Colin Farrell

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Research Interests

- Understanding gene regulation dynamics through the study of epigenetic modifications, mainly DNA methylation.

- Explore the physiological response to cancer immunotherapies to understand contributors to disease relapse and how alternative immunotherapies can slow, or prevent, relapse.

Education

University of California, Los Angeles, Los Angeles, California
Ph.D., Human Genetics   **August 2016 - Spring 2021**
- Advisor: Prof. Matteo Pellegrini
- Thesis Topic: *Assessing human health using DNA methylation based predictive models*
- Thesis Committee: Matteo Pellegrini, Xia Yang, Jae-Hoon Sul, Aldons J. Lusis
- Supported by NIH T32 CA201160-01 Biomedical Big Data (2018 - 2019)

University of Utah, Salt Lake City, Utah
M.P.H., Public Health   **August 2011 - June 2013**
- Advisors: Prof. Lisa Gren, Prof. 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

Experience

University of California, Los Angeles

Graduate Student Researcher, Pellegrini Lab   **August 2016 – Current**

- Designed an integrated measure of type two diabetes and fit a DNA methylation based predictive model to 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 analysis pipeline to assess inactivation of CAR T-cell therapy vectors following product infusion using accumulation of DNA methylation levels and vector integration location
- Designed targeted bisulfite sequencing capture library and implemented optimized analysis pipeline
- Actively worked 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 subordinates
- Implement analysis pipelines for use on high performance computing clusters
- 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 – Current**

- 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
  - Fluent - Python
  - Competent - C, C++, Rust, R, Bash
- Unit Testing
- System Administration Linux/UNIX, MacOS
- Tools - Git, Jupyter, SGE, AWS, SLURM, Anaconda, Vim

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 workflow utilized to perform a quarter long genome annotation project. (Review 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.
- **Ibrahime Wone (Santa Monica College Summer Scholars, Summer 2019)** built a non-linear DNA methylation based predictive model for type two diabetes progression.
- **Adewale Oytetunde (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)** working towards developing a simulation framework for modeling epigenetic age acceleration in response to physiological stress and is validating the framework using publicly available methylation datasets.

Publications

- **Farrell, C**., Thompson, M., Tosevska, A., Oyetunde, A. & Pellegrini, M. BiSulfite Bolt: A BiSulfite Sequencing Analysis Platform. 2020.10.06.328559 (2020). doi:10.1101/2020.10.06.328559
- 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., Lusis, 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., Lusis, 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).