Jonathan Perrie

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Education

PhD, Bioinformatics | UCLA (2020–2025)

Dissertation (embargoed): *Granuloma gradients*

- Supervised by Matteo Pellegrini and in all but name Robert Modlin
- https://escholarship.org/uc/item/3bf2h046

MMath, Computer Science | UWaterloo (2016–2019)

Thesis: *Modelling chart trajectories using song features*

- Supervised by Dan Brown and Peter van Beek
- http://hdl.handle.net/10012/14937

BSc (Honours), Computer Science & Statistics | Dalhousie (2012–2016)

- Supervised by Robert Beiko, mentored by Michael Hall

Experience

Grad student, Pellegrini Lab | UCLA (2022–2025)

- Analyzed large spatial sequencing data sets (GeoMx, CosMx transcriptomic, proteomic) to map immune architecture in pulmonary tuberculosis
- Characterized macrophage identity gradients (TREM2–SPP1) underlying foamy macrophage propagation and granuloma formation
- Built reproducible workflows for QC, enrichment, spatial visualization, and cross-modality comparison

Pre-grad intern, Laboratory of Epigenome Biology | NHLBI (2018–2020)

- Benchmarked single-cell epigenomic assays based on how they separate out PBMC subtypes
- Ran pipelines for sequence alignment, QC, and data visualizations

Grad student | UWaterloo (2016–2019)

- Modeled song chart trajectories using time-series and clustering methods
- Integrated audio and lyric features to profile song features

Research assistant, Beiko Lab | Dalhousie (2015–2016)

- Developed heuristics and sub-clustering approaches for profiling metagenomic time series data

Teaching

MCD BIO 187 Research Immersion Laboratory in Genomic Biology | UCLA (2024, 2025)
C&S BIO 185 Thesis Research Opportunities in Computational and Systems Biology | UCLA (2022)
BIOF 045 Bioinformatic Analysis of NGS Data | FAES-NIH (2020, 2021)
CS 492 Social Implications of Computing | UWaterloo (2018)
CS 486 Introduction to Artificial Intelligence | UWaterloo (2017)
CS 330 Management Information Systems | UWaterloo (2016, 2017)
CS 1100 Computer Science I | Dalhousie (2015)

Technical

Languages: Python, R, Bash • **Sequencing:** spatial transcriptomics (GeoMx, CosMx), scRNA-seq, bulk RNA-seq, single-cell epigenomics (scATAC-seq, scDNase-seq), CellScape • **Data science:** regression, classification, feature engineering, time series analysis • **Libraries:** Scanpy, scikit-learn, matplotlib, ggplot2 • **Other:** Git, Jupyter