

Elisabeth Rebboah, Ph.D.
San Diego, CA
erebboah@gmail.com
(858) 722-6370
GitHub: github.com/erebboah

Summary

Scientist specializing in optimizing and developing NGS-based assays, including single-cell barcoding, multiomic, and spatial transcriptomics assays. Proficient in both molecular biology and bioinformatics, with expertise in assay optimization, project management, and data analysis. Experienced in managing projects, presenting results, and collaborating with multidisciplinary teams.

Education

Ph.D. in Mathematical, Computational, and Systems Biology
University of California, Irvine

2024
Irvine, CA

B.S. in Bioengineering
University of California, San Diego

2015
San Diego, CA

Research Experience

Postdoctoral Scholar

Advisor: Ali Mortazavi

May 2024-present

University of California, Irvine, CA

- Conducting integrative analysis of single-cell RNA-seq and multiome assays across barcoding platforms (10x, SHARE-seq, Parse Split-seq); optimizing SHARE-seq multiome assay for our lab
- Developed and implemented a pipeline for single-cell RNA-seq data processing in Python (https://github.com/mortazavilab/parse_pipeline).

Graduate Student Researcher

Advisor: Ali Mortazavi

Jan. 2019-April 2024

University of California, Irvine, CA

- Developed long-read sequencing assay for split-pool barcoding (Split-seq) single-cell RNA-seq.
- Validated cluster marker gene expression with RNA FISH (RNAscope) in a differentiating cell line.
- Modeled regulatory topics using single-nucleus RNA-seq in 5 diverse mouse tissues during postnatal development with Latent Dirichlet Allocation (LDA).
- Led production and analysis teams for over 25 large-scale snRNA-seq experiments, building high-resolution single-nucleus atlases for more than 10 mouse tissues.

Skills

- Optimization of single-nucleus assays and spatial transcriptomics methods (RNAscope, MERSCOPE) in various tissues and cell lines.
- Experienced in automation using liquid handlers for RNA-seq library preparation, operation of sequencing platforms such as Illumina NextSeq 500 and 2000, Oxford Nanopore MinION
- Experienced in cell culture, differentiation, mouse husbandry, and mouse dissection.
- Proficient in R, Python, shell scripting, and Snakemake workflow management.
- Experienced in analysis of both short- and long-read sequencing data (Illumina, PacBio, Oxford Nanopore) using contemporary bioinformatics tools.
- Strong project management, written, and oral communication skills, with experience collaborating in large consortia like ENCODE and IGVF.
- Teaching and training experience with undergraduates and technicians in genomics assays and basic bioinformatics.

Publications

1. **Rebboah, E.**, Weber, R., Liang, H. Y., et al. (2024). Characterizing the impact of genetic diversity on gene expression across adult cell types and states in mice. *In preparation*.
2. Loving, R. K., Sullivan, D. K., Reese, F., **Rebboah, E.**, et al. (2024). Long-read sequencing transcriptome quantification with Ir-kallisto. *bioRxiv*. <https://doi.org/10.1101/2024.07.19.604364>
3. **Rebboah, E.**, Rezaie, N., Williams, B. A., et al. (2024). The ENCODE mouse postnatal developmental time course identifies regulatory programs of cell types and cell states. *bioRxiv*. <https://doi.org/10.1101/2024.06.12.598567>
4. Rezaie, N., **Rebboah, E.**, Williams, B. A., et al. (2024). Identification of robust cellular programs using reproducible LDA that impact sex-specific disease progression in different genotypes of a mouse model of AD. *bioRxiv*. <https://doi.org/10.1101/2024.02.26.582178>
5. Reese, F., Williams, B. A., Balderrama-Gutierrez, G., Wyman, D., Celik, M. H., **Rebboah, E.**, et al. (2023). The ENCODE4 long-read RNA-seq collection reveals distinct classes of transcript structure diversity. *bioRxiv*. <https://doi.org/10.1101/2023.05.15.540865>
6. Balderrama-Gutierrez, G., Liang, H. Y., Rezaie, N., Carvalho, B., Forner, S., Matheos, D., **Rebboah, E.**, et al. (2021). Single-cell and nucleus RNA-seq in a mouse model of AD reveal activation of distinct glial subpopulations in the presence of plaques and tangles. *bioRxiv*. <https://doi.org/10.1101/2021.09.29.462436>
7. **Rebboah, E.**, Reese, F., et al. (2021). Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq. *Genome Biology*, 22(286). <https://doi.org/10.1186/s13059-021-02505-w>
8. Carvalho, B., **Rebboah, E.**, et al. (2021). Uncovering the Gene Regulatory Networks Underlying Macrophage Polarization Through Comparative Analysis of Bulk and Single-Cell Data. *bioRxiv*. <https://doi.org/10.1101/2021.01.20.427499>

Selected Presentations

- 2022 ASHG Annual Meeting: *The ENCODE mouse postnatal developmental time course identifies regulatory signatures of cell type maturation*
- 2024 ASHG Annual Meeting: *Exploring the impact of genetic diversity on cell type- and state-specific gene expression in mice*

Teaching Experience

Teaching Assistant — University of California, Irvine

- | | |
|---|-------------------------|
| • COSMOS (Genes, Genomes, and Skeletal Muscle Dystrophies) | 2021, 2022, 2023 |
| • Intro to Precision Medicine (D132) | 2021, 2022 |
| • COSMOS (Tissue, Tumor Biology, and Mathematical Modeling) | 2019 |