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, UCSF Discovery — *Sept. 2015 – Apr. 2018*
- **B.S. (Honors) - University of Central Florida** — Orlando, FL
  Biotechnology; GPA: 4.0/4.0; National Merit Scholar: Full Tuition & Stipend Scholarship — *Aug. 2012 – Apr. 2015*

EXPERIENCE

Calico Life Sciences — South San Francisco, CA
Computational Fellow — *March 2020 - Present*
- Leading a research program focused on programming cell identity to address age-related diseases
- Developed `scNym` semi-supervised adversarial neural networks for classifying cell types in single cell genomics, improving the state-of-the-art – scnym.research.calicolabs.com

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 that revealed a decision point where old stem cells fail to differentiate – myo.research.calicolabs.com
- Developed an analysis platform for pooled functional genomics screens, leveraged pooled functional genomics screens to guide early stage discovery
- 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 of cell states from cell motility measurements and prediction of cell motility 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. 2018*
- 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 acquisition

University of Central Florida — Orlando, FL
Research and Mentoring Program Scholar; Principal Investigator: Kiminobu Sugaya — *Aug. 2012 - Apr. 2015*
- Characterized induced pluripotent reprogramming from mesenchymal cells using image classification models
- Applied polarized optical torques to guide cell motility in primary neuronal cell populations

University of California, San Francisco — San Francisco, CA
Amgen Scholar; Principal Investigator: K. Mark Ansel — *May. 2014 - Aug. 2014*
- Investigated the role of microRNA-29 in the regulation of cytokine production in T-cells

National Institute on Aging — Baltimore, MD
Summer Fellow; Image Informatics and Computational Biology Unit — *May 2012 - Aug. 2012*
- Identified differential aging rates across the anatomy of C. elegans using image classification models

SKILLS

- **Data Analysis**: Experimental design, linear modeling, time series analysis, multivariate statistics
- **Machine Learning**: Neural networks, 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

1. **Kimmel JC**, Kelley DR. scNym: Semi-supervised adversarial neural networks for single cell classification. 2020. *bioRxiv*. doi: https://doi.org/10.1101/2020.06.04.132324.
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.
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. A murine aging cell atlas 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*.
9. Constant C, **Kimmel JC**, Sugaya K, Dogariu A. Optically controlled subcellular diffusion. 2015. *Frontiers in Optics & Laser Science*. doi: 10.1364/FIO.2015.FW5E.7.

Selected Presentations

1. **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.
2. **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.
3. **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.
4. **Kimmel JC**, Hwang A, Brack AS, Marshall WF. Inferring cell state dynamics with machine learning models. Invited talk at the *Machine Learning in Cell Biology* session at ASCB-EMBO 2018. San Diego, CA. 2018.
5. **Kimmel JC**, Brack AS, Marshall WF. Deep neural networks for cell motility analysis. Presentation to Nvidia Deep Learning in Biomedicine Workshop. San Francisco, CA. 2018. Awarded: Nvidia Most Innovative Use of Deep Learning in Biomedicine.

Service

- **Peer Reviewer:** *Bioinformatics*, *IEEE Journal of Biomedical & Health Informatics*, *Nature Medicine*, *PLoS Computational Biology*, *Proc. of the National Academy of Sciences*

Selected Honors & Awards

- 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, 2015