

Nuri Teresa Pierce-Ward

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EMPLOYMENT	University of California, Davis , Davis, California Assistant Researcher, Population Health and Reproduction	2023-present
TRAINING	University of California, Davis , Davis, California <i>Advisor:</i> C. Titus Brown (Lab for Data-Intensive Biology) NSF Postdoctoral Fellowship 2017-2020	2017-2023
EDUCATION	Scripps Institution of Oceanography, UCSD , La Jolla, California Ph.D., Marine Biology <i>Advisors:</i> Terry Gaasterland, Ron Burton <i>Specialization:</i> Interdisciplinary Environmental Research <i>Dissertation Topic:</i> Developmental Transcriptomics of the California market squid, <i>Doryteuthis opalescens</i>	June 2017
	Stanford University , Stanford, California M.S., Biology <i>Advisor:</i> Fiorenza Micheli	2009
	B.S. with Honors, Biological Sciences <i>Advisor:</i> William Gilly <i>Honors Thesis:</i> Venom Synthesis and Gene Expression Analysis of Toxins in the Venom Ducts of <i>Conus californicus</i> Maintained in Tissue Culture	2009
RESEARCH INTERESTS	microbial metagenomics, bioinformatics, genomics	
PREPRINTS & PUBLICATIONS	Mazloom, R., Pierce-Ward, N.T. , Pritchard, L., Brown, C.T., Vinatzer, B.A., and Heath, L.S. (2023). LINgroups as a principled approach to compare and integrate multiple bacterial taxonomies. bioRxiv. Portik, D.M., Brown, C.T., and Pierce-Ward, N.T. (2022). Evaluation of taxonomic classification and profiling methods for long-read shotgun metagenomic sequencing datasets. BMC bioinformatics, 23(1), 541. Pritchard, L., Brown, C.T., Harrington, B., Heath, L.S., Pierce-Ward, N.T. and Vinatzer, B.A., (2022). Could a Focus on the “Why” of Taxonomy Help Taxonomy Better Respond to the Needs of Science and Society? Frontiers in Microbiology, p.1817. Roach, M.J., Pierce-Ward, N.T. , Suchecki, R., Mallawaarachchi, V., Papudeshi, B., Handley, S.A., Brown, C.T., Watson-Haigh, N.S. and Edwards, R.A.. (2022). Ten simple rules and a template for creating workflows-as-applications. PLoS computational biology, 18(12), p.e1010705. Rahman-Hera, M.R., Pierce-Ward, N.T. and Koslicki, D., (2022). Debiasing FracMinHash and deriving confidence intervals for mutation rates across a wide range of evolutionary distances. BioRxiv. Irber, L.C., Brooks, P.T., Reiter, T.E., Pierce-Ward, N.T. , Rahman Hera, M., Koslicki, D., and	

- Brown, C.T. (2022). Lightweight compositional analysis of metagenomes with FracMinHash and minimum metagenome covers. Preprint bioRxiv: 10.1101/2022.01.11.475838.
- Irber, L.C., **Pierce-Ward, N.T.**, and Brown, C.T. (2022). Sourmash Branchwater Enables Lightweight Petabyte-Scale Sequence Search. Preprint bioRxiv.
- Lumian, J., Sumner, D., Grettenberger, C., Jungblut, A.D., Irber, L.C., **Pierce-Ward, N.T.**, and Brown, C.T. (2022). Biogeographic Distribution of Five Antarctic Cyanobacteria Using Large-Scale k-mer Searching with sourmash branchwater. Preprint bioRxiv: 10.1101/2022.10.27.514113
- Reiter, T.E., **Pierce-Ward, N.T.**, Irber, L.C., Botvinnik, O.G., and Brown, C.T. (2022). Protein k-mers enable assembly-free metapangenomics. Preprint bioRxiv: 10.1101/2022.06.27.497795.
- Reiter, T.E., Irber, L.C., Gingrich, A.A., Haynes, D., **Pierce-Ward, N.T.**, Brooks, P.T., Mizutani, Y., Moritz, D., Reidl, F., Willis, A.D., Sullivan, B.D., and Brown, C.T. (2022). Meta-analysis of metagenomes via machine learning and assembly graphs reveals strain switches in Crohn's disease. Preprint bioRxiv: 10.1101/2022.06.30.498290.
- Reiter, T., Brooks, P.T., Irber, L., Joslin, S.E., Reid, C.M., Scott, C., Brown, C.T. and **Pierce-Ward, N.T.** (2021). Streamlining data-intensive biology with workflow systems. *GigaScience*, 10(1), p.giaa140.
- Pereira, R.J., Lima, T.G., **Pierce-Ward, N.T.**, Chao, L. and Burton, R.S., (2021). Recovery from hybrid breakdown reveals a complex genetic architecture of mitonuclear incompatibilities. *Molecular Ecology*, 30(23), pp.6403-6416.
- Botvinnik, O.B., Vemuri, V.N.P., **Pierce, N.T.**, Logan, P.A., Nafees, S., Karanam, L., Travaglini, K.J., Ezran, C.S., Ren, L., Juang, Y. and Wang, J., (2021). Single-cell transcriptomics for the 99.9% of species without reference genomes. bioRxiv.
- Love, M. I., Soneson, C., Hickey, P. F., Johnson, L. K., **Pierce, N.T.**, Shepherd, L., Morgan, M., and Patro, R. (2020). Tximeta: Reference sequence checksums for provenance identification in RNA-seq. *PLoS computational biology*, 16(2), e1007664.
- Pierce, N.T.**, Irber, L., Reiter, T., Brooks, P., and Brown, C. T. (2019). Large-scale sequence comparisons with sourmash. *F1000Research*, 8, 1006. <https://doi.org/10.12688/f1000research.19675.1>
- Mascuch, S. J., Boudreau, P. D., Carland, T. M., **Pierce, N.T.**, Olson, J., Hensler, M. E., Choi, H., Campanale, J., Hamdoun, A., Nizet, V. and Gerwick, W. H. Marine Natural Product Honaucin A Attenuates Inflammation by Activating the Nrf2-ARE Pathway. *Journal of natural products* (2017).
- Lindström J. B., **Pierce N.T.** and Latz M. I. Role of TRP channels in dinoflagellate mechanotransduction. *Biological Bulletin* (2017).
- Navarro, M.O., Kwan, G.T., Batalov, O., Choi, C., **Pierce, N.T.**, Levin, L.A. "Development of embryonic market squid, *Doryteuthis opalescens*, under chronic exposure to low environmental pH and [O₂]." *PLoS One* (2016).
- Pereira, R.J., Barreto, F.S., **Pierce, N.T.**, Carneiro, M., Burton, R.S. "Transcriptome-Wide Patterns of Divergence During Allopatric Evolution." *Molecular Ecology* (2016).
- Elliger, C.A., Richmond, T.A., Lebaric, Z.N., **Pierce, N.T.**, Sweedler, J.V., Gilly, W.F. "Diversity of conotoxin types from *Conus californicus* reflects a diversity of prey types and a novel evolutionary history." *Toxicon*. 57 (2): 311-322 (2011).

GRANTS & AWARDS

Fellowships

National Science Foundation Postdoctoral Research Fellowship in Biology, 2017-2020, \$207,000

National Science Foundation Graduate Research Fellowship in Biology, 2010-2016
 National Science Foundation Integrative Graduate Education and Research Traineeship (IGERT):
 Global Change, Marine Ecosystems and Society 2010-2013
 San Diego Fellowship, 2010-2012
 UCSD Center for Marine Biodiversity and Conservation Diversity Fellowship, 2010-2012

Grants and Awards

PI, XSEDE Research "Improving reference genomes and transcriptomes towards gene expression profiling of sequencing data sets containing multiple eukaryotic species" \$50,040 2019
 co-PI, XSEDE Educational Resource Allocation, genomics workshop \$6,729 2018
 XSEDE Research Startup Allocation \$16,834 2017
 co-PI, XSEDE Educational Resource Allocation, RNAseq workshop at SIO \$6,729 2017
 Center for Marine Biodiversity and Conservation Mentoring Award \$500 2014,5
 Ocean Global Change Biology GRC: Carl Storm Underrep. Minority Fellowship \$520 2014
 Scripps Institution of Oceanography Graduate Student Excellence Travel Award \$700 2014
 Center for Marine Biodiversity and Conservation IGERT Research Grant, \$11,500 2012
 Stanford University VPUE Summer Research Grant, \$5200 2008
 Stanford University Howard Hughes Medical Institute Summer Research Grant, \$5200 2007
 Chicano & Latino Community Awards, Stanford University 2005-2009

SELECTED INVITED TALKS & CONFERENCE PRESENTATIONS

International Society for Computational Biology, MICROBIOME COSI, 2022. **N.T Pierce-Ward**, M. Rahman Hera, L. Irber, T.E. Reiter, D. Koslicki, and C. Titus Brown. "Average Nucleotide Identity estimation from FracMinHash sketches" *Talk*

International Society for Computational Biology, BOSC Bioinformatics Open Source Conference, 2021. **N.T Pierce-Ward**, L. Irber, O. Botvinnik, T.E. Reiter, C. Titus Brown. "Sourmash protein k-mer sketches for large-scale sequence comparisons" *Talk*

Society for Integrative and Comparative Biology, 2018. **N.T Pierce**, M.O. Navarro, R.S. Burton, and T. Gaasterland. "Gene expression response of California Market Squid to high-CO₂, low-O₂ conditions" *Poster*

Ocean To Table Fish and Fisheries Event by SIO-UCSD, NOAA Southwest Fisheries, August 2016. "Biology of the California Market Squid, *Doryteuthis opalescens*" *Invited talk*

SIO 242C: Big Data Analysis in Computational Molecular Biology, 2015. "Techniques for Differential Expression Analysis of *de novo* RNA-Seq Data" *Invited lecture*

Plant and Animal Genome Conference, San Diego, CA, 2015. Waksmundski, A., **N.T Pierce**, Gaasterland, T. "Automated *de novo* Transcriptome Analysis of Eukaryotic Organisms" *Poster*

Scripps Institution of Oceanography Student Symposium, San Diego, CA 2014. "Gene Expression Response of California Market Squid to high-CO₂, low-O₂ conditions" *Winner, best poster*

Ocean Global Change Biology Gordon Research Conference, Waterville Valley, NH, 2014. "Gene Expression Response of California Market Squid to high-CO₂, low-O₂ conditions" *Poster*

Scripps Institution of Oceanography, La Jolla, CA, 2013. "Gene Expression Response of California Market Squid to Ocean Acidification and Hypoxia Conditions" *Invited talk*

CSU Fullerton English as a Second Language Marine Science Symposium. "Global Change Impacts to Marine Organisms" 2012 *Invited lecture*

Society for the Advancement of Chicanos and Native Americans in Science (SACNAS), Seattle, WA, 2012. **N.T Pierce**, M.O. Navarro, and R.S. Burton. "Gene Expression Response of California Market Squid, *Doryteuthis opalescens*, to high-CO₂/low-pH, low O₂ conditions" *Poster*

	Evolution, Ottawa, Canada, 2012. N.T. Pierce and R.S. Burton. "Variation-Aware Transcriptome Alignment Improves Gene Expression Analyses in <i>Tigriopus californicus</i> " <i>Poster</i>	
	Evolution, Norman, OK, 2011. N.T. Pierce and R.S. Burton. "High Resolution Melting (HRM) Genotyping in <i>Tigriopus californicus</i> : An Application to Heat Stress Response" <i>Poster</i>	
BIOINFORMATICS TRAINING	<i>Instructor</i>	2022-2023
	Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS)	
	Marine Biological Laboratory, Woods Hole, MA	
	Course materials: https://github.com/mblstamps/stamps2023/wiki , https://github.com/mblstamps/stamps2022/wiki	
	<i>Assistant Instructor, Pangenomics</i>	2023
	Plant and Animal Genome Conference	
	Course materials: https://github.com/dib-lab/workshop_12Jan_2023	
	<i>Guest Instructor, Introduction to Bioinformatics</i>	2020
	University of California, Davis	
	Course materials: https://github.com/ngs-docs/2020-ggg-201b-rnaseq	
	<i>Instructor, Metatranscriptomics</i>	2018
	Centro de Investigación Científica y de Educación Superior de Ensenada	
Course materials: https://ngs-docs.github.io/2018-cicese-metatranscriptomics		
<i>Instructor, Data Carpentry Genomics</i>	2018	
California State University, Monterey Bay		
Course materials: https://bluegenes.github.io/2018-03-22-csumb		
<i>ANGUS: Analyzing High Throughput Sequencing Data</i>	2017	
Data Intensive Biology Summer Institute, UC Davis		
Course materials: https://angus.readthedocs.io/en/2017		
<i>Instructor, Nonmodel mRNAseq Data Analysis</i>	2017	
Scripps Institution of Oceanography, UCSD		
Course materials: https://rnaseq-workshop-2017.readthedocs.io		
<i>Instructor and Developer, Nonmodel mRNAseq Data Analysis</i>	2017	
Data Intensive Biology Summer Institute		
Course materials: http://dibsi-rnaseq.readthedocs.io/en/latest		
<i>Instructor, Intermediate RNA-Seq Analysis</i>	2015	
University of California, Davis		
Course materials: http://dib-training.readthedocs.io/en/pub/2015-11-02-mRNAseq-intermediate.html		
<i>Instructor, Software Carpentry</i>	2015	
University of California, San Diego		
Course materials: https://github.com/sdsc-scicomp/2015-10-27-ucsd		
<i>Organizer & Assistant, Software Carpentry, UCSD</i>	2016	
<i>Organizer & Assistant, Software Carpentry, SIO</i>	2014	
SELECTED SERVICE & OUTREACH	NSURP National Summer Undergraduate Research Project - <i>Research Advisor</i>	2020-2021
	SACNAS National Diversity in STEM Conference - <i>Abstract Reviewer</i>	2018
	The Carpentries - <i>Instructor</i>	2015-Present
	SIO Team for Inclusion, Engagement, and Diversity in Science (TIDES)	2010-2017
	Expanding Your Horizons (EYH) STEM Conference for Girls - <i>Co-led Workshop</i>	2016-2017
	Open Data Science at SIO - <i>Co-founder</i>	2016
	SIO Diversity Initiatives Coordinator - <i>Hiring Committee Member</i>	2016
	Ocean Discovery Institute - <i>Occasional Volunteer scientist</i>	2011-2016

SIO Bioinformatics Users Group - <i>Co-founder</i>	2015-2017
Birch Aquarium at Scripps SEA Days - <i>Volunteer scientist</i>	2014
NOAA Climate Change Student Summit - <i>Volunteer Scientist</i>	2012
Birch Aquarium - <i>Volunteer</i>	2009

SKILLS

Add'l Languages: Spanish

Computing: Python, Rust (beginner), Snakemake, Git, GitHub, Bash, R, L^AT_EX

Updated September 27, 2023