

Shao-shan Carol Huang

Curriculum Vitae

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📍 Center for Genomics and Systems Biology
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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

- 2020-current Mentoring Faculty, PhD program in Developmental Genetics, NYU School of Medicine
2019-current Affiliate Faculty, Center for Data Science, New York University
2018-current 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
- 2011 Postdoctoral associate, Department of Biological Engineering
Massachusetts Institute of Technology
- 2005-2011 Graduate student, Program in Computational and Systems Biology
Massachusetts Institute of Technology
- 2004-2005 Undergraduate research assistant, Center for Molecular Medicine and Therapeutics
University of British Columbia
- 2003-2005 Undergraduate research assistant, Department of Mathematics
University of British Columbia

Funding

Ongoing Grant Support

NIH - 1R35GM138143 Huang (PI) 2020/07/01 - 2025/04/30

National Institutes of Health, National Institute of General Medical Sciences

Title: Dissecting natural variation in transcription factor - DNA interactions

Description: This grant aims to study the mechanisms of genome-wide transcription factor binding site changes and the resulting regulatory networks using diverse genomes and epigenomes of natural

strains of *Arabidopsis* as model. We will build computational models of DNA sequence and non-sequence features for predicting binding variations, and experimentally validate the biological functions of selected binding site variants.

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.

Reviews

1. Qian, Y. and **S.-s. C. Huang** (2020). Improving plant gene regulatory network inference by integrative analysis of multi-omics and high resolution data sets. *Current Opinion in Systems Biology*.
2. **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. Cancelled due to COVID-19.
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

Postdoctoral scholars

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| 2020-current | Abbas Shojaee |
| 2018-current | Miaomiao Li |
| 2020 | Yichun Qian |

Graduate students

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|--------------|--------------------------------------------|
| 2020-current | Michelle Saavedra, M.S. in Biology, NYU. |
| 2020-current | Nabilla Zaman, M.S. in Biology, NYU. |
| 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 | Yuhan Wang, M.S. in Biology, NYU. |

Teaching

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| 2020-current | Instructor, Fundamentals of Bioinformatics (Course BIOL-UA 124), NYU Department of Biology. |
| 2018-current | Module instructor, Developmental and Stem Cell Systems II (Course DSCSII), NYU School of Medicine. |
| 2018-current | Co-instructor, Bio Core III: Molecules and Cells (Course BIOL-GA 2003), 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. |

Professional activities

- Member, International Society for Computational Biology.

- ▶ Member, American Society of Plant Biologists.
- ▶ Reviewer for BMC Biology, BMC Bioinformatics, eLife, Genome Research, IEEE Transactions on Biomedical Engineering, Nature, Nature Plants, npj Systems Biology and Applications, Nucleic Acids Research, Plant J, The Plant Cell, PNAS.

Committees

NYU Biology Department

- ▶ Co-chair, PhD recruitment committee, 2021
- ▶ Member, PhD recruitment committee, 2018-2020
- ▶ Organizer, Departmental postdoc seminar series, 2019-2020
- ▶ PhD student thesis committees
 - Ornob Alam, PhD student, committee member
 - Jose Antonio Salome correa, PhD student, committee member
 - Xinyi (Cathy) Guo, PhD student, committee member
 - 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