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Integrating theory and population data to forecast the spatiotemporal spread of COVID-19

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Background

The outbreak of COVID-19 has led to a surge of interest in **computational simulation of infectious disease outbreaks** using:

- **Mechanistic compartmental models based on the classical SIR (susceptible-infected-recovered) and SEIR (susceptible-exposed-infected-recovered) paradigms**, which leverage a system of ordinary differential equations (ODEs) to describe the temporal dynamics of disease spread.
- **Purely data-driven statistical approaches**, which predict future trends in the outbreak evolution based on incoming data of the current epidemic.

These **forecasting technologies** have been useful in **monitoring COVID-19 outbreaks**. However, **their predictive ability is limited** by:

- **A heavy reliance on time series of epidemiologic data.**
- **An inherent lack of spatial information;** i.e., they are unable to explain the mechanisms by which the disease propagates in space over the study area.

Research vision and aim

Vision | We believe that **a partial differential equation (PDE) model constrained with available demographic, geographic, and epidemiologic data** may overcome the previous limitations by offering:

- A more powerful mechanistic approach to **predict the spread of COVID-19 in both space and time.**
- The ability to capture complex phenomena based on **human habits, public health interventions, and population features.**

Aim | To construct, calibrate, and validate **an SEIRD (susceptible-exposed-infected-recovered-deceased) mathematical model featuring a diffusion term with heterogeneous coefficient to describe the spread of living-person model compartments**, and hence the local spatial propagation of COVID-19.

Mathematical model

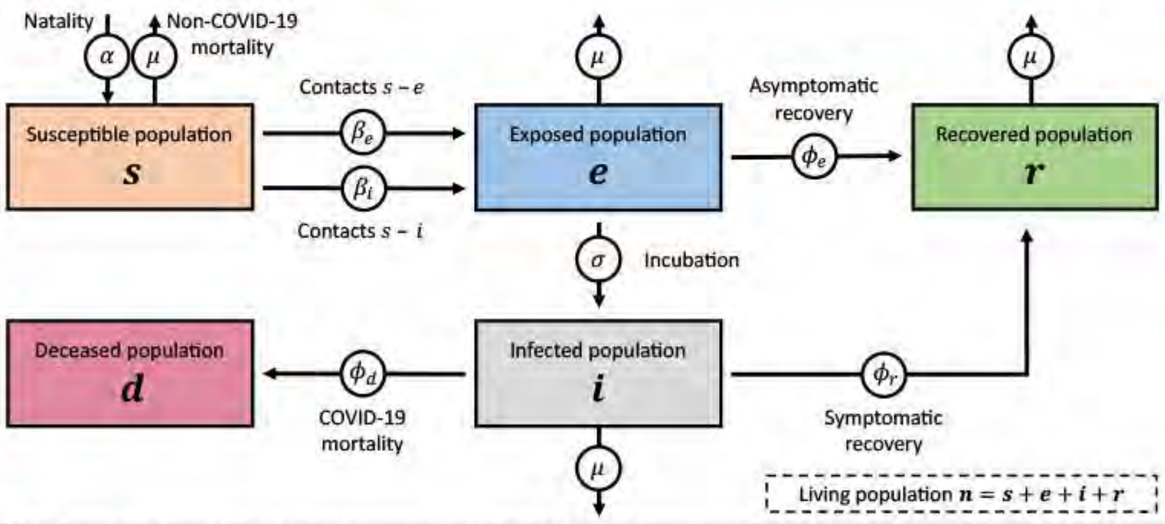

Fig.1. Flowchart describing the baseline demographics and COVID-19 contagion dynamics across the model compartments.

Given a certain geographical area, **we distribute its population into different compartments according to COVID-19 status,** as shown in **Fig. 1**. We model the **change in disease status and the movement of the individuals in each compartment in space and time with the PDE system in Eqs. (1)-(5).**

$$\partial_t s = \alpha n - (1-A/n)\,\beta_i s i - (1-A/n)\,\beta_e s e - \mu s + \nabla\cdot(n\,\nu_s \nabla s) \quad (1)$$

$$\partial_t e = (1-A/n)\,\beta_i s i + (1-A/n)\,\beta_e s e - \sigma e - \phi_e e - \mu e + \nabla\cdot(n\,\nu_e \nabla e) \quad (2)$$

$$\partial_t i = \sigma e - \phi_d\, i - \phi_r i - \mu i + \nabla\cdot(n\,\nu_i \nabla i) \quad (3)$$

$$\partial_t r = \phi_r i + \phi_e e - \mu r + \nabla\cdot(n\,\nu_r \nabla r) \quad (4)$$

$$\partial_t d = \phi_d\, i \quad (5)$$

Our model has the following **salient features**:

- **Asymptomatic transmission**, a pivotal driver of COVID-19 outbreaks.
- **Clustering of outbreaks towards larger population centers** *via* **Allee effect (*A*).**
- **Inhomogeneous diffusivity coefficients** to accomodate **higher mobility of individuals in larger population centers.**

Computational study: Lombardy (Italy)

We tested our model to **describe the dynamics of COVID-19 contagion during the 2020 outbreak in Lombardy (Italy)**. We adopted the following **problem definition, calibration scheme,** and **computational setup,** which we implemented in **FreeFEM:**

- Initial conditions for the model compartments. **Gaussian circular functions** centered at the **latitute and longitude of the municipalites** with more than 10,000 inhabitants, weighted by their corresponding **population according to demographic and the COVID-19 epidemiological data** on February 27, 2020.
- Boundary conditions. **Homogeneous Neumann,** i.e., absolute isolation.
- Model calibration. We **fixed the parameters describing COVID-19 incubation, recovery and death** from the literature; **neglected the effect of natality and non-COVID-19 mortality**; and **estimated the remaining parameters** *via* iterative simulations constrained by the available **data for the deceased compartment** from February 27 to April 27, 2020 (see **Table 1** and **Fig.2**).
- Spatial discretization. **Unstructured finite-element mesh** consisting of 30,407 linear triangular elements.
- Time discretization. **Backward Euler method,** with Picard iteration to solve the nonlinear algebraic equations. The resulting linear systems were solved with the GMRES algorithm.

Parameter	Value	Units
σ	1/7	day^{-1}
ϕ_r	1/24	day^{-1}
ϕ_e	1/6	day^{-1}
ϕ_d	1/160	day^{-1}
α	0	day^{-1}
μ	0	day^{-1}
A	1000	ps
ν_i	$1.0\cdot10^{-4}$	km$^2\cdot$ ps$^{-1}\cdot$ day^{-1}

Table 1. Constant model parameters (ps=persons).

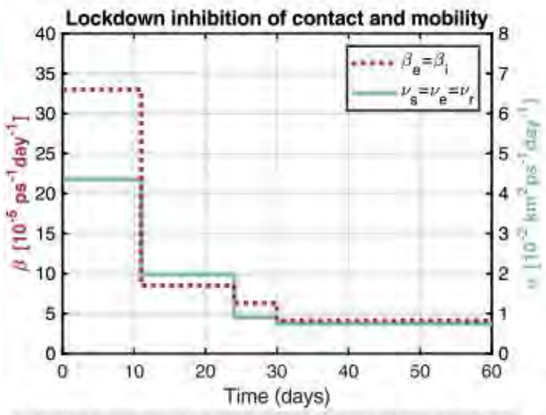

Fig. 2. Time-varying model parameters (ps=persons).

Results

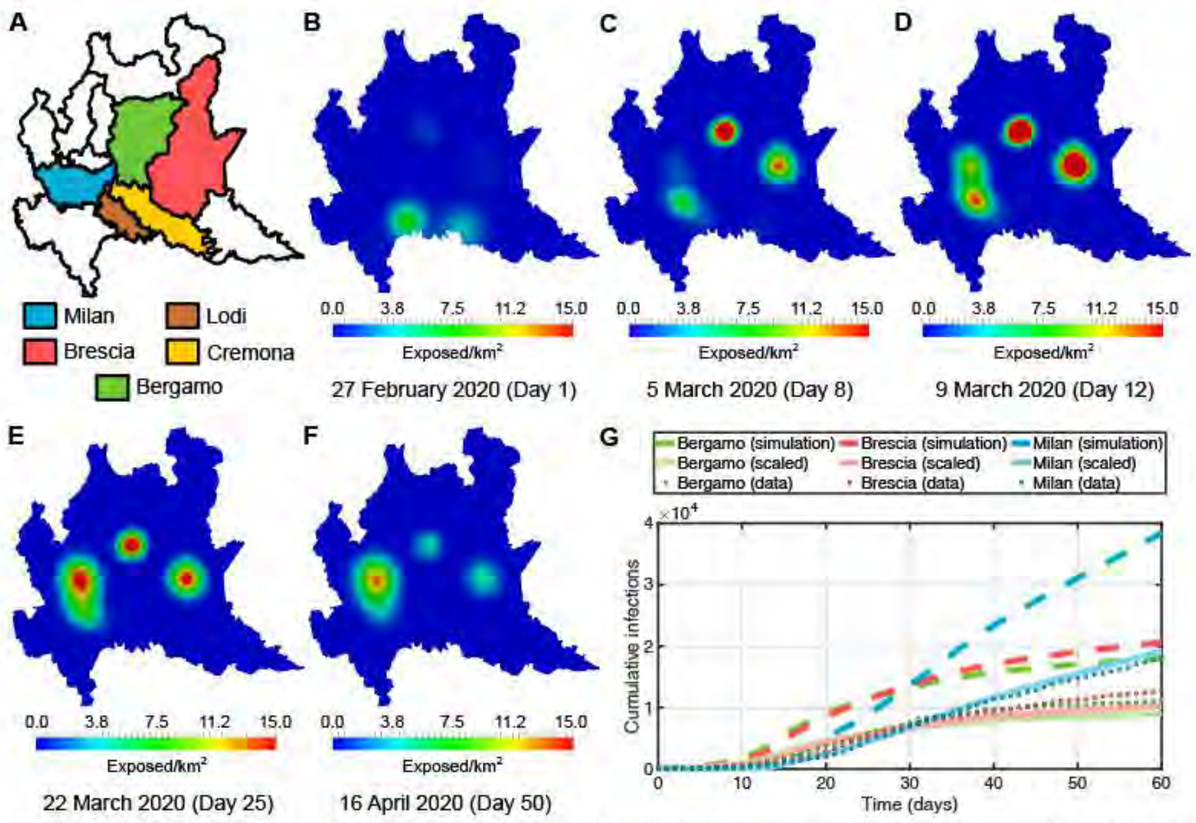

Fig.3. Model forecast of COVID-19 spread in Lombardy. (A) Main affected provinces. (B-F) Spatiotemporal evolution of exposed individuals. (G) Cumulative infection curves over most affected areas obtained from simulations and data.

Fig. 3 shows the simulation results. Our model predicts a **larger number of infections** because it was calibrated against death data. This suggests **undetected transmission**. In **Fig. 3**, we scaled the predicted infection to the corresponding data to highlight the **remarkable qualitative agreement** (R^2>0.95). **Model predictions were also notably accurate in the deceased compartment** (R^2>0.95, range-normalized RMSE=7.6%).

Conclusions

We believe that **data-driven forecasts of our model** could ultimately assist public health officials to quickly **design pandemic-arresting strategies from local to region-wise levels** and to **anticipate the geographical allocations of crucial medical resources.**

References

[1] Viguerie A *et al* (2020), *Appl Math Lett*, 111: 106617.
[2] Viguerie A *et al* (2020), *Comput Mech*, available online.