

Youfang Cao, PhD

Postdoctoral Research Associate

Theoretical Biology and Biophysics (T-6), Center for Nonlinear Studies (CNLS)
 Los Alamos National Laboratory, PO Box 1663 MS B258, Los Alamos NM, 87545
 Office: 505-667-7135, Cell: 312-395-0455, Email: ycao@lanl.gov

EDUCATION

Los Alamos National Laboratory

Postdoctoral Research Associate in Mathematical Biology **2017**

Mentor: Alan S. Perelson, Ruy M. Ribeiro

University of Illinois at Chicago

Postdoctoral Research Associate **2015**

Mentor: Jie Liang

Shanghai Jiao Tong University

Ph.D. in Biomedical Engineering **2007-2011**

Dissertation: "Theoretical modeling methods of stochastic biological networks and applications"

Advisor: Jie Liang (University of Illinois at Chicago)

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

Shanxi University

M.S. in Biochemistry and Molecular Biology **2002**

Area of concentration: Bioinformatics

Area of research: Microbial genomics

Shanxi University

B.S. in Computational Mathematics **1999**

RESEARCH EXPERIENCE

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

Postdoc Research Associate **05/2015-Present**

(1) *Modeling HIV viral dynamics controlled by immune response.*

(2) *Investigate the **stochastic control of latency** in HIV infected cells.*

University of Illinois at Chicago, Department of Bioengineering

Research Assistant Professor **09/2012–04/2015**

(1) *Built the Accurate Chemical Master Equation (**ACME**) method for high-resolution modeling of gene regulatory networks.*

(2) *Built a multi-scale modeling framework for tissue pattern formation.*

University of Illinois at Chicago, Department of Bioengineering

Postdoctoral Research Associate **09/2011–08/2012**

*Developed the **adaptively biased sequential importance sampling (ABSIS)** method for rare event sampling in biological networks.*

University of Illinois at Chicago, Department of Bioengineering

Research Scholar **03/2009–08/2011**

(1) *Developed finite buffer method for directly solving chemical master equation.*

(2) *Studied **stochastic bistable control of phage λ** lysogenic-lytic genetic switch.*

Shanghai Jiao Tong University, Shanghai Center for Systems Biomedicine

Assistant Research Scientist

08/2002–03/2009

(1) Studied metagenomics of human gut microbiota by analyzing big sequencing data. (2) Developed a novel protein structural class prediction method using the rough sets theory. (3) Discovered novel genes for plant stress responses using large-scale sequence data analysis.

RESEARCH AREAS AND INTERESTS

1. Mathematical and computational modeling of biological networks.
2. Stochastic cell fate determination in infectious diseases and immune responses.
3. Mathematical modeling of within-host viral dynamics in infectious diseases.
4. Integrative multi-scale modeling for tissue-level cell dynamics in infectious diseases.
5. Development of modeling methodology, algorithms and computational tools.

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

2015-2017

“Dynamic multi-scale cell model for spatio-temporal tissue pattern in wound healing”

Role: PI

Awarded (declined)

This award was declined as I was moving from University of Illinois at Chicago to Los Alamos National Laboratory. This is a competitive campus wide grant competition for early career scientists, including tenure track assistant professors. 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 (*EQUAL CONTRIBUTIONS)

1. **Youfang Cao**, Jessica M. Conway, Stephen Mason, James B. Whitney, and Alan S. Perelson (2017). Control of SIV with transient anti-PD-L1 treatment. **Manuscript in preparation.**
2. **Youfang Cao**, Emily Cartwright, Guido Silvestri, and Alan S. Perelson (2017). Modeling viral dynamics of CD8+ depletion in SIV infected Rhesus Macaques. **Manuscript in preparation.**
3. **Youfang Cao** and Jie Liang (2017). ACME: a software package for high-resolution stochastic modeling of biological networks. **Manuscript in preparation.**
4. **Youfang Cao**, Xue Lei, and Jie Liang (2017). Stochastic control of latency and activation in HIV-1 infected cells. **Manuscript in preparation.**

5. **Youfang Cao**, (2017). Precise control in noise: stochastic control of transcription and translation in simple genetic circuits. *Manuscript in preparation*.
6. **Youfang Cao**, Carrie A. Manore, and Ethan Romero-Severson (2017). High-resolution modeling for stochastic epidemiology using Accurate Chemical Master Equation (ACME) method. *Manuscript in preparation*.
7. **Youfang Cao** and **Eduardo Sontag** (2017). Control of stochastic transitions in genetic toggle switch. *Manuscript in preparation*.
8. **Youfang Cao***, Jieling Zhao*, Luisa A. DiPietro, and **Jie Liang** (2017). Control of skin wound healing through ECM chemotaxis gradient buffering effect. *Manuscript in preparation*.

PUBLICATIONS (TOTAL OVER 1000 CITATIONS BY GOOGLE SCHOLAR, H-INDEX: 13)

[Link to my Google Scholar profile](#)

1. J. B. Honeycutt, W.O. Thayer, C. E. Baker, R.M. Ribeiro, S.M. Lada, **Youfang Cao**, R.A. Cleary, M. G. Hudgens, D.D. Richman, J. V. Garcia (2017). HIV persistence in tissue macrophages of humanized myeloid only mice during antiretroviral therapy. *Nature Medicine*. **Accepted**.
2. Jieling Zhao*, **Youfang Cao***, Luisa A. DiPietro, and **Jie Liang** (2017). Dynamic cellular finite element method for modeling large scale cell migration and proliferation under the control of mechanical and biochemical cues: A study of reepithelialization. *Journal of the Royal Society Interface*. **Accepted**.
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. ([PDF](#))
4. **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. ([PDF](#))
5. **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. ([PDF](#))
6. 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. ([PDF](#))
7. Jie Liang, **Youfang Cao**, Gamze Gursoy, Hammad Naveed, Anna Terebus and Jieling Zhao (2015), 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*, 43 (4), 323-346. ([PDF](#))
8. 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. ([PDF](#))
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. ([PDF](#))

10. Xiaojun Zhang, Siqing Yue, Huihui Zhong, Weiying 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.
11. **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. ([PDF](#))
12. Chenhong Zhang, Menghui Zhang, Shengyue Wang, Ruijun Han, **Youfang Cao**, Weiying 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. **Highly Cited: 303** ([PDF](#))
13. **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. ([PDF](#))
14. **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. ([PDF](#))
15. 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.
16. 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.
17. 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.
18. **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. **Highly Cited: 127** ([PDF](#))
19. 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.
20. 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.
21. 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.
22. 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.

23. 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.
24. 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.
25. 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.
26. **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. ([PDF](#))
27. 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.
28. 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.
29. 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.
30. 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.
31. 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.
32. 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.
33. 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.
34. **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.

PEER-REVIEWED CONFERENCE PAPERS

1. 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.* 5228-5231. ([PDF](#))
2. 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.* 1166-1169. ([PDF](#))
3. **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. ([PDF](#))
4. **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. ([PDF](#))
5. 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.
6. **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. ([PDF](#))
7. **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.* 611–614. ([PDF](#))
8. **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.* 4599-4602. ([PDF](#))

TALKS

- 2016 Lecturer at the Tenth q-bio Summer School, Albuquerque, NM
- 2016 Selected Talk at the Symposium on Cell Signaling, Santa Fe, NM
- 2016 Invited Talk at the Center for Nonlinear Studies (CNLS) External Committee Review, Los Alamos, NM (**One of four selected presentations in CNLS to the external review committee**)
- 2015 Invited Speaker at 37th Annual International Conference of the IEEE Engineering in Medicine & Biology Society, Milan, Italy
- 2015 Lecturer at The Ninth q-bio Summer School, Albuquerque, NM
- 2014 Invited Speaker at 36th Annual International Conference of the IEEE Engineering in Medicine & Biology Society, Chicago, IL
- 2014 Invited talk in Kean University, Union, NJ
- 2013 Invited Speaker at 35th Annual International Conference of the IEEE Engineering in Medicine & Biology Society, Osaka, Japan
- 2013 Selected Talk at 35th Annual International Conference of the IEEE Engineering in Medicine & Biology Society, Osaka Japan

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

2012 Invited Speaker at Department of Physics, University of Illinois at Chicago

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

2010 Selected Talk at the 21th International Conference on Genome Informatics (GIW 2010), Hangzhou, China

CONFERENCE POSTERS

2017 Keystone Symposia on Molecular and Cellular Biology: “Modeling Viral Infections and Immunity”, Estes Park, CO

2017 Gordon Research Conference “Stochastic Physics in Biology -- Landscapes, Stochastic Dynamics, and Heterogeneity in Biology”, Ventura, CA

2016 The 4th Systems Approaches in Immunology and Infectious Diseases Conference, Santa Fe, NM

2016 The 36th CNLS Annual Conference: Energy Landscapes: From Protein Folding to Molecular Assembly, Santa Fe, NM

2016 The 23rd HIV Dynamics and Evolution, Woodshole, MA

2015 The Duke Center for HIV/AIDS Vaccine Immunology and Immunogen Discovery (CHAVI-ID), Durham, NC

2015 The 59th Biophysical Society Annual Meeting, Baltimore, MD

2014 The 4th Annual Meeting of the American College of Wound Healing and Tissue Repair, Chicago, IL

2014 The 36th Annual International Conference of the IEEE Engineering in Medicine & Biology Society, Chicago, IL

2014 The 58th Biophysical Society Annual Meeting, San Francisco, CA

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

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

2011 The 9th Annual Chicago Biomedical Consortium (CBC) Symposium, Chicago, IL

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

2009 The 53rd Biophysical Society Annual Meeting, Boston, MA

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

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

TEACHING AND MENTORING EXPERIENCE

2012-2015 Graduate students mentoring in the Liang Lab, Department of Bioengineering, University of Illinois at Chicago.

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

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

2006 Course development and teaching, *Introductions to Bioinformatics*, Shanghai Jiao Tong University, 2 hours/week for 1 semester.

HONORS

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

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

PLoS Computational Biology, Journal of Chemical Physics, Journal of Theoretical Biology, SIAM Multiscale Modeling and Simulation, Journal of Cell Science, Nature Scientific Reports, Mathematical Biosciences, BMC Bioinformatics, BMC Systems Biology, Transactions on Biomedical Engineering, IEEE EMBC 2009-2016