

# James Chuang, PhD

77 Avenue Louis Pasteur  
New Research Building, Room 239  
Boston, MA 02115

[james\\_chuang@hms.harvard.edu](mailto:james_chuang@hms.harvard.edu)  
(617) 432-7557

[james-chuang.github.io](https://james-chuang.github.io)  
[github.com/james-chuang](https://github.com/james-chuang)

---

A bioinformatics data scientist with experience analyzing complex datasets to investigate biological questions. Created software pipelines to process, visualize, and perform statistical analyses on multiple types of genomic data. Familiar with UNIX, the Python and R data science stacks, and cluster computing. Skilled at technical writing and communicating complex ideas to collaborators.

## relevant skills

- genomic data analysis
- Python (NumPy, Pandas, SciPy, etc.)
- R (tidyverse)
- UNIX
- version control (git)
- workflow management (Snakemake)
- distributed computing (Slurm)

## post-doctoral experience

**2020** Fred Winston lab, Department of Genetics, Harvard Medical School

- Analyzed datasets including RNA-seq, transcription start site sequencing (TSS-seq), native elongating transcript sequencing (NET-seq), ChIP-seq, and MNase-seq for the following projects:
  1. Studying the interaction between Spt6 and Spn1, two histone chaperones involved in transcription elongation.
  2. Studying the requirement for Spn1 by depleting it from cells and assaying various aspects of transcription and chromatin state.
  3. Studying the role of intragenic transcripts, transcripts which initiate from within gene bodies, during yeast stress responses.

## education

**2019** PhD, Biomedical Engineering, Boston University

advisor: Fred Winston, PhD  
Professor of Genetics  
Harvard Medical School

- summary: Analyzed datasets including TSS-seq, ChIP-nexus (high-resolution ChIP-seq), NET-seq, and MNase-seq for the following projects:
1. Studying the mechanisms of widespread intragenic transcription observed in mutants of Spt6, a histone chaperone and transcription elongation factor.
  2. Studying the requirement for Spt5, a critical transcription elongation factor, by depleting it from cells and assaying various aspects of transcription and chromatin state.

**2013** BSc, Biomedical Engineering, Johns Hopkins University

advisor: Jef D. Boeke, PhD, Dsc  
Director, Institute for Systems Genetics  
Professor of Biochemistry and Molecular Pharmacology  
NYU Langone Health

summary: Contributed to the development of methods for the modular assembly of multi-gene circuits for expression in yeast. Also assembled DNA for SC2.0, a project to design and build a novel eukaryotic genome based on the yeast genome.

## **publications** (\*equal contribution)

- 2020** Reim NI\*, **Chuang J\***, Jain D\*, Alver BH, Park PJ, Winston F (2020). **The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in *Saccharomyces cerevisiae*.** Nucleic Acids Research, doi:[10.1093/nar/gkaa745](https://doi.org/10.1093/nar/gkaa745)
- 2018** Doris SM\*, **Chuang J\***, Viktorovskaya O, Murawska M, Spatt D, Churchman LS, Winston F (2018). **Spt6 is required for the fidelity of promoter selection.** Molecular Cell, doi:[10.1016/j.molcel.2018.09.005](https://doi.org/10.1016/j.molcel.2018.09.005)
- 2018** **Chuang J**, Boeke JD, Mitchell LA (2018) **Coupling yeast golden gate and VEGAS for efficient assembly of the violacein pathway in *Saccharomyces cerevisiae*.** Synthetic Metabolic Pathways, doi:[10.1007/978-1-4939-7295-1\\_14](https://doi.org/10.1007/978-1-4939-7295-1_14)
- 2017** Aquino P, Honda B, Jaini S, Lyubetskaya A, Hosur K, Chiu JG, Ekladios I, Hu D, Jin L, Sayeg MK, Stettner AI, Wang J, Wong BG, Wong WS, Alexander SL, Ba C, Bensussen SI, Chou K, **Chuang J**, Gastler DE, Grasso DJ, Greifenberger JS, Guo C, Hawes AK, Israni DV, Jain SR, Kim J, Lei J, Li H, Li D, Li Q, Mancuso CP, Mao N, Masud SF, Meisel CL, Mi J, Nykyforchyn CS, Park M, Peterson HM, Ramirez AK, Reynolds DS, Rim NG, Saffie JC, Su H, Su WR, Su Y, Sun M, Thommes MM, Tu T, Varongchayakul N, Wagner TE, Weinberg BH, Yang R, Yaroslavsky A, Yoon C, Zhao Y, Zollinger AJ, Stringer AM, Foster JW, Wade J, Raman S, Broude N, Wong WW, Galagan JE (2017). **Coordinated regulation of acid resistance in *Escherichia coli*.** BMC Systems Biology, doi:[10.1186/s12918-016-0376-y](https://doi.org/10.1186/s12918-016-0376-y)
- 2015** Mitchell, LA\*, **Chuang J\***, Agmon N, Khunsriraksakul C, Phillips NA, Cai Y, Truong DM, Veerakumar A, Wang Y, Mayorga M, Blomquist P, Sadda P, Trueheart J, Boeke JD (2015). **Versatile genetic assembly system (VEGAS) to assemble pathways for expression in *S. cerevisiae*.** Nucleic Acids Research, doi:[10.1093/nar/gkv466](https://doi.org/10.1093/nar/gkv466)
- 2015** Agmon N, Mitchell LA, Cai Y, Ikushima S, **Chuang J**, Zheng A, Choi W, Martin JA, Caravelli K, Stracquadanio G, Boeke JD (2015). **Yeast golden gate (yGG) for the efficient assembly of *S. cerevisiae* transcription units.** ACS Synthetic Biology, doi:[10.1021/sb500372z](https://doi.org/10.1021/sb500372z)
- 2013** Mitchell LA, Cai Y, Taylor M, Noronha AM, **Chuang J**, Dai L, Boeke JD (2013). **Multi-change isothermal mutagenesis: a new strategy for multiple site-directed mutations in plasmid DNA.** ACS Synthetic Biology, doi:[10.1021/sb300131w](https://doi.org/10.1021/sb300131w)