

# Shao-shan Carol Huang

## Curriculum Vitae

December 2016

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

- 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. 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.

2. 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.
3. 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.
4. 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).
5. 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.
6. **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.
7. 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.
8. 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.
9. 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.
10. **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.
11. **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. Academia Sinica Institute of Cellular and Organismic Biology. Taipei, Taiwan. December 21, 2016.
2. Carnegie Institution of Science Department of Plant Biology. Stanford, CA. December 2, 2016.
3. Salk Featured Fellow Series. The Salk Institute for Biological Studies. La Jolla, CA. August 10, 2016.

4. 22nd International Conference on Plant Growth Substances. Toronto, Canada. June 22, 2016.
5. UCLA Department of Molecular, Cell, and Developmental Biology and the Institute for Quantitative and Computational Biosciences. Los Angeles, CA. April 25, 2016.
6. Cold Spring Harbor conference on Systems Biology: Global Regulation of Gene Expression. Cold Spring Harbor, NY. March 19, 2016.
7. University of Toronto Department of Cell and Systems Biology. Toronto, Canada. March 14, 2016.
8. University of New Hampshire Department of Molecular, Cellular, and Biomedical Sciences. Durham, NH. July 15, 2015.
9. San Diego Center for Systems Biology: Cytoscape and Network Analysis Workshop. San Diego, CA. April 17, 2015.
10. 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.

#### 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                                                      |
| 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