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*Structural Identifiability of Biological Models.*

The parameter identifiability problem in biological modeling concerns finding which unknown parameters of a model can be determined from data. An important step in this problem is to determine the structural identifiability of the model, which concerns identifiability of the model parameters under the ideal circumstances of perfect data, i.e. data that is noise-free and of any time duration required. If all of the parameters can be determined from perfect data, then the model is said to be structurally identifiable. However, many models arising in systems biology are structurally unidentifiable, which means that some of the parameters of the model can take on an infinite number of values and yet yield the same input-output data, even under the ideal circumstances of perfect data. We explore the structural identifiability problem using a differential algebra approach and apply tools from computational algebra to find sufficient conditions for identifiability. (Received September 21, 2015)