

Eamon O'Connor

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[Github \(Code Samples\)](#) | [Portfolio \(Result Samples\)](#) | [LinkedIn](#)

San Francisco, CA

EDUCATION

Northeastern University, Boston, Massachusetts

M.S. in Bioinformatics, May 2025

GPA 3.893

Relevant Coursework: Bioinformatics Programming, Unsupervised Machine Learning, Molecular Modeling

B.S. in Biology, Minor in Philosophy, June 2024

GPA 3.889

Relevant Coursework: Biostatistics, Calculus 2 & 3, Differential Equations & Linear Algebra

SKILLS

Programming Languages: R, Python, SQL, Bash

Statistics: Hypothesis testing, Experimental design, ANOVA, Regression analysis, Data visualization (ggplot2, Matplotlib)

Tools & Software: AWS HPC, Git, Docker, Nextflow, Linux, Bioconductor, FastQC, Bowtie, STAR, Samtools, DESeq2

Databases: NCBI, Ensembl, UCSC Genome Browser

Machine Learning: Data mining, Clustering (DBScan, K-means), Dimensionality reduction (PCA, tSNE)

Laboratory Techniques: NGS, PCR, Gel electrophoresis, Western blotting, Bacterial transformation, Protein purification

PROFESSIONAL EXPERIENCE

Metaphore Biotechnologies, Cambridge, MA

Computational Biology Co-op

January - June 2025

- Performed differential expression analysis using R to identify receptor-specific agonists for therapeutic candidate selection
 - Collaborated with wet lab scientists to evaluate novel methods for agonist library preparation
- Executed NGS read alignment and quality control workflows with Nextflow pipelines on AWS HPC infrastructure
 - Assessed feasibility of sequencer-integrated pre-processing tools for use by wet lab scientists
- Compared a novel DNA ligation-based Illumina sequencing workflow against PacBio, reducing sequencing time and cost
- Presented findings to computational and wet lab scientists to inform experimental design and research decisions
- Debugged Nextflow pipelines using git-based version control to improve accuracy and efficiency

NGS & Protein Sciences Co-op

July - December 2024

- Prepared NGS libraries for Illumina and PacBio sequencers
- Synthesized and purified protein samples based on in-house experimental designs for translational research
- Analyzed protein samples using gel electrophoresis and western blots to assess purity and molecular weight
- Performed Bio-Layer Interferometry (BLI) to quantify protein concentration
- Conducted kinetics assays to evaluate binding performance and interaction strength

Metrovet Veterinary Clinic, Boston, MA

Veterinary Assistant Co-op

July - December 2023

- Recorded detailed clinical data from surgeries and medical exams for case analysis
- Processed and interpreted in-house diagnostic tests to enable data-informed treatment plans

RESEARCH & PROJECTS

Microbiome-Disease Correlation Analysis

September - December 2024

Developed a Python program to analyze the correlation between gut microbiome composition and disease phenotypes

- Integrated APIs for automated data retrieval from Ensembl and GMrepo
- Normalized data and applied Welch's t-test to assess difference in bacterial abundance between disease and healthy groups
- Found significant negative correlation between Depression and relative abundance of Bifidobacterium in the gut

SLE-RA Immune Heterogeneity

March - May 2024

Reproduced analysis of immune system signaling in systemic lupus erythematosus (SLE) and rheumatoid arthritis (RA)

- Analyzed single-cell RNA sequencing data for immune cell communication using the R packages *Seurat* and *Cellchat*
- Visualized changes in the Migration Inhibitory Factor and Galectin-9 pathways using heatmaps and circle plots
- Identified global changes in signaling activity for both SLE and RA