

Daniel B. Munro

Computational biologist at UC San Diego
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EDUCATION

- 2019 **Ph.D.** Quantitative and Computational Biology, Princeton University
Thesis: Revealing disease-relevant alteration patterns through data aggregation. Advisor: Mona Singh
- 2013 **B.S.** Biology, University of North Texas

RESEARCH EXPERIENCE

- 05/2025–Present **Assistant Project Scientist**, UC San Diego and
Visiting Scientist, Seattle Children’s Research Institute
Continuing postdoctoral research with Abraham Palmer and Pejman Mohammadi • Quantitative genetics and regulatory genomics • Integrating genetic variation, multi-modal transcriptomics, and complex traits
- 05/2023–04/2025 **Bioinformatics Programmer**, UC San Diego and
Visiting Scientist, Seattle Children’s Research Institute
Continuing postdoctoral research with Abraham Palmer and Pejman Mohammadi • Quantitative genetics and regulatory genomics • Integrating genetic variation, multi-modal transcriptomics, and complex traits
- 03/2020–04/2023 **Postdoctoral Fellow**, Scripps Research and
Postdoctoral Scholar, UC San Diego
Advisors: Pejman Mohammadi & Abraham Palmer • Quantitative genetics and regulatory genomics • Integrating genetic variation, multi-modal transcriptomics, and complex traits
- 03/2019–10/2019 **Postdoctoral Associate**, New York University
Advisor: Christine Vogel • Computational research in proteomics and cancer genomics
- 01/2014–12/2018 **Graduate Research Assistant**, Princeton University
Advisor: Mona Singh • Computational research in cancer genomics, protein variant impact, and histological image analysis
- 01/2011–05/2013 **Undergraduate Research Assistant**, University of North Texas
Advisor: Qunfeng Dong • Computational microbiome research and genomics software development

PEER-REVIEWED PUBLICATIONS

N Santhanam, S Sanchez-Roige, S Mi, Y Liang, AS Chitre, **D Munro**, D Chen, et al. RatXcan: A framework for cross-species integration of genome-wide association and gene expression data. *PLOS Genetics* (2025). 21(3): e1011583.

EK Hebda-Bauer, MH Hagenauer, **DB Munro**, P Blandino Jr., F Meng, K Arakawa, JDH Stead, et al. Bioenergetic-related gene expression in the hippocampus predicts internalizing vs. externalizing behavior in an animal model of temperament. *Frontiers in Molecular Neuroscience* (2025). 18:1469467.

D Munro, N Ehsan, SM Esmaili-Fard, A Gusev, AA Palmer, P Mohammadi. Multimodal analysis of RNA sequencing data powers discovery of complex trait genetics. *Nature Communications* (2024). 15: 10387.

F Okamoto, AS Chitre, TM Sanches, D Chen, **D Munro**, AT Aron, A Beeson, et al. Y and mitochondrial chromosomes in the heterogeneous stock rat population. *G3 Genes/Genomes/Genetics* (2024). jkae213.

TV de Jong, Y Pan, P Rastas, **D Munro**, M Tutaj, H Akil, C Benner, et al. A revamped rat reference genome improves the discovery of genetic diversity in laboratory rats. *Cell Genomics* (2024). 4 (4): 100527.

R Clifford, **D Munro**, D Dochtermann, P Devineni, S Pyarajan, Million Veteran Program, F Telese, et al. Genome-wide association study of chronic dizziness in the elderly identifies loci implicating *MLLT10*, *BPTF*, *LINC01224*, and *ROS1*. *JARO* (2023). 24: 575-591.

JL Zhou, G de Guglielmo, AJ Ho, M Kallupi, N Pokhrel, H-R Li, AS Chitre, **D Munro**, et al. Single-nucleus genomics in outbred rats with divergent cocaine addiction-like behaviors reveals changes in amygdala GABAergic inhibition. *Nature Neuroscience* (2023). 26: 1868–1879.

AS Chitre, O Polesskaya, **D Munro**, R Cheng, P Mohammadi, K Holl, J Gao, et al. Exponential increase in QTL detection with increased sample size. *GENETICS* (2023). 224 (2): iyad054.

S Fowler, T Wang, **D Munro**, A Kumar, AS Chitre, TJ Hollingsworth, A Garcia Martinez, et al. Genome-wide association study finds multiple loci associated with intraocular pressure in HS rats. *Frontiers in Genetics* (2023). 13: 1029058.

D Munro, T Wang, AS Chitre, O Polesskaya, N Ehsan, J Gao, A Gusev, LC Solberg Woods, LM Saba, H Chen, AA Palmer, P Mohammadi. The regulatory landscape of multiple brain regions in outbred heterogeneous stock rats. *Nucleic Acids Research* (2022). 50 (19): 10882–10895.

JT Ash*, G Darnell*, **D Munro***, BE Engelhardt. Joint analysis of gene expression levels and histological images identifies genes associated with tissue morphology. *Nature Communications* (2021). 12 (1): 1–12.

* These authors contributed equally

D Munro, M Singh. DeMaSk: A deep mutational scanning substitution matrix and its use for variant impact prediction. *Bioinformatics* (2020). 36 (22–23): 5322–5329.

GXL Li, **D Munro**, D Fermin, C Vogel, H Choi. A protein-centric approach for exome variant aggregation enables sensitive association analysis with clinical outcomes. *Human Mutation* (2020). 41 (5): 934–945.

D Munro, D Gherzi, M Singh. Two critical positions in zinc finger domains are heavily mutated in three human cancer types. *PLoS Comput Biol* (2018). 14 (6): e1006290.

C Cohen, E Toh, **D Munro**, Q Dong, H Hawlena. Similarities and seasonal variations in bacterial communities from the blood of rodents and from their flea vectors. *The ISME Journal* (2015). 2015-01-09.

Y Gavish, H Kedem, I Messika, C Cohen, E Toh, **D Munro**, Q Dong, C Fuqua, K Clay, H Hawlena. Association of host and microbial species diversity across spatial scales in desert rodent communities. *PLoS ONE* (2014). 9: e109677.

JS Kuehn, PJ Gorden, **D Munro**, R Rong, Q Dong, PJ Plummer, C Wang, GJ Phillips. Bacterial community profiling of milk samples as a means to understand culture-negative bovine clinical mastitis. *PLoS ONE*. 8: e61959.

M Zhou, R Rong, **D Munro**, C Zhu, X Gao, Q Zhang, Q Dong (2013). Investigation of the effect of type 2 diabetes mellitus on subgingival plaque microbiota by high-throughput 16S rDNA pyrosequencing. *PLoS ONE* (2013). 8: e61516.

H Hawlena, E Rynkiewicz, E Toh, A Alfred, LA Durden, MW Hastriter, DE Nelson, R Rong, **D Munro**, Q Dong, C Fuqua, K Clay. The arthropod, but not the vertebrate host or its environment, dictates bacterial community composition of fleas and ticks. *The ISME Journal* (2013). 7: 221-223.

K Revanna, **D Munro**, A Gao, C Chiu, A Pathak, Q Dong. A web-based multi-Genome Synteny Viewer for customized data. *BMC Bioinformatics* (2012). 13: 190.

PREPRINTS

KR Ganapathy, E Song, **D Munro**, A Torkamani, P Mohammadi. Allele Specific Expression Quality Control Fills Critical Gap in Transcriptome Assisted Rare Variant Interpretation. Preprint: <https://www.biorxiv.org/content/10.1101/2025.05.30.657086v2>

L Phan, A Gatti, Z Han, N Li, J Hu, H Zhang, S Shi, et al. (**D Munro** is 196th author). Humanity's Last Exam. Preprint: <https://arxiv.org/abs/2501.14249>

HONORS & AWARDS

- 2019 Runner-up, Symbiosis Competition at Imagine Science Film Festival, New York, NY, in collaboration with Jin Angdoo
- 2013 **National Science Foundation Graduate Research Fellowship**
- 2013 Phi Kappa Phi National Fellowship (\$5000)

TEACHING EXPERIENCE

- Spring 2016 Assistant in Instruction, “An Integrated, Quantitative Introduction to the Natural Sciences II”, Princeton University
- Fall 2015 Assistant in Instruction, “An Integrated, Quantitative Introduction to the Natural Sciences I”, Princeton University

PRESENTATIONS

- 2024 “Multimodal analysis of RNA sequencing data powers discovery of complex trait genetics”, platform talk at RECOMB-Genetics, April 28, 2024
- 2022 “The regulatory landscape of multiple brain regions in outbred heterogeneous stock rats”, talk at the Complex Trait Consortium-Rat Genomics 2022 meeting, September 29, 2022
- 2021 “Identification of regulatory landscape in multiple brain regions of outbred heterogeneous stock rats”, talk at the Complex Trait Consortium-Rat Genomics 2021 meeting, September 1, 2021
- 2021, 2023 “Techniques for algorithmic graphics”, guest lecture for Honors Colloquium on Complex Systems, University of Nebraska Omaha, March 2, 2021 and March 28, 2023
- 2020 “Mapping eQTLs in five rat brain regions”, talk at the 6th Annual Retreat for P50 Center for GWAS in Outbred Rats, La Jolla, CA, November 2, 2020

PROFESSIONAL SERVICE & MEMBERSHIPS

Active member of the Multi-Omics and Human analysis working groups for the NASA Open Science Data Repository. <https://awg.osdr.space/u/danielmunro>

Ad hoc peer reviewer for:

Developmental Biology (2019)
PLOS Computational Biology (2020)
PLOS ONE (2020)
BMC Bioinformatics (2021)

Journal of Computational Biology (2021)
Genome Biology (2023)
IEEE/ACM Transactions on Computational Biology and Bioinformatics (2023)
The American Journal of Human Genetics (2023)
Neuropsychopharmacology (2024)
Nature Communications (2024)

Memberships:

Society for Neuroscience (Since 2025)
American Society of Human Genetics (Since 2020)
International Society for Computational Biology (Since 2019)

CERTIFICATIONS

Initial Physiological Training Course – NASA (Houston, TX, 2024-11-07)
Open Water Diver – PADI (2024-07-28)
Amateur Radio License, General Class – FCC (2024-06-25)