Jacob C. Kimmel

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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

Calico Life Sciences — South San Francisco, CA
Computational Fellow — *March 2020 - Present*

- Leading a research program focused on repurposing developmental programs to address aging
- Lead the development of a computational & experimental platform for pooled screening of cell reprogramming strategies, successfully completing a company-wide goal
- 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
- Recruited & managed PhD-level intern, mentored Data Scientists, selected for Leadership Development

Calico Life Sciences — South San Francisco, CA
Data Scientist, Computing — *May 2018 - February 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 an analysis platform for pooled genomics screens, guided target ID & biomarker development
- Developed timelapse image analysis methods for oncology applications, enabling multi-day cell tracking

University of California, San Francisco — San Francisco, CA
PhD Candidate; Thesis: Inferring cell state from cell behavior; Advisor: Wallace Marshall — Sept. 2015 - Apr. 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 — *Sept. 2017 - Dec. 2017*

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

Skills

- **Data Analysis**: Experimental design, linear modeling, time series analysis, multivariate statistics
- **Machine Learning**: Neural networks, semi-supervised learning, adversarial learning, PyTorch, Tensorflow
- **Programming**: Python (scipy, scikit-learn, statsmodels), R, Matlab, git, bash, LaTeX
- **NGS**: Single cell and bulk RNA-seq analysis, variant calling, samtools, IGV
- **Image Analysis**: Image segmentation, classification, particle tracking
- **Experimental Biology**: Single cell RNA-seq, primary cell culture, molecular biology, automated microscopy

Selected Publications

Author Links: `Google Scholar`, `PubMed`, `bioRxiv`

1. **Kimmel JC**, Kelley DR. scNym: Semi-supervised adversarial neural networks for single cell classification. 2020. doi: https://doi.org/10.1101/2020.06.04.132324. Accepted at *Genome Research*.
2. **Kimmel JC**, Hendrickson DG, Kelley DR. Differentiation reveals the plasticity of age-related change in murine muscle progenitors. 2020. *bioRxiv*. doi: 10.1101/2020.03.05.979112. In revision at *Cell Reports*.

3. **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. **Chosen as a Research Highlight** by *Development*: Muscling in on Stem Cell Aging.

4. **Kimmel JC**. Disentangling latent representations of single cell RNA-seq experiments. 2020. *bioRxiv.* doi: 10.1101/2020.03.04.972166.

5. Deuker M, Lewis Hardell KL, Ingaramo M, **Kimmel JC**, Buffenstein R, Settleman J. Unprovoked Stabilization and Nuclear Accumulation of the Naked Mole-Rat p53 Protein. 2020. *Scientific Reports.*

6. **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.***

7. **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. Preprint featured in *Company of Biologists: the Node*.

8. **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**, Kelley DR. scNym: Semi-supervised adversarial neural networks for single cell classification. Contributed talk at the International Conference on Machine Learning (ICML) 2020, Workshop on Computational Biology. Awarded: Contributor Award for best reviewed papers.

2. **Kimmel JC**, Hendrickson DG, Kelley DR. Differentiation reveals latent features of aging and an energy barrier in murine myogenesis. Selected talk at Cold Spring Harbor Mechanisms of Aging 2020.

3. **Kimmel JC**, Kelley DR. scNym: Semi-supervised adversarial neural networks for single cell classification. Selected talk at Intelligent Systems for Molecular Biology (ISMB) 2020, Machine Learning in Computational & Systems Biology session.

4. **Kimmel JC**, Penland L, Rubinstein ND, Hendrickson DG, Kelley DR, Rosenthal AZ. Cell type and tissue-specific aging trajectories. Invited talk at California QB3 Institute's *Aging and the Single Cell* event. San Francisco, CA. 2019.

5. **Kimmel JC**, Penland L, Rubinstein ND, Hendrickson DG, Kelley DR, Rosenthal AZ. Cell type and tissue-specific aging trajectories. Invited talk at Mission Bay Capital Biolabs. San Francisco, CA. 2019.

6. **Kimmel JC**, Hwang A, Brack AS, Marshall WF. Inferring cell state dynamics with machine learning. Invited talk at the *Machine Learning in Cell Biology* session at ASCB-EMBO. San Diego, CA. 2018.

7. **Kimmel JC**, Brack AS, Marshall WF. Deep neural networks for cell motility analysis. Nvidia Deep Learning in Biomedicine Workshop. San Francisco, CA. 2018. Awarded: Nvidia Most Innovative.

Scientific Service

- **Peer Reviewer:** *Bioinformatics, eLife, IEEE Journal of Biomedical & Health Informatics, Nature Medicine, PLoS Computational Biology, Proc. of the National Academy of Sciences*
- **Open Source:** `statsmodels`, `gseapy`, `CellBender`, `scnym`[†], `heteromotility`[†], `velodyn`[†]. [†]Maintainer.
- **Experimental Oversight:** Reviewed all pre-clinical *in vivo* work at Calico as an Animal Committee member.

Selected Honors & Awards

- Contributor Award for top submission, *ICML Computational Biology*, 2020
- Selected as an *eLife* Early Career Reviewer, 2020
- Nvidia Most Innovative Use of Deep Learning in Biomedicine, *Nvidia Deep Learning in Biomedicine*, 2018
- National Science Foundation, Graduate Research Fellowship, $138,000/3 years, 2017
- PhRMA Foundation Informatics Fellowship, $40,000/2 years, 2017
- UCSF Discovery Fellowship, 2017
- Nvidia GPU Grant, 2017 & 2018
- National Institutes of Health T32 Appointee, $82,000/2 years, 2015