HIV\_multiomics

Files verified =

SNF\_cross\_validation.Rmd

Produced files

“relative\_abundance\_table.csv”

"processing/cluster\_SNF\_3\_omics\_3\_clusters.csv"

“cluster\_SNF\_3\_omics\_3\_clusters\_plusHC.csv”

"results/LIMMA\_results\_lipids\_with\_HC.csv"

"results/LIMMA\_results\_lipids\_with\_HC.csv"

"processing/MDM\_clean\_list\_2.txt"

"processing/processing\_microbione\_derived\_metabolomics.csv"

"processing/list\_microbiome\_derived\_metabolites\_heatmap\_all\_comparisons.csv"

"processing/table\_nodes\_first\_neigbors.xlsx"

"processing/extracted\_MOFA\_features.xlsx"

"processing/metabolomics\_data\_HIV\_correlations.csv"

"processing/table\_GSEA\_MOFA\_factors.csv"

"processing/table\_pathway\_analysis\_MOFA\_Factor\_2.csv"

"processing/clinical\_data\_clean\_for\_regression\_models.csv"

"results/clinical/COCOMO\_3\_layers\_normal\_distrib\_numeric\_values\_ANOVA.xlsx"

"results/clinical/COCOMO\_3\_layers\_non\_norm\_numeric\_values\_kruskal.xlsx"

"results/clinical/X2\_results\_results\_cocomo\_3\_groups.xlsx"

"processing/data\_phylum\_clean.csv"

"processing/data\_family\_clean.csv"

"processing/data\_genus\_clean\_relative\_abundance.csv"

"processing/data\_count\_microbiome.csv"

"processing/table\_alpha\_diversity\_filtered\_model.csv"

"processing/table\_alpha\_diversity\_filtered\_model\_clusters.csv"

"processing/alpha\_diversity\_clusters\_pvalues.csv"

"results/Adonis-Results\_phylum.csv"

"processing/coefficient\_permanova\_group\_2\_vs\_group\_1.csv"

"results/DGE\_family.csv"

"results/microbiome/association\_otu\_clinical\_parameters.xlsx"

Missing files

SNF

"processing/table\_clinical\_data.csv"

DGE LIMMA

"/home/flomik/Desktop/Code-PHD/3\_layers\_integration/processing/lipidomics\_log2\_plusHC.csv"

"/home/flomik/Desktop/Code-PHD/3\_layers\_integration/processing/final\_list"

MDM

"/home/flomik/Desktop/Code-PHD/3\_layers\_integration/data/microbiome\_derived\_metabolites.xlsx"

"processing/table\_node\_super\_network\_MDM.csv"

Clinical

"processing/duration\_ART\_COCOMO\_3.csv"

"processing/clinical\_ordered\_microbiome\_project.csv"

"processing/summary\_data\_interest\_COCOMO\_microbiome.csv"

MOFA

"processing/clinical\_data\_microbiome\_project.csv"

processing/MOFA\_correlation\_clinical\_parameters.csv

Changes

Data → change “Original\_Scale\_Data\_CLP.xlsx” no IDs → right file : clp\_lipidomics\_data.csv

Data → change “Supplementary Data 1.xlsx” no IDs → right file : cocomo\_norm\_data\_filt.csv

Data → add clp\_um\_new\_data.csv

Code making network co-expression metabolomics ?

Code making consensus co-expression network