Modeling the spatiotemporal epidemic spreading of multiple virus strains

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The mathematical modeling of epidemic diseases allows us to investigate the role of fundamental aspects in the spreading of infectious diseases. Compartimental models have been used with great success to describe different diseases and their aspects [1]. Network science has contributed with its convenient framework to represent the complex interactions of individuals and populations. The recent availability of large datasets, such as about human mobility and social behavior, has improved the accuracy of predictions achieved with epidemic modeling. In particular, the data-driven approach has been adopted by building analytically tractable models, but at the same time use explicit real data [2]. For example, origin-destination (OD) matrices are obtained by capturing the daily mobility of the population at different levels, from global with the airport networks, to the local scale, measuring the urban rhythms inside a country, state, or municipality. The mobility of spatially separated subpopulations can be represented by metapopulations, in which subpopulations are placed in different patches as nodes of a directed network whose interactions or edges quantify the flow of individuals from a patch i to j by an OD matrix W_{ij}. These approaches were successful in the context of COVID-19 such as in measuring the effects of non-pharmaceutical intervetions [3] and the outbreak diversity across different geographical scales [4].

In this work, we investigate a metapopulation modeling for the spread of multiple strains of the same virus, such as the SARS-CoV-2 variants. We assume that the population is distributed in Ω patches, each patch i containing a subset of n_i individuals, while the flow of individuals is governed by a normalized OD matrix $R_{ij} = W_{ij}/\sum_l W_{il}$ in a movement-interaction-return (MIR) model [2]. We assume a susceptible-exposed-infected-recovered compartmental dynamics in which individuals can be susceptible and infected by different strains, one at a time. The number of individuals in a given compartment $Z = \{S, E, I, R\}$, patch i, susceptible state ν and last infection state σ is represented by $Z_i^{\nu,\sigma}$. For three different strains, for example, we can define $\sigma = \{\sigma_1, \sigma_2, \sigma_3\}$ and $\nu = (\nu_1, \nu_2, \nu_3)$ in which $\nu_i = 1$ when the individual is not immune for the variant σ_i, and 0 otherwise, $i \in [1, 3]$. The model and rates are schematically shown in Fig. 1(a). Dynamical equations are written using a Microscopic Markov Chain Approach (MMCA) approach [2, 3]. We find multiple waves of infection governed by the existence of different variants, shown in Fig. 1(b,top) for three patches, and measure the impact of seeding a new variant in

different patches of the networks, measured by the number of exposed and infected individuals by each strain in each patch, Fig. 1(b,bottom). We compare the results with real data of the prevalence of each variant in the largest municipality of Brazil, Sao Paulo, for 10 months of 2021, sampled in different districts of the city with geo-referenced data. The empirical results are shown in Fig. 1(c), showing the replacement of one variant to another as in the simulated results. The perspective of this work is to calibrate the model together with a real OD network within the municipality via mobile geolocation data [5] and time-evolving rates as a function of vaccination.

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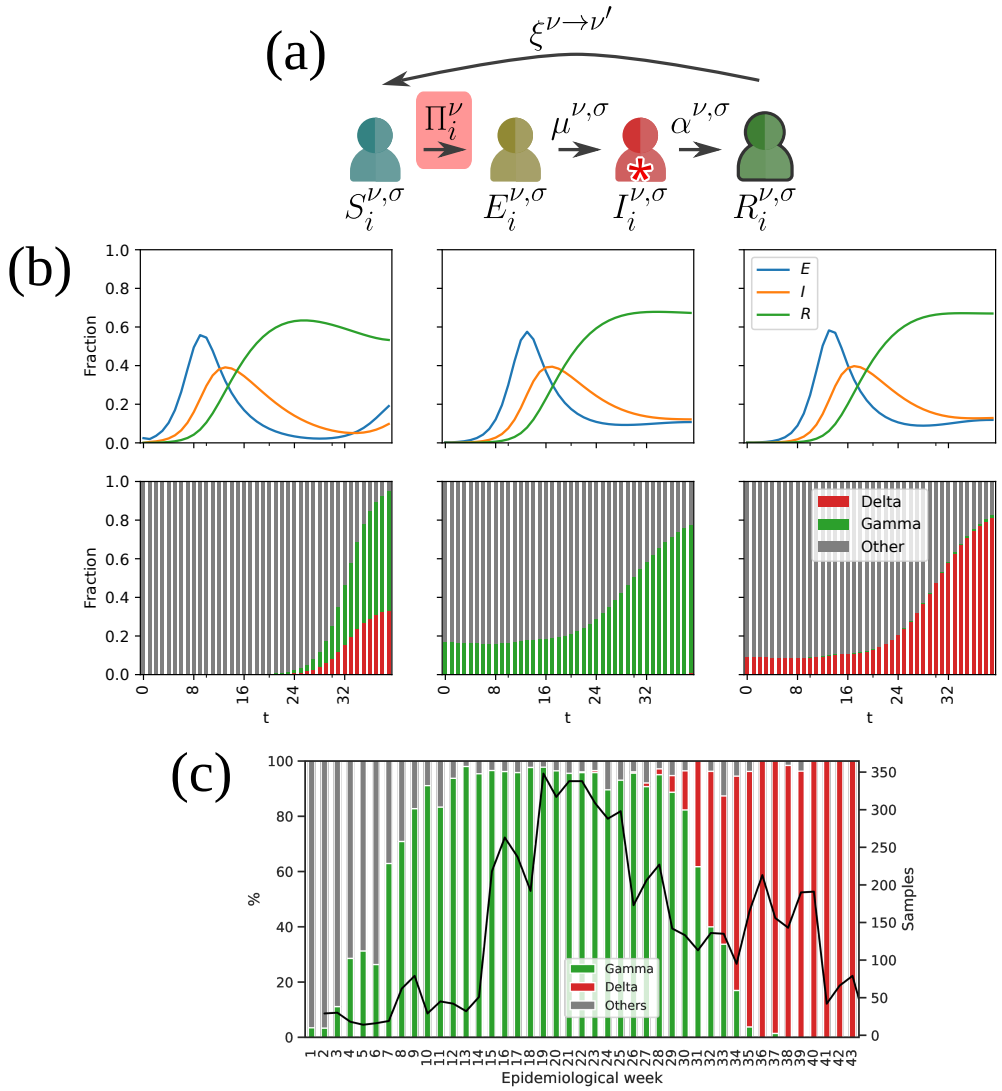

Figure 1: (a) Schematic representation of the model, its compartments and transition rates. Susceptible individuals are infected by a probability Π_i^ν, becoming an exposed individual $E_i^{\nu,\sigma'}$ with probability $\Pi_i^{\sigma'}$, that takes into account all infectious individuals with the strain σ' and the susceptibility ν currently in a patch i (residents or visitors), while recovered individuals become again susceptible to a new strain with probability $\xi^{\nu\to\nu'}$ spontaneously. (b) Multiple waves of infection (top) and prevalence of the variants in exposed and infected individuals (bottom) for three patches of a random geometric network with $\Omega = 50$ patches with subpopulations of size n_i given uniformly from 100 to 1000, and out-going flow $\sum_j R_{ij}$ sampled uniformly from 0.1 to 0.4. (d) Real data of the prevalence of distinct strains of SARS-CoV-2 in the municipality of Sao Paulo, Brazil.

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