

Shao-shan Carol Huang

Curriculum Vitae

June 2019

📍 Center for Genomics and Systems Biology
Department of Biology, New York University
12 Waverly Pl, New York, NY 10003
🏠 huanglab.rbind.io
☎ +1 212 998 8286
✉ s.c.huang@nyu.edu
🐦 @shhuang1
🌐 hlab1

Education and qualifications

- 2018 **Workshop on Leadership in Biosciences**
Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA.
- 2011 **Ph.D., Computational and Systems Biology**
Massachusetts Institute of Technology, Cambridge, MA, USA
Advisor: Dr. Ernest Fraenkel
Thesis: A constraint optimization framework for discovery of cellular signaling and regulatory networks
- 2005 **B.Sc., Combined Honors Computer Science and Biology, Co-op Option**
University of British Columbia, Vancouver, BC, Canada
Advisor: Dr. Wyeth Wasserman
Honors thesis: Computational identification of over-represented combinations of transcription factor binding sites in sets of co-expressed genes

Current position

- 2018- Assistant Professor, Center for Genomics and Systems Biology, Department of Biology
New York University

Past research positions

- 2011-2017 Postdoctoral associate, Genomic Analysis Laboratory & Plant Biology Laboratory
The Salk Institute for Biological Studies
Advisor: Dr. Joseph Ecker
- 2011 Postdoctoral associate, Department of Biological Engineering
Massachusetts Institute of Technology
Advisor: Dr. Ernest Fraenkel
- 2005-2011 Graduate student, Program in Computational and Systems Biology
Massachusetts Institute of Technology
Advisor: Dr. Ernest Fraenkel
- 2004-2005 Undergraduate research assistant, Center for Molecular Medicine and Therapeutics
University of British Columbia
Advisor: Dr. Wyeth Wasserman
- 2003-2005 Undergraduate research assistant, Department of Mathematics
University of British Columbia
Advisor: Dr. Leah Edelstein-Keshet

Publications

Refereed research papers

1. Procko, C., S. Morrison, C. Dunar, S. Mills, B. Maldonado, C. Cockrum, N. Peters, **S.-s. Huang**, and J. Chory (2019). Big Data to the Bench: Transcriptome Analysis for Undergraduates. *CBE-Life Sciences Education* (in press).

2. Bartlett, A., R. C. O'Malley, **S.-s. C. Huang**, M. Galli, J. R. Nery, A. Gallavotti, and J. R. Ecker (2017). Mapping genome-wide transcription-factor binding sites using DAP-seq. *Nature Protocols* **12**(8), 1659–1672.
3. Trigg, S. A., R. M. Garza, A. MacWilliams, J. R. Nery, A. Bartlett, R. Castanon, A. Goubil, J. Feeney, R. O'Malley, **S.-s. C. Huang**, Z. Zhang, M. Galli, and J. R. Ecker (2017). CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. *Nature Methods* **14**(8), 819.
4. Kawakatsu, T. *, **S.-s. C. Huang***, F. Jupe*, E. Sasaki*, R. J. Schmitz, M. A. Urich, R. Castanon, J. R. Nery, C. Barragan, Y. He, H. Chen, M. Dubin, C.-R. Lee, C. Wang, F. Bemm, C. Becker, R. O'Neil, R. C. O'Malley, D. X. Quarless, The 1001 Genomes Consortium, N. J. Schork, D. Weigel, M. Nordborg, and J. R. Ecker (2016). Epigenomic Diversity in a Global Collection of *Arabidopsis thaliana* Accessions. *Cell* **166**(2), 492–505.
*co-first author.
5. O'Malley, R. C. *, **S.-s. C. Huang***, L. Song, M. G. Lewsey, A. Bartlett, M. Galli, J. R. Nery, A. Gallavotti, and J. R. Ecker (2016). Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. *Cell* **165**(5), 1280–1292.
*co-first author.
6. Pedmale, U. V., **S.-s. C. Huang**, M. Zander, B. J. Cole, J. Hetzel, K. Ljung, P. A. Reis, P. Sridevi, K. Nito, J. R. Nery, J. R. Ecker, and J. Chory (2016). Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. *Cell* **164**(1-2), 233–245.
7. Song, L., **S.-s. C. Huang**, A. Wise, R. Castanon, J. R. Nery, H. Chen, M. Watanabe, J. Thomas, Z. Bar-Joseph, and J. R. Ecker (2016). A transcription factor hierarchy defines an environmental stress response network. *Science* **354**(6312).
8. Chang, K. N., S. Zhong, M. T. Weirauch, G. Hon, M. Pelizzola, H. Li, **S.-s. C. Huang**, R. J. Schmitz, M. A. Urich, D. Kuo, et al. (2013). Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in *Arabidopsis*. *eLife* **2**, e00675.
9. **Huang, S.-s. C.**, D. C. Clarke, S. J. Gosline, A. Labadorf, C. R. Chouinard, W. Gordon, D. A. Lauffenburger, and E. Fraenkel (2013). Linking proteomic and transcriptional data through the interactome and epigenome reveals a map of oncogene-induced signaling. *PLoS Computational Biology* **9**(2), e1002887.
10. Tuncbag, N., A. Braunstein, A. Pagnani, **S.-S. C. Huang**, J. Chayes, C. Borgs, R. Zecchina, and E. Fraenkel (2013). Simultaneous reconstruction of multiple signaling pathways via the Prize-Collecting Steiner Forest problem. *Journal of Computational Biology* **20**(2), 124–136.
11. Qiao, H., Z. Shen, **S.-s. C. Huang**, R. J. Schmitz, M. A. Urich, S. P. Briggs, and J. R. Ecker (2012). Processing and subcellular trafficking of ER-tethered EIN2 control response to ethylene gas. *Science* **338**(6105), 390–3.
12. Tuncbag, N., S. McCallum, **S.-s. C. Huang**, and E. Fraenkel (2012). SteinerNet: a web server for integrating 'omic' data to discover hidden components of response pathways. *Nucleic Acids Research* **40**(W1), W505–W509.
13. **Huang, S.-s. C.** and E. Fraenkel (2009b). Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. *Science Signaling* **2**(81), ra40.
14. **Huang, S.-s.**, D. L. Fulton, D. J. Arenillas, P. Perco, S. Ho Sui, J. R. Mortimer, and W. W. Wasserman (2006). Identification of over-represented combinations of transcription factor binding sites in sets of co-expressed genes. *Advances in Bioinformatics and Computational Biology* **3**, 247–56.

Review

1. **Huang, S.-s. C.** and J. R. Ecker (2017). Piecing together cis-regulatory networks: insights from epigenomics studies in plants. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, e1411.

Book chapter

1. **Huang, S.** and E. Fraenkel (2012). Swimming upstream: identifying proteomic signals that drive transcriptional changes using the interactome and multiple '-omics' datasets. *Computational Methods in Cell Biology* **110**, 57.

Patent

1. Fraenkel, E., **S.-S. C. Huang**, D. R. Karger, L. Riva, and E. Yeger-Lotem (2012). *Identifying biological response pathways*. US Patent No. 8612160. Issued December 17, 2013.

Invited talks

1. University of Cambridge Sainsbury Laboratory Seminar Series. Cambridge, UK. November 27, 2019.
2. University of Maryland Department of Cell Biology and Molecular Genetics. College Park, MD. September 20, 2019.
3. Iowa State University Bioinformatics and Computational Biology Symposium. Ames, IA. April 19, 2019.
4. CNRS - Jacques Monod Conference: First International Plant Systems Biology Meeting. Roscoff, France. September 12, 2018.
5. Workshop on Construction of Gene Regulatory Networks in Arabidopsis in the 29th International Conference on Arabidopsis Research. Turku, Finland. June 26, 2018.
6. Boyce Thompson Institute. Ithaca, NY. May 8, 2018.
7. University of California, Riverside Data Science Center. Riverside, CA. March 22, 2017.
8. Cornell University School of Integrative Plant Science. Ithaca, NY. March 9, 2017.
9. New York University Department of Biology. New York, NY. March 7, 2017.
10. Washington University at St. Louis Department of Biology. St. Louis, MO. January 9, 2017.
11. Academia Sinica Institute of Cellular and Organismic Biology. Taipei, Taiwan. December 21, 2016.
12. Carnegie Institution of Science Department of Plant Biology. Stanford, CA. December 2, 2016.
13. Salk Featured Fellow Series. The Salk Institute for Biological Studies. La Jolla, CA. August 10, 2016.
14. 22nd International Conference on Plant Growth Substances. Toronto, Canada. June 22, 2016.
15. UCLA Department of Molecular, Cell, and Developmental Biology and the Institute for Quantitative and Computational Biosciences. Los Angeles, CA. April 25, 2016.
16. Cold Spring Harbor Conference on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY. March 19, 2016.
17. University of Toronto Department of Cell and Systems Biology. Toronto, Canada. March 14, 2016.
18. University of New Hampshire Department of Molecular, Cellular, and Biomedical Sciences. Durham, NH. July 15, 2015.
19. San Diego Center for Systems Biology: Cytoscape and Network Analysis Workshop. San Diego, CA. April 17, 2015.
20. Oregon State University Center for Genome Research and Biocomputing. Corvallis, OR. April 15, 2015.

Selected conference posters

1. Li, M., N. Angeles, and **S.-s. C. Huang** (2019). Mapping cis-regulatory variations in plant genomes. Maize Genetics Conference. St. Louis, MO. March 2019.
2. **Huang, S.-s. C.**, R. C. O'Malley, A. Bartlett, L. S. Song, and J. R. Ecker (2018). Base resolution atlases of the Arabidopsis cistrome and epicistrome. International Conference on Arabidopsis Research. Turku, Finland. June 2018.
3. **Huang, S.-s. C.**, T. Kawakatsu, F. Jupe, E. Sasaki, M. Nordborg, and J. R. Ecker (2018). Epigenome and transcriptome diversity in a global collection of Arabidopsis thaliana accessions. Plant Molecular Biology Gordon Research Conference. Holderness, NH. June 2018.
4. **Huang, S.-s. C.** and J. R. Ecker (2012). Chromatin accessibility profiles and transcriptional regulation in ethylene hormone response of Arabidopsis thaliana. HHMI Science Meeting - Nucleic Acids and Interacting Proteins. Ashburn, VA. September 2012.
5. **Huang, S.-s. C.**, P. Huang, F. White, and E. Fraenkel (2011). Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks in glioblastoma. AACR-NCI Conference on Systems Biology. San Diego, CA. February 2011.

6. **Huang, S.-s. C.** (2010). A computational approach integrating proteomic, transcriptional, and interactome data for discovery of cellular signaling networks. Selected talk at the Systems Biology of Human Disease 2010. Boston, MA. June 2010.
7. **Huang, S.-s. C.** and E. Fraenkel (2009a). A computational approach integrating proteomic, transcriptional, and interactome data for discovery of cellular signaling networks. First AACR International Conference on Frontiers in Basic Cancer Research. Boston, MA. October 2009.

Press

1. Salk Researchers Say Plant May Hold Key To Drought Resistance (2016). *KPBS Midday Edition*. <https://www.kpbs.org/news/2016/dec/05/salk-researchers-say-plant-may-hold-key-drought-re/>.
2. SCI-TECH: Local scientists find clues to how fruit ripens (2012). *The San Diego Union-Tribune*. <https://www.sandiegouniontribune.com/sdut-sci-tech-local-scientists-find-clues-to-how-fruit-2012sep02-story.html>.

Honors and awards

2014	Pioneer Fund Fellow, Salk Institute for Biological Studies
2007-2011	Graduate Fellowship, NCI Center for Cancer Systems Biology at MIT
2011	Scholar-in-Training Award, AACR-NCI Conference on Systems Biology
2005-2009	Post-graduate Scholarship at Foreign Universities, Natural Sciences and Engineering Research Council of Canada (NSERC)
2005	Amy E. Sauder Scholarship and Jean Craig Smith Scholarship, UBC
2004, 2005	Undergraduate Student Research Award in Industry and University, NSERC
2004	Wesbrook Scholar, UBC
2004	AstraZeneca Undergraduate Scholarship, UBC
2002-2003	Women in Engineering and Science Program, National Research Council of Canada
2000-2004	Chancellor's Entrance Scholarship, UBC
2000-2004	IBM Canada Pacific Development Center Scholarship

Graduate students and postdoctoral scholars

Current postdoctoral scholars

2018- Miaomiao Li

Graduate students mentored

2018-2019 Ziyan Lin, M.S. in Biology, NYU.
 2018-2019 Ruxin Dai, M.S. in Biology, NYU.
 2018-2019 Diogo Mesquita, M.S. in Data Science, NYU.
 2018-2019 Yuhuan Wang, M.S. in Biology, NYU.

Teaching

- 2019 Co-instructor, Fundamentals of Bioinformatics (Course BIOL-UA 124), NYU Department of Biology.
- 2018-2019 Module instructor, Developmental and Stem Cell Systems II (Course DSCSII), NYU School of Medicine.
- 2018 Co-instructor, Bio Core III: Molecules and Cells (Course BIOL-GA 2003), NYU Department of Biology.
- 2007 Teaching assistant, Introduction to Computer Science and Programming (Course 6.00), MIT.
- 2004 Teaching assistant, Introduction to Software Development (Course CPSC 211), UBC.
- 2003 Teaching assistant, Program Design and Data Structures (Course CPSC 216), UBC.

Committees

Biology Department

- 2018,2019 Graduate Student recruitment committee

PhD Student thesis committees

- Akash Sookdeo, PhD student, committee member
- Chang Wang, PhD student, committee member
- Victoria Le, PhD student, committee member

Professional activities

- Member, International Society for Computational Biology.
- Member, American Society of Plant Biologists.
- Review editor for Frontiers in Genetics and Plant Science.
- Reviewer for BMC Bioinformatics, eLife, Genome Research, IEEE Transactions on Biomedical Engineering, Nature, Nucleic Acids Research.