
Preface to the second edition

It was keen to write a second edition of this book even before the first edition was published in the spring of 2006. The first edition was written during the latter half of 2004 and the first half of 2005 when the use of stochastic modelling within computational systems biology was still very much in its infancy. Based on an inter-disciplinary Masters course I was teaching I saw an urgent need for an introductory textbook in this area, and tried in the first edition to lay down all of the key ingredients needed to get started. I think that I largely succeeded, but the emphasis there was very much on the “bare essentials” and accessibility to non-mathematical readers, and my goal was to get the book published in a timely fashion, in order to help advance the field. I would like to think that the first edition of this text has played a small role in helping to make stochastic modelling a much more mainstream part of computational systems biology today. But naturally there were many limitations of the first edition. There were several places where I would have liked to have elaborated further, providing additional details likely to be of interest to the more mathematically or statistically inclined reader. Also, the latter chapters on inference from data were rather limited and lacking in concrete examples. This was partly due to the fact that the whole area of inference for stochastic kinetic models was just developing, and so it wasn't possible to give a coherent overview of the problem from an introductory viewpoint. Since publishing the first edition there have been many interesting developments in the use of “likelihood-free” methods of Bayesian inference for complex stochastic models, and so the latter chapters have now been re-written to reflect this more modern perspective, including a detailed case study accompanied by working code examples.

Of course the whole field has moved on considerably since 2005, and so the second edition is also an opportunity to revise and update, and to change the emphasis of the text slightly. The Systems Biology Markup Language (SBML) has continued to evolve, and SBML Level 3 is now finalised. Consequently, I have updated all of the examples to Level 3, which is likely to remain the standard encoding for dynamic biological models for the foreseeable future. I have also taken the opportunity to revise and update the R code examples associated with the book, and to bundle them all together as an R package (`smfsb`). This should make it much easier for people to try out the examples given in the book. I have also re-written and re-structured all of the code relating to simulation, analysis and inference for stochastic kinetic models. The code is now structured in a more modular way (using a functional programming style), making it easy to “bolt together” different models, simulation algorithms, and analysis tools. I've created a new website specific to this second edition (<http://www.staff.ncl.ac.uk/d.j.wilkinson/smfsb/2e/>), where

I will keep links, resources, an errata, and up-to-date information on installation and use of the associated R package.

The new edition contains more background material on the theory of Markov processes and stochastic differential equations, providing more substance for mathematically inclined readers. This allows discussion of some of the more advanced concepts relating to stochastic kinetic models, such as random time-change representations, Kolmogorov equations, Fokker–Planck equations and the linear noise approximation. It also enables simple modelling of “extrinsic” in addition to “intrinsic” noise. This should make the text suitable for use in a greater range of courses. Naturally, in keeping with the spirit of the first edition, all of the new theory is presented in a very informal and intuitive way, in order to keep the text accessible to the widest possible readership. This is not a rigorous text on the theory of Markov processes (there are plenty of other good texts in that vein) — the book is still intended for use in courses for students with a life sciences background.

I’ve also updated the references, and provided new pointers to recent publications in the literature where this is especially pertinent. However, it should be emphasised that the book is not intended to provide a comprehensive survey of the stochastic systems biology literature — I don’t think that is necessary (or even helpful) for an introductory textbook, and I hope that people working in this area accept this if I fail to cite their work.

So here it is, the second edition, completed at last. I hope that this text continues to serve as an effective introduction to the area of stochastic modelling in computational systems biology, and that this new edition adds additional mathematical detail and computational methods which will provide a stronger foundation for the development of more advanced courses in stochastic biological modelling.

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