Original files

/home/flomik/Desktop/Code-PHD/COCOMO\_txn/data/clinical/COCOMID\_LabelID Negin.xlsx

/home/flomik/Desktop/Code-PHD/COCOMO\_txn/data/Olink/Q-01546\_Neogi\_NPX\_2022-06-09.csv

/home/flomik/Desktop/Code-PHD/data\_COCOMO\_txn/salmon.merged.gene\_counts.tsv

/home/flomik/Desktop/Code-PHD/data\_COCOMO\_txn/salmon.merged.gene\_tpm\_length\_scaled.tsv

data/clinical/COCOMO\_Master File\_SK.xlsx

/home/flomik/Desktop/Code-PHD/COCOMO\_txn/data/clinical/U.Neogi\_21\_01\_sample\_info.txt

data/metabolomics/cocomo\_norm\_data\_filt.csv

/home/flomik/Desktop/Code-PHD/COCOMO\_txn/data/clinical/data\_base\_200\_patients\_COCOMO\_filtered.csv

CIBERSORTxGEP\_Job34\_Fractions.txt

data/whole\_patients/CO\_HIV\_new.xlsx

data/whole\_patients/Characteristics.xlsx

data/clinical/cocomo\_drug\_comorbidities\_data.csv

To find

/home/flomik/Desktop/Code-PHD/COCOMO\_txn/data/clinical/clinical\_data\_microbiome\_project.csv

GSEA → KEGG\_1 (proteomics), co-expression network C3 (proteomics)

MSEA → co-expression network C3 (metabolomics)

all\_genes default edge.csv (BINGO)

All\_genes default node.csv(BINGO)

produced

COCOMO\_transcriptomics\_vsd\_data\_deseq2.csv

processing/cluster\_SNF\_transcriptomics\_metabolomics\_olink\_3.csv

processing/clinical\_data\_whole\_data.csv

olink\_data\_new\_ids.csv

processing/clinical\_data\_clean.csv x3 (made from PHD/COCOMO\_txn/data/clinical/clinical\_data\_microbiome\_project.csv)

processing/clinical\_data\_clean\_with\_clusters\_and\_categories.csv (made from processing/clinical\_data\_clean.csv)

processing/COCOMO\_metabolomics\_pathways.csv

COCOMO\_metabolomics\_log2\_norm\_filt.csv

processing/factor\_differing\_groups\_3.csv

processing/numeric\_differing\_groups\_3.csv

processing/clinical\_data\_PCA\_3.csv

clinical\_data\_clean\_2.csv (olink)