Computational science in the COVID-19 pandemic

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Image: Nextstrain
Quantitative understanding of epidemics: History

- **1610/1611**: Felix Platter writes ‘Pestbericht’ in Basel

- **1766**: Daniel Bernoulli uses differential calculus to study impact of variolation against small pox

- **1927**: Kermack & McKendrick develop basic SIR model

- **Since 2000**: Global Epidemic and Mobility Model (GLEAMviz) and genomic epidemiology (Nextstrain)

*Images: Wikipedia, Nextstrain*
Early January 2020

Image: The New York Times
Simulating early outbreak trajectories in Wuhan (Hubei, China)

Human-to-human transmission of influenza viruses is characterised by $R_0$ values between 1.5 and 2 and a larger value of $k$, implying a more steady transmission without superspreading. The emergence of new strains of influenza, for which human populations carried little to no immunity contrary to seasonal influenza, led to pandemics with different severity such as the ones in 1918, 1957, 1968 and 2009. It is notable that coronaviruses differ from influenza viruses in many aspects, and evidence for the 2019-nCoV with respect to case fatality rate, transmissibility from asymptomatic individuals and speed of transmission is still limited. Without speculating about possible consequences, the values of $R_0$ and $k$ found here during the early stage of 2019-nCoV emergence and the lack of immunity to 2019-nCoV in the human population leave open the possibility for pandemic circulation of this new virus.

Strengths and limitations

The scarcity of available data, especially on case counts by date of disease onset as well as contact tracing, greatly limits the precision of our estimates and does not yet allow for reliable forecasts of epidemic spread. Case counts provided by local authorities in the early stage of an emerging epidemic are notoriously unreliable as reporting rates are unstable and vary with time. This is due to many factors such as the initial lack of proper diagnosis tools, the focus on the more severe cases or the overcrowding of hospitals. We avoided this surveillance bias by relying on an indirect estimate of epidemic size on 18 January, based on cases identified in foreign countries before quarantine measures were implemented on 23 January. This estimated range of epidemic size relies itself on several assumptions, including that all infected individuals who travelled from Wuhan to other countries have been detected [6].

This caveat may lead to an underestimation of transmissibility, especially considering the recent reports about asymptomatic cases [4]. Conversely, our results do not depend on any assumption about the existence of asymptomatic transmission, and only reflect the possible combinations of transmission events that lead to the situation on 18 January.

Figure: Riou & Althaus (2020, Euro Surveill)
Comparison to MERS, SARS and influenza

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Transmission characteristics appear to be of similar magnitude to severe acute respiratory syndrome-related coronavirus (SARS-CoV) and pandemic influenza, indicating a risk of global spread.

The World Health Organization (WHO) declared the novel coronavirus outbreak a public health emergency of international concern (PHEIC) on 30 January 2020.
Digital contact tracing: D3-PT (Decentralized Privacy-Preserving Proximity Tracing)

A similar protocol was later implemented into the Google/Apple Exposure Notification (GAEN) system.

Figure PT: proximity tracing process.

Figure: Troncoso et al. (2020, arXiv)
Effectiveness of digital contact tracing for SARS-CoV-2 in Switzerland

From 23 July to 10 September 2020, 65 (imputed) of 12,456 cases (0.5%) reported the SwissCovid app as the reason for the test, corresponding to around 3,000 cases during second wave.

Provided that both the index case and the exposed contacts use the app, we estimate 0.24 (95% CI: 0.20-0.27) identified positive contacts per index case.

Figure: Salathé et al. (2020, Swiss Medical Wkly)
Epidemiological impact of digital contact tracing in the UK

“We estimated that for every 1% increase in app users, the number of infections can be reduced by 0.8% (from modelling) or 2.3% (from statistical analysis).”

Figure: Wymant et al. (2021, https://github.com/BDI-pathogens/covid-19_instant_tracing)
Interfaculty Platform for Data and Computational Science

- Collaboration between Institute for Social and Preventive Medicine (ISPM) and the Center for Space and Habitability (CSH)

- Aim: Development and application of computational methods in epidemiology, medicine and the natural sciences

- Synergies with ARTORG, IDSC, CAIM, and the newly founded multidisciplinary center for research into infectious diseases and immunity

⇒ “Planetary Health”