# Results using simulated data used to conduct power analyses

**Website**: https://www.bco-dmo.org/dataset/877456
**Data Type**: model results
**Version**: 1
**Version Date**: 2022-10-14

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


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**Abstract**
Spatial covariance between genotypic and environmental influences on phenotypes (CovGE) can result in the nonrandom distribution of genotypes across environmental gradients and is a potentially important factor driving local adaptation. However, a framework to quantify the magnitude and significance of CovGE has been lacking. We develop a novel quantitative/analytical approach to estimate and test the significance of CovGE from reciprocal transplant or common garden experiments, which we validate using simulated data. We demonstrate how power to detect CovGE changes over a range of experimental designs. We confirm an inverse relationship between gene-by-environment interactions (GxE) and CovGE, as predicted by first principles, but show how phenotypes can be influenced by both. The metric provides a way to measure how phenotypic plasticity covaries with genetic differentiation and highlights the importance of understanding the dual influences of CovGE and GxE on phenotypes in studies of local adaptation and species' responses to environmental change.

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## Table of Contents


- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Supplemental Files
- Related Publications
- Related Datasets
- Parameters
- Project Information
- Funding


### Methods & Sampling

To validate the and G×E& sampling estimates, we created simulations that mimicked experimental data, and provided an array of scenarios to understand how effect size, presence of GxE, total sample size, experimental design, and variability were affected, as well as the ability to detect and measure these patterns. We simulated datasets with total sample sizes (number of environments x number of genotypes x sample size) between 32 and 500 individuals.

For reciprocal transplant data, we simulated genotypic effects that increased linearly at rate y along an environmental variable (e) for genotypes equally spaced from environment j = [1, 2, ... nenv]. We generated unitless phenotypic data based on an equation in the Supplemental File "Equation for power output results" (power_analyses_pasted_graphic.pdf).

In this equation, the phenotype of individual k from genotype i in environment j is given by the genotypic effect, the reaction norm (where ej is the value of the environment and beta is the slope of the reaction norm), an interaction term for genotype i in environment j that describes the deviation of the reaction norm from linearity, and error.

Interaction terms were drawn from a normal distribution with mean of zero and variance equal to the number of genotypes. Random error was added by sampling from a normal distribution with a mean of zero and standard deviation of either 0.5 (low residual variation) or 1 (high residual variation). Scenarios with no random error (= 0) were used to assess population parameters.

For common garden designs, we adjusted this approach to model designs in which different numbers of genotypes were reared in two common environments. We generated a single phenotypic reaction (see supplemental docs) norm for each group of genotypes (i.e., genotypes native to the same environment) based on the first terms of Eqn. 4. Then we generated reaction norm data for individual genotypes by adding the interaction term and error to the overall reaction norms.

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

**Data Processing Description**

**BCO-DMO Processing:**
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Added a conventional header with dataset name, PI names, version date

[ table of contents | back to top ]

## Data Files

| File |
|---|
| **power_output_results.csv** (Comma Separated Values (.csv), 4.48 MB) MD5:d9dc39a0b9301e1c8e6d0577c4b2c17f<br>Primary data file for dataset ID 877456 |

[ table of contents | back to top ]

## Supplemental Files

| File |
|---|
| **Equation for power output results**<br>filename: power_analyses_pasted_graphic.pdf (Portable Document Format (.pdf), 10.81 KB) MD5:feaf1a0a6cbb775a8b50d98352a9a825 |

[ table of contents | back to top ]

## 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*

[ table of contents | back to top ]

## Related Datasets

**IsRelatedTo**

Albecker, M., Trussell, G. C., Lotterhos, K. (2025) **Metadata for studies from meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2) Version Date 2025-06-05 doi:10.26008/1912/bco-dmo.877414.2 [view at BCO-DMO]

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]

**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

[ table of contents | back to top ]

## Parameters

| Parameter | Description | Units |
|---|---|---|
| row | identifier | unitless |
| replicate | identifier | unitless |
| env_scenario | identifies whether reciprocal transplant (1) or common garden design (2) was used | unitless |
| delta_env | degree of environmental change | unitless |
| delta_gen | degree of genetic change | unitless |
| sample_size | sample size | unitless |
| total_samples | total sample | unitless |
| n_env | total number of environments | unitless |
| n_pop | total number of genotypes | unitless |
| std_dev | degree of error | unitless |
| interaction | deviation from linearity | unitless |

| | | |
|---|---|---|
| Sim_time | minutes to complete simulation | unitless |
| true_cov | population covGE | unitless |
| covariance | sample covGE estimate | unitless |
| covariance_lwrCI | lower confidence interval for CovGE sample estimate | unitless |
| covariance_uprCI | upper confidence interval for CovGE sample estimate | unitless |
| covariance_pvalue | significance of sample estimate from 0 | unitless |
| true_cov_means | population CovGE for data in means format | unitless |
| cov_means | sample estimate for CovGE for data in means format | unitless |
| cov_means_lwrCI | lower confidence interval for CovGE sample estimate for means data | unitless |
| cov_means_uprCI | upper confidence interval for CovGE sample estimate for means data | unitless |
| cov_means_pvalue | significance of sample estimate from 0 for means data | unitless |
| GxE_Anova | magnitude of interaction | unitless |
| true_GxE_emm | population interaction magnitude | unitless |
| GxE_emm | sample estimate for interaction magnitude | unitless |
| GxE_emm_lwrCI | lower confidence interval for interaction magnitude | unitless |
| GxE_emm_uprCI | upper confidence interval for interaction magnitude | unitless |
| GxE_emm_pvalue | significance of sample estimate for GxE | unitless |
| true_GxE_omega | population GxE using omega squared approach | unitless |
| GxE_omega | sample GxE estimate using omega squared approach | unitless |

| | | |
|---|---|---|
| GxE_omega_lwrCI | lower confidence interval for interaction using omega squared approach | unitless |
| GxE_omega_uprCI | upper confidence interval for interaction using omega squared approach | unitless |
| GxE_omega_pvalue | significance of sample estimate for interaction using omega squared approach | unitless |
| true_GxE_means | populations GxE using means approach | unitless |
| GxE_means | sample estimate for GxE using means approach | unitless |
| GxE_means_lwrCI | lower confidence interval for interaction for means data | unitless |
| GxE_means_uprCI | upper confidence interval for interaction for means data | unitless |
| GxE_means_pvalue | significance of interaction term for means data | unitless |

[ table of contents | back to top ]

## 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.

[ table of contents | back to top ]

## Funding


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


[ table of contents | back to top ]