Nuri Teresa Pierce-Ward

Contact Information

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Training

University of California, Davis, Davis, California 2017-present

NSF Postdoctoral Fellowship, Lab for Data-Intensive Biology (CT Brown)

Education

Scripps Institution of Oceanography, UCSD, La Jolla, California
Ph.D., Marine Biology June 2017

Advisors: Terry Gaasterland, Ron Burton

Specialization: Interdisciplinary Environmental Research

Dissertation Topic: Developmental Transcriptomics of the California market squid, *Doryteuthis opalescens*

Stanford University, Stanford, California
M.S., Biology 2009
Advisor: Fiorenza Micheli
B.S. with Honors, Biological Sciences 2009
Advisor: William Gilly
Honors Thesis: Venom Synthesis and Gene Expression Analysis of Toxins in the Venom Ducts of *Conus californicus* Maintained in Tissue Culture

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. Waksmunski, 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 *Tigriopus californicus*” *Poster*

Evolution, Norman, OK, 2011. **N.T Pierce** and R.S. Burton.“High Resolution Melting (HRM) Genotyping in *Tigriopus californicus*: An Application to Heat Stress Response” *Poster*

Bioinformatics Training

Assistant Instructor, Pangenomics **2023**
Plant and Animal Genome Conference
Course materials: `https://github.com/dib-lab/workshop_12Jan_2023`

Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) **2022**
Marine Biological Laboratory, Woods Hole, MA
Course materials: `https://github.com/mblstamps/stamps2022/wiki`

Guest Instructor, Introduction to Bioinformatics **2020**
University of California, Davis
Course materials: `https://github.com/ngs-docs/2020-ggg-201b-rnaseq`

Instructor, Metatranscriptomics **2018**
Centro de Investigación Científica y de Educación Superior de Ensenada
Course materials: `https://ngs-docs.github.io/2018-cicese-metatranscriptomics`

Instructor, Data Carpentry Genomics **2018**
California State University, Monterey Bay
Course materials: `https://bluegenes.github.io/2018-03-22-csumb`

ANGUS: Analyzing High Throughput Sequencing Data **2017**
Data Intensive Biology Summer Institute, UC Davis
Course materials: `https://angus.readthedocs.io/en/2017`

Instructor, Nonmodel mRNAseq Data Analysis **2017**
Scripps Institution of Oceanography, UCSD
Course materials: `https://rnaseq-workshop-2017.readthedocs.io`

Instructor and Developer, Nonmodel mRNAseq Data Analysis **2017**
Data Intensive Biology Summer Institute
Course materials: `http://dibsi-rnaseq.readthedocs.io/en/latest`

Instructor, Intermediate RNA-Seq Analysis **2015**
University of California, Davis
Course materials:
`http://dib-training.readthedocs.io/en/pub/2015-11-02-mRNAseq-intermediate.html`

Instructor, Software Carpentry **2015**
University of California, San Diego
Course materials: `https://github.com/sdsc-scicomp/2015-10-27-ucsd`

Organizer & Assistant, Software Carpentry, UCSD **2016**
Organizer & Assistant, Software Carpentry, SIO **2014**

Selected Service & Outreach

NSURP National Summer Undergraduate Research Project - *Research Advisor*	2020-2021
SACNAS National Diversity in STEM Conference - *Abstract Reviewer*	2018
The Carpentries - *Instructor*	2015-Present
SIO Team for Inclusion, Engagement, and Diversity in Science (TIDES)	2010-2017
Expanding Your Horizons (EYH) STEM Conference for Girls - *Co-led Workshop*	2016-2017
Open Data Science at SIO - *Co-founder*	2016
SIO Diversity Initiatives Coordinator - *Hiring Committee Member*	2016
Ocean Discovery Institute - *Occasional Volunteer scientist*	2011-2016
SIO Bioinformatics Users Group - *Co-founder*	2015-2017
Birch Aquarium at Scripps SEA Days - *Volunteer scientist*	2014
NOAA Climate Change Student Summit - *Volunteer Scientist*	2012
Birch Aquarium - *Volunteer*	2009

Skills

Add'l Languages: Spanish
Computing: Snakemake, Python, Git, GitHub, Bash, R, LaTeX

Updated April 6, 2023