

The basic reproduction number for discrete- and continuous-time models

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Abstract

For a disease model, the basic reproduction number R_0 is the expected number of secondary cases directly caused by an infected individual which is introduced into an otherwise susceptible population. Mathematically, it is defined as the spectral radius of a next-generation operator that tracks disease from one generation to the next.

I will start by reviewing how mathematical analysis of the basic reproduction number has been key in understanding the continuous-time dynamics of emerging infectious diseases. As an example, I will focus on recent progress regarding West Nile Virus models. R_0 can also be formulated for discrete-time models, where it sometimes interpreted as the net reproductive rate, the mean number of offspring per individual over its lifetime. I will connect discrete and continuous versions of R_0 and derive a new method for calculating R_0 directly by applying graph reduction rules to a modified life-cycle graph representation of the discrete-time model.

The last part of the talk involves recent work with Tomas de Camino Beck (Alberta).