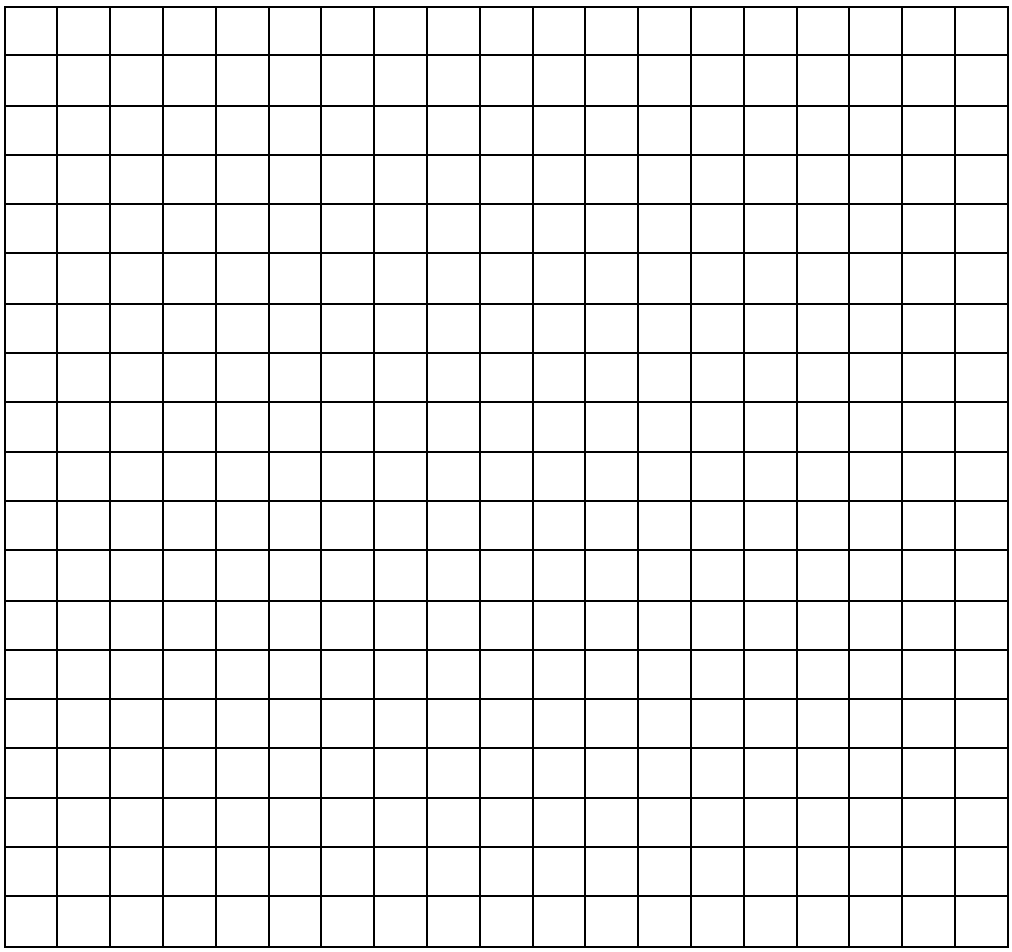
Alignments by Hand

Use the directions and grid below to align the following sequences to the best of your ability.

1. Place the longest sequence (4) on the graph below to be used as a reference. This sequence should not contain any gaps.
2. Label each additional sequence placed on the graph with its identifying number.
3. Use dashes to represent gaps in the sequence.
4. Mismatches are allowed, but not preferable.
   - Changes between (C and T) and (G and A) are preferred over others. Why do you think that is?
5. The goal is to maximize similarity, i.e., as many similar letters and as few gaps in each column as possible.
6. Calculate the overall percent similarity between these sequences. (Percent similarity consists of the number of sites with identical bases/total length of longest sequence.)

1 GAATCTGCTC
2 GAATCCTGCCC
3 GAAATCTCTC
4 GAATCCTTGCTC
5 GATCCGCTC



Adapted from *Science Research Mentoring Program: GENETICS*
American Museum of Natural History © 2011. All Rights Reserved.