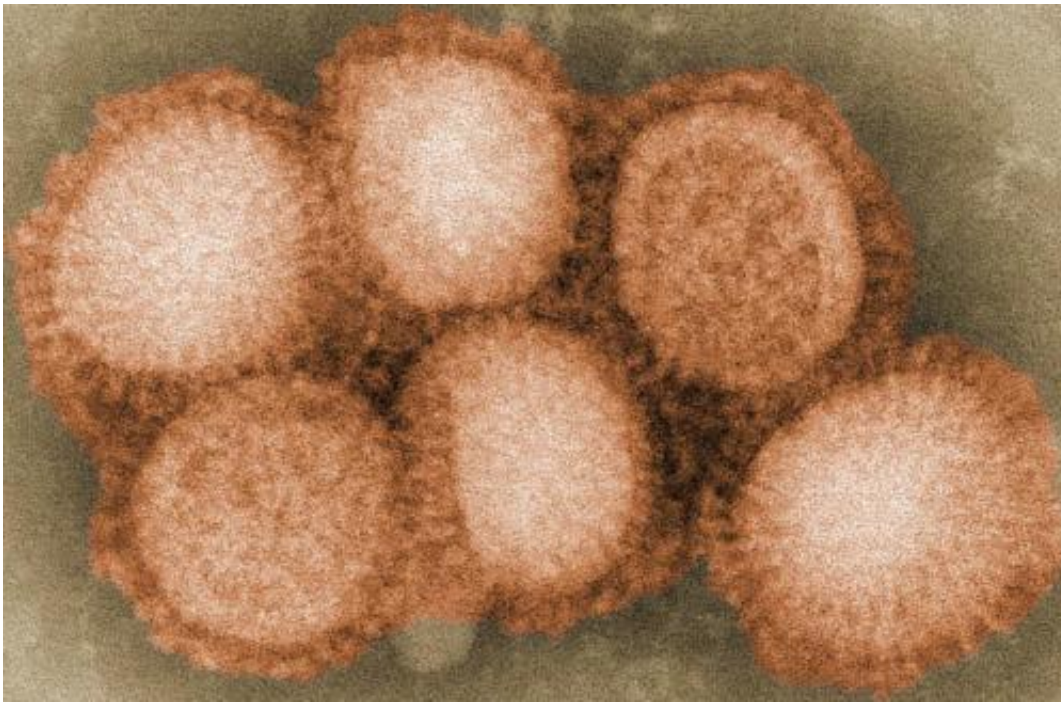


Waging a more effective war against viral outbreaks

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H1N1 virus. Credit: C. S. Goldsmith and A. Balish, CDC

HIV, SARS, Ebola, H1N1, Zika, the list of communicable global health threats seems ever growing. And all too often, the limited resources available to fight these diseases must be picked up and redeployed, often haphazardly, as the next new threat emerges.

But what if there were ways to wage a more effective war against all [communicable diseases](#), using new combinations of proven complex

sociological and statistical mathematic models to tell where an outbreak might occur, how it might spread, and how it could best be rolled back or even eliminated by a more tactical application of resources?

That's exactly what Carlos Castillo-Chavez, a regent's professor of mathematical biology at Arizona State University's School of Human Evolution and Social Change, and colleagues propose the need for in a new article published this month in the *Proceedings of the National Academy of Sciences*.

As executive director of the Simon A. Levin Mathematical and Computational Modeling Sciences Center, Castillo-Chavez isn't satisfied with the traditional mathematical epidemiological approach to tracking these diseases, which relies heavily on the amount of per capita points of "collisions" between those with a disease and others not yet infected. These models often fall short because they fail to take into account the unique complicating factors of what is referred to in the study as a "patch" (or a zone of shared socioeconomic, geographic or other traits) where those interactions occurred.

Instead, Castillo-Chavez is now looking at and prompting others in his field to consider the intersection of two evolving approaches that could be used to better address the problem.

The first is economic epidemiological modeling (EEM), which includes examining information flow in affected areas and the financial risk/reward perceptions that may drive movement of individuals to, from, and within affected "patches." An example might be someone having to choose between self-quarantine as a protection strategy versus leaving home during an outbreak to go to work and receive income—which can also be a matter of life and death.

The second is the Lagrangian approach, which also assists with

projecting human crowd movement and behavior, but broadens the scope of patches considered related to a disease and allows them be assigned their own associated risk of infection per residency time. This information can then be layered over EEM-driven population mobility calculations for more accurate transmission projections.

"The Lagrangian perspective has helped increase our understanding of the consequences of the deliberate release of biological agents in 2003 and most recently in the study of Ebola in West Africa and Zika in the Americas," Castillo-Chavez notes.

Both the development and the application of these types of new, complex mathematical and social theories would be no easy feat. But it might be a first step towards the goal of identifying consistent patterns—such as those starting to emerge in the study of host-parasite systems—that can account for not just known and recurrent variables, but also emergent natural and social shifts in a world where people can move anywhere, at nearly any time.

"These efforts emerged as the result of multi-institutional collaborators that met regularly at NIMBioS in Tennessee with the support of NSF for more than two years," Castillo-Chavez says. "The research has been carried out with my former students and postdoctoral associates Benjamin Morin, now at Vassar and Derdei Bichara, now at Cal State Fullerton."

More information: Carlos Castillo-Chavez et al, Perspectives on the role of mobility, behavior, and time scales in the spread of diseases, *Proceedings of the National Academy of Sciences* (2016). [DOI: 10.1073/pnas.1604994113](https://doi.org/10.1073/pnas.1604994113)

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