

## Supplementary Materials

### Supplementary Table 1: Recommended methods for fixed gene set enrichment analysis.

#### (A) Recommended methods:

Method	Algorithm	Platform	Data	URL	Ref
g:Profiler	ORA+FET (modified for ordered gene lists)	WT, RP	GL	<a href="http://biit.cs.ut.ee/gprofiler">http://biit.cs.ut.ee/gprofiler</a>	1
CAMERA	ORA+FET (corrected for gene correlation)	RP	GL, EXP	<a href="http://www.bioconductor.org/packages/release/bioc/html/limma.html">http://www.bioconductor.org/packages/release/bioc/html/limma.html</a>	2
GO	DB	WT, DS	NA	<a href="http://geneontology.org">http://geneontology.org</a>	3
GSEA, ssGSEA	FCS+KS	DS, CL, RP	GLV	<a href="http://www.broadinstitute.org/gsea">http://www.broadinstitute.org/gsea</a>	4
GSVA	FCS+KS	RP	GLV	<a href="http://www.bioconductor.org/packages/release/bioc/html/GSVA.html">http://www.bioconductor.org/packages/release/bioc/html/GSVA.html</a>	5
HumanCyc	DB	WT	NA	<a href="http://humancyc.org">http://humancyc.org</a>	6
KEGG	DB	WT, DS	NA	<a href="http://www.genome.jp/kegg/pathway.html">http://www.genome.jp/kegg/pathway.html</a>	7
REACTOME	DB	WT, DS	NA	<a href="http://www.reactome.org">http://www.reactome.org</a>	8
SLEA	FCS+Z	DS, CL	GLV	<a href="http://bg.upf.edu/slea">http://bg.upf.edu/slea</a>	9

#### (B) Additional methods:

Method	Algorithm	Platform	Data	URL	Ref
Babelomics	ORA, FCS+FET	WT	GL	<a href="http://www.babelomics.org">http://www.babelomics.org</a>	10
BiNGO	ORA+HT	CP	GL	<a href="http://www.psb.ugent.be/cbd/papers/BiNGO">http://www.psb.ugent.be/cbd/papers/BiNGO</a>	11
ConceptGen	ORA+FET	WT	GL	<a href="http://conceptgen.ncibi.org">http://conceptgen.ncibi.org</a>	12
Gitools	ORA+FET, FCS+Z	DS, CL	GL, GLV	<a href="http://www.gitools.org">http://www.gitools.org</a>	13
GoMiner	ORA+FET	WT	GL	<a href="http://discover.nci.nih.gov/gominer">http://discover.nci.nih.gov/gominer</a>	14
GOstats	ORA+HT	RP	GL	<a href="http://www.bioconductor.org/packages/release/bioc/html/GOstats.html">http://www.bioconductor.org/packages/release/bioc/html/GOstats.html</a>	15
iPAGE	ORA+MI	DS, CL, WT	GL	<a href="https://tavazoielab.c2b2.columbia.edu/iPAGE">https://tavazoielab.c2b2.columbia.edu/iPAGE</a>	16
ToppGene	ORA	WT	GL	<a href="http://toppgene.cchmc.org">http://toppgene.cchmc.org</a>	17

**Supplementary Table 2: Recommended methods for *de novo* network construction and clustering.**

**(A) Recommended methods:**

Method	Algorithm	Platform	Data	URL	Ref
BioGRID	DB	WT, DS	NA	<a href="http://thebiogrid.org">http://thebiogrid.org</a>	18
EnrichNet	RWR	DS, WT, CP	GL	<a href="http://www.enrichnet.org">http://www.enrichnet.org</a>	19
GeneMANIA	DB, RR	CP, WT	GL	<a href="http://www.genemania.org">http://www.genemania.org</a>	20
Hypermodules	GS+CC	CL, CP	GL, CD	<a href="http://apps.cytoscape.org/apps/hypermodules">http://apps.cytoscape.org/apps/hypermodules</a>	21
INTACT	DB	WT, DS	NA	<a href="http://www.ebi.ac.uk/intact">http://www.ebi.ac.uk/intact</a>	22
iRefIndex	DB	DS	NA	<a href="http://irefindex.org/wiki/index.php">http://irefindex.org/wiki/index.php</a>	23
MEMo	ME	CL, DS	SSM, SNA	<a href="http://cbio.mskcc.org/tools/memo">http://cbio.mskcc.org/tools/memo</a>	24
NetBox	EB	CL, DS	GL	<a href="http://cbio.mskcc.org/tools/netbox">http://cbio.mskcc.org/tools/netbox</a>	25
ReactomeFIViz	GC, FG, MCL	CP	GL, GLV	<a href="http://apps.cytoscape.org/apps/reactomefiviz">http://apps.cytoscape.org/apps/reactomefiviz</a>	26
ResponseNet	MCFL	CP, WT	GLV (gene weights)	<a href="http://bioinfo.bgu.ac.il/respnet">http://bioinfo.bgu.ac.il/respnet</a>	27
STRING	DB	WT, DS	NA	<a href="http://string-db.org">http://string-db.org</a>	28

**(B) Additional methods:**

Method	Algorithm	Platform	Data	URL	Ref
Dendrix	ME	CP, DS, WT	SM	<a href="http://compbio.cs.brown.edu/projects/dendrix">http://compbio.cs.brown.edu/projects/dendrix</a>	29
iCluster+	GLV	RP	SSM, SNA, EXP	<a href="http://www.mskcc.org/research/epidemiology-biostatistics/biostatistics/iclusplus">http://www.mskcc.org/research/epidemiology-biostatistics/biostatistics/iclusplus</a>	30
Pathifier	PDS	CL, RP	EXP	<a href="http://www.weizmann.ac.il/complex/compphys/software/yotam/pathifier">http://www.weizmann.ac.il/complex/compphys/software/yotam/pathifier</a>	31
SIRENE	BC	ML	EXP	<a href="http://cbio.ensmp.fr/sirene">http://cbio.ensmp.fr/sirene</a>	32

**Supplementary Table 3: Recommended methods for network-based modeling.**

**(A) Recommended methods:**

Method	Algorithm	Platform	Data	URL	Ref
HotNet	UD	ML	GLV	<a href="http://compbio.cs.brown.edu/projects/hotnet">http://compbio.cs.brown.edu/projects/hotnet</a>	33
TieDIE	UD	CL, ML	SSM, SCNA, EXP	<a href="https://sysbiowiki.soe.ucsc.edu/tiedie">https://sysbiowiki.soe.ucsc.edu/tiedie</a>	34
SPIA	RW	RP	EXP	<a href="http://www.bioconductor.org/packages/devel/bioc/html/SPIA.html">http://www.bioconductor.org/packages/devel/bioc/html/SPIA.html</a>	35
ARACNE	DPI	CL, DS, RP	EXP	<a href="http://wiki.c2b2.columbia.edu/califanolab/index.php/Software/ARACNE">http://wiki.c2b2.columbia.edu/califanolab/index.php/Software/ARACNE</a>	36
GENIE3	LR	ML, RC	EXP	<a href="http://homepages.inf.ed.ac.uk/vhuynht/software.html">http://homepages.inf.ed.ac.uk/vhuynht/software.html</a>	37
PARADIGM	PGM	WT, DS, CL	SSM, SCNA, EXP, METH	<a href="http://paradigm.five3genomics.com">http://paradigm.five3genomics.com</a>	38
PARADIGM-Shift	PGM	DS	SSM, SCNA, EXP, METH	<a href="http://github.org/sng87/paradigmshift">http://github.org/sng87/paradigmshift</a>	39
PathOlogist	PGM	CL, ML	EXP	<a href="ftp://ftp1.nci.nih.gov/pub/pathologist">ftp://ftp1.nci.nih.gov/pub/pathologist</a>	40
DataRail	BKRM	DS, RP, CP	EXP+PD	<a href="https://code.google.com/p/sbpipeline/wiki/DataRail">https://code.google.com/p/sbpipeline/wiki/DataRail</a>	41

**(B) Additional methods:**

Method	Algorithm	Platform	Data	URL	Ref
PSA	NF	CA	EXP, CHIP	<a href="http://apps.cytoscape.org/apps/pathwayscoringapplication">http://apps.cytoscape.org/apps/pathwayscoringapplication</a>	42
NetPhorest	NF	WT	GL	<a href="http://netphorest.info">http://netphorest.info</a>	43
NetworkKIN	NF	WT	GL	<a href="http://networkin.info">http://networkin.info</a>	44
CellNet-Optimizer	BKRM	DS, RP, CP	EXP+PD	<a href="http://www.cellnopt.org">http://www.cellnopt.org</a>	45

**Code for platform type:**

CL: Command line tool  
CP: Cytoscape plugin  
DS: Downloadable software/database  
ML: Matlab code available  
RC: R code  
RP: R package (Bioconductor)  
WT: Web tool

**Code for Method Type:**

BC: Binary classifier  
BHC: Bayesian hierarchical clustering  
DB: Reference Database  
EB: Edge-betweenness subnetwork detection  
FCS+KS: Functional class scoring using Kolmogorov–Smirnov rank statistics  
FCS+Z: Functional class scoring using z-score rank statistics  
FG: Factor-graph subnetwork detection  
GLV: Gaussian latent variable model subnetwork detection  
LR: Linear regression  
MCFL: Minimum-cost flow optimization subnetwork detection  
MCL: Markov-chain clustering  
MDPI: Mutual information + data processing inequality  
ME: Mutually exclusive subnetworks  
MIP: Mixed integer programming  
NF: Network flow type, incorporates direction and inhibitory/excitatory  
ORA+FET: Over-representation analysis using Fisher's exact test  
ORA+MI: Over-representation analysis using mutual information statistic  
PDS: Pathway deregulation score based on tumor RNA expression data  
PGM: Probabilistic Graphical Model  
REA: Recursive enumeration algorithm on network weighted for predicted oncogenicity of edges  
RR: Ridge regression clustering  
RW: Random walk  
UD: Undirected diffusion; incorporates undirected links

**Code for data type:**

CD: Clinical data  
CHIP: ChIP-seq  
EXP: Gene list with RNA expression values  
GL: Gene list (e.g. mutated genes, thresholded RNA fold-change)  
GLV: Gene list with values (typically RNA fold-change)  
SSM: Simple somatic mutations  
SCNA: Somatic copy number alterations  
PD: Perturbation data (e.g. small molecule screens)  
METH: DNA methylation  
NA: Not applicable

## Supplementary references

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