This initial documentation is more of a conceptual understanding of the methodology to generate two graphs: connectivity and ACE matrix.

Functions Involved in Plot Generation

1. Heatmap of Species Pair Frequencies

This plot visualizes the frequency of species pairs appearing together. The key functions involved in this process are:

• repeated_call_causal_data_all_up_to_pc_101: This function runs the PC algorithm multiple times to generate a collection of causal graphs (DAGs), which include relationships between species pairs.

• convert_cpdag_into_dag: Converts the output of the PC algorithm (CPDAG) into a Directed Acyclic Graph (DAG), which is needed to check species pairs.

• filter_dags_by_edges: Filters the DAGs to only keep those that have a certain number of edges, ensuring that only graphs with enough connections are considered.

• find_components: Finds connected components in the filtered DAGs. These components represent groups of species that are linked by causal or undirected edges.

• two_species_count_normalized: This is the main function for the pair frequency heatmap. It counts how often pairs of species co-occur across the different DAGs. The matrix of pair frequencies is generated here.

• plotACEMatrix: This function is reused to visualize the pair frequency matrix as a heatmap, although it is originally designed for the ACE plot.

2. ACE (Average Causal Effect) Matrix Plot

This plot shows the estimated causal effect of one species on another. The key functions involved here are:

• computeACEForAllDAGs: This is the main function that calculates the Average Causal Effect (ACE) between species pairs across all the DAGs. It loops over the DAGs and computes the ACE for each pair where a causal edge exists.

• mapIndicesToSpeciesNames: After computing the ACE, this function maps the numeric indices in the ACE matrices to the actual species names, ensuring that the resulting ACE matrix is labeled correctly with species names.

• combine_and_normalize_ace: Once the ACE values are computed for all DAGs, this function combines them into a single ACE matrix, normalizing the values across multiple DAGs.

• plotACEMatrix: This function visualizes the combined and normalized ACE matrix, showing the strength of causal effects between species pairs.