Package ‘aPCoA’

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Type Package

Title Covariate Adjusted PCoA Plot

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Description In fields such as ecology, microbiology, and genomics, non-Euclidean distances are widely applied to describe pairwise dissimilarity between samples. Given these pairwise distances, principal coordinates analysis (PCoA) is commonly used to construct a visualization of the data. However, confounding covariates can make patterns related to the scientific question of interest difficult to observe. We provide ‘aPCoA’ as an easy-to-use tool to improve data visualization in this context, enabling enhanced presentation of the effects of interest. Details are described in Yushu Shi, Liangliang Zhang, Kim-Anh Do, Christine Peterson and Robert Jenq (2020) <arXiv:2003.09544>.

License GPL (>= 2)

Imports vegan, randomcoloR, mvabund, ape, car, cluster

NeedsCompilation no

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Description

Adjusted confounding covariates to show the effect of the primary covariate in a PCoA plot. This method is designed for non-Euclidean distance. This function will plot the original PCoA plot along with the covariate adjusted PCoA plot.

Usage

\texttt{aPCoA(formula, data, maincov, drawEllipse=TRUE, drawCenter=TRUE)}

Arguments

- \texttt{formula}: A typical formula such as \texttt{Y~ A}, but here \texttt{Y} is a dissimilarity distance. The formula has the same requirements as in \texttt{adonis} function of the \texttt{vegan} package.
- \texttt{data}: A dataset with the rownames the same as the rownames in distance. This dataset should include both the confounding covariate and the primary covariate.
- \texttt{maincov}: the covariate of interest in the dataset, must be a factor
- \texttt{drawEllipse}: Do you want to draw the 95\% confidence ellipse for each cluster?
- \texttt{drawCenter}: Do you want to show the connection between cluster center (medoid) and cluster members?

Value

Two PCoA plots. One is the original one, while the other is the PCoA plot after adjusting for the confounding covariate.

- \texttt{plotMatrix}: The matrix for plotting the adjusted PCoA plot.

Source


Examples

\begin{verbatim}
library(mvabund)
library(vegan)
library(aPCoA)
data("Tasmania")
data<-data.frame(treatment=Tasmania$treatment, block=Tasmania$block)
bray<-vegdist(Tasmania$abund, method="bray")
rownames(data)<-rownames(as.matrix(bray))
opar<-par(mfrow=c(1,2),
       mar=c(3.1, 3.1, 3.1, 5.1),
       lwd=3)
par(new=TRUE)
plot(aPCoA(~ treatment | block, data))
par(opar)
\end{verbatim}
result <- aPCoA(bray~block, data, treatment)
par(opar)
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