Q3: Sequence assembly, Milestone 2

Copy paste your code from the previous milestone into get\_best\_nucleotide(nucleotide1, nucleotide2, nucleotide3) and write assemble\_sequence(sequence1, sequence2, sequence3) to do the actual sequence assembly! The main() function we provide for you, which you should not modify, does the housekeeping of loading the sequences, and then calls assemble\_sequence() to do the real work. You can assume that all three sequences passed into this function are the same size (have the same height and width).

Your function should create a new (blank) sequence of the same size as the grids passed into the function and then appropriately set the nucleotides in this new sequence to construct the solution sequence. The solution sequence is generated by simply placing the best nucleotide (most common, non-blank nucleotide, at that position across all three sequences) at each position. For example, if you're given 'AA\_', 'ATA', and 'AT\_', you will be able to discern that the solution sequence is 'ATA'.

We've given you a couple folders with three sequences each that will be used to test your code when you press the Mark button. You can view the sequences in these folders by clicking the upper left icon in your file workspace (directly to the left of the tab for the file sequence\_assembly.py your code is in!). To change the folder you run your code on, change the value of the SEQUENCES\_FOLDER constant at the top of the file to one of the other folder names, either 'tiny' , 'no\_blanks', 'long', or 'large' .