Table 5. Results of maximum likelihood analyses. Analyses are distinguished by combination of alignment and outgroup(s) used. Summary statistics shown are: the final log likelihood of each analysis; their AIC, AICc and BIC scores; the total number of free parameters in the analysis; the alignment size (total number of character traits); whether or not trees were able to be successfully rooted in the maximum likelihood tree search and bootstrap analyses; and whether or not bootstraps converged in the bootstopping test.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Analysis Dataset | Outgroup(s) Used | Final Log Likelihood | AIC Score | AICc Score | BIC Score | Free Parameters (model + branch length) | Alignment Size | Search Trees Rooted | Bootstrap Trees Rooted | Bootstrap Convergence |
|
| Concatenated Alignment | Zerg\_OG Tyranids\_OG Xenomorphs\_OG | -2544.78 | 5227.56 | 14887.56 | 5382.71 | 69 | 70 | Rooted | Not Rooted | Yes |
|
|
| Physiological Alignment | Zerg\_OG | -636.42 | 1398.84 | 9462.84 | 1491.18 | 63 | 32 | Rooted | -- | -- |
| Behavioral Alignment | Zerg\_OG | -- | -- | -- | -- | -- | -- | -- | -- | -- |
| Archetypal Alignment | Zerg\_OG | -639.63 | 1405.26 | 9469.26 | 1461.36 | 63 | 18 | Rooted | Rooted | No |
| Physiological Alignment | Protoss\_OG | -627.05 | 1380.10 | 9444.10 | 1472.44 | 63 | 32 | Rooted | Rooted | No |
| Behavioral Alignment | Protoss\_OG | -- | -- | -- | -- | -- | -- | -- | -- | -- |
| Archetypal Alignment | Protoss\_OG | -632.35 | 1390.70 | 9454.70 | 1446.80 | 63 | 18 | Rooted | Rooted | Yes |