Removal_pipeline

↳ input

data/GeneECAnnotation.txt

data/GeneTaxonomicAnnotation.txt

data/count_table_contigs.txt

output →

results/removal_pipline/EC_contig_taxa_ctable.tsv

results/removal_pipline/contig_taxa_ctable.tsv

results/removal_pipline/gene_func_ec_contig_ctable.tsv

results/removal_pipline/gene_functional_EC.txt

results/removal_pipline/get_contig_taxonomy_ranked.txt

split_count_table_by_treatment

↳ input

results/removal_pipline/EC_contig_taxa_ctable.tsv

results/removal_pipline/contig_taxa_ctable.tsv

results/removal_pipline/gene_func_ec_contig_ctable.tsv

output →

results/split_ctable/{treatment}_EC_contig_taxa_ctable.tsv

claculate_enzyme_diversity_score

↳ input

results/split_ctable/{treatment}_EC_contig_taxa_ctable.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

enzyme_diversity

↳ input

results/enzyme_divierisy/NCF_EC_w_taxaon_dominant.txt

results/enzyme_divierisy/cf_EC_w_taxaon_dominant.txt

output →

results/enzyme_divierisy/merged.txt

determine_diffenetial_abundance

↳ input

data/contrasts.txt

data/sample_metadata.tsv

results/enzyme_divierisy/merged.txt

results/removal_pipline/gene_func_ec_contig_ctable.tsv

output →

results/edgeR/EC_diff_abundance.png

results/edgeR/EC_diff_abundance.tsv