**Supplementary Table 1**: Number of OTUs whose membership (identity) matched perfectly to expected membership found in the Grinder simulated datasets, as determined using different combinations of the tree reconstruction methods and phylogenetic delimitation models. Expected species membership indicates number of species used to generate a given network. Shaded cells represent models that perform adequately for a given mock network. ML = maximum likelihood solution; BI = most supported Bayesian inference; BI mean = average Bayesian inference; ST = single threshold; MT = multiple threshold. NA denotes cases where the webserver failed to complete analysis.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Network** | **Total Reads** | **Total OTUs** | **RaxML** | | | | **BEAST** | | | |
| **PTP** | | **GMYC** | | **PTP** | | **GMYC** | |
| **ML** | **BI** | **ST** | **MT** | **ML** | **BI** | **ST** | **MT** |
| **Mock 2** | 60 | 32 | 15 | 15 | 18 | 14 | NA | NA | 18 | 18 |
| **Mock 3** | 44 | 15 | 13 | 11 | 1 | 4 | NA | NA | 11 | 10 |
| **Mock 4** | 14 | 10 | 6 | 6 | 8 | 3 | 7 | 6 | 8 | 3 |
| **Mock 5** | 19 | 3 | 3 | 3 | 2 | 0 | 3 | 3 | 3 | 2 |