

Youfang Cao, PhD

Postdoctoral Research Associate
 Theoretical Biology and Biophysics (T-6)
 Center for Nonlinear Studies (CNLS)
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EDUCATION

Shanghai Jiao Tong University

Ph.D. in Biomedical Engineering

2011

Dissertation: "Theoretical modeling methods of stochastic biological networks and their applications", Advisor: Jie Liang

Honor: Anthony James Leggett and Haruko Kinase-Leggett Graduate Awards

Shanxi University

M.S. in Biochemistry and Molecular Biology

2002

Minor: Bioinformatics

Area of Concentration: Microbial genomics analysis

Shanxi University

B.S. in Computational Mathematics

1999

RELATED EXPERIENCE

Los Alamos National Laboratory, Theoretical Biology and Biophysics (T-6), Center for Nonlinear Studies (CNLS)

Postdoc Research Associate

2015/05-Present

Research on viral dynamics in HIV and HCV infections based on clinical data and multi-scale stochastic modeling; Study regulatory mechanisms of stochastic biological networks through exact computation and efficient biased sampling.

University of Illinois at Chicago, Department of Bioengineering

Research Assistant Professor

2012/09–2015/04

Studied cell pattern formation using novel multi-scale mechano-geometric modeling methodology; Developed multi-buffer dCME method for direct solution of chemical master equation.

University of Illinois at Chicago, Department of Bioengineering

Postdoc Research Associate

2011/09–2012/08

Developed efficient Monte Carlo sampling method for rare events in biological networks;

University of Illinois at Chicago, Department of Bioengineering
Research Scholar **2009/03–2011/08**

Developed finite buffer method for direct solutions of chemical master equation; Studied efficiency and stability of phage λ bistable lysogenic-lytic epigenetic switch.

Shanghai Jiao Tong University, Shanghai Center for Systems Biomedicine
Assistant Research Scientist **2006/08–2011/08**

Design of data analysis system and pipelines for metagenomics study of human gut microbiota.

Shanghai Jiao Tong University, College of Agriculture and Biology
Assistant Research Scientist **2002/08–2006/07**

Development of a novel prediction method for protein structural classes; Discovery of novel genes from EST databases important for plant stress responses.

RESEARCH AREAS AND INTERESTS

Mathematical and computational modeling of biological networks;
 Stochastic control of genetic circuits of cellular fate;
 Multi-scale modeling for tissue pattern formation;
 Theoretical Immunology;
 Computational systems biology.

GRANT PROPOSALS

XSEDE Research Allocation 2016-2017
 “Multiscale Simulation and Complex Data Fitting of HIV Latency-Reactivation Control and Viral Dynamics”
 Role: Co-PI, TG-BIO160026 2,555,333 Service Units (SU: core hours) Awarded.
 According to XSEDE, the value of these awarded resources is \$88,145.99.

XSEDE Startup Allocation 2015-2016
 “Stochastic Control of HIV Latency-Reactivation and Viral/Immune System Dynamics”
 Role: PI, TG-BIO150068 50,000 Service Units Awarded.

UIC Chancellor’s Discovery Fund for Multidisciplinary Pilot Research 2015
 “Dynamic multi-scale cell model for spatio-temporal tissue pattern in wound healing”
 Role: PI Awarded and declined.
This award was declined as I left UIC. This is a competitive campus wide grant competition for early career scientists. Only 4-5 applications are awarded each year.

NIH R21 1R21AR069177-01
 “Dynamic multiscale cell model for spatio-temporal tissue pattern in wound healing”
 Role: PI Submitted.

MANUSCRIPTS IN REVIEW AND IN PREPARATION

1. Jieling Zhao, **Youfang Cao**, and Jie Liang (2016). Difference and relevance of mechanical and chemical microenvironment effects on re-epithelialization of human skin wound healing. **Submitted.**
2. **Youfang Cao**, Jessica Conway, and Alan Perelson (2016). Control of SIV with transient anti-PD-L1 treatment. **Manuscript.**
3. **Youfang Cao**, Jieling Zhao, Luisa DiPietro, and Jie Liang (2016). Dynamic cellular pattern formation in regenerative wound healing of human skin. **Manuscript.**
4. **Youfang Cao**, Xue Lei, and Jie Liang (2016). Stochastic control of latency and activation in HIV-1 infected cells. **Manuscript.**
5. **Youfang Cao**, Wei Tian and Jie Liang (2016). Reaction-coupling stochastic differential equation: an approximation to the Chemical Master Equation. **Manuscript.**

PUBLICATIONS (TOTAL 961 CITATIONS FROM GOOGLE SCHOLAR, H-INDEX: 13)

1. Jie Liang, **Youfang Cao**, Gamze Gursay, Hammad Naveed, Anna Terebus and Jieling Zhao (2016), Multiscale modeling of cellular epigenetic states: stochasticity in molecular networks, chromatin folding in cell nuclei, and tissue pattern formation of cells. **Critical Reviews in Biomedical Engineering, In press.**
2. **Youfang Cao**, Anna Terebus and Jie Liang (2016), Modeling stochastic gene regulatory networks using direct solutions of chemical master equation and rare event sampling. **Emerging Research in the Analysis and Modeling of Gene Regulatory Networks. IGI Global.**
3. **Youfang Cao**, Anna Terebus and Jie Liang (2016). State space truncation with quantified errors for accurate solutions to discrete chemical master equation. **Bulletin of Mathematical Biology.** 78:617–661.
4. Amber Ismael, Wei Tian, Nicholas Waszczak, Xin Wang, **Youfang Cao**, Dmitry Suchkov, Eli Bar, Metodi V. Metodiev, Jie Liang, Robert A. Arkowitz, and David E. Stone (2016). G β promotes receptor polarization and chemotropism by inhibiting receptor phosphorylation, **Science Signaling.** 9(423): ra38.
5. **Youfang Cao**, Anna Terebus and Jie Liang (2016). Accurate Chemical Master Equation solution using multi-finite buffers. **SIAM: Multiscale Modeling and Simulation.** 14(2): 923–963.
6. Sema Kachalo, Hammad Naveed, **Youfang Cao**, Jieling Zhao, and Jie Liang (2015). Mechanical Model of Geometric Cell and Topological Algorithm for Cell Dynamics from Single-Cell to Formation of Monolayered Tissues with Pattern. **PLoS One.** 10(5): e0126484.
7. Anna Terebus, **Youfang Cao** and Jie Liang (2014). Exact Computation of Probability Landscape of Stochastic Networks of Single Input and Coupled Toggle Switch Modules. **Conf Proc IEEE Eng Med Biol Soc.** Accepted.
8. Wei Tian, **Youfang Cao**, Amber Ismael, David Stone and Jie Liang (2014). Roles of Regulated Internalization in the Polarization of Cell Surface Receptors. **Conf Proc IEEE Eng Med Biol Soc.** Accepted.

9. **Youfang Cao** and Jie Liang (2013). Adaptively biased sequential importance sampling for rare events in reaction networks with comparison with exact solutions from finite buffer dCME method. *Journal of Chemical Physics* 139, 025101.
10. **Youfang Cao**, Hammad Naveed, Claire Liang and Jie Liang (2013). Modeling spatial population dynamics of stem cell lineage in wound healing and cancerogenesis. *Conf Proc IEEE Eng Med Biol Soc.* 5550-5553.
11. **Youfang Cao**, Claire Liang, Hammad Naveed, Yingzi Li, Meng Chen and Qing Nie (2012). Modeling spatial population dynamics of stem cell lineage in tissue growth. *Conf Proc IEEE Eng Med Biol Soc.* 5502–5505.
12. Hongyuan Zhu, Tianqi Chen, Xue Lei, Wei Tian, **Youfang Cao** and Ping Ao (2012). Understand the noise of CI expression in phage λ lysogeny. *Control Conference (CCC), 31st Chinese*, 7432-7436.
13. Xiaojun Zhang, Siqing Yue, Huihui Zhong, Weiyang Hua, Ruijia Chen, **Youfang Cao**, Liping Zhao (2011). A diverse bacterial community in an anoxic quinoline-degrading bioreactor determined by using pyrosequencing and clone library analysis. *Applied microbiology and biotechnology*, 91(2), 425-434.
14. **Youfang Cao**, Hsiao-Mei Lu and Jie Liang (2010). Probability landscape of heritable and robust epigenetic state of lysogeny in phage lambda. *Proceedings of the National Academy of Sciences USA*, 107(43), 18445–18450.
15. Chenhong Zhang, Menghui Zhang, Shengyue Wang, Ruijun Han, **Youfang Cao**, Weiyang Hua, Yuejian Mao, Xiaojun Zhang, Xiaoyan Pang, Chaochun Wei, Guoping Zhao, Yan Chen and Liping Zhao (2010). Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. *The ISME Journal* 4:232–241.
16. **Youfang Cao** and Jie Liang (2010). Nonlinear Langevin model with product stochasticity for biological networks: the case of the Schnakenberg model. *Journal of Systems Science and Complexity*, 23:896–905.
17. **Youfang Cao** and Jie Liang (2009). Nonlinear coupling for improved stochastic network model: A study of Schnakenberg model. *The Third International Symposium on Optimization and Systems Biology (OSB'09) ORSC & APORC* 379–386.
18. **Youfang Cao** and Jie Liang (2008). Optimal enumeration of state space of finitely buffered stochastic molecular networks and accurate computation of steady state landscape probability. *BMC Systems Biology* 2:30.
19. **Youfang Cao**, Hsiao-Mei Lu, and Jie Liang (2008). Stochastic probability landscape model for switching efficiency, robustness, and differential threshold for induction of genetic circuit in phage lambda. *Conf Proc IEEE Eng Med Biol Soc.* 1:611–614.
20. **Youfang Cao** and Jie Liang (2007). An optimal algorithm for enumerating state space of stochastic molecular networks with small copy numbers of molecules. *Conf Proc IEEE Eng Med Biol Soc.* 1:4599-4602.
21. Kai-Jing Zuo, Jie Qin, Jing-Ya Zhao, Hua Ling, Li-Da Zhang, **Youfang Cao**, Ke-Xuan Tang (2007). Over-expression GbERF2 transcription factor in tobacco enhances brown spots disease resistance by activating expression of downstream genes. *Gene* 391(1-2), 80-90.

22. Jin Wang, Kai-Jing Zuo, Jie Qin, Lida Zhang, Lan Su, Junrong Liu, Hua Ling, Jing-Ya Zhao, **Youfang Cao**, Ke-Xuan Tang (2007). Isolation and bioinformatics analyses of a COR413-like gene from *Gossypium barbadense*. *Acta Physiologiae Plantarum* 29(1), 1-9.
23. Lida Zhang, Kaijing Zuo, Fei Zhang, **Youfang Cao**, Jiang Wang, Yidong Zhang, Xiaofen Sun, Kexuan Tang (2006). Conservation of noncoding microsatellites in plants: implication for gene regulation. *BMC genomics* 7(1), 323.
24. **Youfang Cao**, Shi Liu, Lida Zhang, Jie Qin, Jiang Wang and Kexuan Tang (2006). Prediction of protein structural class with Rough Sets. *BMC Bioinformatics* 7:20.
25. Yidong Zhang, Zeyun Wang, Lida Zhang, **Youfang Cao**, Danfeng Huang, Kexuan Tang (2006). Molecular cloning and stress-dependent regulation of potassium channel gene in Chinese cabbage (*Brassica rapa* ssp. *Pekinensis*). *Journal of Plant Physiology* 163(9), 968-978.
26. Lida Zhang, Shunwu Yu, **Youfang Cao**, Jiang Wang, Kaijing Zuo, Jie Qin, Kexuan Tang (2006). Distributional gradient of amino acid repeats in plant proteins. *Genome* 49 (8), 900-905.
27. Jie Qin, Kaijing Zuo, Jingya Zhao, Hua Ling, **Youfang Cao**, Chengxiang Qiu, Fupeng Li, Xiaofen Sun and Kexuan Tang (2006). Overexpression of GbERF confers alteration of ethylene-responsive gene expression and enhanced resistance to *Pseudomonas syringae* in transgenic tobacco. *Journal of Biosciences* 31(2):255–263.
28. Yidong Zhang, Zeyun Wang, Lida Zhang, **Youfang Cao**, Danfeng Huang, Kexuan Tang (2006). Molecular cloning and stress-dependent regulation of a glutamine synthetase gene in Chinese cabbage. *Russian Journal of Plant Physiology* 53 (2), 231-237.
29. Jiang Wang, Lida Zhang, Kai-Jing Zuo, Hong-Mei Qian, **Youfang Cao**, Kexuan Tang (2006). Cloning and Expressional Studies of the Voltage - dependent Anion Channel Gene from *Brassica rapa* L. *Journal of Integrative Plant Biology* 48 (2), 197-203.
30. Guoan Shen, Yongzhen Pang, Weisheng Wu, Zhongxiang Deng, Lingxia Zhao, **Youfang Cao**, Xiaofen Sun, Kexuan Tang (2006). Cloning and characterization of a flavanone 3-hydroxylase gene from *Ginkgo biloba*. *Bioscience Reports* 26(1), 19-29.
31. Lingxia Zhao, Jingfu Li, Yourong Chai, Guoyin Kai, **Youfang Cao**, Xiaofen Sun, Kexuan Tang (2006). Investigation on Genetic Relationship and Cross Compatibility of *S. lycopersicoides* and *Lycopersicon*. *Pakistan Journal of Biological Sciences* 9, 1160-1168.
32. **Youfang Cao**, Lianjie Wang, Kexue Xu, Chunhai Kou, Yulei Zhang, Guifang Wei, Junjian He, Yunfang Wang and Liping Zhao (2005). Information theory-based algorithm for in silico prediction of PCR products with whole genomic sequences as templates. *BMC Bioinformatics* 6:190.
33. Jie Qin, Jingya Zhao, Kaijing Zuo, **Youfang Cao**, Hua Ling, Xiaofen Sun, Kexuan Tang (2004). Isolation and characterization of an ERF-like gene from *Gossypium barbadense*. *Plant Science* 167(6):1383–1389.
34. Zhugang Li, Lingxia Zhao, Guoyin Kai, Shunwu Yu, **Youfang Cao**, Yongzhen Pang, Xiaofen Sun, Kexuan Tang (2004). Cloning and expression analysis of a water stress-induced gene from *Brassica oleracea*. *Plant Physiology and Biochemistry* 42 (10), 789-794.

35. Dongqin Tang, Hongmei Qian, Shunwu Yu, **Youfang Cao**, Zhihua Liao, Lingxia Zhao, Xiaofen Sun, Danfeng Huang, Kexuan Tang (2004). cDNA cloning and characterization of a new stress-responsive gene BoRS1 from *Brassica oleracea* var. *acephala*. *Physiologia Plantarum* 121(4):578-585.
36. Lida Zhang, Dejun Yuan, Shunwu Yu, Zhugang Li, **Youfang Cao**, Zhiqi Miao, Hongmei Qian, Kexuan Tang (2004). Preference of simple sequence repeats in coding and non-coding regions of *Arabidopsis thaliana*. *Bioinformatics* 20 (7), 1081.
37. Lingxia Zhao, Lixin Jin, Zhugang Li, **Youfang Cao**, Chengxiang Qiu, Dongqin Tang, Hongmei Qian, Kexuan Tang (2004). Cloning and DNA sequence Analysis of Element Responsive to Ethylene in E8 Promoter of the Tomato. *Acta Horticulturae Sinica* 31 (2), 204-208.
38. Jingya Zhao, Kaijing Zuo, Jin Wang, **Youfang Cao**, Lida Zhang, Kexuan Tang (2003). cDNA cloning and characterization of a cotton peptide methionine sulfoxide reductase (cMsrA). *Mitochondrial DNA* 14 (4), 303-310.
39. Yingchun Chen, **Youfang Cao**, Liping Zhao (2002). Non-random nature of genomic DNA amplification of *E. coli* K-12 MG1655 via ERIC-PCR. *Microbiology China* (Chinese) 29 (6), 28-32.
40. **Youfang Cao**, Liping Zhao (2001). Computational analysis of the distribution of ERIC (IRU) in different bacterial genomes. *Journal of Shanxi University (Natural Science Edition)* (Chinese) 25 (4), 354-357.

ORAL PRESENTATIONS

"Multistable Physiological States from Simple Stochastic Gene Regulatory Network Motifs"

Invited Speaker at 37th Annual International Conference of the IEEE

Engineering in Medicine & Biology Society, Milan, Italy 2015

"Using the Finite Buffer method (fb-dCME) to model stochastic viral dynamics"

Lecturer at The Ninth q-bio Summer School, Albuquerque, NM 2015

"Multiscale Simulation of Wound Healing with Dynamics Cell Model with Embedded Gene Networks"

Invited Speaker at 36th Annual International Conference of the IEEE

Engineering in Medicine & Biology Society, Chicago, IL 2014

"Multi-scale computational modeling of cellular processes: from genetic circuits to cell pattern formation"

Invited talk in Kean University, Union, NJ 2014

"Spatio-Temporal Dynamics of Cell Population in Models of Human Skin Wound Healing"

Invited Speaker at 35th Annual International Conference of the

IEEE Engineering in Medicine & Biology Society, Osaka, Japan 2013

"Modeling Spatial Population Dynamics of Stem Cell Lineage in Wound Healing and Cancerogenesis"

Paper presented at 35th Annual International Conference of the

IEEE Engineering in Medicine & Biology Society, Osaka Japan 2013

“Modeling Spatial Population Dynamics of Stem Cell Lineage in Wound Healing”
Invited Speaker at 34th Annual International Conference of the
 IEEE Engineering in Medicine & Biology Society, San Diego, CA 2012

“Multiscale dynamic processes in biological systems: epigenetic circuits for lysogeny maintenance, cell signal responses, and tissue development.”
Invited presentation at Department of Physics, University of Illinois
 at Chicago 2012

“Modeling spatial population dynamics of stem cell in tissue growth and regeneration.”
Selected Presenter at Regenerative Biology and Tissue
 Engineering Workshop at University of Illinois, Urbana-Champaign 2011

“Computing probability landscapes of stochastic biological networks through discrete Chemical Master Equation: Maintenance of phage lambda epigenetic state.”
 The 21th International Conference on Genome Informatics (GIW
 2010), Hangzhou, China 2010

CONFERENCE POSTERS

“Stochastic bistable control of latency and transactivation in HIV-1 Tat circuit: implications from probability landscapes”
 36th CNLS Annual Conference: Energy Landscapes: From Protein Folding to Molecular
 Assembly, Santa Fe, NM 2016

“HIV-1 Tat circuit: stochastic bistable control of latency and transactivation”
 The 23rd HIV Dynamics and Evolution, Woodshole, MA 2016

“Post-treatment control of HIV-1 and immune check-point blockade”
 The Duke Center for HIV/AIDS Vaccine Immunology and
 Immunogen Discovery (CHAVI-ID), Durham, NC 2015

“Stochastic Control of Intracellular Latency and Transactivation in Human Immunodeficiency Virus Type 1 (HIV-1)”
 Biophysical Society Annual Meeting, Baltimore, MD 2015

“Spatio-temporal cell pattern formation during skin wound healing”
 The Fourth Annual Meeting of the American College of
 Wound Healing and Tissue Repair, Chicago, IL 2014

“Roles of Regulated Internalization in the Polarization of Cell Surface Receptors”
 36th Annual International Conference of the IEEE
 Engineering in Medicine & Biology Society, Chicago, IL 2014

“Multi-Finite Buffer Method for Direct Solution of Discrete Chemical Master Equation”
 Biophysical Society Annual Meeting, San Francisco, CA 2014

“Role of Internalization of Cell Surface Receptors in Regulation of Cell Polarity”
 Biophysical Society Annual Meeting, San Francisco, CA 2014

“Modeling Spatial Population Dynamics of Stem Cell Lineage in Tissue Growth”

Paper presented at 34th Annual International Conference of the
IEEE Engineering in Medicine & Biology Society, San Diego, CA 2012

“Stochastic temporal-spatial population dynamics of stem cell in tissue growth and regeneration”

Stem Cell and Regenerative Medicine, University of Illinois at
Chicago 2012

“Computing probabilistic landscape of stochastic network for maintenance of epigenetic states of cell and for regulation of cellular fate”

Ninth Annual Chicago Biomedical Consortium (CBC) Symposium 2011

“Cholesky-Langevin Model for Biochemical Networks with Accurate Account of Stochastic Effects of Couplings between Molecular Species”

Biophysical Society 54th Annual Meeting, San Francisco, CA 2010

“A Study of Cro’s Role in the Induction of Phage Lambda Switch by Stochastic Probability Landscape Model”

Biophysical Society 53th Annual Meeting, Boston, MA 2009

“Stochastic probability landscape model for switching efficiency, robustness, and differential threshold for induction of genetic circuit in phage lambda”

Engineering in Medicine and Biology Society, 30th Annual
International Conference of the IEEE, Vancouver, BC, Canada 2008

“An optimal algorithm for enumerating state space of stochastic molecular networks with small copy numbers of molecules”

Engineering in Medicine and Biology Society, 29th Annual
International Conference of the IEEE, Lyon, France 2007

AWARDS

Travel Award for the 2015 Annual Computational Genomics Workshop
The Center for Cell Circuits at the Broad Institute. 2015

Anthony James Leggett and Haruko Kinase-Leggett Graduate Awards, First Place
Shanghai Jiao Tong University 2011

Selected Presenter at Regenerative Biology and Tissue Engineering Workshop
University of Illinois, Urbana-Champaign 2011

TEACHING AND MENTORING EXPERIENCES

Facilitator, BIOE 250 Clinical Problems in Bioengineering, University of Illinois at Chicago
1 contact hour/week for 1 semester. 2015

Student Research Advisor, Scientific Inquiry and Research Course, Illinois Mathematics and
Science Academy (IMSA). Advising research of local high school student.
1 day/week for 48 weeks. 2011-2013

PROFESSIONAL MEMBERSHIPS

Society for Industrial and Applied Mathematics, Early Career Membership
American Association for the Advancement of Science
Biophysical Society, Early Career membership

JOURNAL REVIEWER

IEEE EMBC 2009-2016
Journal of Theoretical Biology
Journal of Chemical Physics
Mathematical Biosciences
BMC Bioinformatics
BMC Systems Biology