

# How ubiquitous are the reproduction numbers for epidemics processes?

Suani T.R. Pinho<sup>(a,b)</sup>, Daniel C.P. Jorge<sup>(a,c,d)</sup>, Robert G.S. de Araújo<sup>(a)</sup>, Filipe C. Ribeiro<sup>(a)</sup>, Caio S. Rauh<sup>(a)</sup>, Arícia F. Pérée<sup>(a)</sup>, Juliane F. Oliveira<sup>(e)</sup>, José G.V. Miranda<sup>(a)</sup>, Roberto F.S. Andrade<sup>(a,b,e)</sup>

<sup>(a)</sup> *Universidade Federal da Bahia, Salvador, Brazil*

<sup>(b)</sup> *National Institute of Science and Technology for Complex Systems, Rio de Janeiro, Brazil*

<sup>(c)</sup> *Instituto de Física Teórica, Universidade Estadual Paulista, São Paulo, Brazil*

<sup>(d)</sup> *Princeton University, Princeton, United States of America*

<sup>(e)</sup> *Center for Data and Knowledge Integration for Health (CIDACS), Fiocruz, Salvador, Brazil*

The idea of measuring the growth of an epidemic process through a well-defined concept is behind the reproduction number. Although it was firstly proposed in 1950's, only in 1990's, the meaning of the (basic) reproduction number,  $R_0$ , as the expected number of people infected by an infectious person in a naive population, was formalized using the next generation method (NGM). The concept of  $R_0$  was generalized to the effective time-dependent reproduction number,  $R(t)$ , for which the population is not naive anymore due to different factors. In general,  $R(t)$  is estimated following the modelling point of view or the epidemics data; our approach considers both model and data, and generalizes the NGM [Jorge et al, RSOS 9 (2022) 220005]. In this talk we present the main steps of the generalized method as well as some applications, such as a metapopulation model of COVID-19, a dengue model with entomological parameters varying with temperature, COVID-19 and dengue models with vaccine.