

Description of mathematical modeling basics and model types:

Mechanically, there are many different ways to construct a model. There are two basic dimensions, however, and these define four classes of models with similar strengths and limitations. First, the underlying processes can be represented in either deterministic or stochastic forms. The difference is analogous to using the mean as a prediction summary versus using the full probability distribution of outcomes. Second, the dynamics over time can be explored either analytically or using computational methods. Analytic, or “closed-form,” solutions isolate the outcome on the left-hand side of an equation, with all of the determinants on the right-hand side, so it is clear how the outcome depends on the inputs. Not all processes can be represented this way. Computational, or “numerical,” solutions must be employed if there are non-trivial feedback loops in the process, so that the outcome ends up on both sides of the equation. Models of this sort are said to be “analytically intractable.” This happens very quickly as simplifying assumptions are relaxed, so most models that attempt to build in realistic heterogeneity need to be solved computationally.

All models divide the population into states (e.g. susceptible and infected) and define the process and rate of movement between those states. Deterministic models are usually built on group aggregates or macro-level states, while stochastic simulation models are usually built to reflect the micro-level states occupied by discrete individual persons. The primary difference between deterministic and stochastic models is how they define the movement between states. Deterministic models define the dynamics using the average *rate* of transition between states. Stochastic models define the dynamics using the *probability* that an individual makes the transition from one state to another.

Analytic models of both sorts (deterministic and stochastic) are typically regarded as the ideal, since they reveal a process in terms of simple cause and effect. Many infectious processes are not simple in that way, however, and the assumptions made to gain tractability often come at the cost of ignoring important parts of the process, and thus failure to properly project the outcomes of interest. As computing power has become more widely available, the need for tractability has declined, and computational-deterministic models have become the workhorse of mathematical epidemiology. Their use has led to substantial insight into the population dynamics of HIV and other STIs, as well as a wide range of other infectious diseases. Increasingly, the limitations of deterministic models are leading to the adoption of computational-stochastic or “microsimulation” methods. These methods are better for representing heterogeneities in the transmission process, behavioral or biological, and they are the only way to accurately represent something as simple as a person having multiple ongoing (“concurrent”) partnerships. The advantages of microsimulation are discussed in detail by van Imhoff and Post.(1998) The primary disadvantages are that it requires richer inputs, and may require significantly more computational capacity.