


Epidemic proximity and imitation dynamics drive infodemic waves during the COVID-19 pandemicValeria d' Andrea ^{1,*}, Oriol Artime,¹ Nicola Castaldo,¹ Pierluigi Sacco,^{2,3,4} Riccardo Gallotti,¹ and Manlio De Domenico^{1,5,†}¹*CoMuNe Lab, Fondazione Bruno Kessler, Via Sommarive 18, 38123 Povo (TN), Italy*²*DiSFiPEQ, University of Chieti-Pescara, Viale Pindaro 42, 65127 Pescara, Italy*³*metaLAB (at) Harvard, 42 Kirkland St, Cambridge, Massachusetts 02138, USA*⁴*Fondazione Bruno Kessler, Via Santa Croce, 77, 38122 Trento, Italy*⁵*Department of Physics and Astronomy, G. Galilei, University of Padua, Via Francesco Marzolo 8, 35131, Padua, Italy*

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An infodemic—an outpouring of information, including misleading and also fake news—is accompanying the current pandemic caused by SARS-CoV-2. In the absence of valid therapeutic approaches, behavioral responses may seriously affect the social dynamics of contagion, so the infodemic may cause confusion and disorientation in the public, leading to possible individually and socially harmful choices. This new phenomenon requires specific modeling efforts to better understand the complex intertwining of the epidemic and infodemic components of a pandemic crisis, with a view to building an integrative public health approach. We propose three models, from epidemiology to game theory, as potential candidates for the onset of the infodemics and statistically assess their accuracy in reproducing real infodemic waves observed in a data set of 390 million tweets collected worldwide. Our results show that evolutionary game-theory models are the most suitable ones to reproduce the observed infodemic modulations around the onset of the local epidemic wave. Furthermore, we find that the number of confirmed COVID-19 reported cases in each country and worldwide are driving the modeling dynamics with opposite effects.

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In the past two decades, the periodic appearance of highly infectious, severe respiratory syndromes with pandemic potential caused by viral agents of the coronavirus family (SARS-CoV-1 in 2003, MERS-CoV in 2012), for which no reliable therapeutic approach was available at the time, has brought the issue of the social containment of epidemics to the attention of both decision makers and the general public. As a response to the previous crises, several mathematical models have been developed to make reliable predictions on the time evolution of an epidemic and at shedding light on key aspects of its drift and shift dynamics [1] as a basis for the design and evaluation of appropriate management and mitigation strategies [2–4].

These developments have proven their importance in the extreme case of the pandemic diffusion of the new virus SARS-CoV-2, that is causing a previously unknown severe acute respiratory syndrome [5], which between early January 2020 and August 2021 has led to a global figure of 216 900 000 confirmed cases and more than 5 500 000 deaths

[6]. In the absence of pharmaceutical treatments such as drugs and vaccines, nonpharmaceutical interventions have been evaluated to control the contagion spreading. Mathematical models allow for nowcasting epidemic dynamics (see Ref. [7] and references therein) and to better understand the role of human behavior to flatten the curve and prepare to face potential future epidemic waves [8,9].

However, one of the most important differences between the current COVID-19 pandemic crisis and SARS-CoV-1 or MERS-CoV is the huge evolution of digital media, driven by the rapid growth and diffusion of social media platforms. The management of a pandemic crisis has to cope with the complexity of the current informational ecosystem [10,11] that tightly interacts and co-evolves with the epidemic one. According to a report of the World Health Organization published in early February 2020 [12], the SARS-CoV-2 epidemic outbreak and response has been accompanied by a phenomenal outpouring of information of all kinds from a multiplicity of sources with various degrees of reliability. This massive phenomenon is named infodemic and is characterized not just by the possibility of spreading misleading or false information, denoted as misinformation or disinformation, but by the very fact that the volume of available information puts both the general public and decision makers under considerable stress, possibly leading to wrong decisions and harmful choices. Infodemics proved to be a potential treat for public health strategies almost two decades ago [13,14], but only more recently started to pose a large-scale public health issue [15,16] and only recently studied in more detail [17,18].

*Corresponding author: vdandrea@fbk.eu†Corresponding author: manlio.dedomenico@unipd.it

Originally defined as an epidemic of misinformation, an infodemic is different from an epidemic in several aspects. Information travels way faster and through very different channels than pathogens, and the resulting informational flows cause emergent phenomena, often as an unintended consequence of human behavioral reactions and cognitive biases. Whereas the spreading of pathogens is an essentially local process that needs a sequence of local contacts to travel to distant geographic areas (mis- and dis-)information can travel anywhere almost instantly, without necessarily relying upon a chain of physical contacts. It is also worth noting that digital media have experimented a rapid evolution recently and that the understanding of how and why misleading information spreads is currently being investigated by the scientific community [19,20]. Furthermore, social media can actively promote dissemination of misleading though sensational news with the aim of making profits [21]. This makes infodemics nonlocal dynamical processes which are more difficult to monitor and control than epidemic outbreaks.

Nevertheless, infodemics and epidemics are inevitably entangled processes. Whereas several studies analyze the spreading of diseases, keeping into account human information processing of the observed levels of contagion and the ensuing behavioral responses [22,23] or human mobility patterns (see Refs. [24–26] and references therein), efforts to mathematically model human behavioral responses to epidemic-related risk perception and awareness have been less frequent [27,28].

The literature provides evidence that—under conditions of information deluge such as those related to the current COVID-19 pandemic—collective attention in sociotechnical systems can be driven by a mechanism of preferential attention toward specific information spreaders [29]. On the other hand, there is increasing evidence that the global interconnectivity and ease of communication enabled by the current global information ecosystem allows for an unprecedented flow of digital data which, at variance with a few years ago, facilitates the massive diffusion of misinformation [21,30], as well as online social manipulation by means of smart deployment of automated bots [31,32]. Moreover, it must also be considered that in the case of COVID-19, there are additional factors that might yield factual misperceptions for people, such as, during the early days of the pandemic, the lack of completely reliable medical information about a new disease, the quest for new pharmaceutical treatments, and the decision makers that are informed by models based on incomplete and uncertain information. These factors certainly pose serious challenges to policy-making for mitigation strategies [33,34].

In this paper, we study the impact of external time-varying processes, such as the epidemic one, on misinformation dynamics. This paper should be regarded as a step toward understanding the mechanisms that drive infodemic dynamics, which is here considered as a dimension that, together with epidemics, shape part of the complex phenomenon of a pandemic.

We focus on a specific time interval, that is, the period around the onset of the local epidemic outbreak when, we hypothesize, external dynamics could be most effective. We compare three models to assess their capacity to reproduce

the empirical infodemic modulation around the inception of a local epidemic.

We first consider as a benchmark a compartmental model, inspired by epidemic processes, which is widely adopted to reproduce the spreading of misinformation and which does not depend on exogenous dynamics. We subsequently move to evolutionary game theoretic models driven by imitation where exogenous epidemics dynamics affect infodemic by modulating an individual's perceived epidemic risk and related perceived benefit of spreading misinformation.

According to our findings, in the days around the onset of the local epidemic outbreak, misinformation diffusion is not properly reproduced by a simple epidemic-inspired model. We find that the best fit is provided by the evolutionary models as a function of epidemic risk awareness, where the latter depends on the geographical proximity to the infection outbreaks.

II. MATERIALS AND METHODS

A. Data overview

To track and then model the amount of misinformation associated to the COVID-19 pandemic circulating in different countries, we use a large database of tweets collected in the Covid19 Infodemics Observatory, described in detail in Ref. [17] and accessible at [35]. Starting from late January 2020, we automatically collected, for 249 countries from the Twitter Filter API, messages containing terms associated with the COVID-19 pandemic from a medical perspective (namely, coronavirus, ncov, Wuhan, covid19, covid-19, sarscov2, covid). These terms have an estimated recall of 40% of all tweets associated with the coronavirus in the period considered, as discussed in Ref. [17] together with a broad discussion of the biases inherent with social data gathering. Other keywords emerged in time to describe other subjects related to online discourse around the social or economical consequences of the pandemic (e.g., stay at home, wear a mask, lockdown...). Topics evolve in time and tracking them progressively might introduce biases similar, or even stronger, than those inherent with a limited keyword selection. All biases associated with the data collection are discussed in detail in the Method section of Ref. [17].

The Twitter Filter API has provided us the totality of tweets associated with these words up until February 25, 2020, when the fraction of tweets included in our filter passed 1% of the total, hitting the limit set by Twitter for basic accounts. The total amount of collected tweets up to August 10, 2020 is more than 390 000 000. To associate tweets with countries, we use both information about the user location and information about the tweet's language included in the information provided by the Twitter API. The user's country has been inferred using the precise coordinates when available for less than 1% of users or, alternatively, the textual user's auto-declared location field that has been successfully used for geocoding with the ArcGIS API for about 50% of users. To ensure that the data were correctly matched, we further selected only messages written in one of the official local languages of the identified country as listed in Ref. [36]. To evaluate the amount of unreliable news circulating every day in each country, we first selected all tweets associated with that country

containing a URL, and then checked whether the associated web domain found a match with a database we created by integrating multiple publicly available databases of manually checked web domains (see Ref. [17] for more details). This database allowed us to classify news in one of seven categories: science, mainstream media, satire, clickbait, political, fake/hoax, and conspiracy/junk science, plus two types of unclassified news (unknown, when not in the database, or shadow, when the link is compressed by nonvanity URL shorteners). News belonging to science and mainstream media have been considered as reliable, whereas news categorized as satire, clickbait, political, fake/hoax, or conspiracy/junk science have been considered unreliable. We remark that it need not be the case that a piece of news belonging to an unreliable domain is necessarily fake; however, it has a higher likelihood of carrying, in the best case, biased content that has to be read and reshared with particular caution.

In our analysis, we aim to model, at a national scale, the infodemic dynamics at the beginning of the local COVID-19 epidemic outbreak. Therefore, we focus upon a time period of 25 days around the onset of the local epidemic. In particular, we set the beginning of local COVID-19 epidemics, in each country, as the date (day_0) at which the first infected individual was detected. Then we select a time window of ($day_0 - 15, day_0 + 10$) days to perform our analysis. We select a subsample of the 249 countries by considering countries with non-null epidemic data and an average unreliable tweet rate in local language greater than 30 tweets/day in the selected 25-days time window. After the application of this filter, we finally obtain a subset of 37 countries, with a total of more than 3 800 000 tweets, on which we carry out our analysis. We aggregate tweets in daily intervals indicated by t , from which we evaluate $n_U(t) = N_U(t)/N(t)$ as the fraction of unreliable tweets with respect to the total (unreliable and reliable) messages, $N(t)$. Likewise, we evaluate the fraction of reliable messages as $n_R(t) = N_R(t)/N(t)$.

Regarding the epidemic data, daily epidemic data were collected from the Our World in Data project by the University of Oxford [6]. In our analysis, we use both the epidemic data reported for a specific country $n_I(t)$ and the global number of confirmed cases, $n_I^W(t)$, that was computed as the sum of daily epidemic curves collected across 249 countries.

Both the epidemic and infodemic data have known limitations. Official epidemic data, such as those collected and aggregated by Our World in Data [6], are often reported with a systematic delay with respect to the date of collection and testing of the samples [37]. Also, the use of automatically collected user-generated content for the study of social phenomena presents a number of known limitations and biases [38]. In our case, the most prominent is a demographic bias toward well-educated males (characteristic of Twitter users), exacerbated by a further bias toward English-speaking users as a consequence of the terms used to filter COVID-19-related messages and of the databases used to evaluate news reliability (see Materials and Methods for further details). Moreover, other demographic attributes such as race, socioeconomic status, and Internet literacy correlate with how likely people use a social platform [38]. Despite these limitations, the time series used here successfully capture, for a specific country, the time evolution of the amount of COVID-19 cases and

misinformation contained in tweets [17], and can be used to study the dynamic coupling between these two phenomena.

B. Infodemic models

To model infodemic waves, we focus our attention on models inspired by both epidemiology and evolutionary biology that are widely used in literature to capture different types of social dynamics in well-mixed populations, as driven by the underlying incentive system. Evolutionary game-theoretic models are able to take into account how individual strategies change and are driven by simple behavioral mechanisms. Here, we assume that, for each individual, the action of sharing (or not) a news item, which is a possible source of misinformation, reflects a decision-making process influenced by the epidemic risk perception of the individual. Local and global epidemic waves are considered as drivers of the ongoing infodemic process, in that they generate the payoff structure associated to different strategies and therefore the underlying incentive system. Since we are primarily interested in the analysis of the infodemic dynamics, we do not model explicitly the epidemic one and, instead, use the epidemic data as exogenous drivers.

We consider three models for modeling the diffusion of the infodemic. First, we consider an epidemics-inspired model, considering a classical susceptible-infected-susceptible (SIS) model [25], which has been widely applied to capture the simple dynamics of adoption in sociotechnical systems and, in particular, to model the spreading of misinformation [39]. Here, individuals either belong to the class of ignorants/stiflers (people who do not spread a piece of misinformation) or to the class of spreaders (people who share messages with unreliable content), and their role is exactly the same as the susceptible versus infected agents of the SIS model. It is worth noting that here we assume a two-compartments model and that people who are sharing reliable news belong to the same class, without fine-grained distinctions between ignorants and stiflers. We assume that the fraction of unreliable messages at time t equals the fraction of spreaders and, according to epidemiclike models, the transition between the two classes is a function of the spreading rate r_{RU} and of the awareness rate r_{UR} . Such rates are estimated for each country with an optimization algorithm (see Optimization algorithm section). Then, the dynamical evolution at a single-day time step of the fraction of unreliable news is given by the differential equation,

$$\frac{dn_U(t)}{dt} = -r_{UR} \cdot n_U(t) + r_{RU} \cdot n_U(t) \cdot n_R(t), \quad (1)$$

where, for each day t it holds:

$$n_R(t) + n_U(t) = 1. \quad (2)$$

We solve the equation using a first-order numerical procedure.

The second model we consider as a candidate to describe the interplay between infodemics and epidemics comes from evolutionary game theory, the so-called double infection (DI) model [40,41]. Here, individual behavior plays an important role in the process of misinformation spreading. We assume that an individual can adopt two different strategies: share unreliable tweets (strategy \mathcal{U}) or share reliable ones (strategy

\mathcal{R}). The fraction of reliable versus unreliable news at time t equals, respectively, the fraction of individuals that adopt strategy \mathcal{R} and \mathcal{U} . The strategy-specific transmission rates are proportional to the perceived payoff that derives from strategy switching, as is typical of evolutionary models. In particular, we assume that the payoff of switching $\mathcal{R} \rightarrow \mathcal{U}$ is proportional to the worldwide epidemic level $n_I^W(t)$, whereas the payoff of switching $\mathcal{U} \rightarrow \mathcal{R}$ is proportional to the local epidemic level $n_I(t)$. The time evolution of the fraction of unreliable news is then given by

$$\frac{dn_U(t)}{dt} = -k_{UR}(t) \cdot n_U(t) \cdot n_R(t) + k_{RU}(t) \cdot n_U(t) \cdot n_R(t), \quad (3)$$

where $n_R(t) + n_U(t) = 1$, $k_{RU}(t) = r_{RU} \cdot n_I^W(t)$ is the payoff from the switching $\mathcal{R} \rightarrow \mathcal{U}$, whereas $k_{UR}(t) = r_{UR} \cdot n_I(t)$ is the payoff from the switching $\mathcal{U} \rightarrow \mathcal{R}$. $n_I^W(t)$ and $n_I(t)$ are, respectively, the global and local epidemic levels. Hence, Eq. (3) reduces to

$$\frac{dn_U(t)}{dt} = n_U(t)[1 - n_U(t)][k_{RU}(t) - k_{UR}(t)]. \quad (4)$$

It is worth noting that the last expression is the standard replicator equation used in evolutionary game dynamics to model evolution and Darwinian selection of population phenotypes, which has been extensively applied in several disciplines [42–44]. The replicator equation allows us to simply capture the trade-off between two processes operating simultaneously, that is, the imitation dynamics and the optimization of the perceived benefit.

The third model we test to capture the observed infodemic waves is again based on evolutionary game theory, but now also taking into account bounded rationality (BR) effects, which have been extensively studied in decision theory from different points of view [45–47]. An underlying assumption in the DI model is that individuals are perfect rational optimizers, whereas the BR model includes a stochastic component in the decision to share reliable or unreliable news. In this context, a BR model accounts for differences in individual attitudes that can be mapped to a heterogeneous risk perception.

Here, we model BR in terms of the deviation from a purely rational decision behavior by means of a Fermi function $P(c, z) = (1 + e^{-cz})^{-1}$, where $P(c, z)$ is the probability of event z , and c indicates how strongly an individual is responsive to the payoff difference. The time evolution of the fraction of unreliable news is then given by

$$\frac{dn_U(t)}{dt} = n_U(t)[1 - n_U(t)]\{P[c, k_{RU}(t)] - P[c, k_{UR}(t)]\}, \quad (5)$$

The effect of BR is to smooth the response function. Thus, the higher the parameter c , the smoother the response. Like all the other parameters of our models, c is estimated separately for each country.

C. Optimization algorithm

The set of model parameters θ are estimated, for each country and for each model, by finding the minimum of the

root mean square error (RMSE) function

$$\text{RMSE} = \sqrt{\frac{1}{n} \text{RSS}} = \sqrt{\frac{1}{n} \sum_{t=1}^n [O_t - E_t(\theta)]^2}, \quad (6)$$

where O_t is the observed data (n_U , fraction of unreliable news) at time t , $E_t(\theta)$ is the expected value at time t (depending on the model parametrized by θ), n is the number of observations, and RSS is the residual sum of squares:

$$\text{RSS} = \sum_{t=1}^n [O_t - E_t(\theta)]^2. \quad (7)$$

To find the global minima, we use a differential evolution algorithm [48]. For the DI and SIS models, we estimate three parameters, namely, n_{U_0} , which is the amount of unreliable news at $t = 0$, the spreading rate r_{RU} , the awareness rate r_{UR} . For the BR model, we also estimate c as an additional model parameter.

D. Model selection

To evaluate the relative prediction performances of the three models, we compute a normalized RMSE, ϵ , defined as the ratio between the RMSE and the standard deviation of infodemic data:

$$\epsilon = \frac{\text{RMSE}}{\sigma_{\text{data}}}. \quad (8)$$

In fact, if ϵ is equal or smaller than one (or, in other words, if $\text{RMSE} \leq \sigma_{\text{data}}$), the prediction at time t is within the data statistical uncertainty σ_{data} .

A popular method to compare multiple models is the Akaike information criterion (AIC) [49,50]. AIC measures the Kullback-Leibler discrepancy between the model that generates data and the tested model and can be interpreted as the probability that a tested model is the best candidate given the data. It is possible to compute AIC using the estimated residuals if they are independent and normally distributed. To test the applicability of AIC to linear regression models, we plot the residual distributions for SIS, DI and BR models. Figure 1 shows the theoretical normal quantiles against the actual quantiles of residuals. Even though the SIS residuals show a more skewed distribution, for all models we obtain distributions that follow the normal theoretical ones.

We compute the raw corrected AIC that has to be preferred to raw AIC when the sample size is small (i.e., the value of the ratio n/p is less than 40) [50,51],

$$\text{AIC} = n \log_{10} \left(\frac{\text{RSS}}{n} \right) + 2p \left(\frac{n}{n-p-1} \right), \quad (9)$$

where p is the number of parameters. Then, for each country, we evaluate the best model with AIC, by computing weights in the following way:

(1) For each model i , we compute the differences between the raw corrected AIC and the AIC of the best model, $\Delta_i(\text{AIC}) = \text{AIC}_i - \min(\text{AIC})$.

(2) Then we estimate the relative likelihood of a model as

$$L_i = \exp \left[-\frac{\Delta_i(\text{AIC})}{2} \right]. \quad (10)$$

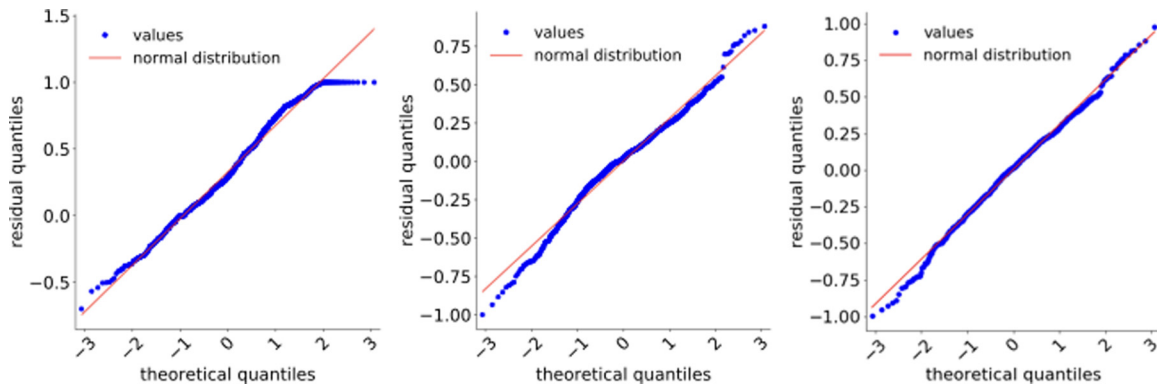


FIG. 1. Quantiles of the normal distribution against the quantiles of residuals for SIS (left panel), double imitation (middle), and bounded rationality (right) models.

(3) Finally, we normalize the relative likelihood and we obtain the Akaike weights:

$$w_i(\text{AIC}) = \frac{\exp\left[-\frac{\Delta_i(\text{AIC})}{2}\right]}{\sum_{k=1}^K \exp\left[-\frac{\Delta_k(\text{AIC})}{2}\right]} \quad (11)$$

We also compute the overall AIC for the three models, where

$$\text{Overall - AIC} = \sum_{j=1}^N \left[n \log_{10} \left((\text{RMSE}_j)^2 \right) \right] + 2pN \left(\frac{nN}{nN - pN - N} \right) \quad (12)$$

and N is the number of considered data sets (countries).

III. RESULTS

A. Modeling infodemic waves

We numerically integrate the dynamical Eqs. (1), (3), and (5), with a single-day time step and report the results in Fig. 2,

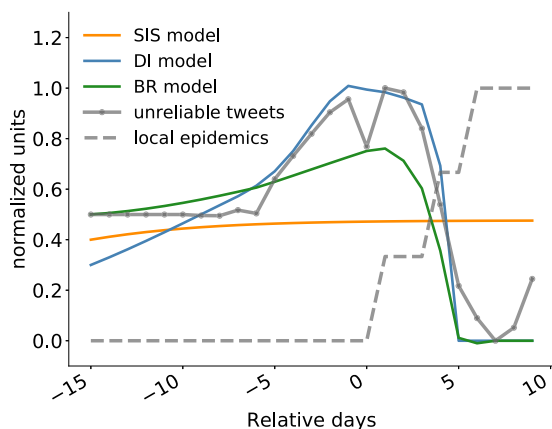


FIG. 2. Modeling dynamics in a sample country. SIS, double infection (DI), and bounded rationality (BR) dynamics are plotted as, respectively, orange, blue, and green lines. The local epidemic level, as cumulative number of reported cases, is represented by a grey dashed line. The empirical fraction of unreliable tweets with respect to the total tweets is represented by grey line. Empirical quantities are normalized in $[0,1]$. The country here considered is India.

along with the real infodemic and epidemic data. We can appreciate how the models studied fit misinformation waves: evolutionary models (blue and green line for, respectively, DI and BR models) are able to capture the ascending and descending trends that characterize infodemic waves around the onset of epidemic outbreak, whereas the SIS model (orange line) fails.

We next evaluate to which extent our models are good at fitting infodemic data. We display in Fig. 3(a) the absolute quality of the fits in terms of normalized RMSE, ϵ , that, as anticipated, is the ratio between the RMSE and the standard deviation of the data. For all tested countries, at least one of the tested models shows $\epsilon < 1$, indicating that modeling dynamics is within statistical uncertainty and, therefore, the performance of our model can be considered satisfactory. Furthermore, Fig. 3(a) shows that model performance may vary across countries, with dynamics that are usually best explained with a DI model. To compare model performances, we compute for each country the AIC weights (see Materials and Methods section) and report our results in Fig. 3(b). AIC analysis shows that the choice of the best model strongly depends upon the actual country being tested. In particular, the DI model is the best candidate to explain infodemic data for most of the countries and the BR model is instead penalized with respect to other models since, even if it presents comparable or even lower residuals, it requires the estimation of one more parameters with respect to the others. Finally, the SIS model is the best candidate model only for 4 out of 37 considered countries.

To summarize and test the significance of the measures of model performance across the whole data set, we show in Fig. 4 the distributions of the normalized RMSE and AIC weights, whose quartile values are reported respectively in Figs. 4(a) and 4(b). Quartile values of ϵ obtained for the SIS model are significantly higher than the ones obtained for the DI and BR ones (two-sided Mann-Whitney U test with Bonferroni correction [52,53]) and medians of those distributions are lower than one (median values are 1.7, 0.94, and 0.89 for the SIS, DI, and BR models, respectively). Figure 4(b) shows that the distributions of AIC weights for the DI and BR models are comparable, whereas the SIS model has the lowest results. To gather conclusive evidence about the best model among the three tested ones, we estimate the overall AIC, which is a way to calculate AIC weights for multiple

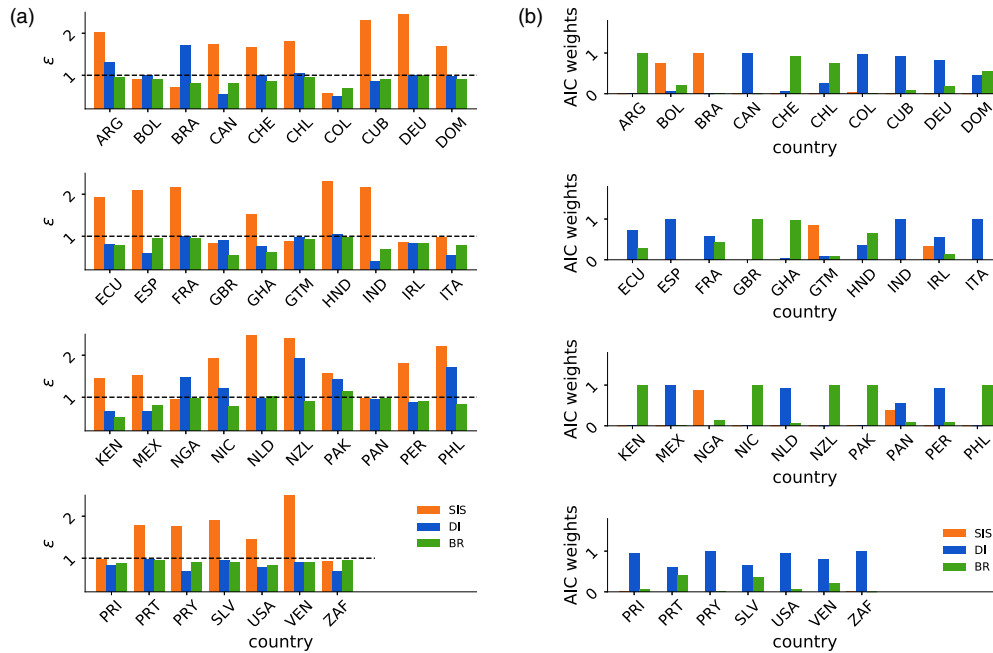


FIG. 3. Model performances across the 37 tested countries. Orange, blue, and green bars refer, respectively, to SIS, double infection, and bounded rationality models. Country names from the list of the current officially assigned ISO 3166-1 alpha-3 codes. (a) Normalized RMSE, ϵ . Dotted black lines mark statistical uncertainty, that is, models with $\epsilon < 1$ are considered to be effective as to the data description (b) AIC weights. For a fixed country, that measure is interpreted as the probability that a model is the best candidate, among the tested ones, to explain infodemic data.

data sets [Fig. 4(c), see Materials and Methods]. We find that the DI model is the best candidate and that it overall performs better than the others in modeling infodemic waves. We also evaluate the performance of the proposed models against a fourth simple model, that is, a constant function $n_U(t) = C$, where parameter C is estimated for each country by finding the minimum RMSE function. Results are reported in the Supplemental Material [54] and show that, even if distributions of AIC are comparable for C, DI and BR models, thanks to

the fact that constant predictor model uses only one parameter for describing infodemics (see Fig. S1B), nevertheless game theoretic models perform better than a simple constant model in terms of normalized RMSE (see Fig. S1A) and are able to capture the dynamics characteristic of infodemic processes where the constant model fails (Fig. S2). Those results suggest the importance of investigating infodemic processes with models that are able to capture their time dependence on other external dynamics.

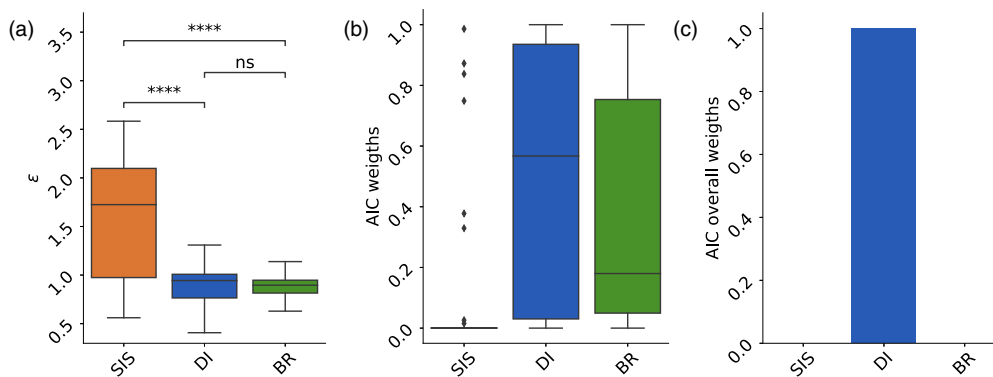


FIG. 4. Distributions and significance tests of model performances. Orange, blue, and green bars refer, respectively, to SIS, double infection (DI), and bounded rationality models. Box plots show the three quartile values of the distributions along with extreme values, bars extend the analysis to points that lie within a 1.5 interquartile range. (a) Normalized RMSE (Mann-Whitney with multiple comparisons test, ns: $p > 0.05$, ****: $p < 10^{-4}$). Results show that the SIS model presents a significantly higher normalized RMSE with respect to DI and BR models, while no significant difference in performance can be found between DI and BR models. (b) Distributions of AIC weights show that the DI has the highest probability to be the best model. (c) Overall AIC weights. This measure is needed when evaluating AIC weights in multiple data sets and shows that the DI model can be selected as the best option among the tested models.

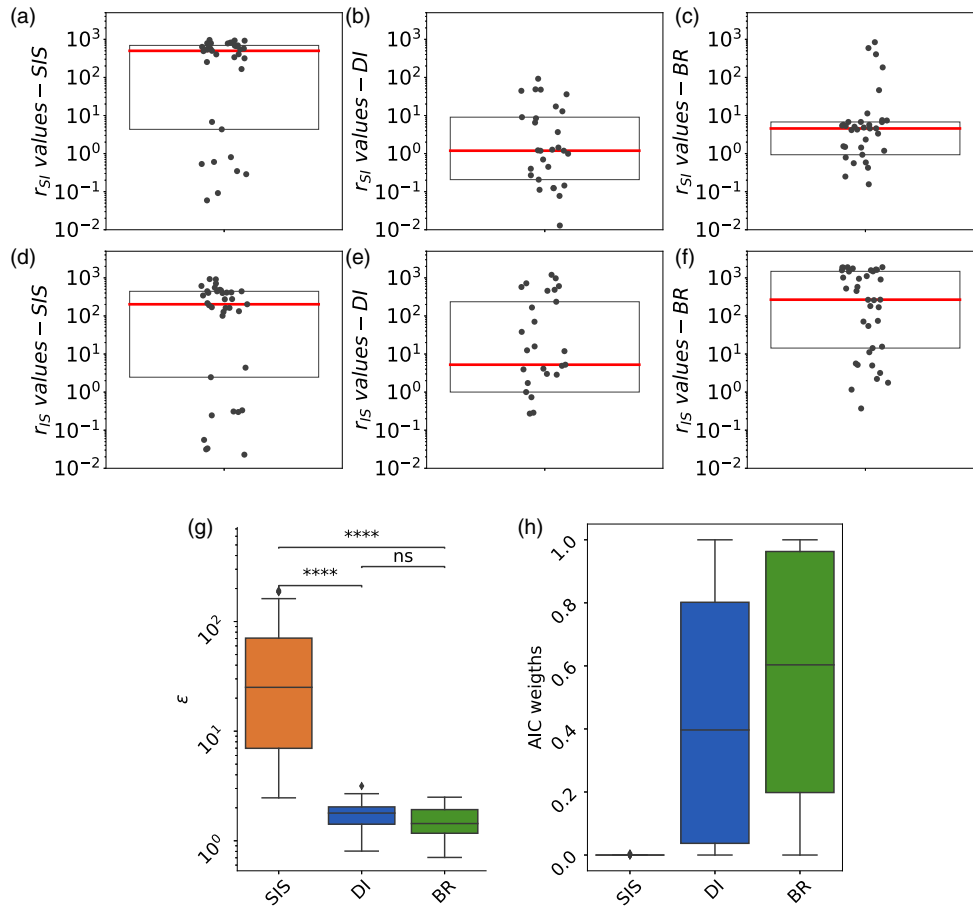


FIG. 5. Out-of-sample validation. (a)–(c) Spreading rate r_{RU} values estimated for, respectively, SIS, double infection, and bounded rationality models. Box plots show the three quartile values of the distributions. Red lines are medians of distributions. Logarithmic scale. (d)–(f) Awareness rate r_{UR} values estimated for, respectively, SIS, SIS, and BR models. Formats as in (a). (g) Distributions of normalized RMSE for leave-one-out validation (Mann-Whitney with multiple comparisons test, see Materials and Methods), ****: $p < 10^{-4}$. Orange, blue, and green bars refer, respectively, to SIS, DI, and BR models. Results show that DI and BR models have the lowest normalized RMSE when they are applied to out-of-sample prediction, whereas the SIS model presents significantly higher errors. (h) Distributions of AIC weights for leave-one-out validation. Results suggest that, among the tested models, game theoretic ones are the best candidates for out-of-sample prediction.

B. Out-of-sample validation

We validate our models by analyzing how they could be generalized to out-of-sample data. We adopt a leave-one-out validation as follows: for each country in our data set and for each tested model, we simulate the dynamics by using as model parameters the median values of the rates r_{RU} and r_{UR} computed from the distributions of the remaining data set. In Fig. 5, we investigate the range of values of the parameters estimated for each model. In particular we focus our attention on the spreading rate r_{RU} [Fig. 5(a)] and on the awareness rate r_{UR} [Fig. 5(b)], since they vary across models and countries. Quartile box plots show that values for the SIS model appear to be less concentrated around the median. This means that the reliability of r_{RU} and r_{UR} estimated for the DI and BR models is higher with respect to the SIS model, and that evolutionary models could be the best candidates for the prediction of infodemic dynamics of an out-of-sample country. To test our hypothesis, we use the leave-one-out validation described above and we find that the normalized RMSE [Fig. 5(g)]

obtained from the SIS model is significantly higher than for DI ($p < 10^{-4}$) and BR ($p < 10^{-4}$). Those results are confirmed by the AIC analysis [Fig. 5(h)]: AIC weights for the SIS model are close to zero, whereas AIC weights related to DI and BR are comparable. Results suggest that game theoretic models are the best candidates among the tested models to predict out-of-sample data.

IV. CONCLUSION

Modeling infodemic waves which spread through online social media during an ongoing epidemic is challenging, and here we provide an exploration of this issue.

To tackle this challenge, we collect more than 390 millions messages posted worldwide to Twitter, a popular microblogging platform, to analyze the infodemic dynamic associated to SARS-CoV-2 epidemic outbreaks across 249 countries.

We first consider as a benchmark a well-known epidemiological model, widely adopted to model social phenomena

such as the spreading of rumors, that does not take into account time-varying processes as drivers of infodemic dynamics. To investigate the role of epidemic drivers, we also consider two additional models derived from evolutionary game theory, widely adopted to model population dynamics in ecological and competitive systems, that present increasing levels of modeling detail of the behavioral processes of agents: the first one based on a simple imitation dynamics, and the second explicitly accounting for a form of limited rationality.

We project social media data over two categories of information: reliable and unreliable news, according to independent expert classification of the majority of their sources. We assume that an individual's choice to share (or not) one piece of content is binary as well, assuming that such a choice is guided by two strategies driven by exogenous events, modulating the payoffs related to different options. This small set of assumptions allow us to integrate in our model the effects of individual behavior at the expense of the description of specific classes of agents, such as ignorants or stiflers, which are usually studied separately in epidemic-like models but whose differential activity cannot be reproduced from the available data.

Interestingly, we find that the infodemic dynamics in the early phase of the epidemic can be successfully described by a DI model borrowed by evolutionary game theory. Its reduced number of parameters avoids the overfitting issue that is characteristic of the BR model, and provides more accurate results than a classic epidemic SIS model, especially when implemented out of sample. This result implies in particular that, for the modeling of the infodemic dynamics, the extra level of behavioral detail provided by the BR model is not worth the extra informational cost that it entails and that, therefore, a more parsimonious evolutionary model works better here. This is a useful insight, also with a view to the future development of more sophisticated infodemic models.

Another important source of insight comes from the global-local tension that drives the social dynamics of the infodemic. According to our findings, the spreading of the epidemic has opposite effects on infodemic waves depending on the geographical proximity to the infection outbreaks and on their incidence. If a country does not report cases of SARS-CoV-2, the local fraction of messages from potentially unreliable sources is proportional to the epidemic increase

registered worldwide. Conversely, when the pandemic wave hits a country, individual risk perception undergoes an abrupt change and the fraction of unreliable sources shared decreases proportionally to the level of the local epidemic. Similar social dynamics are well-known in evolutionary game models of the emergence of cooperation [55]. Recent studies have also explicitly linked the emergence of cooperation within a population to the epidemic level of a disease [56].

It is worth stressing here that our results refer to a time window around the onset of the local epidemic outbreak. However, further studies are needed to analyze the complex unfolding of infodemic processes for longer time periods or characterized by different interplays with epidemic processes unfolding at different scales.

Our results can be considered as a step toward the comprehension of the dynamic coevolution between epidemic and infodemic processes that represents the necessary baseline to design and test integrated epidemic/infodemic public health interventions during pandemic crises. We obtain some insights into some macro-level mechanisms that could drive infodemic dynamics that are worth further attention.

From an evolutionary game-theoretic perspective, the spreading of unreliable content may be considered as anti-social behavior. However, we find that such behavior can be driven by nonlocal forces and can therefore fail to reflect local social conditions, as happens, e.g., when the disease is spreading worldwide but not locally. This is radically different from what it is usually assumed in canonical epidemiological models, where the spreading of a piece of (mis)information fades away and spontaneously decays whenever individuals lose their interest in disseminating it. Our results suggest, instead, that such forms of antisocial behavior have their own characteristic dynamics, driven by perceived payoff, and that other external forces influencing an individual's perceived benefit have to come into play to actively mitigate it.

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