Efficient Sampling of Probabilistic Program for Biological Systems

Authors : Keerthi S. Shetty, Annappa Basava

Abstract : In recent years, modelling of biological systems represented by biochemical reactions has become increasingly important in Systems Biology. Biological systems represented by biochemical reactions are highly stochastic in nature. Probabilistic model is often used to describe such systems. One of the main challenges in Systems biology is to combine absolute experimental data into probabilistic model. This challenge arises because (1) some molecules may be present in relatively small quantities, (2) there is a switching between individual elements present in the system, and (3) the process is inherently stochastic on the level at which observations are made. In this paper, we describe a novel idea of combining absolute experimental data into probabilistic model using tool R2. Through a case study of the Transcription Process in Prokaryotes we explain how biological systems can be written as probabilistic program to combine experimental data into the model. The model developed is then analysed in terms of intrinsic noise and exact sampling of switching times between individual elements in the system. We have mainly concentrated on inferring number of genes in ON and OFF states from experimental data.

Keywords : systems biology, probabilistic model, inference, biology, model

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