

TABLE 3. Protein Network Visualization and Analysis Tools

	Cytoscape V2.0	Osprey V1.2.0	Pajek V1.01	ProViz V1.0	WebInterViewer
General					
Web site	http://www.cytoscape.org	http://biodata.mshri.on.ca/osprey	http://vlado.fmf.uni-lj.si/pub/networks/pajek	http://cbl.labri.fr/eng/proviz.htm	http://interviewer.inha.ac.kr
License	Free	Free for educational, research, and not-for-profit	Free for noncommercial use	Free	Free
Platform	Linux, Mac, Windows	Linux, Mac, Windows	Windows	Linux	Linux, Mac, Windows
Data Exchange					
Import					
<i>Files</i>	Flat file (space-delimited interactions, node and edge attributes, gene functional annotations), GML	Flat file (tab-delimited gene names, interactions, experimental system, source, literature evidence)	Flat file (space-delimited gene names, interactions), Vega graphs, Gedcom, Ucinet DL	Tulip, PSI-MI (XML)	Flat file (tab-delimited gene names and interactions), GML, XML
<i>Databases</i>	—	GRID interaction data	—	IntAct interaction data	DB on InterViewer3 server or local data server
<i>Additional</i>	Expression data, arbitrary data attributes on nodes and edges	—	—	—	—
Export					
<i>Text files</i>	Flat file (space-delimited, genes, interactions), GML	Flat file (tab-delimited, genes and interactions)	Flat file (space-delimited, node and edge attributes), Vega graphs, Gedcom, Ucinet DL	Tulip, PSI-MI	Flat file (tab-delimited, genes and interactions), XML, EdgeCnt, IG1
<i>Image files</i>	EPS, JPEG, PDF, PNG, PS, SVG	JPEG, PNG, SVG	BMP, EPS/PS, Kinemage, MDL, SVG, VRML	PNG	BMP (with copyright note)
Visualization					
Graph layout	5 algorithms	7 algorithms	7 algorithms	3 algorithms	2 algorithms
Data attributes					
<i>Proteins</i>	All imported properties	GO terms	All imported properties	GO terms	—
<i>Interactions</i>	All imported properties	Source, experimental system (e.g., two-hybrid), literature evidence	All imported properties	PSI-MI terms	—
Visual mappings					
<i>Proteins</i>	Color, shape, line type, size, label, font	Color	Color, line type, size	—	—
<i>Interactions</i>	Color, line type, arrow, label, font	Color	Color, line type, arrow	—	—
Analysis					
Filters					
<i>Proteins</i>	Attribute values	GO terms	Attribute values	GO terms	—
<i>Interactions</i>	Type (e.g., protein–DNA)	Experimental system, source	Attribute values	PSI-MI terms	—
<i>Network</i>	Node degree, distance	Node degree, distance	Node degree, distance	Node distance	Node distance
Multiple data superposition	—	+	+	+	+
Subnetwork identification	MCODE, ActiveModules plug-ins	—	—	—	—
Group and collapse nodes	—	—	—	—	Group cliques, nodes with same interactions
Network comparison	PathBLAST plug-in	—	Intersection, union, difference	Find shared nodes and edges	Find shared nodes and edges
Extras	Many plug-ins for extended analysis, e.g., network comparison via PathBLAST	—	Many operations on graphs and metric computation	URL links to external source for node and edge properties	Data server for central data storage; List of connected groups
Conclusions					
Pros	<ul style="list-style-type: none"> • Flexible and extensible through many existing and user defined plug-ins • Superposition of gene expression and other data 	<ul style="list-style-type: none"> • Direct import and quick visualization from GRID DB • Superposition of different data sets 	<ul style="list-style-type: none"> • General network visualization and analysis tool • Multiple formats for exporting images • Rich set of operations on graphs and metric computation 	<ul style="list-style-type: none"> • Interaction filter based on PSI-MI controlled vocabulary terms • New analyses as plug-ins using the Tulip graph management platform 	<ul style="list-style-type: none"> • Central storage of data on server
Cons	<ul style="list-style-type: none"> • Requires substantial preprocessing of data, e.g., special network formats and data attribute lists 	<ul style="list-style-type: none"> • Limited visualization possibilities for external data sets (outside of GRID) 	<ul style="list-style-type: none"> • Single platform • Not specifically designed for molecular interaction networks • Requires much data preprocessing 	<ul style="list-style-type: none"> • Single platform • Limited visualization functionality 	<ul style="list-style-type: none"> • No visualization of protein or interaction attributes (e.g. expression) • Only one filter • Very brief documentation