Package: F2Adonis2 (via r-universe)

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Title PERMANOVA using the F2 Statistic

Version 0.1.1

Language en-US

Description Implements the F2 statistic of Anderson et al. (2017) <doi:10.1111/anzs.12176> for permutational multivariate analysis of variance (PERMANOVA) on dissimilarity matrices. The F2 statistic uses group-specific dispersion estimates, so group centroids can be compared when dispersions differ and group sizes are unequal. P-values are obtained by permutation, bootstrap, or bias-adjusted bootstrap. The formula interface follows 'adonis2()' in the 'vegan' package.

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Encoding UTF-8

Imports stats, vegan (>= 2.7-3)

RoxygenNote 7.3.3

Depends R (>= 4.1.0)

LazyData true

Suggests knitr, rmarkdown, dplyr, ggplot2, onewaytests, yarrr, combinat, kableExtra, testthat (>= 3.0.0)

VignetteBuilder knitr

URL https://github.com/LakviruPerera/F2Adonis2

BugReports https://github.com/LakviruPerera/F2Adonis2/issues

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`F2_adonis2` *Permutational Multivariate Analysis of Variance Using the F2 Statistic*

Description

Analysis of variance using distance matrices for partitioning variation among sources. Unlike standard PERMANOVA, this function uses the F2 statistic (Anderson 2017) which accounts for heterogeneous dispersions (Behrens-Fisher problem).

Usage

```
F2_adonis2(
  formula,
  data,
  permutations = 999,
  method = "euclidean",
  sqrt.dist = FALSE,
  add = FALSE,
  by = NULL,
  parallel = getOption("mc.cores"),
  na.action = na.fail,
  strata = NULL,
  bootstrap = FALSE,
  bias.adjust = FALSE,
  plot.dist = TRUE,
  ...
)
```

Arguments

`formula`	Model formula. The LHS must be a community data matrix or a dissimilarity matrix. The RHS must define a single factor predictor.
`data`	A data frame containing the independent variables.
`permutations`	Number of permutations for the test, or a permutation matrix.
`method`	Pairwise distance method used in `vegdist`. Common options include "jaccard" (for binary data), "bray" (for abundance data), or "euclidean".
`sqrt.dist`	Logical; take square root of dissimilarities to "euclidify" them.

add	Add a constant to dissimilarities to avoid negative eigenvalues. Options are "lingoes" or "cailliez".
by	Validation restricted to NULL. F2 currently only supports global tests.
parallel	Number of parallel processes to use.
na.action	Handling of missing values on the RHS.
strata	Groups within which to constrain permutations.
bootstrap	Logical; perform separate-sample residual bootstrapping in dissimilarity space (Anderson 2017).
bias.adjust	Logical; apply empirical bias correction to bootstrap variances.
plot.dist	Logical; if TRUE (default), plot the permutation distribution of the F2 statistic.
...	Other arguments passed to vegdist.

Details

F2_adonis2 implements the multivariate F2 statistic and the matrix-based bootstrap procedure derived in Anderson et al. (2017).

Value

An object of classes F2_adonis2, anova.cca, anova and data.frame: an ANOVA-style table with rows Model, Residual and Total, and columns Df, SumOfSqs, F2 and Pr(>F2). If bootstrap = TRUE, the column Pr(>F2.boot) is added, and if bias.adjust = TRUE, Pr(>F2.ba) as well. The permutation values of the F2 statistic are stored in the attribute F.perm.

Author(s)

Lakviru Perera (based on logic by Marti J. Anderson)

References

Anderson, M. J., Walsh, D. C., Clarke, K. R., Gorley, R. N., & Guerra-Castro, E. (2017). Some solutions to the multivariate Behrens–Fisher problem for dissimilarity-based analyses. *Australian & New Zealand Journal of Statistics*.

Examples

```
# Load internal package data objects
data("pkd_metadata", package = "F2Adonis2")
data("pkd_metabolites", package = "F2Adonis2")

# Set up a data frame for the group factor
pkd_meta <- data.frame(Group = factor(pkd_metadata$Group))

# Example using 99 permutations
fit <- F2_adonis2(
  formula = as.matrix(pkd_metabolites) ~ Group,
  data = pkd_meta,
  method = "euclidean",
```

```
  permutations = 99,
  plot.dist = FALSE
)
print(fit)
```

`norway_metadata` *Norway Benthic Macrofauna Metadata*

Description

Metadata containing geographical location assignments for the 101 sampled sites in the Norway benthic community dataset.

Usage

```
norway_metadata
```

Format

A data frame with 101 rows and 1 column:

Area A grouping factor with 5 levels indicating the specific geographical region.

Source

Ellingsen, K.E. and Gray, J.S. (2002), *Journal of Animal Ecology*, 71(3), 373-389, doi:10.1046/j.13652656.2002.00606.x. Data as provided with Anderson et al. (2017), doi:10.1111/anzs.12176 (Data S1).

`norway_pa` *Norway Benthic Macrofauna Presence-Absence Data*

Description

A presence-absence matrix for 809 marine macrofauna species across 101 sites, utilized as a baseline biological validation dataset.

Usage

```
norway_pa
```

Format

A matrix with 101 rows (sites) and 809 columns (species).

Source

Ellingsen, K.E. and Gray, J.S. (2002), *Journal of Animal Ecology*, 71(3), 373-389, doi:10.1046/j.13652656.2002.00606.x. Data as provided with Anderson et al. (2017), doi:10.1111/anzs.12176 (Data S1).

`pkd_metabolites` *Polycystic Kidney Disease (PKD) Metabolites*

Description

An auto-scaled, log-transformed intensity matrix of urinary profiles (metabolites) from early-stage Polycystic Kidney Disease patients and healthy controls.

Usage

```
pkd_metabolites
```

Format

A matrix with 95 rows (samples) and 1554 columns (metabolites).

Source

Derived from the urinary metabolomics cohort in Houske et al. (2023), *American Journal of Physiology-Renal Physiology*, 324(6), F590-F602, doi:10.1152/ajprenal.00301.2022.

`pkd_metadata` *Polycystic Kidney Disease (PKD) Metadata*

Description

A dataset containing group categories for the Polycystic Kidney Disease (PKD) cohort, used to demonstrate multivariate testing under biological heterogeneity.

Usage

```
pkd_metadata
```

Format

A data frame with 95 rows (samples) and 1 column:

Group A factor indicating disease classification status (Ctrl vs PKD).

Source

Derived from the urinary metabolomics cohort in Houske et al. (2023), *American Journal of Physiology-Renal Physiology*, 324(6), F590-F602, doi:10.1152/ajprenal.00301.2022.

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