

Package: OmicsBraid (via r-universe)

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Type Package

Title Covariance-Aware Inference of Cross-Omic Effect Trajectories

Version 0.2.2

Description A research-oriented statistical framework for comparing standardized biological effects across matched omics layers. It estimates layer-specific standardized effects, accounts for cross-omic dependence using matched-subject bootstrap correlations, tests multivariate omnibus evidence, synthesizes consensus effects with generalized least squares, quantifies cross-omic heterogeneity, performs practical-equivalence testing, fits covariance-aware ordered GLS effect trajectories, classifies hierarchical cross-layer effect patterns with separate confirmatory and suggestive states, supports analytic and subject-bootstrap confidence intervals for layer and consensus effects, supports empirical matched-subject permutation and centered-bootstrap calibration of omnibus and heterogeneity tests for non-Gaussian settings, and creates evidence-forest and effect-braid visualizations. The package is designed for analysis-ready bulk multi-omics data or externally estimated summary statistics. It does not perform raw sequencing or mass-spectrometry preprocessing.

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as_omics_braid_data	<i>Coerce supported objects to OmicsBraid data</i>
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Description

Coerce supported objects to OmicsBraid data

Usage

```
as_omics_braid_data(x, ...)
```

Arguments

x	Object to coerce.
...	Additional arguments.

bootstrap_consensus_intervals	<i>Bootstrap confidence intervals for GLS consensus effects</i>
-------------------------------	---

Description

Uses matched subject-bootstrap layer-effect draws from ‘bootstrap_effect_covariance()’ and the fitted covariance structure to form a bootstrap distribution of the GLS consensus effect. The hypothesis tests and analytic standard errors remain unchanged; these intervals are intended for robust uncertainty reporting and coverage validation.

Usage

```
bootstrap_consensus_intervals(
  effects,
  bootstrap,
  integrated = NULL,
  method = c("percentile", "basic"),
  conf_level = 0.95,
  min_boot = 100L,
  min_omics = 2L
)
```

Arguments

effects	Layer-specific effect table.
bootstrap	An 'omics_braid_covariance' object.
integrated	Optional output of 'integrate_effects()'.
method	"percentile" or "basic".
conf_level	Confidence level.
min_boot	Minimum usable bootstrap consensus draws.
min_omics	Minimum finite omic layers required in an individual bootstrap replicate.

Value

One row per entity with bootstrap consensus interval diagnostics.

bootstrap_effect_covariance

Estimate cross-omic effect covariance by matched-subject bootstrap

Description

Biological subjects are resampled as whole units, preserving their matched measurements across omics. Bootstrap correlations are estimated for each entity and combined with analytic marginal standard errors from 'estimate_effects()': $V = \text{diag}(\text{SE}) R_{\text{boot}} \text{diag}(\text{SE})$. This stabilizes marginal uncertainty while retaining empirically estimated cross-layer dependence.

Usage

```
bootstrap_effect_covariance(
  data,
  group,
  reference,
  comparison,
  effects = NULL,
  entities = NULL,
  B = 500L,
  seed = 1L,
  min_n = 3L,
  shrinkage = 0.05,
  min_complete = 50L,
  stratified = TRUE
)
```

Arguments

data	An 'omics_braid_data' object.
group	Metadata group column.
reference	Reference group.
comparison	Comparison group.
effects	Optional output of 'estimate_effects()'.
entities	Optional entities to bootstrap. By default, entities present in at least two omics.
B	Number of subject-level bootstrap replicates.
seed	Random seed.
min_n	Minimum observations per group within an omic.
shrinkage	Correlation shrinkage toward the identity in [0,1].
min_complete	Minimum usable bootstrap pairs to estimate a correlation.
stratified	Logical; resample subjects separately within reference and comparison groups. This preserves the observed group sizes and is recommended for fixed two-group designs.

Value

Object of class 'omics_braid_covariance' containing a covariance matrix per entity.

bootstrap_effect_intervals

Bootstrap confidence intervals for layer-specific standardized effects

Description

Constructs nonparametric confidence intervals for Hedges' g using the matched, group-stratified subject bootstrap draws generated by 'bootstrap_effect_covariance()'. Percentile and basic intervals reuse those bootstrap draws. BCa intervals additionally estimate the acceleration term from leave-one-subject-out jackknife effects within each omic.

Usage

```
bootstrap_effect_intervals(
  effects,
  bootstrap,
  method = c("percentile", "basic", "bca"),
  conf_level = 0.95,
  min_boot = 100L,
  data = NULL,
  group = NULL,
  reference = NULL,
  comparison = NULL,
  min_n = 3L
)
```

Arguments

effects	Output of 'estimate_effects()' after any scientifically justified orientation has been applied.
bootstrap	An 'omics_braid_covariance' object containing 'boot_effects'.
method	One of "percentile", "basic", or "bca".
conf_level	Confidence level.
min_boot	Minimum number of finite bootstrap draws required per entity-by-omic effect.
data	Required only for 'method = "bca"'; an 'omics_braid_data' object used to calculate leave-one-subject-out jackknife effects.
group	Metadata group column, required for BCa.
reference	Reference-group label, required for BCa.
comparison	Comparison-group label, required for BCa.
min_n	Minimum observations per group used for jackknife effects.

Details

These intervals are an uncertainty-reporting option. They do not replace the analytic standard errors or p-values used by the current OmicsBraid hypothesis tests unless a future method version explicitly validates such a change.

Value

A data frame with one row per usable entity-by-omic effect and bootstrap interval diagnostics.

braid_pattern_probabilities

Quantify uncertainty in effect-braid geometry

Description

Draws from a multivariate normal approximation to the estimated cross-omic effects and reports how often each practical geometric pattern occurs. These frequencies propagate estimation uncertainty; they are not Bayesian posterior probabilities and they do not replace the confirmatory inferential braid label.

Usage

```
braid_pattern_probabilities(
  effects,
  covariance = NULL,
  omic_order,
  margin = 0.3,
  n_draws = 2000L,
  trajectory_margin = 0.15,
  seed = 1L,
  min_slope = NULL
)
```

Arguments

effects	Effect table.
covariance	Optional bootstrap covariance object/list. If absent, omics are treated as independent.
omic_order	Ordered omics.
margin	Equivalence/negligible-effect margin; scalar or named by omic.
n_draws	Number of Monte Carlo draws per entity.
trajectory_margin	Practical trajectory threshold per layer transition.
seed	Random seed.
min_slope	Deprecated alias for ‘trajectory_margin’.

Value

Long data frame of geometric pattern frequencies per entity.

braid_results_table	<i>Create a one-row-per-entity master result table</i>
---------------------	--

Description

Create a one-row-per-entity master result table

Usage

```
braid_results_table(result)
```

Arguments

result	An ‘omics_braid_result’.
--------	--------------------------

Value

Data frame merging integrated inference, braid classification, and compact layer summaries.

classify_braids

Classify cross-omic braid patterns using inferential evidence

Description

Braid labels are deliberately conservative. Opposite statistically supported layer directions confirm inversion. Buffering and emergence require practical equivalence in the appropriate downstream/upstream layers. Concordance, attenuation, and amplification require all observed layers to support one direction and use a covariance-aware GLS trajectory test. If the joint-null omnibus test is not rejected and practical equivalence is not established, the result is labelled ‘no_detectable_effect’ rather than incorrectly claiming equivalence.

Usage

```
classify_braids(
  equivalence,
  omic_order,
  covariance = NULL,
  integrated = NULL,
  trend = NULL,
  trajectory_margin = 0.15,
  alpha = 0.05,
  min_slope = NULL
)
```

Arguments

equivalence	Output of ‘test_equivalence()’.
omic_order	Ordered character vector describing the biological/display order of omics.
covariance	Optional covariance object used when a trend table must be computed internally.
integrated	Optional output of ‘integrate_effects()’. Supplying it allows ‘no_detectable_effect’ to be distinguished from generic uncertainty.
trend	Optional output of ‘test_braid_trend()’. If absent it is computed.
trajectory_margin	Smallest meaningful effect change per one-layer transition for attenuation/amplification.
alpha	Local inferential significance level.
min_slope	Deprecated alias for ‘trajectory_margin’ retained for early OmicsBraid prototypes.

Details

A separate ‘suggestive_pattern’ is derived from effect geometry only. It can be useful when the inferential pattern is unresolved because the data are too imprecise, but it is not a confirmatory conclusion.

Value

One row per entity containing confirmatory and suggestive labels plus trajectory diagnostics.

empirical_omics_tests *Empirically calibrate OmicsBraid omnibus and heterogeneity tests*

Description

Provides resampling-based p-values for the two cross-omic quadratic tests. The omnibus test can be calibrated by matched-subject label permutation or by a centered matched-subject bootstrap. The heterogeneity test can be calibrated by a raw-data null-shift matched bootstrap (recommended) or by an effect-level centered bootstrap under the fitted common-effect null.

Usage

```
empirical_omics_tests(
  data,
  group,
  reference,
  comparison,
  effects = NULL,
  entities = NULL,
  B = 499L,
  seed = 1L,
  min_n = 3L,
  min_omics = 2L,
  min_complete = 100L,
  omnibus_method = c("permutation", "centered_bootstrap"),
  heterogeneity_method = c("null_shift_bootstrap", "centered_bootstrap"),
  orientation = NULL,
  p_adjust = "BH"
)
```

Arguments

data	An ‘omics_braid_data’ object containing sample-level assays.
group	Metadata column containing the two groups.
reference	Reference-group label.
comparison	Comparison-group label.
effects	Optional layer-specific effect table. If supplied after ‘orient_omics()’, pass the same ‘orientation’ so resampled effects receive the identical sign transformation.
entities	Optional entities to calibrate. By default, entities observed in at least ‘min_omics’ layers are used.
B	Number of resampling replicates for each empirical null.

seed	Random seed.
min_n	Minimum observations per group within an omic.
min_omics	Minimum omic layers per entity.
min_complete	Minimum complete resampling draws required for a p-value.
omnibus_method	Either "permutation" or "centered_bootstrap". Permutation is appropriate for the global null in an exchangeable two-group design. Centered bootstrap is a nonparametric alternative.
heterogeneity_method	"null_shift_bootstrap" (recommended robust calibration) or "centered_bootstrap". Ordinary label permutation is not used because the heterogeneity null permits a common non-zero effect.
orientation	Optional named +1/-1 vector applied to the resampled layer effects. This must match any scientific orientation already applied to 'effects'.
p_adjust	Multiple-testing method for empirical p-values.

Details

The resampling is performed at the biological-subject level: all available omic measurements belonging to a subject remain linked. This preserves the cross-omic dependence that would be destroyed by shuffling individual assay matrices independently.

Empirical calibration is intended as a robust alternative when the chi-square reference distributions used by 'integrate_effects()' may be inaccurate, for example under heavy-tailed sampling distributions. The asymptotic statistics remain available and are not overwritten by this function.

Value

A data frame containing asymptotic-independent empirical omnibus and heterogeneity p-values, empirical critical values, and resampling diagnostics.

estimate_effects	<i>Estimate layer-specific standardized effects</i>
------------------	---

Description

Estimates Hedges' g for a two-group contrast in each feature/pathway and omic. Inputs should already be quality-controlled and normalized appropriately for their assay technology. Hedges' g is scale-free but does not repair poor raw preprocessing, severe censoring, or inappropriate transformations.

Usage

```
estimate_effects(
  data,
  group,
  reference,
  comparison,
  entities = NULL,
  min_n = 3L,
  conf_level = 0.95,
  p_adjust = "BH"
)
```

Arguments

<code>data</code>	An 'omics_braid_data' object.
<code>group</code>	Metadata column containing the two groups.
<code>reference</code>	Reference group label.
<code>comparison</code>	Comparison group label. Positive effects mean comparison > reference.
<code>entities</code>	Optional character vector limiting features/pathways.
<code>min_n</code>	Minimum non-missing observations per group and omic.
<code>conf_level</code>	Confidence level.
<code>p_adjust</code>	Multiple-testing method applied separately within each omic.

Value

Data frame of effect estimates and uncertainty.

<code>harmonize_entities</code>	<i>Harmonize assay-specific feature identifiers to common entities</i>
---------------------------------	--

Description

Maps feature IDs within each omic to a shared entity identifier for entity-level cross-omic analysis (for example Ensembl RNA identifiers and UniProt proteins to a common gene symbol). Many-to-one mappings are rejected by default because collapsing isoforms/probes changes the scientific estimand.

Usage

```
harmonize_entities(
  data,
  mapping,
  collapse = c("error", "mean", "median"),
  min_mapped = 1L
)
```

Arguments

data	An 'omics_braid_data' object.
mapping	Data frame with columns 'omic', 'feature_id', and 'entity'.
collapse	How to handle multiple assay features mapping to one entity: "error" (default), "mean", or "median".
min_mapped	Minimum mapped entities required per retained omic.

Value

An 'omics_braid_data' object with harmonized entity row names and a mapping report stored in 'attr(x, "entity_harmonization")'.

integrate_effects	<i>Integrate effects across omic layers and quantify heterogeneity</i>
-------------------	--

Description

Uses generalized least squares (GLS) to estimate a common cross-omic effect. A generalized Cochran Q statistic tests whether the layer-specific effects are compatible with a common effect after accounting for their sampling covariance. A separate multivariate Wald-type omnibus statistic tests the joint null that all layer effects are zero; unlike the consensus effect, this test does not cancel equally strong effects occurring in opposite directions. The reported I2-like statistic is descriptive and should not be interpreted as literal between-study heterogeneity because omics layers are not studies.

Usage

```
integrate_effects(
  effects,
  covariance = NULL,
  min_omics = 2L,
  p_adjust = "BH",
  conf_level = 0.95
)
```

Arguments

effects	Data frame containing 'entity', 'omic', 'effect', and 'se'.
covariance	Optional output of 'bootstrap_effect_covariance()' or a named list of covariance matrices.
min_omics	Minimum omics per entity.
p_adjust	Multiple-testing method for integrated and heterogeneity p-values.
conf_level	Confidence level for the analytic GLS consensus interval.

Value

Data frame of integrated effects and heterogeneity diagnostics.

omics_braid_data	<i>Construct an OmicsBraid data object</i>
------------------	--

Description

Construct an OmicsBraid data object

Usage

```
omics_braid_data(assays, metadata, sample_id = "sample_id", annotation = NULL)
```

Arguments

assays	Named list of numeric matrices. Features are rows and samples are columns.
metadata	Data frame containing one row per biological sample.
sample_id	Column in 'metadata' holding sample identifiers.
annotation	Optional feature annotation data frame.

Value

An object of class 'omics_braid_data'.

orient_omics	<i>Harmonize the sign orientation of omic-layer effects</i>
--------------	---

Description

Some omic measurements have an interpretation whose natural direction is opposite to an activity/abundance scale used in other layers. This helper multiplies selected omic effects by +1 or -1 and applies the corresponding sign transformation to covariance matrices. Use it only when the orientation is scientifically justified; it must not be used to force apparent agreement.

Usage

```
orient_omics(effects, covariance = NULL, orientation)
```

Arguments

effects	Effect table with 'omic' and 'effect' columns.
covariance	Optional OmicsBraid covariance object or named covariance list.
orientation	Named numeric vector with one value (+1 or -1) per omic to be re-oriented. Omics not named default to +1.

Value

A list with oriented 'effects' and 'covariance'.

plot_braid_heatmap	<i>Plot a braid heatmap across entities and omics</i>
--------------------	---

Description

Plot a braid heatmap across entities and omics

Usage

```
plot_braid_heatmap(
  result,
  entities = NULL,
  omic_order = result$settings$omic_order
)
```

Arguments

result	An 'omics_braid_result'.
entities	Optional entities; default top 25 by integrated adjusted p-value.
omic_order	Optional omic order.

Value

A ggplot object.

plot_concordance_map	<i>Plot concordance versus integrated significance</i>
----------------------	--

Description

Plot concordance versus integrated significance

Usage

```
plot_concordance_map(
  result,
  label_top = 0L,
  metric = c("evidence_direction_agreement", "direction_agreement", "i2_consistency"),
  significance = c("omnibus", "consensus")
)
```

Arguments

result	An 'omics_braid_result'.
label_top	Number of most significant entities to label.
metric	Concordance metric: evidence-qualified directional agreement (default), raw weighted directional agreement, or descriptive I2-based consistency.
significance	Evidence axis: multivariate omnibus (default) or GLS consensus-effect significance.

Value

A ggplot object.

plot_effect_braid	<i>Plot an Effect Braid</i>
-------------------	-----------------------------

Description

Plot an Effect Braid

Usage

```
plot_effect_braid(  
  result,  
  entity,  
  omic_order = result$settings$omic_order,  
  show_ci = TRUE,  
  show_equivalence_region = TRUE  
)
```

Arguments

result	An 'omics_braid_result'.
entity	Entity/pathway to display.
omic_order	Optional omic order.
show_ci	Show confidence intervals.
show_equivalence_region	Shade the negligible-effect region.

Value

A ggplot object.

plot_evidence_forest *Plot an Omics Evidence Forest*

Description

Plot an Omics Evidence Forest

Usage

```
plot_evidence_forest(result, entity, omic_order = result$settings$omic_order)
```

Arguments

result	An 'omics_braid_result'.
entity	Entity/pathway to display.
omic_order	Optional omic order.

Value

A ggplot object.

read_omics_braid *Read OmicsBraid input files*

Description

Read OmicsBraid input files

Usage

```
read_omics_braid(
  metadata_file,
  assay_files,
  sample_id = "sample_id",
  sep = NULL,
  annotation_file = NULL
)
```

Arguments

metadata_file	CSV/TSV file containing sample metadata.
assay_files	Named character vector or named list mapping omic names to CSV/TSV files.
sample_id	Metadata sample identifier column.
sep	Separator. If 'NULL', inferred from file extension ('.tsv'/''.txt' -> tab; otherwise comma).
annotation_file	Optional annotation CSV/TSV file.

Value

An 'omics_braid_data' object.

run_omics_braid	<i>Run the complete OmicsBraid workflow on sample-level data</i>
-----------------	--

Description

Run the complete OmicsBraid workflow on sample-level data

Usage

```
run_omics_braid(
  data,
  group,
  reference,
  comparison,
  omic_order = names(data$assays),
  entities = NULL,
  pathway_mapping = NULL,
  pathway_method = "mean_z",
  min_pathway_features = 3L,
  bootstrap_B = 500L,
  bootstrap_shrinkage = 0.05,
  empirical_tests = FALSE,
  empirical_B = 499L,
  empirical_omnibus_method = c("permutation", "centered_bootstrap"),
  empirical_heterogeneity_method = c("null_shift_bootstrap", "centered_bootstrap"),
  empirical_use_as_primary = FALSE,
  ci_method = c("analytic", "percentile", "basic", "bca"),
  integrated_ci_method = c("analytic", "percentile", "basic"),
  ci_conf_level = 0.95,
  ci_min_boot = 100L,
  orientation = NULL,
  equivalence_margin = 0.3,
  alpha = 0.05,
  state_basis = c("local", "adjusted"),
  equivalence_p_adjust = "BH",
  trajectory_margin = 0.15,
  trend_p_adjust = "BH",
  min_slope = NULL,
  pattern_draws = 2000L,
  seed = 1L
)
```

Arguments

data	An 'omics_braid_data' object.
group	Metadata group column.
reference	Reference group.
comparison	Comparison group.
omic_order	Biological/display order of omics. Defaults to assay order.
entities	Optional entities to analyze.
pathway_mapping	Optional mapping passed to 'score_pathways()'; if supplied, analysis is performed on pathway scores.
pathway_method	Pathway scoring method.
min_pathway_features	Minimum pathway features per omic.
bootstrap_B	Bootstrap replicates for cross-omic covariance. Set to 0 to assume independence.
bootstrap_shrinkage	Correlation shrinkage.
empirical_tests	Logical; if 'TRUE', calculate additional resampling- calibrated omnibus and heterogeneity p-values using 'empirical_omics_tests()'.
empirical_B	Number of empirical resampling replicates.
empirical_omnibus_method	"permutation" or "centered_bootstrap".
empirical_heterogeneity_method	"null_shift_bootstrap" (recommended) or "centered_bootstrap".
empirical_use_as_primary	Logical; if 'TRUE', empirical p-values replace asymptotic p-values when available for downstream omnibus evidence. The original asymptotic p-values are retained in separate columns.
ci_method	Layer-effect confidence interval method: "analytic", "percentile", "basic", or "bca". Bootstrap intervals change interval reporting only; analytic SEs and p-values remain available.
integrated_ci_method	Consensus-effect confidence interval method: "analytic", "percentile", or "basic".
ci_conf_level	Confidence level for analytic/bootstrap intervals.
ci_min_boot	Minimum finite bootstrap draws required before a bootstrap interval replaces the analytic interval.
orientation	Optional named +1/-1 vector to harmonize omic effect directions.
equivalence_margin	Smallest effect size of interest for practical equivalence.
alpha	Significance level for local difference/equivalence and braid inference.

state_basis	Use local or multiplicity-adjusted inferential states for deterministic braid labels.
equivalence_p_adjust	Multiple-testing method retained for adjusted equivalence/difference evidence.
trajectory_margin	Smallest meaningful standardized-effect change per one-layer transition.
trend_p_adjust	Multiple-testing method retained for adjusted trajectory evidence.
min_slope	Deprecated alias for 'trajectory_margin'.
pattern_draws	Monte Carlo draws for geometric uncertainty propagation.
seed	Random seed.

Value

An object of class 'omics_braid_result'.

run_omics_braid_summary

Run OmicsBraid from externally estimated summary statistics

Description

Run OmicsBraid from externally estimated summary statistics

Usage

```
run_omics_braid_summary(
  effects,
  covariance = NULL,
  omic_order,
  orientation = NULL,
  equivalence_margin = 0.3,
  alpha = 0.05,
  state_basis = c("local", "adjusted"),
  equivalence_p_adjust = "BH",
  trajectory_margin = 0.15,
  trend_p_adjust = "BH",
  min_slope = NULL,
  pattern_draws = 2000L,
  seed = 1L
)
```

Arguments

effects	Data frame with at least 'entity', 'omic', 'effect', and 'se'.
covariance	Optional named list of entity-specific covariance matrices.
omic_order	Ordered omics.

orientation	Optional named +1/-1 vector to harmonize omic effect directions.
equivalence_margin	Smallest effect size of interest.
alpha	Significance level.
state_basis	Use local or multiplicity-adjusted inferential states for deterministic braid labels.
equivalence_p_adjust	Multiple-testing method retained for adjusted equivalence/difference evidence.
trajectory_margin	Smallest meaningful standardized-effect change per one-layer transition.
trend_p_adjust	Multiple-testing method retained for adjusted trajectory evidence.
min_slope	Deprecated alias for 'trajectory_margin'.
pattern_draws	Monte Carlo draws.
seed	Random seed.

Value

'omics_braid_result' without sample-level data.

score_pathways	<i>Score pathways within each omic layer</i>
----------------	--

Description

This convenience function z-standardizes each feature across samples within an omic and then aggregates features assigned to the same pathway. OmicsBraid's inferential core can also accept externally computed pathway/activity scores, which is recommended when a domain-specific scoring method is preferred.

Usage

```
score_pathways(
  data,
  mapping,
  method = c("mean_z", "median_z"),
  min_features = 3L,
  center = TRUE,
  scale = TRUE
)
```

Arguments

data	An 'omics_braid_data' object.
mapping	Data frame with columns 'omic', 'feature_id', and 'pathway'.
method	Aggregation method: "mean_z" or "median_z".
min_features	Minimum mapped features per pathway within an omic.
center	Logical; center feature values before aggregation.
scale	Logical; scale feature values before aggregation.

Value

An 'omics_braid_data' object whose assay rows are pathways.

simulate_braid_data	<i>Simulate multi-omics data with known braid patterns</i>
---------------------	--

Description

Generates matched sample-level data for method development and validation. Residuals are correlated across omic layers for each entity, allowing the covariance, heterogeneity, equivalence, and classification procedures to be tested against known cross-layer effects.

Usage

```
simulate_braid_data(
  n_per_group = 60L,
  n_reference = NULL,
  n_comparison = NULL,
  omics = c("RNA", "Protein", "Metabolite"),
  patterns = NULL,
  rho = 0.4,
  missing_rate = 0,
  modality_missing_rate = 0,
  residual_distribution = c("normal", "t"),
  t_df = 5,
  seed = 1L
)
```

Arguments

n_per_group	Default samples per group when 'n_reference' and 'n_comparison' are not supplied.
n_reference	Optional reference-group sample size.
n_comparison	Optional comparison-group sample size.
omics	Ordered omic names.
patterns	Named list of true standardized mean shifts, one numeric vector per entity.
rho	Scalar equicorrelation or an omic-by-omic residual correlation matrix.
missing_rate	Independent value-level missingness probability.
modality_missing_rate	Probability of an entire subject modality being absent; scalar or named by omic.
residual_distribution	"normal" or heavy-tailed "t" residuals.
t_df	Degrees of freedom for t residuals; must exceed 2 for finite variance.
seed	Random seed.

Value

List with 'data' ('omics_braid_data') and 'truth' table.

test_braid_trend	<i>Test ordered cross-omic effect trajectories with generalized least squares</i>
------------------	---

Description

Fits a covariance-aware linear trajectory to standardized effects across an explicitly ordered set of omic layers. Effects are aligned to the dominant observed direction before fitting, so a positive slope represents increasing absolute effect magnitude (amplification) and a negative slope represents decreasing magnitude (attenuation). Three practical hypotheses are evaluated: a meaningfully positive slope, a meaningfully negative slope, and practical equivalence of the slope to a flat trajectory within '[-trajectory_margin, +trajectory_margin]'.

Usage

```
test_braid_trend(  
  effects,  
  covariance = NULL,  
  omic_order,  
  trajectory_margin = 0.15,  
  alpha = 0.05,  
  min_omics = 2L,  
  p_adjust = "BH"  
)
```

Arguments

effects	Data frame containing 'entity', 'omic', 'effect', and 'se'.
covariance	Optional output of 'bootstrap_effect_covariance()' or a named list of entity-specific covariance matrices. If omitted, layer estimates are treated as independent for this calculation.
omic_order	Ordered character vector describing the layer trajectory.
trajectory_margin	Smallest meaningful change in standardized effect per one-layer transition. A scalar greater than zero.
alpha	Local significance level used to define the trend state.
min_omics	Minimum observed layers required.
p_adjust	Multiple-testing method used for confirmatory adjusted trend p-values across entities. Local states remain the default for braid geometry.

Details

The trend test is intended for ordered layers when attenuation/amplification is scientifically meaningful. It does not establish causality or temporal direction.

Value

One row per entity containing the aligned GLS slope, uncertainty, practical trend tests, and local/adjusted trajectory states.

test_equivalence	<i>Test practical equivalence to a negligible effect region</i>
------------------	---

Description

Performs two one-sided tests (TOST) for whether each standardized effect lies within ‘[-margin, +margin]’. It reports both local (entity-specific) and multiplicity-adjusted inferential states. Local states are recommended for describing the geometry of an individual braid because they do not change merely when unrelated entities are added to the analysis; adjusted states are retained for confirmatory screening across many entities.

Usage

```
test_equivalence(  
  effects,  
  margin = 0.3,  
  alpha = 0.05,  
  p_adjust = "BH",  
  state_basis = c("local", "adjusted")  
)
```

Arguments

effects	Effect table from ‘estimate_effects()’ or compatible summary statistics.
margin	Smallest effect size of interest on the standardized-effect scale; scalar or named by omic.
alpha	Significance level.
p_adjust	Multiple-testing adjustment applied separately within each omic.
state_basis	Which inferential state is copied to the legacy ‘state’ column: “local” (default) or “adjusted”.

Value

Effect table with TOST p-values, local/adjusted difference p-values, and both local and multiplicity-adjusted practical states.

`validate_omics_braid_data`*Validate an OmicsBraid data object*

Description

Validate an OmicsBraid data object

Usage

```
validate_omics_braid_data(x)
```

Arguments

`x` An 'omics_braid_data' object.

Value

Invisibly returns 'TRUE' or throws an informative error.

`write_omics_braid`*Export OmicsBraid results*

Description

Export OmicsBraid results

Usage

```
write_omics_braid(result, dir, save_plots = TRUE, top_n = 20L)
```

Arguments

`result` An 'omics_braid_result'.
`dir` Output directory.
`save_plots` Save overview PDF figures.
`top_n` Number of top entities for heatmap and individual plots.

Value

Invisibly returns the output directory.

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