Thoughts on NAFLD

I got gene count table for Low (stage < 3)vs normal and High(stage > 2)vs normal. After this I did obtain differentially expressed genes by using DESeq2 (in R). But I didn’t obtain much information like the module of genes which are getting upregulated simultaneously (because a group of Transcription factor bind in the upstream) and getting downregulated. So, I was told to use WGCNA (Weighted Gene Co-expression Network Analysis) to identify such modules.   
I did obtain more than 8 significant modules.

Now, I need to find the genes in each module and obtain their gene ontology. For gene ontology I’m thinking to develop a tree in python. There are several methods for visualizing the gene ontology like the bubble chart, categorical bar chart. Through this type of chart, we are mainly trying to understand the Gene count in the biological pathway, p-value associated with it. But it doesn’t represent under what categories they are the part of, for example: Copper detoxification pathway lies under metabolic pathway. Thus I decided to built a tree in python.  
For building the tree, I will be making use of the pvalue of the biological pathways, the gene count of the pathway. I have to take care that the leave nodes size will be altered but what about the parent nodes? How do we alter the size of the parent node?

The parent node size will be based on the number of biological pathways \* *constant*. I haven’t decided the value of the constant but will figure it out.