Vignette1 - Introduction & Main

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9/1/2022

Part 1: Interpreting Global Scores

MCIA calculates a global scores matrix that is $n \times k$ where n is the number of samples and k is the number of factors. Each entry M_{ik} represents the strength of factor k to sample i. As such, you may be interested in further dissecting the global scores matrix in order to understand, for a given sample, what factors capture the most the MCIA decomposition. . . (to be continued)

Running MCIA on NCI60 Data

```
library(nipalsMCIA)
data(NCI60)
results <- nipals_multiblock(data_blocks, preprocMethod='colprofile',num_PCs = 10,
             plots='none', tol=1e-12)
```

```
## Performing centered column profile pre-processing...

## Pre-processing completed.

## Computing order 1 scores

## Computing order 2 scores

## Computing order 3 scores

## Computing order 4 scores

## Computing order 5 scores

## Computing order 6 scores

## Computing order 7 scores

## Computing order 8 scores

## Computing order 9 scores

## Computing order 10 scores
```

Projection Plot: Understanding the relationships between factors

. . . (to be continued)

Scree Plot with Global Score eigenvalues

. . . (to be continued)

Heatmap of the Global Score Matrix (G): Visualizing the clustering of samples and factors

```r
gs_scores = results$global_scores
colnames(gs_scores) = paste0('F', seq(1, ncol(results$global_scores)))
p = ComplexHeatmap::Heatmap(gs_scores,
    name = "GS Score",
    column_title = "Factors",
    row_title = "Samples",
    row_names_gp = grid::gpar(fontsize = 7),
    show_column_names = T,
    show_row_names = T,
    row_names_side = "right"
)
p
```
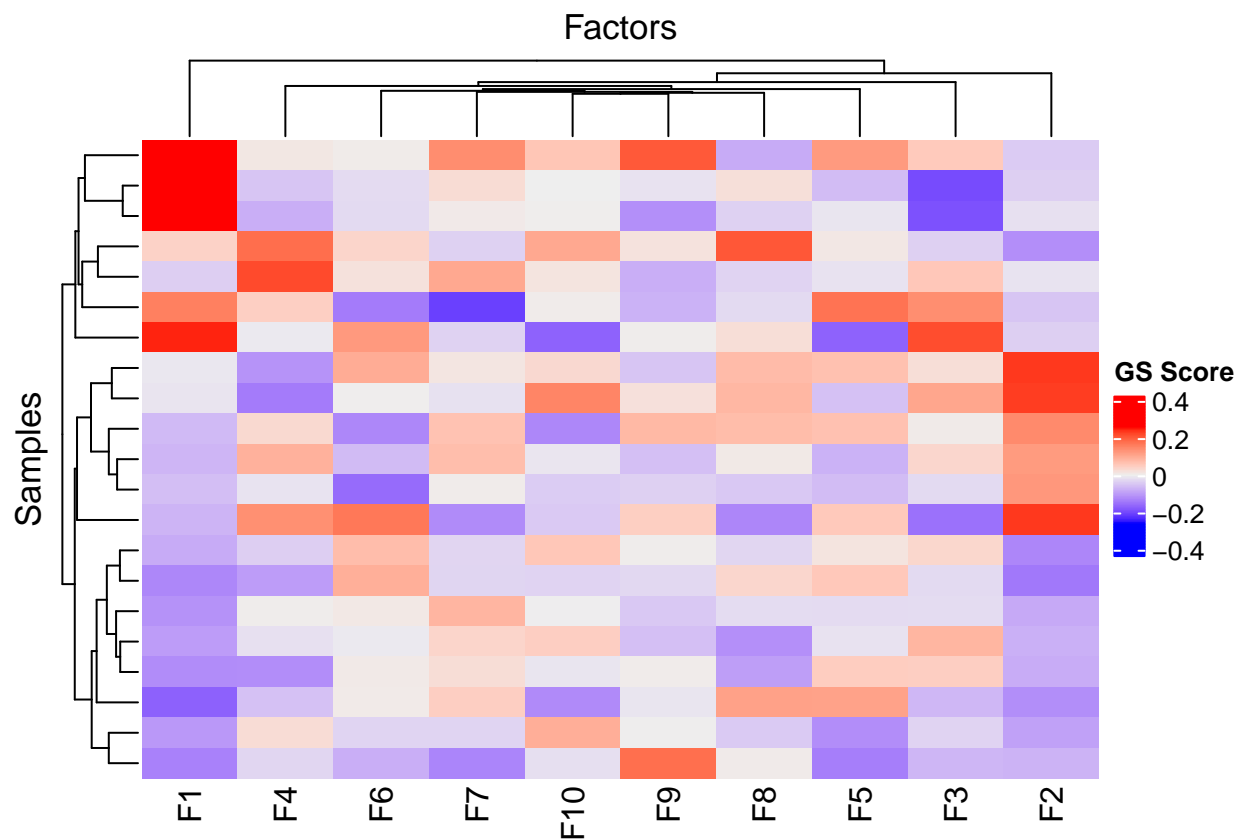

Part 2: Interpreting Global Loadings

In addition to the global scores matrix, MCIA also calculates a global loadings matrix that is $(m_1 + ... + m_j + ... + m_R) \times k$ where m_j is the number of features within the omics matrix X^j and K is the number of factors calculated. This second matrix provides information as to the contribution

Heatmap of Omic Contributions to block scores

...(to be continued)

Scree Plot: Determining the variance explained per factor

. . . (to be continued)

Pathway analysis for the top factors using data from gene-centric omics blocks

. . . (to be continued)