Modeling Infectious Behaviors: The Need to Account for Behavioral Adaptation in COVID-19 Models

Raffaele Vardavas[1], Pedro Nascimento de Lima[1], Paul K. Davis[1], Andrew M. Parker,[2] and Lawrence Baker[1]

[1]RAND Corporation, Santa Monica, CA 90401, USA

[2]RAND Corporation, Pittsburgh, PA 15213, USA

Modelado de conductas infecciosas: la necesidad de tener en cuenta la adaptación conductual en los modelos COVID-19

传染性行为建模：衡量新冠肺炎模型中的行为适应

The current COVID-19 pandemic affects billions of people worldwide, and its unprecedented scale and duration are causing extraordinary disruptions to lives and livelihoods. Policymakers have taken comparably extraordinary measures to mitigate the spread of the virus (SARS-CoV-2) by implementing a range of nonpharmaceutical public health interventions (NPIs), from partial closings of business to complete lockdown and mask-wearing (Aledort et al., 2007). NPIs continue to be critically important

as new vaccines roll out in an attempt to reach herd immunity as quickly as possible. Several models have been developed to help policymakers compare interventions such as NPIs and vaccination. Such models attempt—dependent on various uncertain assumptions—to forecast cases, deaths, and medical supply needs; predict the timing of peaks in cases; and estimate if and when to expect additional waves or surges. However, a key limitation of many existing models is that they do not directly integrate adaptive behavioral components to account for how risk perceptions, protective behaviors, and compliance with interventions change over time and ultimately influence transmission. Patterns of COVID-19 transmission shape the subsequent patterns of behavioral responses to the disease and, in turn, are shaped by such responses. Changes in risk perceptions during the pandemic affect behaviors, including adherence to NPIs and willingness to vaccinate. Also, the effects that NPIs have on a population activities have led to pandemic fatigue and a decline in compliance with recommended restrictions (Alagoz et al., 2020; Crane et al., 2021; Kantor and Kantor, 2020). Moreover, perceptions of the risks and benefits of vaccination change, increasing or decreasing the vaccine hesitancy that undermines attempts to reach herd immunity (Yaqub et al., 2014). Decision-makers are faced with the daunting task of interpreting model predictions while simultaneously estimating how the behavioral responses should alter predictions. Despite considerable uncertainties, it may be possible to improve these estimates by explicitly modeling behavioral responses to intervention, rather than merely varying parameters such as willingness to be vaccinated. Useful explicit modeling will require tapping new sources of data as we recommend in this article.

To elaborate, because the anticipation of behavioral responses can change policy recommendations, new transmission models that factor in the interplay between behaviors and disease dynamics are needed. To properly investigate the trade-offs of different policies, models must be grounded in causal epidemiological and behavioral theory and data (Manheim et al., 2016). Further, models need to factor in the many interacting uncertainties surrounding the virus and the vaccines, such as seasonal effects, the duration of natural and vaccine-based immunity, and the emergence of more transmissible strains. Early evidence suggests that immunity generated by the vaccines could be short-lived and that the vaccine is somewhat more effective at reducing severity than transmission (Hall et al., 2021; Tande et al., 2021). Emerging evidence also suggests that current vaccines may be less effective in protecting against specific variants, although they effectively prevent the most severe reactions and death (Wibmer et al., 2021). Hence, it seems increasingly likely that the virus will enter long-term circulation and become endemic, and that people will need to be vaccinated regularly with updated vaccines, as for seasonal influenza (Kissler et al., 2020; Scudellari, 2020).

Existing COVID-19 models use one of two general mathematical approaches for projections: statistics-based models that rely largely on data and curve fitting, and mechanistic models grounded in epidemiological micro-foundations and causal mechanisms. Purely data-driven statistical models (including those based on machine learning (ML) algorithms) generally have better short-term predictive performance, but limited capacity to explain counterfactual conditions and policy interventions. To explore and compare trade-offs of different policies and "what if" scenarios relative to each other, models need to be grounded in causal epidemiological and behavioral theory and data (Pearl, 2009).

Two types of mechanistic epidemiological models are (i) population-based models (PBM) and (ii) individual-level agent-based models (ABMs). Most of the COVID-19 mechanistic models have been deterministic PBM variants of the SEIR model, where the population is divided into such compartment classes as susceptible, exposed (latent), infectious, and removed (e.g., recovered and died) (Adiga et al., 2020). More recently, ABMs based on SEIR-type classes have been developed to explore intervention policies at the individual-level. Both the PBMs and the ABMs have been very useful for comparing policy interventions affecting testing, tracing, NPI, and vaccine prioritization strategies.

A PBM uses a top-down approach to depict disease dynamics at a macroscopic, system level. The ABM approaches have used less abstraction and been more bottom-up, considering each individual in the environment as an agent with its own infection state and behavior (Auchincloss and Garcia, 2015). Deterministic PBMs are formulated using coupled ordinary differential equations (ODEs) and are less computationally demanding, quicker to develop, and faster to run than ABMs, and their results are often easy to interpret. PBMs are therefore valuable for exploring and comparing a large set of intervention policies. They also relate well to the macro-level factors that policymakers deal with. However, since they model aggregate groups of people, they are not well-suited to addressing individual-level disease transmission dynamics. A PBM's disease transmission rate assumes the law of mass-action (i.e., that rate is proportional to the product of relevant concentrations). It also makes assumptions about how different groups of people, or population strata mix and under what circumstances (e.g., home, school, work). These are generally modeled using mode-specific mixing-matrices that control the different levels of homogeneous mixing between the population strata. In contrast, ABMs can better reflect a broader range of epidemiological heterogeneities that affect transmission patterns, such as the role of super-spreaders; importantly, they can explicitly model contact networks (Pastor-Satorras et al., 2015). Hence, ABMs allow individuals belonging to the same population group to have very different social mixing properties. Depending on data availability, ABMs can have better predictive

power than PBMs and can be used to explore more targeted intervention policies (Bonabeau, 2002). However, this improved predictiveness depends on numerous assumptions and, thus, requires more data. PBMs and ABMs can complement each other when used together in a multi-model approach and mitigate some structural uncertainties (Gambhir et al., 2015). Ideally, ABMs can generate simulated data permitting recognition of developments that can then be abstracted for inclusion in the analytically convenient PBMs (Davis and O'Mahony, 2019). Towards this goal, modelers have combined ABMs and PBMs into hybrid models of infectious disease transmission (Bobashev et al., 2007). These hybrid models switch between the two approaches over time and allow integration across multiple scales of description. Hybrid models are computationally faster than pure ABMs but still allow for individual-level analysis of emerging population structures.

Despite the rapid advancements in COVID-19 models and forecast tools, very few models directly include adaptive behavioral effects and how risk perceptions influence transmission dynamics. Both PBMs and ABMs can be coupled with models describing behaviors that are affected by and affect the disease transmission dynamics (Manfredi and D'Onofrio, 2013). For example, in PBMs behavioral changes that influence the contact rate during the epidemic can be modeled by allowing the transmission rate parameter to change in response to observed epidemiological state variables such as model outputs for reported cases and deaths

(Kwuimy et al., 2020). Simple parametric models of behavior consider an exponential or a reverse-sigmoid decline in transmission rate with increasing deaths (Getz and Dougherty, 2018). These models consider how contact rate declines in the early stages of the epidemic. Other behavioral effects can be included to model increased mixing due to fatigue in complying with NPIs. However, PBMs models use equations intended to be descriptive of entire groups of people: individuals that belong to the same population group are described by the same behavioral equations and parameter values. Moreover, the adaptive behaviors of each population group only respond to the current epidemiological state variables. Hence, PBMs do not allow for different behaviors to develop due to different histories of otherwise identical individuals that belong to the same population group. ABMs allow explicit specification of micro-level behavioral mechanisms that affect public risk perceptions and individual protective behaviors and attitudes. Moreover, similar individuals in an ABM develop different behaviors due to their different histories.

Whether people are willing to vaccinate strongly affects disease transmission dynamics. Hence, modeling how vaccination willingness is affected by context, events, and policies is crucial in estimating a voluntary vaccination policy's effectiveness. Coupling transmission models of infectious diseases with models of vaccination decisions has been a growing field of research. Early models in behavioral epidemiology considered rationally self-interested

individuals who use deductive reasoning and maximize their utility function when deciding to vaccinate for pathogens that provide permanent immunity (Bauch and Earn, 2004). Subsequent models considered influenza, where vaccination provides only temporary immunity and where individuals use inductive reasoning to make their yearly vaccination-related decisions by adapting to the changing epidemiology that they, in part, help form (Vardavas et al., 2007). For example, individuals choose to vaccinate based on their personal histories with influenza and the vaccine. If they did not vaccinate in the previous year and think they contracted the flu, they are more likely to vaccinate in the current season. On the other hand, if they were vaccinated in the previous season but think that they contracted the flu anyway, or perceive a low risk of contracting the flu because unvaccinated friends did not get the flu, they will be less likely to vaccinate in the current season. These models showed how heterogeneities in vaccination behaviors could emerge in otherwise homogeneous populations and some authors conclude that influenza epidemics cannot be prevented by voluntary vaccination without incentive-based programs (Breban et al., 2007).

Researchers have since been adding more realism to these models by including important sources of heterogeneities. Most notably, they consider how people's behaviors spread over complex social contact networks and affect disease transmission chains (Bhattacharyya and Bauch, 2012; Wang et al., 2016). This is also partly due to

how risk perceptions and protective behaviors are affected by social networks (Bruine de Bruin et al., 2019). For example, through a process of imitation, influenza vaccination behaviors and hesitancy can spread over social networks, further affecting disease transmission dynamics (Cornforth et al., 2011). If COVID-19 becomes endemic, there will be a growing need for new COVID-19 models that consider how behaviors spread over networks and explore incentive-based policies that target key people to vaccinate. These could be a combination of the most vulnerable to severe COVID-19 and those identified as highly connected and most likely to spread the virus. Prevailing models that consider the current acute phase of COVID-19 disease transmission have favored targeting the most vulnerable (Bubar et al., 2021; Kohli et al., 2021). However, other studies have shown that under certain conditions (high vaccine availability, high vaccine effectiveness to prevent transmission), prioritization of vaccinating the highly connected could rapidly cut transmission chains and indirectly protect the most vulnerable (Gulden et al., 2021; Matrajt et al., 2020).

Generally, disagreements between COVID-19 model projections and policy recommendations are due to differences in model architecture, assumptions and how data informs the models. A diverse set of publicly available data-sets have been used to inform COVID-19 models. These include time-series of case reporting and deaths, transmission estimation, and prognosis from epidemiological, de-

mographic, and mobility data, as well as social media data used for sentiment analysis and knowledge-based semantic analysis from the collection of scholarly articles covering COVID-19. Mixing matrices and the contact networks and how these change over time are critical model inputs. To better fit time-series data, modelers often use time-varying mixing parameters that are either informed by proxies to mixing (e.g., mobility data) or directly fitted to data. This approach allows modelers to fit case and death time-series. The reasoning behind this method is that infectious mixing is an unobserved process affected by many time-varying variables such as individual preferences, policy, and fatigue. Therefore, instead of modeling the relevant processes that affect mixing endogenously, one should use the available data such that the effective mixing time-series fits observed time-series. However, this approach does not result in an endogenous explanation of why the behavior changed in the past, and how it might change in the future. Moreover, if modelers are not careful, they may attribute changes in other parts of the system to changes in mixing. For example, if modelers use death time-series to calibrate a mixing parameter, they might attribute changes in mortality rates to changes in mixing. This problem, known as omitted variable bias in causal inference, is often not discussed in papers employing mechanistic models.

Better data-sets containing behavioral information are required to address the pressing need for new reliable COVID-19 models that include adaptive responses. We argue that interdisciplinary researchers should work together to design and field longitudinal surveys tailored to inform simulation models for this purpose. These surveys would capture how public perceptions of risk, protective and preparedness behaviors, public trust, knowledge, and misinformation change with the evolving epidemic, social network influences and personal experiences. Interdisciplinary research teams designing the surveys should bring together behavioral scientists, epidemiologists, policy researchers, mathematicians, and statisticians. The RAND Corporation is using this approach to develop an ABM of influenza vaccination decision. It has conducted a 4-year, 8-wave longitudinal survey fielded from Fall 2016 to Spring 2020 on the decision to vaccinate for influenza and influenza infection outcomes. The study is called FluPaths and its data is freely publicly available through RAND's American Life Panel (RAND Corporation, 2014). Pre-season questions included respondents' intentions to vaccinate, risk perceptions of catching influenza, and whether they received a recommendation to vaccinate from a health care professional. Post-influenza season questions included whether respondents were vaccinated, whether vaccination resulted from a healthcare professional's advice, whether they thought they caught influenza (and if so, whether they were tested for it and were prescribed antiviral medication). FluPaths surveys collected detailed information on each respondent's social network structure (including alter-alter ties) and assessed the influence of net-

work experiences on the respondent's risk perceptions and attitudes regarding influenza and vaccination over time.

Novel ML methods can generate network structures informing the ABM. For example, they can combine egocentric network data sets from the surveys like FluPaths containing the behavioral responses to socio-centric large-scale networks representing large U.S. cities with socio-demographic features (Hartnett et al., 2020). Further, the surveys inform the adaptive behavioral mechanism of the ABM, which can be based on an Adaptive Control of Thought - Rational (ACT-R) framework. ACT-R provides a realistic and mechanistic behavioral model of human cognition grounded in reinforcement learning (i.e., an area of ML), representing the evolution of individuals' experiences, perceptions, and preferences in disease protective measures (Ritter et al., 2019). It brings together multiple psychological theories that account for human perception, learning, memory, decision making, and action. ACT-R models memory activation, retrieval, and mismatch (i.e., retrieval of the wrong information) based on experience frequency and recency, which is well-aligned to modeling how behaviors change in response to changing epidemiological outcomes, information, and risk perceptions. Hence, these tailored surveys lead to a natural convergence between computational simulation modeling, large data, and ML.

So far, in this paper, we have not addressed the pervasive problem of uncertainty. Even if the modeling improvements we suggest prove to be valid, there will be profound limitations on how well they will predict the course of disease under alternative interventions (Steinmann et al., 2020). Actual developments will depend on many factors such as actual infectiousness by pathogen variant, which population groups are most affected, the actual effectiveness of public-service announcements, government credibility, and world events. This will be another instance when public policy reasoning is beset with deep uncertainty (Lempert, 2019; Marchau et al., 2019). Model-based analysis may still be very insightful for describing and understanding what has happened, the many possible ways in which matters may unfold under different interventions, and what intervention packages (including built-in monitoring and preparation for adaptation) will be most robust across the uncertainties. A variety of methods are now well developed for what is now called robust decision-making (RDM). However, they are most effective when the model being used is relatively simple, with perhaps ten rather than dozens or hundreds of uncertain inputs. In such cases, it is possible to explore the consequences of all the combinations of input values and find relatively robust strategies. With this in mind, we see great value in pursuing the enhanced ABM approach that we have described above to represent better the complicated cause-effect relationships among interventions, events, entities and their reasoning, agent networks, agent behavioral changes, and the course of the disease. However, we also urge that

experiments with such a relatively detailed model be used to suggest a much simpler model useful for exploratory analysis of policy options (Davis, 2019). Even the simplified model might have aggregate agents, a primitive network or a simplified equivalent, and different contexts reflecting "phase transitions" in the more microscopic model.

In summary, since public willingness to embrace such measures as social distancing, mask-wearing, and vaccination will be so crucial in managing the continuing COVID epidemic over time, and since deep uncertainties afflict many assumptions about the models and their parameter values, we conclude that

1. New agent-based COVID-19 models should include explicit causal mechanisms reflecting how policies affect public behaviors (in both desirable and undesirable ways), affecting subsequent disease epidemiology; these models should be approximated by somewhat simpler models that are amenable to wide-ranging uncertainty analysis;

2. New tailored longitudinal surveys should be conducted and analyzed with novel machine-learning methods specifically designed to inform empirically these enriched models with difficult-to-predict adaptive behaviors;

3. Policy analysis should use the models and the methods of decision-making under deep uncertainty (DMDU) to compare alternative COVID-19 policies—identifying robust policies, i.e., policies that seem likely to prove effective under a broad range of assumptions.

Such improved models, data, and analytical methods could substantially improve the ability to compare alternative intervention strategies.

References

Adiga, A., Dubhashi, D., Lewis, B., Marathe, M., Venkatramanan, S., & Vullikanti, A. 2020. Mathematical Models for COVID-19 Pandemic: A Comparative Analysis. Journal of the Indian Institute of Science 100, 793–807. https://doi.org/10.1007/s41745-020-00200-6

Alagoz, O., Sethi, A.K., Patterson, B.W., Churpek, M., & Safdar, N. 2020. Effect of Timing of and Adherence to Social Distancing Measures on COVID-19 Burden in the United States. Ann. Intern. Med. 174, 50–57. https://doi.org/10.7326/M20-4096

Aledort, J.E., Lurie, N., Wasserman, J., & Bozzette, S.A. 2007. Non-pharmaceutical public health interventions for pandemic influenza: an evaluation of the evidence

base. BMC Public Health 7, 208. https://doi.org/10.1186/1471-2458-7-208

Auchincloss, A.H., & Garcia, L.M.T. 2015. Brief introductory guide to agent-based modeling and an illustration from urban health research. Cad. Saude Publica 31 Suppl 1, 65–78. https://doi.org/10.1590/0102-311X00051615

Bauch, C.T., & Earn, D.J. 2004. Vaccination and the theory of games. Proc Natl Acad Sci U A 101, 13391–4.

Bhattacharyya, S., & Bauch, C.T. 2012. Mathematical models of the interplay between individual vaccinating decisions and disease dynamics: a need for closer integration of models and data. Hum. Vaccines Immunother. 8, 842–844. https://doi.org/10.4161/hv.19616

Bobashev, G.V., Goedecke, D.M., Feng Yu, & Epstein, J.M. 2007. A Hybrid Epidemic Model: Combining the Advantages Of Agent-Based And Equation-Based Approaches, in: 2007 Winter Simulation Conference. Presented at the 2007 Winter Simulation Conference, pp. 1532–1537. https://doi.org/10.1109/WSC.2007.4419767

Bonabeau, E. 2002. Agent-based modeling: Methods and techniques for simulating human systems. Proc. Natl. Acad. Sci. 99, 7280–7287. https://doi.org/10.1073/pnas.082080899

Breban, R., Vardavas, R., & Blower, S. 2007. Mean-field analysis of an inductive reasoning game: application to influenza vaccination. Phys. Rev. E Stat. Nonlin. Soft Matter Phys. 76, 031127. https://doi.org/10.1103/PhysRevE.76.031127

Bruine de Bruin, W., Parker, A.M., Galesic, M., & Vardavas, R. 2019. Reports of social circles' and own vaccination behavior: A national longitudinal survey. Health Psychol. Off. J. Div. Health Psychol. Am. Psychol. Assoc. 38, 975–983. https://doi.org/10.1037/hea0000771

Bubar, K.M., Reinholt, K., Kissler, S.M., Lipsitch, M., Cobey, S., Grad, Y.H., & Larremore, D.B. 2021. Model-informed COVID-19 vaccine prioritization strategies by age and serostatus. Science 371, 916–921. https://doi.org/10.1126/science.abe6959

Cornforth, D.M., Reluga, T.C., Shim, E., Bauch, C.T., Galvani, A.P., & Meyers, L.A. 2011. Erratic flu vaccination emerges from short-sighted behavior in contact networks. PLoS Comput Biol 7, e1001062. https://doi.org/10.1371/journal.pcbi.1001062

Crane, M.A., Shermock, K.M., Omer, S.B., & Romley, J.A. 2021. Change in Reported Adherence to Nonpharmaceutical Interventions During the COVID-19 Pandemic, April-November 2020. JAMA. https://doi.org/10.1001/jama.2021.0286

Davis, P.K., & O'Mahony, A. 2019. Improving Social-Behavioral Modeling.

Gambhir, M., Bozio, C., O'Hagan, J.J., Uzicanin, A., Johnson, L.E., Biggerstaff, M., & Swerdlow, D.L. 2015. Infectious Disease Modeling Methods as Tools for Informing Response to Novel Influenza Viruses of Unknown Pandemic Potential. Clin. Infect. Dis. 60, S11–S19. https://doi.org/10.1093/cid/civ083

Getz, W.M., & Dougherty, E.R. 2018. Discrete Stochastic Analogs of Erlang Epidemic Models. J. Biol. Dyn. 12, 16–38. https://doi.org/10.1080/17513758.2017.1401677

Gulden, T.R., Hartnett, G.S., Vardavas, R., & Kravitz, D. 2021. Protecting the Most Vulnerable by Vaccinating the Most Active. RAND Corp. https://doi.org/10.7249/PEA1068-1

Hall, V., Foulkes, S., Charlett, A., Atti, A., Monk, E.J.M., Simmons, R., Wellington, E., Cole, M.J., Saei, A., Oguti, B., Munro, K., Wallace, S., Kirwan, P.D., Shrotri, M., Vusirikala, A., Rokadiya, S., Kall, M., Zambon, M., Ramsay, M., Brooks, T., Group, S.S., Brown, C.S., Chand, M.A., & Hopkins, S. 2021. Do antibody positive healthcare workers have lower SARS-CoV-2 infection rates than antibody negative healthcare workers? Large multi-centre prospective cohort study (the SIREN study), England: June to November 2020. medRxiv 2021.01.13.21249642. https://doi.org/10.1101/2021.01.13.21249642

Hartnett, G.S., Vardavas, R., Baker, L., Chaykowsky, M., Gibson, C.B., Girosi, F., Kennedy, D.P., & Osoba, O.A. 2020. Deep Generative Modeling in Network Science with Applications to Public Policy Research. RAND Corp. https://doi.org/10.7249/WRA843-1

Kantor, B.N., & Kantor, J. 2020. Non-pharmaceutical Interventions for Pandemic COVID-19: A Cross-Sectional Investigation of US General Public Beliefs, Attitudes, and Actions. Front. Med. 7. https://doi.org/10.3389/fmed.2020.00384

Kissler, S.M., Tedijanto, C., Goldstein, E., Grad, Y.H., & Lipsitch, M. 2020. Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. Science 368, 860–868. https://doi.org/10.1126/science.abb5793

Kohli, M., Maschio, M., Becker, D., & Weinstein, M.C. 2021. The potential public

health and economic value of a hypothetical COVID-19 vaccine in the United States: Use of cost-effectiveness modeling to inform vaccination prioritization. Vaccine 39, 1157–1164. https://doi.org/10.1016/j.vaccine.2020.12.078

Kwuimy, C.A.K., Nazari, F., Jiao, X., Rohani, P., & Nataraj, C. 2020. Nonlinear dynamic analysis of an epidemiological model for COVID-19 including public behavior and government action. Nonlinear Dyn. 101, 1545–1559. https://doi.org/10.1007/s11071-020-05815-z

Lempert, R.J. 2019. Robust Decision Making (RDM). https://www.rand.org/pubs/external_publications/EP67834.html

Manfredi, P., & D'Onofrio, A. 2013. Modeling the interplay between human behavior and the spread of infectious diseases. Springer, New York.

Manheim, D., Chamberlin, M., Osoba, O.A., Vardavas, R., & Moore, M. 2016. Improving Decision Support for Infectious Disease Prevention and Control: Aligning Models and Other Tools with Policymakers' Needs. RAND Corporation.

Marchau, V.A., Walker, W., Bloemen, P.J., & Popper, S.W. 2019. Decision Making Under Deep Uncertainty: From Theory to Practice. Springer, New York.

Matrajt, L., Eaton, J., Leung, T., & Brown, E.R. 2020. Vaccine optimization for COVID-19: Who to vaccinate first? Sci. Adv. 7, eabf1374. https://doi.org/10.1126/sciadv.abf1374

Pastor-Satorras, R., Castellano, C., Van Mieghem, P., & Vespignani, A. 2015. Epidemic processes in complex networks. Rev. Mod. Phys. 87, 925–979. https://doi.org/10.1103/RevModPhys.87.925

Pearl, J. 2009. Causality. Cambridge University Press.

RAND Corporation, 2014. The American Life Panel. https://www.rand.org/research/data/alp.html

Ritter, F.E., Tehranchi, F., & Oury, J.D. 2019. ACT-R: A cognitive architecture for modeling cognition. WIREs Cogn. Sci. 10, e1488. https://doi.org/10.1002/wcs.1488

Scudellari, M. 2020. How the pandemic might play out in 2021 and beyond. Nature 584, 22–25. https://doi.org/10.1038/d41586-020-02278-5

Steinmann, P., Wang, J.R., van Voorn, G.A., & Kwakkel, J.H. 2020. Don't try to

predict COVID-19. If you must, use deep uncertainty methods. Rev. Artif. Soc. Soc. Simul. 17.

Tande, A.J., Pollock, B.D., Shah, N.D., Farrugia, G., Virk, A., Swift, M., Breeher, L., Binnicker, M., & Berbari, E.F. 2021. Impact of the COVID-19 Vaccine on Asymptomatic Infection Among Patients Undergoing Pre-Procedural COVID-19 Molecular Screening. Clin. Infect. Dis. https://doi.org/10.1093/cid/ciab229

Vardavas, R., Breban, R., & Blower, S. 2007. Can influenza epidemics be prevented by voluntary vaccination? PLoS Comput. Biol. 3, e85. https://doi.org/10.1371/journal.pcbi.0030085

Wang, Z., Bauch, C.T., Bhattacharyya, S., d'Onofrio, A., Manfredi, P., Perc, M., Perra, N., Salathé, M., & Zhao, D. 2016. Statistical physics of vaccination. Phys. Rep., Statistical physics of vaccination 664, 1–113. https://doi.org/10.1016/j.physrep.2016.10.006

Wibmer, C.K., Ayres, F., Hermanus, T., Madzivhandila, M., Kgagudi, P., Oosthuysen, B., Lambson, B.E., de Oliveira, T., Vermeulen, M., van der Berg, K., Rossouw, T., Boswell, M., Ueckermann, V., Meiring, S., von Gottberg, A., Cohen, C., Morris, L., Bhiman, J.N., & Moore, P.L. 2021. SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. Nat. Med. 1–4. https://doi.org/10.1038/s41591-021-01285-x

Yaqub, O., Castle-Clarke, S., Sevdalis, N., & Chataway, J. 2014. Attitudes to vaccination: a critical review. Soc. Sci. Med. 1982 112, 1–11. https://doi.org/10.1016/j.socscimed.2014.04.018