Table S1.　The comparison of seven network-based pathway analysis methods

NO.	Methods	Databases	Program Languages	Availability	Open or not	Advantages and Disadvantages
1	SPIA[15]	GEO, LaborC, Vessels, LaborM and KEGG	R and C	http://vortex.cs.wayne.edu/ontoexpress/	Yes	Advantages: SPIA combines the information of the complex gene interactions based on differentially expressed genes. It has the increased sensitivity compared with GSEA. Disadvantages: The topology information is relatively simple and priori knowledge is not abundant.
2	PARADIGM [16]	GEO, TCGA and NCI PID	C	http://sbenz.github.com/Paradigm	Yes	Advantages: PARADIGM integrates part of the pathway-level interactive information, and can be used to infer hidden quantities by combining multiple '-omics' data. It has fewer false-positives compared with SPIA. Disadvantages: It needs analysts who have enough biological knowledge to draw out entities with biological significance.
3	PathOlogist [17]	BioCarta、 TCGA and NCI PID	Matlab	ftp://ftp1.nci.nih.gov/pub/pathologist/	Yes	Advantages: PathOlogist includes 2 descriptive metrics - 'activity' and 'consistency'. It provides a tool to both laboratory researchers and informatics analysts. Disadvantages: It can only be used to analyze established pathways. Additionally, small subsets of interactions that have real association to a clinical feature may be overshadowed.
4	Active Modules[18]	BIND and TRANSFAC	Java	http://www.cytoscape.org	Yes	Advantages: Active Modules is simple and intuitive, and is a milestone of many methods developed based on its principle. Disadvantages: The priori knowledge is not taken full advantage and does not guarantee to find the optimally scoring subgraph.
5	AMBIENT [19]	KEGG and BioCyc	Python	http://www.theosysbio.bio.ic.ac.uk/ambient.	Yes	Advantages: AMBIENT is an effective and flexible tool for the analysis of high-throughput data in a metabolic context. It converts the metabolic network into a bipartite network and treats all metabolites equivalently. Disadvantages: AMBIENT does not extract all of the information possible from transcriptomic data, but just the information from genes with known functions and does not in any way take into account regulation.
6	GIGA[20]	GO and KEGG	Perl script	http://www.biomedcentral.com/content/supplementary/1471-2105-5-100-S2.pl	Yes	Advantages: GiGA method is simple, robust and cost saving based on statistical methods, it can be used as a stand-alone tool, and it can be integrated into existing microarray analysis software. Disadvantages: The method does not guarantee to find the optimally scoring subgraph and is difficult to apply to very noisy or unreplicated experiments.
7	neXus[21]	GEO and GO	Python	http://csbio.cs.umn.edu/neXus	Yes	Advantages: The neXus algorithm is a scalable approach for discovering conserved active subnetworks across species and it is an effective means of filtering noise from the active subnetwork discovery problem. Disadvantages: The method is time-consuming.

*The third column describes databases employed by the corresponding method, the fourth column describes Program Language implemented by the corresponding method, the sixth column tells us whether the code is open source, and the last column pinpoints their limitations and performance of the methods.