
8 Open Issues

In conclusion, we successfully constructed a precise knowledge graph that effectively represents the interactions between individuals and their respective microbiome species, as well as interactions among species themselves. However, while our teleology includes an entity for cancer, our dataset contained only one type of cancer. This is not necessarily a limitation, as other studies can integrate additional data with multiple cancer types using the same knowledge graph.

A notable weakness of this study is the inability to statistically and significantly evaluate the results of the queries. In particular, the threshold used to classify species' relative abundances as high or low was chosen arbitrarily based on the average, making it unreliable for hypothesis-driven studies. Therefore, future research should incorporate machine learning techniques for a more comprehensive analysis of this knowledge graph, allowing for the extraction of meaningful insights from the data.

Additionally, other studies may be interested in grouping specific classes or families of microbiome species and comparing them by aggregating their relative abundances across different individuals. Another potential extension, that was present in this study due to the lack of data is the integration of time-series data for the same individuals, which could provide deeper insights into species-species interactions over time.