Package 'OmicsBraid'

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Type Package

Title Covariance-Aware Inference of Cross-Omic Effect Trajectories

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. Methodological components draw on standardized mean-difference estimation described by Hedges (1981) <doi:10.3102/10769986006002107>, bootstrap resampling described by Efron (1979) <doi:10.1214/aos/1176344552>, and two one-sided equivalence testing described by Schuirmann (1987) <doi:10.1007/BF01068419>.

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Contents

as_omics_braid_data *Coerce supported objects to OmicsBraid data*

Description

Converts supported input objects into the standardized data structure used by OmicsBraid for downstream cross-omic analyses.

Usage

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

Arguments

x	Object to coerce.
...	Additional arguments passed to the appropriate coercion method.

Value

An object of class `omics_braid_data` containing the harmonized omics assays, sample metadata, and optional feature annotation, ready for downstream OmicsBraid analyses.

bootstrap_consensus_intervals *Bootstrap confidence intervals for GLS consensus effects*

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 = diag(SE) R_boot diag(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 *Create a one-row-per-entity master result table*

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 *Estimate layer-specific standardized effects*

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

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

Value

Data frame of effect estimates and uncertainty.

---

harmonize_entities *Harmonize assay-specific feature identifiers to common entities*

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 *Integrate effects across omic layers and quantify heterogeneity*

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 *Construct an OmicsBraid data object*

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 *Harmonize the sign orientation of omic-layer effects*

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 *Plot a braid heatmap across entities and omics*

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 *Plot concordance versus integrated significance*

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 *Plot an Effect Braid*

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` *Run the complete OmicsBraid workflow on sample-level data*

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` *Score pathways within each omic layer*

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` *Simulate multi-omics data with known braid patterns*

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` *Test ordered cross-omic effect trajectories with generalized least squares*

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 *Test practical equivalence to a negligible effect region*

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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