Bioinformatics III

Fifth Assignment

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Exercise 5.1: Cliques and Network Evolution

(a) Listing 1 shows source code.

Listing 1: Listing of source code

```python
0  import random
   from os.path import exists
   from AbstractNetwork import AbstractNetwork
   import matplotlib.pyplot as plt


5
   class CliqueNetwork(AbstractNetwork):
       def __createNetwork__(self, filename, dummy):
           """
           Create a network from a file
10         """
           if exists(filename):
               # "with" closes the file again after reading
               with open(filename) as openfile:
                   for line in openfile:
15                     # get entries of a line as list
                       content = line[0:(len(line)-1)].split("\t")
                       # and store them
                       if len(content) == 2:
                           n1 = self.getNode(content[0])
20                         n2 = self.getNode(content[1])
                           n1.addLinkTo(n2)
                           n2.addLinkTo(n1)
           else:
               print(filename, "does_not_exist")

25
       def findCliques(self):
           cliques = []
           for node1 in self.nodes.values():
               for node2 in node1.nodelist:
30                 candidates = list()
                   candidates.append(node1)
                   candidates.append(node2)
                   clique = set(self.extendClique(candidates, 3))
                   if clique not in cliques and len(clique) > 2:
35                     cliques.append(clique)
           return cliques

       def extendClique(self, candidates, depth):
           if depth <= 5:
40             for nextnode in candidates[0].nodelist:
                   if nextnode not in candidates:
                       if all(nextnode.hasLinkTo(x) for x in candidates):
                           candidates.append(nextnode)
                           self.extendClique(candidates, depth+1)
```

```python
45                            else:
                                  return candidates
                      return candidates
                else:
                      return candidates
50
        def evolve(self, t):
              cliques = list()
              for c in range(3):
                    cliques.append(t * [0])
55          for i in range(t):
                    clique = cn.findCliques()
                    r = random.random()
                    node1id = random.choice(list(self.nodes))
                    node1 = self.nodes[node1id]
60              if r <= 0.5:
                        while True:
                              node2id = random.choice(list(self.nodes))
                              node2 = self.nodes[node2id]
                              if not node1.hasLinkTo(node2):
65                                  node1.addLinkTo(node2)
                                    node2.addLinkTo(node1)
                                    break
                    else:
                        while len(node1.nodelist)==0:
70                            node1id = random.choice(list(self.nodes))
                              node1 = self.nodes[node1id]
                        node2 = random.choice(node1.nodelist)
                        node1.removeLinkTo(node2)
                    cliques = self.plot(clique, i, cliques)
75          for index, item in enumerate(cliques):
                    plt.plot(range(len(item)), item, marker='x')
                    plt.xlabel('t')
                    plt.ylabel('amount of cliques')
                    plt.title('Evolving Networks')
80                  plt.legend('345')
                    plt.tight_layout()
              plt.show()

        def printClique(self, clique):
85          for line in clique:
                    s = ''
                    for c in line:
                          s += str(c)
                    print(s)
90
        def plot(self, clique, t, cliques):
              if t == 999:
                    for c in clique:
                          cliques[len(c)-3][t] = cliques[len(c)-3][t] + 1
95                return cliques
              else:
                    for c in clique:
                          cliques[len(c)-3][t] = cliques[len(c)-3][t] + 1
                    return cliques
100


    cn = CliqueNetwork("rat_network.tsv", "dummy")
    #cn = CliqueNetwork("test.txt", "dummy")
105 #print(cn.size())
    clique = cn.findCliques()
    #cn.printClique(clique)
    cn.evolve(1000)
    clique = cn.findCliques()
110 #cn.printClique(clique)
```
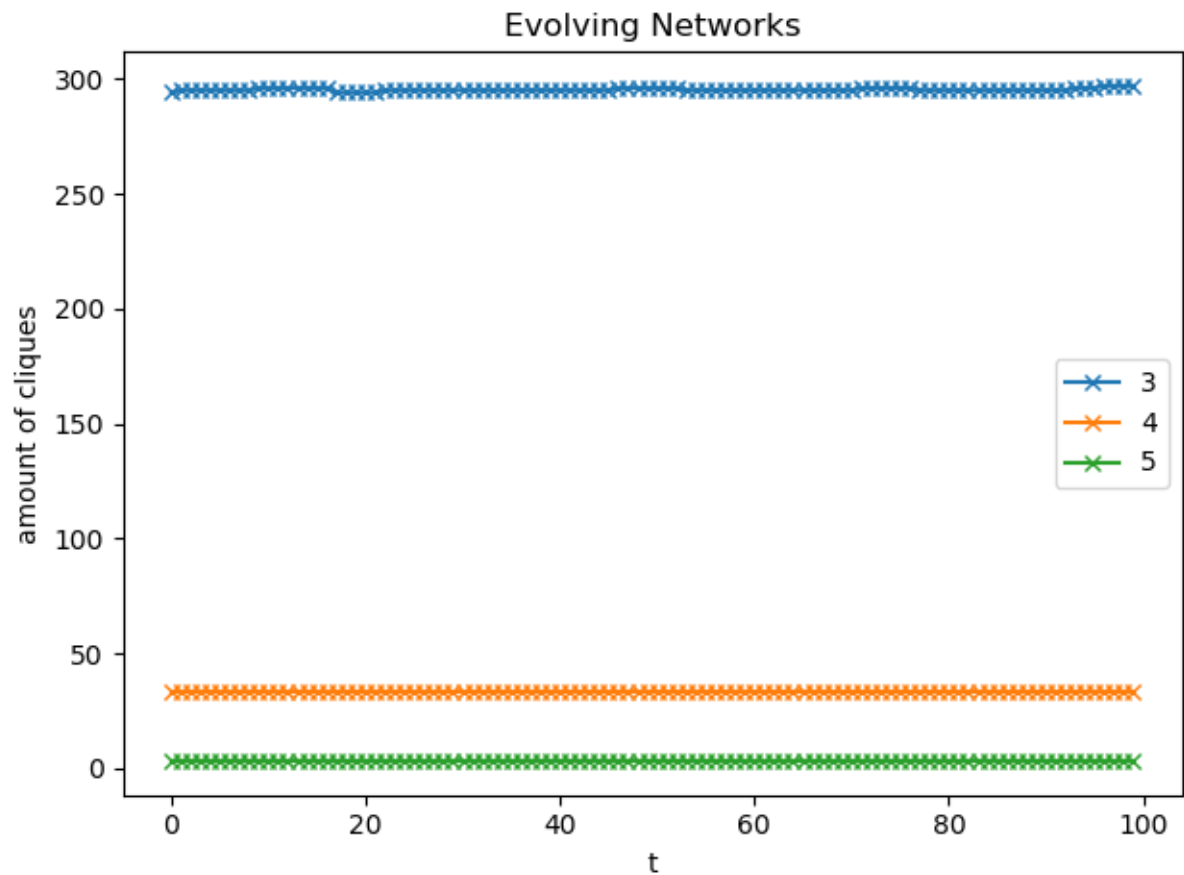
Figure 1: Number of cliques of size 3, 4 and 5 at the beginning and after each time step as a function of time with t = 100

(b) Listing 1 shows source code.

(c) Listing 1 shows source code.

(d) The number of cliques stays approximately the same independent of the time step because approximately the same amount of edges are added which are removed as shown in figure 1. The amount of cliques of size 3 increases rather than the one of larger cliques because a less edges added may result in a small clique.

clique size	number of cliques before evolution	number of cliques after evolution
3	294	300
4	33	33
5	3	3

Table 1: Number of cliques of size 3, 4 and 5 at the beginning and after letting it evolve for 100 time steps

(e)

(f)

clique size	number of cliques before evolution	number of cliques after evolution
3	294	327
4	33	27
5	3	3

Table 2: Number of cliques of size 3, 4 and 5 at the beginning and after letting it evolve for 1000 time steps

Exercise 5.2: Annotations in Protein Protein Interaction Networks

(a)

(b)

(c)

(d)

(e)