
Boolean: One of the simplest possible modelling techniques is to represent a network using Boolean logic (?). This approach has been used to model gene networks.

Ordinary differential equations (ODEs): This is the commonest and arguably most useful representation. Although based on a continuum model, ODE models have proved to be excellent descriptions of many biological systems. Another advantage to using ODEs is the wide range of analytical and numerical methods that are available. The analytical methods in particular provide a means to gain a deeper insight into the workings of the model.

Deterministic hybrid: A deterministic hybrid model is one which combines a continuous model (e.g ODE model) with discrete events. These models are notoriously difficult to solve efficiently and require carefully crafted numerical solvers. The events can occur either in the state variables or parameters and can be time dependent or independent. A simple example involves the division of a cell into two daughter cells. This event can be treated as a discrete event which occurs when the volume of the cell reaches some preset value at which point the volume halves.

Differential-algebraic equations (DAEs): Sometimes a model requires constraints on the variables during the solution of the ODEs. Such a situation is often termed a DAE system. The simplest constraints are mass conservation constraints, however these are linear and can be handled efficiently and easily using simple assignment equations (see equation ??). DAE solvers need only be used when the constraints are nonlinear.

Partial differential equations (PDEs): Whereas simple ODEs model well stirred reactors, PDEs can be used model heterogenous spatial models.

Stochastic: At the molecular level concentrations are discrete, but as long as the concentrations levels are sufficiently high, the continuous model is perfectly adequate. When concentrations fall below approximately one hundred molecules in the volume considered (e.g. the cell or compartment) one has to consider using stochastic modelling. The great disadvantage in this approach is that one loses almost all the analytical methods that are available for continuous models, as a result stochastic models are much more difficult to interpret.

Figure 1: A non-exhaustive selection of mathematical techniques for modelling biological systems.