Northeastern
College of Science

# Combating COVID-19 With Innovative Research

Since the onset of the COVID-19 pandemic, faculty investigators at the College of Science have been conducting cutting-edge research to help impede the virus's spread, lessen its impact, and shape prevention strategies–ultimately uncovering treatments that may save lives.

## MODELING THE SPREAD OF COVID-19 AND EVALUATING CONTROL STRATEGIES

When the fight against COVID-19 began, stringent social distancing, robust testing, contact tracing, and quarantining helped to control the virus's spread long enough to allow some social and economic activity to restart. Months on, researchers continue to track the virus and are simulating and assessing the impact of mitigation strategies. Leading these efforts is **Alessandro Vespignani,** director of the Network Science Institute and the Sternberg Family Distinguished University Professor.

Vespignani is collecting data from mobile devices and census records to create a sample of the synthetic population of the Boston metropolitan area. This model explores scenarios of how COVID-19 may spread in the future, and examines ways to mitigate more severe outbreaks while reopening the economy and society. The study's results use two different scenarios: LIFT and LET. In the LIFT scenario, the stay-at-home order is lifted after eight weeks and all work and community places, except for restaurants, theaters, schools, and similar locations with mass gatherings, are reopened. In the LET scenario, the same stay-at-home order is lifted after eight weeks and the same places are reopened, in conjunction with significant contact tracing and precautionary quarantining of potentially exposed individuals. Those individuals, along with their households, would be quarantined.

The study shows that when 40 percent or more of the contacts of people with detected COVID-19 symptomatic infections are traced, and those households are quarantined, the reduction in transmission leads to a noticeable flattening of the epidemic curve. And importantly, this approach appears to effectively limit the virus's resurgence. If the LET scenario is implemented with crowd control, working from home, and mask wearing, it could lead to a further decline of virus transmissibility. This scenario also allows for loosening social distancing measures while retaining hospital demands at levels close to availability and capacity. Vespignani's study demonstrates a method for managing and mitigating the spread of COVID-19, while continuing to reopen society without suffering significant economic losses, widespread social disruptions, or a healthcare system collapse.

The Bill and Melinda Gates Foundation has selected Vespignani's MOBS Lab to model the outcomes of two scenarios of vaccine distribution. In the first scenario, 50 high-income countries monopolize limited doses of the COVID-19 vaccine; in the second, doses are distributed based on each country's population. The lab's results show that cooperation

between countries is the most effective way to minimize the global death rate: 61 percent of deaths could be avoided if the vaccine is distributed to all countries proportional to population, versus 33 percent of deaths avoided if high income countries receive the vaccine first. "You see immediately that the second scenario is far superior," says Vespignani.

In a new, data-driven model, the MOBS Lab affirms that global collaboration is necessary to paint a comprehensive picture of the COVID-19 outbreak and forecast future epidemics. The lab is drawing from global public sources–everything from census figures to data sets about where people work and who they live with–to identify interpersonal behavior down to the state or province level. By splitting populations into smaller settings, epidemiologists and public health officials will be better able to make informed decisions about which disease interventions would be most effective in specific regions.

**COLLABORATING WITH THE GLOBAL COMMUNITY IN THE FIGHT AGAINST COVID-19**

**Samuel Scarpino,** assistant professor and director of the Emerging Epidemics Lab has been collecting data and creating models forecasting the spread of COVID-19. Since the outbreak of the virus, it has been difficult to collect data due to regulations and mandates regarding data-sharing agreements between member countries of the World Health Organization. Because of this, a new international consortium, in which Northeastern plays a major part, was created to build a comprehensive data set.

Researchers and professors worldwide began contributing vast amounts of health data, epidemiologic data, and other records to provide information about COVID-19. Engineers, designers, and product managers have also been offering support with overseeing the technology and infrastructure of the database–and about two million individual records from 150 countries have been entered.

Scarpino and his team are using the information gathered from the international consortium to build and tailor COVID-19 models specifically for the benefit of the city of Boston and the state of Massachusetts. He hopes to provide local and state leaders and lawmakers with accurate information in order to successfully manage the pandemic.

In addition to being a researcher, Scarpino has become an advocate for and communicator of science. He translates data into insights for members of the media, including news anchors, to stress the importance of using scientific data in the battle to combat COVID-19.

"We are providing information, data points, and model forecasts to aid and support decision making," says Scarpino. "It is to paint a picture and provide the resources necessary for policymakers to make the decisions on how they want to move forward to best protect their populations, try to support the economy, and ensure that individuals have the health services that they need."

**USING MACHINE LEARNING TO PINPOINT COVID-19'S WEAK SPOTS**

Few things in the world would function without proteins–not the cells within our bodies and not SARS-CoV-2, the coronavirus that causes COVID-19. These building blocks are among the human body's most sophisticated molecules, catalyzing biochemical reactions that support the structure, function, and regulation of tissues and organs. The 29

proteins in COVID-19 enable it to infect cells without triggering noticeable symptoms, and to learn why **Mary Jo Ondrechen** and **Penny Beuning** are researching the role each protein plays.

Ondrechen and Beuning, both professors of chemistry and chemical biology, want to identify all of the amino acids responsible for the abilities of the coronavirus to infect and thrive at the expense of human cells. They received a grant from the National Science Foundation to use machine learning algorithms and experimental lab work to do just that. By learning more about each protein at the molecular level, the researchers hope their findings will serve as the basis for developing drugs that inhibit chemical reactions from the start, with minimal side effects to patients, and render SARS-CoV-2 ineffective.

Ondrechen's computational program, which her lab invented in 2009, analyzes the chemical properties of each amino acid within a protein. It could predict the roles of important but subtle interactions in SARS-CoV-2 involving amino acids that are not directly linked to the main reaction sites, and which would be too difficult to analyze with conventional bioinformatic research.

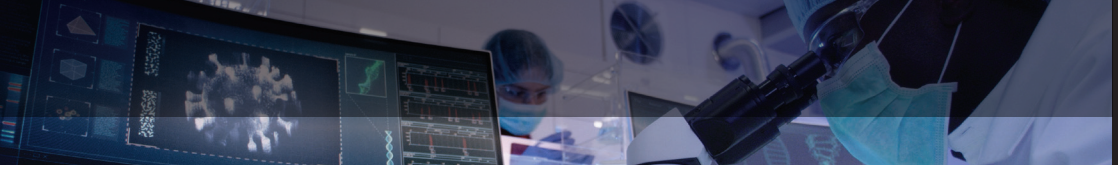
Once Ondrechen's program runs the analysis to find candidate proteins to inhibit SARS-CoV-2, it will guide Beuning's experimental tests in her lab. Buening is searching for compounds that bind to those proteins, and scrutinizing whether they modulate the activity of the protein and impair the coronavirus. Ultimately, the researchers plan to move on from in vitro testing to tests in live organisms to uncover a way to render the coronavirus ineffective.

## REPURPOSING DRUGS TO FIND A CURE FOR COVID-19

As the COVID-19 pandemic continues, researchers are working to develop pharmaceutical drugs that slow the virus's reach and may cure those who are infected. But what if promising therapies already exist? Scientists are racing to identify approved and experimental drugs that may benefit patients, and network medicine is our most powerful platform to identify candidate therapies.

**Albert-László Barabási,** Robert Gray Dodge Professor of Network Science, Distinguished Professor of Physics, and director of the Center for Complex Network Research, has assembled a multidisciplinary team that uses network medicine to hunt for a COVID-19 treatment. Barabási is exploring repurposing approved drugs with known toxicity and side effects that may have a therapeutic effect on COVID-19 patients.

Last year, the Barabási Lab began re-curating its past work on the human interactome, an intracellular and intercellular network of protein interaction. Less than 10 days after starting, the team identified 40 medications that target the cellular areas where COVID-19 works. The virus latches on to a healthy cell's proteins, then disrupts functions within





that cell and generates millions more copies of itself. The lab developed a network model of the 332 proteins targeted by COVID-19 and examined how the virus's perturbing activity might affect tissues and organs. Using this model to examine how COVID-19 binds with host proteins, the lab predicted that the virus could attack cells in the brain–which may explain why early symptoms in people with COVID-19 include loss of the senses of smell and taste.

After forecasting the cellular progression of COVID-19, Barabási began looking for drugs and experimental compounds that could fight the virus by targeting proteins in its network vicinity. Through computation, network modeling, and experimental validation, he hopes to better locate candidate therapies, understand the virus's spread, and observe how repurposed drugs can target areas where the virus works.

**FIT, FABRIC, AND FILTRATION: THE EFFICACY OF FACEMASKS**

Wearing a facemask is one of the chief precautions we can take in controlling the spread of COVID-19. Doing so minimizes the reach of viral particles leaving a person's airway, even if that person is asymptomatic–but researchers are discovering that not all masks are equally effective. **Loretta Fernandez and Amy Mueller,** professors of civil and environmental engineering, are testing the fit and filtration capabilities of different facemasks made with materials commonly available at home or from fabrics sold by crafts and fabric retailers.

Fernandez and Mueller are using tools designed to test tight-fitting respirators, such as N95 masks, to compare their particle removal efficiency to masks sewn from fabric and other alternative face coverings. In doing so, they are intending to fill a gap where no formal testing procedure exists to benchmark facemasks. Realizing that a mask's effectiveness is a combination of both material and fit, separate tests are run using practical techniques to optimize the fit of any mask. The researchers have found that sewn fabric masks can, in some cases, come close to the filtration efficiency provided by commercially produced masks. However, the results of hand-sewn masks have been highly variable and can be so low as to be practically useless.

Fernandez and Mueller have found that with some masks, especially surgical-style masks, using an elastic overlayer can improve the fit on the face and provide greater filtration. With a tighter seal, microscopic viral particles do not pass through the gaps and openings a person would normally get from a mask that fits poorly. Instead, as they breathe in, the particles are pulled onto the mask, which can help filter them out. While wearing a facemask, combined with other preventive measures, helps slow the spread of COVID-19, Fernandez and Mueller's research reveals the critical importance of evaluating every detail of a mask–no matter how seemingly minor.

**To learn more about faculty research in the College of Science, contact Kevin Thompson, Associate Dean for Development, at k.thompson@northeastern.edu.**