Metadata for studies from meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results

Website: https://www.bco-dmo.org/dataset/877414
Data Type: model results
Version: 2
Version Date: 2025-06-05

Project
» RCN: Evolution in Changing Seas (RCN ECS)

Contributors	Affiliation	Role
Lotterhos, Katie	Northeastern University	Principal Investigator
Trussell, Geoffrey C.	Northeastern University	Co-Principal Investigator
Albecker, Molly	Northeastern University	Contact
Heyl, Taylor	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager
Soenen, Karen	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

Covariance can exist between the genetic and environmental influences on phenotype (CovGE) and can have an important role in ecological and evolutionary processes in nature and population responses to environmental change. CovGE is commonly called countergradient variation (CnGV; negative CovGE)or cogradient variation (CoGV; positive CovGE)and has been recognized in classic studies that have established several long-standing hypotheses about CnGV and CoGV. For instance, it is hypothesized that CnGV is more prevalent in nature than CoGV, that CnGV is more prevalent in fish, amphibian, and invertebrate taxa, across latitudinal or altitudinal environmental gradients, and more frequently occurs in metabolic compensation traits, including development, growth, feeding, metabolism, and activity, while CoGV is more commonly observed in morphological traits. The recent development of a standardized method to measure CovGE allows for the first rigorous quantitative exploration of these hypotheses. We use meta-analysis and apply the novel quantitative method to test whether the above hypotheses are supported in the literature. We found no differences in frequency of CnGV and CoGV, and no systematic patterns relative to taxa, environmental gradient, or trait type. However, our analyses suggest that CovGE may be as common as gene by environment (GxE) interactions. Given that CovGE is likely to have a strong impact on future outcomes for organisms experiencing environmental change, that significant CovGE occurred frequently, and the lack of systematic patterns in the occurrence of CovGE, we encourage a more widespread application of measuring CovGE.

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Methods & Sampling

We searched the Web of Science database for experimental studies that evaluated differences in phenotypic responses across different genotypes and environments. We conducted the initial search on June 24, 2019.

We used the search terms, ("cogradient variation" OR "countergradient variation" OR" cogradient selection" OR "countergradient selection" OR "co-gradient variation" OR "counter-gradient variation" OR "co-gradient selection" OR "counter-gradient selection") OR ("GxE" OR "genotype by environment" or "gene by environment") OR ("nonadaptive plast*" OR "non-adaptive plast*" OR "maladaptive plast*" OR "adaptive plast*") OR ("phenotypic plast*" AND "adapt*") AND ("common garden" OR "reciprocal transplant"). Initial searches returned approximately 5,900 hits. Results were further refined by including only those articles within Web of Science categories that related to ecology, evolution, or any ecological or evolutionary subdiscipline (e.g., papers categorized as engineering or biomedical were excluded). Refining reduced the search results to 4,458 studies. We also added studies that were included in previously published meta-analyses by Murren et al. (2015) and Hereford (2009) for screening.

After compiling studies, we measured CovGE and GxE magnitude on phenotypic data. More methods can be found in the manuscript published in Ecology Letters in 2022.

See Related Dataset Albecker et al. (2022) for model code.

BCO-DMO Processing Description

Version 1:
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Missing data identifier ‘NA’ replaced with 'nd' (BCO-DMO's default missing data identifier)
- Added a conventional header with dataset name, PI names, version date
- Replaced commas with semi-colons in column "table_Number"

Version 2:
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Missing data identifier ‘NA’ replaced with 'nd' (BCO-DMO's default missing data identifier)

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Data Files

File
877414_v2_metaanalysis.csv (Comma Separated Values (.csv), 205.17 KB) MD5:e9453ac11377b8439f0104471ed4dba1 Primary data file for dataset ID 877414, version 2

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Related Publications

Albecker, M. A., Trussell, G. C., & Lotterhos, K. E. (2022). A novel analytical framework to quantify co-gradient and countergradient variation. Ecology Letters, 25(6), 1521–1533. Portico. https://doi.org/10.1111/ele.14020
Results

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Related Datasets

IsRelatedTo

Albecker, M., Lotterhos, K., Trussell, G. C., Bittar, T. (2024) **Model code and output for a comparison of**

methods for meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-08-06 doi:10.26008/1912/bco-dmo.934896.1 [view at BCO-DMO]
Relationship Description: These "Metadata from a meta-analysis on CovGE in phenotypic results" (doi:10.26008/1912/bco-dmo.877414.1) data were used in the "CovGE MetaAnalysis" (doi:

Albecker, M., Trussell, G. C., Lotterhos, K. (2025) **Results from a meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results in published literature.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2) Version Date 2025-06-05 doi:10.26008/1912/bco-dmo.877425.2 [view at BCO-DMO]

Albecker, M., Trussell, G., Lotterhos, K. (2022) **Results using simulated data used to conduct power analyses.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-10-14 doi:10.26008/1912/bco-dmo.877456.1 [view at BCO-DMO]

Lotterhos, K., Trussell, G. C., Albecker, M. (2025) **Input data and code to test hypotheses between genetic and environmental effects on phenotypes.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-06-05 doi:10.26008/1912/bco-dmo.963375.1 [view at BCO-DMO]
Relationship Description: Dataset 963375 holds the input file for the code that is also is in this dataset.

Software

Albecker, M. A., Casalott, & Lotterhos, K. (2022). *RCN-ECS/CnGV: Archived CGV data and code - April 2022* (Version 1.0) [Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.6470547
https://doi.org/10.5281/zenodo.6470547

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Parameters

Parameter	Description	Units
STUDY_ID	numerical identifier	unitless
First_Author	name of first author	unitless
Data_file_name	identifier - study ID with first author	unitless
G_match_E	denotes whether genetic information matches native environment in paper blank	unitless
natural_env_type	whether environmental data is continuous or categorical	unitless
GxE_sig	true if paper reports significant GxE in phenotype	unitless
phylum_division	phylum of study organism	unitless
genus	genus of study organism	unitless
species	species of study organism	unitless

gen_number	number of populations included in study	unitless
gen_number_knownenvs	number of native environments able to be matched to populations	unitless
phenotype	the phenotype measured in the study	unitless
phenotype_unit	the units defining phenotype measurement	unitless
life_stage	life stage investigated	unitless
exp_env_type	whether experimental treatments were categorical or continuous	unitless
experimental_comparison	the comparison of environments in the experiment	unitless
Experimental_environment	the environmental conditions tested	unitless
experimental_env_unit	the units of the experimental treatments	unitless
natural_env	the native environment	unitless
natural_env_unit	the units used to measure native environment	unitless
Study_ID_phenotype	identifier used to link results	unitless
Raw_data_available	whether raw data is accessible	unitless
Proportion	is data proportion? (yes/no)	unitless
Mention_CGV	does the study mention CovGE? (yes/no)	unitless
Data_source	where did data originate from paper	unitless
figure_Number	figure from which data was collected	unitless
table_Number	table from which data was collected	unitless
Comments	notes, if necessary	unitless

Checked	noting whether the study was double checked	unitless

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Project Information

RCN: Evolution in Changing Seas (RCN ECS)

Website: https://rcn-ecs.github.io/

Coverage: United States

NSF abstract:
How marine species will react to changing environment and climate is not well understood. While the interaction between oceanographic and ecological processes has yielded considerable insight into the ecology of marine species, the evolutionary responses of marine species are not well integrated into this framework. This project research coordinated network on "Evolution in Changing Seas" (ECSRCN), will bring marine scientists together with evolutionary biologists having expertise in population genetics, eco-evolutionary dynamics, and phylogenetics to better understand and predict the evolutionary responses of marine species to climate stressors. ECS-RCN will increase the impact of evolutionary studies in marine systems through increased collaboration among scientists from diverse fields. Furthermore, the empirical robustness of these studies will also be improved through the development of standards for experimental design and statistical analysis, especially for genomics data analysis. ECS-RCN will build a diverse network through a dedicated workshop for early-career participants, by advertising with diversity groups, and by dedicating funds to increase diversity. This project will support one postdoctoral researcher who will play a key role in coordinating scientific activities of the network as well as receive interdisciplinary training through network activities, strongly positioning them to become a leader in the field. ECS-RCN will also build the foundation for a lasting network through establishment of a listserv, open access to publications, development of a website, and development of teaching modules for undergraduate and graduate curriculum.

Specifically, ECS-RCN will consider how coupling between oceanographic and evolutionary processes shape adaptive and plastic responses to climate change, from the fundamental level of genomes scaled up to entire populations. Under this theme, the objectives of ECS-RCN are to synthesize the current state of knowledge, to prioritize lines of inquiry that will advance knowledge in marine and evolutionary biology, to determine the appropriate experimental designs and statistical approaches for robustly testing these lines of inquiry (including genomics approaches), and to build a foundation for a diverse and lasting network. These goals will be realized over the course of 3 years, starting with a Synthesis Workshop in Year 1 where working groups will be established, followed by working group meetings and formation of a Genomics Subcommittee in Year 2, and ending with an Integration and Training Workshop aimed at early career scientists in Year 3. To promote synthesis and self-organization at workshops, the workshops will employ the Open Space format. ECS-RCN will promote evolutionary thinking in biological oceanography and integrate unique aspects of marine life-histories into evolutionary principles. ECS-RCN will also advance knowledge in both marine and evolutionary biology through synthesis and the development of frameworks for merging genomics and ecology. The activities will provide novel insights into pressing questions in both marine and evolutionary ecology, such as: what drives geographic patterns of local (mal)adaptation and plasticity?; what are the mechanisms that generate adaptive vs. nonadaptive plasticity?; what is the role of genotype dependent dispersal in adaptation?; what are the genetic constraints on adaptation of function-valued traits to climate change?; and how do epigenetic modifications act as a mediator between adaptation and plasticity? Ultimately, the RCN aims to develop a quantitative understanding of the relative importance of ecological versus evolutionary responses to climate change.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1764316

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