

Jacob C. Kimmel

San Francisco, California – jck.bio

jacob@jck.bio
(321)-536-1919

EDUCATION

- **Ph.D. – University of California, San Francisco** San Francisco, CA
Dept. of Biochemistry & Biophysics; Fellowships: NSF GRFP, PhRMA, NIH T32, Discovery Sept. 2015 – Apr. 2018

RECENT EXPERIENCE

NewLimit South San Francisco, CA
Head of Research 2022 - Present

- Leading Research to enable therapeutic applications of epigenetic reprogramming

Calico Life Sciences South San Francisco, CA
Principal Investigator, R&D 2021 - 2022
Computational Fellow, Computing 2020 - 2021

- Led a research laboratory focused on programming cell identity to address age-related diseases
- Coordinated a cross-functional team, mentored Data Scientists, recruited Ph.D.-level scientists
- Led the development of a computational & experimental platform for pooled screening of cell reprogramming strategies, completing a company-wide goal – reprog.research.calicolabs.com
- Developed `scNym` semi-supervised adversarial neural networks for classifying single cell genomics profiles. Set new state of the art for performance, used by the Human Cell Atlas – scnym.research.calicolabs.com

Data Scientist I & II, Computing 2018 - 2020

- Lead an investigation of cell type and tissue environment influences on aging using single cell genomics across three murine tissues – mca.research.calicolabs.com
- Lead an investigation of skeletal muscle aging using single cell genomics & dynamical systems modeling that revealed a critical point where old stem cells fail to differentiate – myo.research.calicolabs.com
- Developed Calico's single cell genomics & screening platform, guided target ID & biomarker development
- Guided biomarker and lead selection decisions for small molecule/mAb programs with functional genomics

University of California, San Francisco San Francisco, CA
PhD Candidate; Thesis: Inferring cell state from cell behavior; Advisor: Wallace F. Marshall 2015 - 2018

- Developed `Heteromotility`, a biological motion analysis package to quantify cell state transitions
- Developed `Lanternfish` deep learning package to enable discrimination and prediction of cell behaviors
- Discovered age-dampened state transitions in myogenesis with single cell RNA-seq & `Heteromotility`

IBM Research San Jose, CA
Deep Learning Intern, Cellular Engineering; Advisor: Simone Bianco Fall 2017

- Developed rapid convolutional neural network segmentation methods for microscopy data
- Implemented a Natural Evolution Strategies (NES) optimization framework to improve multi-cell tracking

SKILLS

- **Data Analysis:** Experimental design, statistics, linear modeling
- **Machine Learning:** Neural networks, semi-supervised learning, adversarial learning, PyTorch, Tensorflow
- **Programming:** Python (scipy, scikit-learn, statsmodels), R, Matlab, git, bash, \LaTeX
- **NGS/Bioinformatics:** Single cell & bulk RNA-seq, ATAC-seq, conv. net. models, variant calling
- **Experimental Biology:** Single cell genomics, primary cell biology, molecular biology, automation

SELECTED PUBLICATIONS

Author links for complete listing: Google Scholar, PubMed, bioRxiv

†: Corresponding

1. Roux A, Zhang C, Zavala-Solorio J, Paw J, Kolumam G, Kenyon C, **Kimmel JC**[†]. Partial reprogramming restores youthful gene expression through transient suppression of cell identity. 2021. *bioRxiv*. doi: <https://doi.org/10.1101/2021.05.21.444556> . Features in *Nature Biotechnology*, MIT Technology Review, Lifespan, Fight Aging, and Tet Systems. *In revision, Cell Systems*.
2. **Kimmel JC**[†], Kelley DR[†]. Semi-supervised adversarial neural networks for single-cell classification. 2021. *Genome Research*. doi: 10.1101/gr.268581.120. **Highlighted** in *Nature Reviews Cancer*.
3. **Kimmel JC**[†], Yi N, Roy M, Hendrickson DG, Kelley DR[†]. Differentiation reveals latent features of aging and an energy barrier in murine myogenesis. 2021. *Cell Reports*. doi: 10.1016/j.celrep.2021.109046. **Featured on the Stem Cell Podcast (StemCell Tech):** Episode 192.
4. **Kimmel JC**, Hwang AB, Scaramozza A, Marshall WF, Brack AS. Aging induces aberrant state transition kinetics in murine muscle stem cells. 2020. *Development*. doi: 10.1242/dev.183855. **Highlighted by Development**.
5. **Kimmel JC**, Penland L, Rubinstein ND, Hendrickson DG, Kelley DR, Rosenthal AZ . Murine single-cell RNA-seq reveals cell-identity- and tissue-specific trajectories of aging. 2019. *Genome Research*. doi: 10.1101/gr.253880.119. **Featured on the cover of Genome Research**.
6. **Kimmel JC**, Brack AS, Marshall WF. Deep convolutional and recurrent neural networks for cell motility discrimination and prediction. 2019. *IEEE Transactions on Computational Biology and Bioinformatics*. doi: 10.1109/TCBB.2019.2919307.
7. **Kimmel JC**, Chang AY, Brack AS, Marshall WF. Inferring cell state by quantitative motility analysis reveals a dynamic state system and broken detailed balance. 2018. *PLoS Computational Biology* 14(1): e1005927. doi: 10.1371/journal.pcbi.1005927. **Chosen as an Editor's Pick** in *PLoS Editor's Collections*.

SELECTED PRESENTATIONS

1. **Kimmel JC**[†]. Partial reprogramming restores youthful gene expression. Invited talk at the Systems Biology of Aging Gordon Research Conference. Newry, ME. 2022.
2. **Kimmel JC**[†]. Reprogramming to restore youthful gene expression. Invited talk at Ai4 Longevity 2021.
3. **Kimmel JC**[†], Kelley DR[†]. Semi-supervised adversarial neural networks for single cell classification. Contributed talk at the Intl Conference on Machine Learning 2020, Computational Biology workshop. Awarded as a top-reviewed paper.
4. **Kimmel JC**[†], et. al. Differentiation reveals latent features of aging and an energy barrier in murine myogenesis. Selected talk at Cold Spring Harbor Mechanisms of Aging 2020.
5. **Kimmel JC**, et. al. Cell type and tissue-specific aging trajectories. Invited talk at California QB3 Institute's *Aging and the Single Cell* event. San Francisco, CA. 2019.

SCIENTIFIC SERVICE

- **Mentorship:** Mentor for Stanford CS273B Deep Learning in Biomedicine (2019), Calico internship mentor
- **Peer Reviewer:** *Bioinformatics*, *eLife*, *EMBO Review Commons*, *Genome Research*, *IEEE Biomed.* & *Health Informatics*, *Nature Medicine*, *Nature Methods*, *PLoS Computational Biology*, *PNAS*
- **Open Source:** statsmodels, CellBender, scnym[†], heteromotility[†], velodyn[†]. [†]Maintainer.

SELECTED HONORS & AWARDS

- Performance Recognition (performance-based spot bonus), Calico Life Sciences, 2020 & 2021
- Contributor Award for top submission, *ICML Computational Biology*, 2020
- Nvidia, Most Innovative Use of Deep Learning in Biomedicine, 2018
- National Science Foundation, Graduate Research Fellowship, 2017
- PhRMA Foundation Informatics Fellowship, 2017
- UCSF Discovery Fellowship, 2017
- National Institutes of Health T32 Appointee, \$82,000/2 years, 2015