

How preventive measures shape generation times in emerging epidemics

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Reproduction numbers

- indicators of transmission -

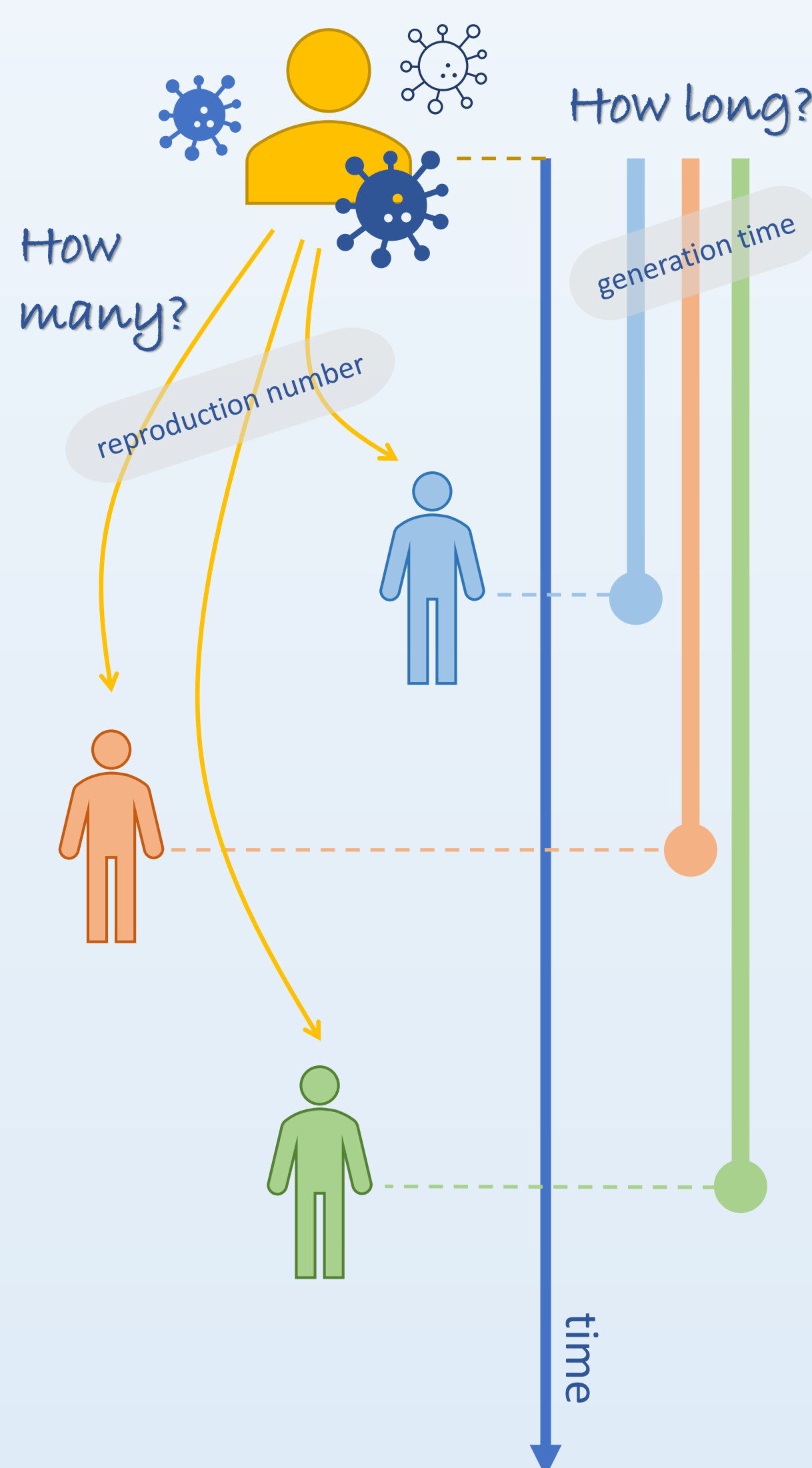
The reproduction number R is the average number of individuals infected by a typical infectious individual.

This number is related to the size of the outbreak

- if R is larger than 1: the epidemic takes off
- if R is smaller than 1: local outbreaks

Example. If $R=1.25$, transmission should be reduced by at least 20% to stop the epidemic from increasing

 Biased estimates of R may lead to improper conclusions regarding control measures



Generation times

- key for estimation -

The generation time is the time interval between the infections of the infector and the infectee.

This time is random and thus can be studied through the tools of probability theory: the **generation time distribution** describes what is the probability of generation times being of a certain length.

Why do we care about generation times?

- an old equation for today's problems -

The generation time distribution g is crucial in linking the to-be-estimated reproduction number R to the easier-to-observe growth rate r , through a century-old equation, the *Euler-Lotka equation*:

$$\int_0^{\infty} e^{-rt} g(t) dt = R^{-1}$$


A new problem

- variations of the generation time distribution -

The deployment of preventive measures, especially drastic world-wide measures such as those we all have experienced during the recent pandemic, may change the generation time distribution.

Why is this important?

Unaccounted variations of the generation time distribution can result in biased estimates of reproduction numbers (crucial for decision making!)

 **Goal:** mathematically describe if and how generation times vary in response to several preventive measures

Results

Measures that cause no variation of generation times:
(while still reducing the reproduction number!)

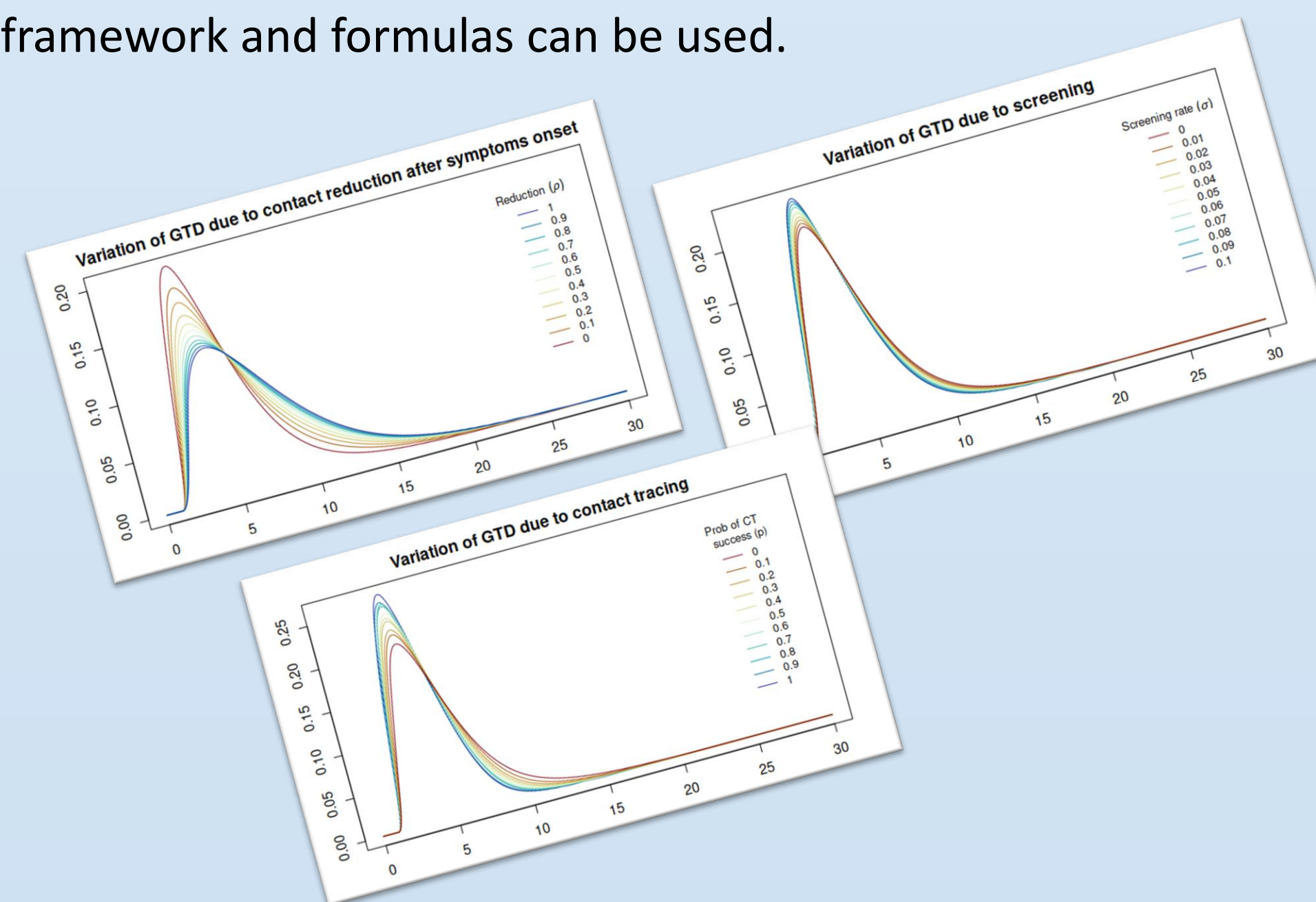
- homogeneous reduction of contact or transmission (e.g., physical distancing, lockdown, face masks)
- vaccination


Measures that affect generation times:

- isolation of symptomatic individuals
- uniform screening (moderate variation)
- contact tracing

To precisely describe the extent of the variations, depending on the specific infectious disease and environment, our mathematical framework and formulas can be used.

In particular, for Covid-19, we provide an illustration of the variations and a study of the deriving biases concerning reproduction numbers.



 Variations of the generation time distribution caused by preventive measures can indeed lead to significant biases in the estimation of reproduction numbers.

Impact

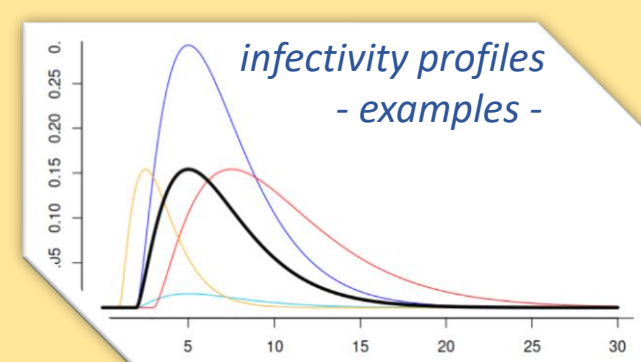
Our findings prove the importance of taking the problem of varying generation times into account when preventive measures are introduced.

The mathematical framework, because of its general nature which captures the properties of various infectious diseases, provides technical tools that can be employed by researchers in their specific analyses.

Our mathematical approach

- a stochastic process -

We define a stochastic (i.e., random) infectivity process. The key components are a stochastic infectiousness profile and contact activity.



- The process is specifically tailored to include several preventive measures.
- Very general: can be used for various infectious diseases.
- We provide formulas under some technical assumptions.

generation time distribution: $g(t) = \frac{\beta(t)}{\int_0^{\infty} \beta(u) du}$
 reproduction number: $R = \int_0^{\infty} \beta(u) du$
 infectivity function:
 $\beta(t) = E[\rho_v \rho_c \rho_x] E[C_1 X(t) G_r(t) + \rho_D C_2 X(t) (1 - G_r(t))]$
 distribution of time of contact reduction:
 $G_r(t) = \exp(-a_s \int_0^t X(u) du - (\sigma + p a_{CT2})(t \wedge 1) - p C_1 \int_0^{t-d} X(u) (1 - \gamma(t-d-u)) du)$
 $\gamma(t) = E[\exp(-a_s \int_0^t X(u) du - \sigma(t \wedge 1))]$

This poster is based on

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