

**Network Calculator** is a GUI based network analysis software implemented by Python, including three main functional modules for analysis, Network localization analysis, Random walking with restart and Network overlap analysis. Please unzip the software file after download and double click the “**Network Calculator.exe**”, then use Network Calculator by this interface as follows:

1. **Network localization analysis**
2. Input:

🞄A text file of total network with the format of gene-gene interaction pairs (one pair per row separated by “Tab”), or use our bulit-in network file “all\_PPIs.txt” (The built-in file of total network was generated by integrating protein-protein interaction network from six databases including CORUM [1], BioPlex [2], CCSB [3], IntAct [4], BioGRID [5],and GeneMANIA [6].

🞄A text file with a column of gene list with human gene symbols or user customized genes.

1. Analysis parameters:

🞄Topological parameters (All edges, mean degree, largest sub-network, mean shortest distance, closeness centrality, betweeness centrality, and clustering coefficient);

🞄Permutation test of each parameter with customized random sampling times

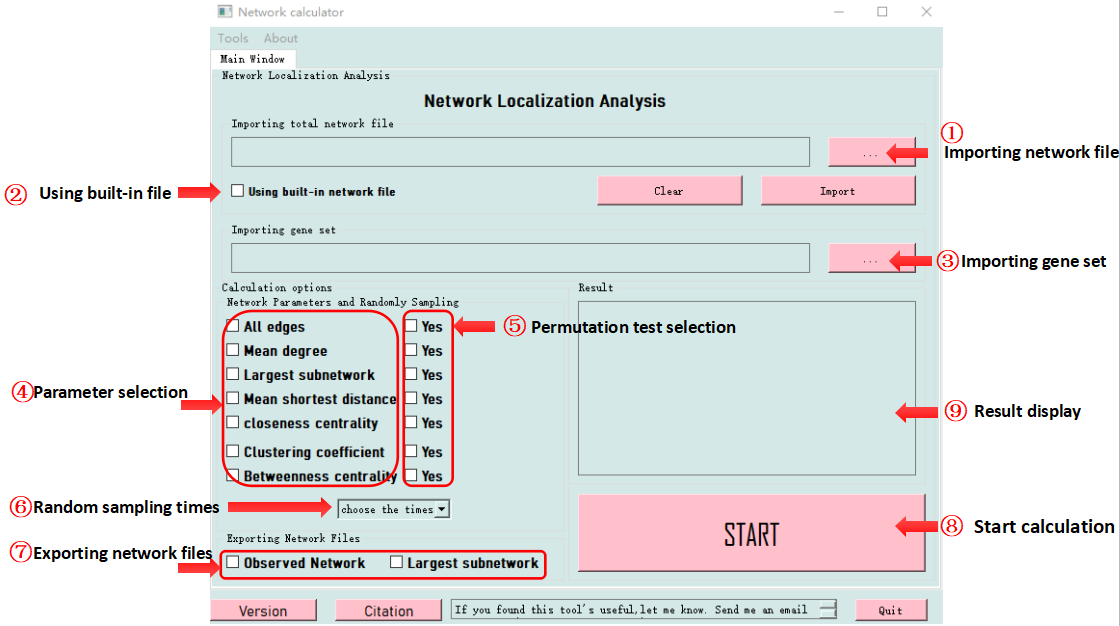
1. Output:

🞄Network parameter calculation results

🞄Randomly sampling distribution figures

🞄Text files of network generated using inputting gene set which could be directly imported in to network visualizing software.

1. Users can perform this analysis according to the following procedures:



1. **Random walking with restart**
2. Input:

🞄A text file of network with the format of gene-gene interaction pairs and related weight separated by “Tab”(e.g. gene1 gene2 1), or use our bulit-in network file “all\_PPIs\_RWR.txt” (The built-in file of total network was generated by “all\_PPIs.txt” with weight of each gene-gene interaction as 1.

🞄A text file with a column of gene list with human gene symbols or user customized genes as seed genes.

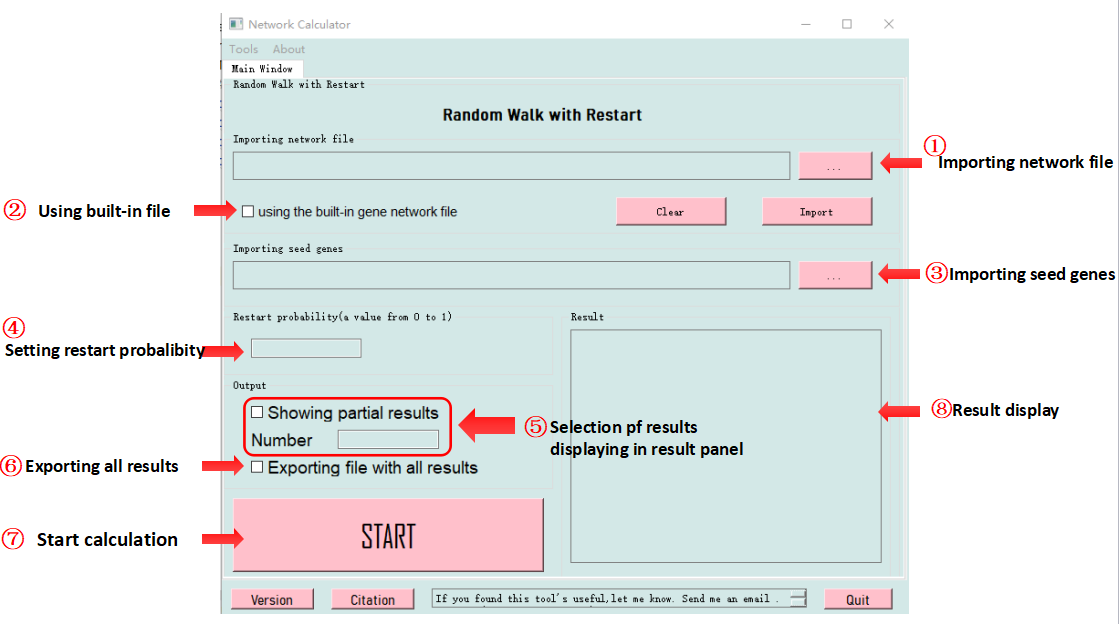
1. Analysis parameters:

🞄Restart probability: A value from 0 to 1.

1. Output:

🞄 Genes and related affinity scores (Users could display customized number of results in result panel or export all results file).

1. Users can perform this analysis according to the following procedures:



1. **Network overlap analysis**
2. Input:

🞄 A text file of total network (or use our bulit-in network file “all\_PPIs.txt”[1-6])

🞄 A text file with a column of gene list with human gene symbols (gene set A) or user customized genes.

🞄 A text file with a column of gene list with human gene symbols (gene set B) or user customized genes.

1. Analysis parameters:

🞄Topological parameters:

Mean shortest distance of gene set A: d\_A

Mean shortest distance of gene set B: d\_B

Mean shortest distance between gene set A and gene set B:d\_AB

Network proximity between gene set A and gene set B: S\_AB=d\_AB-(d\_A+d\_B)/2 [7]

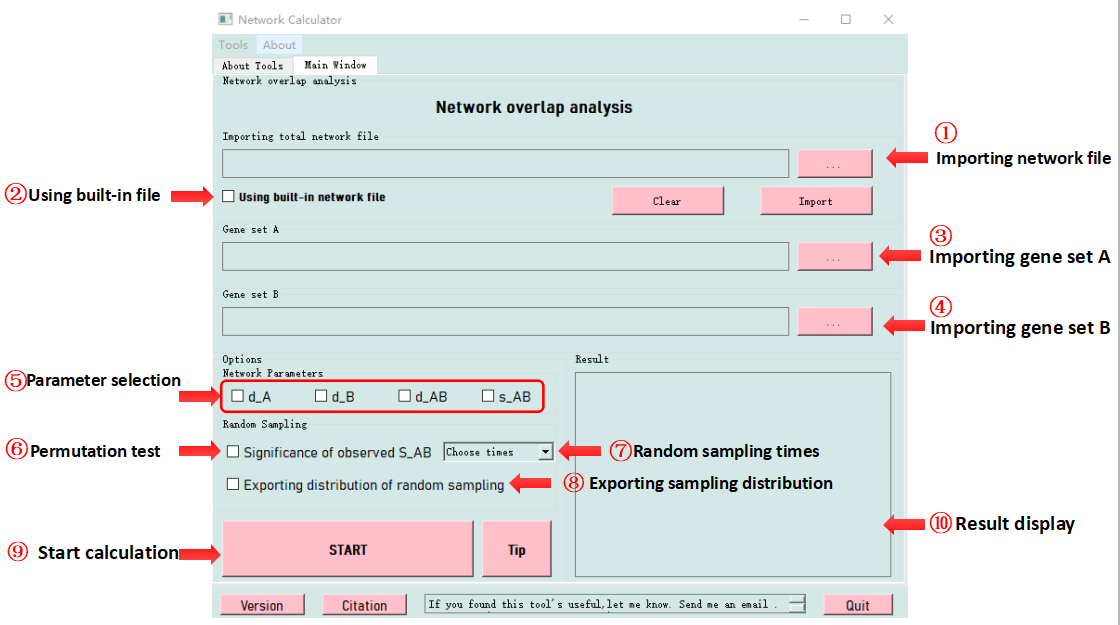
🞄Permutation test of each parameter with customized random sampling times

1. Output:

🞄Network parameter calculation results

🞄Randomly sampling distribution figures

1. Users can perform this analysis according to the following procedures:



Any question about usage of Network Calculator, please contact gaolei\_tsmu@163.com.

**Reference**

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