

Assignment 1

Arvind Iyer
MT16122

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1 Introduction

"Network integration of Parallel Metabolic and Transcriptional Data" uses concepts of network and graph theory to understand the metabolic and transcriptional networks of an organism in integrated fashion in order to understand the relationship between them leading to the cause of rapid growth of macrophage(a type of white blood cells).

2 Answers

1] The nodes in the network are metabolites represented in using circle symbol in the web app dataset while in paper there are square symbols also representing enzymes. The edges are the reaction taking place between two nodes in presence of an enzyme. In literature the macrophage are divided into two main groups M1 and M2 on the basis of activation of macrophage and functionality they do. The differential expression of metabolite and enzyme determine the size of node and the red and green colour in the network determine the fold change(M2 to M1)(As per paper Red is for M2 and green for M1). The

3] From playing around with the parameters what I could understand that the the scoring of nodes is done using p values based on which module are created. Now the size of the network would vary as as we add more reaction between two nodes. In nutshell we alter the network by increasing or decreasing the weight of edge and that would alter how nodes are regulated. Due to this we get different shape and size of network.

2] As per my understanding we had to show the module found in the paper to the given data set. I have used cytoscape tool to visualize the network and tried to show the region/module as mentioned in paper to best if could have. The images are as follows:



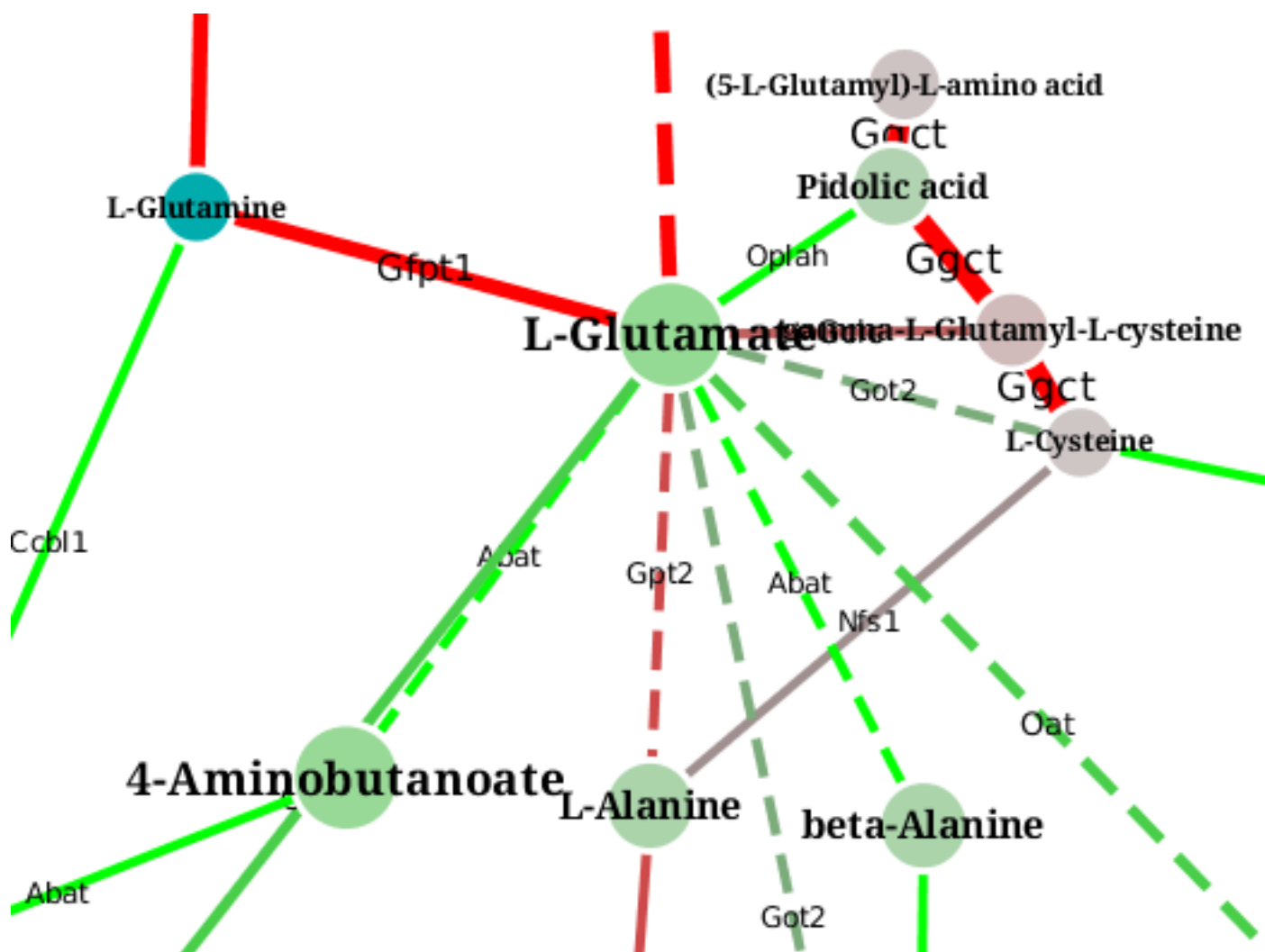


Figure 3: Glutamine

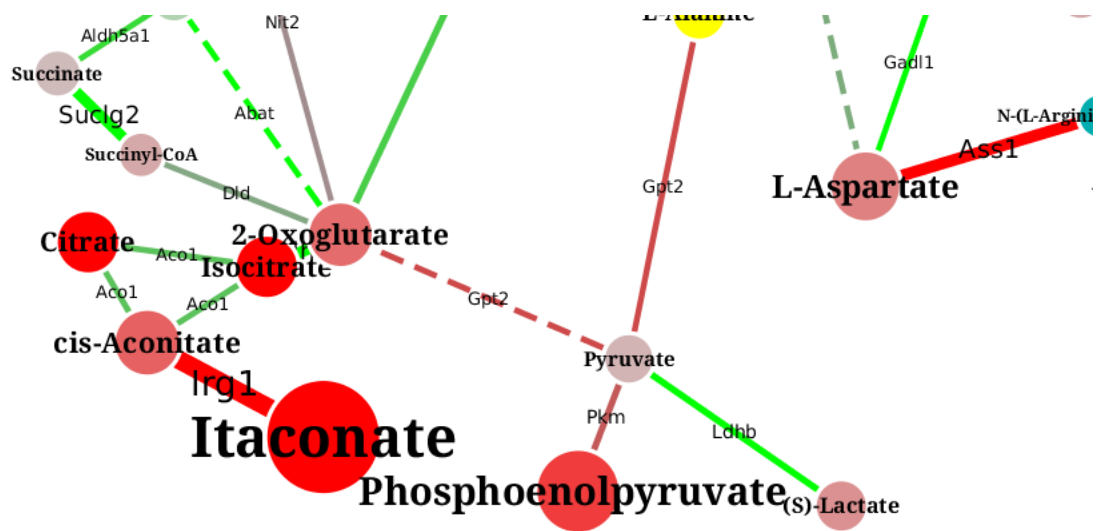


Figure 4: TCA

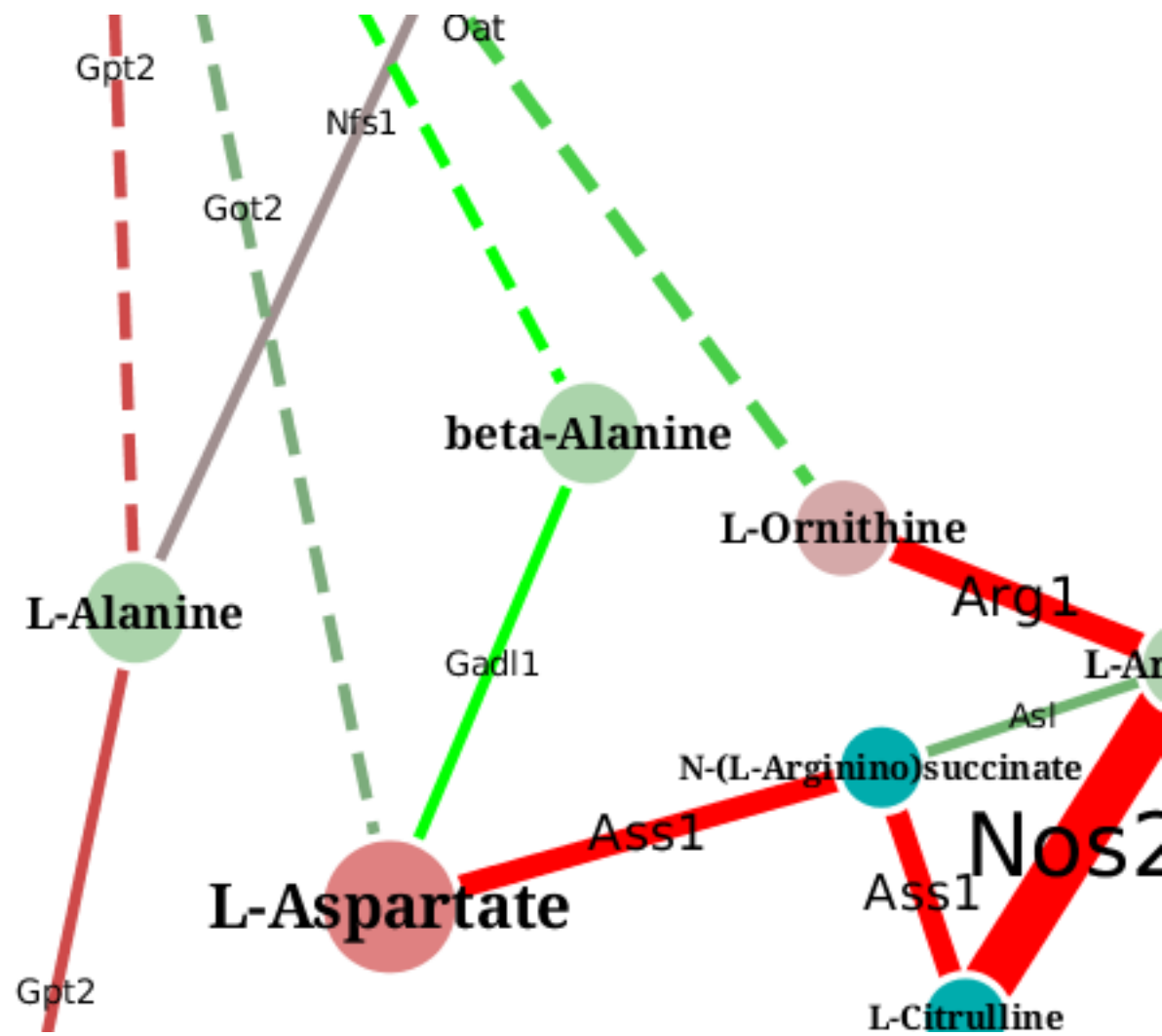


Figure 5: Urea



Figure 6: Fatty

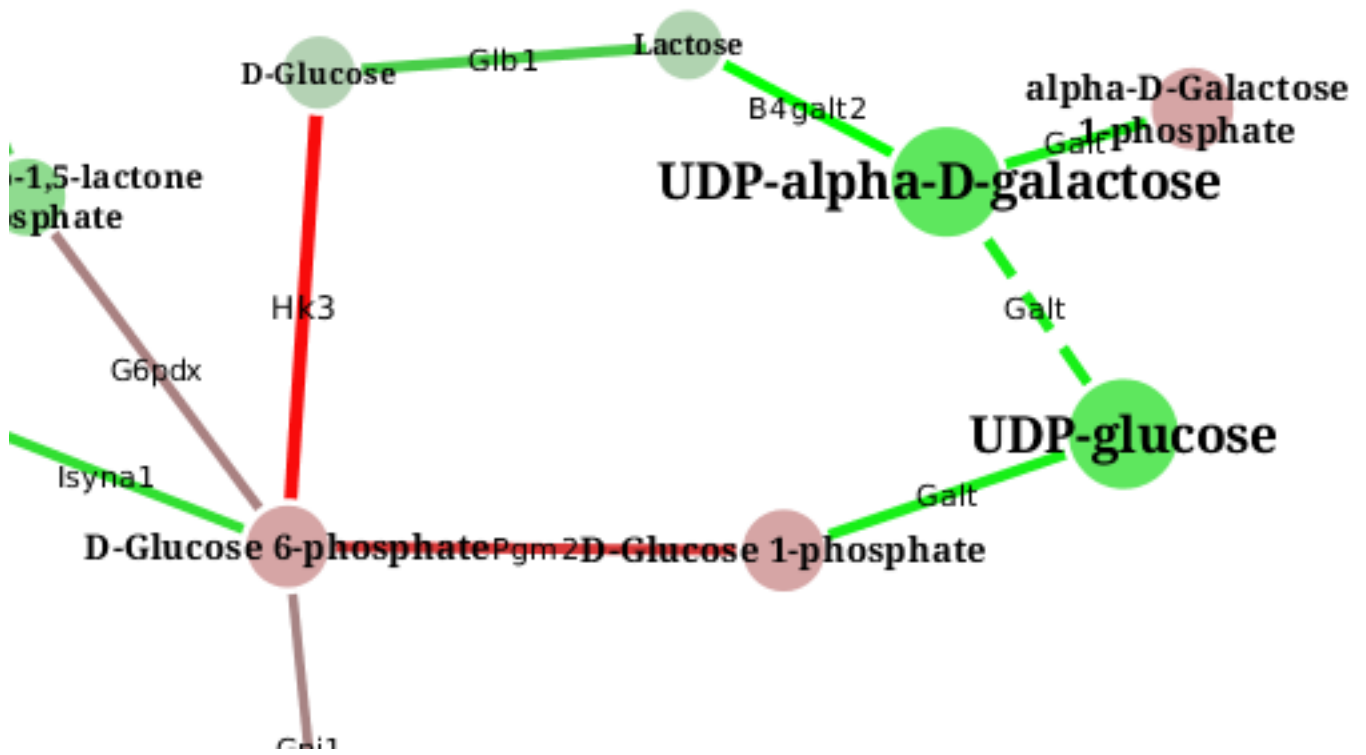


Figure 7: UDP-GLcNAc