

# James Chuang, PhD

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A computational biologist experienced in deriving insights from complex datasets to advance research and development projects. Writes software pipelines to reproducibly process, visualize, and perform statistical analyses on varied data types. Familiar with the Unix shell, Python and R for data science, and workflow orchestration on compute clusters and cloud platforms. Skilled at scientific communication and technical writing.

## skills

- -omics data analysis
- CRISPR screen design and analysis
- Bayesian statistical modeling
- Python (NumPy, Pandas, SciPy, etc.)
- R (tidyverse)
- version control (git)
- workflow orchestration (Snakemake)
- cloud computing (AWS)
- distributed computing (Slurm)
- Unix shell

## experience

### 2021- Senior Computational Biologist, **64x Bio**

Design and analysis of pooled CRISPR screens for viral productivity  
Bayesian modeling of viral titer digital PCR data  
Development of Python libraries to support data analysis and automate repetitive lab tasks  
Analysis of internal and external datasets to support research projects

### 2020-21 Computational Biologist, **Freenome**

Data analysis supporting assay development for early cancer detection by liquid biopsy

### 2019-20 Postdoctoral researcher, **Fred Winston lab, Harvard Medical School Department of Genetics**

Analysis of 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:

- Studying the interaction between Spt6 and Spn1, two histone chaperones involved in transcription elongation.
- Studying Spn1 functions by depleting it from cells and assaying transcription and chromatin state.
- 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

research: Analysis of datasets including TSS-seq, ChIP-nexus (high-resolution ChIP-seq), NET-seq, and MNase-seq for the following projects:

- Studying the mechanisms of widespread intragenic transcription observed in mutants of Spt6, a histone chaperone and transcription elongation factor.
- Studying the transcription elongation factor Spt5 by depleting it from cells and assaying transcription and chromatin state.

Analysis of RNA-seq and ChIP-seq data to characterize genetic circuits with low off-target misregulation via cooperative binding of low-affinity synthetic transcription factors

### 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

research: Methods for the modular assembly of multi-gene circuits for expression in yeast  
DNA assembly for the Sc2.0 synthetic yeast genome project

## publications

### 2023 Context-dependent neocentromere activity in synthetic yeast chromosome VIII

S Lauer, J Luo, L Lazar-Stefanita, W Zhang, LH McCulloch, V Fanfani, E Lobzaev, MAB Haase, N Easo, Y Zhao, F Yu, J Cai, L Anne, JS Barger, N Belkaya, K Boulier, K Butler, M Callaghan, C Chang, J Chen, XJ Chen, IY Cho, E Choi, WJ Choi, **J Chuang**, AL Cook, E Cooper, NT Culbertson, J Dunn, C Floria, BG Anderson, NP Held, E Hsiao, JK Igwe, K Kang, J Karanxha, M Kelly, A Khakhar, C Khunsriraksakul, JJ Kim, D Kim, JW Kim, A Lamb, DSH Lee, YK Lee, J Lim, S Liu, J Lopez, ZA Lu, H Ma, JA Mandel, J Mao, J Matelsky, J Merran, R Mohan, C Montoya, S Murugan, L Ni, WC Oh, Y Park, L Paulsen, N Phillips, S Pinglay, VA Rajan, G Ransom, E Rhoads, P Sanna, E Scher, J Shah, A Sharma, MC Shepardson, J Song, S Sontha, V Srinivas, S Tan, AA Tu, S Uhl, W Xiaoyue, J Yu, A Zhu, JS Bader, G Stracquadanio, JD Boeke  
Cell Genomics 3 (11)

### 2023 Cooperative assembly confers regulatory specificity and long-term genetic circuit stability

MDJ Bragdon, N Patel, **J Chuang**, E Levien, CJ Bashor, AS Khalil  
Cell 186 (18), 3810-3825. e18

### 2022 Suppressor mutations that make the essential transcription factor Spn1/lws1 dispensable in *Saccharomyces cerevisiae*

F López-Rivera, **J Chuang**, D Spatt, R Gopalakrishnan, F Winston  
Genetics 222 (2), iyac125

### 2021 Essential histone chaperones collaborate to regulate transcription and chromatin integrity

O Viktorovskaya, **J Chuang**, D Jain, NI Reim, F López-Rivera, M Murawska, D Spatt, LS Churchman, PJ Park, F Winston  
Genes & Development 35 (9-10), 698-712

- 2020 The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in *Saccharomyces cerevisiae***  
 NI Reim\*, **J Chuang\***, D Jain\*, BH Alver, PJ Park, F Winston  
 Nucleic Acids Research 48 (18), 10241-10258
- 2018 Spt6 is required for the fidelity of promoter selection**  
 SM Doris\*, **J Chuang\***, O Viktorovskaya, M Murawska, D Spatt, LS Churchman, F Winston  
 Molecular Cell 72 (4), 687-699
- 2018 Coupling yeast golden gate and VEGAS for efficient assembly of the violacein pathway in *Saccharomyces cerevisiae***  
**J Chuang**, JD Boeke, LA Mitchell  
 Synthetic Metabolic Pathways: Methods and Protocols, 211-225
- 2017 Coordinated regulation of acid resistance in *Escherichia coli***  
 P Aquino, B Honda, S Jaini, A Lyubetskaya, K Hosur, JG Chiu, I Ekladios, D Hu, L Jin, MK Sayeg, AI Stettner, J Wang, BG Wong, WS Wong, SL Alexander, C Ba, SI Bensussen, K Chou, **J Chuang**, DE Gastler, DJ Grasso, JS Greifengberger, C Guo, AK Hawes, DV Israni, SR Jain, J Kim, J Lei, H Li, D Li, Q Li, CP Mancuso, N Mao, SF Masud, CL Meisel, J Mi, CS Nykyforchyn, M Park, HM Peterson, AK Ramirez, DS Reynolds, NG Rim, JC Saffie, H Su, WR Su, Y Su, M Sun, MM Thommes, T Tu, N Varongchayakul, TE Wagner, BH Weinberg, R Yang, A Yaroslavsky, C Yoon, Y Zhao, AJ Zollinger, AM Stringer, JW Foster, J Wade, S Raman, N Broude, WW Wong, JE Galagan  
 BMC Systems Biology 11 (1), 1-15
- 2015 Versatile genetic assembly system (VEGAS) to assemble pathways for expression in *S. cerevisiae***  
 LA Mitchell\*, **J Chuang\***, N Agmon, C Khunsriraksakul, NA Phillips, Y Cai, DM Truong, A Veerakumar, Y Wang, M Mayorga, P Blomquist, P Sadda, J Trueheart, JD Boeke  
 Nucleic Acids Research 43 (13), 6620-6630
- 2015 Yeast golden gate (yGG) for the efficient assembly of *S. cerevisiae* transcription units**  
 N Agmon, LA Mitchell, Y Cai, S Ikushima, **J Chuang**, A Zheng, W Choi, JA Martin, K Caravelli, G Stracquadanio, JD Boeke  
 ACS Synthetic Biology 4 (7), 853-859
- 2013 Multichange isothermal mutagenesis: a new strategy for multiple site-directed mutations in plasmid DNA**  
 LA Mitchell, Y Cai, M Taylor, AM Noronha, **J Chuang**, L Dai, JD Boeke  
 ACS Synthetic Biology 2 (8), 473-477