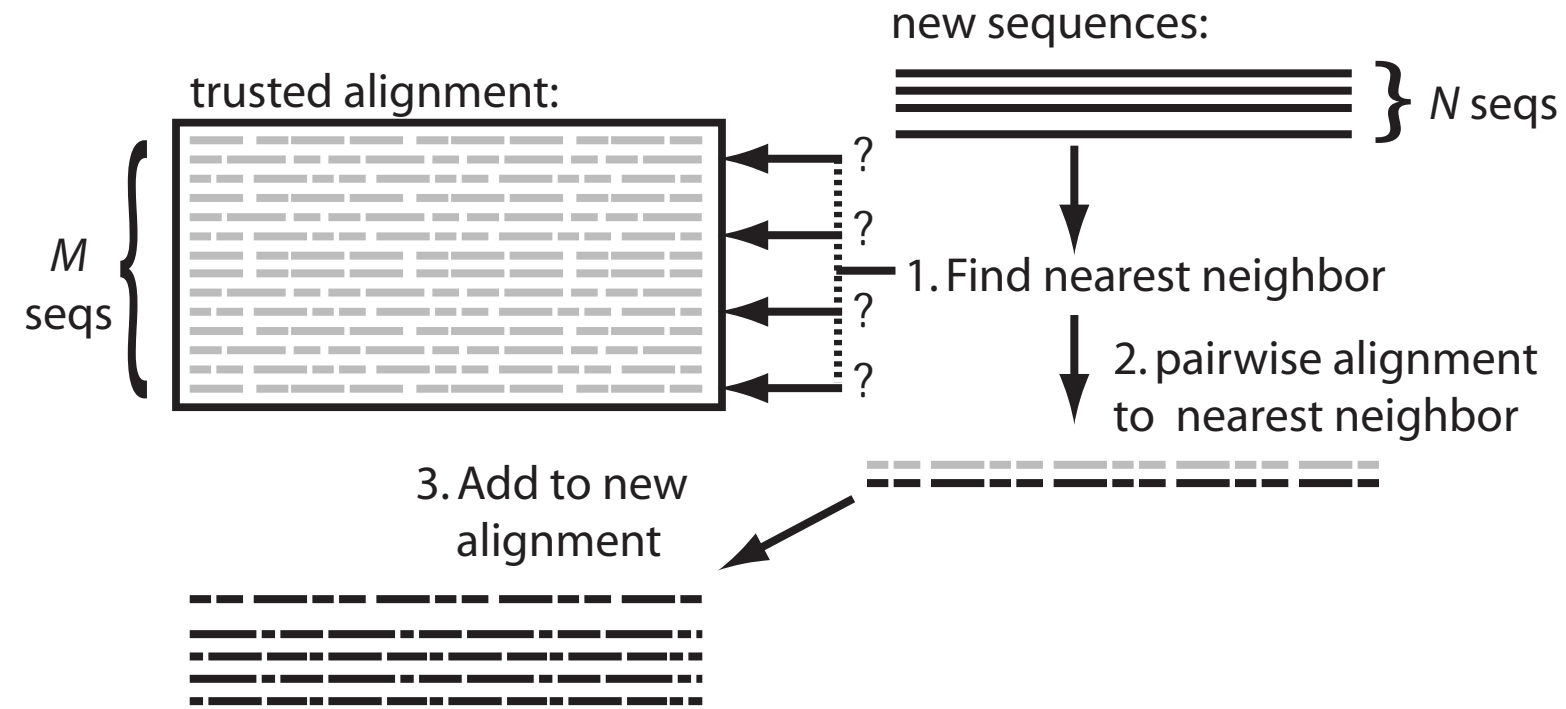


"nearest neighbor" strategy:



Potential drawbacks:

- M may need to be large ($\sim 5,000$ SSU rRNA seqs for Greengenes(*))
- errors in reference alignment will be propagated
- pairwise alignment ignores varying conservation across alignment