RACHEL BOZADJIAN

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EDUCATION

Boston University Boston, MA
M.S. Bioinformatics Expected May 2025
  GPA: 4.0

University of California Santa Barbara Santa Barbara, CA
B.S. Biopsychology March 2016

SKILLS

Programming: Python, R, Bash, Workflow management (Snakemake, Nextflow), HPC, Git, scikit-learn, SQL
NGS Technologies: DNA-seq, RNA-seq, scRNA-seq
Molecular Biology: DNA Library Prep and NGS, Molecular Cloning, DNA and RNA Extraction

ACADEMIC PROJECTS

Supervised Classifier for Prostate Cancer Severity November 2024
- Built a Boosted Random Forest model with scikit-learn to classify early and late stage prostate tumors based on gene expression data, using labeled pathological T scores
- Identified RNF185, CDNF, and APOBEC3B as the model's most important features and potential biomarkers
- Achieved a 79% model accuracy with 75% precision and 70% recall for early stage cancer, and 81% precision and 85% recall for late stage cancer

Bulk and scRNA-Seq Analysis of Glioblastoma-Associated Endothelial Cells November 2024
- Created an RShiny App to analyze differential gene expression with DESeq2, use unsupervised learning to reduce dimensionality with PCA, and visualized differentially expressed genes with ggplot2
- Calculated and plotted single-cell trajectories using Monocle3 to study gene expression over pseudotime in Glioblastoma

Variant Calling Workflow for Genes Implicated in Alzheimer's Disease May 2024
- Developed a Snakemake-based workflow on the HPC to identify and annotate SNPs with BCFtools and SnpEff
- Visualized SNP counts per individual with Matplotlib for APP, SOD1, and DYRK1A genes on Chromosome 21

WORK EXPERIENCE

Asimov Boston, MA
Supervisors: Dr. Kat Tarasova, Julie Hachey
Associate Scientist I May 2019 - August 2023
- Utilized EGF CUBA Python libraries (Primavera and BandWitch) to automate Sanger Sequencing primer and restriction enzyme selection for ~100 plasmids/week, reducing hands-on time for team
- Created and implemented Python script using Pandas to track metadata for hundreds of plasmid samples, which minimized sample loss and streamlined troubleshooting
- Prepared NGS libraries and sequenced ~700 plasmids per week on MiSeq to quality control plasmids for use in downstream cloning workflow
- Optimized, automated, deployed, and trained team on fluorescence-based DNA quantification assay with Echo acoustic liquid handler resulting in >7-fold increase in concentration measurement throughput

Ocean State Research Institute | Brown University Providence, RI
Principal Investigator: Dr. Alan Morrison
Research Assistant August 2018 - May 2019
- Tested potential miRNA candidates involved in IL1-R signaling pathway with qRT-PCR in bone-marrow-derived macrophages in a mouse aging model

UCSB Neuroscience Research Institute Santa Barbara, CA

Principal Investigator: Dr. Benjamin Reese
Laboratory Technician   August 2016 - August 2018
- ● Searched the UCSC Genome Browser to rank candidate genes and identified DTX4 and DIXDC1 as key regulatory genes controlling AII amacrine cell number in the mouse retina (Kulesh et al., 2023)
- ● Developed a retinal dissociation protocol in mouse cholinergic amacrine cells for FACS analysis and sequencing

UCSB Center for Stem Cell Biology and Engineering   Santa Barbara, CA
Principal Investigator: Dr. James Thomson
Laboratory Technician   August 2016 - June 2017
- ● Established a novel rat model for diabetic retinopathy by measuring weight and random blood glucose (mg/dL) via tail vein of ~200 Nile Grass Rats (Toh et al., 2019)

UCSB Psychological and Brain Sciences Department   Santa Barbara, CA
Principal Investigator: Dr. Tod Kippin
Laboratory Technician   September 2014 - May 2016
- ● Restraint-stressed ~20 prenatal mice and monitored daily dam-pup contact which discovered a strain-dependent propensity for cocaine dependence in offspring (Bagley et al., 2019)
- ● Administered subcutaneous estradiol injections to ~40 castrated male rats, trained them in operant conditioning chambers, and tracked cocaine vs. food preference, demonstrating that estradiol enhances cocaine preference (Bagley et al., 2017)

SELECTED COURSEWORK
- ● Linear Algebra, Univariate Data Modeling in R, Management of Large-Scale Omics Data (Snakemake), Translational Bioinformatics (Nextflow), Biological Database Analysis (SQL), Applied Genetic Analysis (GWAS)

AWARDS
- ● Boston University Bioinformatics Program Merit Scholarship

PUBLICATIONS
Kulesh B, **Bozadjian R**, Parisi RJ, Leong SA, Kautzman AG, Reese BE, Keeley PW. Quantitative trait loci on chromosomes 9 and 19 modulate AII amacrine cell number in the mouse retina. Front Neurosci. 2023 Feb 2;17:1078168. doi: 10.3389/fnins.2023.1078168. PMID: 36816119; PMCID: PMC9932814

Bagley JR, Adams J, **Bozadjian RV**, Bubalo L, Kippin TE. Strain differences in maternal neuroendocrine and behavioral responses to stress and the relation to offspring cocaine responsiveness. Int J Dev Neurosci. 2019 Nov;78:130-138. doi: 10.1016/j.ijdevneu.2019.06.009. Epub 2019 Jun 22. PMID: 31238105; PMCID: PMC6824979

Toh H, Smolentsev A, **Bozadjian RV**, Keeley PW, Lockwood MD, Sadjadi R, Clegg DO, Blodi BA, Coffey PJ, Reese BE, Thomson JA. Vascular changes in diabetic retinopathy-a longitudinal study in the Nile rat. Lab Invest. 2019 Oct;99(10):1547-1560. doi: 10.1038/s41374-019-0264-3. Epub 2019 May 17. PMID: 31101854; PMCID: PMC6788790

Bagley JR, Adams J, **Bozadjian RV**, Bubalo L, Ploense KL, Kippin TE. Estradiol increases choice of cocaine over food in male rats. Physiol Behav. 2019 May 1;203:18-24. doi: 10.1016/j.physbeh.2017.10.018. Epub 2017 Oct 19. PMID: 29056351; PMCID: PMC5908759