Analysis of Multi-Omics Data with Multiple Co-Inertia Analysis via Nonlinear Iterative Partial Least Squares (NIPALS)

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Quick Start

The package can be installed directly from Github via the `devtools` package:

```r
install.packages("devtools",repos = "http://cran.us.r-project.org")
library(devtools)# required for install_github

install_github("Muunraker/NIPALS-MCIA")
library(nipalsMCIA)
```

A test dataset of NCI60 cancer cell line data with 3 blocks (mRNA, proteins, and micro-RNA) is included to illustrate how the main MCIA function works with multi-omics data:

```r
data(NCI60) # loads data as data_blocks
summary(data_blocks)
```

```
##       Length Class      Mode
## mrna  12895  data.frame list
## miRNA   537  data.frame list
## prot   7016  data.frame list
```

The main NIPALS function includes a pre-processing option for the data. The results include a plot of the first two global scores as well as an eigenvalue scree plot to aid variable selection.

```r
# Main NIPALS function
results <- nipals_multiblock(data_blocks, preprocMethod='colprofile',num_PCs = 10,
                             plots='all', tol=1e-12)
```

Score Projection Plot

Order 2 Scores

Order 1 Scores

mrna
miRNA
prot
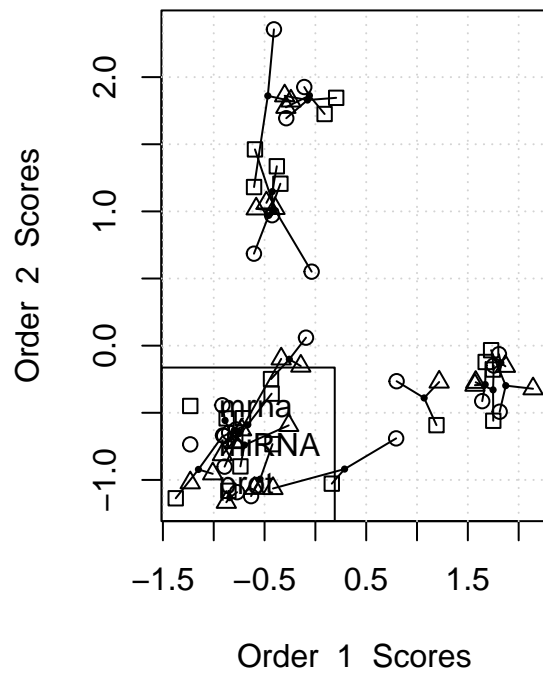
Global Score Eigenvalues

Global Score Order