S. Carol Huang
Curriculum Vitae

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Center for Genomics and Systems Biology
Department of Biology, New York University
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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-present   Mentoring Faculty, PhD program in Developmental Genetics, NYU School of Medicine
2019-present   Affiliate Faculty, Center for Data Science, New York University
2018-present   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

Preprints

1. Yin, L., M. Zander, **S.-S. C. Huang**, M. Xie, L. Song, J. P. Saldierna Guzmán, E. Hann, B. K. Shanbhag, S. Ng, S. Jain, B. J. Janssen, N. M. Clark, J. W. Walley, T. Beddoe, Z. Bar-Joseph, M. G. Lewsey, and J. R. Ecker (2023). Transcription Factor Dynamics in Cross-Regulation of Plant Hormone Signaling Pathways. *bioRxiv : the preprint server for biology*.

Refereed research papers

1. Zhang, C., Z. Dai, T. Ferrier, L. Orduña, A. Santiago, A. Peris, D. C. J. Wong, C. Kappel, S. Savoi, R. Loyola, A. Amato, B. Kozak, M. Li, A. Liang, D. Carrasco, C. Meyer-Regueiro, C. Espinoza, G. Hilbert, R. Figueroa-Balderas, D. Cantu, R. Arroyo-Garcia, P. Arce-Johnson, P. Claudel, D. Errandonea, M. Rodríguez-Concepción, E. Duchêne, **S.-S. C. Huang**, S. D. Castellarin, G. B. Tornielli, F. Barrieu, and J. T. Matus (2023). MYB24 orchestrates terpene and flavonol metabolism as light responses to anthocyanin depletion in variegated grape berries. *The Plant cell* **35** (12), 4238–4265.

2. Shojaee, A. and **S.-S. C. Huang** (2023). Robust discovery of gene regulatory networks from single-cell gene expression data by Causal Inference Using Composition of Transactions. *Briefings in bioinformatics* **24** (6).

3. Li, M., T. Yao, W. Lin, W. E. Hinckley, M. Galli, W. Muchero, A. Gallavotti, J.-G. Chen, and **S.-S. C. Huang** (2023). Double DAP-seq uncovered synergistic DNA binding of interacting bZIP transcription factors. *Nature Communications* **14**(1), 2600.

4. Orduña, L., M. Li, D. Navarro-Payá, C. Zhang, A. Santiago, P. Romero, Ž. Ramšak, G. Magon, J. Höll, P. Merz, K. Gruden, A. Vannozzi, D. Cantu, J. Bogs, D. C. J. Wong, **S.-s. C. Huang**, and J. T. Matus (2022). Direct regulation of shikimate, early phenylpropanoid and stilbenoid pathways by Subgroup 2 R2R3-MYBs in grapevine. *The Plant Journal* **110**(2), 529–547.

5. Plant Cell Atlas Consortium, S. Ghosh Jha*, A. T. Borowsky*, B. J. Cole*, N. Fahlgren*, A. Farmer*, **S.-s. C. Huang***, P. Karia*, M. Libault*, N. J. Provart*, S. L. Rice*, M. Saura-Sanchez*, P. Agarwal, A. H. Ahkami, C. R. Anderton, S. P. Briggs, J. A. Brophy, P. Denolf, L. F. Di Costanzo, M. Exposito-Alonso, S. Giacomello, F. Gomez-Cano, K. Kaufmann, D. K. Ko, S. Kumar, A. V. Malkovskiy, N. Nakayama, T. Obata, M. S. Otegui, G. Palfalvi, E. H. Quezada-Rodríguez, R. Singh, R. G. Uhrig, J. Waese, K. Van Wijk, C. R. Wright, D. W. Ehrhardt, K. D. Birnbaum, and S. Y. Rhee (2021). Science Forum: Vision, challenges and opportunities for a Plant Cell Atlas. *eLife* **10**, e66877.
   *equal contribution.

6. Scherma, M., J. S. Qvist, A. Asok, **S.-s. C. Huang**, P. Masia, M. Deidda, Y. B. Wei, R. K. Soni, W. Fratta, P. Fadda, E. R. Kandel, D. B. Kandel, and P. A. Melas (2020). Cannabinoid exposure in rat adolescence reprograms the initial behavioral, molecular, and epigenetic response to cocaine. *Proceedings of the National Academy of Sciences* **117**(18), 9991–10002.

7. 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), ar19.

8. Ursu, O., S. J. C. Gosline, N. Beeharry, L. Fink, V. Bhattacharjee, **S.-s. C. Huang**, Y. Zhou, T. Yen, and E. Fraenkel (Oct. 2017). Network modeling of kinase inhibitor polypharmacology reveals pathways targeted in chemical screens. *PLOS ONE* **12**(10), 1–22.

9. 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.

10. 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.

11. 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).

12. 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.

13. 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.

14. 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.

15. 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.

16. **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.

17. 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.

18. 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.

19. 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.

20. **Huang, S.-s. C.** and E. Fraenkel (2009). Integrating proteomic, transcriptional, and interactome data reveals hidden components of signaling and regulatory networks. *Science Signaling* **2**(81), ra40.

Reviews

1. Hajheidari, M. and **S.-s. C. Huang** (2022). Elucidating the biology of transcription factor–DNA interaction for accurate identification of cis-regulatory elements. *Current Opinion in Plant Biology* **68**, 102232.

2. Shojaee, A., M. Saavedra, and **S.-s. C. Huang** (2021). Potentials of single-cell genomics in deciphering cellular phenotypes. *Current Opinion in Plant Biology* **63**, 102059.

3. 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* **22**, 8–15.

4. **Huang, S.-s. C.** and J. R. Ecker (2018). Piecing together cis-regulatory networks: insights from epigenomics studies in plants. *WIREs Systems Biology and Medicine* **10**(3), e1411.

Book chapters

1. Li, M. and **S.-S. C. Huang** (2022). "DNA Affinity Purification Sequencing (DAP-Seq) for Mapping Genome-Wide Transcription Factor Binding Sites in Plants". In: *Accelerated Breeding of Cereal Crops*. Ed. by A. Bilichak and J. D. Laurie. New York, NY: Springer US, pp. 293–303.

2. **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 (Dec. 2012). *Identifying biological response pathways*. US Patent No. 8612160. Issued December 17, 2013.

Invited talks

1. Michigan State University Genetics and Genome Sciences Symposium. East Lansing, MI. (May 7, 2024).
2. University of British Columbia Centre for Molecular Medicine and Therapeutics. Vancouver, BC, Canada. (April 5, 2024).
3. University of British Columbia Department of Botany. Vancouver, BC, Canada. (April 2, 2024).
4. Cincinnati Children's Hospital Research Foundation. Cincinnati, OH. (March 6, 2024).
5. Cold Spring Harbor Laboratory Meeting in Plant Genomes, Systems Biology Engineering. Cold Spring Harbor, NY. (November 30, 2023).
6. 2023 Gordon Research Conference Single-Cell Approaches in Plant Biology. Ventura, CA. (August 3, 2023).
7. 19th Annual NYU Center for Genomics and Systems Biology Symposium. New York, NY. (June 7, 2023).
8. 2023 Society of Developmental Biology Mid-Atlantic Regional Meeting. Princeton, NJ. (April 21, 2023).
9. University of Texas Austin Department of Molecular Biosciences. Austin, TX. (March 22, 2023).
10. University of Georgia Department of Genetics. Athens, GA. (March 15, 2023).

11. University of Florida Department of Horticultural Sciences (October 31, 2022).

12. 32nd International Conference on Arabidopsis Research. Belfast, Northern Ireland. (June 23, 2022).

13. Annual Meeting of Mid-Atlantic section of the American Society of Plant Biologists (ASPB). College Park, MD. (May 24, 2022).

14. European Cooperation in Science and Technology: INTERGRAPE 3rd Annual Meeting. Virtual. (July 28 and 30, 2021). Attended virtually.

15. Annual Meeting of Mid-Atlantic section of the American Society of Plant Biologists (ASPB). College Park, MD. (May 2020). Cancelled due to COVID-19.

16. University of Cambridge Sainsbury Laboratory. Cambridge, UK. (November 27, 2019).

17. University of Maryland Department of Cell Biology and Molecular Genetics. College Park, MD. (September 20, 2019).

18. Iowa State University Bioinformatics and Computational Biology Symposium. Ames, IA. (April 29, 2019).

19. CNRS - Jacques Monod Conference: First International Plant Systems Biology Meeting. Roscoff, France. (September 12, 2018).

20. Workshop on Construction of Gene Regulatory Networks in Arabidopsis in the 29th International Conference on Arabidopsis Research. Turku, Finland. (June 26, 2018).

21. Boyce Thompson Institute. Ithaca, NY. (May 8, 2018).

22. University of California, Riverside Data Science Center. Riverside, CA. (March 22, 2017).

23. Cornell University School of Integrative Plant Science. Ithaca, NY. (March 9, 2017).

24. New York University Department of Biology. New York, NY. (March 7, 2017).

25. Washington University at St. Louis Department of Biology. St. Louis, MO. (January 9, 2017).

26. Academia Sinica Institute of Cellular and Organismic Biology. Taipei, Taiwan. (December 21, 2016).

27. Carnegie Institution of Science Department of Plant Biology. Stanford, CA. (December 2, 2016).

28. Salk Featured Fellow Series. The Salk Institute for Biological Studies. La Jolla, CA. (August 10, 2016).

29. 22nd International Conference on Plant Growth Substances. Toronto, Canada. (June 22, 2016).

30. UCLA Department of Molecular, Cell, and Developmental Biology and the Institute for Quantitative and Computational Biosciences. Los Angeles, CA. (April 25, 2016).

31. Cold Spring Harbor Laboratory Meeting in Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY. (March 19, 2016).

32. University of Toronto Department of Cell and Systems Biology. Toronto, Canada. (March 14, 2016).

33. University of New Hampshire Department of Molecular, Cellular, and Biomedical Sciences. Durham, NH. (July 15, 2015).

34. San Diego Center for Systems Biology: Cytoscape and Network Analysis Workshop. San Diego, CA. (April 17, 2015).

35. Oregon State University Center for Genome Research and Biocomputing. Corvalis, OR. (April 15, 2015).

Students and postdoctoral scholars mentored

Postdoctoral scholars

2018-present	Miaomiao Li
2020-2023	Abbas Shojaee
2021-2022	Mohsen Hajheidari
2020	Yichun Qian

Graduate students

2023-present	José A. Galván, Ph.D. in Biology, NYU.
2023-present	Aurelia Li, B.S. and M.S. in Biology, NYU.
2022-present	Graeme Vissers, Ph.D. in Biology, NYU (joint with Ken Birnbaum).
2021-present	Will Hinckley, Ph.D. in Biology, NYU (joint with Gloria Coruzzi).
2021-2022	Wanru Lin, M.S. in Biology, NYU.
2020-2021	Michelle Saavedra, M.S. in Biology, NYU.
2020-2021	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.

Research assistants

2023-present	Tara Ghandour
2022-2023	Yilin Zhou
2018-2019	Nathaniel Angeles

Undergraduate students

2023-present	Vera Vecherskaia, B.S. in Chemical and Biomolecular Engineering, NYU.
2023-present	Sean Doyle, B.S. in Computer Science, NYU.

High school intern

2021-2023	Hannah Will, The Packer Collegiate Institute, Brooklyn, NY.

Teaching

2020-present	Instructor, Fundamentals of Bioinformatics (Course BIOL-UA 124), NYU Department of Biology.
2018-present	Module instructor, Developmental and Stem Cell Systems II (Course DSCSII), NYU School of Medicine.
2018-present	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

➤ Scientific Advisory Board, DOE Research Center - BioPoplar: A tunable chassis for diversified bioproduct production.

➤ Computational/Modeling/AI Committee Lead, The Plant Cell Atlas Research Coordination Network.

➤ Reviewer for National Sciences and Engineering Research Council of Canada Discovery Grant, 2021.

➤ Reviewer for BMC Biology, BMC Bioinformatics, Current Opinion in Plant Biology, eLife, Frontiers in Plant Science, Genome Biology, Genome Research, IEEE Transactions on Biomedical Engineering, iScience, Molecular Cell, Nature, Nature Communications, Nature Plants, npj Systems Biology and Applications, Nucleic Acids Research, The Plant Journal, The Plant Cell, Plant Communications, PLoS ONE, PNAS, Science.

➤ Member, International Society for Computational Biology.

➤ Member, American Society of Plant Biologists.

Committees

NYU Biology Department

➤ Member, PhD Admissions Committee, AY 2018-2019, AY 2021-present.

➤ Organizer, Biology Faculty Exchange Seminar Series, AY 2021.

➤ Co-chair, PhD Admissions Committee, AY 2020.

➤ Organizer, Biology Postdoc Seminar Series, AY 2019-2021.

➤ PhD Student Thesis Committees

  − Shaili Regmi, committee member, 2024-present.

  − Isabel Bojanini, committee member, 2024-present.

- Eric Laderman, committee member, 2023-present.
- Wells Burrell, committee member, 2023-present.
- Dylan Fitzmaurice, committee member, 2023-present.
- Maggie Beheler-Amass, committee chair, 2022-present.
- Julie Chuong, committee member, 2022-present.
- Yingzhen Pei, committee chair, 2021-present.
- Ornob Alam, committee member, 2021-present.
- Jose Antonio Salome correa, committee member, 2020-present.
- Xinyi (Cathy) Guo, committee member, 2020-present.
- Xinhe Xue, committee member, 2020-2023.
- Yuhan Hao, committee member, 2020-2023.
- Cassandra Buzby, committee member, 2020-present.
- Akash Sookdeo, committee member, 2019-2022.
- Victoria Le, committee member, 2019-2022.
- Chang Wang, committee member, 2019-2021.

Honors and awards

2022	NYU Whitehead Fellowship for Junior Faculty in Biomedical and Biological Sciences
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