A stochastic epidemic model to study the impact of non-pharmaceutical interventions on basic reproduction number and generation time distribution

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Based on ongoing work with T. Britton (Stockholm University) and G. Scalia Tomba (University of Rome Tor Vergata)

Understanding the Generation Time for COVID-19,
Newton Gateway to Mathematics, July 28, 2021

Introduction

- We present a stochastic model that is akin to Kermack-McKendrik theory [1], i.e. based on an infectivity process
- Various non-pharmaceutical interventions can be included in the model
- Goal: monitoring the generation time distribution
  - which affect the estimates of the basic and effective reproduction numbers

Note: The model is general, but we tuned it for Covid-19

[1] Kermack, McKendrick 1927. A contribution to the mathematical theory of epidemics, Proceedings of the Royal Society London Ser. A 115, 700-721

The model

- Homogeneously mixing population
- Individuals are first (equally) suceptibles, they might get infected and later removed
- Infectious individuals have independent and identically distributed infectivity profiles that are the realization of a stochastic process $\lambda(t)$[2]

$\lambda(t) = C(t)X(t)$: infectivity process

$C(t)$: contact process
$X(t)$: infectiousness process
(time is measured since infection)

[2] Svensson 2007. A note on generation times in epidemic models, Mathematical biosciences, 208, 300-311

The model

of τ, C_1, C_2, allow

Contact process:

$C = \{C(t)\}_{t \geq 0}$ with $C(t)$ C_1, if $t \leq \tau$ C_2, if $t > \tau$
=

Different definitions

modelling contacts in several scenarios, with or without non-pharmaceutical interventions

C_1: base contact rate (r.v)

C_2: reduced contact rate (r.v) τ: time of contact reduction (r.v) due to e.g. symptoms or detection

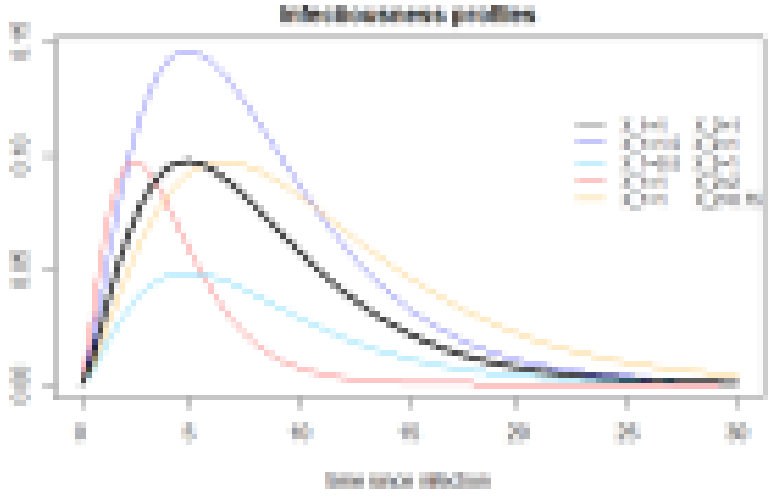
Infectiousness process:

$X = \{X(t)\}_{t \geq 0}$: probability of infection at time t (strength of infectiousness)

e.g. $X(t) = I_{[0,\tau]}(t)$ (SIR)

e.g. $X(t) = X_1 h(X_2 t)$,

h deterministic function, X_1, X_2 r.v.'s



Infectivity process: $\lambda(t) = C(t)X(t)$

Quantities of interest

Letting $G(t) = P(\tau > t \mid X, C_1, C_2) = \exp\{-\int_0^t \alpha_\tau(u)du\}$,

- $\beta(t) = E[C(t)X(t)] = E[C_1X(t)G(t) + C_2X(t)(1-G(t))]$ [infectivity function]
- $R_0 = \int_0^\infty \beta(t)dt = R^{(1)}_0 + R^{(2)}_0$ [basic reproduction number]

with $R^{(1)}_0 = E\left[C_1 \int_0^\infty X(t)(1-G(t))dt\right]$

- $g(t) = \frac{\beta(t)}{R_0}$ [generation time pdf]

and $R^{(2)}_0 = E\left[C_2 \int_0^\infty X(t)G(t)dt\right]$

Without interventions

$\tau = T_S$: time to symptoms onset

rate: $\alpha_S(t) = \xi X(t), \xi \in \mathrm{R}_{>0}$

$$\mathrm{P}^{\mathrm{i}} T_S = \infty \mid X^{\not\in} = \exp\{-\xi^{\mathrm{R}}{}_{\infty}{}_0 X(u)du\}.$$

With interventions...

Non-pharmaceutical interventions

$\rho \in [0, 1]$

Contact-reducing interventions (with $\tau = T_S$)

1. Uniform reduction of contacts (e.g. social distancing, lockdown): $C \nrightarrow \rho C$

   Bdoes not affect generation time distribution

2. Isolation of symptomatic individuals:

   $C_2 \nrightarrow \rho C_2$

Transmission-reducing interventions (with $\tau = T_S$)

3. face masks:

   $X \,, \rightarrow \rho X$

   Bmathematically equivalent to 1.

Shortening-detection-time interventions $T_S \,, \rightarrow T_D$

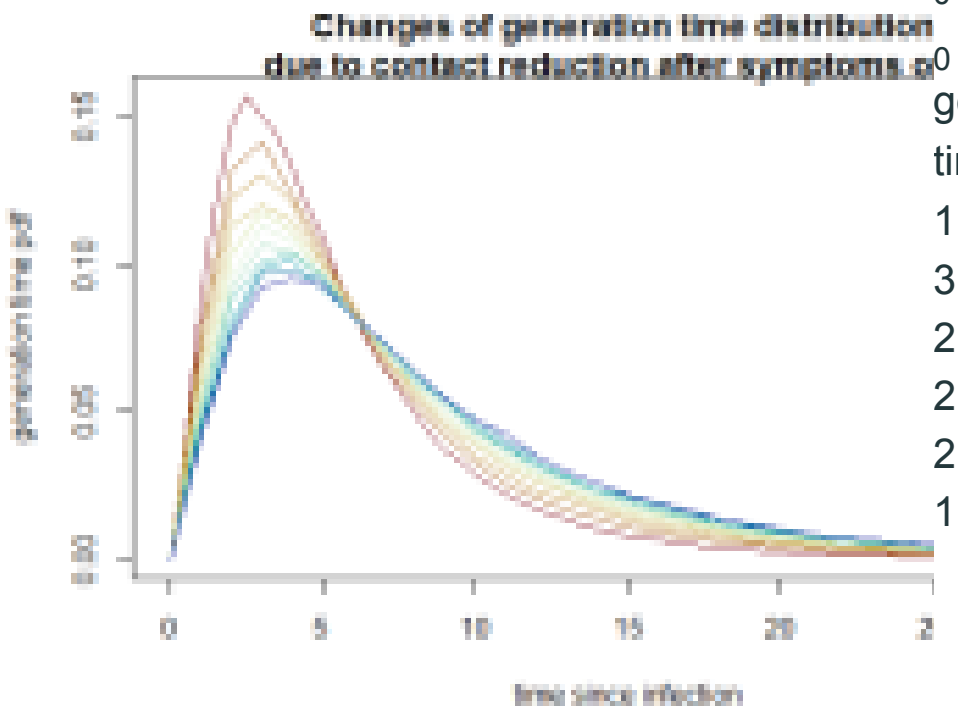
4. screening: $T_D = \min\{T_S \,, T_{scr\ e}\}$
5. contact tracing: $T_D = \min\{T_S \,, T_{CT}\}$

Isolating symptomatic individuals

$\tau = T_S$

$C_2 = \rho C_1$

$X(t) = X_1 h(t\ X_2)$



$_0R^{(2)}$

$_0$ mean gen. time

1 3.76 1.64 2.11 8.24 0.9 3.54 1.64 1.90 8.11 0.8 3.33 1.64 1.69 7.96 0.7 3.12 1.64 1.48 7.79 0.6 2.91 1.64 1.27 7.60 0.5 2.70 1.64 1.06 7.38 0.4 2.49 1.64 0.84 7.12 0.3 2.39 1.64 0.63 6.81 0.2 2.07 1.64 0.42 6.44 0.1 1.85 1.64 0.21 5.98 0 1.64 1.64 0 5.41

Asymptomatic cases: about 1/3

ρ R_0 $R^{(1)}$

Screening (+ isolating symptomatic individuals)

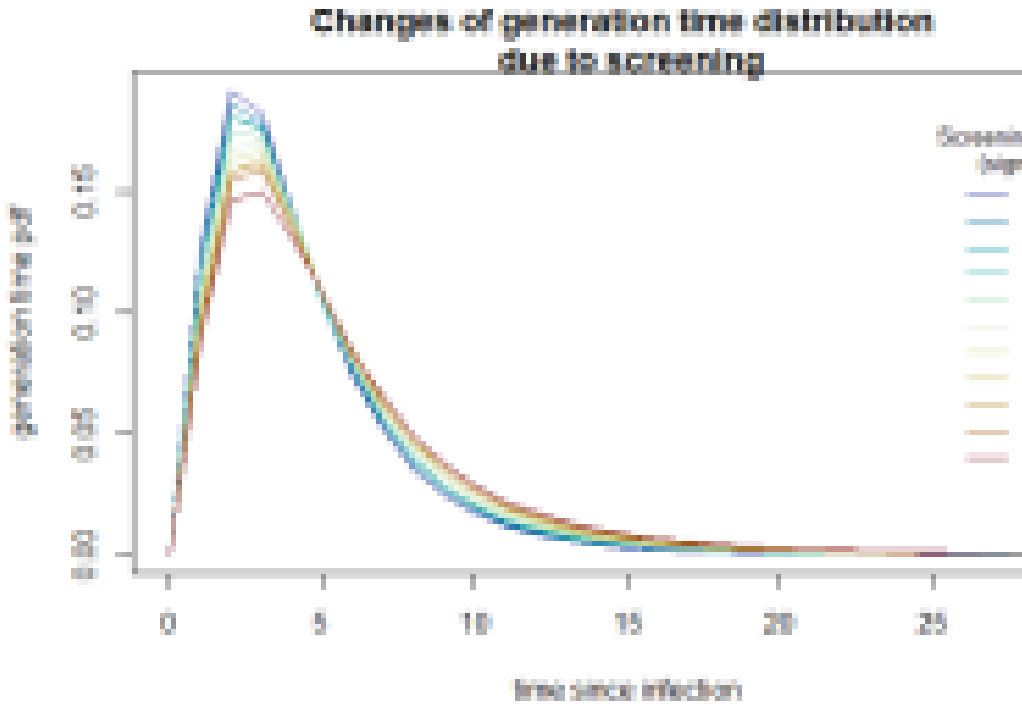
$\tau = \min\{T_S, T_{scr\,e}\}$

Constant rate of being screened: $\alpha_{scr\,e}(t) = \sigma \in R_{>0}$

$\alpha_T(t) = \alpha_S(t) + \alpha_{scr\,e}(t) = \xi X(t) + \sigma$

σ R_0 mean

$\rho = 0$



gen.
time
0 1.64 5.41 0.01 1.56 5.26 0.02 1.48 5.09 0.03 1.41 4.95 0.04 1.34 4.82 0.05 1.28 4.70 0.06 1.22 4.58 0.07 1.17 4.48 0.08 1.16 4.37 0.09 1.07 4.29 0.1 1.03 4.18

Ongoing work: contact tracing

$\tau = \min\{T_S, T_{scre}, T_{CT}\}$

$\alpha_\tau(t) = \alpha_S(t) + \alpha_{scre}(t) + \alpha_{CT}(t)$

$\alpha_{CT}(t) = \alpha_{CT1}(t) + \alpha_{CT2}(t)$

- α_{CT1}: rate at which an individual is detected through people they have infected
- α_{CT2}: rate at which an individual is detected through the person who has infected them

Heuristically, $\alpha_{CT1}(t) = \int_0^t C_{1X(u)} \bar{f}_\tau(t-u)du$, $\alpha_{CT2}(t) = \int_0^t \bar{f}_{i(u)} \bar{f}^*_\tau(t+u \mid u)du$, where

- $\bar{f}_\tau$: pdf of τ for a general infectious individual

- $f^*_\tau(\cdot \mid u)$: pdf of τ for a general infector who infects at time u since their infection

- f_i: pdf of infector's age

⇒ integro-differential equation for α_τ

Conclusions

Non-pharmaceutical interventions can significantly shorten generation times

Using estimates of the generation time distribution from the early phases of the Covid-19 pandemic leads to biased estimates of reproduction numbers.

There is a need to either collect data for up-to-date estimates of the

generation time distribution, or to account for biases through models that include interventions

References

Britton, Favero, Scalia Tomba 2021+. A stochastic epidemic model to study the impact of non-pharmaceutical interventions on basic reproduction number and generation time distribution, *In preparation*

Kermack, McKendrick 1927. A contribution to the mathematical theory of epidemics, *Proceedings of the*

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Thank you!

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