

Genetic relatedness estimates calculated from SNP genotype data of oysters from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2018-2020

Website: <https://www.bco-dmo.org/dataset/1003777>

Data Type: Other Field Results

Version: 1

Version Date: 2026-08-05

Project

» [CAREER: Linking genetic diversity, population density, and disease prevalence in seagrass and oyster ecosystems](#) (Seagrass and Oyster Ecosystems)

Contributors	Affiliation	Role
Hughes, A. Randall	Northeastern University	Principal Investigator
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Abstract

This dataset contains pairwise individual relatedness estimates for eastern oysters (*Crassostrea virginica*, urn:lsid:marinespecies.org:taxname:140657) sampled from 12 experimental restored reefs in Ninigret Pond, Rhode Island, USA in fall 2018 and fall 2020, as part of a multi-year oyster reef restoration experiment using oysters sourced from four commercial hatcheries along the U.S. Atlantic coast. Pairwise relatedness was estimated for every unique pair of individuals within the same reef and assigned genetic cluster using the Wang estimator applied to the SNP genotype data. Genetic clusters broadly correspond to the four commercial hatchery sources (Maine, Massachusetts, New York, and Virginia) as described in the related genetic assignments dataset. These data enable assessment of fine-scale relatedness patterns within the assigned genetic clusters on individual reefs across the two sampling time points

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Coverage

Location: Ninigret Pond, Charlestown, Rhode Island

Spatial Extent: Lat:41.3549 Lon:-71.6929

Temporal Extent: 2018-11 - 2020-10

Methods & Sampling

These data were published in Truskey et al. 2025 (Evolutionary Applications).

This dataset contains pairwise individual relatedness estimates for eastern oysters (*Crassostrea virginica*, urn:lsid:marinespecies.org:taxname:140657) sampled from 12 experimental restored reefs in Ninigret Pond, Rhode Island, USA in fall 2018 and fall 2020, as part of a multi-year oyster reef restoration experiment using oysters sourced from four commercial hatcheries along the U.S. Atlantic coast. We sampled live oysters from

each reef on scuba or snorkel. Oysters were put on ice and transported to the Northeastern University Marine Science Center where they were held at -80°C until DNA extraction.

Raw sequence reads for this study are deposited in the NCBI SRA (BioProject ID PRJNA1280068) and linked in the Related Datasets section. Also see Related Datasets for sequence metadata for all sampled oysters and individual genetic assignments source data.

Estimating pairwise individual relatedness

Pairwise relatedness was estimated for all individuals within the same genetic cluster on each reef using the Wang estimator (Wang 2002) implemented in the R package related v0.8 (Pew et al. 2015), applied to the primary SNP dataset (4679 SNPs filtered for $\text{MAF} > 0.01$ and fall 2020 batch missingness, and pruned for linkage disequilibrium). The Wang estimator was selected for its reduced bias at small sample sizes and among highly related individuals (Wang 2017), as expected within hatchery-bred lineages.

BCO-DMO Processing Description

- Loaded table Truskey_EVA2025_ind_relatedness_reefxgeneticcluster.csv
- Output as 1003777_v1_ind_relatedness_reefxgeneticcluster.csv

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Related Publications

Pew, J., Muir, P. H., Wang, J., & Frasier, T. R. (2015). related: an R package for analysing pairwise relatedness from codominant molecular markers. *Molecular Ecology Resources*, 15(3), 557–561. Portico.

<https://doi.org/10.1111/1755-0998.12323>

Software

Truskey, S., Sotka, E., Grabowski, J., Kollars-Kjersten, N. M., Lotterhos, K. E., Schneider, E., & Hughes, A. R. (2025). Non-Random Mortality in an Experimental Oyster Restoration. *Evolutionary Applications*, 18(7). Portico.

<https://doi.org/10.1111/eva.70128>

Results

Wang, J. (2002). An Estimator for Pairwise Relatedness Using Molecular Markers. *Genetics*, 160(3), 1203–1215.

<https://doi.org/10.1093/genetics/160.3.1203>

Methods

Wang, J. (2017). Estimating pairwise relatedness in a small sample of individuals. *Heredity*, 119(5), 302–313.

<https://doi.org/10.1038/hdy.2017.52>

Methods

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Related Datasets

IsRelatedTo

Hughes, A. R., Truskey, S. (2026) **Genetic diversity metrics for oyster genetic clusters from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2018-2020**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-12 <http://lod.bco-dmo.org/id/dataset/1004745> [[view at BCO-DMO](#)]

Relationship Description: Related dataset with genetic diversity estimates at the oyster genetic cluster-level from restored reefs

Hughes, A. R., Truskey, S. (2026) **Oyster genetic assignment data from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2017-2020**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-07 <http://lod.bco-dmo.org/id/dataset/1004242> [[view at BCO-DMO](#)]

Relationship Description: Companion dataset with individual genetic cluster assignments for oysters

Hughes, A. R., Truskey, S. (2026) **Oyster morphometric, condition, and parasite infection data from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2018-2020.**

Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-11 <http://lod.bco-dmo.org/id/dataset/1004478> [[view at BCO-DMO](#)]

Relationship Description: Related dataset with trait measurements for oysters from restored reefs

Hughes, A. R., Truskey, S. (2026) **Sequence metadata for all sampled oysters from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2017-2020.**

Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-07 <http://lod.bco-dmo.org/id/dataset/1003894> [[view at BCO-DMO](#)]

Relationship Description: Sequence metadata for all archived genetic samples associated with this project

References

Northeastern University. Non-random mortality in an experimental oyster restoration. 2025/06. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA1280068>. NCBI:BioProject: PRJNA1280068.

Truskey, S. B., & Hughes, A. R. (2025). Non-random mortality in an experimental oyster restoration [Data set]. Northeastern University. <https://hdl.handle.net/2047/D20775066>

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Parameters

Parameter	Description	Units
yearcoll	Year and season of sample collection (e.g., F2018 = Fall 2018, F2020 = Fall 2020, Init = hatchery-sourced samples taken before reef deployment).	unitless
block	Experimental block in which a restored reef was situated (A - D)	unitless
reef	Restored reef from which an individual was collected. Letter refers to experimental block and number refers to the reef number within a block (e.g., D3)	unitless
primary_genetic_assignment	Assigned genetic cluster for an individual using the primary genetic assignment set applied to all main text analyses (DAPC approach, SNP set filtered for MAF > 0.01, LD pruning, and Fall 2020 missing data). Label names correspond to the state of origin of the hatchery source associated with a given genetic cluster (gME, gMA, gNY, gVA).	unitless
geneticcluster_year_reef	Identifier combining the shared genetic cluster, year, and reef for a pairwise relatedness comparison of two individual oysters (e.g., gMA_F2018_D3)	unitless
ind_id_1	Unique identifier for the first individual in the relatedness pair. This identifier corresponds to the associated FASTQ sequence file name for individual 1.	unitless
ind_id_2	Unique identifier for the second individual in the relatedness pair. This identifier corresponds to the associated FASTQ sequence file name for individual 2.	unitless
wang_relatedness	Pairwise relatedness estimate using Wang estimator (Wang, 2002); calculated only among individuals within the same assigned genetic cluster and reef	unitless

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 2500
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	See Related Datasets for individual genetic assignments from hatchery samples and restored reefs and sequence metadata for NCBI dataset. The initial and fall 2020 batches were sequenced on a single lane of the Illumina HiSeq 2500 at Tufts University Core Facility Genomics; the fall 2018 batch was sequenced on two lanes of the Illumina NovaSeq 6000 at the University of Texas at Austin Genomic Sequencing and Analysis Facility.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	See Related Datasets for individual genetic assignments from hatchery samples and restored reefs and sequence metadata for NCBI dataset. The initial and fall 2020 batches were sequenced on a single lane of the Illumina HiSeq 2500 at Tufts University Core Facility Genomics; the fall 2018 batch was sequenced on two lanes of the Illumina NovaSeq 6000 at the University of Texas at Austin Genomic Sequencing and Analysis Facility.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	
Generic Instrument Name	Manual Biota Sampler
Dataset-specific Description	We haphazardly sampled live oysters from each reef on scuba or snorkel. Oysters were put on ice and transported to the Northeastern University Marine Science Center where they were held at -80°C until DNA extraction.
Generic Instrument Description	"Manual Biota Sampler" indicates that a sample was collected in situ by a person, possibly using a hand-held collection device such as a jar, a net, or their hands. This term could also refer to a simple tool like a hammer, saw, or other hand-held tool.

Dataset-specific Instrument Name	scuba
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
Dataset-specific Description	We haphazardly sampled live oysters from each reef on scuba or snorkel. Oysters were put on ice and transported to the Northeastern University Marine Science Center where they were held at -80°C until DNA extraction.
Generic Instrument Description	The self-contained underwater breathing apparatus or scuba diving system is the result of technological developments and innovations that began almost 300 years ago. Scuba diving is the most extensively used system for breathing underwater by recreational divers throughout the world and in various forms is also widely used to perform underwater work for military, scientific, and commercial purposes. Reference: https://oceanexplorer.noaa.gov/technology/technical/technical.html

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Project Information

CAREER: Linking genetic diversity, population density, and disease prevalence in seagrass and oyster ecosystems (Seagrass and Oyster Ecosystems)

Coverage: Coastal New England

NSF Award Abstract:

Disease outbreaks in the ocean are increasing, causing losses of ecologically important marine species, but the factors contributing to these outbreaks are not well understood. This 5-year CAREER project will study disease prevalence and intensity in two marine foundation species - the seagrass *Zostera marina* and the Eastern oyster *Crassostrea virginica*. More specifically, host-disease relationships will be explored to understand how genetic diversity and population density of the host species impacts disease transmission and risk. This work will pair large-scale experimental restorations and smaller-scale field experiments to examine disease-host relationships across multiple spatial scales. Comparisons of patterns and mechanisms across the two coastal systems will provide an important first step towards identifying generalities in the diversity-density-disease relationship. To enhance the broader impacts and utility of this work, the experiments will be conducted in collaboration with restoration practitioners and guided by knowledge ascertained from key stakeholder groups. The project will support the development of an early career female researcher and multiple graduate and undergraduate students. Students will be trained in state-of-the-art molecular techniques to quantify oyster and seagrass parasites. Key findings from the surveys and experimental work will be incorporated into undergraduate courses focused on Conservation Biology, Marine Biology, and Disease Ecology. Finally, students in these courses will help develop social-ecological surveys and mutual learning games to stimulate knowledge transfer with stakeholders through a series of workshops.

The relationship between host genetic diversity and disease dynamics is complex. In some cases, known as a dilution effect, diversity reduces disease transmission and risk. However, the opposite relationship, known as the amplification effect, can also occur when diversity increases the risk of infection. Even if diversity directly reduces disease risk, simultaneous positive effects of diversity on host density could lead to amplification by increasing disease transmission between infected and uninfected individuals. Large-scale field restorations of seagrasses (*Zostera marina*) and oysters (*Crassostrea virginica*) will be utilized to test the effects of host genetic diversity on host population density and disease prevalence/intensity. Additional field experiments independently manipulating host genetic diversity and density will examine the mechanisms leading to dilution or amplification. Conducting similar manipulations in two marine foundation species - one a clonal plant and the other a non-clonal animal - will help identify commonalities in the diversity-density-disease relationship. Further, collaborations among project scientists, students, and stakeholders will enhance interdisciplinary training and help facilitate the exchange of information to improve management and restoration efforts. As part of these efforts, targeted surveys will be used to document the perceptions and attitudes of managers and restoration

practitioners regarding genetic diversity and its role in ecological resilience and restoration.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1652320

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