

# Unravelling Age-Specific Transmission Dynamics of COVID-19 through a Formal Sensitivity Analysis

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## Abstract

The stability analysis of the linearization of a system of ordinary differential equations around its equilibrium points traditionally traces back to examining the sign of the spectral bound of the associated Jacobi matrix. However, when analysing infectious disease spread through compartmental models, an alternative approach is employed. This approach scrutinises the spectral radius modulus of the next-generation matrix (NGM)[1], derived via an appropriate decomposition of the Jacobi matrix. The NGM embodies the generational contribution to new infections from distinct categories of infected individuals. Essentially, it is the product of the contact matrix (representing the interactions each category has with the rest of the population) and two vectors. These vectors capture the epidemiological characteristics of the potential receiver and transmitter of the infection, modelling the per-contact probability of contagion, [2]. Moreover, the spectral radius of the NGM characterizes the transmission potential (or basic reproduction number) and guides the stability of the disease-free equilibrium in the host population. This methodology, versatile across compartmental models of any size, allows for analysing the varied contributions from different population categories to the transmission potential. This is achieved through a formal perturbation or sensitivity analysis of the NGM entries [3]. The presented study [4] employs this approach to an age-structured Susceptible, Exposed, Infectious, and Recovered model [5] to examine COVID-19 dynamics in Belgium. We introduce indices to gauge the distinct impacts of different age cohorts on disease spread and uncover epidemiological information from the matrix's eigenstructure. Our findings substantiate the hypothesis that from April to July 2020, COVID-19 transmission was only marginally influenced by children aged 0-18 years and adults older than 60 years.

## Keywords

Next generation matrix, Linear stability analysis, Sensitivity, Infectious disease modelling, Basic reproduction number.

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