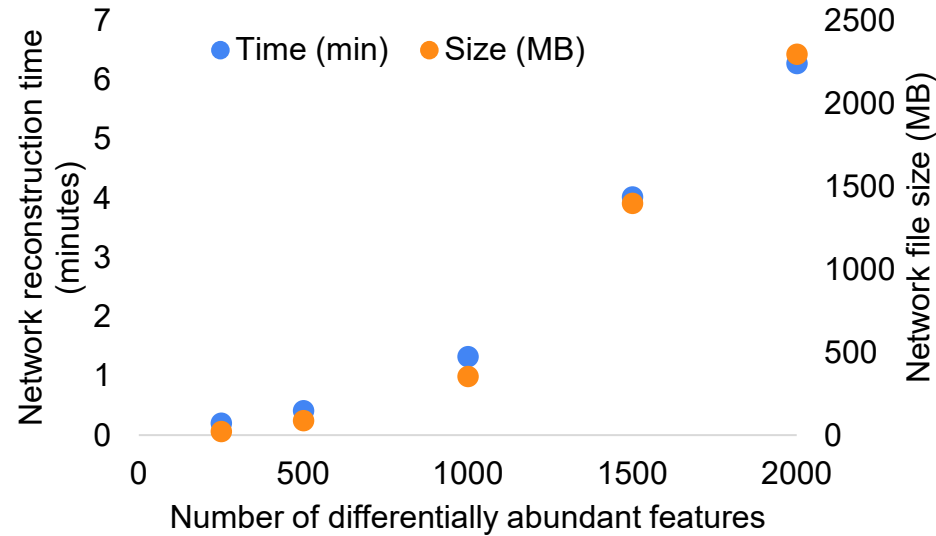

Transkingdom Network Analysis (TkNA): a systems framework for inferring causal factors underlying host–microbiota and other multi-omic interactions

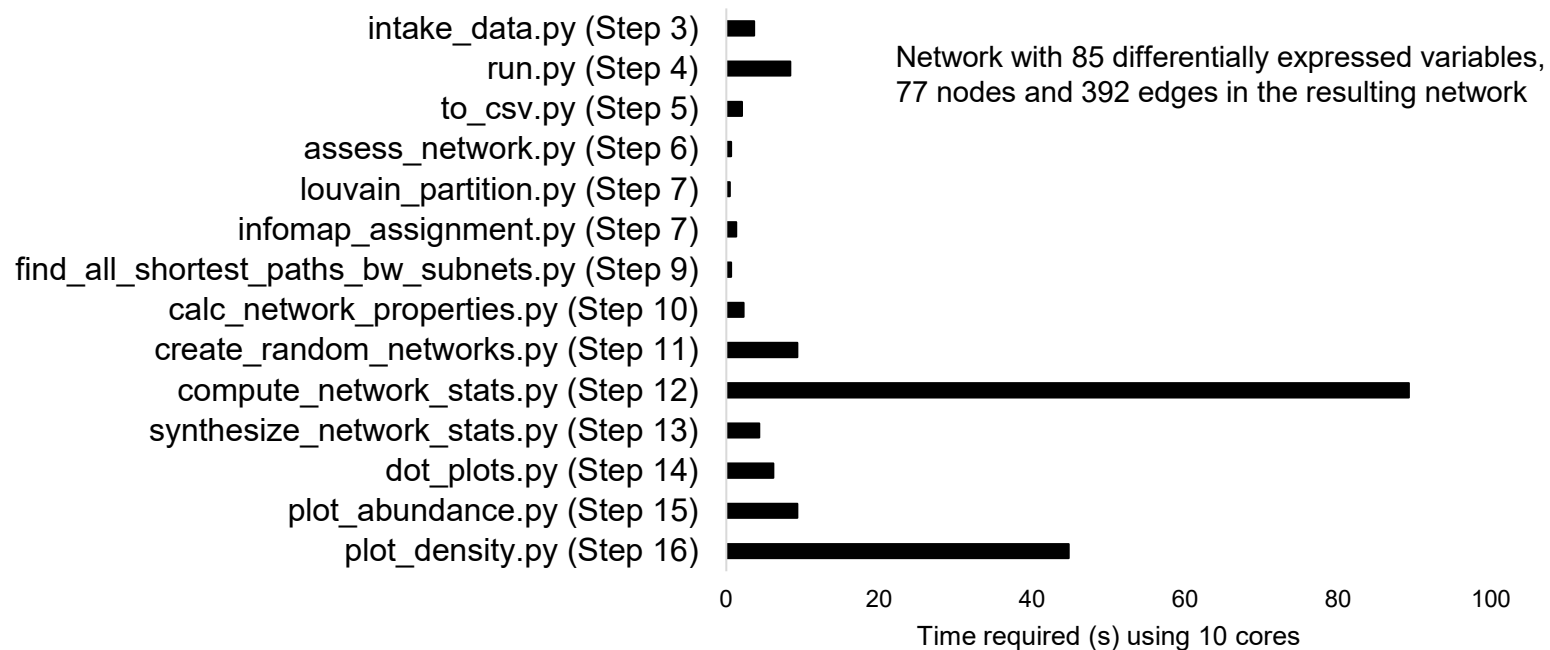
In the format provided by the authors and unedited

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Supplementary Figure 1. Benchmarking of TkNA. Amount of time (left y axis, blue dots) and storage space (right y axis, orange dots) required to reconstruct a network (Stage 1 of TkNA) as a function of the number of differentially abundant features (x axis). Differentially abundant features include those that pass all user-defined statistical thresholds and that are consistent in fold change direction across the user-defined number of experiments.



Supplementary Figure 2. Timing estimates for each step using a network of moderate size. Note that time will vary depending on the number of cores used by the user. The most time-consuming step is step 12, `compute_network_stats.py`, due to the need to perform many shortest paths calculations in thousands of random networks.