Mathematical modeling of metal ion homeostasis and signaling systems

Cui, J.

Citation for published version (APA):
Acknowledgements:

Firstly I would like to thank my promoter Peter Sloot for providing me the opportunity to work as a PhD candidate researcher in his group and for his sustaining support on my research. As mentioned in Chapter 1 of this thesis, one of the greatest challenges of systems biology is the challenge of collaboration. Thank Peter for his enormous efforts of developing Section Computational Science into a comprehensive computational group with a number of international collaborators. The close collaborations within the group and among the international collaborators make the possibilities for tackling various complex biological problems and will surely bring bright prospect in the future (Chapter 3 of this thesis illustrates a good example of the power of collaborations).

Secondly I would like to thank my supervisor Jaap Kaandorp for his appreciation, patience and enthusiasm. His wide relations in the circle of biologists help me to know all kinds of biologists. Thank Peter and Jaap for making me one of the most frequent speakers in ISNB (International Symposium on Networks in Bioinformatics) symposium. It is obvious that ISNB symposium provides us a good platform to develop collaborative relations with pioneering biologists and other important researchers all over the world and to magnify the influence of our research achievements.

Thirdly I would like to thank the Dutch Science Foundation (NWO) for funding my research and for funding ISNB symposium. The research in the field of system biology is like rolling the snow ball during which the initial start may be quite difficult, but once the snow ball gets running, things become easier. Thank NWO and EU again for the funding which delivers the initial push on my research career.

My full respect and gratitude go to Professor Kyle W. Cunningham whose valuable data constitute the basis of Chapter 2 and Chapter 3 of this thesis. The work presented in Chapter 4 will also be impossible without his kind suggestion of the topic.

Special thanks to all the collaborators involved in the works presented in this thesis, including Y. Fomekong Nanfack, Olufisayo O. Ositelu, Olufisayo O. Ositelu, Veronica Beaudry, Alicia Knight and Dr. Catherine M. Lloyd. Thank Catherine again for translating three models (Chapter 2, 4, 5) in this thesis into CellML codes and include them into the CellML Model Repository.

I would also like to thank Dr. Peter Willems, Dr. Leen Torensvliet, Dr. Walter Hoffmann and Dr. Pia Pfluger for their appreciation of my research and mathematical abilities. Thank many members in our group for all kinds of forms of support and thank many biologists and other scientists whom I ever met in person (particularly Prof. Bastien Chopard, Prof. Daan Frenkel, Dr. Nan-nan Zhang, Dr. Drew D. Dudgeon, Drs. Joke blom, Dr. L.J. van den Horn, Dr. Gertien J. Smits, Dr. Sylvia Tambutté, Prof. Matthias Mann, Prof. David Yue, Prof. David Miller, Prof. Denis Allemand, Prof. Sjoerd Verduyn Lunel) or contacted through emails (Dr. Caryn E. Outten, Dr. C.L. Woldringh, Prof. David M.
Bedwell, Prof. Patrick Gervais, Prof. Dietrich H. Nies) in these several years for their advice and discussions.

Finally many thanks to the reading committee of my PhD thesis. Thank you for your time and patience to read such a big bulk of research stuff.