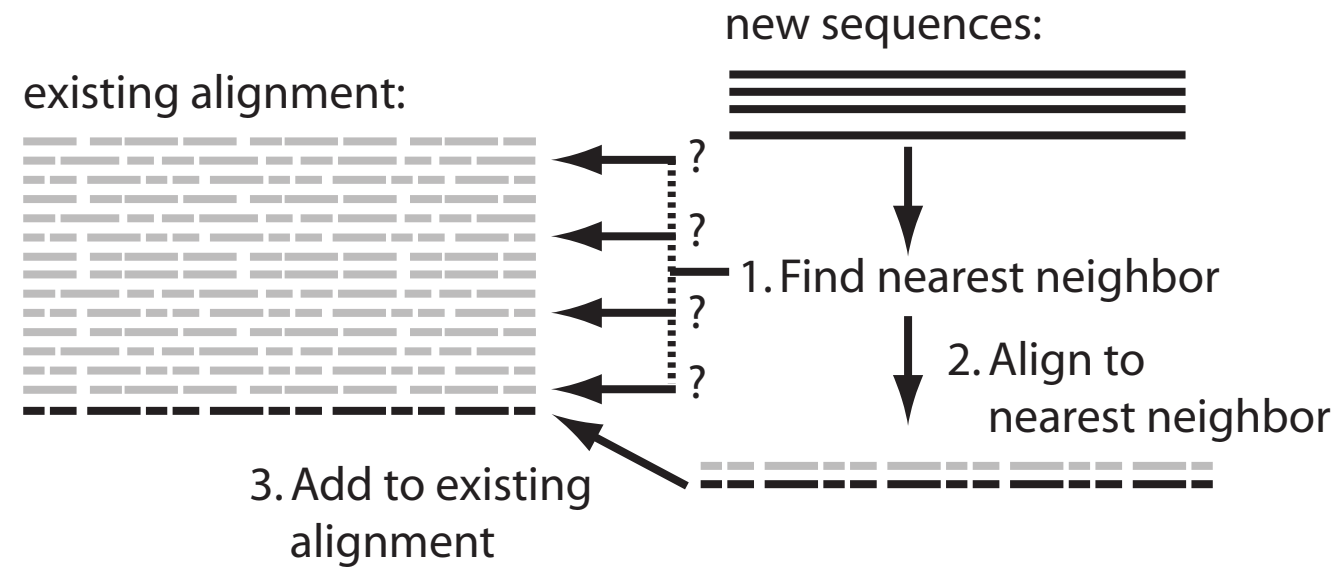# Generic "nearest neighbor" strategy:

- align each sequence to it's nearest neighbor in the existing alignment

- novel, divergent sequences are difficult to align

- errors can easily propagate

- flexible, but doesn't scale well

existing alignment:

new sequences:

1. Find nearest neighbor

2. Align to nearest neighbor

3. Add to existing alignment

NAST "nearest neighbor" strategy:

- use fixed, trusted alignment of ~10,000 sequences

- tradeoff between speed of NN search and accuracy of pairwise alignments

- flexible and scalable

trusted alignment:

new sequences:

1. Find nearest neighbor

2. Align to nearest neighbor

3. Add to new alignment