

## Biographical Sketch (Template)

Name: Cliff Shaffer	Title: Professor
Email: shaffer@vt.edu	Department: Computer Science

### Education/Training:

Institution/Location	Degree/Postdoc	Year(s)	Field of Study
University of Maryland, College Park	BS	1980	Computer Science
University of Maryland, College Park	MS	1982	Computer Science
University of Maryland, College Park	PhD	1986	Computer Science

### Personal Statement:

(One paragraph on your interests and experiences in systems biology.)

I have been working with John Tyson's group since approximately 2000. My primary interest is in tools and visualizations that support the process by which modelers develop biochemical reaction models. The principle goal is to support the modeler in the process of developing larger scale models. This includes visualizations and automated optimization tools, as well as model design and editing tools. I see many parallels between the process of developing, maintaining, and analyzing a model based on a collection of chemical reaction equations and the software development process.

### Selected Publications:

(5-10 recent publications in the area of systems biology; with hotlinks to the journal article or pubmed, please.)

- A. Palmisano, S. Hoops, L.T. Watson, T.C. Jones Jr, J.J. Tyson, and C.A. Shaffer, JigCell Run Manager (JC-RM): a tool for managing large sets of biochemical model parametrizations, to appear in BMC Systems Biology, 2016.
- B. T.-H. Ahn, A. Sandu, L.T. Watson, C.A. Shaffer, Y. Cao, and W.T. Baumann, A framework to analyze the performance of load balancing schemes for ensembles of stochastic simulations, International Journal of Parallel Programming 43, 4(August 2015), 597–630.
- C. Alida Palmisano, Stefan Hoops, Layne T. Watson, Thomas C. Jones Jr, John J. Tyson, and Clifford A. Shaffer Multistate Model Builder (MSMB): a flexible editor to write compact biochemical models, BMC Systems Biology 8, 42(April 2014), 13 pages.
- D. Z. Liu, Y. Pu, C.A. Shaffer, S. Hoops, J.J. Tyson, and Y. Cao, Hybrid Modeling and Simulation of Stochastic Effect on Progression through the Eukaryotic Cell Cycle, Journal of Chemical Physics 136, 3(January) 2012.
- E. R. Randhawa, C.A. Shaffer, and J.J. Tyson, Model Composition for Macromolecular Regulatory Networks, IEEE/ACM Transactions on Computational Biology and Bioinformatics 7, 2(April-June 2010), 278–287.
- F. R. Randhawa, C.A. Shaffer, and J.J. Tyson, Model Aggregation: a building-block approach to creating large macromolecular regulatory networks, Bioinformatics 25, 24(2009), 3289–3295.
- G. Clifford A. Shaffer, Jason W. Zwolak, Ranjit Randhawa, and John J. Tyson Modeling Molecular Regulatory Networks with JigCell and PET, in Systems Biology 500, Ivan Maly, ed., Humana Press, 2009, 81-111.

H. T.-H. Ahn, L.T. Watson, Y. Cao, C.A. Shaffer, and W.T. Baumann, Cell Cycle Modeling for Budding Yeast with Stochastic Simulation Algorithms, Computer Modeling in Engineering and Sciences 51, 1(2009), 27–52.

**Current and/or Recently Completed Research Grants:** (as applicable)

Agency	Grant Number	PI	Dates
NIH	2-R01-GM078989-05	J.J. Tyson	2010-2014
Stochastic Models of Cell Cycle Regulation in Eukaryotes			
(brief description of goals)			
Agency	Grant Number	PI	Dates
Title:			
(brief description of goals)			