

The evidence profiled below was selected from credible academic and grey literature sources and based on potential applicability to the Ontario Modelling Consensus Table.

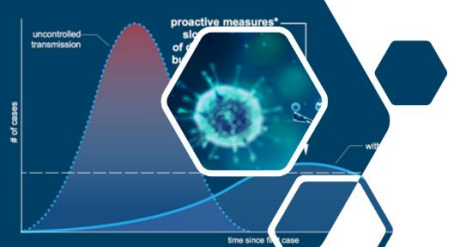
CONFOUNDING FACTORS

Crowding and the shape of COVID-19 epidemics. *Nature Medicine. Oct 5, 2020.*

This study analyzed highly resolved spatial variables in cities, together with case count data, to investigate the role of climate, urbanization, and variation in interventions. Using detailed case count data from COVID-19 among cities in China and Italy, the study fit multiple regression models to explain variability in the shape of epidemics among them. The study shows that the degree to which cases of COVID-19 are compressed into a short period of time (i.e., peakedness of the epidemic) is strongly shaped by population aggregation, and heterogeneity, such that epidemics in crowded cities are more spread over time, and crowded cities have larger total attack rates than less populated cities. Observed differences in the peakedness of epidemics are consistent with a meta-population model of COVID-19 that explicitly accounts for spatial hierarchies. This work essentially provides empirical support for the role of spatial organization in determining infectious disease dynamics and, specifically, spatial variability in transmission parameters. The study paired its estimates with globally comprehensive data on human mobility and predicted that crowded cities worldwide could experience more prolonged epidemics, even after the implementation of lockdowns. Cities that are less crowded and have lower attack rates might be more susceptible to experiencing future outbreaks if SARS-CoV-2 is successfully re-introduced. [Read.](#)

Reconciling model predictions with low reported cases of COVID-19 in Sub-Saharan Africa (SSA): insights from Madagascar. *Global Health Action. Oct 5, 2020.*

So far, SSA has reported lower incidence and fatalities compared to the predictions of standard models and the experience of other regions of the world. There are three leading explanations, each with different implications for the final epidemic burden: 1) low case detection, 2) differences in epidemiology (e.g., low R_0), and 3) policy interventions. The low number of cases have led some SSA governments to relax their policy interventions. To understand how to interpret the lower- than-expected COVID-19 case data in Madagascar, the study used a simple age-structured model to explore each of these explanations and predict the epidemic impact associated with them. The study showed that the incidence of COVID-19 cases, as of July 2020, can be explained by any combination of the late introduction of first imported cases, early implementation of non-pharmaceutical interventions (NPIs), and low case detection rates. The study then re-evaluated these findings in the context of the COVID-19 epidemic in Madagascar through August 2020. This analysis reinforced that Madagascar, along with other countries in SSA, remains at risk of a growing health crisis. If NPIs remain enforced, up to 50,000 lives may be saved. Even with NPIs, without vaccines and new therapies, COVID-19 could infect up to 30% of the population, making it the largest public health threat in Madagascar for the coming year, hence the importance of clinical trials and continually improving access to healthcare. The authors concluded that currently there is not enough evidence to suggest that the epidemiology of COVID-19 is different in Madagascar than elsewhere. [Read.](#)



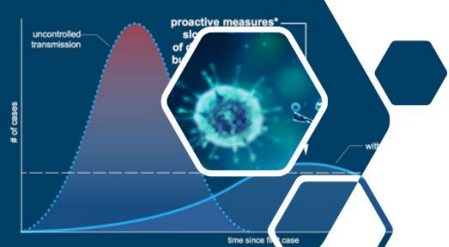
Virus evolution affected early COVID-19 spread. *medRxiv. Sep 30, 2020.*

This preprint study provides new evidence for an evolutionary effect on the COVID-19 growth rate early in the pandemic. As the SARS-Cov-2 virus spreads around the world afflicting millions of people, it has undergone divergent genetic mutations. Although most of these mutations are expected to be inconsequential, some mutations in the spike protein structure have been hypothesized to affect the critical stage at which the virus invades human cells, which could affect transmission probability and disease expression. If true, then we expect an increased growth rate of reported COVID-19 cases in regions dominated by viruses with these altered proteins. The study modelled early global infection dynamics based on clade assignment along with other demographic and meteorological factors previously found to be important. The study noted that clade, but not variant D614G which has been associated with increased viral load, enhanced our ability to describe early COVID-19 growth dynamics. Including clade identity in models significantly improved predictions over earlier work based only on weather and demographic variables. In particular, higher proportions of clade 19A and 19B were negatively correlated with COVID-19 growth rate, whereas higher proportions of 20A and 20C were positively correlated with growth rate. A strong interaction between the prevalence of clade 20C and relative humidity suggests that the impact of clade identity might be more important when coupled with certain weather conditions. In particular, 20C and 20A generate the highest growth rates when coupled with low humidity. Projections based on data through April 2020 suggest that, without intervention, COVID-19 has the potential to grow more quickly in regions dominated by the 20A and 20C clades, including most of South and North America. [Read](#).

MODELLING DRUGS

A multimodal deep learning-based drug repurposing approach for treatment of COVID-19. *Molecular Diversity. Sep 30, 2020.*

Recently, various computational methods have been proposed to find new therapeutic applications of existing drugs. The Multimodal Restricted Boltzmann Machine approach (MM-RBM), which has the capability to connect the information about the multiple modalities, can be applied to the problem of drug repurposing. The present study used MM-RBM to combine two types of data, including the chemical structure data of small molecules and differentially expressed genes as well as small molecules perturbations. In the proposed method, two separate RBMs were applied to find out the features and the specific probability distribution of each datum (i.e., modality). Further, RBM was used to integrate the discovered features, resulting in the identification of the probability distribution of the combined data. The results demonstrated the significance of the clusters acquired by the model. These clusters were used to discover medicines, which were remarkably similar to the proposed medications to treat COVID-19. Moreover, the chemical structures of some small molecules, as well as dysregulated genes' effect, led the researchers to suggest using these molecules to treat COVID-19. The results also showed that the proposed method might prove useful in detecting the highly promising remedies for COVID-19 with minimum side effects. [Read](#).



COMPARATIVE MODELLING

Control of a multigroup COVID-19 model with immunity: treatment and test elimination. *Nonlinear Dynamics. Sep 30, 2020.*

This study introduces a multigroup COVID-19 model with immunity, in which the total population of each group is partitioned into five compartments: susceptible, exposed, infective, infective in treatment, and recovered. If the basic reproduction number is less than or equal to one, and the infection graph is strongly connected, then the disease-free equilibrium is globally asymptotically stable, and the disease dies out. However, COVID-19 is already in a pandemic state, and the basic reproduction number is larger than one. Hence, in order to make COVID-19 die out in some groups in an area, some appropriate control strategies were designed which should reduce the number of exposed people and increase the number of people treated. These two methods have been proved to be the most effective methods at present. The authors propose an algorithm to identify the groups that need to be controlled. Finally, the actual limited data of Hubei, Guangdong, and Zhejiang provinces in China were used to illustrate the effectiveness of the obtained results. [Read.](#)

MODELLING TECHNIQUES

Verification of infection prevention control using a spatial random walk model. *International Journal of Social Science Studies. Sep 30, 2020.*

To stop pandemic of COVID-19, "an 80 percent reduction of person to person contact opportunities" was proposed by the Japanese government. This guideline was based on the result of a macroscopic differential equation model akin to the SIR (Susceptible-Infected-Recovered) model. A new model was built to calculate infections between two persons who are in contact each other, in order to indicate the person-to-person infection mechanism intuitively. This model adopted a spatial random walk model to express random movement of people in a specific 2-D geographical space. This model was applied to verify the effect of the proposed infection control procedure, "80 percent reduction". The result of the numerical simulation supported a proposed infection control procedure of "an 80 percent reduction" derived by the SIR model. [Read.](#)