

You are provided with two journal publications for discussion:

J. Chem. Inf. Comput. Sci. 2003, 43, 1011–1019

DiMSim: A Discrete-Event Simulator of Metabolic Networks

Xiao-Qin Xia and Michael J. Wise*

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Answer the following questions for Xia and Wise (2003). You only need to read the abstract, introduction and discussion (!):

1. Reading the **abstract** and **discussion** what do the authors suggest their simulator can do? What is your impression do they emphasize; what makes their simulator possibly special or better than others?
2. In the **abstract**, is there any particular claim in the abstract that strikes you as bold?
3. In the **introduction** how do the authors motivate/justify their work, compared to other simulation systems?
4. Would you consider modeling and simulation as two different concepts?
5. What is a mathematical model, what does it consists of and where does the information come from to construct/simulate a mathematical model?
6. Which concepts are most widely used for modeling metabolic networks?
7. What do the authors criticize about differential equation models?
8. Looking at **Figure 3** (Dynamics of metabolites) and **Figure 4** (Lotka-Volterra system), do these examples/plots suggest a “discrete-event” approach for modeling?
9. Has this paper had any impact? How widely is their simulator DimSim used?

insight review articles

Control, exploitation and tolerance of intracellular noise

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NATURE | VOL 420 | 14 NOVEMBER 2002

Answer the following questions for Rao et al. (2002):

1. What is noise? Are there degrees of randomness; can there be pattern in noise?
2. When is noise a nuisance and when are chance events meaningful for the functioning of a cell?
3. Consider the notion of “robustness” vs. “sensitivity” to noise.
4. What are the main arguments for stochastic models and what arguments are made against alternative approaches?
5. Considering the expression of a gene, the initiation of transcription can be determined by single molecules, while the consequences involve very large quantities. What consequence has this on the modeling approaches we could choose to study gene expression?
6. When should single-cell experiments/measurements be preferred over population based experiments? For single-cell experiments, how do we remove uncertainty in data?
7. Looking at Figure 1, what is the message of this plot? Does it make a difference whether a single simulation run of a stochastic process is shown or an average?
8. Are rate equations (mass-action or Michaelis-Menten type) deterministic?
9. In general terms, what is the difference between a deterministic, respectively stochastic model/system?
10. What is the advantage of an “analytical approach” over a “numerical approach”?
11. Should a model be a simplification/abstraction or a realistic replica representation of a real system?