



VISUALIZATIONS

How coronavirus spread in Europe over time: national probabilities based on migration networks

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Global migration trends (Hatton–Williamson 2005, Bálint et al 2017, Farkas–Dövényi 2018) today differ from those in previous centuries in terms of both the number of people migrating (as of 2017, 272 million people live in a country other than their country of origin) as well as the geographical, economic, and cultural distance between sending regions and destination countries. The interconnection between countries is constantly growing, relationships are expanding through migration, and people's movement is increasing.

Migration shows strong territorial concentration (Winders 2014); in 2019, half of the global migrant population lived in nine countries. In international migration, there are centres (large host countries) and global migration destinations, which attract migrants over long distances. Such hubs include the USA, Canada, Australia, the UK, Germany, France and Spain.

Close migration relationships mean strong exposure and vulnerability to the spread of infectious diseases. The calculation does not assume that infection can only be caused by migration, but states that migration relationships between countries, that is, their network, well represent the spread of infections between countries.

Keywords:

international migration,
migration networks,
coronavirus

Methodological notes for establishing migration links

There is a close relationship between two countries when there is international migration (Wimmer–Schiller 2002, Novotný–Pregi 2018, Lados–Hegedűs 2019) between them, that is, someone moved from one (birth) place to another (current residence). Only movements above a threshold are considered by the network (Ba-

rabási 2016), as a small number of international migrants between two large countries does not necessarily represent a real migration link (Castles 2010; Castles–Miller 2013). In other words, the network connects two countries only if the number of migrants between them is relevant and asymmetric. That is,

$$q(A, B) = \frac{M[A \rightarrow B] - M[B \rightarrow A]}{N(A) + N(B)}$$

is above a fixed threshold μ . Here, $M[X \rightarrow Y]$ is the population density of country Y born in country X and $N(X)$ is the population of country X , $\mu \in \{-1; +1\}$, $\mu \in \mathbb{R}$.

If $q(A, B) > \mu$, a migration link from country A to country B is created; if not, there is no such link between the two countries. This allows different grids to be edited depending on the μ parameter.

Situation in Europe

1.2 million people born in China live in Europe (UN 2019). European countries most densely populated by Chinese people (Italy, the UK, Spain, Germany, and France) are home to 120-300,000 Chinese per country. Italy, the UK, Spain, Germany (Glorius 2018), and France are global migration centres and also the countries most infected with coronavirus.

In the following, we estimate the magnitude of the Chinese migration impact on European countries by creating scenarios for the temporal spread of the coronavirus at the national level.

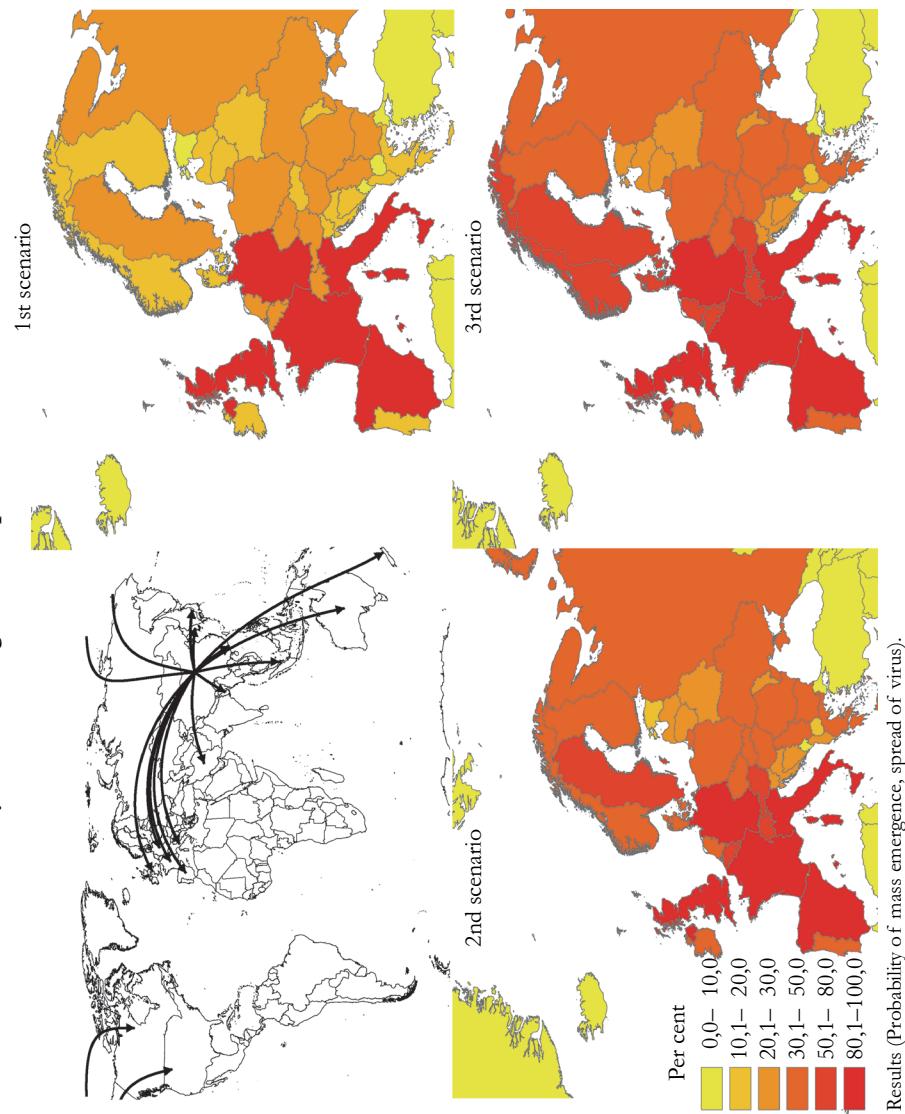
Set up scenarios

Within real migration networks (Barabási 2016), their topology shows the „distance” between countries, that is how “far away” they are from China and how many countries they are connected to. There is an inverse relationship between the distance in the network and the probability of propagation.

(Figure 1 (top left) shows the most important target areas for migration from China) With a longer migration distance, the rate at which the infection appears is as follows:

- Scenario 1: 5% (Lower values for Wuhan and surrounding regions) (top right)
- Scenario 2: 15% (Average spread for Lombardy and neighbouring regions in the case of Italy) (bottom left)
- Scenario 3: 25% (Highest penetration rate among regions of Italy) (bottom right)

Figure 1

Probability of mass emergence and spread of coronavirus over time

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DATA:

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