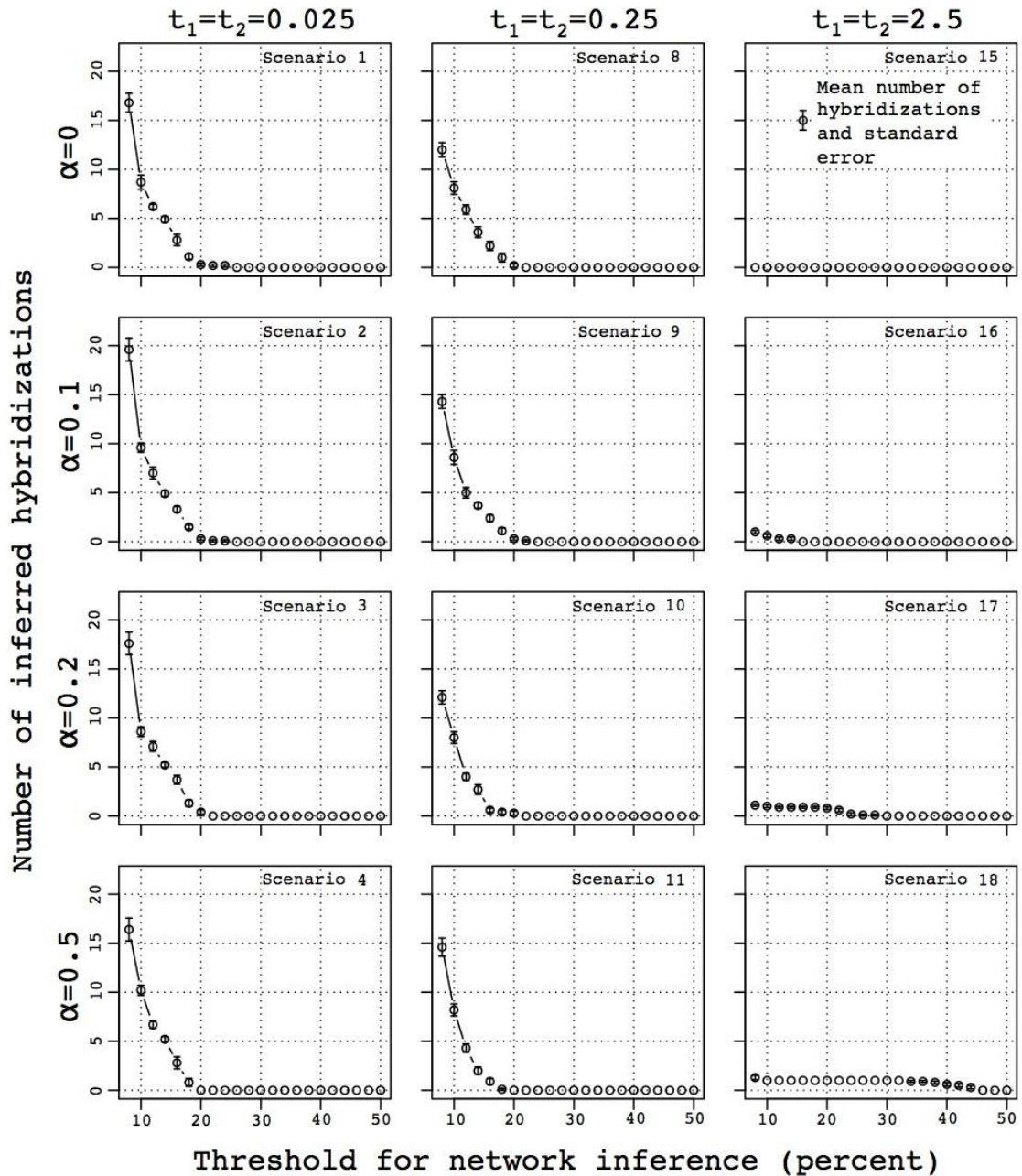
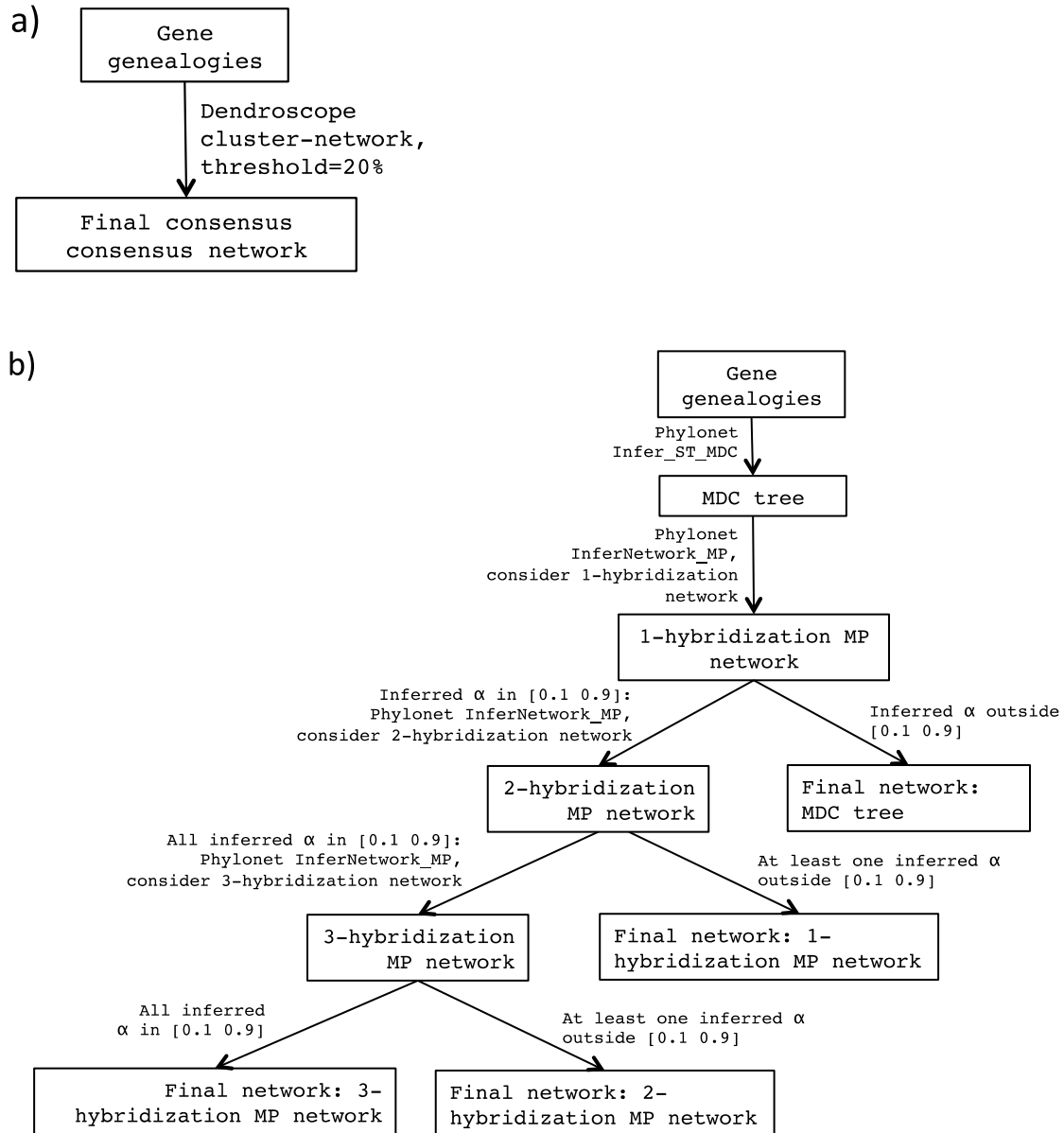


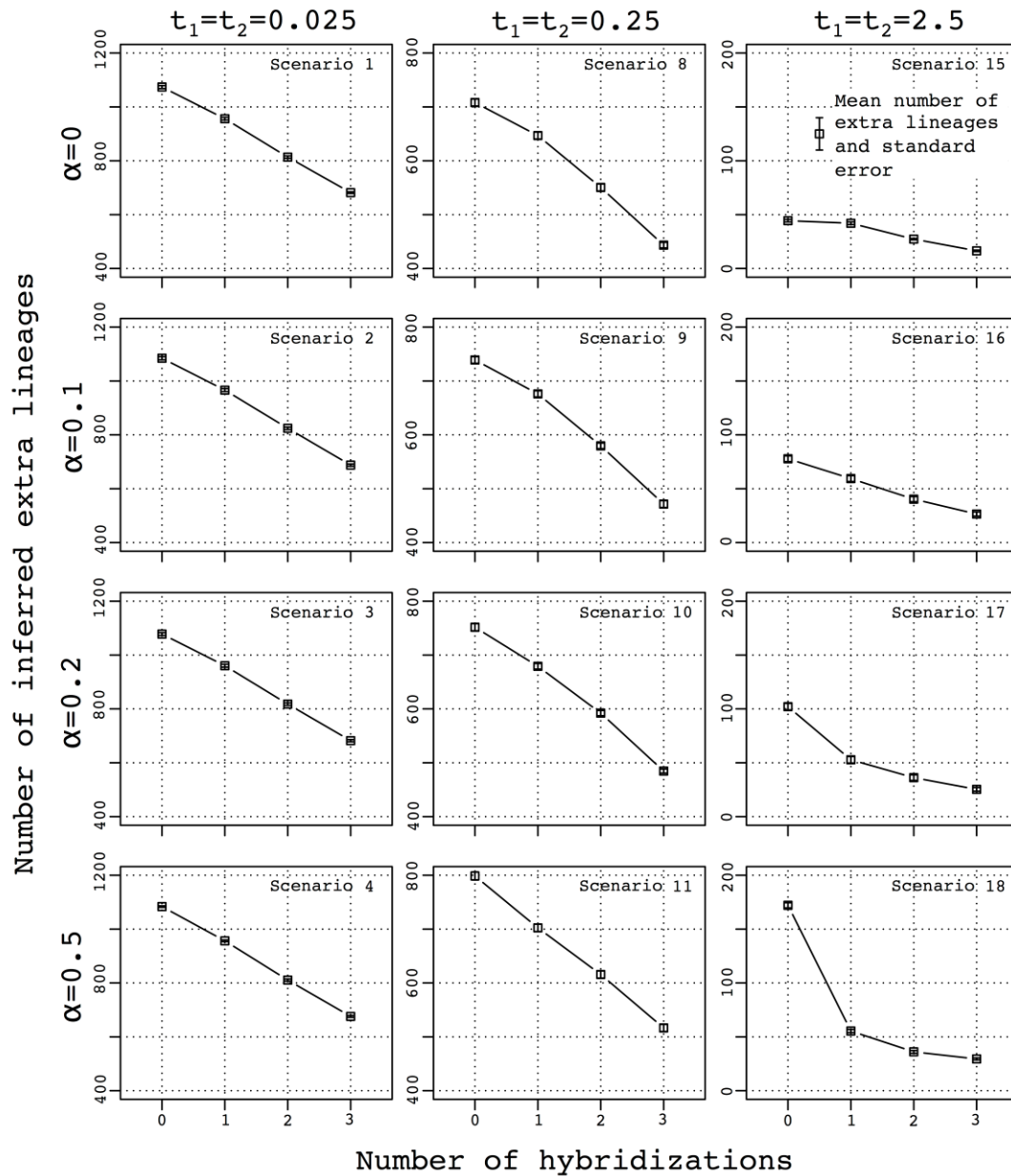
**Figure S1. Schematic representation of the procedure employed to simulate erroneous gene genealogies.**



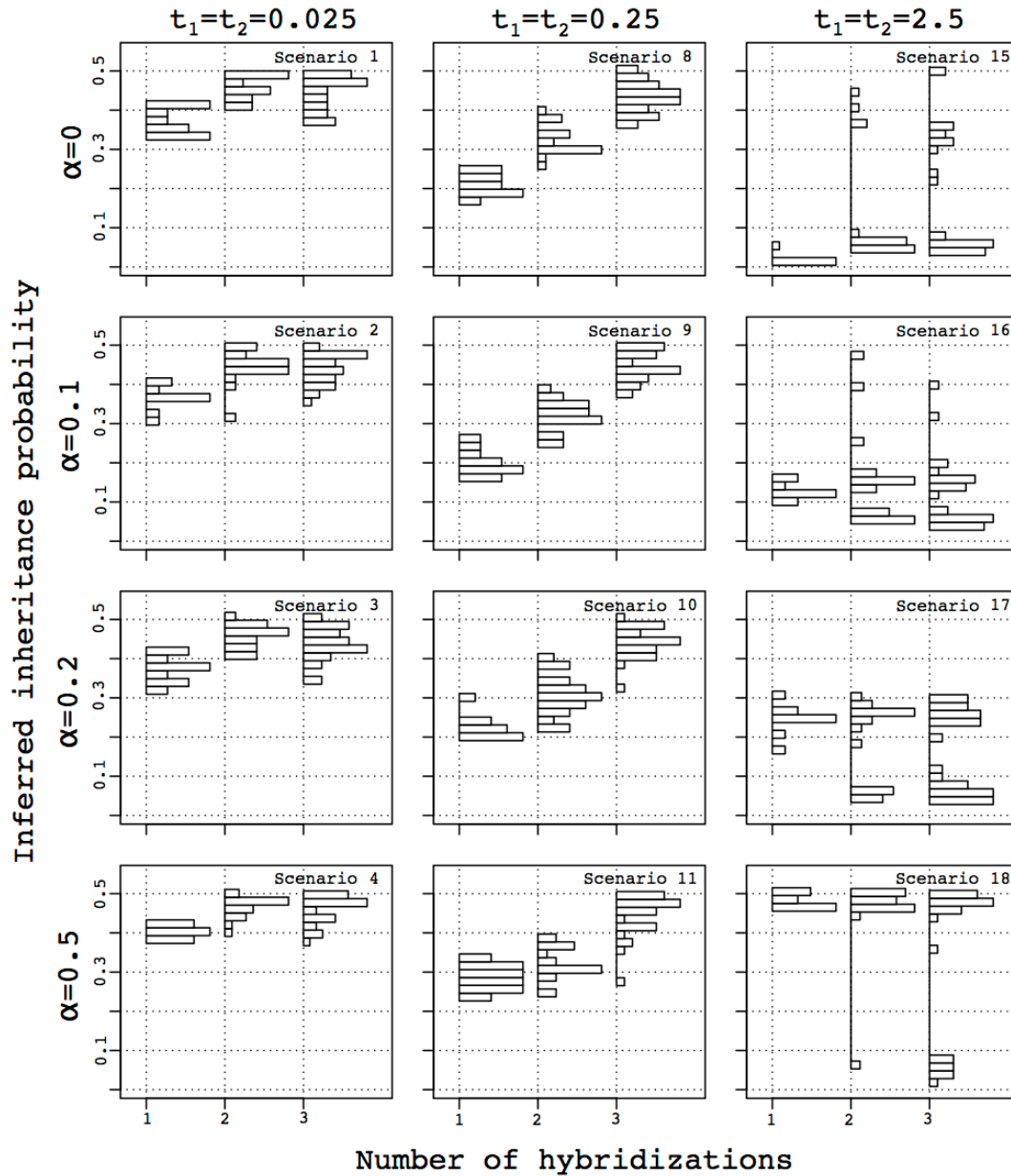
**Figure S2. Number of hybridizations in consensus networks inferred using different threshold values.** The threshold is defined as the minimal number of gene trees required to contain a cluster in order for it to be included into the inferred consensus network. The number of inferred hybridizations was averaged across 10 replicates. Standard errors of the means are also shown.



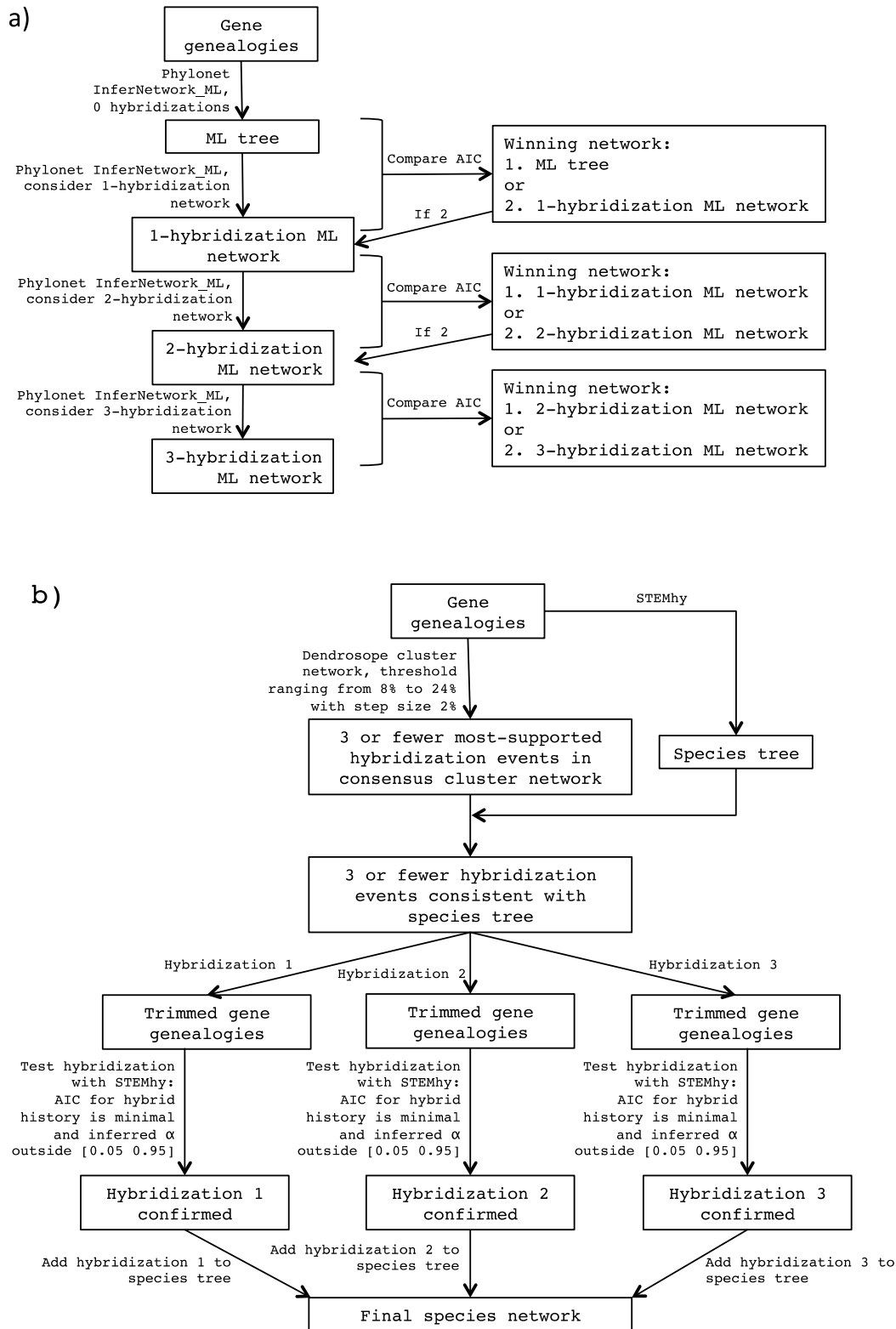
**Figure S3. Schematic representation of strategies implemented to infer species networks.** (A) Consensus network. (B) Maximum parsimony network in PhyloNet.



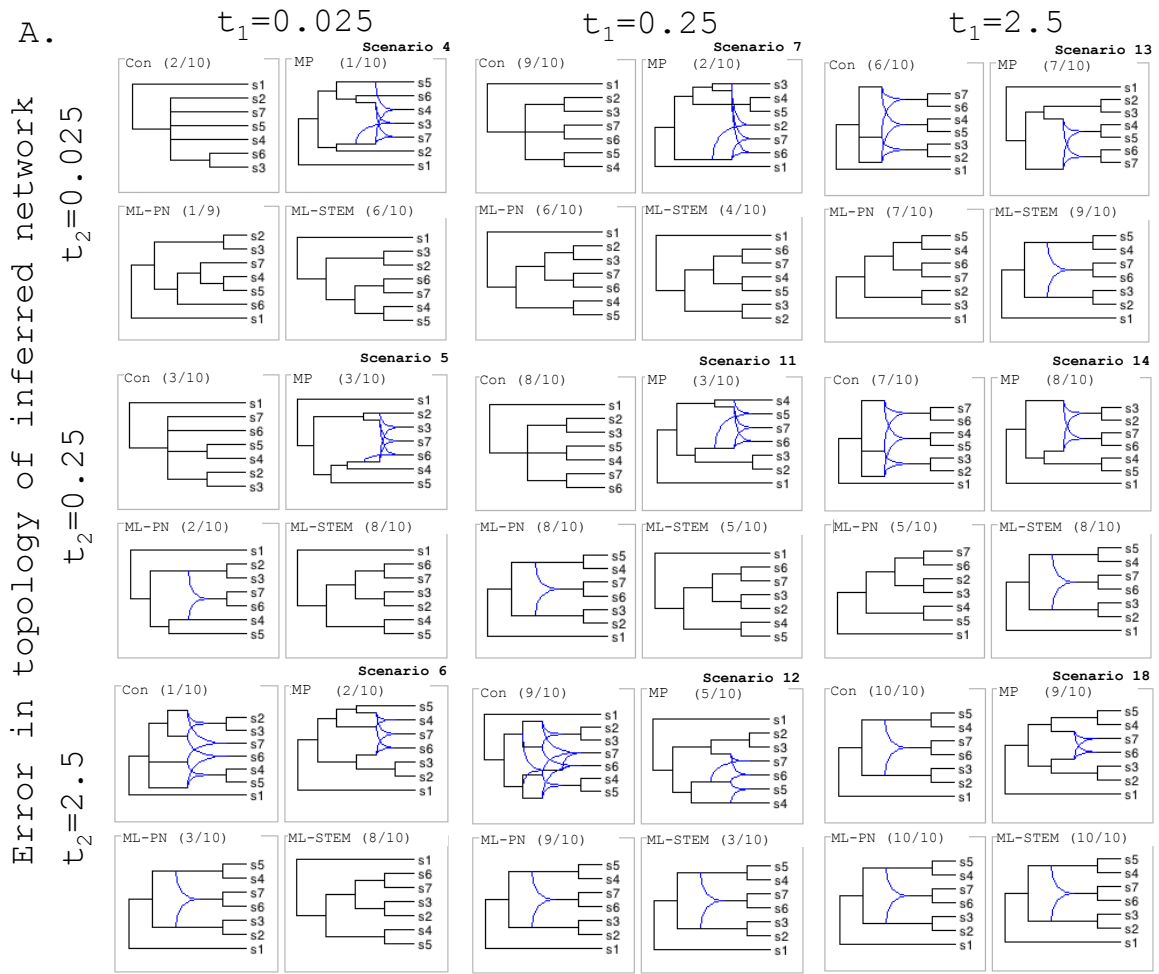
**Figure S4. Number of extra lineages in MP-PhyloNet species networks, allowing for varying numbers of hybridization events.** The number of extra lineages was evaluated for every inferred species network using MP-PhyloNet and averaged across 10 replicate simulations. Standard errors of the means are also shown.



**Figure S5. Values of the parameter  $\alpha$  inferred by MP-PhyloNet, allowing for varying numbers of inferred hybridizations.** Species contributions associated with every hybridization event were recorded for every species network inferred by MP-PhyloNet for 10 replicate simulations. The smaller species contribution is shown for every hybridization.

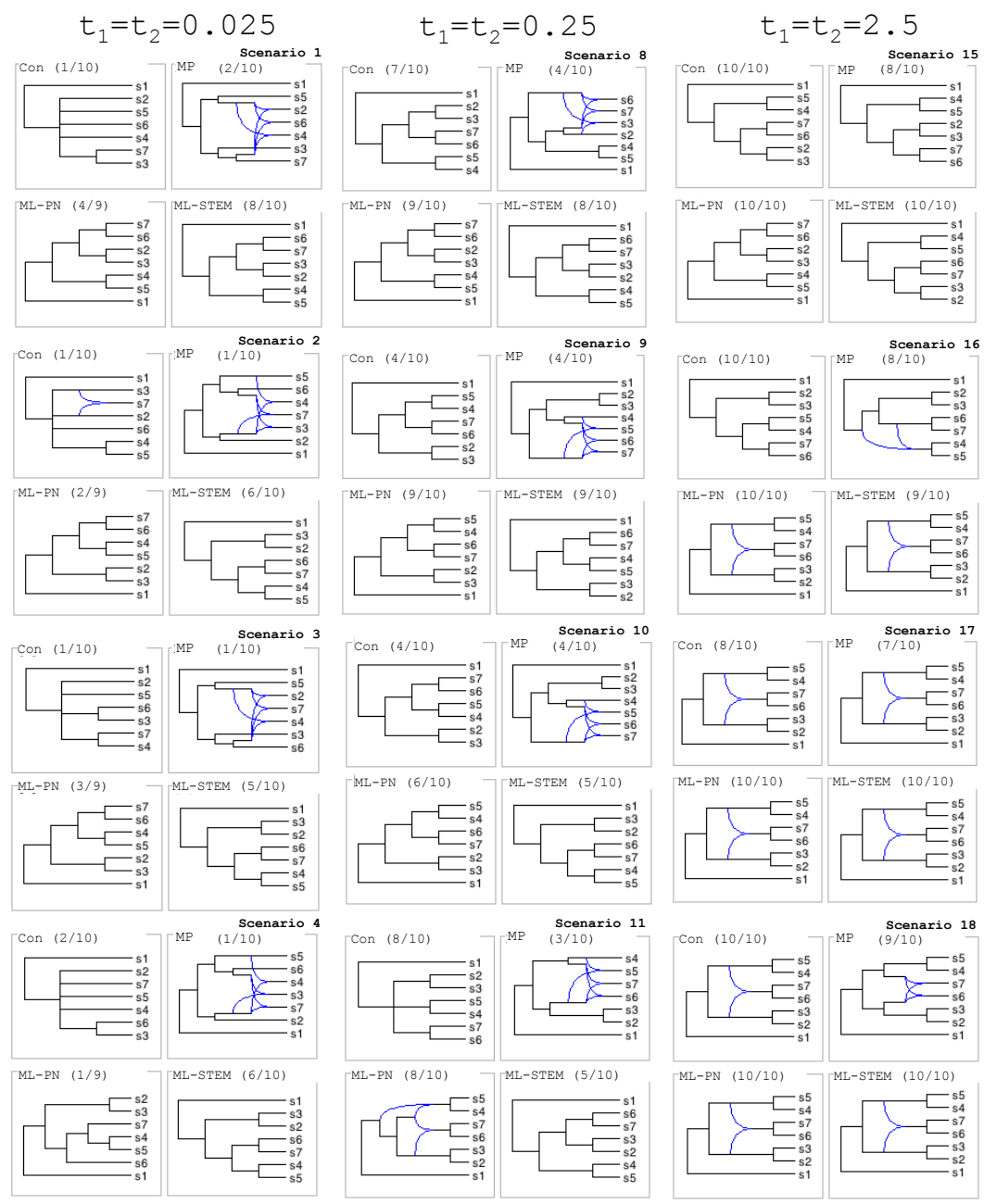


**Figure S6. Schematic representation of strategies implemented to infer species networks. (A) Maximum likelihood network in PhyloNet. (B) Maximum likelihood network with STEMhy.**

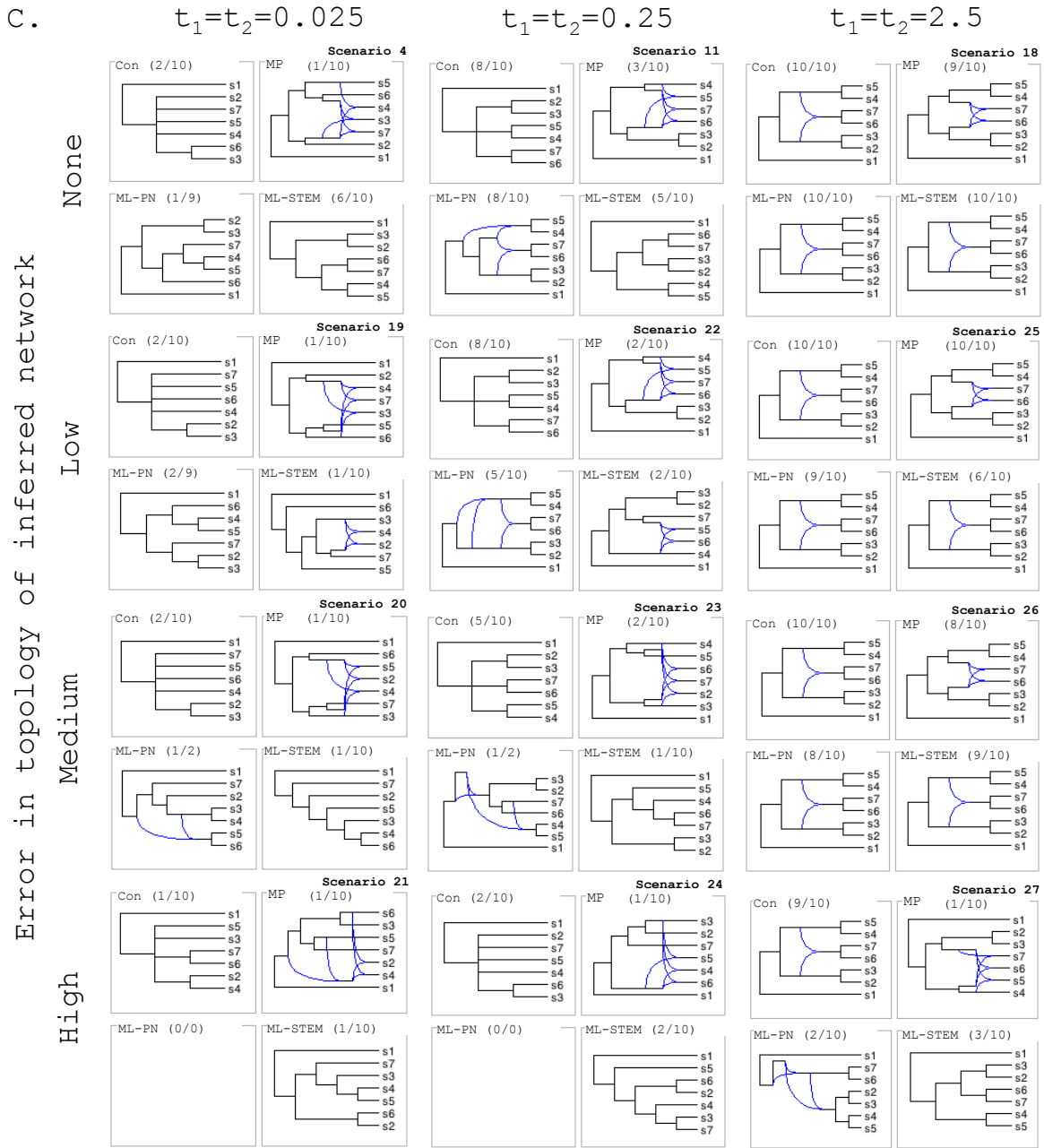


B.

Error in topology of inferred network







**Figure S7. Most frequently observed species network topologies.** The species network topology inferred most frequently among 10 replicates is shown for four species network inference methods, for inferences performed on sets of 250 loci. Con: consensus network; MP: MP network inferred using PhyloNet; ML-PN: ML network inferred using PhyloNet; ML-STEM: ML network inferred using STEMhy. The three panels show the influence of different variables. The number of times the topology was recovered among replicates for which inference was completed appears in parentheses. In case of ties, one topology was chosen at random. Note that in some cases with ML-PN, fewer than 10 replicates were analyzed. PhyloNet failed to terminate or produced computing errors in

some replicates with short branch lengths; here and in the main text, we proceeded by analyzing those replicates that completed successfully. (A) Species divergence times (see Figs. 3 and 4). (B) Species contributions to the hybridization event (see Figs. 5 and 6). (C) Level of error in gene tree estimation (see Figs. 7 and 8).