Data: 1) a matrix of gene expression data (TCGA data). The samples are in the columns and the genes in the rows; 2) a matrix where the pathways are in the columns and the genes inside the pathways are in the rows

Result: pathway interactions that are able to classify two groups of samples with the best performances

Being a and b two pathways in a set of pathways P;

for *all nodes(a,b) in P* **do**

    a score distance between the nodes a and b;

    if *AUC > cut-off* **then**

        keep (a,b) as edge;

    else

        remove (a,b) as edge;

    end

end