

Removal_pipeline
↔ input data/GeneECAnnotation.txt data/GeneTaxonomicAnnotation.txt data/count_table_contigs.txt
output → results/removal_pipeline/EC_contig_taxa_c table.tsv results/removal_pipeline/contig_taxa_c table.tsv results/removal_pipeline/gene_func_ec_contig_c table.tsv results/removal_pipeline/gene_functional_EC.txt results/removal_pipeline/get_contig_taxonomy_ranked.txt

split_count_table_by_treatment
↔ input results/removal_pipeline/EC_contig_taxa_c table.tsv results/removal_pipeline/contig_taxa_c table.tsv results/removal_pipeline/gene_func_ec_contig_c table.tsv
output → results/split_c table/{treatment}_EC_contig_taxa_c table.tsv

claculate_enzyme_diversity_score
↔ input results/split_c table/{treatment}_EC_contig_taxa_c table.tsv
output → results/enzyme_divierisy/{treatment}_EC_w_taxaon_dominant.txt results/enzyme_divierisy/{treatment}_EC_w_taxaon_dominant_knockout.txt results/enzyme_divierisy/{treatment}_RscriptOutput.csv results/enzyme_divierisy/{treatment}_RscriptOutput_filter_IdentMostFreq.csv results/enzyme_divierisy/{treatment}_RscriptOutput_filter_IdentMostFreqbyEnzyme.csv results/enzyme_divierisy/{treatment}_RscriptOutput_filter_dominance.csv

Community_knockouts_simulations
↔ input results/enzyme_divierisy/{treatment}_EC_w_taxaon_dominant_knockout.txt results/netcom/{treatment}_resources.txt
output → results/community_konckouts_simulation/{treatment}_compounds.txt results/community_konckouts_simulation/{treatment}_compounds_complementary_list.txt results/community_konckouts_simulation/{treatment}_compounds_complementary_table.txt

prepare_pathway_compounds_for_visual
↔ input results/community_konckouts_simulation/{treatment}_compounds_complementary_list.txt results/netcom/{treatment}_Compounds_pathway.csv
output → results/netcom/{treatment}_vis_Compounds_pathway.txt

visualize_knockout_network
↔ input results/community_konckouts_simulation/{treatment}_compounds_complementary_table.txt results/enzyme_divierisy/{treatment}_EC_w_taxaon_dominant_knockout.txt results/netcom/{treatment}_compounds.txt results/netcom/{treatment}_resources.txt results/netcom/{treatment}_vis_Compounds_pathway.txt results/removal_pipeline/gene_func_ec_contig_c table.tsv
output → results/community_konckouts_simulation/{treatment}_compounds_complementary_pathway_count_table.tsv results/community_konckouts_simulation/{treatment}_compounds_complementary_pathway_table.tsv results/community_konckouts_simulation/{treatment}_compounds_network_notFiltered.csv results/community_konckouts_simulation/{treatment}_treatment_removal_network_knockout_pdf.pdf results/community_konckouts_simulation/{treatment}_treatment_removal_network_knockout_png.png

merge_netcom2
↔ input results/community_konckouts_simulation/NCF_compounds_network_notFiltered.csv results/community_konckouts_simulation/NCF_treatment_removal_network_knockout_pdf.pdf results/community_konckouts_simulation/NCF_treatment_removal_network_knockout_png.png results/community_konckouts_simulation/cf_compounds_network_notFiltered.csv results/community_konckouts_simulation/cf_treatment_removal_network_knockout_pdf.pdf results/community_konckouts_simulation/cf_treatment_removal_network_knockout_png.png
output → results/merged_netcom2.txt