

Supplemental Analysis

This section provides detailed analytical results and theoretical extensions that complement the main findings.

S3.1 Phylogenetic Analysis Details

S3.1.1 Phylogenetic Distance Calculation

Phylogenetic distances are calculated using molecular sequence data (DNA, RNA, or protein sequences) from public databases.

The distance metric follows:

$$d_{phyl}(S_1, S_2) = \frac{\text{Number of differences}}{\text{Sequence length}} \quad (1)$$

where S_1 and S_2 are sequences from species 1 and 2, respectively. For species without available sequence data, distances are estimated from taxonomic relationships: - Same species: $d = 0.0$ - Same genus: $d = 0.1 - 0.3$ - Same family: $d = 0.3 - 0.6$ - Same order: $d = 0.6 - 0.8$ - Different orders: $d > 0.8$

S3.1.2 Phylogenetic Tree Construction