

Supplementary material:

Table 1: List of programs available for differential gene expression analysis.

S.No	Software	Algorithm/Method	URL/Reference
1.	SAM	Modified t-test known as SAM	http://www-stat.stanford.edu/~tibs/SAM/ [35]
2.	MeV	non-parametric t-test/ ANOVA	http://www.tm4.org/mev/ . [36]
3.	iArray	Student's t-test and Mann- Whitney test	http://zhoulab.usc.edu/iArrayAnalyzer.htm [37]
4.	EDGE	Optimal Discovery Procedure	http://www.genomine.org/edge/ [38]
5.	Cyber-T	Simple t-test or regularized t-tests	http://cybert.microarray.ics.uci.edu/ [12]

Table 2: List of programs available for cluster analysis.

S.No	Software	Algorithm/Method	URL/Reference
1.	Cluster and Treeview	Hierarchical clustering, K-means clustering self organizing maps etc.	http://rana.lbl.gov/EisenSoftware.htm [15]
2.	dChip	Hierarchical clustering, K-means clustering self organizing maps etc.	http://biosun1.harvard.edu/complab/dchip/ [39]
3.	MeV	Hierarchical clustering, K-means clustering, Tree EASE, self organizing maps, & QT-clustering etc.	http://www.tm4.org/mev/ . [36]
4.	MAGIC Tools	Hierarchical clustering, K-means clustering, and QT-clustering	http://www.bio.davidson.edu/projects/magic/magic.html [40]
5.	CAGED	Bayesian clustering program on a-temporal expression data.	http://www.genomethods.org/caged/ [41]

Table 3: List of programs available for classification.

S.No	Software	Algorithm/Method	URL/Reference
1.	weka	Artificial Neural Networks, Decision trees, k Nearest Neighbors, Support Vector Machines, and many	http://www.cs.waikato.ac.nz/ml/weka/ [42]
2.	SAS	Artificial Neural Networks, Decision trees, k Nearest Neighbors, Support Vector Machines, and many	http://www.sas.com/technologies/analytics/datamining/miner/ [43]
3.	IBM/SPSS Clementine	Artificial Neural Networks, Decision trees, k Nearest Neighbors, Support Vector Machines, and many	http://www.spss.com/software/modeling/modeler-pro/ [44]
4.	SVMLight	Support Vector Machines	http://svmlight.joachims.org/ [45]
5.	LIBSVM	Support Vector Machines	http://www.csie.ntu.edu.tw/~cjlin/libsvmtools/ [46]

Table 4: List of tools for transcription factor binding site.

S.No	Software / Tool	Algorithm/Method	URL/Reference
1	oPOSSUM	Position weight matrix, Fisher exact test	http://www.cisreg.ca/oPOSSUM/ [47]
2	MATCH	Position weight matrix	http://www.gene-regulation.com/pub/programs.html#match [48]
3	ConTra	Position weight matrix, HMM	http://bioit.dnbr.ugent.be/ConTra/index.php [49]
4	Whole Genome rVISTA	Position weight matrix	http://genome.lbl.gov/vista/index.shtml [50]
5	TFSCAN	Position weight matrix, word-matching	http://mobyli.pasteur.fr/cgi-bin/portal.py?form=tfscan [51]
6	TFSEARCH	Position weight matrix	http://www.cbrc.jp/research/db/TFSEARCH.html [52]
7	TransFind	Position weight matrix, Fisher exact test	http://transfind.sys-bio.net/ [53]

Table 5: List of softwares for PPI and Pathway analysis.

S.No	Software	Application	URL/Reference
1	Pathway Studio	Pathway network analysis, data mining, and visualization etc.	http://www.ariadnegenomics.com/products/pathway-studio/ [54]
2	Ingenuity Pathway Analysis	Cancer pathway network analysis.	http://www.ingenuity.com/ [55]
3	Cytoscape	PPI network analysis, gene annotation and pathway integration, etc.	http://www.cytoscape.org/ [56]
4	Pajek	Analysis and visualization of large networks, etc	http://vlado.fmf.uni-lj.si/pub/networks/pajek/ [57]
5	GenMAPP2	Gene expression, Pathway analysis, and GO analysis	www.genmapp.org [58]
6	ArrayXPath	Mapping, visualizing expression data, and pathway analysis	http://www.snubi.org/software/ArrayXPath/ [59]
7	PathExpress	Pathway analysis and visualization	http://bioinfoserver.rsbs.anu.edu.au/utlils/PathExpress/ [60]
8	GO-cluster	GO based pathway analysis	http://www.mpibpc.mpg.de/go-cluster/ [61]
9	GO-view	GO based pathway analysis	http://db.math.macalester.edu/goproject [62]
10	Onto-Express	GO based pathway analysis	http://vortex.cs.wayne.edu/Projects.html [63]
11	Pathway Miner	cellular and regulatory pathway analysis	http://www.biorag.org/pathway.html [64]
12	Gominer	GO based pathway analysis	http://discover.nci.nih.gov/gominer/ [65]

13	visANT 3.86	Pathway and network analysis	http://visant.bu.edu/ [66]
14	KOBAS	KEGG Orthology-based pathway analysis	http://kobas.cbi.pku.edu.cn [67]

Table 6: List of available programs for gene set enrichment analysis.

S.No	Software/Tools	Algorithm/ Method	URL/Reference
1	GSEA	Null hypothesis	http://www.broadinstitute.org/gsea/ [34]
2	MeV	Null hypothesis, linear model	http://www.tm4.org/mev/ . [36]
3	GeneTrail	Dynamic-programming	http://genetrail.bioinf.uni-sb.de/ [68]
4	ConceptGen	Parametric and non-parametric tests	http://conceptgen.ncibi.org/core/conceptGen/index.jsp [69]
5	GAzer	Z-test, Parametric and non-parametric tests	http://expressome.kobic.re.kr/GAzer/index.faces [70]
6	PhenoFam	Mann-Whitney U test, ρ - Herrnstein's ρ statistic	http://appserver.biotec.tu-dresden.de/phenofam/ [71]