Jacob C. Kimmel

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Profile

Computational biologist with extensive experience in data analysis, machine learning, and image analysis.
Deep biological domain knowledge, from molecules to mouse trials.
Passionate about finding value in overlooked places.

Experience

PhD Candidate, University of California San Francisco, San Francisco, CA, 2015 - Present
Dept. of Biochemistry and Biophysics
Thesis: Inferring stem cell state from cell behavior by quantitative image analysis

- Developed Heteromotility biological motion analysis package, including feature extraction, unsupervised clustering, and time-series analysis tools to quantify dynamic state transitions in cellular systems
- Quantified rates of muscle stem cell differentiation with single cell resolution for the first time using Heteromotility
- Developed Lanternfish deep learning package to enable the analysis of biological motion using convolutional neural networks for the first time
- Demonstrated classification of stem cell differentiation states and cancerous transformation detection using Lanternfish

Summer Intern, National Institute on Aging, Baltimore, MD, 2012 Summer
Image Informatics and Computational Biology Unit

- Identified that tissues age at different rates across the anatomy of C. elegans with machine learning image classifiers
- Investigated the relationship between cognitive and age related morphologies in the primate hippocampus with machine learning image classifiers

Burnett Research Scholar, University of Central Florida, Orlando, FL, 2011 - 2015

- Utilized machine-learning image classifiers to characterize the timing of induced pluripotent reprogramming – the process of generating new embryonic-like stem cells from normal adult cells
- Developed a data processing pipeline for mouse behavioral testing data
- Examined the use of polarized optical torques to guide cell motility in collaboration with U. of Central Florida's optics research center

Amgen Scholar (Summer), University of California San Francisco, San Francisco, CA, 2014

- Implemented quantitative PCR normalization algorithms to enable robust analysis of gene expression
- Investigated the role of microRNA-29 in the regulation of cytokine production in T-cells

Skills

Data Analysis: Experimental design, hypothesis testing, time series analysis, multivariate statistics
Machine Learning: Supervised, unsupervised, feature engineering, distributed computing (MPI, SGE)
Deep Learning: Convolutional neural networks, Tensorflow, Theano, Keras
Image Analysis: Image segmentation, classification, object detection, particle tracking
Programming: Python (scipy stack, pandas, scikit-learn), Matlab, R, git, shell scipt, LaTeX

Education

Ph.D. — Dept. of Biochemistry & Biophysics, UC San Francisco, 2015 - Present
Funding: NSF Graduate Fellowship, PhRMA Informatics Fellowship, NIH T32 Awardee
GPA: 4.0 / 4.0

B.S. — Biotechnology, University of Central Florida, 2012 - 2015
Distinctions: Summa Cum Laude, Top Honors, University Honors
GPA: 4.0 / 4.0

Selected Publications & Presentations

1. Deep convolutional neural networks allow analysis of cell motility during stem cell differentiation and neoplastic transformation. **Jacob C. Kimmel**, Andrew S. Brack, and Wallace F. Marshall. 2017. bioRxiv. doi: https://doi.org/10.1101/159202. *(Submitted for publication)*.
2. Inferring cell state by quantitative motility analysis reveals a dynamic state system and broken detailed balance. **Jacob C. Kimmel**, Amy Y. Chang, Andrew S. Brack, Wallace F. Marshall. 2017. bioRxiv 168534; doi: https://doi.org/10.1101/168534. *(Submitted for publication)*.
3. Inferring cell state from cell motility behavior. **Jacob C. Kimmel**, Amy Y. Chang, Andrew S. Brack, Wallace F. Marshall. Selected oral presentation to the NSF Quantitative Cell Biology Network Workshop. Allen Institute for Cell Science, Seattle, WA. 2016.
4. Characterization of induced pluripotent reprogramming in mesenchymal stem cells by quantitative image analysis. **Jacob C. Kimmel**, B. Yuan, C. Constant, D. Dogariu, H. Foroosh, K. Sugaya. U. of Central Florida, Showcase of Research Excellence. 2014.
5. Do different tissues age at different rates? Machine-learning based characterization of aging rates in C. elegans and rhesus macques. **Jacob C. Kimmel**, D. Mark Eckley, Chris Colleta, John Long, Nikita Orlov, Peter Rapp, Ilya G. Goldberg. National Institute on Aging, Baltimore, MD. 2012.

Honors and Awards

- National Science Foundation Graduate Research Fellowship, 2017
- PhRMA Informatics Fellowship, PhRMA Foundation, 2017
- Amgen Scholar, University of California San Francisco, 2014
- Burnett Research Scholar, U. of Central Florida, 2013
- Florida Academic Scholar, State of Florida, 2012-2015
- National Merit Scholar, 2012

Outreach & Volunteering

Science Education Partnership, UCSF/SFUSD, 2016 - 2017

- Partnered with San Francisco public school teachers to design and implement science lessons for elementary school students

Bay Area Maker Faire Exposition, 2016 - Present

- Bay Area festival to present creative science and technology to the public, 100,000+ attendees
- Presented an exhibit demonstrating adaptive cellular responses to engage the public with life science research