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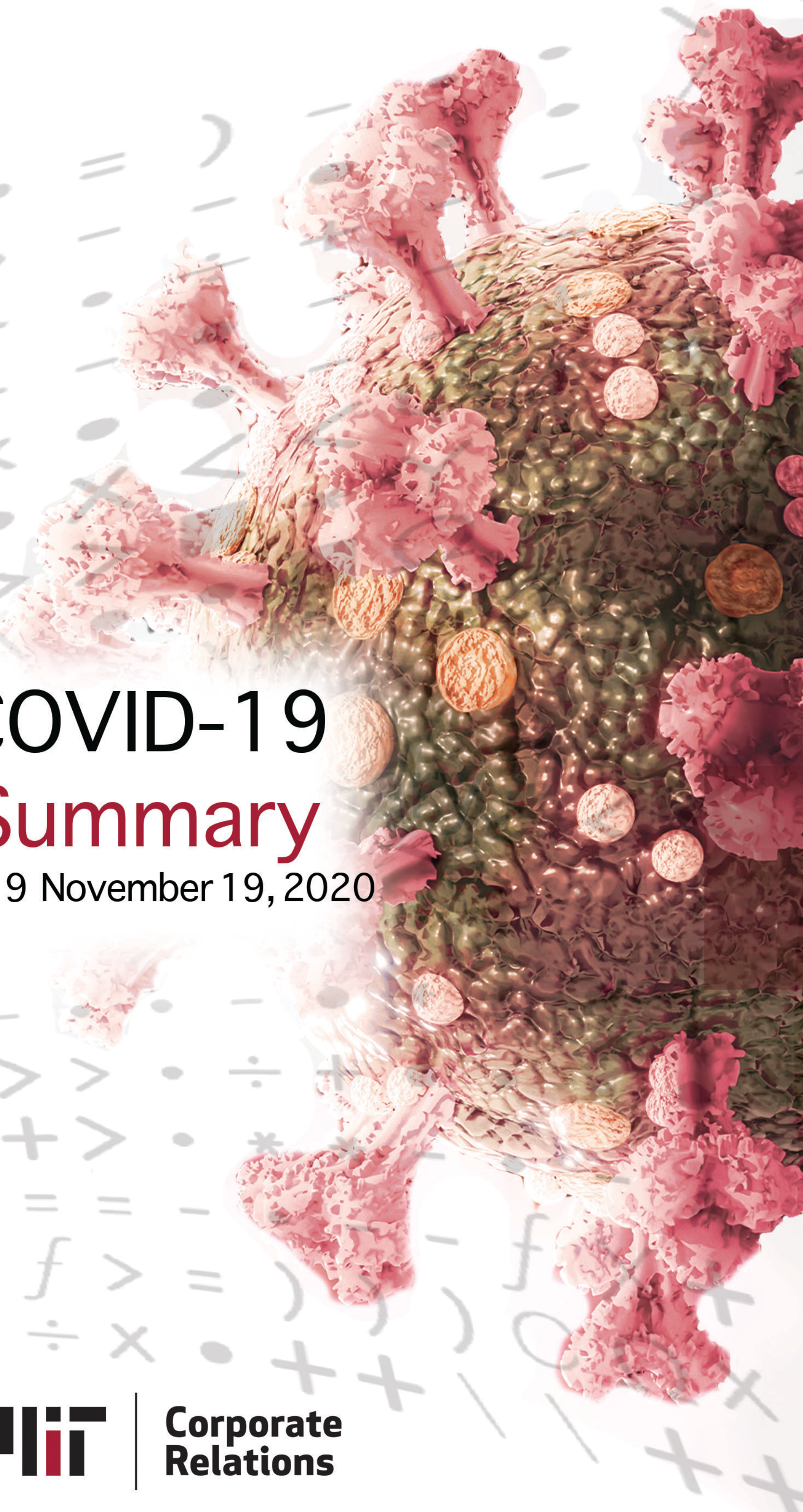

COVID-19
Summary

Vol. 19 November 19, 2020

MIT Corporate Relations

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MIT ILP UPDATES // COVID-19 RELATED

This is a very brief collection of current resources and information from MIT's Industrial Liaison Program covering a range of issues related to COVID-19 and is offered to help us all navigate during this ongoing unprecedented and disruptive time.

UPCOMING EVENTS

MIT ILP WEBINARS

See: https://ilp.mit.edu/search/event?f%5B0%5D=event_type_term%3A24

TUESDAY, 1 DECEMBER, 11:00 AM – 12:30 PM: SUPPLY CHAIN CHALLENGES

MIT Corporate Relations / ILP
Agenda: https://ilp.mit.edu/attend/supply-chain-challenges

THURSDAY, 3 DECEMBER, 11:00 AM – 1:00 PM: THE CHANGING URBAN ENVIRONMENT

MIT Corporate Relations / ILP
Agenda: https://ilp.mit.edu/attend/changing-urban-environment

TUESDAY & WEDNESDAY, 8 & 9 DECEMBER: 2020 U.S. C3E WOMEN IN CLEAN ENERGY SYMPOSIUM AND AWARDS

12 noon - 4:30 pm each day, https://www.c3eawards.org/2020
For the first time, this normally invitation-only event is open to all who would like to attend
Register (free): https://www.eventbrite.com/e/2020-us-c3e-women-in-clean-energy-symposium-and-awards-tickets-124298200263

MONDAY, 14 DECEMBER, 11:00 AM – 12:30 PM: HACKING HEALTHCARE TRANSFORMATION WITH DIGITAL TECHNOLOGY + OPEN INNOVATION

MIT Corporate Relations / ILP
Agenda: https://ilp.mit.edu/attend/hacking-healthcare-transformation-digital-technology-open-innovation

PROJECTS, INITIATIVES, RESEARCH

COLLINS LAB

James J. Collins, Termeer Professor of Medical Engineering and Science, IMES, Professor of Biological Engineering, https://be.mit.edu/directory/james-j-collins; http://imes.mit.edu/people/faculty/collins-james-j/
Lab: https://collinslab.mit.edu/index.html

The Collins Lab works in synthetic biology and systems biology, with a particular focus on using network biology approaches to study antibiotic action, bacterial defense mechanisms, and the emergence of resistance. In synthetic biology, we have used techniques and principles from nonlinear dynamics and molecular biology to design and construct synthetic gene networks. We have created genetic toggle switches, RNA switches, programmable cells, genetic counters, genetic timers, kill switches for microbes, engineered bacteriophage to combat bacterial infections, and tunable mammalian genetic switches, each with broad applications in medicine and biotechnology. In systems biology, we have developed and implemented dynamical techniques to reverse engineer and analyze naturally occurring gene regulatory networks. We have shown that these reconstructed networks can be used to identify the genetic mediators of a given disease or biological process, as well as the biomolecular targets of a therapeutic compound.

Covid-19 “super-spreading” events play outsized role in overall disease transmission

Mathematical analysis suggests that preventing large gatherings could significantly reduce Covid-19 infection rates.
Anne Trafton I MIT News Office, November 2, 2020, https://news.mit.edu/2020/super-spreading-covid-transmission-1102

Interventions limiting superspreading may be particularly effective at controlling the ongoing COVID-19 pandemic, according to an analysis of SARS-CoV and SARS-CoV-2 superspreading events….

Related paper:

Evidence that coronavirus superspreading is fat-tailed

Felix Wong (postdoc, Collins Lab) and James J. Collins, Proceedings of the National Academy of Sciences USA, PNAS first published November 2, 2020
https://www.pnas.org/content/early/2020/10/30/2018490117
https://doi.org/10.1073/pnas.2018490117
http://www.mit.edu/~wongf/publications.html

Superspreaders, infected individuals who result in an outsized number of secondary cases, are believed to underlie a significant fraction of total SARS-CoV-2 transmission. Here, we combine empirical observations of SARS-CoV and SARS-CoV-2 transmissin and extreme value statistics to show that the distribution of secondary cases is consistent with being fat-tailed, implying that large superspreading events are extremal, yet probable, occurrences. We integrate these results with interaction-based network models of disease transmission and show that superspreading, when it is fat-tailed, leads to pronounced transmission by increasing dispersion. Our findings indicate that large superspreading events should be the targets of interventions that minimize tail exposure.

HONG LAB

Mei Hong, Professor of Chemistry, http://meihonglab.com/professor-mei-hong/
Research: http://meihonglab.com/honglabresearch/

The Hong group develops and applies magic-angle-spinning solid-state NMR spectroscopy to elucidate the structure and dynamics of biological macromolecules. We seek to understand how molecular conformation, motion, and intermolecular interactions enable proteins and carbohydrates to carry out their functions such as ion conduction across lipid membranes, membrane fusion between viruses and cells, membrane scission during virus budding, and maintenance and expansion of plant cell walls. We also investigate the structure and dynamics of amyloid proteins in neurodegenerative diseases. To answer these mechanistic biophysical questions, we innovate multinuclear (1H, 13C, 15N, 19F, 2H, & 31P) and multidimensional solid-state NMR techniques that measure molecular structure, inter-atomic distances, and amplitudes and rates of molecular motions with high sensitivity.

MIT News: Chemists discover the structure of a key coronavirus protein
The protein, which acts as an ion channel, could be a target for new drugs against the SARS-CoV-2 virus.
Anne Trafton I MIT News Office, November 12, 2020
https://news.mit.edu/2020/chemists-discover-structure-key-coronavirus-protein-1112

Using nuclear magnetic resonance (NMR), MIT chemists have determined the molecular structure of a protein found in the SARS-CoV-2 virus. If researchers could devise ways to block this ion channel, they may be able to design drugs that would interfere with viral replication. The illustration on the right shows the five-helix bundle of the envelope protein E with a gray water column inside.

Related paper:
Structure and drug binding of the SARS-CoV-2 envelope protein transmembrane domain in lipid bilayers
V.S. Mandala, M.J. McKay, A.A. Shcherbakov, A.J. Dregni, A. Kolocouris, and **Mei Hong**, (2020) Nat. Struct. Mol. Biol., Published: 11 November 2020, https://doi.org/10.1038/s41594-020-00536-8
Hong Lab members: http://meihonglab.com/people/
Related story: https://spectrum.mit.edu/fall-2020/tiny-molecules-big-impacts/

An essential protein of the SARS-CoV-2 virus, the envelope protein E, forms a homopentameric cation channel that is important for virus pathogenicity. Here we report a 2.1-Å structure and the drug-binding site of E's transmembrane domain (ETM), determined using solid-state NMR spectroscopy. In lipid bilayers that mimic the endoplasmic reticulum–Golgi intermediate compartment (ERGIC) membrane, ETM forms a five-helix bundle surrounding a narrow pore. The protein deviates from the ideal α-helical geometry due to three phenylalanine residues, which stack within each helix and between helices. Together with valine and leucine interdigitation, these cause a dehydrated pore compared with the viroporins of influenza viruses and HIV. Hexamethylene amiloride binds the polar amino-terminal lumen, whereas acidic pH affects the carboxy-terminal conformation. Thus, the N- and C-terminal halves of this bipartite channel may interact with other viral and host proteins semi-independently. The structure sets the stage for designing E inhibitors as antiviral drugs.

SENSEABLE CITY LAB

Carlo Ratti, Director and Professor of the Practice, https://carloratti.com/
http://senseable.mit.edu/

Q&A: A smarter way of working

IPE Real Assets, September / October 2020 (Magazine)
https://realassets.ipe.com/offices/qanda-a-smarter-way-of-working/10047986.article

Italian architect and professor Carlo Ratti directs the MIT Senseable City Lab, which explores how technology is changing cities. How does he see the future of the office post-COVID-19? Maha Khan Phillips reports

What long-term impact will the COVID-19 pandemic have on the way people work?

In as early as 1973, urban theorist Melvin Webber proclaimed that ‘for the first time in history, it might be possible to locate on a mountain top and to maintain intimate, real-time, and realistic contact’.

I don’t think we will work from the mountain top, but certainly COVID-19 has sped up the transition to smart working. I believe that smart working is here to stay.

Twitter, amongst others, is giving its employees the choice to practice smart working, even after the pandemic and all activities reopen. To push the conversation a step further, we can leverage the liberty given to us by technology not only to work from home, but to work from everywhere. A more flexible professional routine could revitalise our social and intellectual fabric damaged by the pandemic.

How will the office environment change as a result?

The crisis is accelerating transitions that have been long in the making. Even before coronavirus, the world had been moving away from the homogenous workplace and professional arrangement.

As a result, we can expect the downsizing of office spaces, and the development of a new working choreography to transmit company culture and connections.

That said, it is unlikely the office would be wiped out completely. It still has important social functions to play, connecting a diverse mix of people and thoughts together. What it needs is a redesign to become more effective.”

You’ve talked about the need for employees to meet and develop ideas, to collaborate, and your research has shown how important this is. Do you think offices of the future will support this?

Initial results of an analysis on the communication networks among the students, professors and administrators of MIT show that interpersonal connections are getting more concentrated on a smaller number of contacts.

A possible explanation is that we are only advancing our strong ties – close relationship forming dense, overlapping networks, according to sociologist Mark Granovetter – while our weak ties with casual acquaintances have been declining.

The office could remedy this situation. Meeting a larger number of acquaintances means a higher likelihood for us to break away from the limited set of beliefs we share with our immediate social circle.

A colleague we do not work directly with could introduce us to a creative approach to tackle an issue, or challenge our long-established preconception. The information we receive from online communicational platforms, sometimes enhanced algorithmically, aligns with our world view or concepts we are familiar with; on the other hand, it is those physical spaces like the office which open us to new learning experiences.

Will employers have to think more about overall wellbeing?

There are different measures employers can take while considering their team's wellbeing. A more flexible work arrangement would be helpful for the employees to strike a better balance of life. In addition, they should also commit to making the office a safer and more social workplace.

For instance, traditional floor plans with their cubicles are designed to facilitate solitary task execution, which today can be more effectively carried out at home. Conversely, we need dynamic spaces to forge ideation and social relations.

Can Open Source Hardware Mechanical Ventilator (OSH-MVs) initiatives help cope with the COVID-19 health crisis? Taxonomy and state of the art

Simone Mora, Fábio Duarte, **Carlo Ratti**, HardwareX, Volume 8, October 2020, e00150
https://doi.org/10.1016/j.ohx.2020.e00150

The field of Open Source Hardware Mechanical Ventilators (OSH-MVs) has seen a steep rise of contributions during the 2020 COVID-19 pandemic. As predictions showed that the number of patients would exceed current supply of hospital-grade ventilators, a number of formal (academia, the industry and governments) and informal (fablabs and startups) entities raced to develop cheap, easy-to-fabricate mechanical ventilators. The presence of actors with very diverse modus operandi as well as the speed at which the field has grown, led to a fragmented design space characterized by a lack of clear design patterns, projects not meeting the minimum functional requirements or showing little-to-no innovation; but also valid alternatives to hospital-grade devices. In this paper we provide a taxonomic system to help researchers with no background in biomedical engineering to read, understand and contribute to the OSH-MV field. The taxonomy is composed of ten properties that are read through the lenses of three reflection criteria: buildability, adoptability and scalability. We applied the taxonomy to the analysis of seventeen OSH-MV projects, which are representative of the current landscape of possibilities available for COVID-19 patients. We discuss the different design choices adopted by each project highlighting strengths and weaknesses and we suggest possible directions for the development of the OSH-MV field.

COVID-19 across United States congressional districts

Priyanka N deSouza, S V Subramanian, J Glob Health Sci. 2020 Dec; 2(2):e22
https://doi.org/10.35500/jghs.2020.2.e22

The congressional district (CD) geography in the United States (US) represents a policy-relevant and a politically important scale at which to monitor the coronavirus disease 2019 (COVID-19) crisis. In this study, we present the first estimates of COVID-19 cumulative cases and deaths (per 1,000 people) and the case fatality rate as of July 13, 2020, as well as for the recent period between June 13 and July 13, 2020 using a population-weighting methodology for the 436 CDs in the US. Access to CD-level information about the impact of COVID-19 can enhance the ability of elected officials and the constituents they represent, to monitor and develop testing strategies and other measures to allow the US to open safely.

PAPERS, ARTICLES, PRESENTATIONS, TALKS'

VACCINES: A COST/BENEFIT ANALYSIS OF CLINICAL TRIAL DESIGNS FOR COVID-19 VACCINE CANDIDATES

Donald A. Berry, Scott Berry, Peter Hale, Leah Isakov, **Andrew W. Lo** (MIT Sloan), Kien Wei Siah & Chi Heem Wong, NBER Working Paper 27882, October 2020, DOI: 10.3386/w27882, https://www.nber.org/papers/w27882

We compare and contrast the expected duration and number of infections and deaths averted among several designs for clinical trials of COVID-19 vaccine candidates, including traditional randomized clinical trials and adaptive and human challenge trials. Using epidemiological models calibrated to the current pandemic, we simulate the time course of each clinical trial design for 504 unique combinations of parameters, allowing us to determine which trial design is most effective for a given scenario. A human challenge trial provides maximal net benefits—averting an additional 1.1M infections and 8,000 deaths in the U.S. compared to the next best clinical trial design—if its set-up time is short or the pandemic spreads slowly. In most of the other cases, an adaptive trial provides greater net benefits.

VACCINES: SHAPING HUMORAL IMMUNITY TO VACCINES THROUGH ANTIGEN-DISPLAYING NANOPARTICLES

Darrell J Irvine (Biological Engineering; MS&E), Benjamin J Read, Current Opinion in Immunology (2020). PMID: 32200132. https://doi.org/10.1016/j.coi.2020.01.007

Strategies to qualitatively and quantitatively enhance the humoral response to immunizations with protein and polysaccharide antigens are of broad interest for development of new and more effective vaccines. A strategy of increasing importance is the formulation of antigens into a particulate format, mimicking the physical form of viruses.The potential benefits of enhanced B cell receptor engagement by nanoparticles have been long been appreciated, but recent studies are defining additional important factors governing how nanoparticle immunogens interact with the immune system in the context of lymphoid organs. This review will discuss findings about how nanoparticles enhance humoral immunity in vivo and factors governing the fate of nanoparticle immunogens in lymph nodes.

Conclusions: Recent studies in both small and large animal models are providing new insights into the impact of particulate formulations of vaccine antigens on humoral immunity. While much effort has focused on engineering antigen display to optimally present neutralizing epitopes, an equally important component will be consideration of engineering nanoparticle designs to exploit natural pathways for optimal entry and localization within lymph nodes. Studies to further our understanding of how the immune system processes particulate antigens should help define improved design strategies for future vaccines.

ALGORITHMS / TRACING: SAMPLING MANHOLES TO HOME IN ON SARS-COV-2 INFECTIONS

Richard C Larson (IDSS), Oded Berman, Mehdi Nourinejad 2020, PLOS One,
5 October 2020, https://doi.org/10.1371/journal.pone.0240007

About 50% of individuals infected with the novel Coronavirus (SARS-CoV-2) suffer from intestinal infection as well as respiratory infection. They shed virus in their stool. Municipal sewage systems carry the virus and its genetic remnants. These viral traces can be detected in the sewage entering a wastewater treatment plant (WTP). Such virus signals indicate community infections but not locations of the infection within the community. In this paper, we frame and formulate the problem in a way that leads to algorithmic procedures homing in on locations and/or neighborhoods within the community that are most likely to have infections. Our data source is wastewater sampled and real-time tested from selected manholes. Our algorithms dynamically and adaptively develop a sequence of manholes to sample and test. The algorithms are often finished after 5 to 10 manhole samples, meaning that—in the field—the procedure can be carried out within one day. The goal is to provide timely information that will support faster more productive human testing for viral infection and thus reduce community disease spread. Leveraging the tree graph structure of the sewage system, we develop two algorithms, the first designed for a community that is certified at a given time to have zero infections and the second for a community known to have many infections. For the first, we assume that wastewater at the WTP has just revealed traces of SARS-CoV-2, indicating existence of a “Patient Zero” in the community. This first algorithm identifies the city block in which the infected person resides. For the second, we home in on a most infected neighborhood of the community, where a neighborhood is usually several city blocks. We present extensive computational results, some applied to a small New England city.

Related MIT News Story: **Testing sewage to home in on Covid-19**
Letting an algorithm decide which maintenance holes to test for evidence of coronavirus could improve pandemic containment efforts.
Scott Murray I Institute for Data, Systems, and Society, October 28, 2020,
https://news.mit.edu/2020/testing-sewage-for-covid-19-1028

A “tree network” of sewage pipelines can be accessed via many maintenance holes (typically about 300 feet apart). A new algorithm can dynamically and adaptively select which maintenance holes in a community to test for evidence of SARS-CoV-2 to lead to areas of outbreak, in this case finding a “hot spot neighborhood” of infections.

ECONOMICS / POLICY: SIZING UP CORPORATE RESTRUCTURING IN THE COVID CRISIS

Robin Greenwood, Benjamin Iverson & **David Thesmar** (MIT Sloan)
NBER Working Paper 28104, November 2020, DOI: 10.3386/w28104,
https://www.nber.org/papers/w28104

In the wake of the COVID-19 pandemic, the financial and legal system will need to deal with a surge of financial distress in the business sector. Some firms will be able to survive, while others will face bankruptcy and thus need to be liquidated or reorganized. Many surviving firms will need to be downsized or acquired. In normal times, this triage is supported by the court system, banks, and financial markets. The goal of this paper is to size up the coming surge of financial distress, list the challenges it presents in the current environment, and offer potential policy solutions. Overall, our analysis suggests that the two key issues will be court congestion and excess liquidation and failure of small firms.

DATA / HEALTH INFORMATICS: UNSUPERVISED LEARNING FOR COUNTY-LEVEL TYPOLOGICAL CLASSIFICATION FOR COVID-19 RESEARCH

Yuan Lai, Marie-Laure Charpignon, Daniel K Ebner, **Leo Anthony Celi**

Intelligence-Based Medicine, Volumes 1–2, November 2020, 100002
https://doi.org/10.1016/j.ibmed.2020.100002

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Marie-Laure Charpignon: PhD student IDSS, https://idss.mit.edu/staff/marie-charpignon/

The analysis of county-level COVID-19 pandemic data faces computational and analytic challenges, particularly when considering the heterogeneity of data sources with variation in geographic, demographic, and socioeconomic factors between counties. This study presents a method to join relevant data from different sources to investigate underlying typological effects and disparities across typologies. Both consistencies within and variations between urban and non-urban counties are demonstrated. When different county types were stratified by age group distribution, this method identifies significant community mobility differences occurring before, during, and after the shutdown. Counties with a larger proportion of young adults (age 20–24) have higher baseline mobility and had the least mobility reduction during the lockdown.

Highlights

- The analysis of county-level COVID-19 pandemic data faces computational and analytic challenges, particularly when considering the heterogeneity of data sources with variation in geographic, demographic, and socioeconomic factors.

- This study presents a method to join relevant data from different sources to investigate underlying typological effects and disparities across typologies. Both consistencies within and variations between urban and non-urban counties are demonstrated.

- Significant community mobility differences occurring before, during, and after the shutdown, based on the types of age group distribution. Counties with a larger proportion of young adults have higher baseline mobility and the least mobility reduction during the lockdown.

Related:
Urban intelligence for pandemic response: Viewpoint
Lai, Yuan, Wesley Yeung, and **Leo A. Celi**. 2020 JMIR Public Health & Surveillance, 6:2, DOI: 10.2196/18873, https://publichealth.jmir.org/2020/2/e18873/

Previous epidemic management research proves the importance of city-level information, but also highlights limited expertise in urban data applications during a pandemic outbreak. In this paper, we provide an overview of city-level information, in combination with analytical and operational capacity, that define urban intelligence for supporting response to disease outbreaks. We present five components (movement, facilities, people, information, and engagement) that have been previously investigated but remain siloed to successfully orchestrate an integrated pandemic response. Reflecting on the coronavirus disease (COVID-19) outbreak that was first identified in Wuhan, China, we discuss the opportunities, technical challenges, and foreseeable controversies for deploying urban intelligence during a pandemic. Finally, we emphasize the urgency of building urban intelligence through cross-disciplinary research and collaborative practice on a global scale.