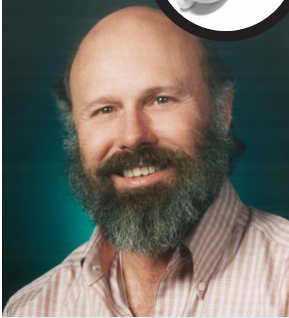




Resisting the Spread of Disease

AMS Podcast Series



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One of the most useful tools in analyzing the spread of disease is a system of evolutionary equations that reflects the dynamics among three distinct categories of a population: those susceptible (S) to a disease, those infected (I) with it, and those recovered (R) from it. This SIR model is applicable to a range of diseases, from smallpox to the flu. To predict the impact of a particular disease it is crucial to determine certain parameters associated with it, such as the average number of people that a typical infected person will infect. Researchers estimate these parameters by applying statistical methods to gathered data, which aren't complete because, for example, some cases aren't reported. Armed with reliable models, mathematicians help public health officials battle the complex, rapidly changing world of modern disease.

Today's models are more sophisticated than those of even a few years ago. They incorporate information such as contact periods that vary with age (young people have contact with one another for a longer period of time than do adults from

different households), instead of assuming equal contact periods for everyone. The capacity to treat variability makes it possible to predict the effectiveness of targeted vaccination strategies—to combat the flu, for instance. Some models now use graph theory and matrices to represent networks of social interactions, which are important in understanding how far and how fast a given disease will spread.

For More Information: *Mathematical Models in Population Biology and Epidemiology*, Fred Brauer and Carlos Castillo-Chavez.



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