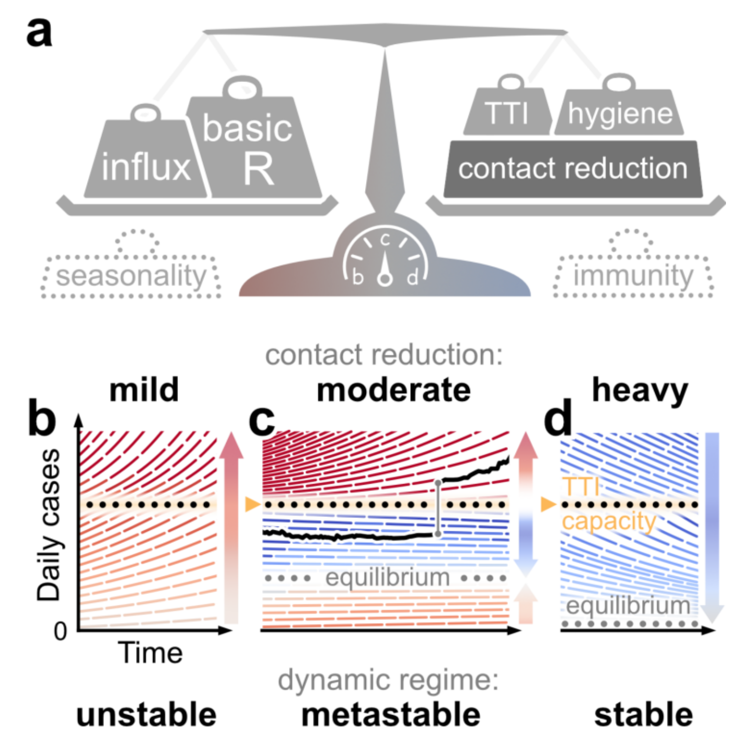
Content

- **Bayesian Inference and short-term forecast**: SIR-Model, Hamiltonian MCMC, weekly change points

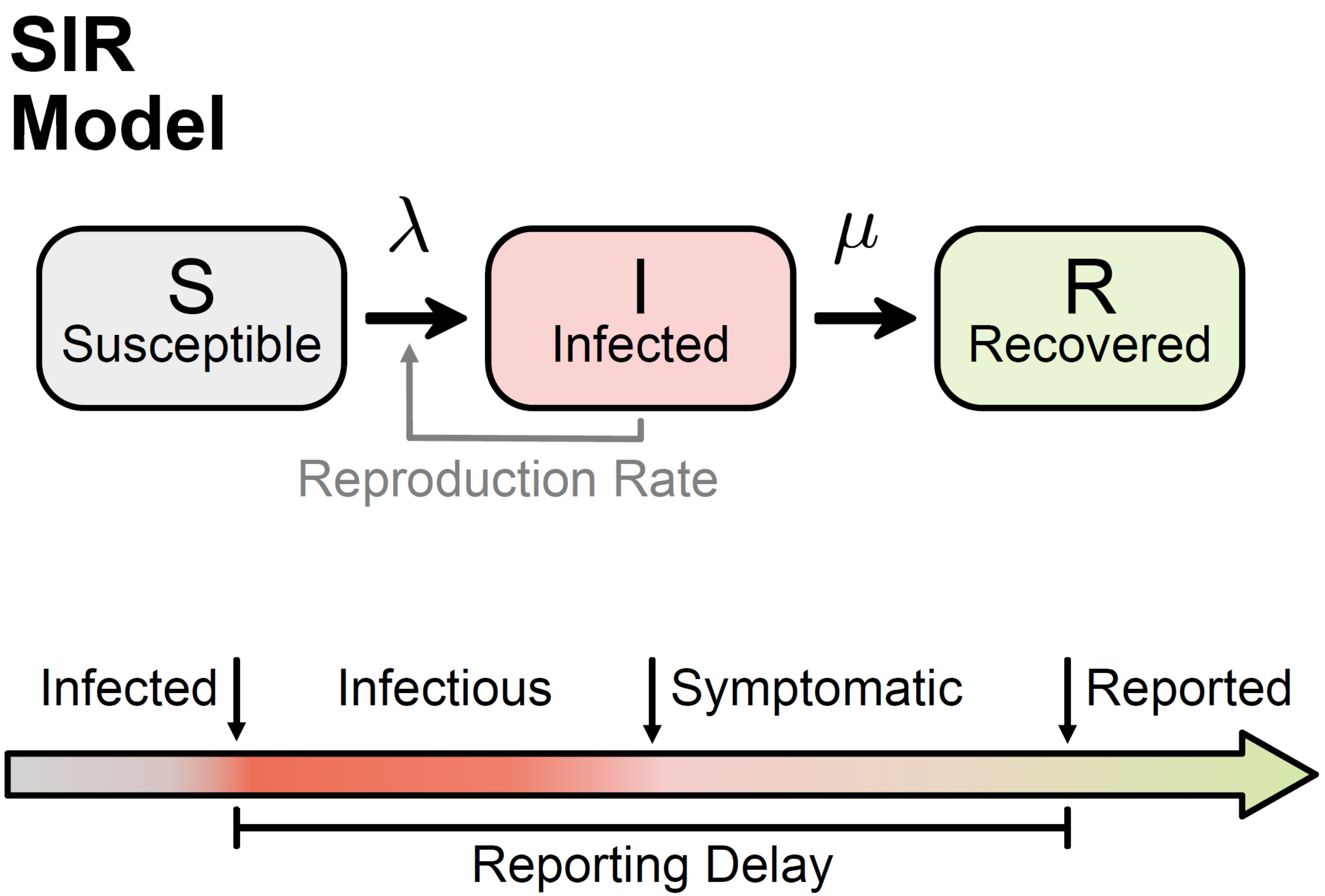
- **Progress of vaccination:** How fast can we lift „non-pharmaceutical intervions“ (NPIs) given the planned vaccination progress?

- **Derive effectiveness of measures**: Contribution of test-trace-isolate (TTI) to containment of COVID-19





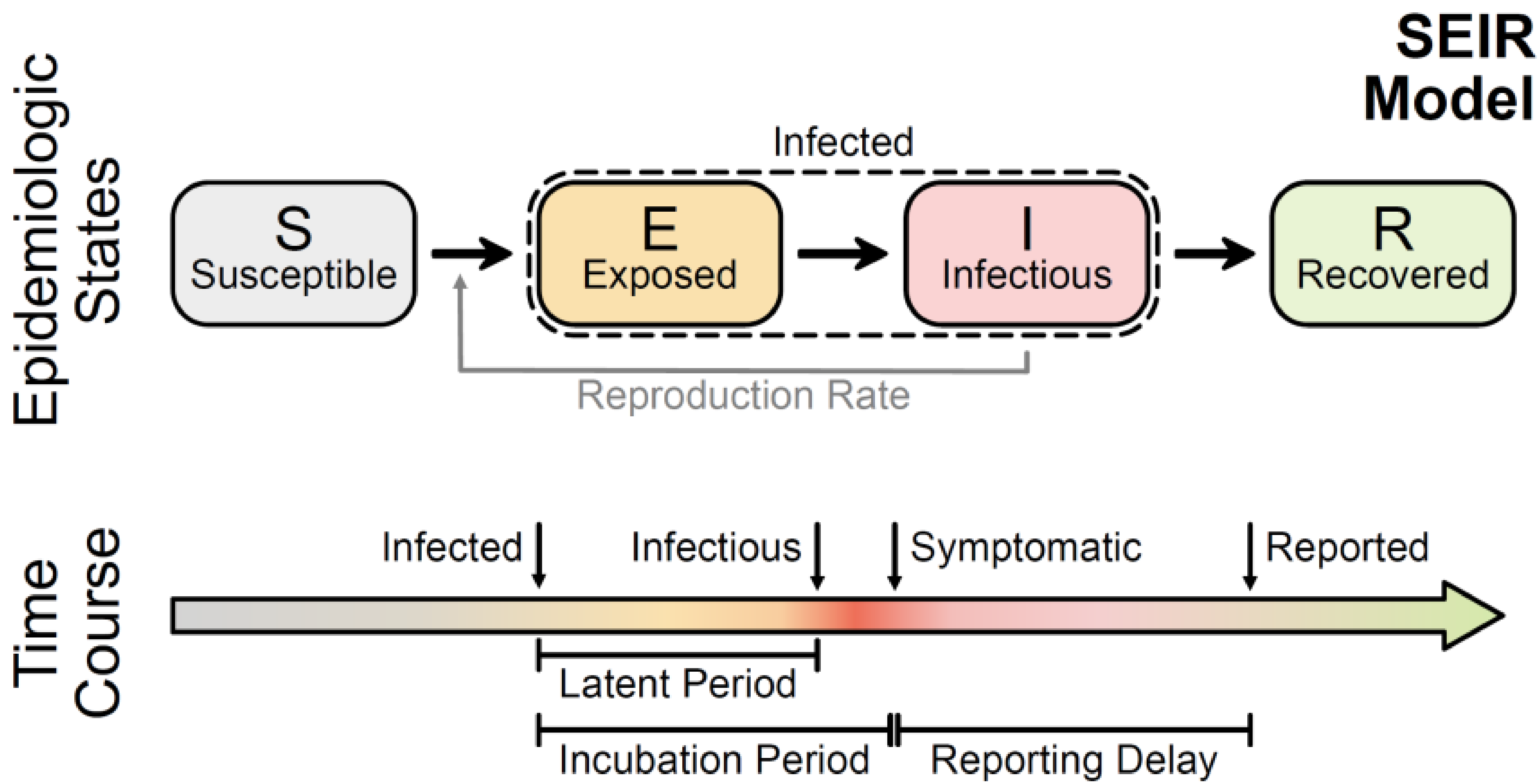
SIR: Susceptible-Infected-Recovered



$$\frac{dS}{dt} = -\lambda \frac{SI}{N}$$
$$\frac{dI}{dt} = \lambda \frac{SI}{N} - \mu I$$
$$\frac{dR}{dt} = \mu I$$

[Dehning et int., Priesemann, medRxiv]
https://www.medrxiv.org/content/medrxiv/early/2020/09/18/2020.09.16.20187484.full.pdf

SEIR: Susceptible-Exposed-Infected-Recovered



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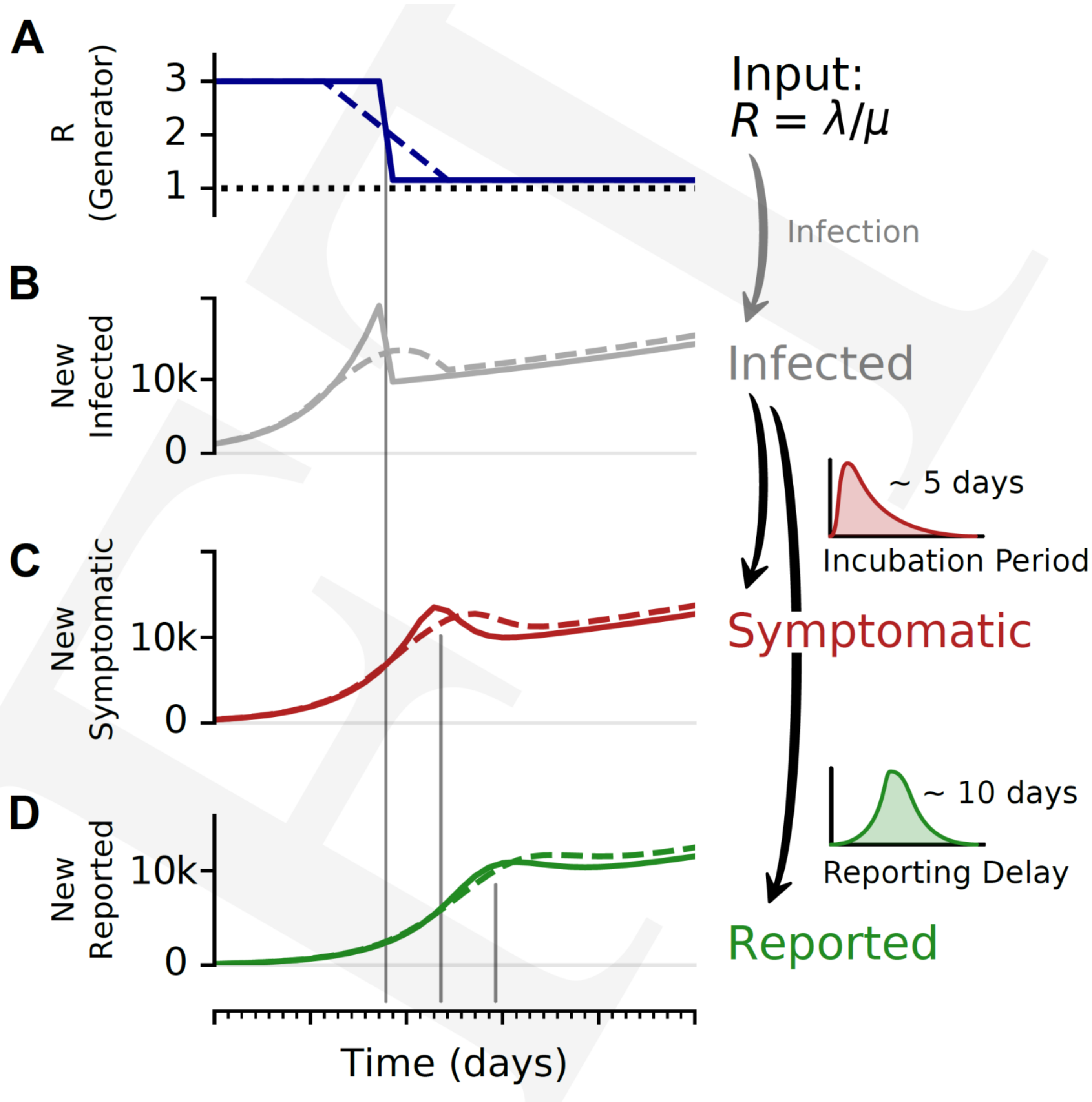
Inference of R under fast changes



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Bayesian Inference of R

- SIR-model:
  - Set begin: $I_0 = I_0$, $S_0 = N - I_0$
  - recursion: $I_{t+1} - I_t = \lambda\, I_t\, \frac{S}{N} - \mu\, I_t$

    $S_{t+1} - S_t = -\,\lambda\, I_t\, \frac{S}{N}$

I_t Infected persons at time t
S_t Susceptible persons at time t
λ Infection rate
μ Recovery rate
N Total number of persons in the population

Adapted from [Dehning et int., Priesemann, Science, 2020]

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- The cases are reported D days later: $C_{t+D} = I_t$
- change points of lambda with times t_i, and length Δt_i
- Weekly modulation with amplitude f_w and offset Φ_w.

$$f(t) = (1 - f_w) \cdot 1 - |sin(\frac{\pi}{7} t - \frac{1}{2} \Phi_w)|)$$

-> Likelihood $P(C_{t,meas} \, | \theta) \sim \mathrm{StudentT}_{\nu=4} \left(\mathrm{mean} = \mathrm{C_t}(\theta), \ \mathrm{width} = \boldsymbol{\sigma} \sqrt{\mathrm{C_t}(\theta)} \right)$

- We use Hamiltonian Monte Carlo which adds a momentum, a modified proposal density and rejection criterion

Adapted from [Dehning et int., Priesemann, Science, 2020]

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I_t Infected persons at time t
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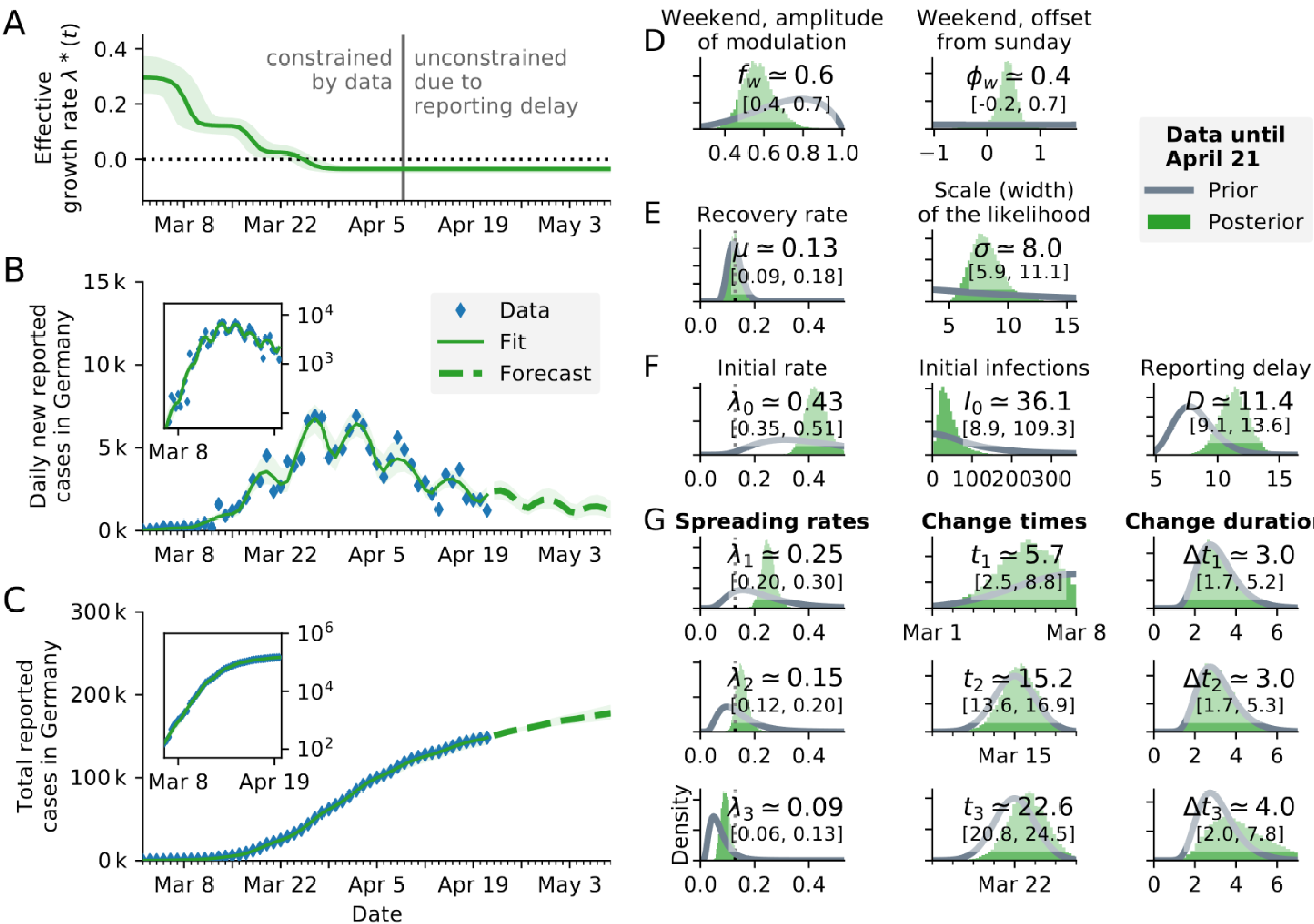
Priors:

Parameter	Variable	Prior distribution
Change points	t_i	Normal(Sunday of week i, 7)
Change duration	Δt_i	LogNormal(log(4),0.5)
Spreading rates	λ_0	LogNormal(log(1/8),0.5)
	λ_i	Relative to $i-1$ with factor (country & week dependent)
Recovery rate	μ	LogNormal(log(1/8),0.2)
Reporting delay	D	LogNormal(log(8),0.2)
Weekly modulation amplitude	f_w	Beta(0.7,0.17)
Weekly modulation phase	Φ_w	vonMises(0,0.01) (nearly flat)
Initially infected	$I(0)$	HalfCauchy(depending on country)

Adapted from [Dehning et int., Priesemann, Science, 2020]

Results March/April 2020



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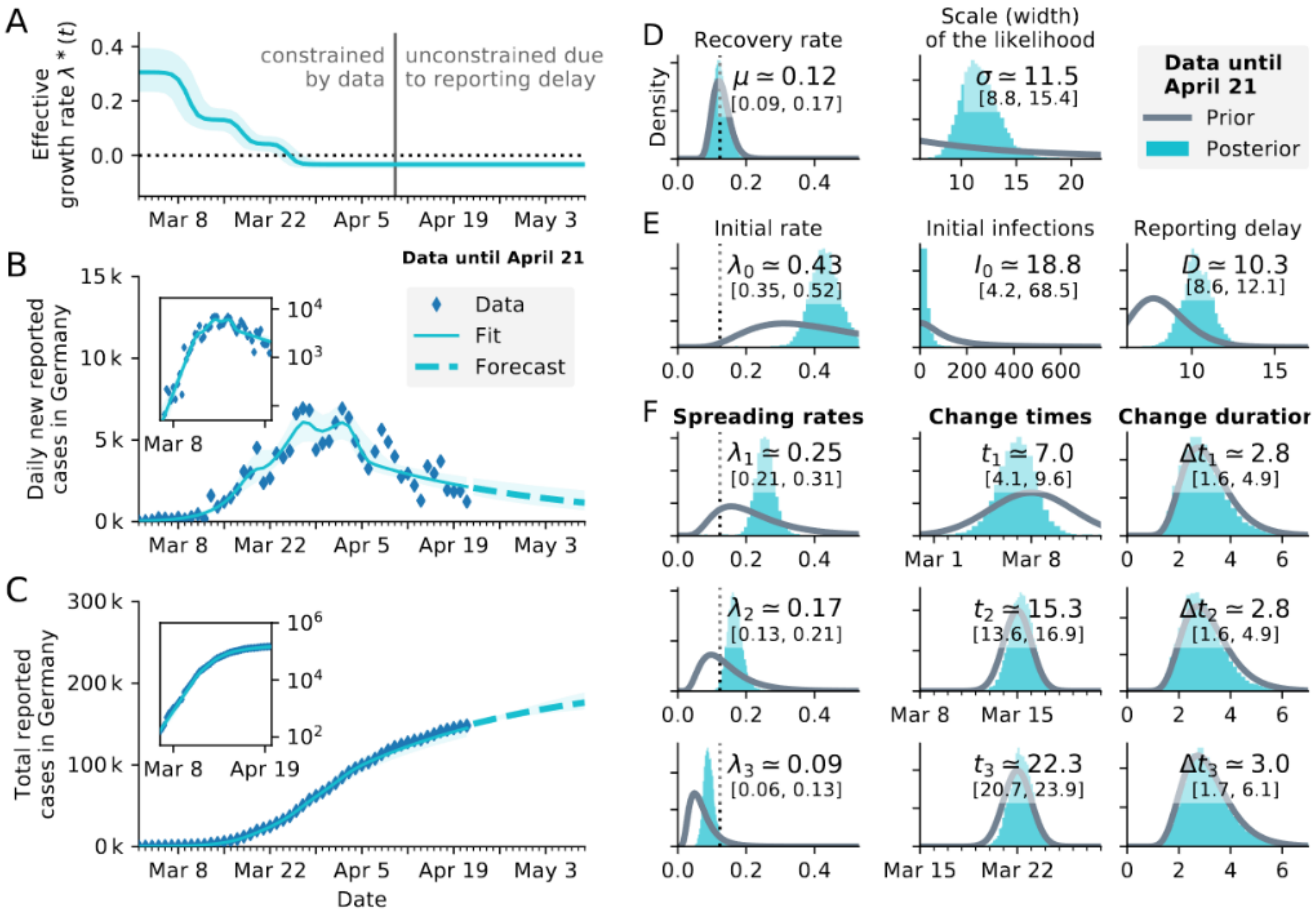
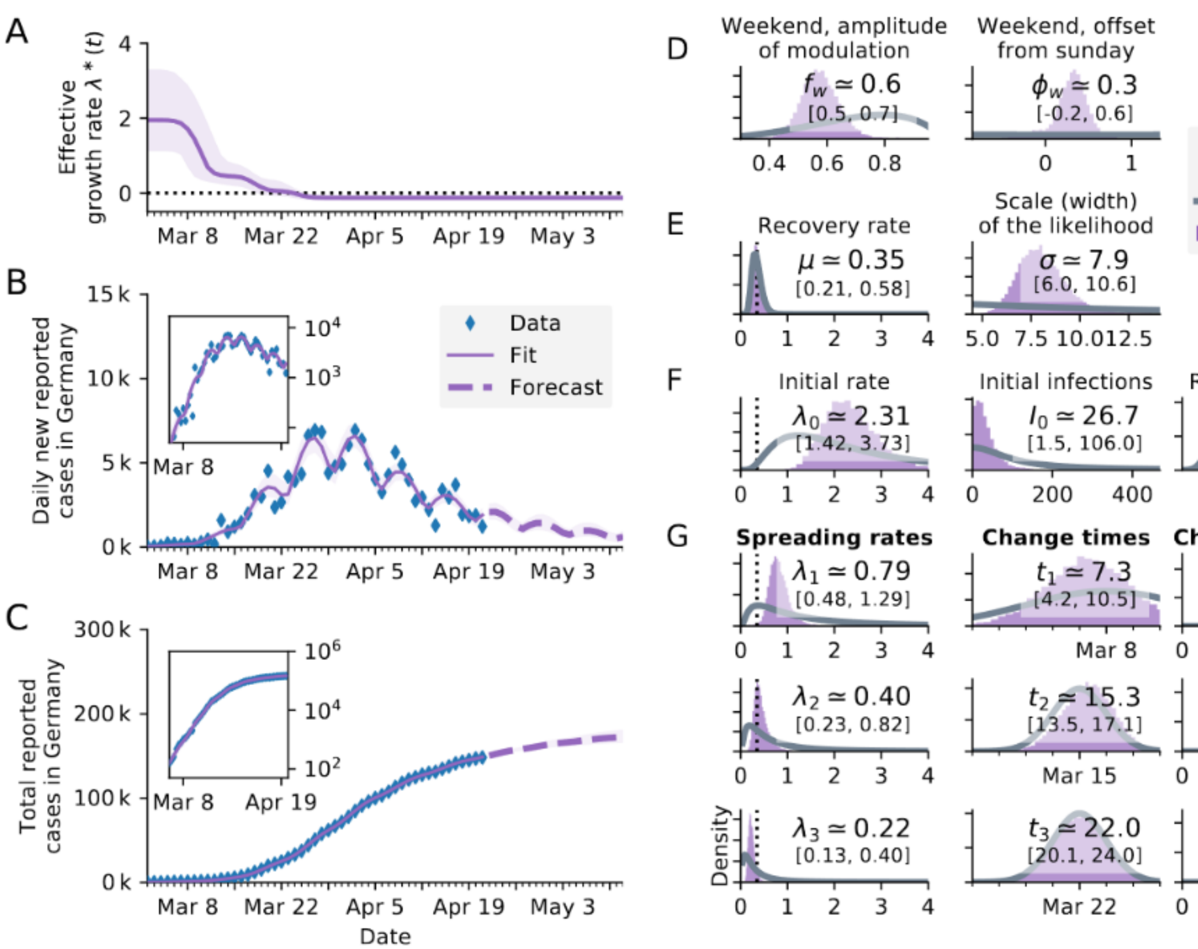
Different Models



Without weekend modulation



With incubation period

Adapted from [Dehning et int., Priesemann, Science, 2020]
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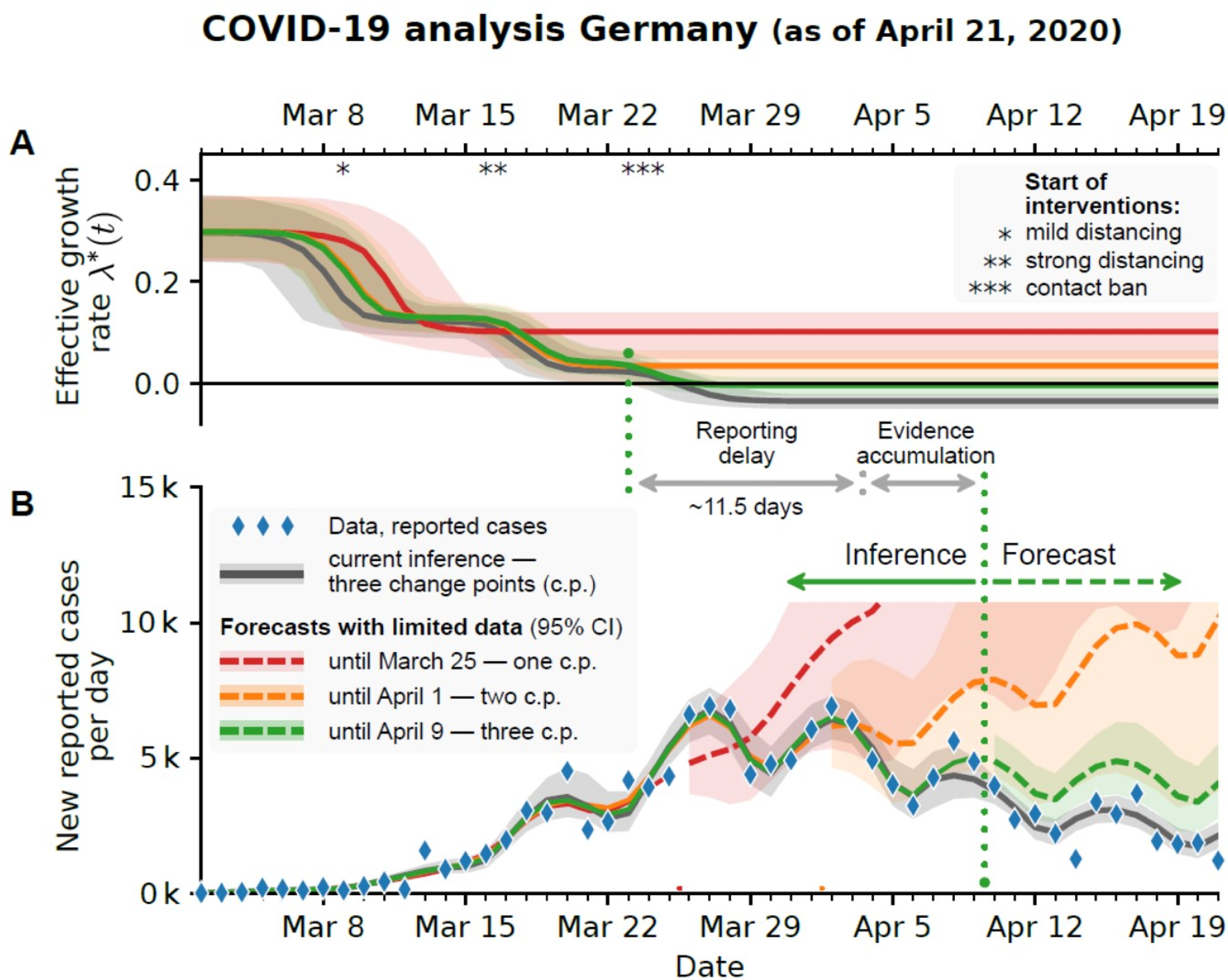
Analysis of the first wave



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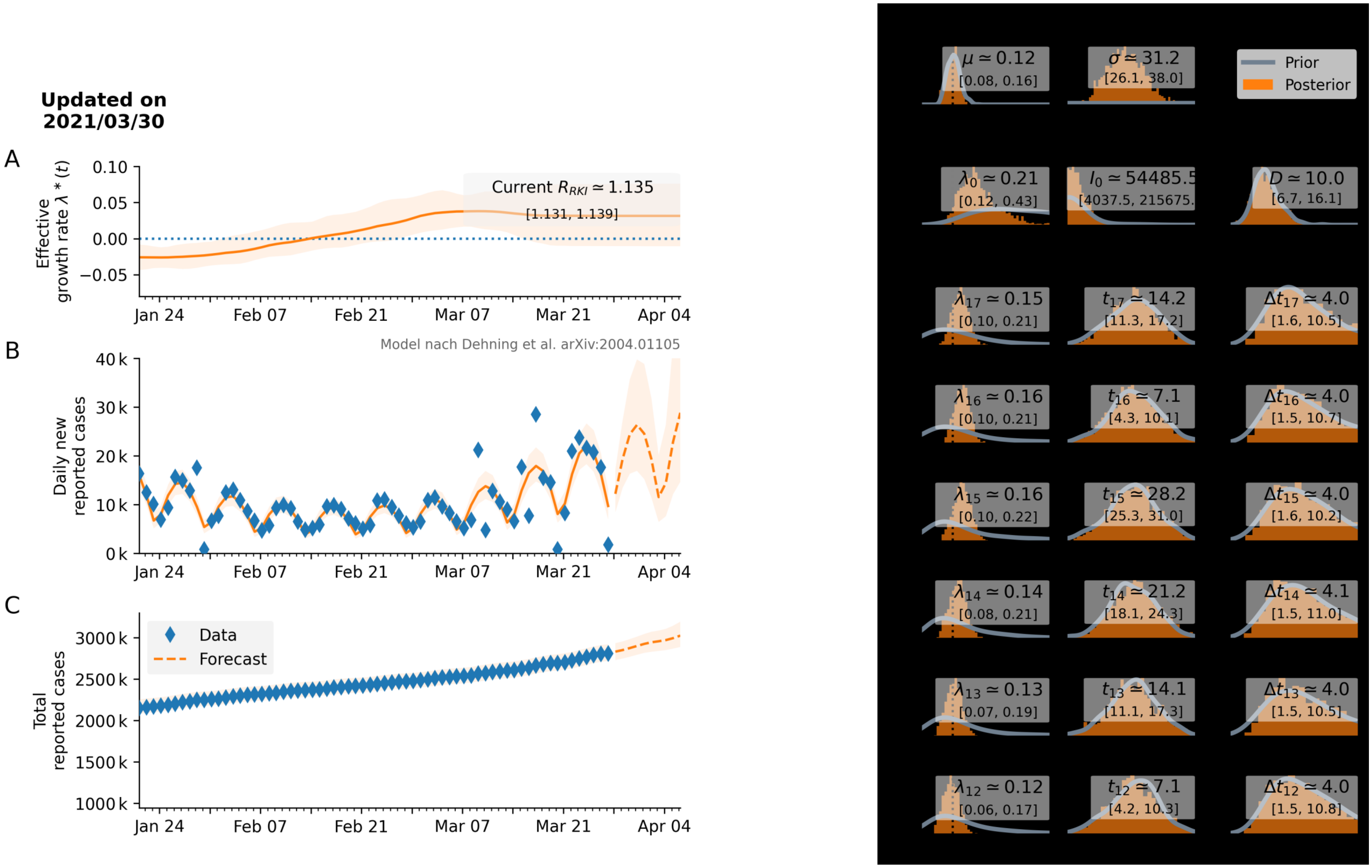
Daily new estimates for Germany



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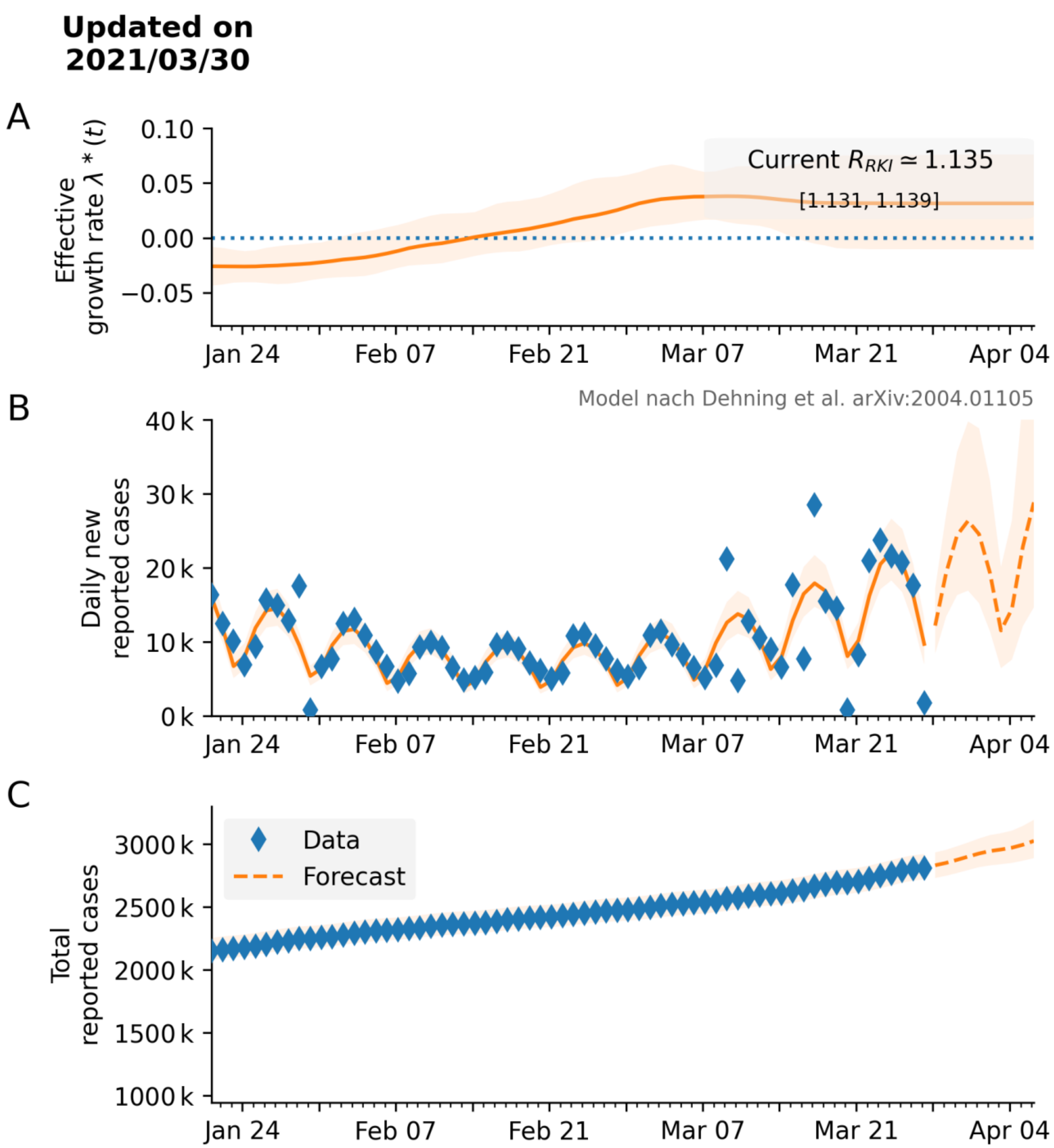
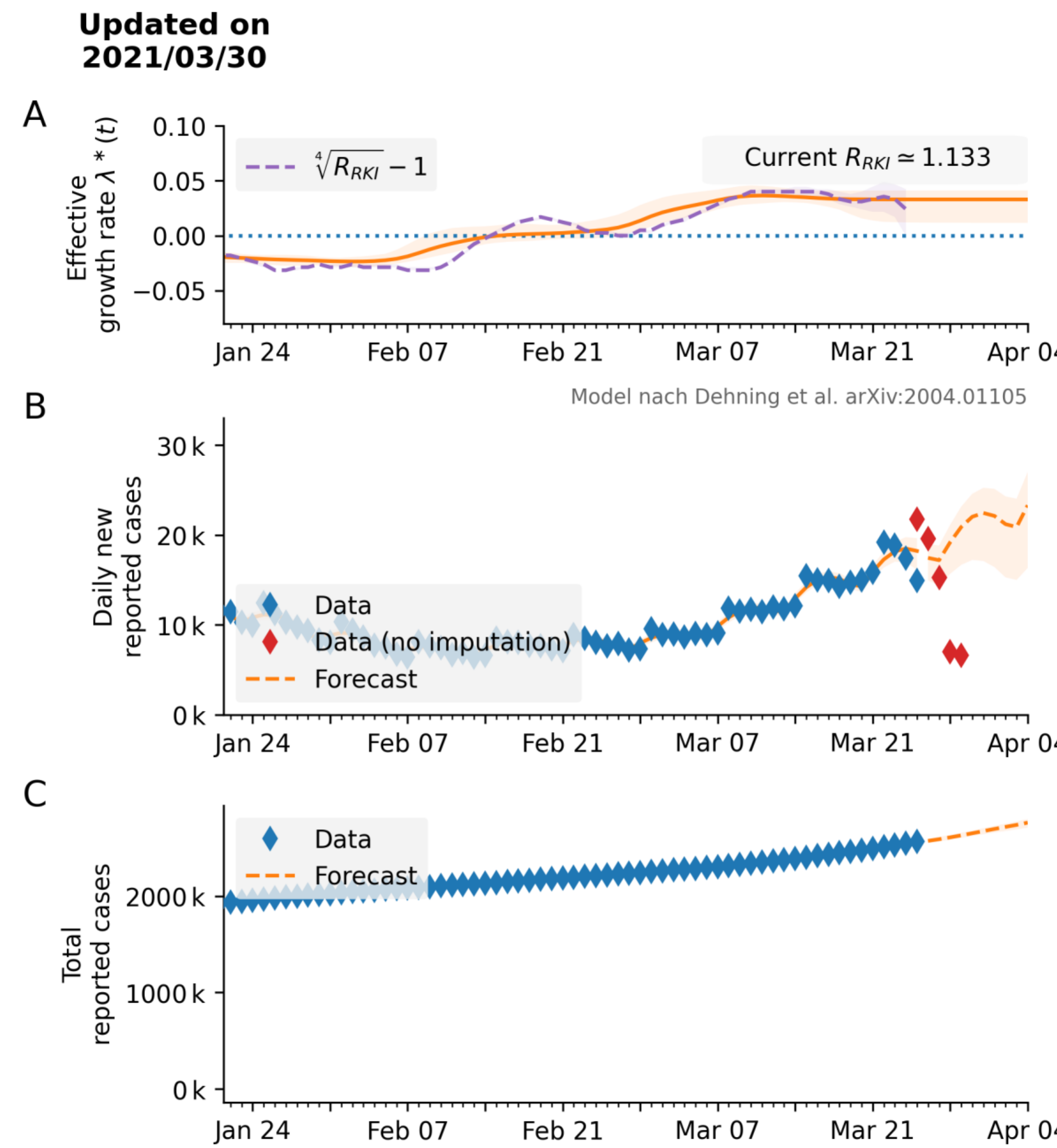


Data Source: OWD



Data Source: RKI Nowcast

Adapted from [Dehning et int., Priesemann, Science, 2020]

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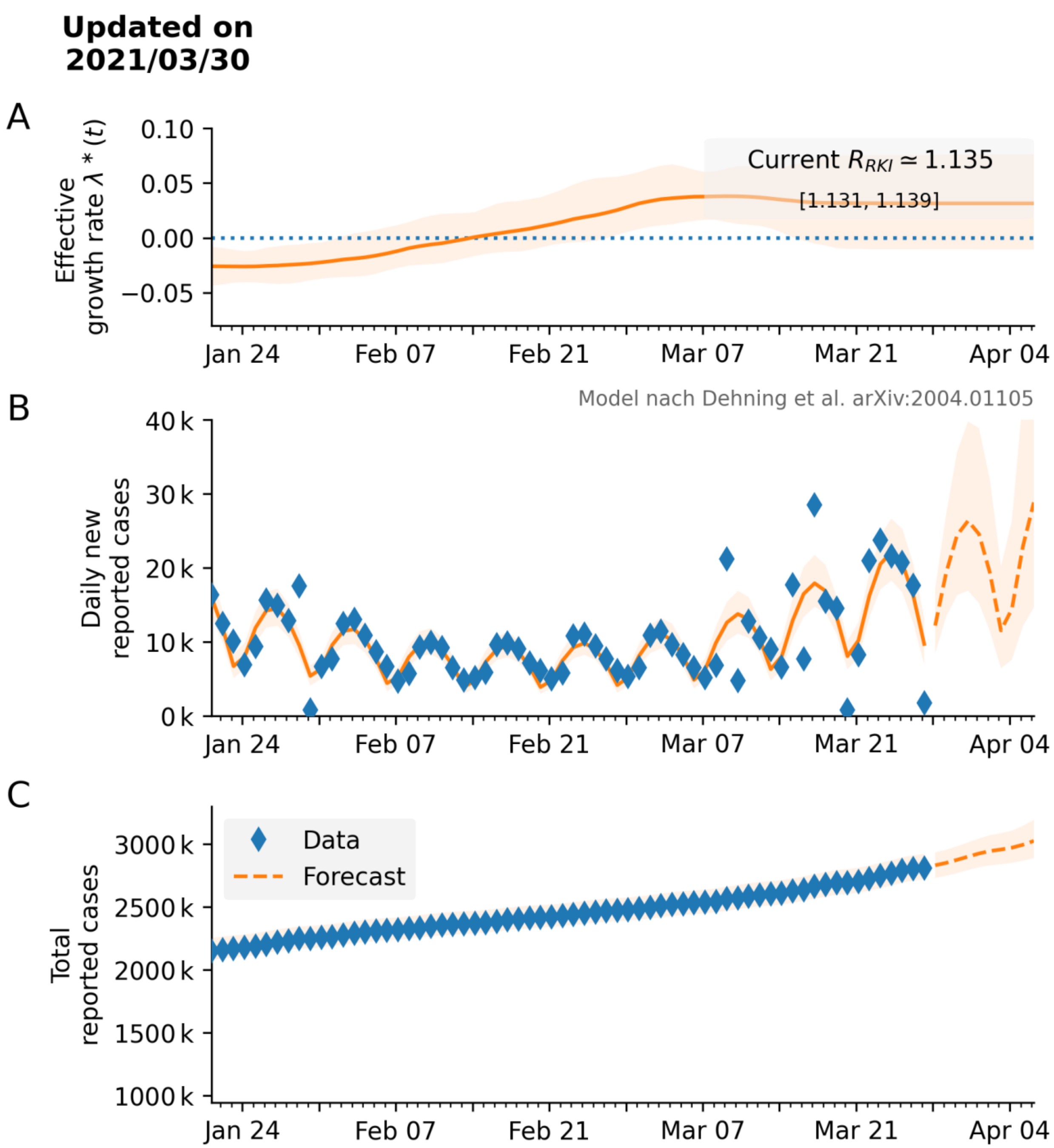

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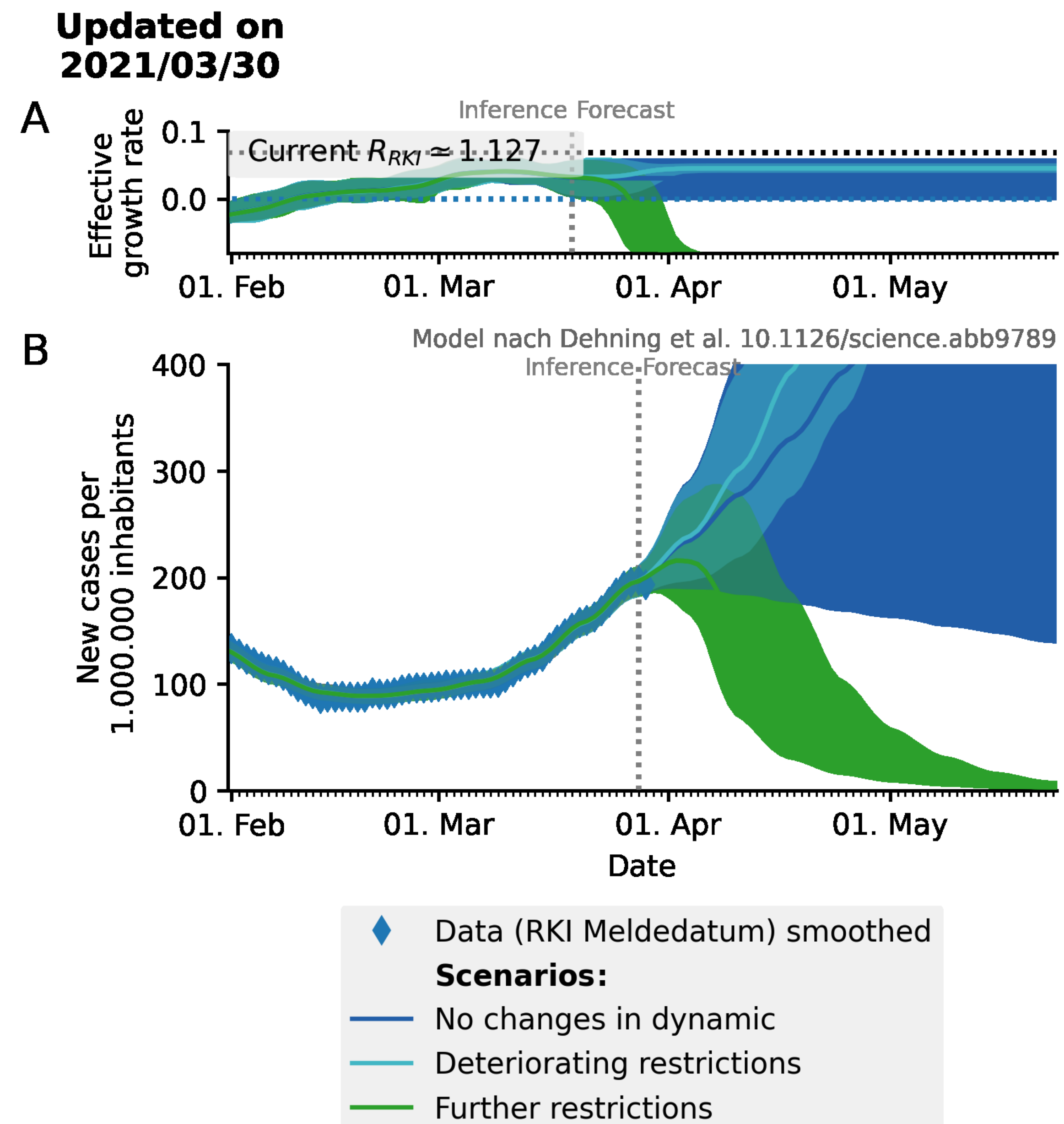

Data Source: RKI Reporting Date

Adapted from [Dehning et int., Priesemann, Science, 2020]

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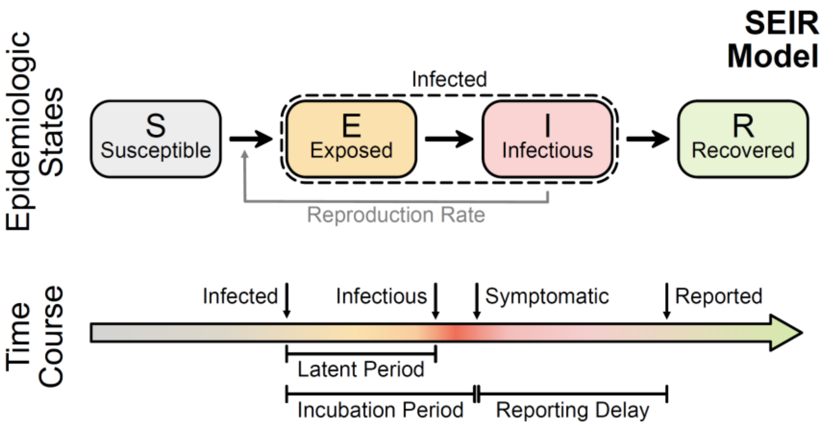

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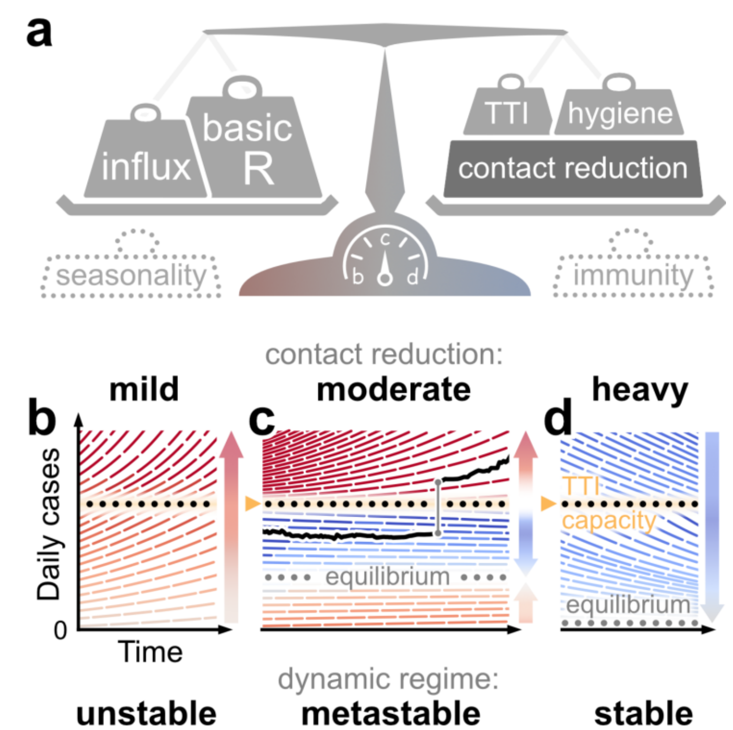
  How fast can we lift „non-pharmaceutical intervions“ (NPIs) given the planned vaccination progress?



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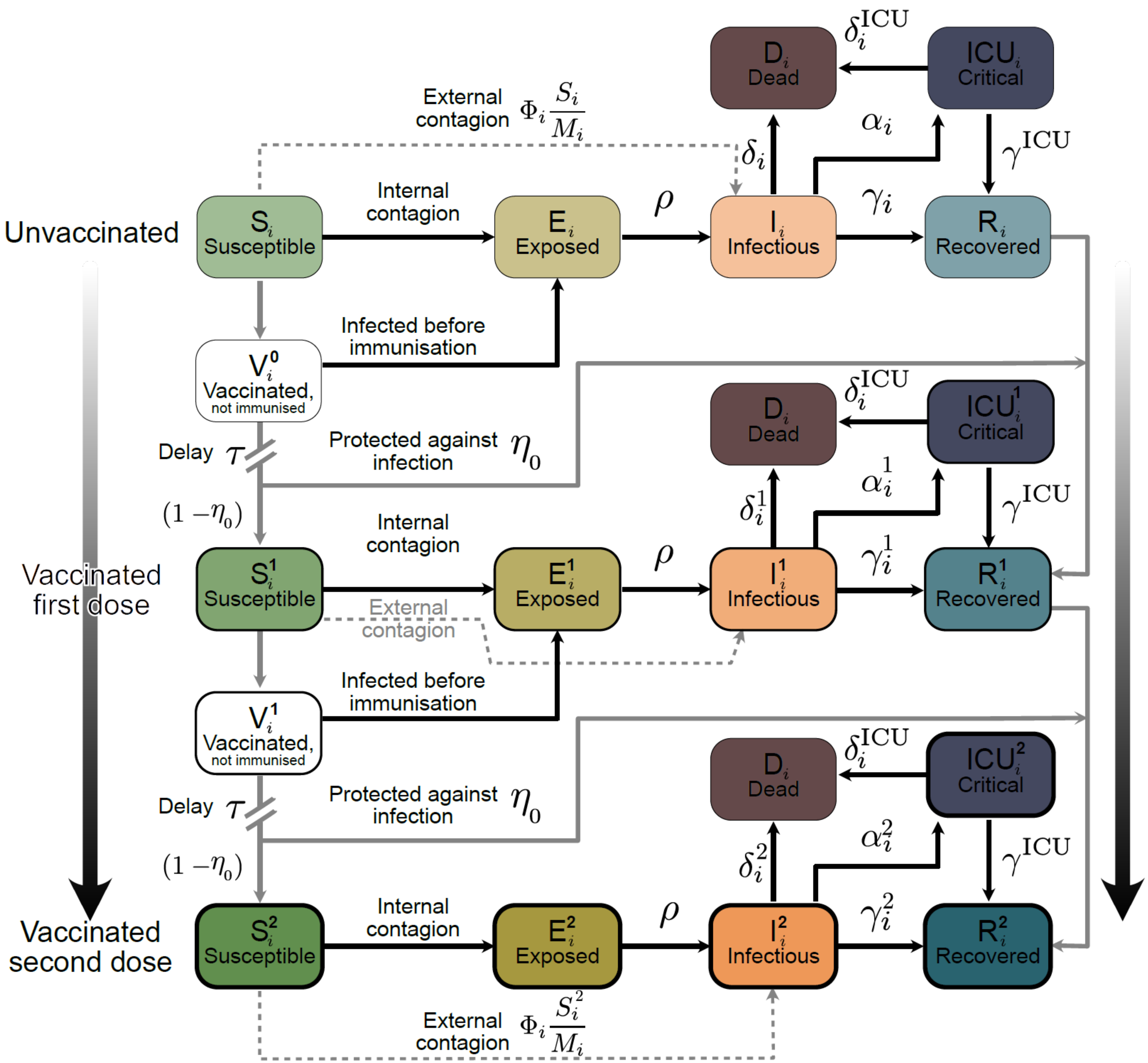
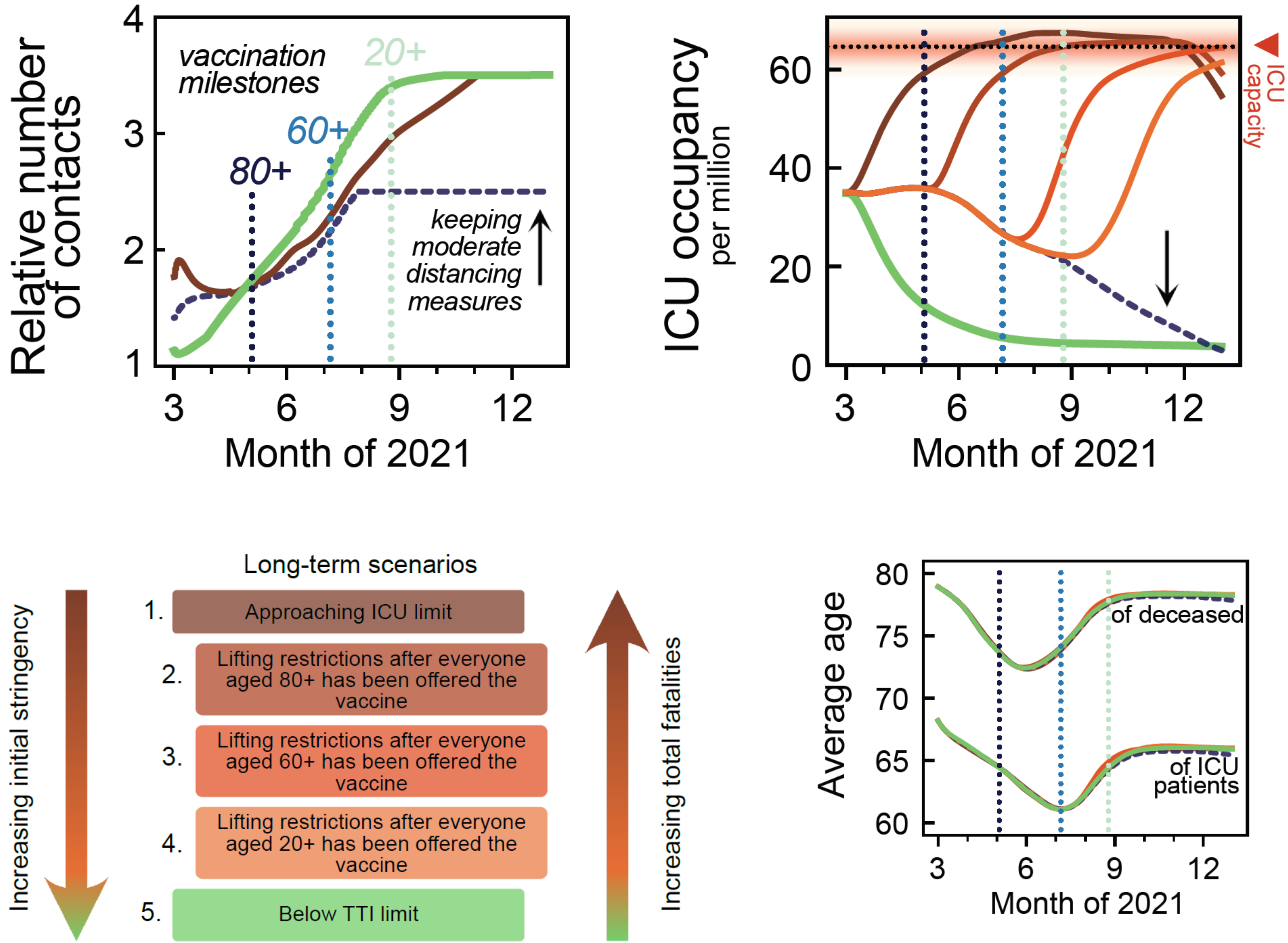
  Contribution of test-trace-isolate (TTI) to containment of COVID-19

Compartmental Vaccination Model – Age Dependent



[Bauer et int., Priesemann, arxiv]

Different Strategies of Opening



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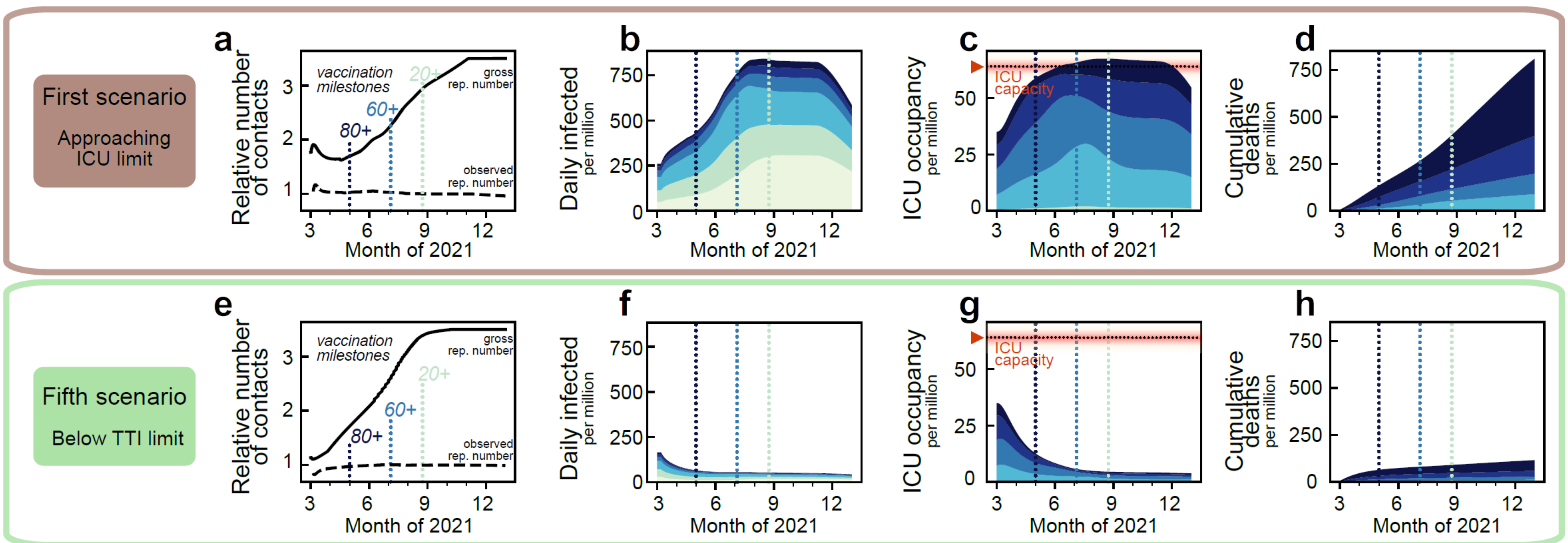

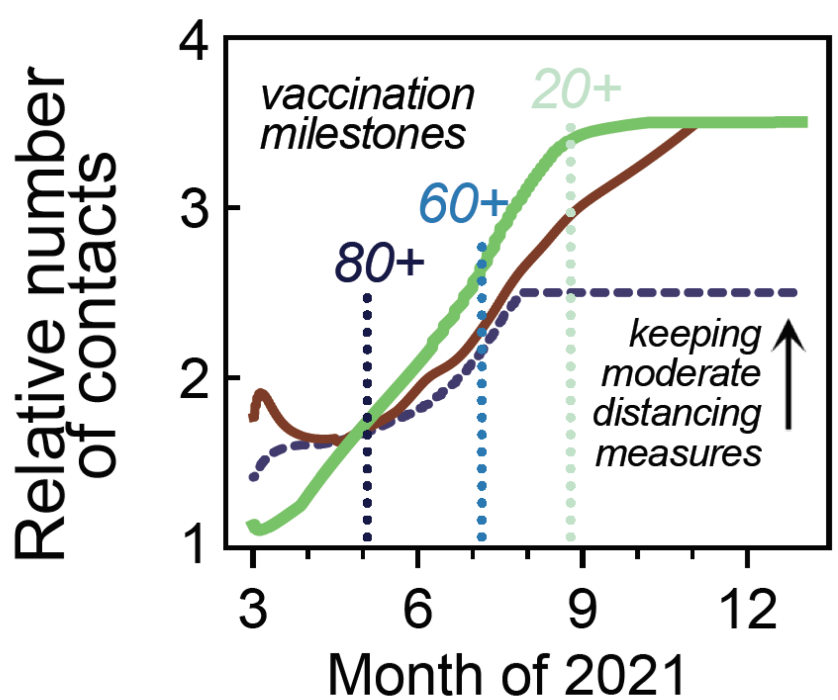

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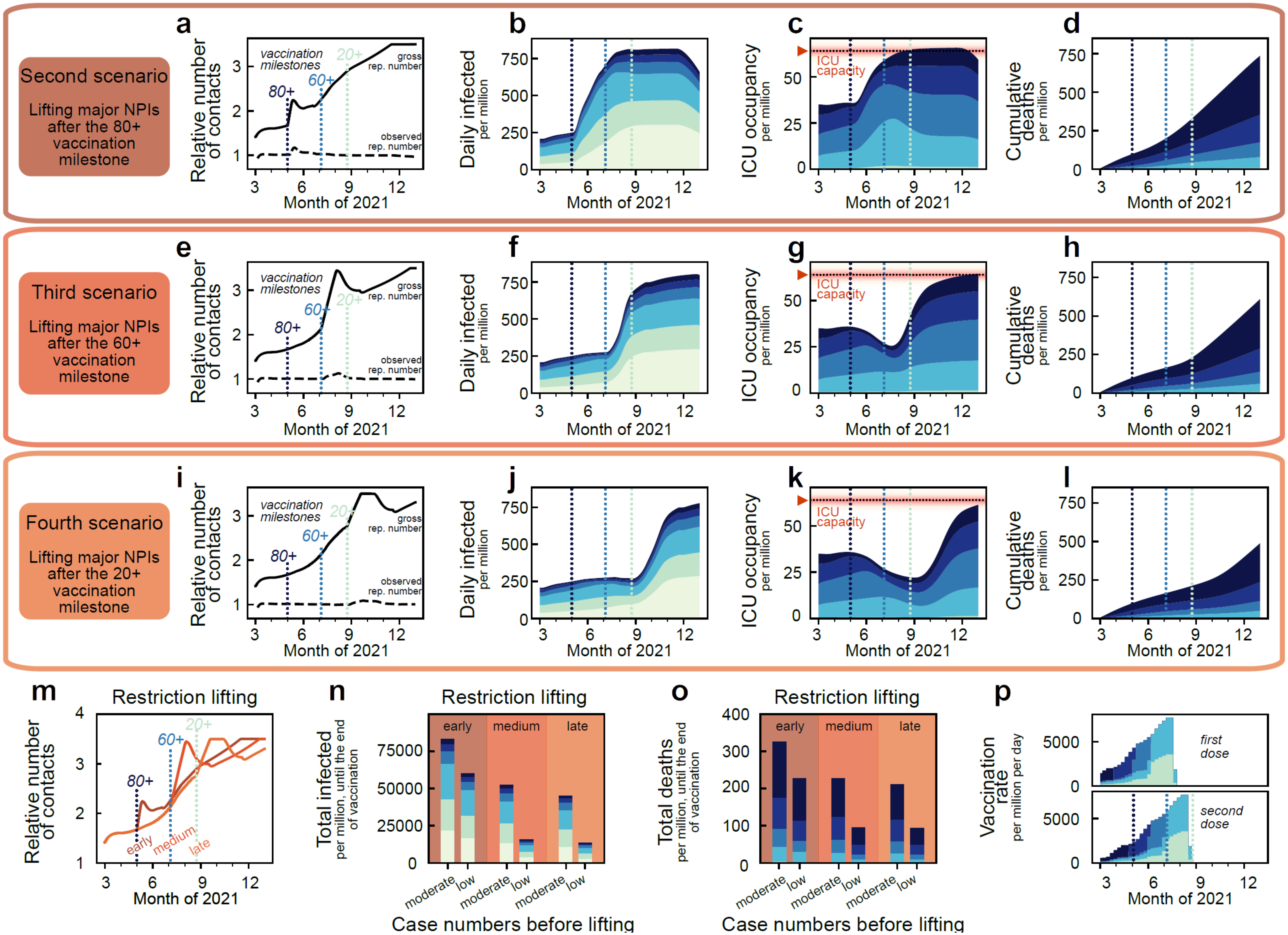

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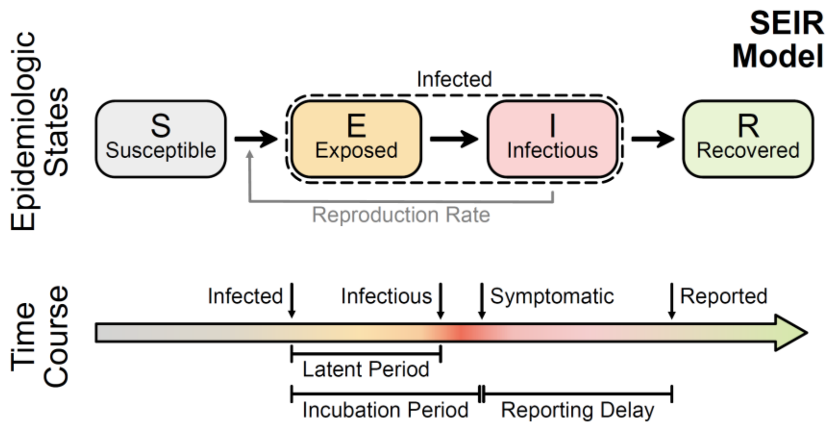

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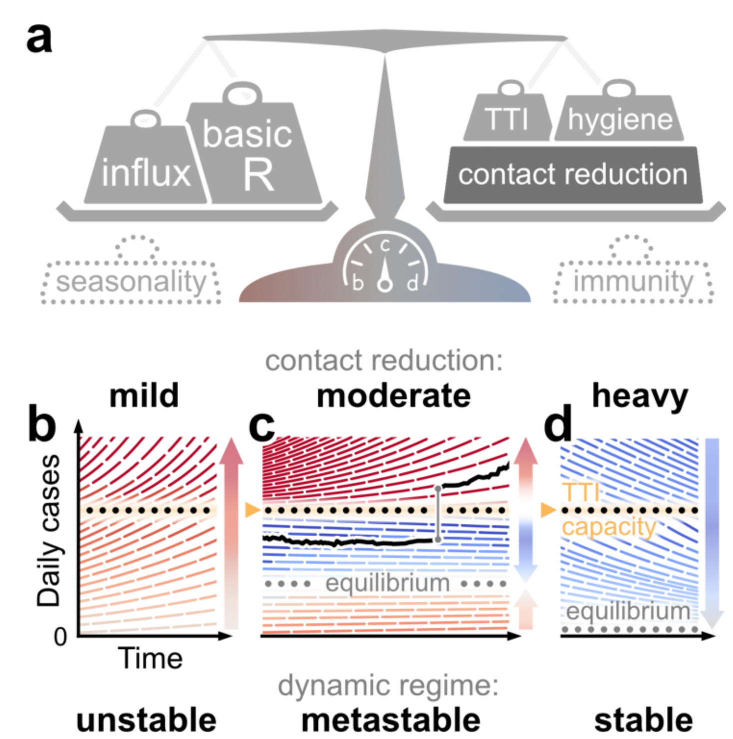

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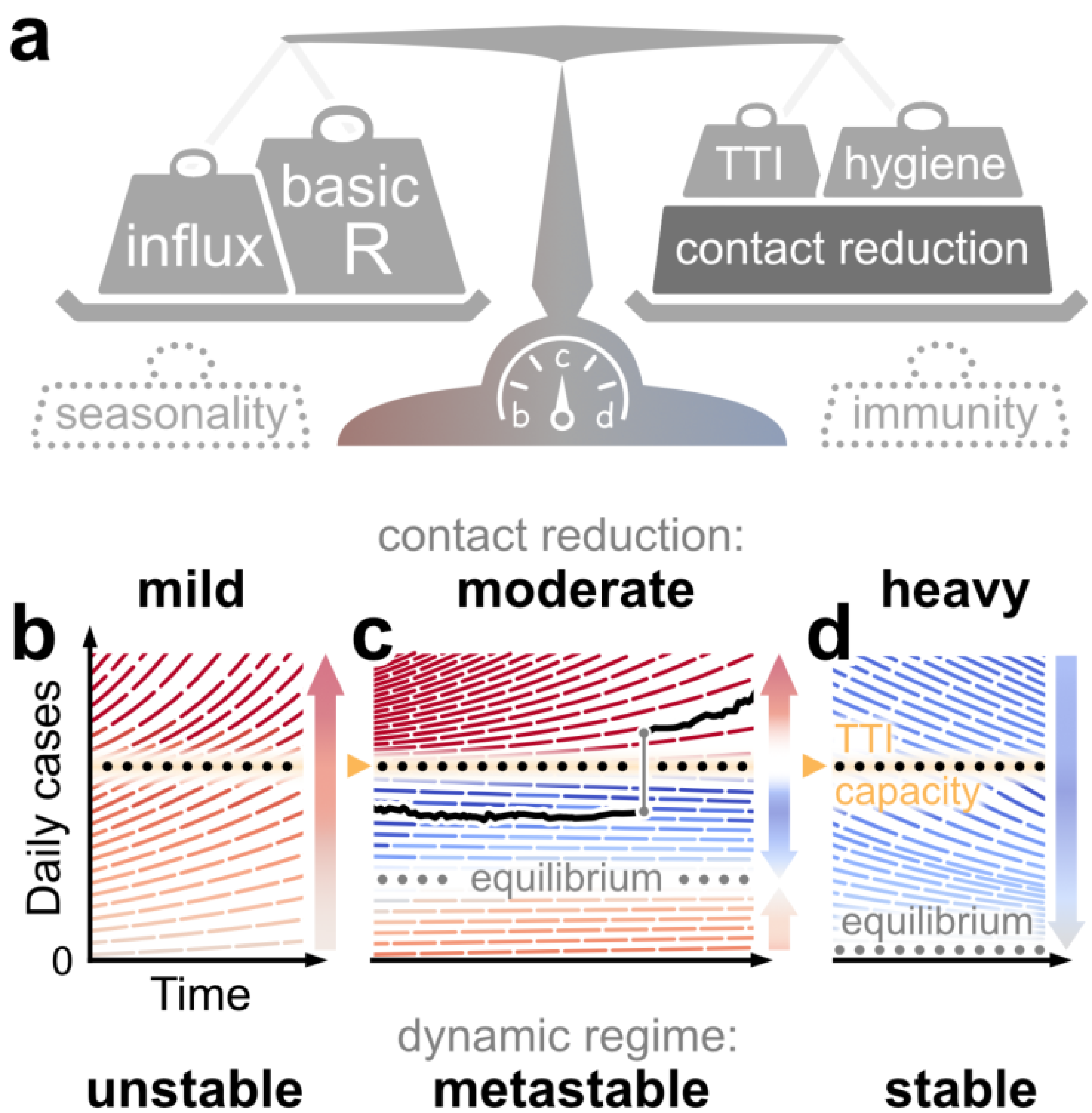
Combined measures to contain COVID-19



[Contreras et int., Priesemann, arxiv / under review]

nature COMMUNICATIONS

ARTICLE

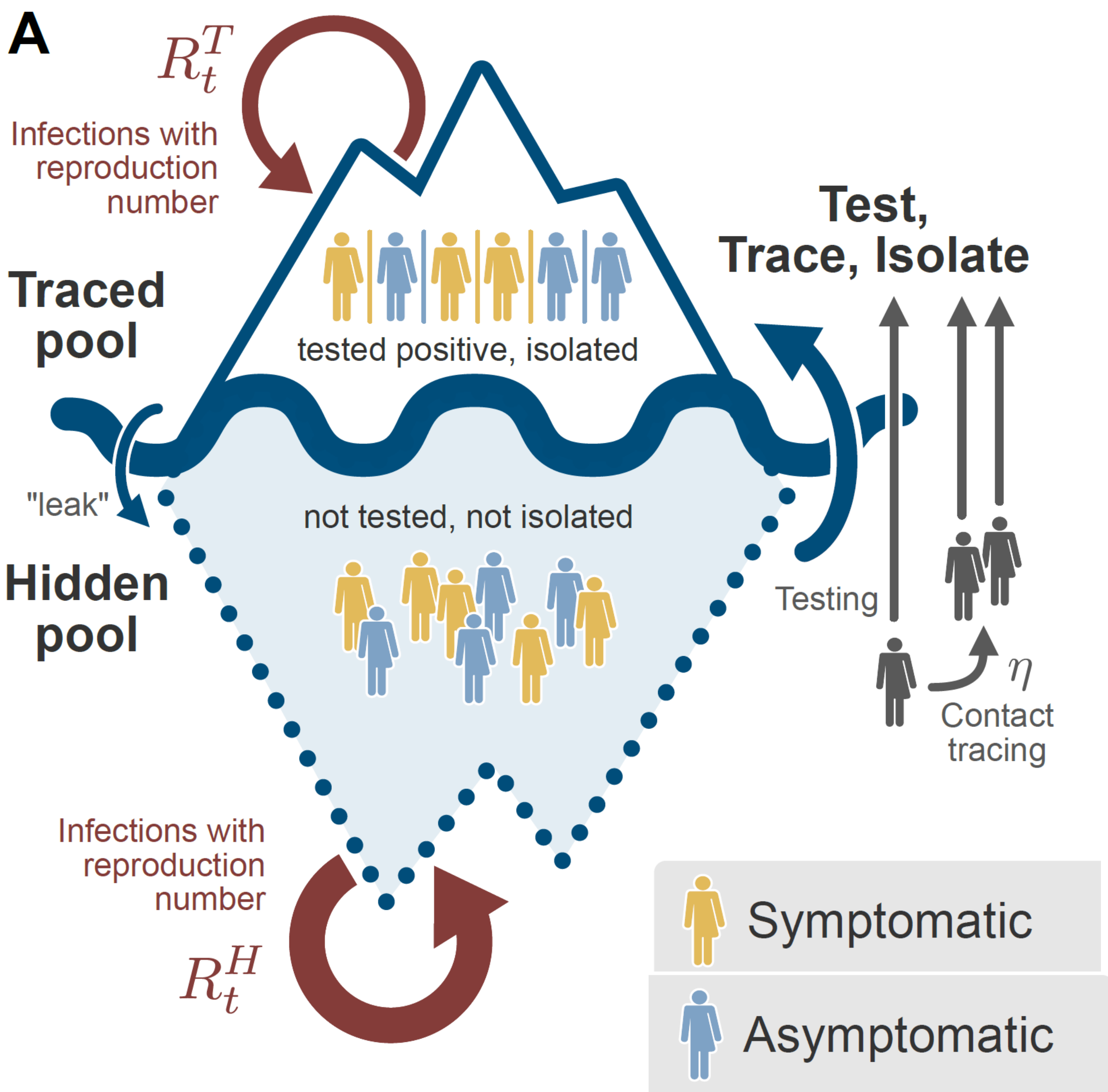
https://doi.org/10.1038/s41467-020-20699-8 OPEN

The challenges of containing SARS-CoV-2 via test-trace-and-isolate

Sebastian Contreras[1,2,5], Jonas Dehning[1,5], Matthias Loidolt[1,5], Johannes Zierenberg[1], F. Paul Spitzner[1], Jorge H. Urrea-Quintero[1], Sebastian B. Mohr[1], Michael Wilczek[1,3], Michael Wibral[4] & Viola Priesemann[1,3]✉

Without a cure, vaccine, or proven long-term immunity against SARS-CoV-2, test-trace-and-isolate (TTI) strategies present a promising tool to contain its spread. For any TTI strategy, however, mitigation is challenged by pre- and asymptomatic transmission, TTI-avoiders, and undetected spreaders, which strongly contribute to "hidden" infection chains. Here, we study a semi-analytical model and identify two tipping points between controlled and uncontrolled spread: (1) the behavior-driven reproduction number R_t^H of the hidden chains becomes too large to be compensated by the TTI capabilities, and (2) the number of new infections exceeds the tracing capacity. Both trigger a self-accelerating spread. We investigate how these tipping points depend on challenges like limited cooperation, missing contacts, and

Test-Trace-and-Isolate (TTI) contributes to containment



Test & isolated

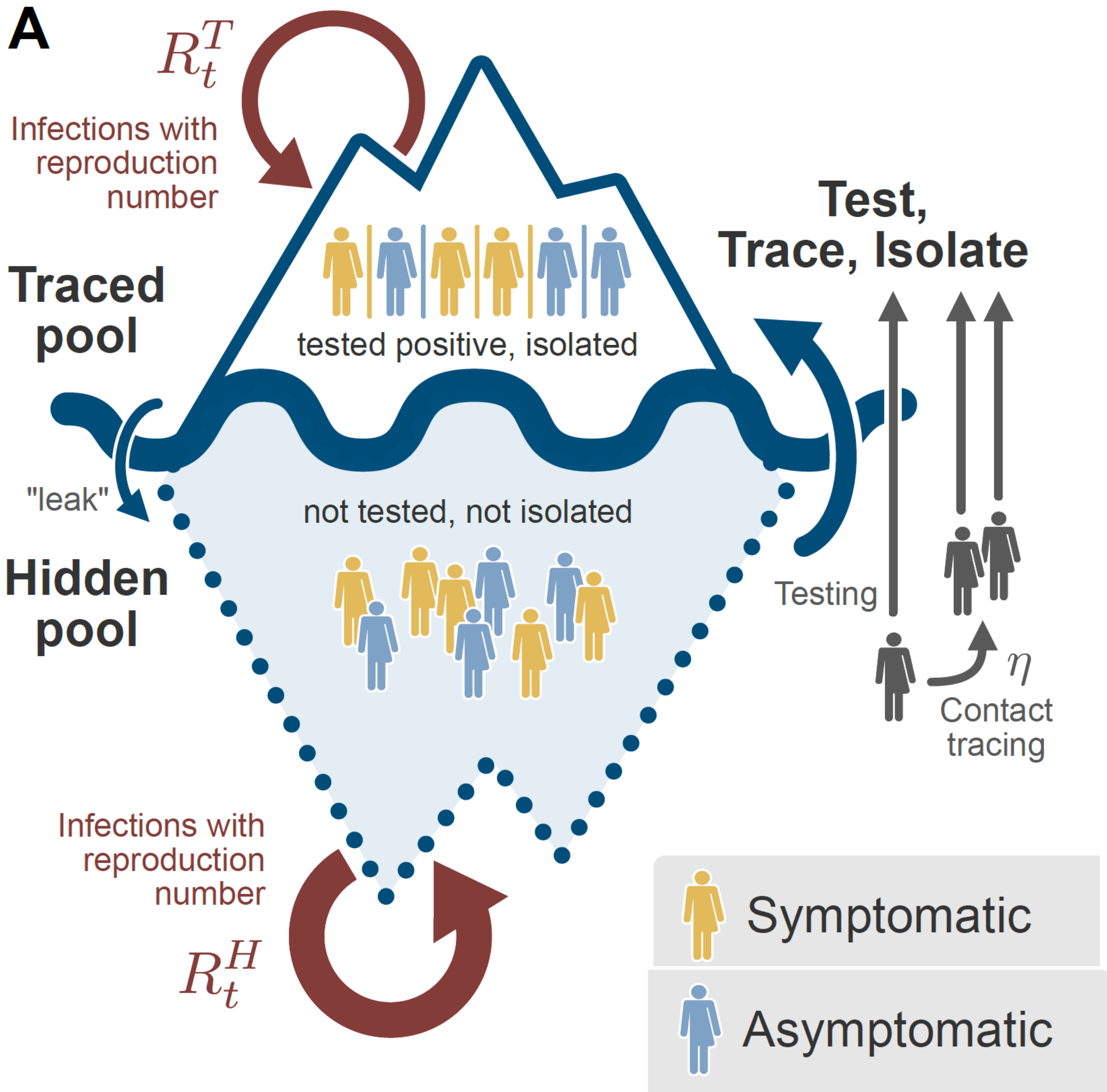
- Random (0)
- Symptoms (50 % of sympt., on average after 5 days)
- Test contact persons

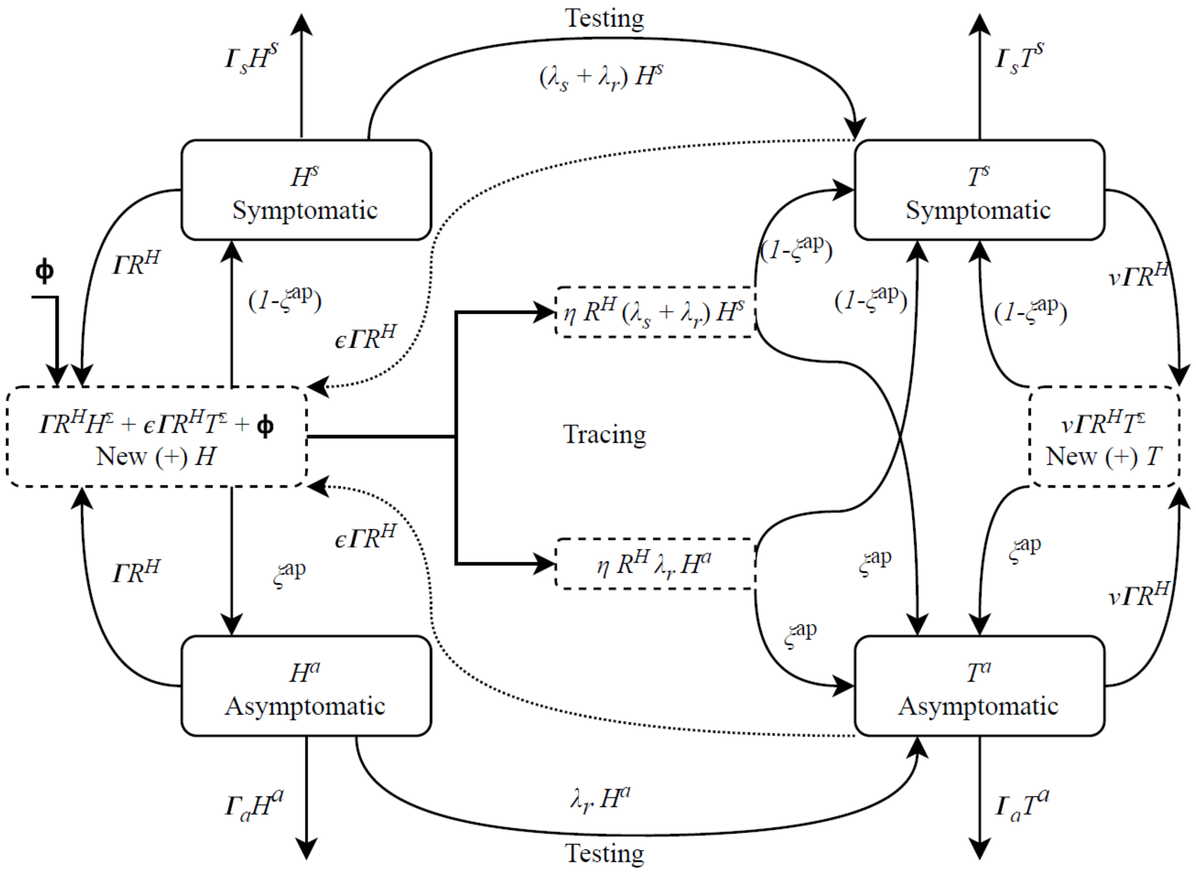
Contact tracing is difficult:

- Pre- und asymptomatic infection
- 1/3 of contacts are overlooked
- Quarantine is not perfect
- People who do not get tested (20%)
- Introduction of new infectious from abroad
- Limited capacities of health offices for testing and tracing

[Contreras et int., Priesemann, Nature Communications, in press]

Test-Trace-and-Isolate (TTI) contributes to containment

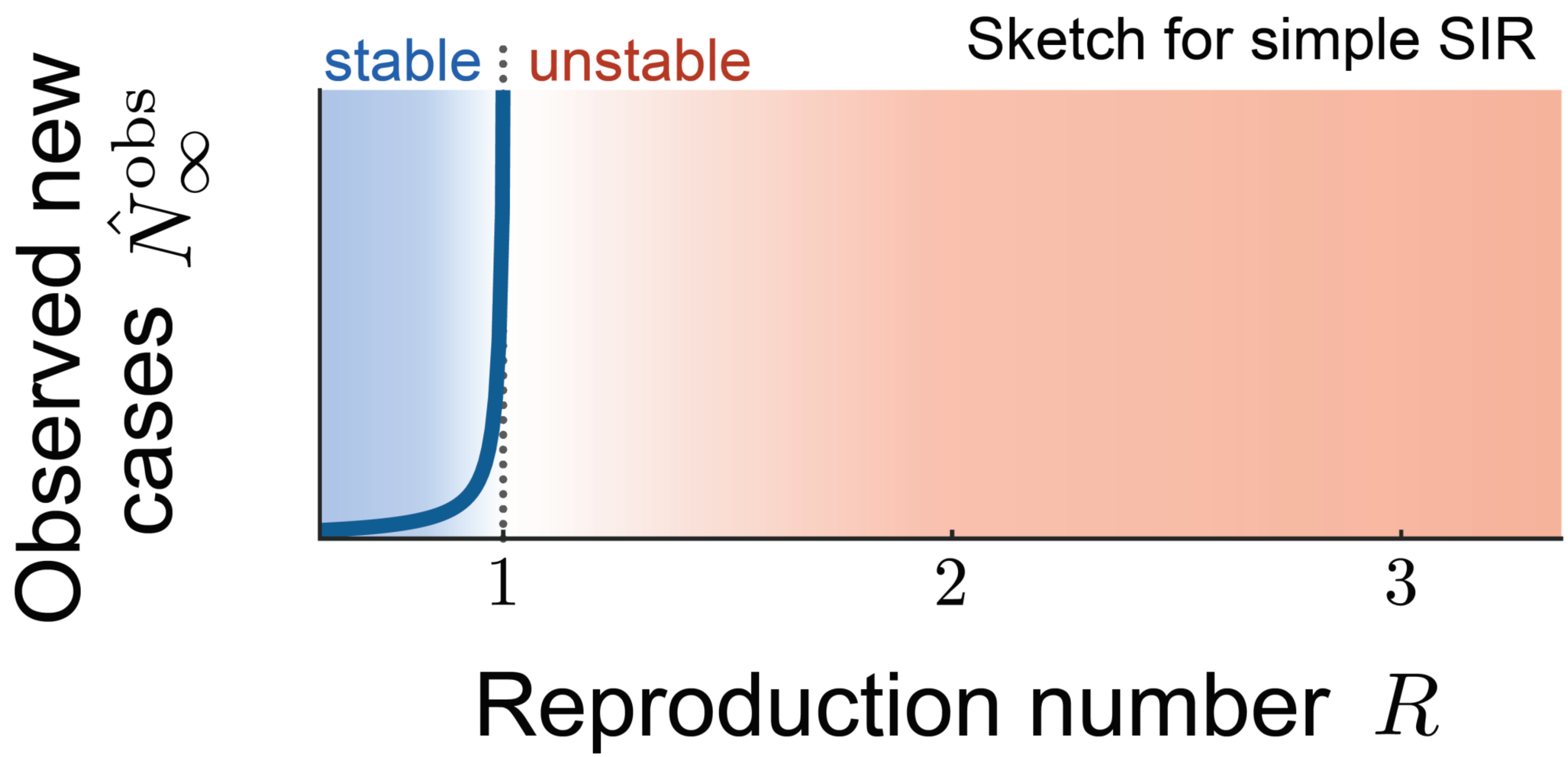


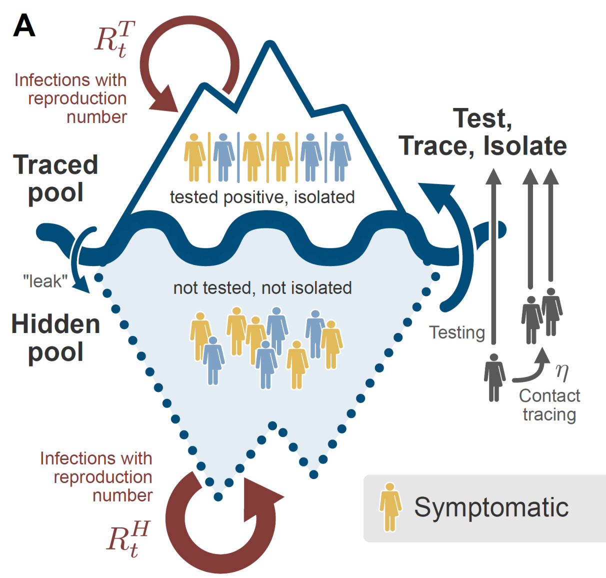


[Contreras et int., Priesemann, Nature Communications, in press]

The reproduction number *R* and the external influx of new cases Φ determine the level of new infections *N*

$$N \approx \frac{\Phi}{R_c - R} = \frac{\Phi}{1 - R}, \qquad \text{für } R < 1$$

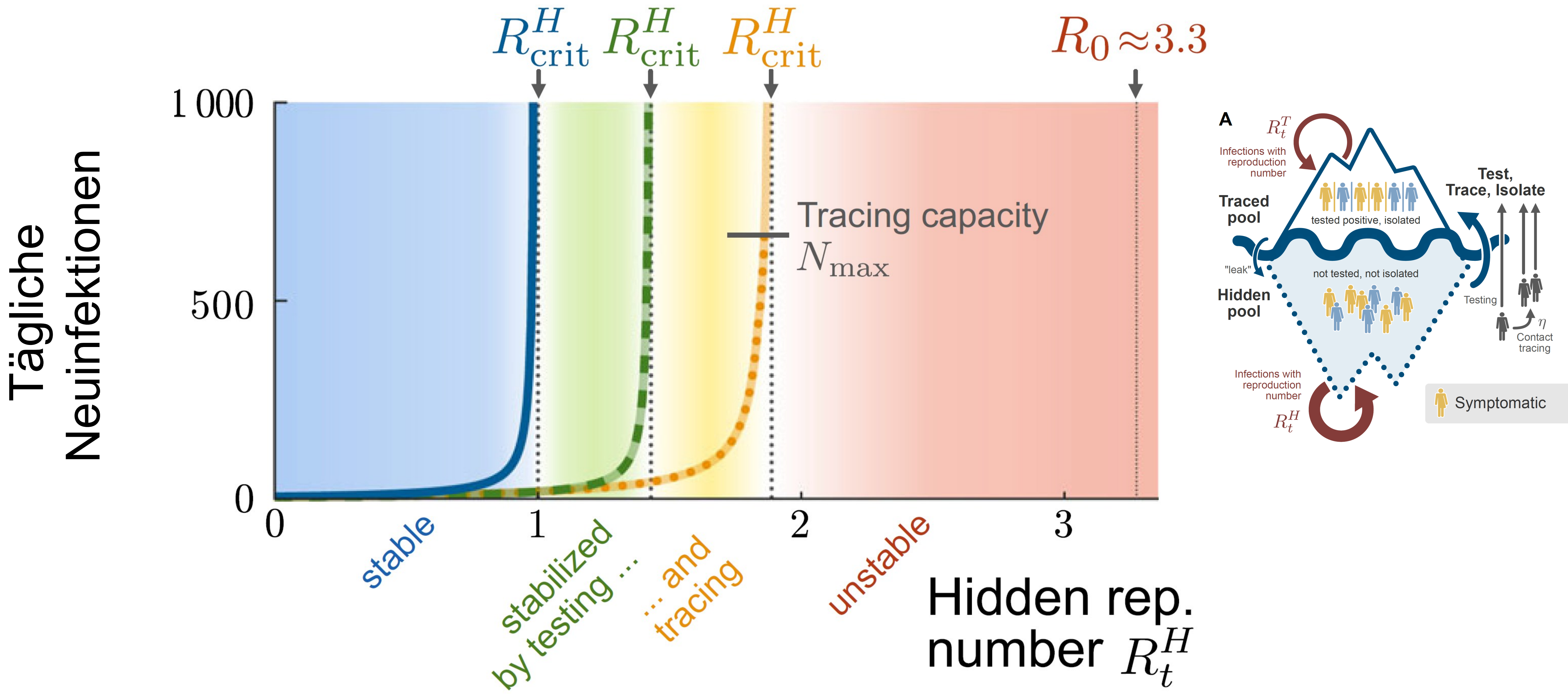




[Contreras et int., Priesemann, Nature Communications, in press]

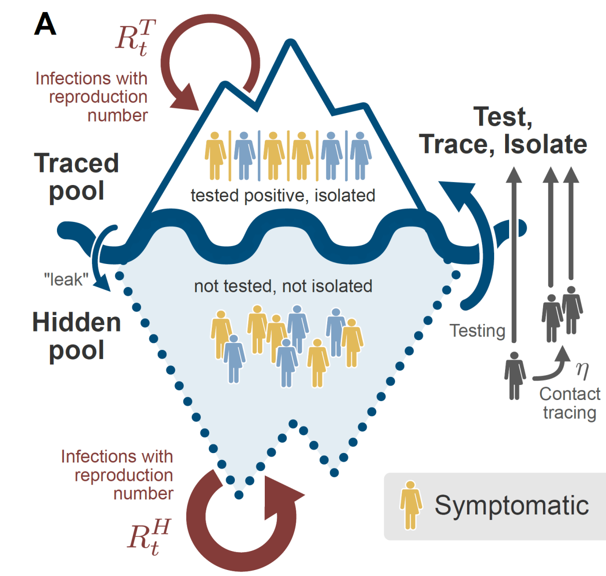
Test-Trace-Isolate (TTI) moves the stability limit:

Without TTI, R must be below 1
With TTI, R in the day to day life can be up to two

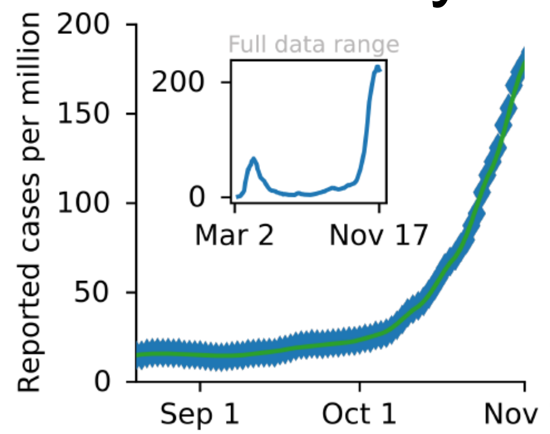


[Contreras et int., Priesemann, Nature Communications, in press]

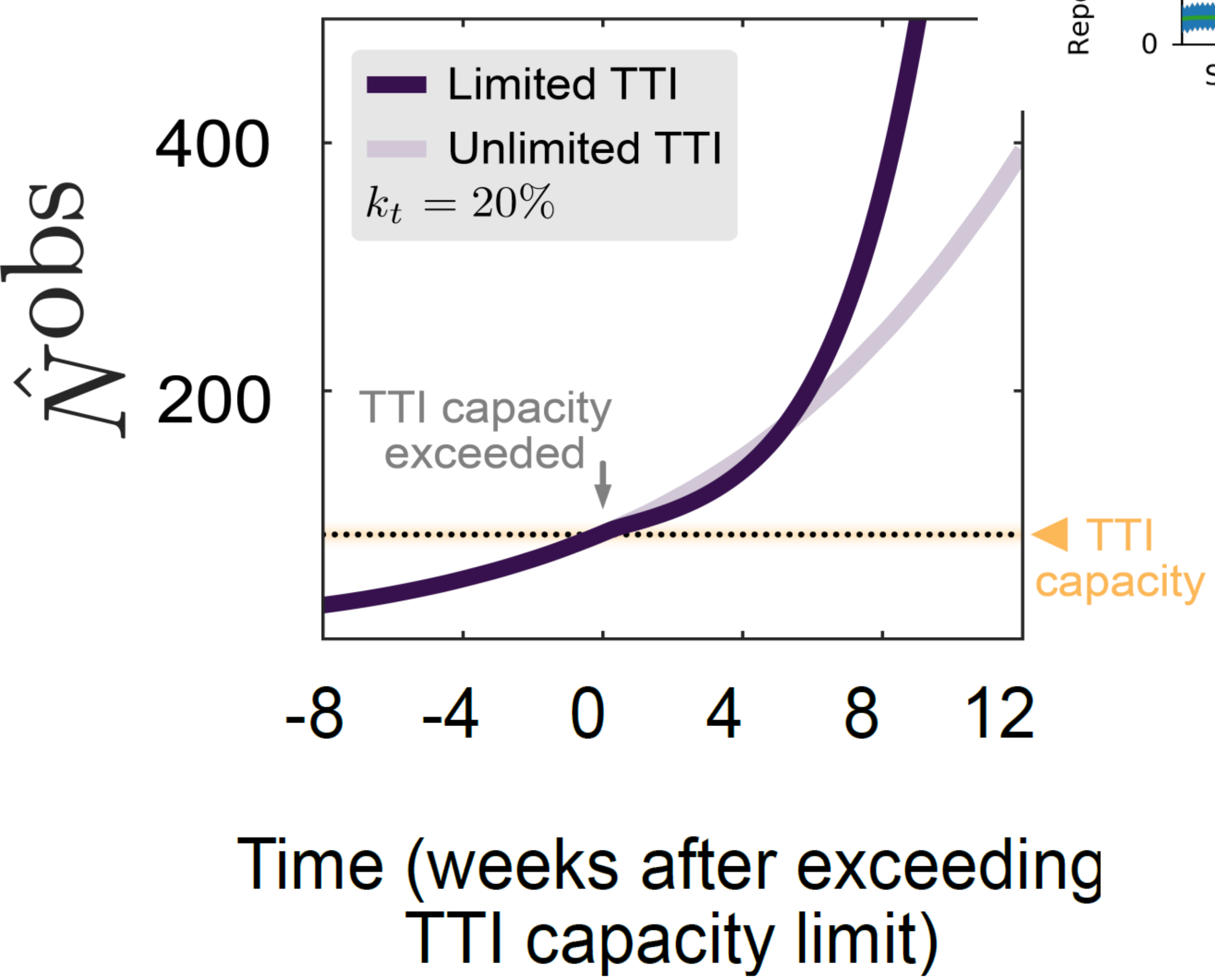
Crossing the TTI Limit: Case numbers grow faster than exponential



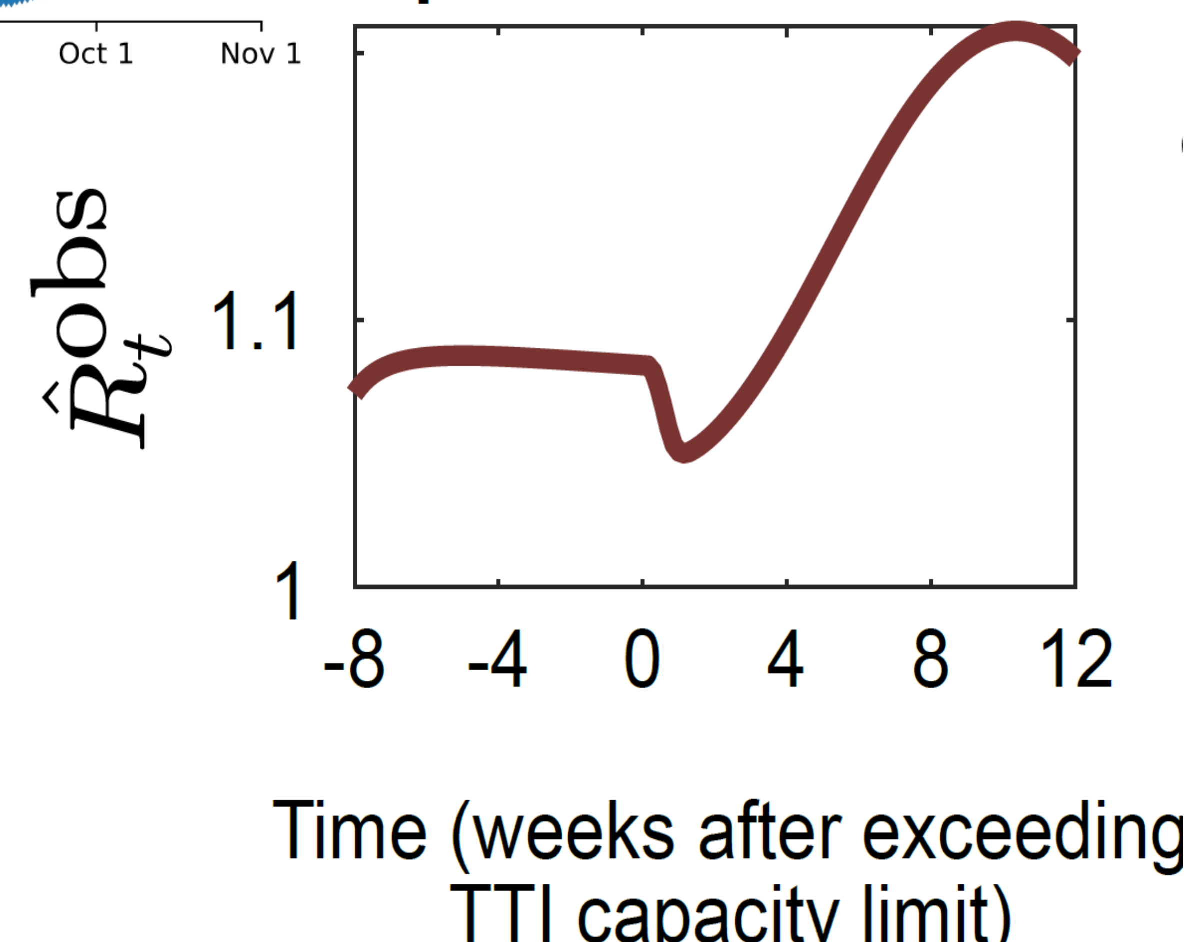
New infections Germany



Daily observed new cases (per million)

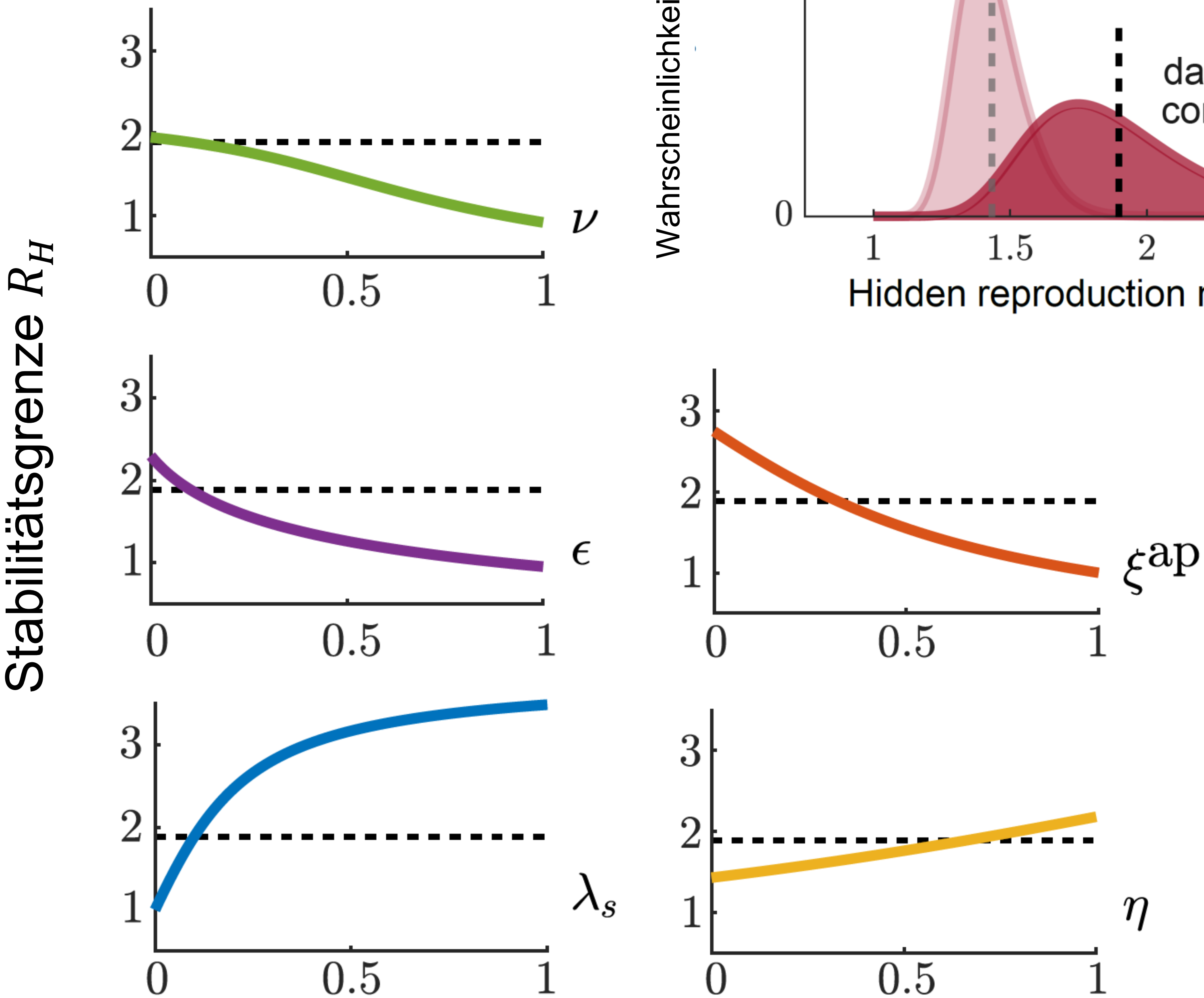


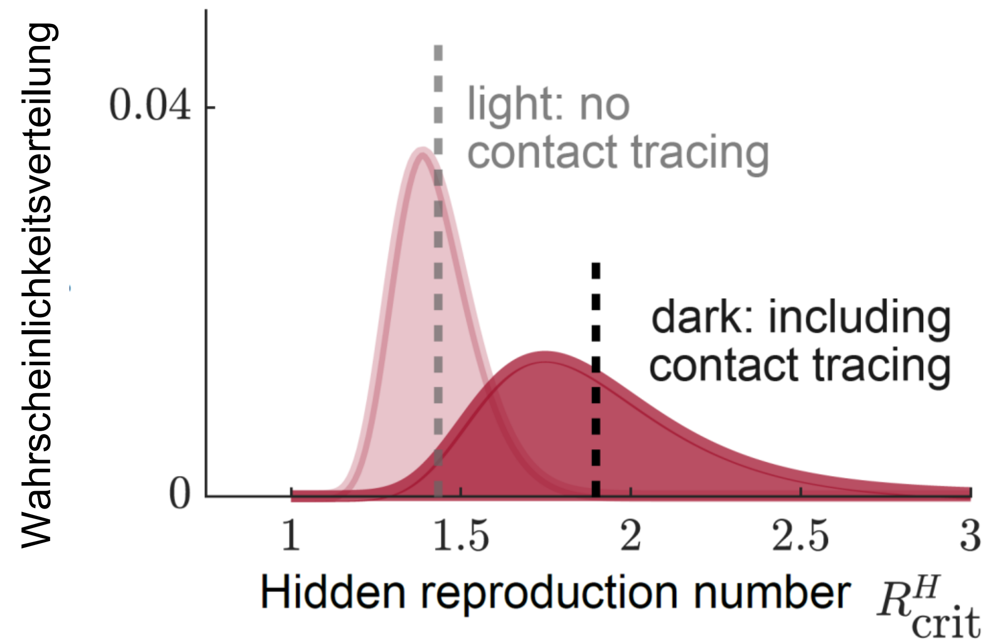
Observed reproduction number

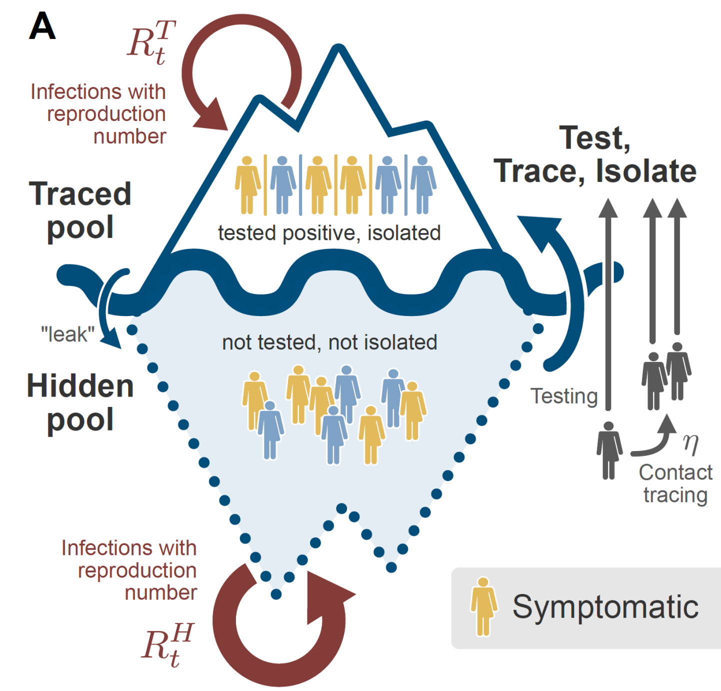


[Contreras et int., Priesemann, Nature Communications, 2021, and arxiv]

Sensitivity Analysis





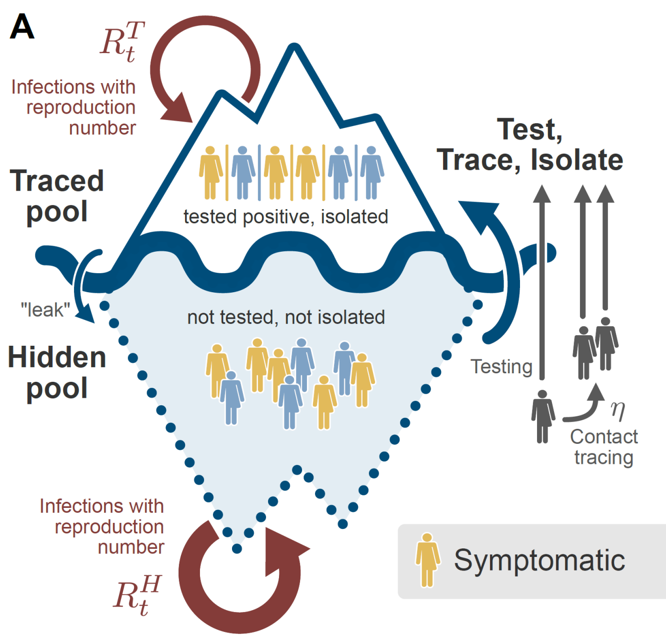


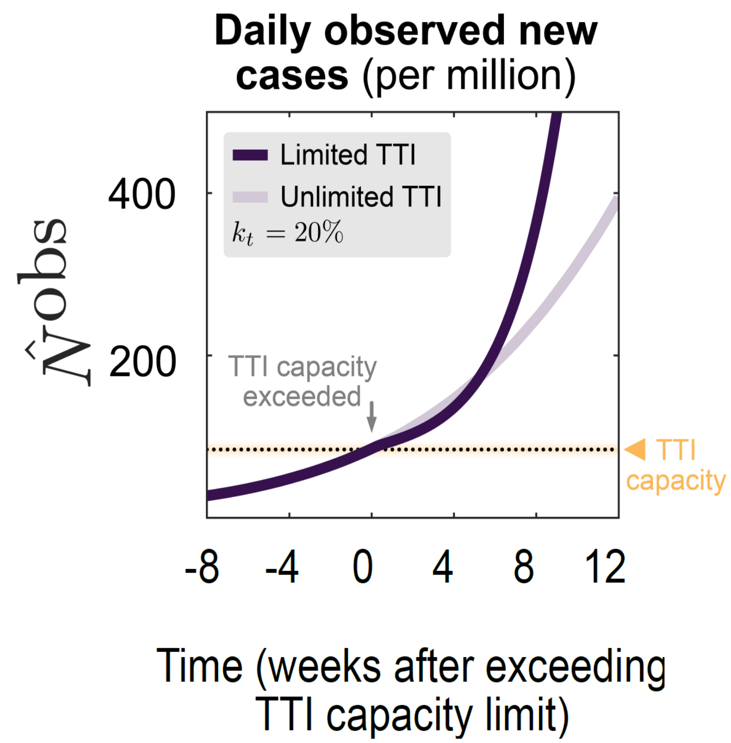
- ν Isolation factor
- ϵ "leak" factor
- λ_s Symptom-driven testing
- ξ^{ap} Apparent asymptomatic fraction
- η Tracing efficiency

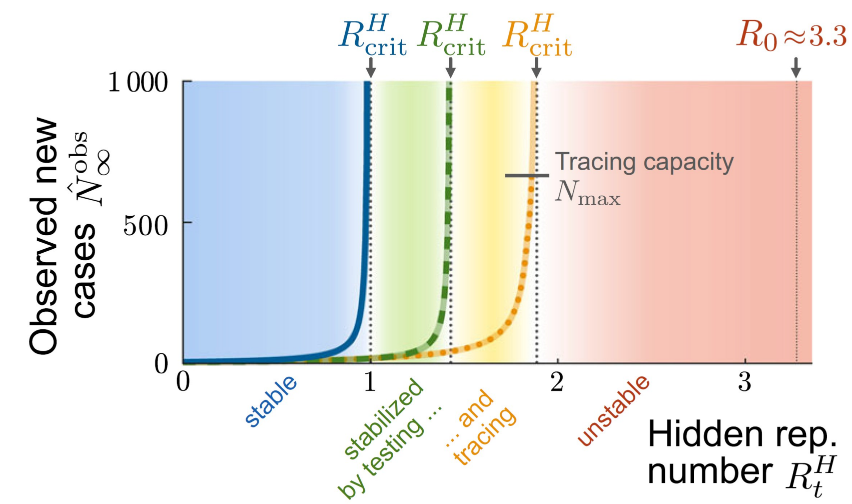
[Contreras et int., Priesemann, Nature Communications, in press]

Summary of the TTI strategy

Test-Trace-Isolate (TTI) contributes to containing COVID-19:







The undetected cases contribute most strongly to the spread

If the TTI capacity is surpassed, a tipping point is crossed, and growth self-accelerates.

TTI enables every single person to have more contacts: Instead of one, about two persons can be infected → Compensaiton by TTI.

https://arxiv.org/pdf/2011.11413 [Contreras et int., Priesemann, arxiv]
https://arxiv.org/pdf/2009.05732 [Contreras et int., Priesemann, Nature Communications, in press]

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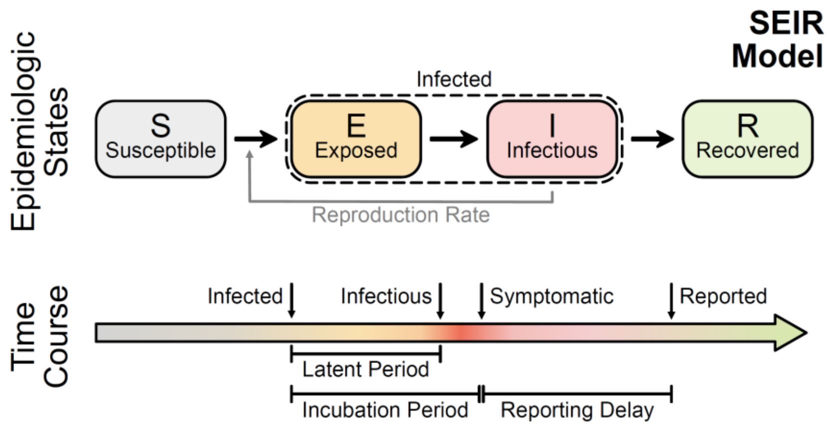

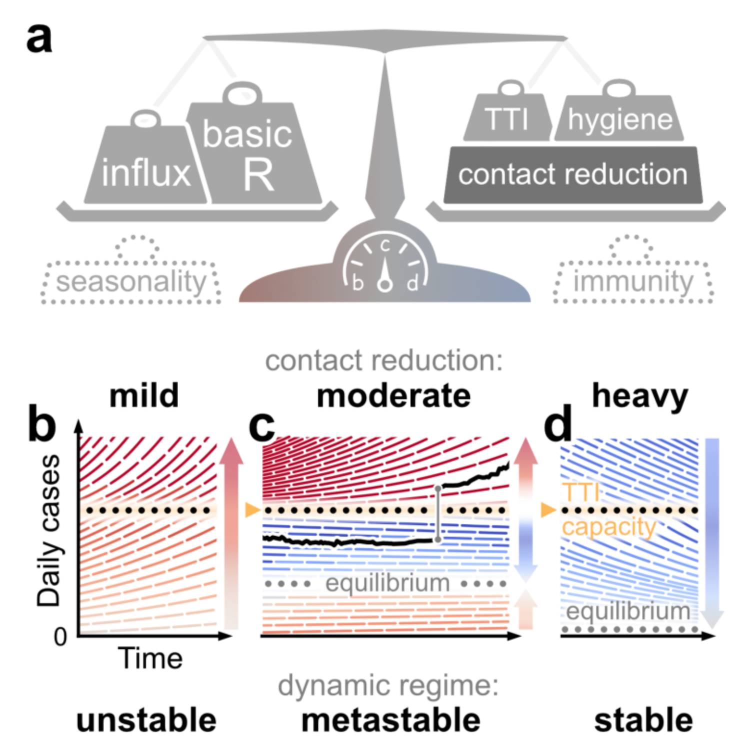

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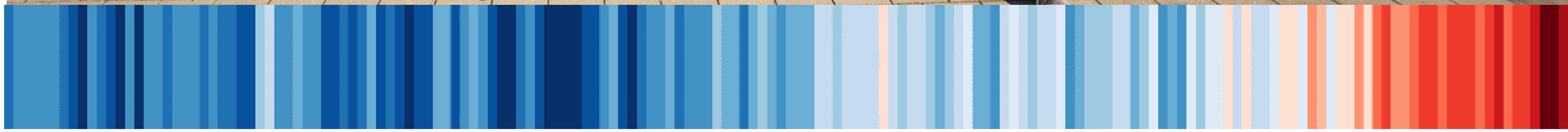

Priesemann Group

Sebastian Contreras
Jonas Dehning
David Ehrlich
Daniel Gonzalez Marx
Benedikt Grüger
Kira Herff
Emil Iftekhar
Matthias Linden
Matthias Loidolt
Fabian Mikulasch
Sebastian Mohr
Valentin Neuhaus
Lucas Rudelt
Alexander Schmidt
Andreas Schneider
Julian Schulz
Paul Spitzner
Patrick Vogt
Johannes Zierenberg
+ you?

External PhD students (co-supervised)

Benjamin Cramer (U Heidelberg)
Madhura Ketkar (ENI Göttingen)
Corentin Nelias (MPI-DS)

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Discussions on COVID within the Göttingen Campus and beyond:
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Bruno del Papa (MERK)
Bettina Royen (Max Planck School)
Mathias Sogorski (PSI, Berlin)
Jens Wilting (Bosch)

Referenzen:

[Dehning et al., Science, May 2020]
[Dehning et al., medRxiv 2020]
[Contreras et al., Nature Commun (2021) / *arXiv:2009.05732*]
[Contreras et al., *arXiv:2011.11413*]
[Alwan et al., The Lancet 2020]
[Linden et al., Dt. Aerzteblatt Int. / *arXiv:2010.05850*]
[Priesemann et al., The Lancet, 2021]
[Priesemann et al., The Lancet, in press]

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