Package ‘lorbridge’

May 8, 2026

Type Package

Title Bridging Log-Odds Ratios and Correspondence Analysis via Closeness-of-Concordance Measures

Version 0.1.0

Date 2026-04-19

Description Provides a unified analytical workflow that bridges conventional binary and multinomial logistic regression with singly-ordered (SONSCA) and doubly-ordered (DONSCA) nonsymmetric correspondence analysis. Log-odds ratios (LORs) from logistic regression are re-expressed as cosine theta estimates and closeness-of-concordance measures (CCMs) -- including Yule's Q, Yule's Y, and r_meta -- on the familiar [-1, +1] scale introduced by Kim and Grochowalski (2019) <doi:10.3758/s13428-018-1161-1>. Bootstrap confidence intervals for cosine theta are provided throughout. The package is intended to help clinical and medical researchers interpret association strength from logistic regression in an intuitive, correlation-like metric, and to connect conventional regression results with geometric correspondence analysis visualisations.

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URL `https://github.com/sekangakim/lorbridge`

BugReports `https://github.com/sekangakim/lorbridge/issues`

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.3.3

Depends R (>= 4.1.0)

Imports CAvariants (>= 5.5), nnet (>= 7.3), stats

Suggests dplyr (>= 1.1.0), ggplot2 (>= 3.4.0), ggrepel (>= 0.9.0), graphics, tidyr (>= 1.3.0), knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

Date/Publication 2026-04-21 21:22:21 UTC

Contents

`blr_categorical` *Binary Logistic Regression with a Categorical (Ordinal) Predictor*

Description

Fits a binary logistic regression model with a categorical predictor (treated as an unordered factor with a user-specified reference level). For each non-reference category, reports the pairwise LOR, OR, Wald confidence interval, p-value, CCMs, and cosine theta from a 2 x J simple correspondence analysis (Kim & Grochowalski, 2019 bridge).

Usage

```
blr_categorical(outcome, predictor, ref_level = NULL, alpha = 0.05)
```

Arguments

`outcome`	Integer or numeric vector. Binary outcome (0/1).
`predictor`	Factor or character vector. Categorical predictor. Will be converted to a factor internally.
`ref_level`	Character. Reference category label (default: first level).
`alpha`	Numeric. Significance level for confidence intervals (default 0.05).

Details

Cosine theta is computed via a 1D singular value decomposition (SVD) of the standardised residual matrix of the 2 x J correspondence table, bypassing `CAvariants` (which requires at least 2 dimensions). In a 2-row table the 1D CA solution is exact, and cosine theta equals +1 or -1 for each non-reference column, with the sign indicating the direction of association relative to the reference category and majority group.

Value

A named list with elements:

model The fitted glm object.

results A data.frame with one row per non-reference category, containing LOR, OR, 95 percent CI, p-value, CCMs, and cosine theta.

tab_2xJ The 2 x J contingency table used for cosine theta.

References

Kim, S.-K., & Grochowalski, J. H. (2019). Gaining from discretization of continuous data: The correspondence analysis biplot approach. *Behavior Research Methods*, 51(2), 589-601. doi:10.3758/s1342801811611

Examples

```
data(lorbridge_data)
res <- blr_categorical(outcome   = lorbridge_data$minority,
                       predictor = lorbridge_data$VMbin,
                       ref_level = "VM4")
print(res$results)
```

`blr_continuous` *Binary Logistic Regression with a Continuous Predictor*

Description

Fits a binary logistic regression model with a single continuous predictor, standardised to unit standard deviation (per 1 SD). Reports the log-odds ratio (LOR), odds ratio (OR), Wald confidence interval, p-value, Nagelkerke R-squared, and the full set of closeness-of-concordance measures (CCMs) on the [-1, +1] scale.

Usage

```
blr_continuous(outcome, predictor, alpha = 0.05)
```

Arguments

`outcome`	Integer or numeric vector. Binary outcome (0/1).
`predictor`	Numeric vector. Continuous predictor variable. Will be standardised internally (mean = 0, SD = 1) before fitting.
`alpha`	Numeric. Significance level for confidence intervals (default 0.05).

Details

The predictor is standardised as `(x - mean(x)) / sd(x)`, so the reported OR and LOR correspond to a one-standard-deviation increase. Nagelkerke R-squared is computed as: (1 - exp((2/n)(LL_null - LL_fit))) / (1 - exp((2/n) * LL_null)).

Value

A named list with elements:

model The fitted `glm` object.

summary_table A `data.frame` with LOR, OR, 95\ Nagelkerke R-squared, and CCMs (YuleQ, YuleY, r_meta) with CIs.

predictor_mean Mean of the predictor used for standardisation.

predictor_sd SD of the predictor used for standardisation.

References

Kim, S.-K., & Grochowalski, J. H. (2019). Gaining from discretization of continuous data: The correspondence analysis biplot approach. *Behavior Research Methods*, 51(2), 589-601. doi:10.3758/s1342801811611

Examples

```
data(lorbridge_data)
res <- blr_continuous(outcome  = lorbridge_data$minority,
                      predictor = lorbridge_data$VM)
print(res$summary_table)
```

`ccm_row` *Closeness-of-Concordance Measures from OR and CI Endpoints*

Description

Computes a full row of closeness-of-concordance measures (CCMs) from an odds ratio (OR), its confidence interval endpoints, and the corresponding log-odds ratio (LOR). CCMs include Yule's Q, Yule's Y, and the meta-analytic correlation r_meta (probit transformation of LOR), all on the [-1, +1] scale introduced by Kim and Grochowalski (2019).

Usage

```
ccm_row(OR, OR_lo, OR_hi, LOR, LOR_lo, LOR_hi)
```

Arguments

`OR`	Numeric. Odds ratio point estimate.
`OR_lo`	Numeric. Lower confidence limit of the odds ratio.
`OR_hi`	Numeric. Upper confidence limit of the odds ratio.
`LOR`	Numeric. Log-odds ratio point estimate.
`LOR_lo`	Numeric. Lower confidence limit of the log-odds ratio.
`LOR_hi`	Numeric. Upper confidence limit of the log-odds ratio.

Details

Yule's Q = (OR - 1) / (OR + 1). Ranges from -1 to +1; equals the Pearson correlation for 2x2 tables under a tetrachoric model.

Yule's Y = (sqrt(OR) - 1) / (sqrt(OR) + 1). A shrunken version of Q with better sampling properties for sparse tables.

r_meta converts LOR to Cohen's d via d = LOR * sqrt(3) / pi, then to a correlation-like metric via d / sqrt(d^2 + 4). Equivalent to the biserial correlation used in meta-analysis.

Value

A one-row `data.frame` with columns: OR, OR_lo, OR_hi, LOR, LOR_lo, LOR_hi, YuleQ, Q_lo, Q_hi, YuleY, Y_lo, Y_hi, r_meta, r_lo, r_hi.

References

Kim, S.-K., & Grochowalski, J. H. (2019). Gaining from discretization of continuous data: The correspondence analysis biplot approach. *Behavior Research Methods*, 51(2), 589-601. doi:10.3758/s1342801811611

Examples

```
lc <- lor_ci_2x2(30, 25, 28, 24)
ccm_row(exp(lc$lor), exp(lc$lo), exp(lc$hi), lc$lor, lc$lo, lc$hi)
```

`cosine_theta_2row` *Cosine Theta from a 2-Row Correspondence Analysis (SVD)*

Description

Computes anchored cosine theta values from a 2 x J contingency table via a direct 1D SVD of the standardised residual matrix, bypassing the `CAvariants` function (which requires at least 2 dimensions). This implements the Kim and Grochowalski (2019) log-odds ratio to cosine theta bridge for 2-row tables.

Usage

```
cosine_theta_2row(tab_2xJ, ref_col)
```

Arguments

`tab_2xJ`	A 2 x J matrix or table. Row 1 = majority/reference group; row 2 = minority/focal group.
`ref_col`	Character. Name of the reference (anchor) column.

Value

A named numeric vector of cosine theta values, one per non-reference column. Values are +1 or -1 in the 1D case (sign carries the direction).

References

Kim, S.-K., & Grochowalski, J. H. (2019). Gaining from discretization of continuous data: The correspondence analysis biplot approach. *Behavior Research Methods*, 51(2), 589-601. doi:10.3758/s1342801811611

Examples

```
data(lorbridge_data)
tab <- table(lorbridge_data$minority, lorbridge_data$VMbin)
rownames(tab) <- c("Majority", "Minority")
cosine_theta_2row(tab, ref_col = "VM4")
```

`donsca_cosines` *Doubly-Anchored Cosine Theta for DONSCA*

Description

Computes doubly-anchored cosine theta values for all non-anchor row and column contrasts in a DONSCA solution. Each cosine theta quantifies the geometric alignment between the direction (row_i - row_anchor) and (col_j - col_anchor) in the full multivariate CA space.

Usage

```
donsca_cosines(fit, col_anchor_idx, row_anchor_idx, dims = "all")
```

Arguments

`fit`	A fitted DONSCA object from `donsca_fit()`.
`col_anchor_idx`	Integer. Column index of the anchor (reference) column.
`row_anchor_idx`	Integer. Row index of the anchor (reference) row.
`dims`	Integer or `"all"`. Number of dimensions to use (default `"all"`).

Value

A `data.frame` with columns: Row, Col, cos_theta.

`donsca_fit` *Fit a DONSCA Model*

Description

Fits a Doubly-Ordered Nonsymmetric Correspondence Analysis (DONSCA) model via `CAvariants`, using all available dimensions.

Usage

```
donsca_fit(tab)
```

Arguments

`tab`	A numeric matrix or table. Both rows and columns must represent ordered categories.

Value

A `CAvariants` fit object containing, among others, `Rprinccoord` (row principal coordinates) and `Cstdcoord` (column standard coordinates).

`inertia_pct` *Percent Inertia from SONSCA*

Description

Computes the percentage of total inertia explained by each dimension in a SONSCA solution, using a direct SVD of the standardised residual matrix.

Usage

```
inertia_pct(tab)
```

Arguments

`tab`	A numeric matrix or table.

Value

Numeric vector of percent inertia values (summing to 100).

`lorbridge_data` *Individual-Level VM and Minority Group Dataset*

Description

An individual-level dataset with N = 900 observations, reconstructed by row expansion from the `vm_raw` grouped data (SONSCA Analysis C). Each row represents one individual with their Vocabulary Meaning (VM) test score, discretised VM bin, binary minority/majority group indicator, and race group label.

Usage

```
lorbridge_data
```

Format

A `data.frame` with 900 rows and 4 columns:

VM Numeric. Raw Vocabulary Meaning score (range 54-149).

VMbin Factor. Discretised VM bin (VM1-VM6), with VM4 as the reference level. Breakpoints: <=64.28, <=81, <=100, <=121, <=138.36, >138.36.

minority Integer. Binary outcome: 1 = minority (Race1 + Race2 + Race3), 0 = majority (Race4).

Race Character. Race group label (Race1, Race2, Race3, Race4).

Source

Reconstructed from the `vm_raw` table in Kim, S.-K. (2026), unified SONSCA/DONSCA analysis script.

`lor_ci_2x2` *Log-Odds Ratio with Haldane-Anscombe Correction*

Description

Computes the log-odds ratio (LOR) and its Wald confidence interval for a 2x2 contingency table, applying the Haldane-Anscombe continuity correction (adding 0.5 to all cells) when any cell count is zero.

Usage

```
lor_ci_2x2(a, b, c, d, alpha = 0.05, cc = 0.5)
```

Arguments

`a`	Numeric. Cell count: row 1 (focal), column 1 (focal).
`b`	Numeric. Cell count: row 1 (focal), column 2 (reference/anchor).
`c`	Numeric. Cell count: row 2 (reference/anchor), column 1 (focal).
`d`	Numeric. Cell count: row 2 (reference/anchor), column 2 (reference/anchor).
`alpha`	Numeric. Significance level for the confidence interval (default 0.05).
`cc`	Numeric. Continuity correction added to all cells when any count is zero (default 0.5, Haldane-Anscombe).

Value

A named list with elements:

lor Point estimate of the log-odds ratio.

se Standard error of the log-odds ratio.

lo Lower bound of the Wald confidence interval.

hi Upper bound of the Wald confidence interval.

References

Haldane, J. B. S. (1956). The estimation and significance of the logarithm of a ratio of frequencies. *Annals of Human Genetics*, 20(4), 309-311.

Examples

```
# Compare Race1 vs Race2 at IQ bin 1 vs IQ bin 4 (reference)
lor_ci_2x2(a = 30, b = 25, c = 28, d = 24)
```

`mlr_ccm` *Multinomial Logistic Regression with CCMs (DONSCA Bridge)*

Description

Fits a multinomial logistic regression model with a single standardised continuous predictor (per 1 SD), using a specified baseline outcome category. Returns log-odds ratios, odds ratios, Wald CIs, and the full set of CCMs for each non-baseline outcome level.

Usage

```
mlr_ccm(outcome, predictor, baseline = NULL, alpha = 0.05)
```

Arguments

`outcome`	Factor or character vector. Polytomous outcome variable.
`predictor`	Numeric vector. Continuous predictor. Standardised internally to unit SD before fitting.
`baseline`	Character. Baseline/reference level of the outcome (default: first level of `outcome` as a factor).
`alpha`	Numeric. Significance level for CIs (default 0.05).

Value

A `data.frame` with one row per non-baseline outcome level, containing LOR, OR, 95% CI, and CCMs (YuleQ, YuleY, r_meta).

`sonsca_bootstrap` *Bootstrap Confidence Intervals for SONSCA Cosine Theta*

Description

Generates bias-corrected and accelerated (BCa-style percentile) bootstrap confidence intervals for doubly-anchored cosine theta estimates from SONSCA. Resamples the contingency table under a multinomial model.

Usage

```
sonsca_bootstrap(
  tab,
  row_anchor,
  col_anchor,
  row_groups,
  col_groups,
  B = 2000,
  alpha = 0.05
)
```

Arguments

`tab`	A numeric matrix or table for SONSCA.
`row_anchor`	Character. Row anchor label.
`col_anchor`	Character. Column anchor label.
`row_groups`	Character vector. Non-anchor row labels to include.
`col_groups`	Character vector. Non-anchor column labels to include.
`B`	Integer. Number of bootstrap replications (default 2000).
`alpha`	Numeric. Significance level for CIs (default 0.05).

Value

A named list with elements:

point Numeric vector of point estimates (flattened row x col).

lo Lower CI bounds.

hi Upper CI bounds.

boot_n Number of successful bootstrap replications.

`sonsca_ccm` *Pairwise CCMs for SONSCA*

Description

Computes pairwise closeness-of-concordance measures (CCMs) for a single (row, column) contrast against the anchor (row_anchor, col_anchor) in a SONSCA contingency table.

Usage

```
sonsca_ccm(tab, row_k, bin_j, row_anchor, col_anchor, alpha = 0.05)
```

Arguments

`tab`	A numeric matrix or table.
`row_k`	Character. Focal row label.
`bin_j`	Character. Focal column label.
`row_anchor`	Character. Row anchor label.
`col_anchor`	Character. Column anchor label.
`alpha`	Numeric. Significance level (default 0.05).

Value

A one-row `data.frame` with columns: Race, Bin, and all CCM columns from `ccm_row()`.

`sonsca_coords` *SONSCA Column-Isometric Coordinates*

Description

Extracts row standard coordinates and column principal coordinates from a Singly-Ordered Nonsymmetric Correspondence Analysis (SONSCA) fit via `CAvariants`. This is the column-isometric scaling recommended for cosine theta computation.

Usage

```
sonsca_coords(tab)
```

Arguments

`tab`	A numeric matrix or table. Rows are nominal categories (e.g., racial groups); columns are ordered categories (e.g., score bins).

Value

A named list with elements:

row_coords Row standard coordinate matrix (rows = row categories).

col_coords Column principal coordinate matrix (rows = column categories).

`sonsca_cosines` *Doubly-Anchored Cosine Theta for SONSCA*

Description

Computes the matrix of doubly-anchored cosine theta values between all non-anchor row and column pairs in SONSCA coordinate space.

Usage

```
sonsca_cosines(row_coords, col_coords, row_anchor, col_anchor)
```

Arguments

`row_coords`	Row coordinate matrix (from `sonsca_coords()`).
`col_coords`	Column coordinate matrix (from `sonsca_coords()`).
`row_anchor`	Character. Row label used as the anchor (reference).
`col_anchor`	Character. Column label used as the anchor (reference).

Value

A matrix of cosine theta values with rows = non-anchor row categories and columns = non-anchor column categories. Anchor rows/ columns yield `NA` (zero displacement).

`tab_IQ` *IQ Contingency Table (4 Races x 6 IQ Bins)*

Description

A 4 x 6 contingency table cross-classifying four racial groups by six discretised IQ score bins. Used in SONSCA Analysis A.

Usage

```
tab_IQ
```

Format

A numeric matrix with 4 rows (Race1, Race2, Race3, Race4) and 6 columns (IQ1-IQ6).

Source

Kim, S.-K. (2026), unified SONSCA/DONSCA analysis script, Analysis A.

`tab_IQ_VM` *IQ x VM Contingency Table (6 IQ Bins x 6 VM Bins)*

Description

A 6 x 6 contingency table cross-classifying six discretised IQ bins by six discretised Vocabulary Meaning (VM) bins. Both rows and columns are ordered, making this suitable for DONSCA.

Usage

```
tab_IQ_VM
```

Format

A numeric matrix with 6 rows (IQ1-IQ6) and 6 columns (VM1-VM6).

Source

Kim, S.-K. (2026), unified SONSCA/DONSCA analysis script, Analysis 3a.

`tab_VM` *VM Contingency Table (4 Races x 6 VM Bins)*

Description

A 4 x 6 contingency table cross-classifying four racial groups by six discretised Vocabulary Meaning (VM) score bins. Used in SONSCA Analysis B.

Usage

```
tab_VM
```

Format

A numeric matrix with 4 rows (Race1, Race2, Race3, Race4) and 6 columns (VM1-VM6).

Source

Kim, S.-K. (2026), unified SONSCA/DONSCA analysis script, Analysis B.

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