

Package ‘ProteinPCA’

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Type Package

Title Principal Component Analysis (PCA) Tool on Protein Expression Data

Version 0.1.1

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Description Analysis of protein expression data can be done through Principal Component Analysis (PCA), and this R package is designed to streamline the analysis. This package enables users to perform PCA and it generates biplot and scree plot for advanced graphical visualization. Optionally, it supports grouping/clustering visualization with PCA loadings and confidence ellipses. With this R package, researchers can quickly explore complex protein datasets, interpret variance contributions, and visualize sample clustering through intuitive biplots. For more details, see Jolliffe (2001) <[doi:10.1007/b98835](https://doi.org/10.1007/b98835)>, Gabriel (1971) <[doi:10.1093/biomet/58.3.453](https://doi.org/10.1093/biomet/58.3.453)>, Zhang et al. (2024) <[doi:10.1038/s41402-024-53239-9](https://doi.org/10.1038/s41402-024-53239-9)>, and Anandan et al. (2022) <[doi:10.1038/s41598-022-07781-5](https://doi.org/10.1038/s41598-022-07781-5)>.

License GPL-3

Encoding UTF-8

Imports stats, ggplot2, gridExtra

Suggests testthat, MASS

Config/testthat/edition 3

RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

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pca_analysis	<i>Principal Component Analysis (PCA) Tool on Protein Expression Data</i>
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Description

This function performs PCA on protein expression data and produces a biplot using ggplot2. Optionally, it supports grouping/clustering visualization with PCA loadings and confidence ellipses.

Arguments

data	A numeric matrix or data frame of protein expression data. Rows are samples, columns are features.
scale	Logical. Should the data be scaled? Default is TRUE.
center	Logical. Should the data be centered? Default is TRUE.
plot	Logical. Should a PCA biplot be generated? Default is TRUE.
groups	Optional. A factor or character vector specifying group memberships of the samples.

Value

A list containing:	
pca	The PCA object from prcomp.
explained_variance	The percentage of variance explained by each principal component.
plot	A ggplot2 PCA biplot (if plot = TRUE).

Author(s)

Paul Angelo C. Manlapaz

References

Jolliffe, I. (2001). Principal Component Analysis (2nd ed.). Springer. <https://doi.org/10.1007/b98835>
Gabriel, K. R. (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, 58(3), 453–467. <https://doi.org/10.1093/biomet/58.3.453>
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Anandan, A., Nagireddy, R., Sabarinathan, S., Bhatta, B. B., Mahender, A., Vinothkumar, M., Parameswaran, C., Panneerselvam, P., Subudhi, H., Meher, J., Bose, L. K., & Ali, J. (2022). Multi-trait association study identifies loci associated with tolerance of low phosphorus in *Oryza sativa* and its wild relatives. *Scientific Reports*, 12(1). <https://doi.org/10.1038/s41598-022-07781-5>

Examples

```
set.seed(123)
data_matrix <- matrix(rnorm(100 * 20), nrow = 100, ncol = 20)
rownames(data_matrix) <- paste0('Sample_', 1:100)
colnames(data_matrix) <- paste0('Protein_', 1:20)
groups <- sample(c("Group A", "Group B"), 100, replace = TRUE)
result <- pca_analysis(data_matrix, groups = groups)
print(result$explained_variance)
print(result$plot)
```

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