



FIGURE 21.2 Schema of the mirror-tree method. Multiple sequence alignments of proteins *A* and *B*, constructed from orthologs of *A* and *B*, respectively, from a common set of species, are used to generate the corresponding phylogenetic trees and distance matrices. The degree of coevolution between *A* and *B* is assessed by comparing the corresponding distance matrices using a linear correlation criteria. Proteins *A* and *B* are predicted to interact if the degree of coevolution, measured by the correlation score, is high (or above a certain threshold).