

Figure 1 displays the results of a 1000-fold bootstrap analysis of the phylogenetic relationships among 1000 simulated datasets. The figure is organized into three main sections, each showing a different set of simulated datasets and their corresponding phylogenetic trees.

Section 1 (Top): This section displays the results for 1000 simulated datasets. The top part shows the sequence alignment for each dataset, with the first 1000 columns representing the simulated sequences. The bottom part shows the phylogenetic tree for each dataset, with the root of the tree at the top and the tips of the tree at the bottom. The trees are color-coded by the number of bootstrap support values, with red indicating high support and blue indicating low support.

Section 2 (Middle): This section displays the results for 1000 simulated datasets. The top part shows the sequence alignment for each dataset, with the first 1000 columns representing the simulated sequences. The bottom part shows the phylogenetic tree for each dataset, with the root of the tree at the top and the tips of the tree at the bottom. The trees are color-coded by the number of bootstrap support values, with red indicating high support and blue indicating low support.

Section 3 (Bottom): This section displays the results for 1000 simulated datasets. The top part shows the sequence alignment for each dataset, with the first 1000 columns representing the simulated sequences. The bottom part shows the phylogenetic tree for each dataset, with the root of the tree at the top and the tips of the tree at the bottom. The trees are color-coded by the number of bootstrap support values, with red indicating high support and blue indicating low support.