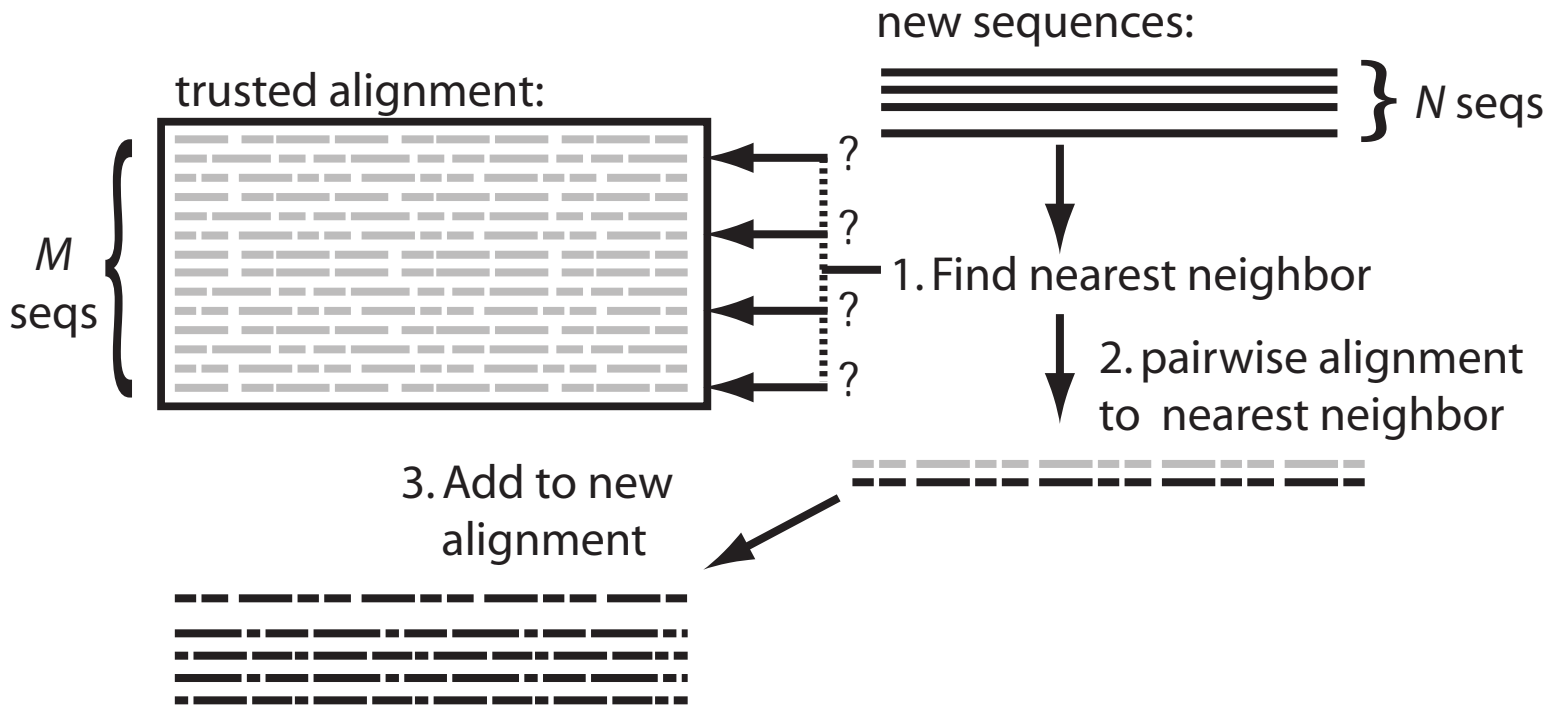


"nearest neighbor" alignment:



Advantages over *de novo*:

1. More scalable ($O(MN)$)
2. Uses existing, trusted SSU alignment

Drawbacks:

1. Still slow if M is large (~ 5000 for Greengenes)
2. Pairwise alignment ignores varying conservation across alignment