

# Daniel B. Munro

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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

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

## PREPRINTS

N Santhanam, S Sanchez-Roige, Y Liang, AS Chitre, **D Munro**, et al. Polygenic transcriptome risk scores can translate genetic results between species.  
Preprint: <https://www.biorxiv.org/content/10.1101/2022.06.03.494719v1>

**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. *Under review at Nucleic Acids Research*.  
Preprint: <https://www.biorxiv.org/content/10.1101/2022.04.07.487560v1>

## PEER-REVIEWED PUBLICATIONS

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.

## HONORS & AWARDS

2019	Runner-up, Symbiosis Competition at Imagine Science Film Festival, New York, NY, in collaboration with Jin Angdoo
2013	<b>National Science Foundation Graduate Research Fellowship</b>
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

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
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- 2021 “Techniques for algorithmic graphics”, guest lecture for Honors Colloquium on Complex Systems, University of Nebraska Omaha, March 2, 2021
- 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)

Genetics Society of America (Since 2020)

International Society for Computational Biology (Since 2019)

American Association for the Advancement of Science (Since 2019)