Biological Computation 2025

חישוב ביולוגי

Exercise #2

הגשה בזוגות עד לתאריך 2.6.25

<u>Note</u>: You can discuss the work with other students however you should write all code by yourself / with your exercise partner. Please document your code and also prepare a short (no more than 2 pages) explanation on how the code works and what were the main design and implementation decisions you made. You must declare if you use any code you did not write on your own or generated using Al.

*In addition to submitting to Moodle prepare a GitHub repository with a readme on how to run the code.

1) a) Write a program (in your favorite programming language) that gets as input a positive integer n and generates all connected sub-graphs of size n.

The output should be a textual file of the following form:

n=2

count=2

#1

12

#2

12

21

The first two lines output n and the total number (count) of different sub-graphs of size n. Then the sub-graphs themselves are given each starting with a line labelled #k for motif number followed by all edges, each line i j means an edge from source i to target j.

b) Output the result of your program for n = 1 to 4.

- c) What is the maximal number n for which your program can complete successfully within no more than 1 hour of computing time?
- d) What is the maximal number n for which your program cancomplete successfully within 2,4,8 hours of computing time?
- 2) Write a program that gets as input positive integer n and a graph of the format:
- 12
- 23
- 14

The graph in the example contains 4 vertices 1,2,3,4 and directed edges (1,2) (2,3) (1,4). The program should output all sub-graphs of size n and count how many instances appear of each motif. The format of the output of the identified sub-graphs should be like in question 1, where in the line after #k should appear the count of number of instances, count=m if the motif appears m times. Output count=0 if a motif does not appear in the graph.