

# Shao-shan Carol Huang

## Curriculum Vitae

April 2020

📍 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

- 2019- Affiliate Faculty, Center for Data Science, New York University  
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

### Funding

## Ongoing Grant Support

NSF - IOS-1916804 Huang (Co-PI) 2019/08/01 - 2023/07/31

### National Science Foundation, Integrative Organismal Systems

**Title:** TRTech-PGR: Mapping and functional characterization of cis-regulatory module variation in plants

**Investigators:** Andrea Gallavotti (Rutgers University; PI), Naden Krogan (American University; Co-PI)

**Description:** This grant develops methods to map transcription factor-DNA interactions that enable comparative analysis of regulatory sequences in multiple genetic backgrounds. The methods will be applied in two species with different genomic properties: maize, a major monocot crop with a large genome, and Arabidopsis, a model eudicot with a compact genome.

## Publications

### Refereed research papers

1. Procko, C., S. Morrison, C. Dunar, S. Mills, B. Maldonado, C. Cockrum, N. E. Peters, **S.-s. C. Huang**, and J. Chory (2019). Big Data to the Bench: Transcriptome Analysis for Undergraduates. *CBE-Life Sciences Education* **18**(2). PMID: 31074696, ar19. eprint: <https://doi.org/10.1187/cbe.18-08-0161>.
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. Annual Meeting of Mid-Atlantic section of the American Society of Plant Biologists (ASPB). College Park, MD. May 2020.
2. University of Cambridge Sainsbury Laboratory. Cambridge, UK. November 27, 2019.
3. University of Maryland Department of Cell Biology and Molecular Genetics. College Park, MD. September 20, 2019.
4. Iowa State University Bioinformatics and Computational Biology Symposium. Ames, IA. April 19, 2019.
5. CNRS - Jacques Monod Conference: First International Plant Systems Biology Meeting. Roscoff, France. September 12, 2018.
6. Workshop on Construction of Gene Regulatory Networks in Arabidopsis in the 29th International Conference on Arabidopsis Research. Turku, Finland. June 26, 2018.
7. Boyce Thompson Institute. Ithaca, NY. May 8, 2018.
8. University of California, Riverside Data Science Center. Riverside, CA. March 22, 2017.
9. Cornell University School of Integrative Plant Science. Ithaca, NY. March 9, 2017.
10. New York University Department of Biology. New York, NY. March 7, 2017.
11. Washington University at St. Louis Department of Biology. St. Louis, MO. January 9, 2017.
12. Academia Sinica Institute of Cellular and Organismic Biology. Taipei, Taiwan. December 21, 2016.
13. Carnegie Institution of Science Department of Plant Biology. Stanford, CA. December 2, 2016.
14. Salk Featured Fellow Series. The Salk Institute for Biological Studies. La Jolla, CA. August 10, 2016.
15. 22nd International Conference on Plant Growth Substances. Toronto, Canada. June 22, 2016.
16. UCLA Department of Molecular, Cell, and Developmental Biology and the Institute for Quantitative and Computational Biosciences. Los Angeles, CA. April 25, 2016.
17. Cold Spring Harbor Conference on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY. March 19, 2016.
18. University of Toronto Department of Cell and Systems Biology. Toronto, Canada. March 14, 2016.

19. University of New Hampshire Department of Molecular, Cellular, and Biomedical Sciences. Durham, NH. July 15, 2015.
20. San Diego Center for Systems Biology: Cytoscape and Network Analysis Workshop. San Diego, CA. April 17, 2015.
21. Oregon State University Center for Genome Research and Biocomputing. Corvallis, OR. April 15, 2015.

## Honors and awards

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|------------|--|
| 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

- 2020- Yichun Qian
- 2018- Miaomiao Li

### Graduate students mentored

- 2018-2019 Ziyang 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 Yuhang Wang, M.S. in Biology, NYU.

## Teaching

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|-----------|--|
| 2020      | Instructor, Fundamentals of Bioinformatics (Course BIOL-UA 124), NYU Department of Biology.        |
| 2020      | Co-instructor, Plant Science and Biotechnology (Course BIOL-UA 560), NYU Department of Biology.    |
| 2019      | Co-instructor, Fundamentals of Bioinformatics (Course BIOL-UA 124), NYU Department of Biology.     |
| 2018-2020 | Module instructor, Developmental and Stem Cell Systems II (Course DSCSII), NYU School of Medicine. |
| 2018-2019 | 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.                     |

## 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 Biology, BMC Bioinformatics, eLife, Genome Research, IEEE Transactions on Biomedical Engineering, Nature, Nucleic Acids Research.

## **Committees**

### **NYU Biology Department**

- PhD recruitment committee, 2018-2020
- Organizer, Departmental postdoc seminar series, 2019-2020
- PhD student thesis committees
  - Xinhe Xue, PhD student, committee member
  - Yuhan Hao, PhD student, committee member
  - Cassandra Buzby, PhD student, committee member
  - Akash Sookdeo, PhD student, committee member
  - Victoria Le, PhD student, committee member
  - Chang Wang, PhD student, committee member