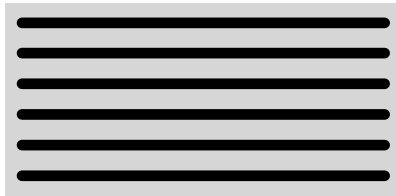


input: unaligned homologous sequences



algorithm:

compute pairwise distance matrix; from this compute a guide tree; follow the guide tree to progressively add more distant sequences to the alignment until all sequences have been aligned



output: globally aligned sequences