

Vignette 1 - Understanding the Results of MCIA

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Part 2: Interpreting Global Loadings

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

First, we compute the first 10 global factors for the dataset:

```
data(NCI60) # this creates the dataset as `data_blocks`
mcia_results <- nipals_multiblock(data_blocks,
                                preprocMethod='colprofile',
                                plots = 'none',
                                num_PCs = 10,
                                tol=1e-12)

# extra gene-centric data
mrna_gfscores <- mcia_results$global_loadings
mrna_rows = str_detect(row.names(mrna_gfscores), '_mrna')
mrna_gfscores <- mrna_gfscores[mrna_rows,]
row.names(mrna_gfscores) <- str_remove(rownames(mrna_gfscores), "_[0-9]*_.*")

# load pathway data
path.database = '../data/c2.cp.reactome.v6.2.symbols.gmt'
pathways <- fgsea::gmtPathways(path.database)

# run the comparison
geneset_report = gsea_report(mrna_gfscores, path.database,
                             factors = c(1,2,3), pval.thr = 0.05)

## [1] "Running GSEA for Factor1"
## [1] "Running GSEA for Factor2"
## [1] "Running GSEA for Factor3"

geneset_report[[1]]

##           min_pval total_pathways
## Factor1 2.461419e-09          119
## Factor2 2.724331e-08           95
## Factor3 1.716512e-20           88

geneset_report[[2]]

## [1] 0.3096026
```