Model code and output for a comparison of methods for meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results

Website: https://www.bco-dmo.org/dataset/934896
Data Type: model results, Synthesis
Version: 1
Version Date: 2024-08-06

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

Contributors	Affiliation	Role
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Abstract
The data for the CovGE meta-analysis from the RCN-ECS project were published as dataset "Metadata for studies from meta-analysis investigating covariance between genetic and environmental (CovGE) effects in phenotypic results (DOI: 10.26008/1912/bco-dmo.877414.1)." However, this dataset contains a meta-analysis comparing our approach with the method described by Stamp and Hadfield (2020) in Ecology Letters. The data tables in this dataset contain output of the model described in forthcoming results publication Albecker et al. (n.d.) "Meta-analysis reveals patterns of cogradient and countergradient variation." This results publication used meta-analysis to measure CovGE and GxE across 354 phenotypes within 64 studies. Katie Lotterhos, with input from the authors, created the "Behavior_of_PL_metric.Rmd" file which provides an in-depth comparison of the two measures and contains R code and rendered figures created with R-Markdown (.Rmd). Dr. Lotterhos documented code and interpretation to demonstrate similarities and contrasts among the two approaches (see Supplemental File "Behavior_of_PL_metric.pdf"). She also uses subsets of simulated data to demonstrate how the two approaches calculate CovGE or PL metric using the same data.

Table of Contents

Methods & Sampling

Simulated data was generated in part with R code (see file "Behavior of PL metric (Supplementary Materials 2)") and in part from simulations taken from Albecker et al. 2022. To create those simulations, we performed the following:

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 affected CovGE, as well

as the ability to detect and measure these patterns. We simulated datasets with total sample sizes (number of environments × number of genotypes × sample size) between 32 and 500 individuals. For reciprocal transplant data, we simulated genotypic effects that increased linearly at rate γ along an environmental variable (e) for genotypes equally spaced from environment $j = [1, 2,... n_{env}]$. We generated unitless phenotypic data based on the equation: In this equation, the phenotype of individual k from genotype i in environment j is given by the genotypic effect (intercept, $(i - 1) \times \gamma$), the reaction norm (where e_j is the value of the environment and β is the slope of the reaction norm), an interaction term for genotype i in environment j (η_{ij}) that describes the deviation of the reaction norm from linearity, and error (ε_{ijk}). When $\eta_{ij} = 0$, GxE is absent. When $\gamma = 0$ (i.e. when $V_p = V_E + V_{GxE}$, Equation 1), $\beta = 0$ (i.e. $V_p = V_G + V_{GxE}$, Equation 1), or η_{ij} is large, CovGE is absent. Interaction terms (η_{ij}) were drawn from a normal distribution with mean of zero and variance equal to the number of genotypes. Random error (ε_{ijk}) 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 (ε_{ijk}) were used to assess population parameters (see file "Supplemental Materials 1", figure 3). For common garden designs, we adjusted this approach to model designs in which different numbers of genotypes were reared in two common environments (see file "Supplemental Materials 1", figure 4, panel c). We generated a single phenotypic reaction norm for each group of genotypes (i.e. genotypes native to the same environment) based on the first terms of Equation 4 (e.g. $(i - 1)\gamma + \beta e_j$). Then we generated reaction norm data for individual genotypes by adding the interaction term (η_{ij}) and error (ε_{ijk}) to the overall reaction norms.

Data Processing Description

R (version 4.3.0)

BCO-DMO Processing Description

BCO-DMO Data Manager Processing Notes:
First column (an index column) of the output files had no column name so added label "row_id" to:
* Power_output_results.csv (text/csv)
* Variance_output_results.csv
* PL_output_results.csv

Files 20231102StampHadfield_KEL.Rmd and 20231102StampHadfield_KEL.pdf
renamed Behavior_of_PL_metric.Rmd and Behavior_of_PL_metric.pdf and attached as supplemental files to this dataset.

[table of contents | back to top]

Data Files

File

phendf: Phenotype output results

filename: phenotype_output_results.csv

(Comma Separated Values (.csv), 55.01 MB)
MD5:ec7144a08ab59d2a0a6e1be1d6167fc5

This datasheet contains the parameters used to generate phenotypic data that produce covariance (and related) estimates in the other Data Files in this dataset (e.g., power_df, etc.)

PLdf: PL output results

filename: PL_output_results.csv

(Comma Separated Values (.csv), 313.62 KB)
MD5:9cb231e1d7dcc6081cbdb0f71adc39d3

This datasheet shows the results where, for 2 genotype/2 environment cases, we calculated Covariance using the PL metric approach described in Stamps and Hadfield (2020) so that we could directly compare to results in Albecker et al. (2022).

powdf: Power output results

filename: Power_output_results.csv

(Comma Separated Values (.csv), 558.00 KB)
MD5:9b0324ec8badd46c91f69689f4258294

This datasheet shows results for the power analysis originally published in Albecker et al. 2022, Ecology Letters. It was used to demonstrate that error rates are similar among covariance estimates using raw data and phenotypic means (see file "Supplemental Materials 1") .

vardf: Variance output results

filename: Variance_output_results.csv

(Comma Separated Values (.csv), 452.01 KB)
MD5:1ee7518473bd784cbe1a2860b6e4b8a8

This datasheet shows the data extracted from simulations showing how phenotypic variation is estimated using traditional variance partitioning methods from Falconer and Mackay 1996 where $V_p = V_g + V_e + V_{gxe} + 2*V_{covGE} + error (V_e)$

[table of contents | back to top]

Supplemental Files

File

Behavior of PL metric (R Markdown File)

filename: Behavior_of_PL_metric.Rmd

(Plain Text, 23.03 KB)
MD5:e1a4fa2bce7c01ea83c6c09e352e3989

See supplemental file "Behavior of PL metric (Supplementary Materials 2)" for more information about this R Markdown file and the model.
title: "Behavior of PL metric," author: "KE Lotterhos, M Albecker, G Trussel, " date: "August 2024"

Behavior of PL metric (Supplementary Materials 2)

filename: Behavior_of_PL_metric.pdf

(Portable Document Format (.pdf), 451.60 KB)
MD5:2f94e6e1d464c1506d1d24785e1e3868

Description of the model that's been used that made these output Data Files and accompanies the R markdown file "Behavior_of_PL_metric.Rmd" (corresponds to Supplementary Materials 2 of Albecker et al. (n.d.) in review).
 "Behavior of PL metric": KE Lotterhos, M Albecker, G Trussel, August 2024.

Parameter (column) information for output data tables

filename: parameter-column-information.txt

(Plain Text, 9.20 KB)
MD5:7629b136092fab15422ce7a709e93256

This file contains the column names and descriptions of the output data tables in this dataset:
PL_output_results.csv
Power_output_results.csv
Variance_output_results.csv
phenotype_output_results.csv

Supplementary Materials 1

filename: Supplemental_Materials1.pdf

(Portable Document Format (.pdf), 440.66 KB)
MD5:dc05453450b6985fdef2471d57ca93a9

Supplementary Materials 1: Meta-analysis reveals patterns of cogradient and countergradient variation. (corresponds to Supplementary Materials 1 of Albecker et al. (n.d.) in review).

[table of contents | back to top]

Related Publications

Albecker, M. A., Bittar, T. B., Trussell, G. C., & Lotterhos, K. E. (n.d.). Meta-analysis reveals patterns of cogradient and countergradient variation. American Naturalist. Manuscript submitted for publication.
Results

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

Hill, W. G., & Mackay, T. F. C. (2004). D. S. Falconer and Introduction to Quantitative Genetics. Genetics, 167(4), 1529–1536. https://doi.org/10.1093/genetics/167.4.1529
Methods

R Core Team (2023). R: A language and environment for statistical computing. R v4.3.0. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Stamp, M. A., & Hadfield, J. D. (2020). The relative importance of plasticity versus genetic differentiation in explaining between population differences; a meta-analysis. Ecology Letters, 23(10), 1432–1441. Portico. https://doi.org/10.1111/ele.13565
Methods

[table of contents | back to top]

Related Datasets

IsRelatedTo

Albecker, M., Trussell, G., Lotterhos, K. (2022) **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 1) Version Date 2022-08-09 doi:10.26008/1912/bco-dmo.877414.1 [view at BCO-DMO]
Relationship Description: Data for this "CovGE MetaAnalysis" (DOI: 10.26008/1912/bco-dmo.934896.1) are in the dataset: "Metadata from a meta-analysis on CovGE in phenotypic results" (DOI: 10.26008/1912/bco-dmo.877414.1).

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[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.

Funding

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