The rules: you can use whatever resources you want, just don't ask other people for answers. This includes online searches of "how do I solve X." Please leave your cameras on (audio off) unless you have a compelling reason to have the camera off. If you do have a compelling reason, please private message the TA (no need to provide a reason).

## Problem 1

```
(10 points total, 2 points each (i).)
```

Below is some code to generate a very simple (uncollapsed) de Bruijn graph. Anywhere there is red text and underscores, fill in the appropriate code. While the code is in Python, it should be readable as pseudocode. The code you write does not need to be syntactically correct, simply logically correct. That is, your answer does not necessarily need to be in Python (but it can be).

To keep things consistent, let's stick to indexing starting at 0, ranges can be provided with ":", and the final value in a sequence is not inclusive. For example, 0:4 would generate the set  $\{0, 1, 2, 3\}$ , as range(4) would in Python.

Some people have asked if they can run the code. Sure, go for it. Given the time constraints, I probably wouldn't.

```
# This is a class for a node in a graph.
# Each node can connect to the next one, thus,
# this is all you should need to make a minimalist graph.
class Node():
    # this is the constructor
    def __init__(self, seq):
        self.seg = seg
        self.edge_seq = None
        self.next = None
    # This is a member function which creates an edge to the next node.
    # For the purpose of this exercise,
    # let's assume there is only one next node.
    def add_edge(self, next_node):
        k = len(self.seq)
        # (c)
        # check if the left and right nodes have the correct matching substring
        if self.seq[\underline{1}:k
                raise Exception("substrings don't match. \{\%s\} - \{\%s\}" %
                            (self.seq, next_node.seq))
        self.edge_seq = self.seq + next_node.seq[k - 1]
        self.next = next_node
        return
def debruijn(seq, k):
    composition = kmer_composition(seq, k)
    graph = None
    position_pointer = None
    for kmer in composition:
        left_right_mers = kmer_composition(kmer, k - 1)
        if graph is None:
            graph = Node(left_right_mers[0])
            position_pointer = graph
        # (d) what is the correct index?
        position_pointer.add_edge(Node(left_right_mers[_____]))
        position_pointer = position_pointer.next
    return graph
```

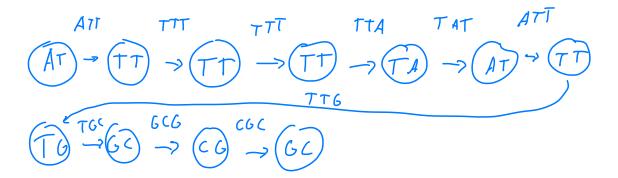
## Problem 2

(15 points)

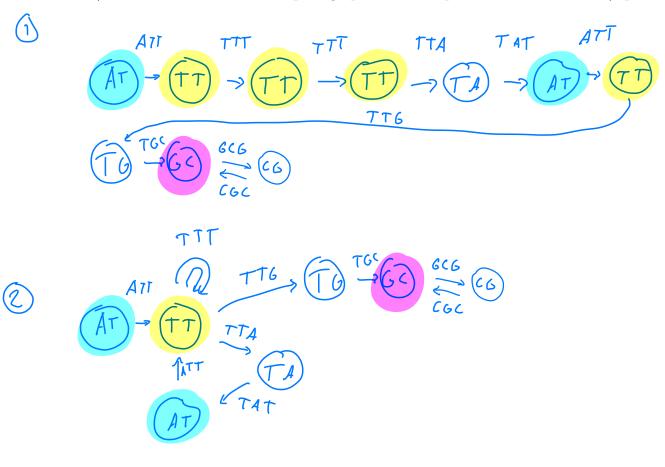
Show work where possible.

Assume the following DNA sequence:

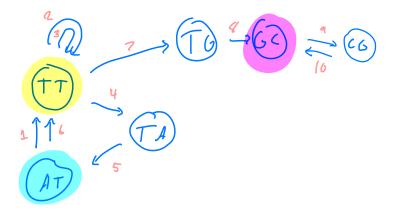
a) Draw the simple de Bruijn graph with k = 3, aka,  $DeBruijn_3(.)$ , that does not collapse any nodes (except the trivial left/right-mers). (3 points)



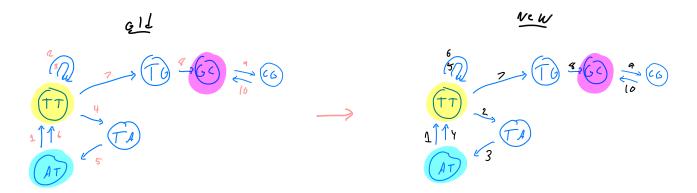
b) Draw all intermediate collapsed graphs that collapse on common nodes. (6 points)



c) Redraw your final graph from (b) and find the Eulerian path that corresponds to the original sequence but do not label the edges with their corresponding k-mer. Instead, label the edges on the Eulerian path edges with with an unique increasing integers starting with 1 (e.g. 1, 2, ...). (3 points)



d) Find an Eulerian path that generates a different sequence. You can simply write down the edge labels here and make sure to write down the corresponding sequence. (2 points)



1,4,5,6,2,3,7,8,9,60

ATT ATTTT 6C6C

e) What's your favorite Power Ranger or Pokémon? (1 point)

I like the blue Power Ransen