

Special Issue on Infectious Disease Modeling

Read about the application of mathematics and computational science to the COVID-19 pandemic in this **special issue**.

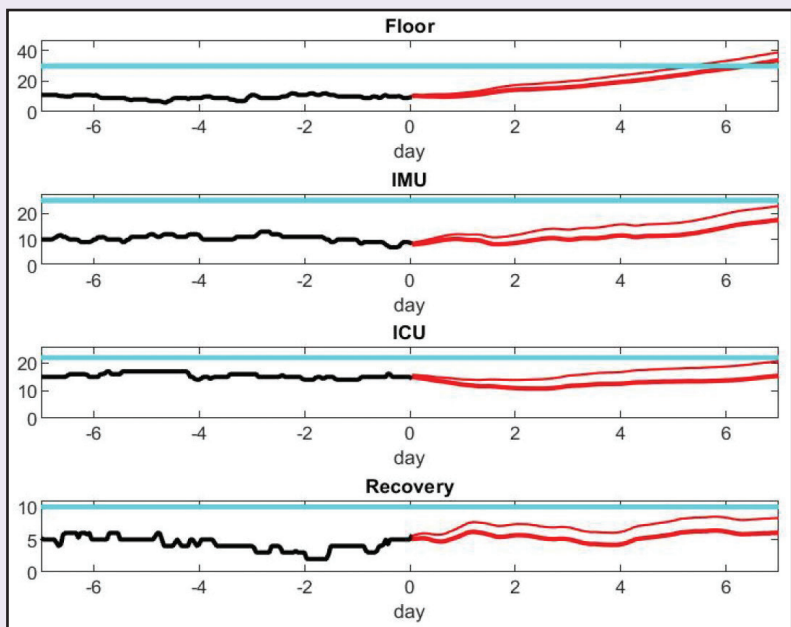


Figure 3. Prediction of unit load in our hypothetical scenario involving a second wave of the pandemic. Figure courtesy of Marc Garbey et al.

In an article on page 5, Marc Garbey, Guillaume Joerger, Shannon Furr, and Vid Fikfak model patient care and resource allocation during COVID-19.

First-principles Machine Learning for COVID-19 Modeling

By Luca Magri and
Nguyen Anh Khoa Doan

In recent months, the novel coronavirus disease 2019 (COVID-19) has affected nearly all corners of the globe. On January 30, 2020, the World Health Organization (WHO) declared the outbreak a Public Health Emergency of International Concern. On March 11, it recognized the outbreak as a pandemic. As of May 4 at 10:00 CEST, WHO reported 3,435,894 confirmed cases of COVID-19, 239,604 confirmed deaths [6], and cases in 215 countries.¹ Government decisions are thus flanked by close scientific advice, perhaps now more than ever.

Mathematical models—which provide predictions about the evolution of the number of infected, recovered, and deceased patients—are central to official advice. The predictions’ accuracy steadily improves as researchers infer the contact rate (β), recovery rate (γ), and death rate (μ) from confirmed cases data. The basic reproduction number (R_0)—the average number of new infections that are generated by a single infected person within a susceptible

population—depends on these rates. In the absence of preventative measures, most accredited sources estimate R_0 to fall within the range of 2-3 [5]. The key epidemic parameters (β, γ, μ, R_0) are crucial in helping governments take appropriate measures to combat the epidemic and *flatten the curve*. Most measures are meant to reduce R_0 , which one can achieve by decreasing the contact rate β or increasing the recovery rate γ [2]. The latter is obtainable with a vaccine or cure, neither of which are currently available. Therefore, governments are presently striving to control COVID-19 by minimizing the contact rate through lockdowns and social distancing. But how can we control a phenomenon about which we know very little?

To start, we must predict the epidemic to stay one step ahead of it—and can do so with modeling techniques. However, how can we model a disease when we only have partial and inaccurate information? The answer to this question is more difficult. Here, we employ a method developed for the prediction of chaotic dynamical systems [1] and apply it to COVID-19 [4]. We combine two sources of past and present

¹ <https://www.who.int/emergencies/diseases/novel-coronavirus-2019>

See **Machine Learning** on page 4

An Alternative System for Curbing COVID-19 Spread in the U.S.

By Samuel Awoniyi

Researchers are currently generating numerous mathematical models that predict both the proliferation and control of the ongoing COVID-19 pandemic. Here I employ Markov chain modeling to compare two possible systems for curbing COVID-19 spread in the U.S. The country is presently utilizing one of these systems, while the other is a proposed alternative system that features a “corps of suppliers and caregivers” to address certain imperfections within the current framework.

My group has designed the alternative system to more effectively control the rate of infection, demand on existing healthcare facilities, overall costs, and disruption to the national economy. One could initiate this method at both the state or community level with only a few weeks of planning, either as a follow-up to—or replacement for—the current system.

The Markov chain model aims to demonstrate the sound mathematical explana-

tion of the proposed alternative system’s superiority. This is followed by a section on practical implementation that would benefit U.S. decision-makers, including state governors’ staff, county commissioners’ personnel, and school system planning committees, among other groups.

Description of the Two Potential Systems

Figure 1 depicts the two possible systems for COVID-19 mitigation in the U.S. In both systems, set B consists of all people in the country who currently test positive for COVID-19, including everyone who is presently hospitalized with COVID-19 symptoms. In the existing system, set A consists of the remaining U.S. population (or community of interest). However, set A is slightly smaller in the alternative method, as it comprises the rest of the population minus set C. And set C encompasses people who are officially commissioned as corps of suppliers and caregivers for everyone in set B.

The official function of individuals in set C is to coordinate and deliver the needs of those in set B, such as food and healthcare supplies, temporary housing, and hospitalization. To minimize infection probability in the proposed system, people in set C—henceforth called “the Red Corps”—will always have all necessary personal protective equipment” (PPE). Detailed guidelines for in-person contacts in this alternative framework are as follows:

Guideline #1: Any person who tests positive for COVID-19 shall promptly move into set B as soon as the test result is known.

Guideline #2: Individuals in set A shall not have any direct, in-person contact with those in set B.

Guideline #3: Everyone in set B shall wear a preventive face mask during all in-person interactions.

Guideline #4: Every member of the Red Corps (set C) shall limit their in-person interactions with people in set B to

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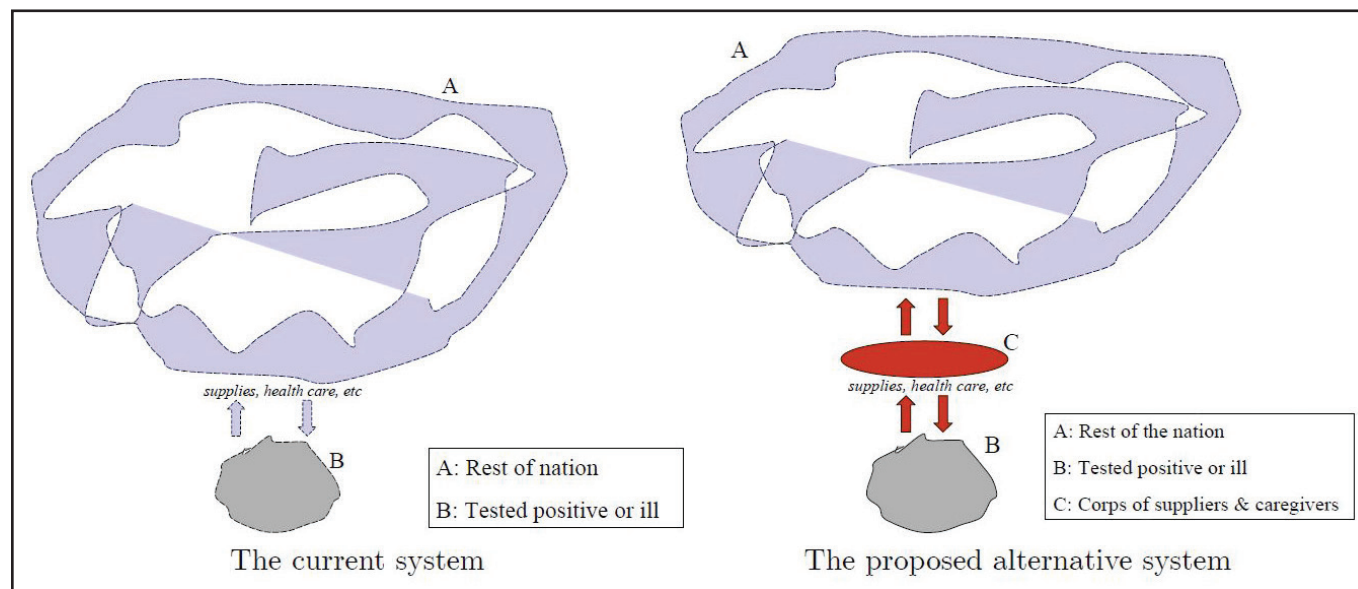


Figure 1. Two possible systems for limiting COVID-19 spread in the U.S. The spongy look of set A is designed to reflect the malleable nature of the country’s relatively free society. Figure courtesy of Samuel Awoniyi.

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8 Florida Students Recognized for Mathematical Model to Forecast the Implementation of Electric Semi-trucks

Each year, high school students from across the U.S. compete in the annual MathWorks Math Modeling (M3) Challenge for over \$100,000 in scholarship funds. The 2020 Challenge problem focused on the trucking industry's eventual transition from diesel fuel to electric power. Students from Pine View School in Osprey, Fla., nabbed the top prize for their complex, multi-part model.

9 Mathematical Modeling in High School: How It Begins and Where It Can Go

Most American high school mathematics programs progress through a standard curriculum without introducing students to the real-world relevance and applicability of math modeling. Alexandra Schmidt, a math teacher at the Emma Willard School in Troy, NY, details her decision to launch a semester-long, project-based math modeling course.



10 Mathematicians Quickly Respond to the COVID-19 Pandemic

The Division of Mathematical Sciences at the National Science Foundation recently requested proposals pertaining to the COVID-19 pandemic. Juan Meza, Zhilan Feng, Tie Luo, and Junping Wang describe the ensuing 15 Rapid Response Research awards that could have a significant impact in mitigating the spread of COVID-19.

11 Computational Science and Mental Health

Joshua Gordon, director of the National Institute of Mental Health (NIMH) at the National Institutes of Health, is dedicated to expanding the boundaries of computational psychiatry. He encourages mathematicians and computational scientists to explore collaborations with the mental health research community and pursue funding opportunities through NIMH's Computational Psychiatry Program.

Message from the Editor-in-chief of SIAM News

By Hans Kaper

As I write this message, the world is still in the midst of the COVID-19 pandemic. The disease has significantly affected our daily lives—both personal and professional—in multiple ways, and the prospect of a speedy return to “normal” is bleak for most countries. If one observation should encourage and cheer us up, however, it is that the word “modeling” has entered mainstream vocabulary. Though it may not always refer to mathematical or computational modeling, the concept has become an integral part of the discussion surrounding SARS-CoV-2 and COVID-19. Mathematical modeling is thus perhaps more important now than ever, as mathematicians and computational scientists have been presented with a unique opportunity to contribute to and shape global dialogue.

The June issue of *SIAM News* is the second of two consecutive special issues

that present various methods and tools of applied and computational mathematics that facilitate our understanding of infectious disease dynamics in numerous contexts. We do not claim that the collection of articles in these two issues provides a comprehensive view of all pertinent topics. Our purpose is to expose a selection of disease-related modeling problems and illustrate the wide range of methods that researchers use to address them. Our main concern in assembling this compilation was timeliness; the articles were solicited (not peer-reviewed) and reflect the authors' opinions. Readers who seek more detailed information should refer to the SIAM Epidemiology Collection, which is freely available for one year and accessible online.¹

We once again thank the authors for their enthusiastic and prompt response to our invitation to contribute articles to

¹ <https://epubs.siam.org/page/EpidemiologyCollection>

this second special issue. The suggestion to publish a series of articles on the spread of infectious diseases originated within the SIAM Activity Group on Mathematics of Planet Earth (SIAG/MPE),² and we appreciate the SIAG's prompt attention to this timely matter.

As your professional society, SIAM is working hard to help facilitate a better understanding of COVID-19 and the research surrounding it. Please visit snews.siam.org for additional posts and relevant mathematical resources.

Hans Kaper, founding chair of the SIAM Activity Group on Mathematics of Planet Earth and editor-in-chief of SIAM News, is affiliate faculty in the Department of Mathematics and Statistics at Georgetown University.

² <https://www.siam.org/membership/activity-groups/detail/mathematics-of-planet-earth>

Obituary: H. Thomas Banks

By William J. Browning

On December 31, 2019, the applied mathematics community lost a prolific researcher, valued collaborator, and thoughtful mentor when Harvey Thomas Banks passed away after a short illness. He was 79 years old. During his long research and teaching career at Brown University, the University of Southern California (USC), and North Carolina State University (NCSU), Tom made seminal contributions

in scientific computing with applications in control and estimation; modeling and control in biomedical systems; smart materials; inverse problems; semi-group theory; and electromagnetic material interrogation. He authored more than 550 peer-reviewed publications and five research monographs. Tom is remembered as an effective teacher and mentor who supervised 51 Ph.D. theses and 40 postdoctoral associates. He was also an outstanding contributor to the applied mathematics community.

Tom was born in Hickory, N.C. on October 30, 1940, and raised in rural North Carolina's Catawba County. He graduated from NCSU in 1963 with a B.S. in applied mathematics before attending graduate school at Purdue University, where he earned his Ph.D. in applied mathematics in 1967. Tom studied under

the guidance of L.D. Berkovitz and wrote his dissertation on control of differential equation systems with delays.

After graduation, Tom joined the Division of Applied Mathematics and the Center for Dynamical Systems at Brown. Solomon Lefschetz had recently founded the latter, which was renowned worldwide for its work in dynamical systems, control theory, and their applications.

From 1969 to 1972, Tom served as director of Brown's Graduate Program in Applied



H. Thomas Banks, 1940-2019. Photo courtesy of Sue Banks.

Mathematics, which led to an early and lifelong interest in mentoring and working with graduate students and postdocs. Though he had a well-deserved reputation as a great teacher at both the undergraduate and graduate levels, Tom occasionally showed limited patience with slackers among his students; this is unsurprising, considering his own amazingly strong work ethic.

In 1970, Tom had the opportunity to work with medical researchers at Rhode Island Hospital on the modeling of glucose homeostasis, which provided a new research direction for him. This stimulated a career-long dedication to teaching and research in biological areas. In the early 1970s, Tom co-taught courses in physiology at Brown's medical school, developed a joint applied mathematics/biomedical sciences program at Brown, and

devoted significant research energy to topics in biology, such as enzyme kinetics, physiological control systems, and enzyme cascades in biochemical pathways.

In 1971, Jacques-Louis Lions invited Tom to spend a month at Inria and lecture on biomedical applications of control and identification. These lectures inspired a long and fruitful collaboration with numerous French applied mathematicians, an honorary faculty position at Université de Technologie de Compiègne (UTC), and multiple exchange visits between the groups at Brown and UTC.

Tom's work in the biological sciences resulted in research contributions to a wide variety of topics, including reaction-diffusion in membranes; protein synthesis; enzyme-regulated pathways in glycogenolysis; insect population growth and dispersal; size-structured models in fish populations; transport in brain tissue; physiologically-based pharmacodynamics kinetic models of toxic agents in animals; detection of coronary stenosis via propagating waves in viscoelastic tissue; and electromagnetic interrogation in tissue by means of natural and/or acoustically generated electrical interfaces.

In 1974, Tom met Franz Kappel in Würzburg, Germany. They quickly became good friends and professional colleagues, initiating a lengthy research collaboration when Kappel and his family visited Brown later that same year. The pair initially focused their joint efforts on approximation methods for delay systems, but subsequent collaboration included semigroup methods for inverse problems — especially those involving size-structured population models for fish populations. An important benefit of their association was exchange visits for many young mathematicians in the research centers at Brown/USC/NCSU and the University of Graz.

In 1980, Milt Rose, director of the Institute for Computer Applications in Science and Engineering (ICASE) at NASA's Langley Research Center, asked Tom to help develop and direct an ICASE program in control theory to provide basic mathematical and computational research for NASA-related scientific and engineering questions. In addition to recruiting and mentoring many excellent postdocs for the program, Tom developed numerous collaborations with NASA engineers. These partnerships significantly affected the directions of his own research, as well as that of his students and postdocs.

At the time of his ICASE involvement, Tom began a series of interactions with scientists and engineers at air force

See H. Thomas Banks on page 6

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Networked Epidemiology for COVID-19

By Jiangzhuo Chen, Simon Levin, Stephen Eubank, Henning Mortveit, Srinivasan Venkatramanan, Anil Vullikanti, and Madhav Marathe

Computational epidemiology aims to develop computer models and decision support systems that understand, predict, and control a disease's spatio-temporal diffusion throughout a population. Researchers can use these models to forecast an epidemic's future course, allocate scarce resources and assess depletion of current resources, infer disease parameters, and evaluate various interventions. Individual behavior and public policy are critical in understanding and controlling infectious diseases, and computational techniques provide a potentially powerful study tool. The COVID-19 pandemic has had significant social, health, economic, and political ramifications worldwide, and its impact will undoubtedly continue to grow in the coming months. Here we outline an approach to support the COVID-19 response with examples that are rooted in network science and data-driven modeling.

Computational Models: From ODEs to Multi-scale Networks

Compartmental mass action models are a cornerstone of mathematical epidemiology. They partition a homogeneous population into a small set of compartments that represent the possible disease states—e.g., susceptible (S), infectious (I), and removed (R)—and specify transition rates between states. Epidemiologists have successfully used these models in the past and continue to do so. Desirable features of comparten-

tal models include their analytical tractability—one can analyze simple dynamic models using scalable numerical simulations, or solve them to yield closed-form solutions or asymptotic limits—and their light demands on computational resources.

An alternative way to study epidemics involves explicit representation of the underlying contact structure that drives them [1-3]. We focus on networked models that consider epidemic spread on an undirected social interaction network $G(V, E)$ over population V . Each edge $e=(u, v) \in E$ implies that individuals (also referred to as nodes) $u, v \in V$ interact. The specific form of interaction depends on the disease in question; for example, sexually transmitted diseases require physical sexual contact, while respiratory illnesses necessitate only physical proximity. Let $N(v)$ denote the set of neighbors of v . The SIR model on graph G is a dynamical process during which each node is in either an S , I , or R state. Infection can potentially spread from u to v along edge $e=(u, v)$ with a probability of $\beta(e, t)$ at time t after u becomes infected, which is conditional on node v remaining uninfected until time t ; this is a discrete version of the infection rate for the aforementioned ordinary differential equation (ODE) model. We allow $I(t)$ to denote the set of nodes that become infected at time t . The random subset of edges on which the infections spread represents a disease outcome and is called a dendrogram. This dynamical system begins with a configuration that features one or more nodes in state I and ultimately reaches a fixed point where all nodes are in states S or R . Some key topics of interest are as follows: (i) Characterization of aspects of $I(t)$ (the *epicurve*)—such as its peak, the time at

which the peak occurs, and its integral (the outbreak size)—as a function of the disease model parameters and network structure; and (ii) the effectiveness of various interventions, including vaccination (which can be modeled as node deletions) and social distancing (which can be modeled as edge deletions).

Networks: Scale, Structure, and Detail

One must treat the network $G(V, E)$ as a first-class model parameter, on equal footing with disease-related parameters like transmissibility and incubation period. This step simply acknowledges the importance of parameters that are swept under the rug by mass action assumption.

Because certain combinations of parameters—such as transmissibility and network structure—are not separately identifiable, problems with mass action assumption are not immediately obvious. Instead, they arise when one attempts to understand the effects of interventions.

For example, consider the following intervention: *reduce contacts by 50 percent*. Figure 1 illustrates three plausible interpretations. Figure 1a reduces the probability of transmission (represented by an edge weight) in each contact by 50 percent, 1b reduces the number of contacts by 50 percent, and 1c cuts the graph in half. The dynamics on each of these graphs are clearly different.

See *Networked Epidemiology* on page 7

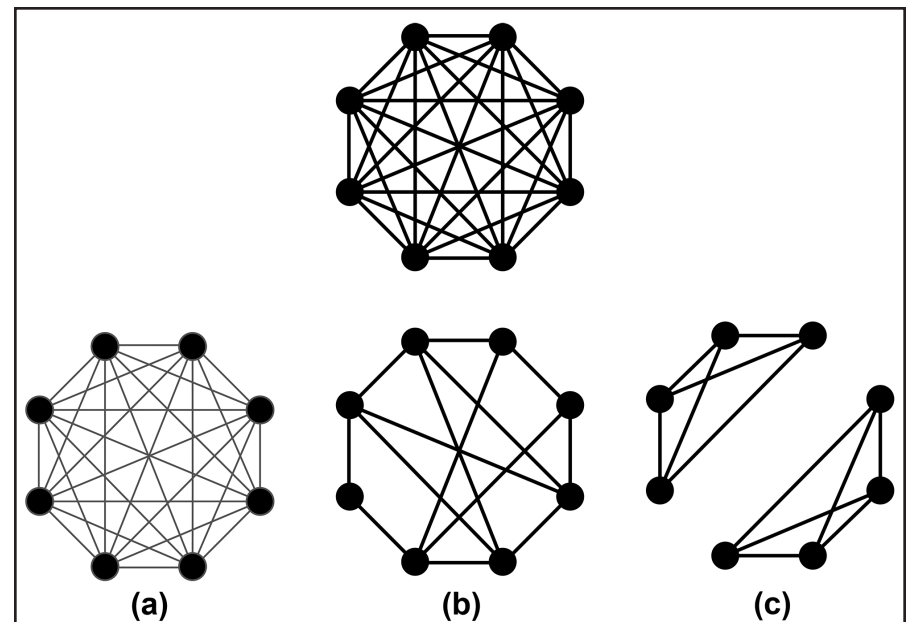


Figure 1. Three interpretations of “reducing contacts by half” in the top network. **1a.** Reducing the strength of each contact by half. **1b.** Reducing the number of contacts by half. **1c.** Reducing the size of connected components by half. Figure courtesy of Stephen Eubank.

Alternative System

Continued from page 1

essential deliveries of needed supplies and healthcare resources.

Guideline #5: Any person in set B shall move to set A after fully recovering from COVID-19; this might include possessing the requisite antibodies.

My team's proposed alternative system somewhat resembles a compartmental model in the area of infectious disease modeling [3]. However, use of a Markov chain sojourn time cycle [1]—rather than mathematical analysis, as with typical compartmental models—makes our modeling efforts unique.

Two Corresponding Markov Chain Models

We utilize two discrete-time Markov chain models, based on the previous guidelines, to explain the superiority of our alternative system. Each model tracks the way in which COVID-19—behaving like a traveling deliverer of harmful packages—moves back and forth between sets B and A in the current system, and sets B and C in the proposed alternative system. This application justifies requisite Markov assumptions because COVID-19's infection rate depends only on society's diligence in following the five aforementioned guidelines.

Figure 2 depicts two discrete-time Markov chains (DTMCs). The meaning of states A, B, and C are the same as in Figure 1 (on page 1), and the probability of 1 in each DTMC is on account of guideline #1: *Any person who tests positive for COVID-19 shall promptly move into set B as soon as the test result is known.*

Probability p_1 reflects the relatively free in-person interactions between individuals in sets A and B in the current system. Similarly, probability p_2 reflects the carefully controlled in-person interactions between the Red Corps (set C) and occupants of set B in the proposed alternative system. Accordingly, one would ordinarily have $p_1 \gg p_2$.

If we let $STC1$ denote the sojourn time cycle for the current system's DTMC and $STC2$ denote the sojourn time cycle for the proposed alternative system's DTMC (see Figure 2), we then have $STC2 \gg STC1$ by virtue of $p_1 \gg p_2$, because $STC1 = 1/p_1 + 1$ and $STC2 = 1/p_2 + 1$. A straightforward introduction to the computation of sojourn time cycles for general Markov chains is available in [1].

For instance, if $p_1 = 0.5$ and $p_2 = 0.1$, then $STC1 = 3$ and $STC2 = 11$. Because STC signifies “average time to next infection” in this application, it is evident that the average time to next infection for the proposed alternative system would ordinarily be much longer than for the current system.

Practical Implementation

Regarding practical implementation, our alternative system first and foremost requires that some form of reliable COVID-19 testing be available to everyone in the U.S. Testing of Red Corps members must be especially prompt; otherwise the proposed framework will not fare much better than the current system in terms of infection probability.

Red Corps members include healthcare teams, grocery and food supply personnel, and communications supply groups. Most Red Corps members will have preferably acquired some COVID-19 antibodies. Each member must wear suitable PPE during in-person interactions with people in set B, and a proper face mask in grocery stores and other shops. This requirement is meant to minimize the probability of a Red Corps worker infecting the general population.

Asymptomatic set B members should be housed in suitable hotels, separate from the members of set B who already show symptoms. These symptomatic individuals should be housed in hospitals that are specialised for COVID-19 patients. Each set B member must wear an appropriate face mask during in-person interactions with Red Corps members. As per guideline #2, people who are currently in set B must not have in-person interactions with those in set A.

Everyone in set A must wear a suitable face mask during in-person interactions involving four or more people. Members of set A who are certified to possess some COVID-19 antibodies can go to work as planned or needed. As such, COVID-19's overall adverse impact on the national economy would likely be much less under the proposed system than the current system.

Since our proposed alternative system involves substantial reduction of human freedom in society, it should be suspended shortly after a viable COVID-19 vaccine or treatment becomes available. One may also suspend the alternative system about one month after set B becomes virtually empty. The fact that an infected person

will either die or recover and develop the necessary antibodies guarantees set B's eventual emptiness.

Ultimately, our proposed method is well-suited to prevent a second wave of COVID-19 infections because the Red Corps will keep set B below *critical community size*—the minimum size of a closed population within which a human-to-human, non-zoonotic pathogen can persist indefinitely [2, 3].

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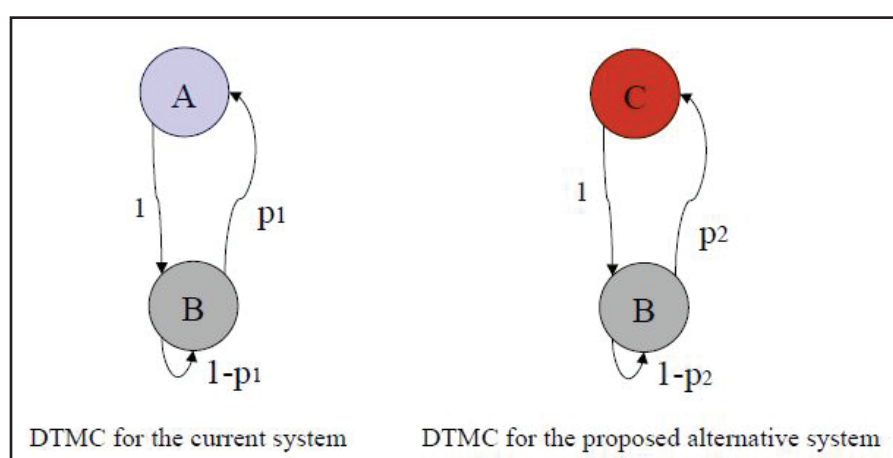


Figure 2. Two discrete-time Markov chains (DTMCs). Figure courtesy of Samuel Awoniyi.

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Machine Learning

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knowledge—first principles of an epidemic model and data on COVID-19 confirmed cases from official databases—to predict the future. While (some) human brains are well suited to capture the first principles that govern a problem, machine learning is more effective at identifying quantitative correlations in data. *First-principles machine learning* synergistically combines the strengths of human brains and machines. We showcase the method on a prototypical epidemic model, but one can apply the technique to more sophisticated models.

A Bit of Maths

To model an epidemic (as with any other phenomenon), we must capture the first principles—assumptions, constraints, laws, and so forth—that govern the dynamics. These principles serve as the “game rules” and should not be violated. We divide a country’s entire population into mutually exclusive groups: population (N) = susceptible (S) + infected (I) + deceased (D) + recovered (R). We assume that the population is constant but the other variables change in time. Each group therefore possesses the same characteristics—i.e., groups are homogeneous—and every susceptible person can contract the virus.

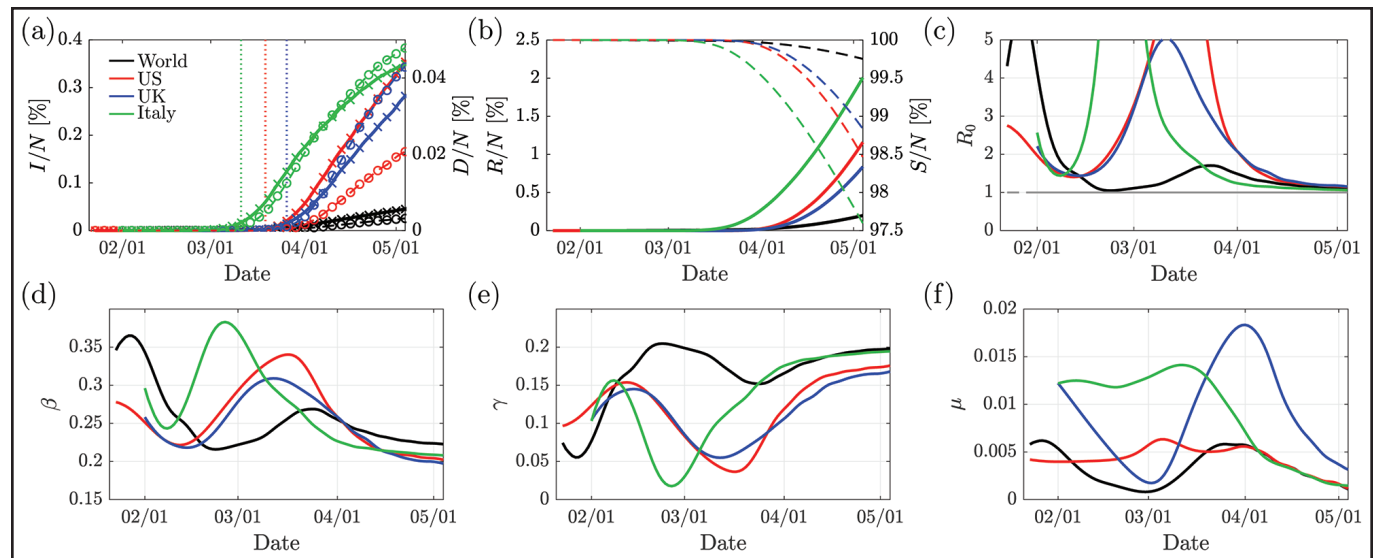


Figure 2. The epidemic’s evolution. **2a.** The left axis represents estimated infected individuals. Crosses indicate data and solid lines indicate the model. The right axis represents deceased cases. Circles indicate data and dashed lines indicate the model. The three dotted vertical lines designate the beginning of lockdown for each country. **2b.** The left axis represents inferred recovered individuals (solid lines). The right axis represents susceptible individuals (dashed lines). **2c.** Basic reproduction rate. **2d.** Contact rate. **2e.** Recovery rate. **2f.** Death rate. Dates are in month/day format. Figure adapted from [4].

demographic model (first principles), and a feed-forward neural network (machine learning) that assimilates the data into the epidemic model to learn the parameters and state (see Figure 1). To begin, the neural network (NN) receives as an input the time histories of the cumulative confirmed infected cases and confirmed deaths up until May 4, 2020. This data is accessible online.² Using the time

and healthcare demand. Imperial College COVID-19 Response Team.

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³ <https://epcced.github.io/ramp/>

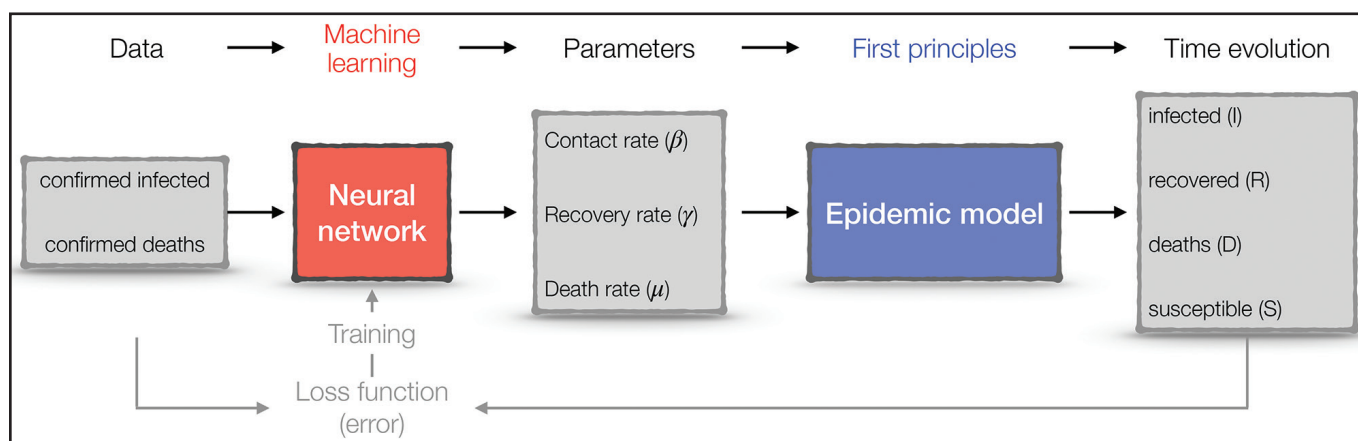


Figure 1. First-principles machine learning for epidemic modeling. Figure adapted from [4].

One can relax these working assumptions in more complex models [2]. This approach is known as the SIR epidemic model with vital dynamics and constant population [3]; we refer to it as the SIRD model for brevity. We use four ordinary differential equations with time-varying parameters (a nonlinear, non-autonomous dynamical system) to mathematically describe the first principles:

$$\begin{aligned} \dot{S} &= -\beta(t) \frac{I}{N} S, & \dot{I} &= -\dot{S} - \dot{R} - \dot{D}, \\ \dot{R} &= \gamma(t) I, & \dot{D} &= \mu(t) I. \end{aligned} \quad (1)$$

These equations are subject to initial conditions. The parameters depend on governmental policies (lockdown, school closures, social distancing, etc.), population heterogeneity (age, lifestyle, herd immunity, hygiene standards, etc.), and the epidemic’s properties (virus genome, spreading mechanisms, etc.). The basic reproduction ratio is $R_0 \equiv \beta / (\gamma + \mu)$. If $R_0 > 1$, the number of infected individuals increases; if $R_0 < 1$, the number of infected individuals decreases on average.

Formalizing the Problem

One can formulate the calculation of the groups’ time evolution and the time-varying epidemic parameters as a constrained optimization problem (or equivalently, a data assimilation problem): *Calculate the number of infected, recovered, deceased, and susceptible individuals; contact rate; recovery rate; and death rate to minimize the error between data and predictions from the epidemic model.* We want to accept only those candidate solutions that are consistent with the epidemic model. More details on the loss function are available in [4].

Solving the Problem

Our proposed first-principles machine learning epidemic model is based on a combination of an ordinary differential equation solver that time-advances the epi-

demographic model (first principles), and a feed-forward neural network (machine learning) that assimilates the data into the epidemic model to learn the parameters and state (see Figure 1). To begin, the neural network (NN) receives as an input the time histories of the cumulative confirmed infected cases and confirmed deaths up until May 4, 2020. This data is accessible online.² Using the time

histories of the confirmed cases, the NN next infers the time evolution of the epidemic model’s parameters. We minimize the loss function—which measures the error between the candidate solution and data—to train the network. We then feed the inferred epidemic parameters into the SIRD model’s time integration. This time integration provides the state’s evolution (number of infected, recovered, deceased, and susceptible individuals). Figure 2 depicts the results. At the epidemic’s inception and in the absence of preventative measures, COVID-19 cases grow exponentially. Implementation of preemptive measures significantly impacts R_0 , which decreases to values that are close to unity. Although the results are consistent with the employed first principles, they are affected by uncertainty because of biases in the data—such as errors in reporting, changes in case definition and testing regime, and, of course, modeling assumptions. However, the fast growth rate and large numbers likely make small biases negligible [5], and multiplicative corrections—such as constant under-reporting—only weakly affect the observed trend. Our proposed data-driven and model-informed methodology reveals new possibilities for inferring an epidemic’s evolution from data (see Figure 1) [4]. Future researchers should utilize more detailed epidemic models and data to improve predictions.

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² <https://github.com/CSSEGISandData/COVID-19>

SIAM to Host a Virtual Career Fair

In light of the ongoing pandemic, we’ll be hosting our annual Career Fair virtually this year since we can’t be together in person. Save the date and check SIAM News Online for details on how to participate as a job seeker, employer, or sponsor!

Virtual Career Fair Happening:
July 7, 2020 from 11am-2pm EST



A Mathematical Model to Support Hospital Workflow Management During a Pandemic

By Marc Garbey, Guillaume Joerger, Shannon Furr, and Vid Fikfak

As with all pandemics, the worldwide spread of COVID-19 is significantly hindering patient flow management and severely straining hospital resources. Therefore, some healthcare professionals must make difficult decisions regarding patient care and resource allocation. While checklists for patient triage do exist, the dynamics of pandemics make efficient execution of these lists especially challenging. Senior management thus requires a tool that facilitates end-to-end demand visibility to identify and predict hospital bed constraints.

Multiple governmental and private agencies have focused on the creation of dashboards to supply the general public with assessments of COVID-19. A significant amount of literature concerning mathematical models in epidemiology provides a rigorous framework for the prediction of COVID-19 dynamics [9, 10]. However, providing the necessary information at the local hospital scale to optimize the management of patient workflow is complex, primarily because researchers still do not fully understand the disease. Every hospital must therefore adapt to COVID-19's daily changes. As guidelines take time to implement, following the most up-to-date information yields significant variety in clinical practices.

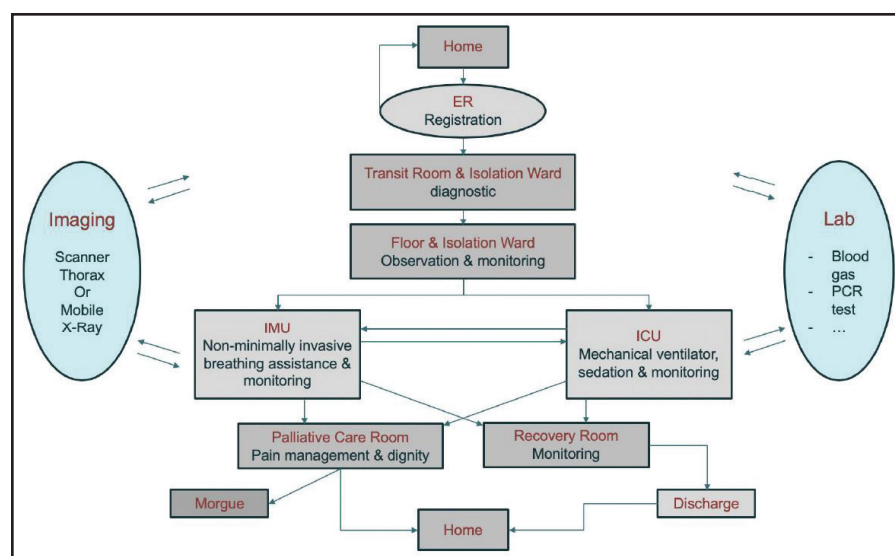


Figure 1. Patient workflow in a hospital.

The Appropriate Data Set and Agile Mathematical Modeling

The French government has released records of most public hospitals around the country during the COVID-19 crisis. This file¹ reveals the number of patients in hospitals, the number of patients in the intensive care unit (ICU), the number of patients that are recovered and discharged, and the number of patients that have died in a medical institution. These numbers are updated daily and date back to March 18, 2020. Because of the sparsity of available data, we begin with a very simple model that reproduces the workflow to match the disease management of each patient (see Figure 1).

Most patients who require hospitalization are first placed on a medicine floor for further assessment and treatment. Non-invasive monitoring, as well as imaging and blood tests, help determine patients' conditions and continue for the duration of their hospital stay. These resources—i.e., imaging and laboratory work—are shared by all patients in the hospital and may slow down the process when overwhelmed with users. Some people who receive medical attention do well with conservative management techniques and are discharged after only a few days. Other patients' health conditions may deteriorate, necessitating a move to the

¹ <https://www.data.gouv.fr/en/datasets/donnees-hospitalieres-relatives-a-lepidemie-de-covid-19/>

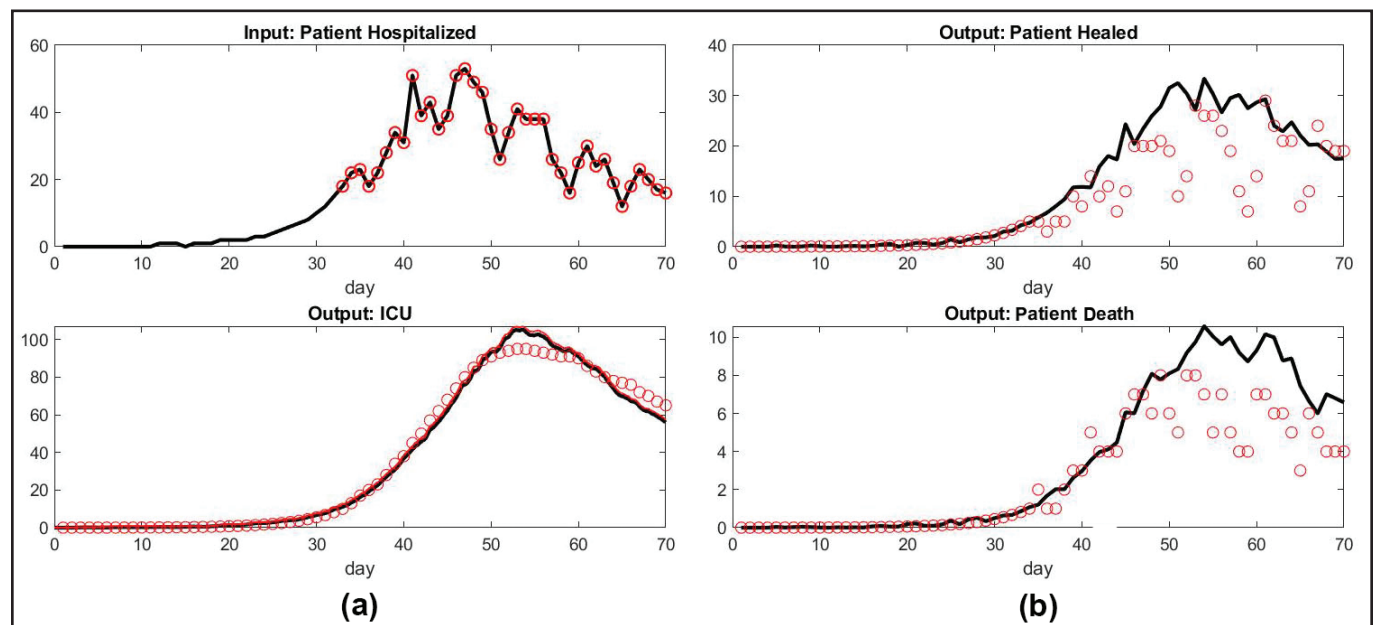


Figure 2. Model compared with data from France hospitals. Day 33 corresponds to March 18, 2020: the first date of our data set. Day 70 corresponds to April 24, 2020. We assume an exponential model of hospital admission for the missing period prior to March 18. **2a.** Top: input of patient hospital admission. Bottom: patients under mechanical ventilation in the intensive care unit (ICU) versus the data set. **2b.** Top: number of recovered patients leaving the hospital each day. Bottom: number of deaths per day.

intermediate care unit (IMU) for additional care or the ICU for ongoing monitoring and sometimes mechanical ventilation.

The IMU and ICU require extensive supplies and resources. Ventilators are not the only limiting factor, as patients under mechanical ventilation need sedation and might be connected to additional systems that handle organ failure. We can add these

hospitals, recovering COVID-19 patients and palliative care patients might share the same floor. To summarize, we create a simple workflow graph that seeks to determine (i) the probability of a patient transitioning from one care unit to another and (ii) a statistical estimate of the patient's duration of stay in each care unit.

The discrete model is stochastic, so we need to run many simulations to build a statistical estimate of quantities of interest. The number of unknown parameters that we must retrieve by fitting the data is relatively large. To avoid overfitting, researchers should devise a strategy that lowers the number of unknowns based on either clinical literature or validated hypothesis. One can retrieve the model's unknown parameters via a stochastic optimization method since the workflow process—like that of the hospital—is discrete, noisy, and nonlinear.

A patient's condition is dominated by the disease's evolution. Furthermore, medical procedures accumulate delays; the durations of both biological and managerial processes are often described by a lognormal distribution with a long tail. This does not contradict the fact that a simple exponential distribution may not ideally depict a patient's length of stay (LOS) in the hospital. Overall, LOS adds up the time distribution of every step in a Markov process and might be described at the convolution of each step's probability distribution [7]. For example, we found it necessary to introduce an artificial two-phase decomposition of patient stay in the ICU to bypass the limitation of a single distribution that may not represent an adequate model of LOS in this unit, according to clinical studies [1].

To guide the optimization process, we employ a stability analysis of the model

that ranks the most sensitive parameters, which should be estimated first. Performance depends on staff conditions and patient population, and the clinicians are clearly experienced with LOS in each step and provide an ad hoc window of time that we can fine-tune as a second pass of the algorithm. It is difficult to recover the true rate of death at the beginning of a new pandemic.

Our first, simplified model essentially requires the calibration of six parameters with a genetic algorithm that compares the model to France's data set [4]. Figure 2 depicts the model's success compared with France's data set from March 18, 2020 to April 24, 2020.

Retrieving Information to Rationalize a Strategy

A manager may have the following simple yet essential questions. How many beds are needed on each floor and how many are available in the critical care unit? How many supplies should be ordered to support patient care and protect staff from infection? How long must the facility operate at maximum capacity, and is there enough staff to sustain this workload? One key factor involves anticipating the load of each care unit and required resources, either to match the patient increase or reallocate resources and begin rescheduling previously cancelled surgeries, for example.

We chose a hypothetical scenario that involves a second wave of the pandemic to illustrate this concept. We assume that the hospital has a nominally low flux of patients from weeks one to seven, and a recurrence with a daily 20 percent increase of new patients at week eight. Figure 3 (on page 1)

See Hospital Workflow on page 6

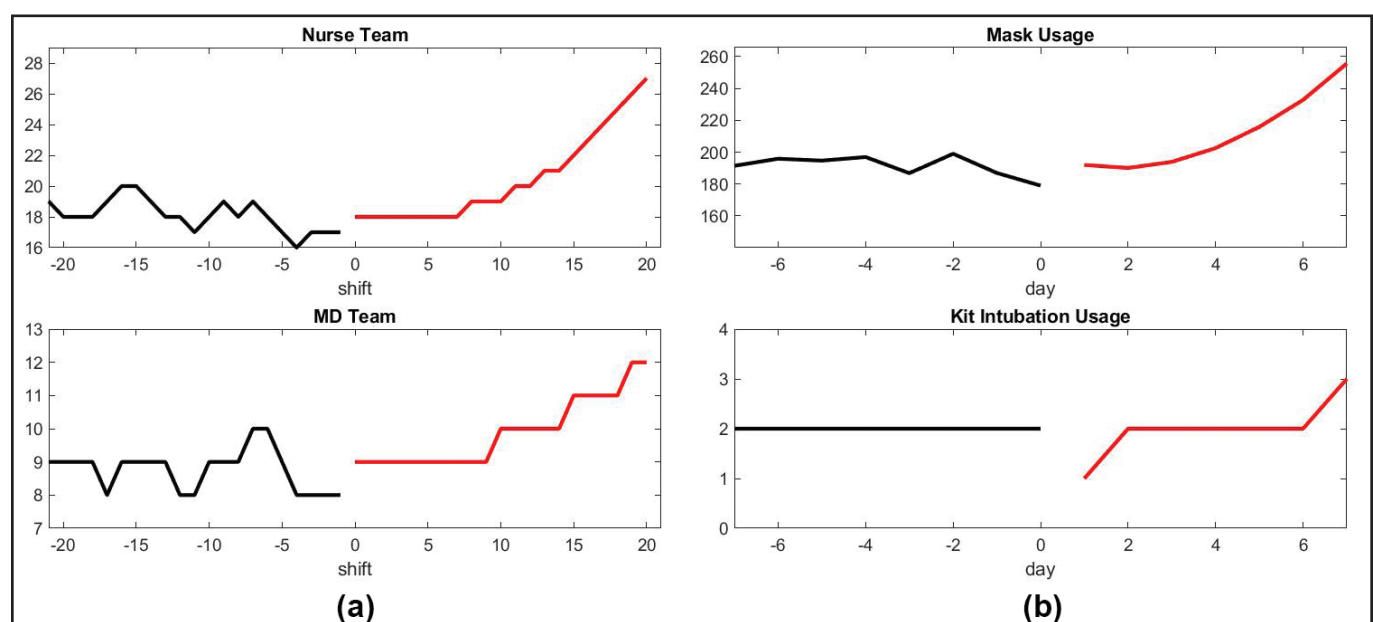


Figure 4. Prediction of required infrastructure for our hypothetical scenario involving a second wave of the pandemic. **4a.** Number of staff required for each eight-hour shift. **4b.** Number of supplies needed per day.

Hospital Workflow

Continued from page 5

displays the load dynamics of each care unit. The black curves mark week seven and the red curves predict week eight, when the second wave hits. The thin uppermost red curve displays the deviation up one standard deviation and provides a sense of the estimate's uncertainty, which grows as the prediction time gets further away. The blue curve depicts the hypothetical capacity of each care unit; the floor would become saturated first and necessitate new beds after just a few days. A manager who sees this prediction would therefore continue cancelling elective surgeries in expectation of COVID-19 patients occupying the floor, and anticipate the need for on-staff recruitment and additional supplies (see Figure 4, on page 5).

Our model could also allow managerial staff to make multiple decisions regarding patient care. Figure 5 compares patient output with and without a shortage of nurses. These results are speculative since it is difficult to quantify patient risk beyond published results [2, 3, 6]. We hope that new data accumulated during the COVID-19 crisis will provide the base for mathematical modeling to rigorously conduct this estimate in future works.

There are admittedly several limitations to our approach. Smaller hospitals yield less predictable outcomes, and the characteristics of the patient population that visits the emergency room change with time. Systematic testing would likely provide early diagnostics and impact the health system's performance, as evidenced by the statistics of countries that adopted this strategy from the onset. Due to the heterogeneity of the patient population and disease patterns that depend heavily on patient characteristics, our next step to improve this model involves the inclusion of patients' medical history from their electronic medical records. We plan to feed our model of hospital workflow with an epidemic model that maintains accuracy in the hospital's ecosystem. Ultimately, we anticipate that the future of computational models in digital health during a pandemic will extensively include sociological and economical modeling components.

The figures in this article were provided by the authors.

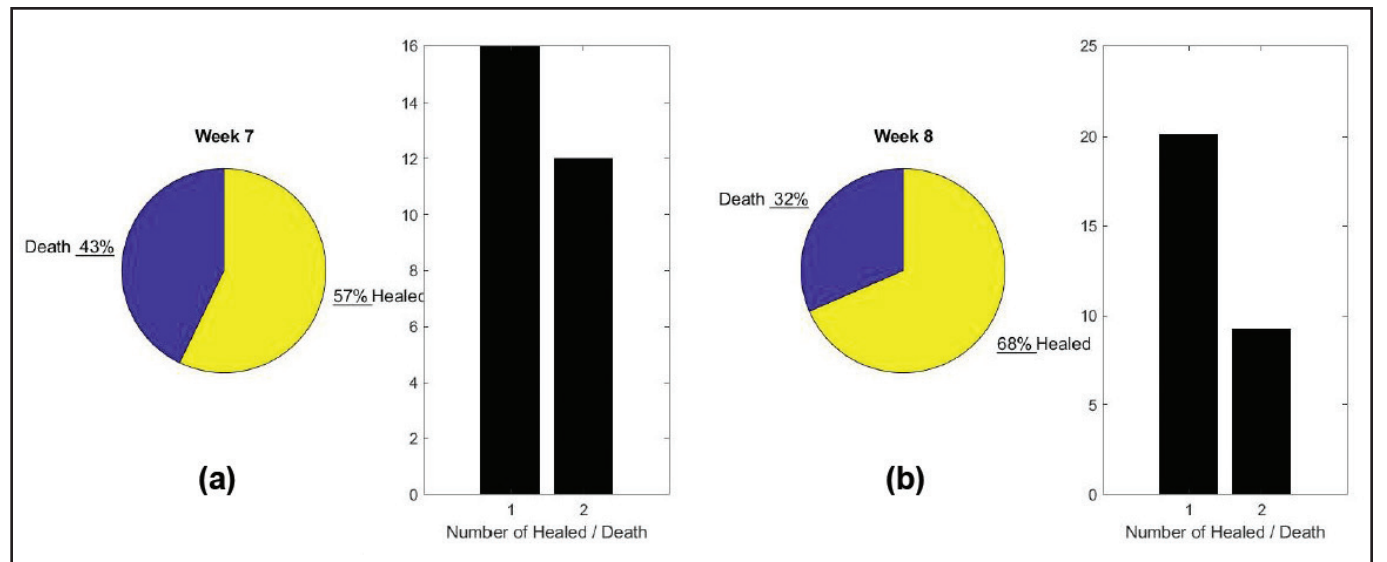


Figure 5. Prediction of performance in our hypothetical scenario involving a second wave of the pandemic. 5a. Patient output for the previous week. 5b. Predicted patient output for the next week.

Acknowledgments: We would like to thank Patrick Doolan for sharing his view on management and risk evaluation based on his experience in the energy sector.

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always worked quickly and accurately, thus attracting many like-minded collaborators from a wide variety of engineering and scientific disciplines. Service to the profession was important to Tom. He was elected to the SIAM Board of Trustees and served as chair of the board. He also held multiple service positions at SIAM, including on the editorial board of the *SIAM Journal on Control and Optimization*; Tom was the managing editor from 1979 to 1981 and 1986 to 1988. In addition, he was the Vice President for Publications and acted as founding editor and editor-in-chief of the SIAM book series on *Frontiers in Applied Mathematics*. Tom received numerous honors for his research and service. These accolades include SIAM's W.T. and Idalia Reid Prize, NCSU's Distinguished Scholarship Achievement Award, and Purdue's Distinguished Alumni Award. He was also an elected Fellow of the Institute of Physics and the Institute of Electrical and Electronics Engineers, as well as an Alumni Distinguished Graduate Professor at NCSU and Professeur Honoraire at Université de Technologie de Compiègne. Students, postdoctoral researchers, and colleagues were extremely significant in Tom's life, but his wife Sue was the most important part of his professional and personal endeavors. It was her efforts that led many of the students, postdocs, and visitors to become members of the Banks' extended family. Tom is survived by his wife Sue, son John, daughter Jennifer, and grandchildren Samantha and Emilie. He was admired and respected by all who knew him for his kindness, collegiality, generosity, and strong work ethic, and is sorely missed by family, students, colleagues, and friends. Please see the online version of this article for additional material.

H. Thomas Banks

Continued from page 2

laboratories. The most significant of these interactions resulted in a project with a group at Brooks Air Force Base, led by Richard Albanese. Tom met Albanese in the early 1990s and enjoyed a substantial and almost immediate scientific rapport, which promoted intense activities in electromagnetics and the health sciences for Tom and his graduate students. Another important influence in the 1980s originated from a chance meeting between Tom and Daniel J. Inman at a workshop on control of flexible structures that was sponsored by the Air Force Office of Scientific Research. Their friendship generated significant collaborative efforts in control and identification, particularly in vibration-based damage detection methods for smart material structures.

In 1989, Tom established the Center for Applied Mathematical Sciences, a research institution in applied mathematics at USC. He became the center's first director. Three years later, Tom joined the faculty of NCSU as University Professor and Drexel Professor of Mathematics. He made a number of important institutional contributions at NCSU, in addition to pursuing a prolific career in both research and education. For example, Tom resuscitated the Center for Research in Scientific Computation and founded the internationally recognized Industrial Applied Mathematics Program, which specializes in research projects and graduate/postdoctoral training with industries and government laboratories.

Tom was also one of the four founding directorate members of the Statistical and Applied Mathematical Sciences Institute (SAMSI) in North Carolina. He served on the directorate from 2002 to 2005, leading the effort in applied mathematics as well as education and outreach. Tom developed the SAMSI Education and Outreach (E&O) Program to foster participation of undergraduates, graduate students, and postdoctoral fellows in joint statistical/mathematical research projects. This program has become the model for similar E&O programs at other institutes of the National Science Foundation.

Throughout his lengthy research career, Tom retained a sharp eye for identifying emerging application areas to which he then made substantial contributions. He

William J. Browning is the CEO and founder of Applied Mathematics, Inc. He studied under L.D. Berkovitz at Purdue University and collaborated with Tom Banks on research projects for many years.

Acknowledgments: The author wishes to thank Wendell Fleming of Brown University for his valuable assistance in putting this tribute together.

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SIAM Members Honored for Notable Achievements

Over the last few months, several SIAM members were recognized in various capacities for their outstanding work in the fields of applied mathematics and computational science. We applaud their accomplishments and thank them for their continuous service to the profession. The subsequent members are those of which we are aware; we of course offer our congratulations to anyone we might have accidentally overlooked.

This spring, **Andrew Stuart** was elected as a Fellow of the Royal Society for his exceptional contributions to scientific understanding, which embody the global nature of science. Stuart is the Bren Professor of Computing and Mathematical Sciences in the Department of Computing and Mathematical Sciences at the California Institute of Technology.

Bonnie Berger was elected as a new member of the National Academy of Sciences for her distinguished and ongoing achievements in original research. Berger is the Simons Professor of Mathematics in the Department of Mathematics at the Massachusetts Institute of Technology (MIT). She also holds joint appointments in electrical engineering and computer science, serves as head of the Computation and Biology group in MIT's Computer Science and Artificial Intelligence Laboratory, and is an associate member of the Broad Institute of MIT and Harvard University.

Finally, **Ioannis G. Kevrekidis**, **Tamara G. Kolda**, and **Jorge Nocedal** were elected to the National Academy of Engineering. Kevrekidis is Bloomberg Distinguished Professor in the Department of Chemical and Biomolecular Engineering at Johns Hopkins University, where he also holds appointments in the Department of Applied Mathematics and Statistics and the Department of Urology. He was recognized for his "research on multiscale mathematical modeling and scientific computation for complex, nonlinear reaction, and transport processes." Kolda is a Distinguished Member of the Technical Staff at Sandia National Laboratories and was honored for her "contributions to the design of scientific software, including tensor decompositions and multilinear algebra." Nocedal is the Walter P. Murphy Professor of Industrial Engineering and Management Sciences and (by courtesy) Engineering Sciences and Applied Mathematics at Northwestern University. He is also the director of Northwestern's Center for Optimization and Statistical Learning. Nocedal was recognized for his "contributions to the theory, design, and implementation of optimization algorithms and machine learning software."

Congratulations to these esteemed members of SIAM!

Networked Epidemiology

Continued from page 3

Figure 2 depicts the probability of a single, randomly selected person infecting as many as three other people on each graph as a function of the probability of transmission. One can calibrate a model’s transmissibility for a range of outbreak sizes to yield the same probability of large outbreaks on each graph: 0.2 in Figure 2. Given only the attack rate, the network structure and transmissibility are thus not separately identifiable.

The *only* way to represent changes in network structure in mass action models is to adjust transmissibility, but this often has unrealistic consequences for model outcomes (in addition to outbreak size). In particular, a “stay at home” policy is best represented by the network in Figure 1c (on page 3). A mass action model of staying at home severely distorts the epidemic curve. The true policy impact is given by the sum of many outbreaks in cliques whose sizes are drawn from the distribution of household sizes; in contrast, a mass action model attempts to fit an outbreak among the entire population with an extremely small transmissibility.

Building Contact Networks

The study of epidemics leads to multi-scale, multi-layer (MSML) networks (see Figure 3). Each network captures different types of interactions and forms the underlying fabric for a distinct contagion process. Constructing social contact networks with sufficient accuracy to model disease spread in cities like Los Angeles or New York City is challenging. Researchers cannot construct such networks by using extensive measurements except in very simple, restricted situations; doing so would require knowledge of every individual’s demographics, activities, and locations, which would be both technologically impossible and ethically questionable. So, how can we accurately represent a city’s populace? One must assemble the networks synthetically by integrating or fusing available datasets with simulation-based generative methods. Unlike simple random graph techniques, these methods synthesize networks by utilizing real-world data sources and combining them with behavioral and social theories.

Scalable Simulations to Study Epidemic Dynamics over Networks

It is difficult to apply an analytical approach in a realistic setting that examines the effects of interventions (which consist of individual and collective behavior at different levels) on epidemics’ dynamics. The complication stems from the unstructured nature of real-world social contact networks, which represent the interactions and heterogeneities between the individuals. Therefore, simulations based on high-performance computing are often the only feasible methods for studying networked epidemic models in large-scale population settings. Our group

has developed a variety of these simulation environments to mimic disease spread in large social contact networks.

Network-based Simulations and Algorithmic Workflows during COVID-19 Response

The ongoing COVID-19 pandemic illustrates the importance of MSML networks in representing the underlying interaction structure. Typical studies demonstrate the utility of network models and algorithmic workflows for managing epidemic response across various scales (international, sub-national, and community-level) and stages (emergence, containment, and mitigation).

We analyzed global airline traffic to ascertain importation risk for various countries during the early stages of a pandemic. Using data on the number of passengers between international airports, we constructed a flow network on which COVID-19 could potentially spread and reach other countries. This representation—coupled with a disease model at each node—allows us to characterize the time for case emergence, assuming a given origin node. Furthermore, a structural characterization of this network (namely effective distance) captures disease emergence times more successfully than purely geographical distance between airports. Such a network representation—with actual flow volumes labeled by airlines—permitted us to implement interventions like airline suspensions and evaluate the subsequent impact on delaying COVID-19’s arrival in various locations.

Networked epidemiology enables the study of social distancing policies, such as voluntary home isolation and school and workplace closures. Improved testing and social distancing—two current responses to COVID-19—work in tandem and must be studied together. Detailed network models help researchers examine better case isolation and household quarantine (products of increased testing) while simultaneously mimicking the effects of workplace and non-essential business closures in reduced mixing within the population. Similarly, an increased push for privacy-preserving contact tracing efforts via smartphones has emerged in Western countries, following its success in China and South Korea. Individual-level contact networks allow for assimilation of such contact traces (equivalent to the dendrograms of disease spread) and evaluation of the effects of coverage and compliance.

A final example involves determining COVID-19’s burden on healthcare infrastructure and exploring possible mitigation strategies. The healthcare burden depends on many factors, including level of social distancing and regional testing, current healthcare resources, and population demographics. Various social distancing measures are attempting to “flatten the curve” and reduce the overload and potential collapse of healthcare systems due to surges in critical cases. Our initial results suggest that

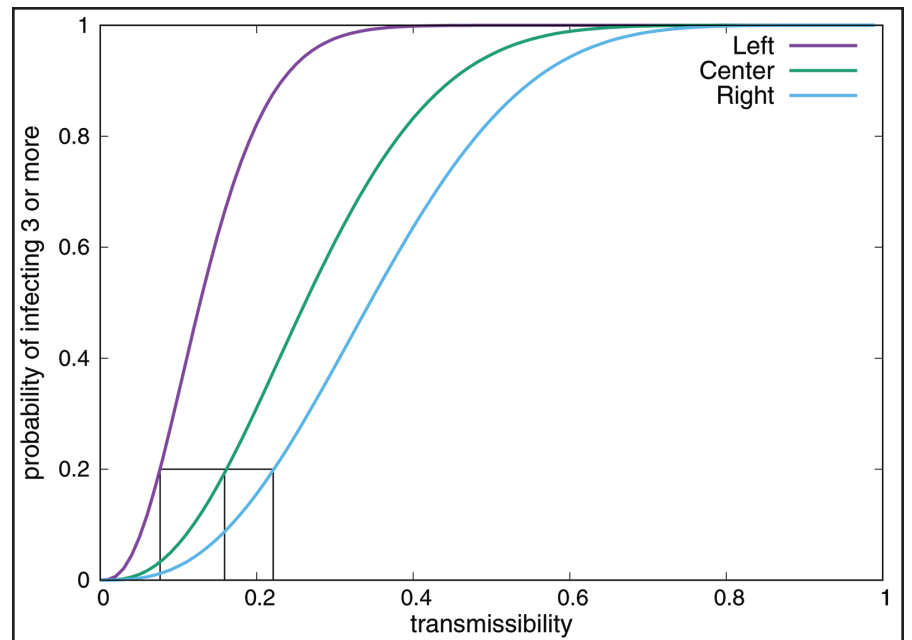


Figure 2. Probability T that the total number of infections exceeds a threshold in the networks in Figure 1 as a function of the probability of transmission across each edge. The underlying network and transmissibility are not separately identifiable from T . Figure courtesy of Stephen Eubank.

patient transfers can have a tangible effect in reducing the healthcare resource deficit.

Traditional ODE models can effectively guide the development of “rules of thumb” for epidemic response. However, when it comes to assessing particular responses to specific outbreaks, a faithful representation in the form of a networked dynamical system is more useful.

Acknowledgments: The authors would like to thank members of the Network Systems Science and Advanced Computing Division at the University of Virginia (UVA) for useful discussion. This work was partially supported by National Institutes of Health Grant 1R01GM109718, National Science Foundation (NSF) BIG DATA Grant IIS-1633028, NSF DIBBS Grant ACI-1443054, NSF Grant No. OAC-1916805, NSF Expeditions in Computing Grant CCF-1918656 and CCF-1917819, U.S. Centers for Disease Control and Prevention 75D30119C05935, DTRA subcontract/ARA S-D00189-15-TO-01-UVA, and a collaborative seed grant from UVA’s Global Infectious Disease Institute.

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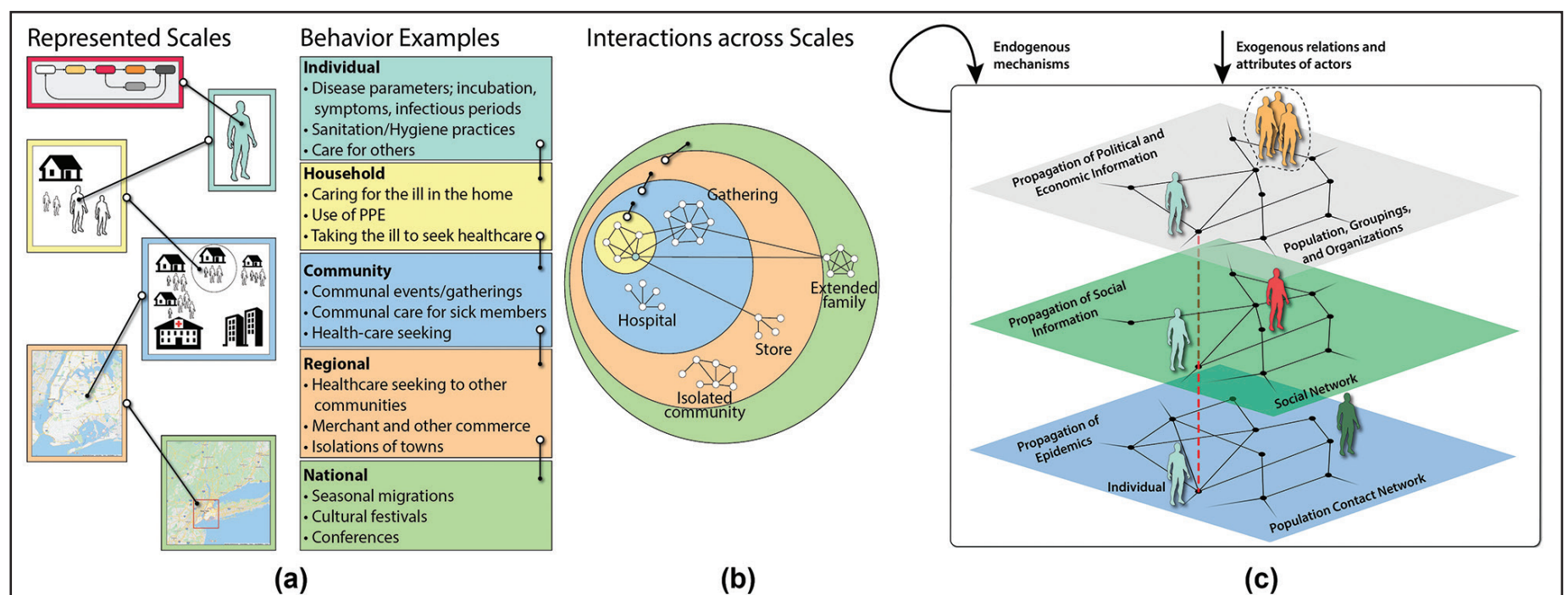


Figure 3. Epidemics are generated by interacting dynamical systems that evolve on multi-scale, multi-layer (MSML) networks. **3a.** Interactions and behaviors in a MSML network, with interactions spanning multiple scales that range from within a household to a community, region, and nation. The specific types of interactions can differ by scale. **3b.** Interactions at different scales yield a complex, multi-scale social contact network. **3c.** Interactions across multiple layers correspond to social and cultural factors. Figure courtesy of Henning Mortveit.

Florida Students Recognized for Mathematical Model to Forecast the Implementation of Electric Semi-trucks

MathWorks Math Modeling Challenge Tackles Trucking's Transition to Electric Power

By Lina Sorg

More than 1.7 million semi-trucks transport nearly every type of imaginable cargo across the country, often from manufacturing plants to retail distribution centers. The continuous movement of raw materials, finished goods, and miscellaneous freight bolsters the economy and keeps society running smoothly. As a result, nearly 7.5 million Americans hold jobs that are related to the trucking industry.¹

Diesel fuel currently powers semi-trucks, which collectively travel an estimated 150 billion miles each year. Unfortunately, these tractor trailers are not known for their fuel efficiency; they average less than seven miles per gallon and are responsible for roughly one third of transport-related carbon emissions.² As battery electric vehicles become increasingly popular, the trucking industry is beginning to explore the viability of electric trucking. Tesla plans to introduce a line of electric semis in 2021, and PepsiCo, Walmart, and UPS have pledged to purchase several hundred. However, more infrastructure is needed to determine whether electric semi-trucks will meet current trucking demands and serve as feasible replacements for traditional diesel vehicles.

"Trucking is a very modest business," Mike Roeth, executive director of the North American Council for Freight Efficiency (NACFE), said. "We go about

getting everything consumers need and want to stores and homes without getting in the way. But trucking is also very complicated due to the many truck configurations, types of freight, and duty cycles, so it requires mathematical modeling to help figure out the details."

The complexity of a potential transition to electric power in U.S. semi-trucks served as the basis for the 2020 MathWorks Math Modeling (M3) Challenge,³ an annual competition for high school juniors and seniors. The contest, which is organized by SIAM and sponsored by MathWorks, invites U.S.-based teams of three to five students to address a multi-layered, real-world problem via mathematical modeling and submit their results in just 14 hours. After two meticulous rounds of online judging by nearly 150 Ph.D.-level mathematicians, six finalist teams emerged. The third and final round of judging—traditionally held in New York City so the top teams can present their work in person—occurred virtually this year due to the ongoing COVID-19 pandemic. Participating students competed for \$107,500 in scholarship funds, which was ultimately split among the six finalist teams and 32 other top performers.

The three-part Challenge problem⁴ asked teams to create a mathematical model to predict the percentage of electric semi-trucks in 2025, 2030, and 2040; calculate the required number of stations and chargers along five different U.S. truck routes to support the current level of traffic; and



From left to right: Nicholas Butakow, Pragnya Govindu, and Kristoffer Selberg of Pine View School in Osprey, Fla., tackle the 2020 MathWorks Math Modeling Challenge trucking problem during Challenge weekend. The Pine View team, which also included Christiana Guan and Michael Gutierrez, took home \$20,000 in scholarship funds for their first-place finish. Photo courtesy of Mark Mattia.

rank the five trucking corridors to determine which should undergo development first. Neil Nicholson (North Central College) authored the problem, with input from Roeth at NACFE and the M3 Challenge Problem Development Committee, which is led by Karen Bliss (Virginia Military Institute).

"This country depends on trucks to move goods around, now more than ever," Bliss said. "Our infrastructure is built around this mode of transporting goods, and yet it's relatively inefficient. A switch to electric trucking seems to be an attractive option, but there are a lot of barriers to converting an entire fleet of trucks."

This year's first-place team, from Pine View School in Osprey, Fla., began by

dividing semi-trucks into three categories: long-haul, regional-haul, and short-haul vehicles. They calculated overall operating costs for both diesel and electric trucks based on existing data, then assumed purchasing costs from the current prices of cab and sleeper semis, as well as base prices for Tesla electric semi-trucks. The students used the differences in operating and purchasing costs to derive the probability values of replacing diesel trucks with electric trucks.

Next, they created three Markov chains—one for each type of truck—to predict the percentage of electric semis in future years. "To execute the three Markov chains, we utilized MATLAB software and determined

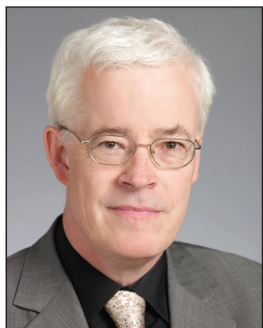
See *Electric Semi-trucks* on page 10

¹ <https://www.rtsinc.com/articles/why-trucking-still-america-s-number-one-job>

² <https://www.iea.org/news/iea-study-unveils-key-role-for-trucks-in-global-oil-demand-growth>

³ <https://m3challenge.siam.org/>

⁴ <https://m3challenge.siam.org/archives/2020/problem>



Approximation Theory and Approximation Practice, Extended Edition

Nick Trefethen on what's new in the Extended Edition: "Approximation Theory and Approximation Practice, Extended Edition (ATAP-EE) corrects some errors and updates some Chebfun syntax, but the real point is a mathematical one."

Applied mathematics is built on three tools:

Chebyshev series for nonperiodic functions

- numerical analysis
- approximation theory

Fourier series for periodic functions

- real analysis
- electrical engineering

Taylor and Laurent series on the unit circle

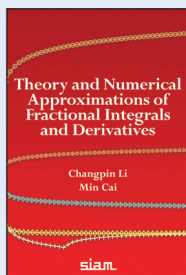
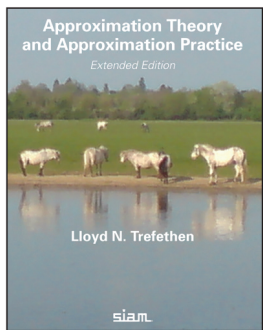
- complex analysis

These settings are equivalent, modulo a certain symmetry, and when I first started to write the book, I conscientiously planned to treat all three in parallel. This proved deadly boring. If I had finished the project, the book would have been 800 pages long.

So ATAP focused on the least widely understood and numerically most useful case, "Chebyshev technology". For the Extended Edition, we've found a way to outline parallel results for the other contexts too without getting bogged down. The new volume reprints a paper by Grady Wright et al. as a kind of "ATAP for periodic functions" and a paper by Anthony Austin et al. as an "ATAP for the unit disk". Both papers share the hands-on style of the rest of ATAP, and in putting this together, I feel I've been privileged to sketch a great cathedral without having to build it all." — Nick Trefethen

Nick Trefethen is professor of numerical analysis at the University of Oxford and a Fellow of the Royal Society. He served as SIAM President in 2011–2012.

2019 • xii + 363 pages • Hardcover • 978-1-611975-93-2 • List \$64.00 • SIAM Member \$44.80 • OT164



Theory and Numerical Approximations of Fractional Integrals and Derivatives

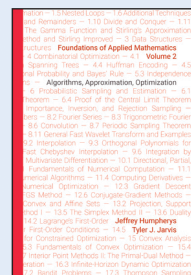
Changpin Li and Min Cai

Fractional calculus has gained momentum in industry and academia, and this monograph is the first to include both fundamental information on fractional calculus and a detailed treatment of existing numerical approximations. It presents an inclusive review of fractional calculus in terms of theory and numerical methods and systematically examines almost all existing numerical approximations for fractional integrals and derivatives. The authors consider the relationship between the fractional Laplacian and the Riesz derivative, a key component absent from other related texts, and highlight recent developments, including their own research and results.

Changpin Li is a professor in the mathematics department at Shanghai University. His research interests include numerical methods and computations for fractional partial differential equations and fractional dynamics. A 2012 recipient of the Riemann–Liouville Award for Best FDA Paper (theory), Li is editor-in-chief of the De Gruyter book series Fractional Calculus in Applied Sciences and Engineering and serves on the editorial boards of several journals.

Min Cai is a Ph.D. student in the mathematics department at Shanghai University whose main research interests include numerical methods and computations for fractional partial differential equations.

2019 • xiv + 312 pages • Softcover • 978-1-611975-87-1 • List \$89.00 • SIAM Member \$62.30 • OT163



Foundations of Applied Mathematics Volume 2: Algorithms, Approximation, Optimization

Jeffrey Humpherys and Tyler J. Jarvis

Geared toward advanced undergraduate and beginning graduate students in mathematics, data science, and machine learning, this textbook presents the foundations of algorithms, approximation, and optimization—essential topics in modern applied and computational mathematics.

The authors provide a unified treatment of several topics that do not usually appear together, and when used in concert with the free supplemental lab materials, this book teaches not only the theory but also the computational practice of modern mathematical methods.

Jeffrey Humpherys is a research professor at the University of Utah School of Medicine, the former Vice Chair of the SIAM Activity Group on Applied Mathematics Education, and a two-term member of the SIAM Education Committee. He is the recipient of a National Science Foundation CAREER award. His research spans a wide range of topics in applied and computational mathematics, from nonlinear partial differential equations to network sciences to machine learning.

Tyler J. Jarvis is a professor of mathematics at Brigham Young University whose research has primarily been in geometric problems arising from physics. He is the recipient of a National Science Foundation CAREER award and the MAA's Deborah and Franklin Tepper Haimo Award for Distinguished University Teaching of Mathematics.

2020 • xviii + 788 pages • Hardcover • 978-1-611976-05-2 • List \$94.00 • SIAM Member \$65.80 • OT166

Mathematical Modeling in High School: How It Begins and Where It Can Go

By Alexandra Schmidt

For most American high school students, interaction with mathematics involves progression through the standard high school math curriculum — typically the higher-level sections of algebra, geometry, trigonometry, precalculus, statistics, and calculus. Students who enjoy challenge and variety sometimes partake in a math club, math circle, or competition team. These extracurriculars typically provide participants with the opportunity to individually solve problems in search of a correct answer, though certain supportive classroom and competition settings allow students to work together to address harder, more complex questions that require teamwork. Many of my students have successfully pursued degrees and careers in various science, technology, engineering, and mathematics (STEM) fields. Unfortunately, few of them actually use mathematics to determine a best course of action or educate themselves about a non-STEM topic until they begin professional internships or careers.

Though I have taught and coached competition mathematics for over 16 years, my previous 15-year career as a control systems engineer found me working with and learning about optimization of locomotive fuel consumption, signal switching at television networks, air traffic path planning, and DVD manufacturing, among other applications. These experiences prefigure my goal that students learn about other fields besides mathematics, consider math's applicability as a decision-making tool, and talk to each other in the process.

While it is possible to create small labs and explorations in the traditional math sequence that let students work toward these goals, SIAM's MathWorks Math Modeling (M3) Challenge¹ implements this on a larger scale. When I first learned about M3 Challenge, I reached out to some of my strongest students who enjoyed mathematics, were omnivorous in their interests, and could write and communicate effectively. The annual contest also inspired me to begin the process of launching a math modeling culture at my high school, the Emma Willard School in Troy, NY.

Apart from student curiosity and persistence, I have identified three important prerequisites for launching a math modeling culture in high school: a thorough understanding of the general process, competency with a basic tool set, and a multitude of interesting problems on which to work.

Although I spent the first part of my professional career developing mathematical models of dynamic systems, I was initially unsure where to begin in teaching the process. The *Guidelines for Assessment and Instruction in Mathematical Modeling*

¹ <https://m3challenge.siam.org/>

Education (GAIMME) report² and SIAM's math modeling handbooks³ helped me create a walk-through for my students. I would also highly recommend notes from the 2019 SIAM-MfA Math Modeling Workshop⁴ for high school teachers, which draw on and distill these materials. All high school students are capable of browsing the internet to obtain information on unfamiliar topics, and Google's suite of collaborative tools facilitates collective contribution to a problem's initial mind mapping. While I do teach basic spreadsheet use for function exploration and data analysis in precalculus, I developed short workshops to familiarize my M3 Challenge teams with the processes of creating more complex formulas and charts and using random functions to simulate outcomes. I have also begun teaching MATLAB, which I particularly enjoy as it is a technology bridge that spans my careers. Because M3 Challenge is only open to juniors and seniors, I ask experienced seniors to provide new team members with a summary of their participation by breaking down, researching, analyzing, developing, quantifying assumptions for, and validating their model from the prior year.

What makes this all “real,” of course, is finding motivating problems on which to practice. These problems should be topical and real; it is even better when they touch on subjects about which the teacher can cheerfully admit to knowing very little! One of the nicest aspects of M3 Challenge is that both past competitions and the website⁵ provide numerous different problems, all of which comprise a multilayered “story” whose relevance extends beyond the competition. One of my students who participated in this year's contest⁶ praised the topic's real-world relevance. “I knew absolutely nothing about electric trucks and very little about charging stations before this experience,” she said. “I really enjoyed being able to apply my math skills while learning about new topics. Although at times the amount of data felt overwhelming, it was so rewarding to see all of our observations and calculations come together in the final product. I will definitely be keeping tabs on the evolution of vehicles and their environmental impact in the future.”

While my school's teams have yet to make it beyond the second round of competition, student response has been remarkably positive. “Being able to apply the knowledge I've gained from my math class-

² <https://www.siam.org/publications/reports/detail/guidelines-for-assessment-and-instruction-in-mathematical-modeling-education>

³ <https://m3challenge.siam.org/resources/modeling-handbook>

⁴ <https://m3challenge.siam.org/newsroom/2019-siam-mfa-math-modeling-teacher-workshop>

⁵ <https://m3challenge.siam.org/>

⁶ Read about the winning solution of this year's M3 Challenge on page 8.



With the right team and the right attitude, 14 hours of math modeling can still include moments that are as fun as a slumber party. Photo courtesy of Alexandra Schmidt.

es to a real-world scenario really interested me, especially given that there wasn't one concrete answer to each question,” another student said. “We could really apply the organizational and math modeling skills—as well as the communication and collaboration skills—that we used during this process to any field or numerical situation.”

The contest's benefits seemed so clear that I suggested that Emma Willard offer a semester-long, project-based course in mathematical modeling for seniors, accessible to any student who has completed precalculus or an advanced algebra course that focused on functions. The course plan, which I developed with several colleagues, introduces students to the use of models to capture the behavior or most important aspects of a messy, real-world problem with many contributing factors. The class's inaugural semester is set for the fall of 2020.

After introducing the basics of the modeling process, the course will allow students to practice defining problems, researching contributing factors, quantifying their assumptions, and developing and testing models. It will also emphasize quantitative writing and oral presentation skills, as these are important components of any high school curriculum or professional setting.

The class will culminate in an individual project that each student chooses for herself, with guidance from the instructor. Students will decide whether experimental or empirical modeling is most appropriate for their problem, and select from model types that correspond with both the problem and their level of mathematical experience. For some, the projects will bring depth and relevance to second-year algebraic models, such as those originating with exponential, power, sinusoidal, and logarithmic functions. Difference equations, smoothed polynomial or spline models, and probabilistic simulations will provide additional depth and challenge for students who have completed a year of calculus. Most (if not all) participants will already be familiar with Desmos or GeoGebra from earlier courses, and we plan to teach and extend existing knowledge of spreadsheets. We may even include MATLAB or Python if enough students have coding experience. As developers of a new course, we as teachers will also be learning from our initial model and changing it to incorporate novel data as it becomes available. While our plan is to utilize GAIMME-based rubrics to assess student models, I expect that the process will require patience, critical thinking, and a willingness to regularly amend small details as necessary.

As a final note, I want to reflect on the very specific experience of teaching math modeling to young women (Emma Willard is an all-girls' high school). As one of my students observed, “an all-female team like ours is a rarity, and we have created a special sisterhood.” Despite the intensity of working within M3 Challenge's regulated time window—which gives participants 14

hours in which to educate themselves on an unfamiliar topic and produce a substantive paper—my students found the process motivating, stimulating, and even empowering. By practicing regularly before the competition, the team developed a collaborative and supportive bond and became comfortable sharing and challenging each other's ideas. As I stopped by during Challenge Weekend to bring the competing students fancy coffee drinks and baked goods and laugh with them during “vibe checks,” I was struck by both the productivity and camaraderie in the room. At the end of the day, my students came away from M3 Challenge with an enhanced sense of math's applicability to their future studies.

Acknowledgments: Special thanks to Caroline Albert, Laszlo Bardos, Judy Price, Chiara Shah, and Yoosong Song for their input and reflections.

Alexandra Schmidt has been a mathematics teacher at the Emma Willard School since 2014. She has taught mathematics at every level from fifth to 12th grade, prior to which she was an electrical engineer. Schmidt holds a Master of Arts in Teaching from Clarkson University and is a National Board Certified Teacher.



Whiteboard walls are the best tools for mind-mapping a problem when the clock is ticking and everyone has something to add. Photo courtesy of Alexandra Schmidt.

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Mathematicians Quickly Respond to the COVID-19 Pandemic

By Juan C. Meza, Zhilan Feng, Tie Luo, and Junping Wang

The Division of Mathematical Sciences (DMS) at the National Science Foundation (NSF) recently participated in an NSF-wide Dear Colleague Letter,¹ which was published on April 3 and requested proposals that address the COVID-19 pandemic. The mathematical sciences community was quick to respond! Ideas ranged from developing tools to help decision-makers better understand the possible outcomes of proposed nonpharmaceutical intervention policies to combining mathematicians' expertise with other disciplines—like biology and chemistry, for example—to study new approaches and accelerate the identification of potential therapeutic treatments.

Overall, the DMS issued a set of 15 Rapid Response Research (RAPID) awards over the span of several weeks that could have a significant impact in mitigating the spread of COVID-19. These awards highlight the critically important need for swift and reliable prediction of epidemics' spatial and temporal risks. Furthermore, many of them use mathematical, statistical, and computational models to evaluate various therapeutic and non-therapeutic mitigation policies, thus allowing policymakers to quickly identify intervention strategies that effectively slow the inevitable. Such strategies can buy additional time to put pandemic plans into effect, reducing peak demand for hospital-based care and ultimately saving lives.

The collection of RAPID awards spans a range of diverse ideas, including novel variations of well-known SIR (susceptible-infected-recovered) models, statistical inference approaches for rapidly changing situations where only partial data is available, and techniques that employ a combination of deep learning and mechanistic methods to quickly improve mathematical models that capture the specific characteristics of COVID-19. Other awards dive deeper into our understanding of how the novel coronavirus infects host cells, targeting the identification of critical areas in the viral genome that could be attacked during drug design. Yet another common theme is the use of data and corresponding mathematical procedures to improve existing models, particularly in situations where the data is incomplete and changes rapidly.

In general, the awards fell into one of two major areas: (i) mathematical models for predicting the spread of COVID-19 and the effects of different mitigation strategies, and (ii) study of the novel coronavirus, the

¹ <https://www.nsf.gov/pubs/2020/nsf20052/nsf20052.jsp>

viral evolution, and subsequent plans for detecting target areas in the viral genome for drug compounds. We can subdivide the awards in the first major area into three general categories: (i) SIR/SEIR (susceptible-exposed-infected-recovered) types of compartmental models with various levels of extensions and complexities; (ii) stochastic, statistical, or probabilistic models; and (iii) network or graph theory-based models.

The DMS made five awards in the first subgroup that will investigate various aspects of the well-known SIR/SEIR model. **Andrea Bertozzi** and **Mason Porter** (DMS – 2027438) plan to integrate a basic SIR framework with high-resolution societal mixing patterns in epidemics and models with self-exciting point processes that are fitted to real-world data. These actions will allow them to study the stochasticity of infection and latency, analyze the uncertainty in disease transmission rates, and evaluate intervention policies. The pair will also examine the outcomes of social distancing using data from a Princess Cruise ship and lecture halls at the University of California, Los Angeles.

Jeffrey Shaman (DMS – 2027369) will utilize SIR-type models with spatial movements and statistical/computational tools to estimate critical epidemiological characteristics that are associated with the transmission of SARS-CoV-2. He will then forecast future COVID-19 incidence, estimate the effectiveness of public health policies (such as school closures and travel restrictions), and project the geographic spread of COVID-19 for given scenarios with various levels of intervention.

Yulia Gel and **Georgiy Bobashev** (DMS – 2027793/2027802) plan to use a predictive approach based on multiple data sources and dynamical SEIR models to train deep learning networks. If one then views simulation SEIR models as surrogate pre-trainers for deep learning models, Gel and Bobashev's work could minimize the amount of real data needed to retrain the predictive model and reflect real-world COVID-19 progression. In contrast, **Grzegorz Rempala** (DMS – 2027001) will employ dynamical survival analysis—which exploits aggregated mean field equations for the underlying large stochastic network approach—to estimate parameters that are similar to those in SIR models. The survival dynamical system may yield new understanding of the pandemic, as it does not require knowledge of the susceptible population's size or overall disease prevalence.

Folashade Augusto (DMS – 2028297) and her collaborators intend to develop disease transmission models that incorporate various factors, including public perception of

risk, age structure within a hospitalized population, population demographics, socioeconomic conditions, and spatial structure. They will then use the models to inform coordination of disease control policies with different scales, ranging from local communities to entire countries. Finally, **Cameron Browne** (DMS – 2028728) and his team will create a modeling framework at the interface of mathematics, epidemiology, and genetics. Their approach may help derive the outbreak size's dependence on contact tracing and broad quarantine intervention parameters, thus quantifying region-specific control characteristics for COVID-19.

Deterministic models are not the only possible tactic. To study systems with high stochasticity, **Jason Xu** and **Allison Aiello** (DMS – 2030355/2030242) will generate new stochastic compartmental models that extend classical mechanisms to explicitly account for changes to the social contact network that underlies disease spread. They will combine these developments with likelihood-based methods to infer key epidemic parameters that offer mechanistic interpretations with uncertainty quantification.

Two other interesting techniques involve modeling the COVID-19 pandemic via network and graph theory. In this group, **Nicole Eikmeier** and **Matthew Junge** (DMS – 2028880/2028892) plan to study quarantine's effect on the network connectivity of graphs to better model societal connections. Individual quarantine is akin to removing a vertex from a graph; the systematic removal of vertices is called site percolation. Eikmeier and Junge will explore biased site percolation's effect on graph structure, particularly the way in which different percolation rules influence the size of a given graph's largest component. The second part of the project will then focus on how an epidemic's critical threshold and size change after percolation for an SIR model.

Faryad Darabi Sahneh's (DMS-2028401) research will take a similar approach but emphasize a data-driven mathematical modeling framework for the forecast of temporal and spatial COVID-19 trends. His team's modeling framework can handle a constantly evolving environment, including individuals' behavioral changes in response to mitigation efforts. Interestingly, Darabi Sahneh borrows this idea from economics.

The second major area of network and graph theory addresses the infectivity and virulence of the novel coronavirus itself, such as the viral evolution, virus structure, and effect on host cells. Here the general line of attack involves studying the RNA viral genome for clues on the way in which it infects the host cells, and determining treatments that might disrupt the infective process.

Gregory Forest's (DMS – 2028758) group has teamed up with two experimental biology laboratories to develop a mathematical modeling platform that will explore the delicate interplay among inhaled loads of SARS-CoV-2 and their diffusion within—and potentially through—the mucus-coated respiratory tract. This will allow the researchers to determine infectivity onset as the virus reaches and invades epithelial cells and propagates the infection. Their ultimate goal is to optimize design of monoclonal antibodies (mAb), characterize efficiency of given mAb affinities to COVID-19 and mucus, and quantify the inhaled mAb dose required to arrest COVID-19 infection at various stages of progression.

Two other awards seek to understand the specific protein that is key to the coronavirus' invasion of host cells: the so-called spike or S-protein in the RNA viral genome. **Tamar Schlick's** (DMS – 2030377) project involves comprehending the COVID-19 RNA viral genome through structural analysis and molecular dynamics studies. The coronavirus is known to mutate over time, but few specifics are currently established. **Javier Arsuaga**, **Raymond Rodriguez**, and **Mariel Vasquez** (DMS – 2030491) intend to employ a combination of Markov processes, graph theory, and topological data analysis to better understand this mutation process and estimate evolutionary parameters and the S-protein's fitness function.

The DMS is thankful to the mathematical sciences community for its incredible response to our call for proposals regarding the worldwide COVID-19 pandemic.

Juan C. Meza is a professor of applied mathematics at the University of California, Merced and currently serves as the division director for the Division of Mathematical Sciences (DMS) at the National Science Foundation (NSF). He became a SIAM Fellow in 2019. Zhilan Feng is a professor of mathematics at Purdue University and presently serves as a program director in the DMS's Mathematical Biology Program. She is an editor for the SIAM Journal on Applied Mathematics. Tie Luo joined the NSF as a program director in the Algebra and Number Theory Program before serving as deputy division director of the DMS. He is currently the Acting Deputy Assistant Director for Mathematical and Physical Sciences. Junping Wang joined the NSF in 2003 and is currently serving as a program director in the Mathematical Biology Program, as well as the acting deputy division director for the DMS. He is also a member of the working group for the NSF's Big Idea on "Understanding the Rules of Life."

Electric Semi-trucks

Continued from page 8

the best estimate of the number of inoperable semi-trucks that would be replaced by electric ones in five, 10, and 20 years," Pragna Govindu of Pine View said. "With these values, we ultimately predicted the percentage of semis that will be electric." The team's model forecasts that electric semi-trucks will comprise 27.39, 69.49, and 97.77 percent of operational semi-trucks in the next five, 10, and 20 years respectively.

The Pine View students then generated another model to discern the mandatory quantity of charging infrastructure for sustainable, large-scale electronic trucking. This task demanded consideration of electric vehicles' varying ranges and charging times. "Electric vehicle batteries are tricky because they charge quickly in the beginning but slowly at the end," team member Michael Gutierrez said. "We didn't want the trucks to use their full charge capacity, as it would waste a lot of time. So we developed a model to find the optimal stopping interval and based our charging station locations around that."

To test their model, the group simulated the resource needs of a large fleet of trucks on the following five major trucking routes: to/from (i) San Antonio, Texas, and New Orleans, La.; (ii) Minneapolis, Minn., and Chicago, Ill.; (iii) Boston, Mass., and Harrisburg, Pa.; (iv) Jacksonville, Fla., and Washington, D.C.; and (v) Los Angeles, Calif., and San Francisco, Calif. "Initially, we created a formula for the number of stations needed along a given route," Nicholas Butakow said. "With this formula, we used the Monte Carlo method to determine the number of stations with randomly generated values, which reflect projected distributions of commercial electric semi-trucks."

Interestingly, Butakow and his teammates found that all five truck routes required charging points roughly every 90 minutes, given the nature of electric batteries. They used a second Monte Carlo simulation—based on the average number of trucks present at each stop at any given time—to determine the necessary number of charging stations per stop, which ranged from 14 to 29.

Finally, the team created an importance score based on three different factors—economic growth, environmental consid-

eration, and total cost of installation—to rank the five corridors. A higher importance score indicated a higher priority for projected development, and the students determined that developers should target the Minneapolis-Chicago corridor first.

The Pine View team—which included Kristoffer Selberg and Christiana Guan, in addition to Govindu, Gutierrez, and Butakow—will split \$20,000 in scholarship funds for their winning solution. The group also nabbed an Outstanding Communication of Results Award, which recognized the excellence and clarity of their video demonstration (submitted in lieu of a physical presentation) and delivered an additional \$1,000.

"It was really different because we had to work over Zoom instead of communicating and presenting in person, which was difficult," Guan said. "But being able to use visuals—which likely wouldn't have been as possible during an in-person presentation—was helpful."

Working together under stringent time and resource constraints provides participating students with unique collaborative modeling experience — much like the type

of projects that computational scientists and professional mathematicians tackle in the real world. In addition to showcasing the vast potential of a career in applied mathematics, M3 Challenge illustrates the practical applicability of mathematical modeling as an acute problem-solving tool, something that most students do not experience in the traditional classroom setting.

"Typically, the math education that I get in school rigorously teaches the fundamentals of mathematics," Selberg, who is interested in pursuing a career in applied mathematics, said. "M3 Challenge takes what students have learned in school and provides a platform for the expression of mathematics in unique ways that are rarely exhibited in classrooms today."

Pine View School's winning paper is available online,⁵ as is their final presentation.⁶

Lina Sorg is the managing editor of SIAM News.

⁵ https://m3challenge.siam.org/sites/default/files/uploads/M3%20CHAMPION_13343.pdf

⁶ <https://youtu.be/uS4JKTfgYVU>

Call for Special Sessions for the 2021 Mathematical Congress of the Americas

By Daniel B. Szyld

We invite you to submit proposals of special sessions for the third Mathematical Congress of the Americas (MCA 2021),¹ which will take place in Buenos Aires, Argentina, from July 19-24, 2021. The deadline for proposal submission is July 31, 2020.

SIAM is a founding member of the Mathematical Council of the Americas,² a network for professional mathematics societies and research institutes throughout the Americas. The organization currently has 32 members from countries ranging from Canada to Argentina and Chile. Both small and large countries—like Costa Rica and Brazil—are represented.

The Council supports several activities—including some “summer schools,” though they do not always occur during the summer—and organizes the Mathematical

Congress of the Americas, a very large quadrennial conference that rotates host countries. The first two conferences were held in Guanajuato, Mexico, and Montreal, Canada. The next conference (MCA 2021) is scheduled for July 2021 in Buenos Aires, Argentina. It will take place in a new building at the University of Buenos Aires’ School of Exact and Natural Sciences.

SIAM members are encouraged to organize special sessions³ (akin to minisymposia) for this meeting. The list of organizers must include affiliations of more than one country in the Americas. The submission period for these proposals is currently open and will close on July 31, 2020.

In addition to the opportunity to network with old and new colleagues, attend talks, and learn about novel trends, conference attendees can experience Buenos Aires during the mild South American winter. To quote a recent article in *The*

New York Times, “The city continues... producing amazing new restaurants; inventing fresh ways to showcase the country’s always-thrilling wine offerings; developing an exceptionally stimulating arts scene; and coming up with creative twists on tradition in everything from aperitifs to bookstores. Visiting Buenos Aires is always filled with new discoveries and beloved stalwarts.”⁴

It is worth noting that the 2021 SIAM Annual Meeting⁵ (AN21) is scheduled for the same week as MCA 2021. AN21, which will take place from July 19-23 in Spokane, Wash., is being held jointly with the SIAM Conference on Control and Its Applications (CT21) and the SIAM Conference on Applied and Computational Discrete Algorithms (ACDA21). The SIAM Activity Groups on Mathematics of Planet Earth and Nonlinear Waves and Coherent Structures will also have tracks at the meeting.

AN21 will feature the SIAM Career Fair, Workshop Celebrating Diversity, Industry Panel and Reception, and Student Days activities, in addition to the standard assortment of minisymposia, minitutorials, contributed talks, invited presentations, panel discussions, and prize lectures. Jonathan Mattingly (Duke University) will deliver the I. E. Block Community Lecture, and several talks and events originally planned for the 2020 SIAM Annual Meeting (which is cancelled with select virtual sessions due to the COVID-19 pandemic) will now take place at AN21.

The organizing committee co-chairs are Fadi Santosa (University of Minnesota) and Elaine Spiller (Marquette University). More details will be released in the coming months, and the call for participation will be made available in September 2020.

Daniel B. Szyld is a SIAM representative to the Mathematical Council of the Americas.

¹ <http://mca2021.org/>

² <http://www.mcofamericas.org/>

³ <http://mca2021.org/news/item/16-mca-2021-call-for-special-sessions>

⁴ <https://www.nytimes.com/2020/01/16/travel/what-to-do-36-hours-buenos-aires.html>

⁵ <https://www.siam.org/conferences/cm/conference/an21>

Computational Science and Mental Health

By Joshua A. Gordon

Since I assumed leadership of the National Institute of Mental Health¹ (NIMH) at the National Institutes of Health (NIH), pushing the boundaries of the possible in computational psychiatry has been among my top priorities.

The science of psychiatry is a study in contrasts. On the one hand, advances in genetics, basic neuroscience, neuroimaging, and integrative computational approaches promise to dramatically improve knowledge of and treatments for mental illnesses. On the other hand, progress in the mental health translational pipeline has been frustratingly slow, leaving us with few reliable biomarkers, indefinite and subjective diagnostic categories, and partially effective treatments.

Why the slow progress? A principal factor involves understanding the complexity of the brain and its influence on behavior. It

is incredibly challenging to connect knowledge gained at genetic, circuit, systems, and behavioral levels. For example, how do the genes that predispose schizophrenia alter function in the circuits that govern the cognitive processes in patients with the disorder? And how might computational approaches help us understand and represent circuit dysfunction in information processing that is visible through neuroimaging? How can we comprehend the incredible heterogeneity in affected patients—even those who share the same genes?

I believe that SIAM and its members can help us answer some of these questions through the application of computational science. Computational approaches allow us to describe and test the way in which complex, high-level phenomena emerge from smaller-scale interactions. Computational models of neural circuits that account for differences in genetic makeup can put testable hypotheses pertaining to gene alterations’ potential effect on circuit function into explicit mathematical terms. Similarly,

computational models of circuit dysfunction can test such dysfunction’s ability to create a progressive, chronic disorder by impacting neural development and plasticity. They can also quantify and explain findings in neural systems’ dysfunctions—captured through neuroimaging—and link them to behavioral manifestations. Finally, computational approaches can take advantage of large data sets, categorizing brain dysfunction in a way that may help predict treatment response and lead to better diagnoses and improved biomarkers.

NIMH’s Computational Psychiatry Program² is the primary engine for this type of research. Through this program, we hope to bring mathematics, biology, and behavioral science into the pathology and physiology of mental illness via the use of theoretical modeling and machine learning. Employing these tools to investigate the underpinnings of neural activity allows us to make discoveries that aid in our fundamental understanding of the way in which mental states develop and change over time.

In addition, data-driven approaches can assist in the evaluation and testing of certain drugs, neuromodulations, and cognitive interventions. This is key because not all patients with similar disorders will react identically to the same treatments. There is increasing interest in the potential of arti-

ficial intelligence to decide the most appropriate drugs for treating common mental illnesses such as depression, a disorder for which there is a wide range of pharmaceutical options. Personalized medicine for more widespread disorders like depression can increase the likelihood that sufferers will seek help and be better equipped to stick with their treatment plans.

Vast potential for advancement exists in these areas, but it will not be possible without robust participation from applied mathematicians and computational scientists. Therefore, I urge computational psychiatrists to explore collaborations with the mental health research community and pursue funding opportunities through the Computational Psychiatry Program. NIMH is constantly seeking chances to leverage expertise in computational psychiatry to make new discoveries in mental health and improve training of researchers that are fluent in data and modeling approaches; these efforts will advance the understanding and treatment of mental disorders. In addition, NIMH is always interested in hearing from researchers who may wish to serve on our study sections and review proposals. Doing so can help the organization hone its approach to computational neuroscience while simultaneously exposing researchers to new funding prospects.

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¹ <https://www.nimh.nih.gov/>

² <https://www.nimh.nih.gov/about/organization/dtr/adult-psychopathology-and-psychosocial-interventions-research-branch/computational-psychiatry-program.shtml>

Call for Papers: *SIAM Journal on Control and Optimization* Special Section on Mathematical Modeling, Analysis, and Control of Epidemics

The *SIAM Journal on Control and Optimization*¹ (*SICON*) is seeking submissions for a **Special Section** that amasses contributions at the intersection of the fields of systems and control theory and the mathematical study of epidemic spread processes. Articles can be related to COVID-19, though the journal welcomes general topics associated with epidemic processes as well. **Submissions will be accepted from July 1 through October 1, 2020.**

The ongoing COVID-19 pandemic has highlighted the critical importance and danger of complex epidemic processes. *SICON*’s Special Section intends to gather recent developments that address the fundamental challenges inherent in the mathematical analysis, estimation, and control of epidemics. Specific topics will include (but are not limited to) the following:

- Mathematical modeling and analysis methods, such as ordinary and partial differential equations as well as deterministic and stochastic systems
- Closed-loop control design strategies, including triggers for enforcing and relaxing nonpharmaceutical intervention strategies
- Optimization algorithms for intervention scheduling and resource allocation
- Computational methods for stochastic simulation
- Learning methods for early tracking, identification, inference, and data-driven analysis.

All interested authors should submit a manuscript and cover letter in PDF format via *SICON*’s online submission site.² Note the block labeled “Special Section” (just under the “keywords” block on your submission screen). Select “Mathematical Modeling, Analysis, and Control of Epidemics” from the dropdown menu.

Anyone with questions should contact Mitch Chernoff, SIAM’s publications manager, at chernoff@siam.org, or Brian Fauth, editorial associate, at sicon@siam.org. Questions about content suitability can be directed to Francesco Bullo, guest editor-in-charge, at bullo@engineering.ucsb.edu.

¹ <https://www.siam.org/publications/journals/siam-journal-on-control-and-optimization-sicon>

² <https://sicon.siam.org>

Mathematics Subject Classification 2020

The 2020 revision of the Mathematics Subject Classification (MSC2020) was published earlier this year. It is a joint project of Mathematical Reviews (MR) and zbMATH, which collectively maintain the MSC. Reviewing services, publishers, funding agencies, and other organizations use this alphanumeric classification scheme to categorize items in the mathematical sciences literature.

Every 10 years, MR and zbMATH request input from the mathematics community and generate an updated MSC based on the resulting comments. MSC2020 contains 63 two-digit classifications, 529 three-digit classifications, and 6,006 five-digit classifications, reflecting updates at both the three-digit and five-digit level. It also accounts for data and computation’s ongoing influence on the mathematical sciences, and features general amendments to class descriptions—which are now more useful to those conducting searches both online and via database interfaces.

MR and zbMATH are now using MSC2020 as their respective classification schemes and invite the mathematics community to do the same. MSC2020 is accessible online at msc2020.org. Searchable versions are available from the zbMATH site¹ and the MathSciNet site.²

¹ <https://zbmath.org/classification/>

² <https://mathscinet.ams.org/msc/msc2020.html>

Mean Field Games 15 Years Later: Where Do We Stand?

By René Carmona
and François Delarue

Since its introduction nearly 15 years ago, the theory of mean field games has rapidly become an exciting source of progress in the study of large dynamic stochastic systems. In 2006, Jean-Michel Lasry and Pierre-Louis Lions proposed a methodology to produce approximate Nash equilibria for stochastic differential games with symmetric interactions and many players. These players feel the impact of other players' states and actions through their empirical distributions only. Researchers extensively studied this type of interaction under the name "mean field interaction" — hence the terminology "mean field game" (MFG) that Lasry and Lions introduced [4]. Peter Caines, Minyi Huang, and Roland Malhamé simultaneously developed a similar approach, calling it the Nash certainty equivalence (NCE) principle [3]. Since its inception, this paradigm has evolved from its seminal principles into a fully-fledged field that attracts theoretically inclined investigators as well as applied mathematicians, engineers, and social scientists.

Early Applications

Early contributors to the field introduced and analyzed some particular applications, primarily to illustrate the explanatory potential of MFG paradigm. To serve their pedagogical purpose, they only captured stylized facts from real-life applications, examples

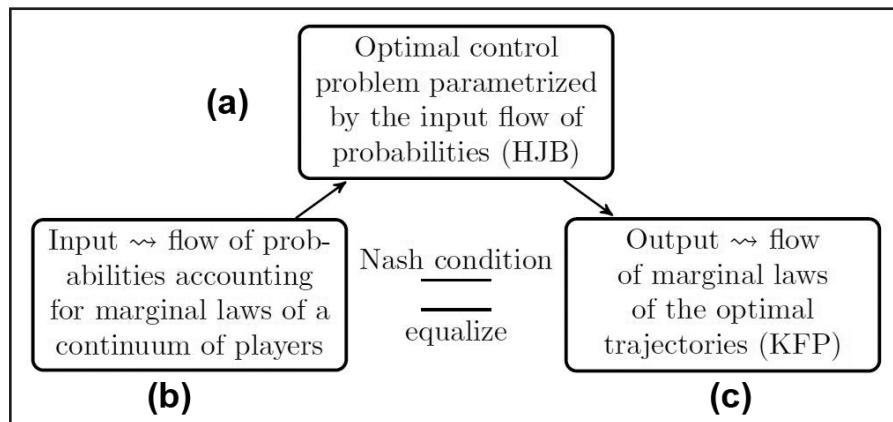


Figure 1. Mean field game (MFG) diagram. **1a.** Optimization problem for each given input. **1b.** Input is a flow of probability measures that describes the statistical state of the population's players. **1c.** Output is the flow of the optimal trajectories' marginal laws. The Nash condition equalizes the input and output flows.

in the form of the following questions: *Why does the Mexican wave have universal features? When does a large meeting begin? Where do I put my towel on the beach?* Realistic engineering applications in wireless communications were concurrently recast as MFG models that showcased the relevance of the search for equilibria in such a framework. Nevertheless, one of MFGs' main attractions is their ability to facilitate the modeling and investigation of large stochastic systems for which standard equilibrium analyses are intractable. Spectacular successes have already occurred (or are expected) in the study of populations in ecology and evolutionary biology—e.g., schooling fish, flocking birds, crowd motion, herding, and swarming—and in financial applications like trading in the presence of price impact (e.g., on high frequency markets) or the quest for better understanding of systemic risk.

However, the number of influential macroeconomic models that foreshadowed the MFG paradigm's introduction is befuddling. Looking back at some of the fundamental works of S. Rao Aiyagari, Per Krusell, and Anthony Smith on macroeconomic growth in the late 1990s, it becomes apparent that these authors were introducing MFG models without identifying them as such. Instead, they proposed to numerically compute approximate solutions by iterating the forward and backward time-stepping of the Hamilton-Jacobi-Bellman (HJB) and Kolmogorov-Fokker-Planck (KFP) equations. In particular, these contributions are a convincing testimony of the importance of a common noise's presence on top of the

idiosyncratic sources of random shocks that are attached to each individual player.

The Analytic Approach

In the spirit of the NCE's original introduction, one can formulate MFGs as a family of standard stochastic control problems that are parameterized by flows of probability measures, which are followed by a fixed point problem on those flows (see Figure 1). This is the typical search for a fixed point of the best response function characteristic of Nash equilibrium. The cornerstone of the analytic approach involves identification of the control problems' value functions as solutions to HJB equations, and then the optimal trajectories' distributions as solutions of KFP equations. One can thus formulate MFGs as a forward-backward system of coupled partial differential equations (PDEs), the analysis of which faces subtle difficulties as the equations' time evolutions run in opposite directions. While researchers may carry out short time analysis via standard contraction fixed point arguments, existence over arbitrary time intervals is much harder and was first completed by Lasry and Lions [4].

The Probabilistic Approach

Probabilists employ several approaches when analyzing MFGs. One approach relies on the theory of backward stochastic differential equations (BSDEs), which are used to handle optimal control problems either through representation of the value process or the stochastic Pontryagin maximum princi-

ple. Combined with the Nash fixed point condition, this leads to the introduction of a new class of forward-backward stochastic differential equations (FBSDEs), called McKean-Vlasov (MKV) FBSDEs. MKV refers to the fact that the coefficients of the stochastic differential equations (SDEs) depend upon their own solutions' distributions. Analysis of these MKV forward-backward equations was essentially nonexistent before MFGs highlighted their role. Their investigation is now a very active field of research.

Practitioners often use linear quadratic models as test beds in classical control and game theory. Their extensions to MFGs form a class of models that one can solve explicitly in the probabilistic approach by solving (possibly matrix) Riccati equations.

Potential Games

MFGs share many similarities with a natural problem that has attracted much attention recently: optimal control of MKV SDEs, also known as mean field control (MFC) (see Figure 2). MFC corresponds to a population of individuals that contribute to an overall cost and take actions according to a control policy chosen by a central planner who minimizes that cost. MFC problems are hence intrinsically optimization problems, while the search for Nash equilibria in MFGs is more of a fixed point problem. Nevertheless, they are linked by their respective Pontryagin principles. Indeed, an MFC problem's Pontryagin system is an MFG's forward-backward system. MFGs that appear this way are called *potential games*, and their variational structure is very useful for both theoretical and numerical purposes.

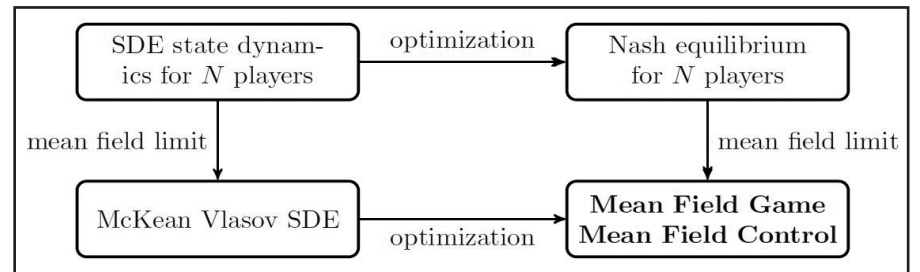


Figure 2. Mean field games (MFGs) versus mean field control (MFC): a non-commutative diagram. In MFC, the mean field limit is taken before optimization is performed. In MFGs, equilibria are reached before the mean field limit is taken.

The Master Equation

Whether the forward-backward system used to handle an MFG is comprised of PDEs or SDEs, one can regard it as the system of characteristics of a PDE, called the master equation. It is set on the product of the physical state space and the space of probability measures. The equation's solution must be understood as the cost in equilibrium of a generic player, beginning from a given state under a given initial probability distribution for the population. This PDE's well-posedness is a difficult question that requires equilibrium uniqueness. The standard condition for uniqueness is a monotonicity condition introduced by Lasry and Lions; monotonicity intuitively encourages players to move away from each other. In fact, it induces a form of strong stability that plays a key role in proving that the characteristics are smooth with respect to the initial condition, whether the latter is a probability measure (as in the PDE approach) or a random variable (as in the BSDE approach).

The Convergence Problem

A mainstay of MFG theory is that one can inject any MFG solution into the N -player version of the game in the form of a distributed strategy (i.e., dependent only on each player's own state, hence of a lower complexity). This provides an approximate equilibrium, the accuracy of which increases with N .

The converse, which aims to show that equilibria of the N -player game converge towards an MFG solution, is known as the convergence problem (see Figure 3). It is much more difficult and remained open until researchers developed an approach based on the master equation [1, 2]. The proof is meant to take advantage of the regularity of the master equation's solution to build an approximate solution to the Nash PDE system of the N -player game, which is the analogue of the HJB equation for games. This approach permits a sharp bound for the error, which leads to a central limit theorem and a large deviation principle for the empirical distributions of the finite player equilibria. In practice, these results produce estimates of finite size effects in the N -player game.

MFGs with Common Noise

Important economic and engineering applications require the presence of an extra source of noise that is common to all players; equilibria become random in these cases. Natural extensions of the aforementioned results merely guarantee the existence of weak solutions that may not be adapted to the common noise. Fortunately, this lack of adaptivity cannot occur under the Lasry-Lions monotonicity condition. Indeed, the resulting MFG system can be uniquely solved by a continuation method — despite the fact that the HJB and KFP equations are stochastic. Outside the monotone regime, researchers seek to understand

whether the common noise can contribute to uniqueness. This is a subject of ongoing research, which raises the question of a possible vanishing viscosity method for selecting solutions to non-uniquely solvable MFGs (without common noise).

Further Developments

Many extensions of MFGs' original form exist. For instance, analysts have focused on the longtime behavior of finite horizon MFGs; they have established convergence towards a stationary MFG under monotonicity conditions, but recent examples indicate that oscillatory behavior may occur in the non-monotone case. Furthermore, both analysts and probabilists have investigated games involving interactions through the laws of the controls, as well as games that feature a major player who interacts with a continuum of minor players. Researchers have also adapted many of the preceding results to finite state games, which are naturally amenable to numerical computations.

Finally, we mention attempts at numerical analysis of MFGs despite their obvious complexity. Early on, finite difference schemes were shown to converge in various situations, and analysts have used optimization methods to solve the corresponding MFC problem. More recently, they have applied ideas from machine learning to parameterize the HJB/KFP system and the master equation via a neural network.

The figures in this article were provided by the authors.

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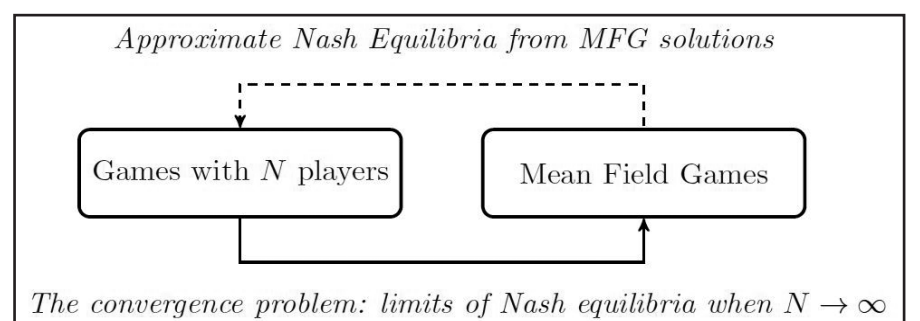


Figure 3. The two ways of connecting finite player games and mean field games (MFGs).