



Resisting the Spread of Disease

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.



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