The routes of COVID-19 in Italy
Past and future scenarios

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Spread and dynamics of the COVID-19 epidemic in Italy: Effects of emergency containment measures

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The spread of coronavirus disease 2019 (COVID-19) in Italy prompted drastic measures for transmission containment. We examine the effects of these interventions, based on modeling of the unfolding epidemic. We test modeling options of the spatially explicit type, suggested by the wave of infections spreading from the initial foci to the rest of Italy. We estimate parameters of a meta-population Susceptible-Exposed-Infected-Recovered (SEIR)-like transmission model that includes a network of 167 provinces connected by mobility at high resolution, and the official contribution of presymptomatic and asymptomatic transmission. We estimate a general reproduction number \( R_0 = 3.60 (3.49 \text{ to } 3.84) \), the spectral radius of a suitable next-generation matrix that measures the potential spread in the absence of containment interventions. The model includes the implementation of progressive restrictions after the first case confirmed in Italy (February 21, 2020) and runs until March 25, 2020. We account for uncertainty in epidemic reporting, and time dependence of human mobility matrices and awareness-dependent exposure probabilities. We draw scenarios of different containment measures and their impact. Results suggest that the sequence of restrictions posed to mobility and human-to-human interactions have reduced transmission by 45% (42% to 48%), Averted hospitalizations are measured by running scenarios obtained by selectively relaxing the imposed restrictions and total about 200,000 individuals (as of March 25, 2020). Although a number of assumptions need to be reexamined, like age structure in social mixing patterns and in the distribution of mobility, hospitalization, and fatalities, we conclude that verifiable evidence exists to support the planning of emergency measures.

The ongoing pandemic of COVID-19 challenges globalized societies. Scientific and technological cross-fertilization yields broad availability of georeferenced epidemiological data and of modeling tools that aid decisions on emergency management. To this end, spatially explicit models of the COVID-19 epidemic are reported.
Summary

• Motivations
• The spatially explicit model
• Model results (up to end of March 2020 and update)
• Future scenarios (lifting containment measures)
• Conclusions
The pathogen: SARS-CoV-2

- RNA virus ad RNA with a crown-like (*corona* in Latin) appearance due to spikes on the surface
- beta coronavirus like SARS-CoV-1
- hosts: bats and rodents (*zoonosis*)
Emerging and re-emerging diseases

Emerging and re-emerging diseases

W. Ian Lipkin, *Nature Reviews Microbiology* 11, 133-141 (February 2013)
Emerging and re-emerging diseases

Hot Spots for Emerging Diseases

Map shows an analysis of the future likelihood of infectious diseases originating in wildlife that have the potential to infect humans.

Key: Greater risk

Factors in the analysis included population density, proximity to and safety of wildlife, and climate.

West Nile virus
A mosquito-borne illness that causes symptoms in about a fifth of those exposed. One in 150 becomes severely ill with encephalitis.

Animal reservoir: Various birds, especially robins in the U.S.
First human case: West Nile district of Uganda, 1937; first U.S. case was in Queens in 1999.
Why it emerged: International air travel.
Susceptible hosts: Humans, birds, especially crows, horses.

SARS
A severe viral respiratory infection that quickly spread from China to many other countries. The outbreak was contained, and since 2004 no new cases have been reported.

Animal reservoir: horseshoe bats.
Why it occurred: Wildlife markets and trade; global travel.
Susceptible: Humans, bats, p, birds.

Bird flu
A deadly strain of the avian influenza virus called H5N1 has spread to humans via contact with live or dead poultry.

Animal reservoir: Wild waterfowl.
Why it occurred: Global expansion of intensive poultry farming; contact with infected birds.
Susceptible: Humans, poultry, cats.

H5N1 influenza
A strain of flu, commonly called avian flu, killed thousands and infected millions in 2005. Humans in turn spread the disease to pigs, triggering a pandemic in livestock.

Animal reservoir: Waterfowl and pigs.
First human case: Vietnam, Mexico, 2009; first U.S. case was in San Diego in 2009.
Why: Livestock production (pigs and poultry) contact with wild waterfowl.
Susceptible: Humans, pigs.

Nipah virus
A highly lethal pathogen for which there is no cure or vaccine. Humans-to-human transmission has been documented; nearly annual outbreaks in Bangladesh since 2001 and in India.

Animal reservoir: Various bats.
Why it occurred: Contact with or eating infected animals, especially bats.
Susceptible: Humans, chimpanzees, gorillas, duikers (small African antelopes, below right).

Hendra virus
A close relative of the Nipah virus, it has killed four people and dozens of horses in Australia.

Animal reservoir: Fruit bats.
First human case: Hendra, a suburb of Brisbane, Australia, 1994.
Why: Urban encroachment on wild habitats.
Susceptible: Humans, horses, dogs.
Why mobility is important: cholera in Haiti

A.Rinaldo et al., PNAS 2012, 109 (17) 6602-6607
The clear spatial signature of the Italian COVID-19 epidemic
In memoriam of my grandfather: the Spanish flu and Katzenau (where he died, Nov. 1918)

Fig. 2 The First and Second Waves of the 1918–1919 Pandemic. First outbreaks and foci of second waves of the pandemic are labeled as red and purple circles, respectively. The lines of spread of the first and second waves of the pandemic are labeled as purple dashed lines and red solid lines, respectively.

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