

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:

```
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:

```
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 preprocessing function and main NIPALS iteration can then be applied to the data. The results include a plot of the first two global scores:

```
# Apply initialization:
data_blocks_norm <- lapply(data_blocks, omicadeInitialization)

# Main NIPALS function
results <- nipals_multiblock(data_blocks_norm, num_PCs = 2, tol=1e-12,
                             deflationMethod = 'block', plots="true")
```

First Two Global Scores

