

# Jacob C. Kimmel

San Francisco, CA – jkimmel.net

jacob@jkimmel.net

(321)-536-1919

## 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; Full Tuition & Stipend Scholarship* Aug. 2012 – Apr. 2015
- **Marine Biological Laboratory** Woods Hole, MA  
*Computational Image Analysis in Cell and Developmental Biology; Fully-funded* Fall 2016

## 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

**Calico Life Sciences** South San Francisco, CA  
*Data Scientist, Computing* May 2018 - February 2020

- Developed an analysis platform for pooled functional genomics screens, leveraged pooled functional genomics screens to guide early stage discovery
- Lead an investigation of cell type and tissue environment influences on aging using single cell genomics across three murine tissues
- Developed timelapse image analysis methods for oncology applications, enabling multi-day cell tracking
- Automated quantification of yeast cell aging using convolutional neural networks
- Developed scNym deep neural networks for cell type classification from single cell genomics data

**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 the **Heteromotility** biological motion analysis package, including feature extraction, unsupervised clustering, and time-series analysis to quantify dynamic state transitions in cellular systems
- Quantified rates of muscle stem cell activation in single cells for the first time using **Heteromotility**
- 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**
- Developed a single cell assay of muscle stem cell age using single cell RNA-seq and machine learning

**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
- Investigated direct reprogramming mesenchymal cells to neuronal fates

**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
- Investigated the relationship between cognitive and age-related morphologies in the primate hippocampus

## SKILLS

---

- **Data Analysis:** Experimental design, linear modeling, time series analysis, multivariate statistics
- **Machine Learning:** Neural networks, PyTorch, Tensorflow
- **Image Analysis:** Image segmentation, classification, particle tracking
- **NGS:** Single cell and bulk RNA-seq analysis, variant calling, samtools, IGV
- **Programming:** Python (scipy, scikit-learn, statsmodels), R, Matlab, git, bash, L<sup>A</sup>T<sub>E</sub>X
- **Experimental Biology:** Microscopy, single cell RNA-seq, primary cell culture, FACS, molecular biology

## SELECTED PUBLICATIONS

---

1. **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.
2. **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. Featured in *Company of Biologists: the Node*.
3. **Kimmel JC**. Disentangling latent representations of single cell RNA-seq experiments. 2020. *bioRxiv*. doi: 10.1101/2020.03.04.972166.
4. **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*.
5. **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*.
6. **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. Featured in *PLoS Editor's Collections*.

## SELECTED PRESENTATIONS

---

1. **Kimmel JC**, Penland L, Rubinstein ND, Hendrickson DG, Kelley DR, Rosenthal AZ. Cell type and tissue-specific aging trajectories. Invited speaker for California QB3 Institute's *Aging and the Single Cell* event. San Francisco, CA. 2019.
2. **Kimmel JC**, Penland L, Rubinstein ND, Hendrickson DG, Kelley DR, Rosenthal AZ. Cell type and tissue-specific aging trajectories. Invited speaker at Mission Bay Capital Biolabs. San Francisco, CA. 2019.
3. **Kimmel JC**, Hwang A, Brack AS, Marshall WF. Inferring cell state dynamics with machine learning models. Invited speaker at the *Machine Learning in Cell Biology* session at ASCB-EMBO 2018. San Diego, CA. 2018.
4. **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. *Nvidia Most Innovative Use of Deep Learning in Biomedicine Award*.

## 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 Best Presentation Award, *Nvidia Deep Learning in Biomedicine*, 2018
- NSF 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
- National Merit Scholar, National Merit Scholarship Corp., 2012