

Daniel B. Munro

Postdoctoral Scholar, UC San Diego
Postdoctoral Fellow, Scripps Research
dmunro@health.ucsd.edu <https://danmun.ro>

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

03/2020–Present **Postdoctoral Fellow**, Pejman Mohammadi, Scripps Research and
Postdoctoral Scholar, Abraham Palmer, UC San Diego
03/2019–10/2019 **Postdoctoral Associate**, Christine Vogel, New York University
01/2014–12/2018 **Graduate Research Assistant**, Mona Singh, Princeton University
01/2011–05/2013 **Undergraduate Research Assistant**, Qunfeng Dong, University of North
Texas

PEER-REVIEWED PUBLICATIONS

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

S Fowler, T Wang, **D Munro**, A Kumar, AS Chitre, TJ Hollingsworth, A Garcia Martinez, et al.
(2023). Genome-wide association study finds multiple loci associated with intraocular pressure
in HS rats. *Frontiers in Genetics*. 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 (2022). The regulatory landscape of multiple
brain regions in outbred heterogeneous stock rats. *Nucleic Acids Research*. 50 (19): 10882-
10895.

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

* These authors contributed equally

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

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

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

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

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

JS Kuehn, PJ Gorden, **D Munro**, R Rong, Q Dong, PJ Plummer, C Wang, GJ Phillips (2013). 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.* 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 (2013). The arthropod, but not the vertebrate host or its environment, dictates bacterial community composition of fleas and ticks. *The ISME Journal.* 7: 221-223.

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

PREPRINTS

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. Preprint: <https://www.biorxiv.org/content/10.1101/2023.04.13.536694v1>

RE Clifford, **D Munro**, D Dochterman, P Devineni, S Pyarajan, F Telese, P Mohammadi, AA Palmer, RA Friedman. GWAS of chronic dizziness in the elderly identifies novel loci implicating MLLT10, BPTF, LINC01225, and ROS1.

Preprint: <https://www.medrxiv.org/content/10.1101/2022.12.14.22283471v3>

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
Fall 2015 Assistant in Instruction, An Integrated, Quantitative Introduction to the Natural Sciences I

PRESENTATIONS

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

Ad hoc reviewer: *Developmental Biology* (2019), *PLOS Computational Biology* (2020), *PLOS ONE* (2020), *BMC Bioinformatics* (2021), *Journal of Computational Biology* (2021)

American Society of Human Genetics (Since 2020)

International Society for Computational Biology (Since 2019)