

## 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:

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

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