

Shao-shan Carol Huang

Curriculum Vitae

September 2017

Address: Genomic Analysis Laboratory &
Plant Biology Laboratory
The Salk Institute for Biological Studies
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Education

- 2011 Ph.D., Program in Computational and Systems Biology
Massachusetts Institute of Technology
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, 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
- 2011- Postdoctoral associate, Genomic Analysis Laboratory & Plant Biology Laboratory
The Salk Institute for Biological Studies
Advisor: Dr. Joseph Ecker
- Project 1: DNA Affinity Purification sequencing (DAP-seq) for *in vitro*, genomic context identification of transcription factor binding sites
 - Project 2: 1,001 (Epi)Genomes Project for *Arabidopsis thaliana*
 - Project 3: Regulatory networks controlling hormone-mediated growth

Past research positions

- 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. 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.

2. 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.
3. 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.
4. O'Malley, R. C. *, **S.-s. C. Huang***, L. Song, M. G. Lewsey, A. Barlett, 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.
5. 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.
6. 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).
7. 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.
8. **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.
9. 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.
10. 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.
11. 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.
12. **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.
13. **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.

Book chapters

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. Univ of California, Riverside Data Science Center. March 22, 2017.
2. New York University Department of Biology. New York, NY. March 7, 2017.
3. Washington University at St. Louis Department of Biology. St. Louis, MO. January 9, 2017.
4. Academia Sinica Institute of Cellular and Organismic Biology. Taipei, Taiwan. December 21, 2016.
5. Carnegie Institution of Science Department of Plant Biology. Stanford, CA. December 2, 2016.
6. Salk Featured Fellow Series. The Salk Institute for Biological Studies. La Jolla, CA. August 10, 2016.
7. 22nd International Conference on Plant Growth Substances. Toronto, Canada. June 22, 2016.
8. UCLA Department of Molecular, Cell, and Developmental Biology and the Institute for Quantitative and Computational Biosciences. Los Angeles, CA. April 25, 2016.
9. Cold Spring Harbor conference on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY. March 19, 2016.
10. University of Toronto Department of Cell and Systems Biology. Toronto, Canada. March 14, 2016.
11. University of New Hampshire Department of Molecular, Cellular, and Biomedical Sciences. Durham, NH. July 15, 2015.
12. San Diego Center for Systems Biology: Cytoscape and Network Analysis Workshop. San Diego, CA. April 17, 2015.
13. Oregon State University Center for Genome Research and Biocomputing. Corvallis, OR. April 15, 2015.

Conference posters

1. **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.
2. **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.
3. **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.
4. **Huang, S.-s. C.** and E. Fraenkel (2009). 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*. <http://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*.
<http://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
2009 First Prize, MIT Center for Environmental Health Sciences Poster Session
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

Teaching

- 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.

Student advising

- 2016- Aaron Rothleder, undergraduate student, UCSD Bioinformatics Program
2016 Lucia Johnson, undergraduate student, Stanford University
2015-2016 Hanfei Shen, undergraduate student, UCSD Bioengineering Program
2014 Benjamin Kellman, rotation graduate student, UCSD Bioinformatics and Systems Biology PhD Program
2010-2011 Oana Ursu, MIT Undergraduate Research Opportunity Program
2010 Jennifer Lai, MIT Undergraduate Research Opportunity Program
2008 Melissa Gymrek, MIT Integrated Cancer Biology Program
2008 Young Eun Choi, MIT Summer Research Program

Professional activities

- Member, International Society for Computational Biology
- Reviewer for BMC Bioinformatics, Nucleic Acids Research
- Review editor for Frontiers in Genetics and Plant Science