

EXPLANATION for THIS CODE

→ From that link stands below a detailed information is kept related with WGCNA Package for R programming.

<https://labs.genetics.ucla.edu/horvath/CoexpressionNetwork/Rpackages/WGCNA/Tutorials/index.html>

WGCNA is an R package for weighted correlation network analysis.

This package was used in my funded company's works. Together with my teammate we handled with Multiple Myeloma (MM) cancer during the project. MM Cancer has specified stages in it such as Gammopathy of Undetermined Significance (MGUS), active stage, metastasis and relapse stages. During the (MGUS) level, the paraproteins are dormant and no treatment is indicated. However, after an undetermined time, some subjects (approx. 1%) switches from the subclinical MGUS condition to clinically active multiple myeloma. Clinicians believe there are likely several biomarkers predicting transition from MGUS to active multiple myeloma. Discovering such biomarkers might enable early detection of multiple myeloma development. Provided those having risk factors can be detected early, clinicians might start therapy beforehand. This way, significant general improvements in multiple myeloma outcomes should be possible. Therefore, with the potential possibilities, we were only able to make real the theoretical experiments. Because of lacking proper database in Turkey related with MM, we have repeated substantial experiment results with R programming with WGCNA package.

- **The code attached with this explanation file covers some modifications related with our experiment.**
- **This code is not totally designed by me but for further analysis, it has been modified.**