# Jacob C. Kimmel

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## EDUCATION

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

**University of Central Florida** — Orlando, FL
*B.S. (Honors) - Biotechnology; GPA: 4.0/4.0* — *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
*Data Scientist, Computing* — *May 2018 - Present*

- 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
- Built an automated targeting system for laser ablation microscopy with sub-millisecond timing
- 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 (CNN) based image segmentation methods for processing of high-throughput timelapse imaging data
- Implemented a Natural Evolution Strategies (NES) optimization framework to improve multi-cell tracking
- Implemented a software interface to custom microscopy hardware, allowing for automation of high-throughput timelapse imaging experiments

**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 by modulation of Nanog

**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**: Supervised discrimination, unsupervised clustering, feature engineering
- **Deep Learning**: Deep convolutional and recurrent neural networks, PyTorch, Tensorflow
- **Image Analysis**: Image segmentation, classification, particle tracking
- **NGS**: Single cell and bulk RNA-seq analysis, samtools, IGV
- **Programming**: Python (scipy, scikit-learn, statsmodels), R, Matlab, git, bash, LaTeX
- **Experimental Biology**: Microscopy, single cell RNA-seq, primary cell culture, FACS, molecular biology

## Selected Publications

1. **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. bioRxiv. doi: 10.1101/657726. Featured in *Company of Biologists: the Node*.
2. **Kimmel JC**, Hwang AB, Marshall WF, Brack AS. Aging induces aberrant state transition kinetics in murine muscle stem cells 2019. bioRxiv. doi: 10.1101/739185.
3. **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*.
4. **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*.
5. 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**, Penland L, Rubinstein ND, Hendrickson DG, Kelley DR, Rosenthal AZ. Cell type and tissue-specific aging trajectories. Invited presentation to California QB3 Institute at *Aging and the Single Cell*. San Francisco, CA. 2019.
2. **Kimmel JC**, Hwang A, Brack AS, Marshall WF. Inferring cell state dynamics with machine learning models. Invited oral presentation to the *Machine Learning in Cell Biology* session at ASCB-EMBO 2018. San Diego, CA. 2018.
3. **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*.
4. **Kimmel JC**, Chang AY, Brack AS, Marshall WF. Inferring cell state from cell motility behavior. Selected oral presentation to the NSF Quantitative Cell Biology Network Workshop. Allen Institute for Cell Science, Seattle, WA. 2016.

## Service

- **Peer Reviewer:** *Bioinformatics*, *IEEE Journal of Biomedical & Health Informatics*, *Nature Medicine*, *PLoS Computational Biology*

## 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
- NIH T32 Appointee, 2015
- National Merit Scholarship, U. of Central Florida, (Full Tuition & Stipend), 2012-2015

## References

Wallace F. Marshall      `Wallace.Marshall@ucsf.edu`
Professor      UC San Francisco

Andrew S. Brack      `Andrew.Brack@ucsf.edu`
Associate Professor      UC San Francisco

Todd Nystul      `Todd.Nystul@ucsf.edu`
Professor      UC San Francisco

Orion Weiner      `Orion.Weiner@ucsf.edu`
Professor      UC San Francisco

Andrew G. York      `agy@calicolabs.com`
Principal Investigator      Calico Life Sciences

David R. Kelley      `drk@calicolabs.com`
Principal Investigator      Calico Life Sciences

Eric Verdin      `eric.verdin@buckinstitute.org`
President & CEO      The Buck Institute