

Data: 1) a matrix where the pathways are in the columns and the genes inside the pathways are in the rows; 2) a data frame where the nodes are presented in the columns and the rows represent the edges

Result: a list of genes with high degree centrality for each pathway
Being $(i \in N)$ & $(i \in P)$ where P is a vector containing the genes inside a pathway of size k and N is an indirect graph of size m ;

for *all nodes i in N* **do**

 | calculate the degree centrality d_{iN} ;

end

for *all nodes i in P* **do**

 | calculate the degree centrality d_{iP} , being the neighbors of i , $i_{ng} \in P$;

end

Calculate degree centrality expected d_{iE} in P

if $d_{iE} < d_{iP} / k_p$ **then**

 | $i \leftarrow$ potential gene drivers of P ;

else

 | $i \leftarrow i + 1$;

end