Biographical Sketch (Template)

Name: Young Cao	Title: Associate Professor
Email: ycao@cs.vt.edu	Department: Computer Science department

Education/Training:

Institution/Location	Degree/Postdoc	Year(s)	Field of Study
U California Santa Barbara	Postdoc	2003-2005	Stochastic modeling and simulation of siological systems
U California Santa Barbara	PhD	2003	Sensitivity and stability analysis of computational systems
Tsinghua University	MS	1998	Computational Mathematics
Tsinghua University	BS	1993	Applied Mathematics

Personal Statement:

Dr. Young Cao's research is in the interdisciplinary area of Computational Biology, which applies mathematical modeling and analysis, as well as computational tools, to study biological systems. Students who work in his lab build mathematical models and develop efficient numerical methods to study underlying mechanisms that help cellular systems survive and reproduce in nature. Dr. Cao is particularly interested in the study of robustness of biological systems when cellular noise cannot be neglected.

Selected Publications (10 papers):

1. Li F, Subramanian K, Chen M, Tyson JJ, Cao Y, A stochastic spatiotemporal model of a response-regulator network in the Caulobacter crescentus cell cycle, Phys Biol. 2016 Jun 25;13(3):035007. doi: 10.1088/1478-3975/13/3/035007, http://www.ncbi.nlm.nih.gov/pubmed/27345750
2. Wang S and Cao Y, The abridgment and relaxation time for a linear multi-scale model based on multiple site phosphorylation, 11 Aug 2015, PLoS One. 2015 Aug 11;10(8):e0133295. doi: 10.1371/journal.pone.0133295. http://www.ncbi.nlm.nih.gov/pubmed/26263559
3. Y Cao and R Erban, Stochastic Turing patterns: analysis of compartment-based approaches, Bulletin of Math Biol, 44, pages 1-19, Nov 2014. DOI: 10.1007/s11538-014-0044-6, http://www.ncbi.nlm.nih.gov/pubmed/25421150
4. Y Pu, S Lee, DC Samuels, LT Watson, Y Cao, The effect of unhealthy-cells on insulin secretion in pancreatic islets, BMC Medical Genomics, 6 (Suppl 3):S6, 2013, doi: 10.1186/1755-8794-6-S3-S6. http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3981690/
5. Z Liu, Y Pu, F Li, CA Shaffer, S Hoops, JJ Tyson, and Y Cao, Hybrid modeling and simulation of stochastic effects on progression through the eukaryotic cell cycle, J. Chem. Phys. 136, 034105, 2012, doi: 10.1063/1.3677190. http://www.ncbi.nlm.nih.gov/pubmed/22280742
6. Ball DA1, Ahn TH, Wang P, Chen KC, Cao Y, Tyson JJ, Peccoud J, Baumann WT, Stochastic exit from mitosis in budding yeast: model predictions and experimental observations, Cell Cycle. 2011 Mar 15;10(6):999-1009. http://www.ncbi.nlm.nih.gov/pubmed/21350333
7. Z Song, Y Cao, DC Samuels, Replication pauses of the wild-type and mutant mitochondrial, PLoS Comput Biol 7(11): e1002287. doi:10.1371/journal.pcbi.1002287, 2011. http://www.ncbi.nlm.nih.gov/pubmed/22125488
8. D Gillespie, Y Cao, K Sanft, and L Petzold, The subtle business of model reduction for stochasticchemical kinetics, J. Chem. Phys. 130, 064103, 2009, http://www.ncbi.nlm.nih.gov/pubmed/19222263
9. Y. Cao, D. Gillespie and L. Petzold, The slow-scale stochastic simulation algorithm, J. Chem. Phys., 122(1), 014116, 2005. http://www.ncbi.nlm.nih.gov/pubmed/15638651
10. Y. Cao, H. Li and L. Petzold, Efficient formulation of the stochastic simulation algorithm for chemically reacting systems, J. Chem. Phys., 121(9), 4059-4067, 2004.

http://www.ncbi.nlm.nih.gov/pubmed/15332951

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

Agency NSF	Grant Number CCF- 1526666	PI: Y Cao	Dates: 2015-2018
Title: AF: Small: Algorithmic Foundations of Hybrid Stochastic Modeling and Simulation Methods with Applications to Cell Cycle Models			
This project is motivated by realistic modeling and simulation of a complex biological control system: the cycle of growth and division in yeast cells. The project focuses on three specific aims. The primary aim is to develop mathematical foundations for error analysis of hybrid methods. The second aim is to develop algorithms for hybrid stochastic simulation of biochemical systems, mechanisms to automatically partition reactions and state variables into different scale regions, and software to efficiently simulate multiscale systems. The third aim of this project is to develop a realistic stochastic model of the budding yeast cell cycle, which will include protein interactions as well as gene and mRNA dynamics and which will be judged with respect to the phenotypes of wild-type budding yeast cells and ~120 mutant strains.			