
RESEARCH INTERESTS

- Understanding gene regulation dynamics through the study of epigenetic modifications, mainly DNA methylation.
 - Understanding contributors to cancer relapse following immunotherapy and how alternative immunotherapies can slow or prevent relapse.
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EDUCATION

University of California, Los Angeles, Los Angeles, California

Ph.D., Human Genetics

August 2016 - Spring 2021

- Advisor: Professor Matteo Pellegrini
- Thesis Topic: *Assessing human health using DNA methylation based predictive models*
- Thesis Committee: Matteo Pellegrini, Xia Yang, Jae-Hoon Sul, Aldons J. Lysis
- Supported by NIH T32 CA201160-01 Biomedical Big Data (2019 - 2020)

University of Utah, Salt Lake City, Utah

M.P.H., Public Health

August 2011 - June 2013

- Advisors: Professors Lisa Gren and David Sundwall
- Practicum: *Disconcerting headache practice patterns in academic primary care.*
- Phi Eta Honor Society

University of Utah, Salt Lake City, Utah

B.S., Chemistry

August 2006 - December 2010

- Delta Omega Honorary Society
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EXPERIENCE

University of California, Los Angeles

Graduate Student Researcher, Pellegrini Lab

August 2016 – Present

- Designed an integrated measure of type two diabetes and built a DNA methylation-based predictive model for this measure
- Built a high performance bisulfite sequencing processing platform written in C, C++, and Python
- Developed a novel statistical model of epigenetic aging to model non-linear epigenetic aging and open-sourced the model as a Python package
- Built an analysis pipeline to assess inactivation of CAR T-cell therapy vectors following product infusion using DNA methylation and vector integration locations
- Designed a targeted bisulfite sequencing method and implemented an optimized analysis pipeline
- Collaborated with researches, clinicians, and support staff to implement research projects and meet project goals
- Managed several parallel research projects, completing simultaneous tasks and delegating appropriate tasks to assistants
- Carried out large scale data processing on high performance computing clusters and AWS
- Instituted lab-wide version control best practice to ease collaboration and foster reproducibility

University of Utah School of Medicine

Lab Specialist, Phillips Lab

February 2014 – Present

- Analyzed sequencing data to identify causative genetic variants in clinical cases diagnosed with iron homeostasis and heme synthesis disorders
- Integrated PacBio, Oxford Nanopore, and Illumina sequencing data to assemble a high quality reference genome for the Babraham pig breed with intact T-Cell Receptor loci for vaccine development
- Performed CRISPR KO analysis to identify ligands targeted by a ubiquitous cancer killing T-Cell line

OPEN SOURCE SOFTWARE TOOLS

BSBolt (Python, C, C++): High performance bisulfite sequencing processing platform; bsbolt.readthedocs.io

Epigenetic Pacemaker (Python): Evolutionary model of epigenetic aging; epigeneticpacemaker.readthedocs.io

COMPUTER SKILLS

- Languages
 - Proficient in Python
 - Competent in C, C++, R, Bash
 - Unit Testing
 - System Administration: Linux/UNIX, MacOS
 - Tools: Git, Jupyter, SGE, AWS, SLURM, Anaconda, Vim
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TEACHING

Research Immersion Laboratory in Genomic Biology at UCLA (Spring 2018, Spring 2019) Instructed laboratory class for upper division molecular biology students at UCLA. In the laboratory class I introduced bioinformatics tools and workflows utilized by the class to perform a quarter long genome annotation project. (Reviews available upon request)

MENTORING

- **Huling Huang (Bruins In Genomics Undergraduate Researcher, summer 2018):** Modeled non-linear epigenetic aging trends in publicly available datasets and compared epigenetic aging trends across distinct populations.
 - **Maria Malikwa (Santa Monica College Summer Scholars, summer 2018):** Designed a DNA methylation based predictor of folic acid levels in pregnant women.
 - **Ibrahim Wone (Santa Monica College Summer Scholars, summer 2019):** Built a non-linear DNA methylation based predictive model for type two diabetes progression.
 - **Adewale Oyetunde (UCLA-CSUN Stem Cell Bridges Program, August 2018 - August 2019):** Modeled methylation dynamics during cellular differentiation and how the DNA methylation landscape is altered by induced pluripotency.
 - **Kalsuda Lapborisuth (UCLA Undergraduate Research Fellow, August 2018 - Present):** Developing a simulation framework for modeling epigenetic age acceleration in response to physiological stress and is validating the framework using publicly available methylation datasets.
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PUBLICATIONS

- **Farrell, C., Thompson, M., Tosevska, A., Oyetunde, A. & Pellegrini, M. BiSulfite Bolt: A BiSulfite Sequencing Analysis Platform.** *GigaScience* (2021, accepted).
- **Li, S., Ma, F., Yokota, T., Jr., G. G., Palermo, A., Wang, Y., Farrell, C., Wang, Y.-C., Wu, R., Zhou, Z., Pan, C., Morselli, M., Teitell, M. A., Ryazantsev, S., Fishbein, G. A., ten Hoeve, J., Arboleda, V. A., Bloom, J., Dillon, B., Pellegrini, M., Lusi, A. J., Graeber, T. G., Arumugaswami, V. & Deb, A. Metabolic reprogramming and epigenetic changes of vital organs in SARS-CoV-2-induced systemic toxicity.** *JCI Insight* 6, (2021).

- **Farrell, C., Snir, S. & Pellegrini, M. The Epigenetic Pacemaker: modeling epigenetic states under an evolutionary framework.** *Bioinformatics* **36**, 4662–4663 (2020).
- Nowicki, T. S., **Farrell, C.**, Morselli, M., Rubbi, L., Campbell, K. M., Macabali, M. H., Berent-Maoz, B., Comin-Anduix, B., Pellegrini, M. & Ribas, A. **Epigenetic Suppression of Transgenic T-cell Receptor Expression via Gamma-Retroviral Vector Methylation in Adoptive Cell Transfer Therapy.** *Cancer Discov.* (2020). doi:10.1158/2159-8290.CD-20-0300
- Morselli, M., **Farrell, C.**, Rubbi, L., Fehling, H. L., Henkhaus, R. & Pellegrini, M. **Targeted bisulfite sequencing for biomarker discovery.** *Methods* (2020). doi:10.1016/j.ymeth.2020.07.006
- Wu, R., Ma, F., Tosevska, A., **Farrell, C.**, Pellegrini, M. & Deb, A. **Cardiac fibroblast proliferation rates and collagen expression mature early and are unaltered with advancing age.** *JCI Insight* **5**, (2020).
- Levine, M., McDevitt, R. A., Meer, M., Perdue, K., Di Francesco, A., Meade, T., **Farrell, C.**, Thrush, K., Wang, M., Dunn, C., Pellegrini, M., de Cabo, R. & Ferrucci, L. **A rat epigenetic clock recapitulates phenotypic aging and co-localizes with heterochromatin.** *Elife* **9**, (2020).
- Crowther, M. D., Dolton, G., Legut, M., Caillaud, M. E., Lloyd, A., Attaf, M., Galloway, S. A. E., Rius, C., **Farrell, C. P.**, Szomolay, B., Ager, A., Parker, A. L., Fuller, A., Donia, M., McCluskey, J., Rossjohn, J., Svane, I. M., Phillips, J. D. & Sewell, A. K. **Genome-wide CRISPR-Cas9 screening reveals ubiquitous T cell cancer targeting via the monomorphic MHC class I-related protein MR1.** *Nat. Immunol.* **21**, 178–185 (2020).
- Snir, S., **Farrell, C.** & Pellegrini, M. **Human epigenetic ageing is logarithmic with time across the entire lifespan.** *Epigenetics* **14**, 912–926 (2019).
- Phillips, J., **Farrell, C.**, Wang, Y., Singal, A. K., Anderson, K., Balwani, M., Bissell, M., Bonkovsky, H., Seay, T., Paw, B., Desnick, R. & Bloomer, J. **Strong correlation of ferrochelatase enzymatic activity with Mitoferrin-1 mRNA in lymphoblasts of patients with protoporphyria.** *Mol. Genet. Metab.* **128**, 391–395 (2019).
- Orozco, L. D., **Farrell, C.**, Hale, C., Rubbi, L., Rinaldi, A., Civelek, M., Pan, C., Lam, L., Montoya, D., Edillor, C., Seldin, M., Boehnke, M., Mohlke, K. L., Jacobsen, S., Kuusisto, J., Laakso, M., Lusi, A. J. & Pellegrini, M. **Epigenome-wide association in adipose tissue from the METSIM cohort.** *Human Molecular Genetics* **27**, 1830–1846 (2018).
- Yaish, H. M., **Farrell, C. P.**, Christensen, R. D., MacQueen, B. C., Jackson, L. K., Trochez-Enciso, J., Kaplan, J., Ward, D. M., Salah, W. K. & Phillips, J. D. **Two novel mutations in TMPRSS6 associated with iron-refractory iron deficiency anemia in a mother and child.** *Blood Cells Mol. Dis.* **65**, 38–40 (2017).
- **Farrell, C. P.**, Overbey, J. R., Naik, H., Nance, D., McLaren, G. D., McLaren, C. E., Zhou, L., Desnick, R. J., Parker, C. J. & Phillips, J. D. **The D519G Polymorphism of Glyceronephosphate O-Acyltransferase Is a Risk Factor for Familial Porphyria Cutanea Tarda.** *PLoS One* **11**, e0163322 (2016).
- **Farrell, C. P.**, Parker, C. J. & Phillips, J. D. **Exome sequencing for molecular characterization of non-HFE hereditary hemochromatosis.** *Blood Cells Mol. Dis.* **55**, 101–103 (2015).