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 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/Iws1 dispensable in *Saccharomyces cerevisiae*
F López-Rivera, **J Chuang**, D Spatt, R Golpalakrishnan, 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 Ekladious, 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 Greifenberger, 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