

February 13, 2014

Welcome

Summary

- Cytoscape v3.1 is now available for immediate download.
- Relative to v3.0.2, it addresses 236 issues.
- It is ready for use by all segments of the Cytoscape community.
- It continues v3.0's core feature set, specifically:
 - It contains improvements for all segments of the Cytoscape community.
 - It is upward compatible and can coexist with previous Cytoscape versions
 - The most popular plugins from previous versions are available, with more to follow.
 - Support offerings have been updated and broadened.
- It includes 10 major feature updates
- 18 more Apps are available in the App Store as compared to the v3.0.2 release
- What to do next ...

Dear Cytoscape User

We are proud and pleased to release Cytoscape v3.1. This new release contains both new features and improvements to functionality and documentation, all of which are described in Section 11.

Additionally, the App Store contains 28 more Apps than were available when v3.0.0 was released, bringing the total to 41. Since v3.0.2, 18 Apps were added, including:

bayelviraApp	eXamine	MetDisease
CoNet	Gasoline	MetScape
CyKEGGParser	GenomeSpace	Pathway Scoring Application
CyTargetLinker	GIANT	PEPPER
CytoNCA	HyperModules	Reactome FI Plugin
Enhanced Graphics	KEGGScape	WikiPathways

*If you are a new or casual Cytoscape user, **welcome aboard!** Feel free to either read on or jump ahead to What to Do Next for a quick start.*

For clarity, references to "Cytoscape 3.x" apply to all Cytoscape versions 3.0.0 and later.

For Cytoscape v2.x Users

Previous Cytoscape releases (through v2.8.3) focused on adding numerous annotation, import, layout, analysis, and visualization features, all of which have combined to deliver critical insights into biological processes of interest to Cytoscape's broad and loyal user community. In fact, many of these features were created and contributed by Cytoscape users, themselves, using Cytoscape's plugin architecture.

Version 3.x marks a major reorganization of Cytoscape program code – it enables us to deliver additional features more quickly and reliably than before, including improvements that benefit new users, casual users, power users, and app developers. Along the way, some features were changed to allow them to better interoperate with other features, some little-used features were dropped, and user interface was

improved. We are particularly excited about the new Cytoscape App Store (described below), which affords users access to the growing collection of *apps* (formerly called *plugins*) produced by fellow Cytoscape users. A table of new features is presented in Section 7.

While version 3.x is upwardly compatible with previous Cytoscape versions (i.e., it can load, analyze, and display networks and attributes stored using previous versions, including v2.x), it can coexist with previous versions on the same workstation. It is not necessary to uninstall previous versions before installing version 3.x, and you can choose to use both on the same workstation.

Version 3.x is still a work in progress and continues to evolve due to the outstanding efforts of its vibrant worldwide development community. Notably, while the Cytoscape team has ported the most popular plugins (as apps) from previous versions, porting less popular plugins was deferred so as to deliver version 3.x sooner and with features that support cutting edge investigation. A table of apps and their status is presented in Section 8.

Finally, we recognize that with all new software (including version 3.x), there are growing pains. While we hope our users will learn to love v3.x's new features, users may also expect to relearn rationalized features and occasionally uncover a bug. With version 3.x, we are rolling out new manuals, tutorials, web pages, and support channels that we hope can create and maintain highly productive experiences for all types of Cytoscape users. A table describing Cytoscape support is presented in Section 9.

We are very excited to make this release, and hope you find it an indispensable tool in your research. To get you started, we have provided additional introductory material to get you started on the right foot, and we have also provided background material for general interest.

Please let us know how we're doing and how we can better advance your research!

The Cytoscape Team

What to Do Next

We hope to help you use Cytoscape in the most productive way. Your next steps depend on how experienced you are with Cytoscape and what you would like to do. In the table below, please find the category that best describes you, and proceed accordingly.

Type of Cytoscape User	Where to Read Next
New	For New Users (Section 1)
Casual	For Casual Users (Section 2)
Power	For Power Users (Section 3)
App Developers	For App Developers (Section 4)
General Interest	Try getting oriented by reading: General Background (Section 5) Cytoscape App Store (Section 6) Then try browsing: New Features (Section 7) App Status (Section 8) Support Offering (Section 9) Future Plans (Section 10) To get your feet wet, try: For New Users (Section 1)

1. For New Cytoscape Users

What is Cytoscape?

Cytoscape is software that can help you visualize complex networks (as *graphs*) representing relationships between genes, proteins, or other entities. Cytoscape tracks and displays these entities (as graph *nodes*) and relationships between them (as graph *edges*). Cytoscape, per se, does not assign meaning to either nodes or edges – you can assign your own meanings to them, and you can add your own node or edge attributes (e.g., name, measurements, states, etc.) that customize your graph to represent semantics important to you. While Cytoscape provides simple analytics and visualizations, others are available as apps from the Cytoscape App store (see Section 6).

What Do I Need Before I Can Use Cytoscape?

At the very least, you must provide Cytoscape with a list of nodes. You can also provide a list of edges and attributes. You can enter your graph manually or import it from your own files – Cytoscape supports a wide variety of file formats, including text and Excel. Cytoscape can also load pre-configured networks (e.g., from BioGRID) so you can leverage them without having to enter them yourself.

Can Cytoscape Help Me Get Started?

Yes! The Cytoscape team had provided many resources tailored for all kinds of users (see Section 9). To start, there is an Installation Guide and numerous tutorials. Once you load your graph, you may find additional useful analytics and visualizations at the App Store (see Section 6).

Which Cytoscape Version Should I Use?

Generally, you should use v3.1 (the newest version). v2.x has been in the field for several years and will be supported into the future, but over time, v3.x and successors will be better supported.

Note that if you have already installed v3.0.0, v3.0.1, or v3.0.2, you can install v3.1 without uninstalling your previous version.

How to Download and Install v3.x

- Surf to <http://www.cytoscape.org>, click on the Download Cytoscape button, and follow the prompts
- ***Be sure to consult with the Release Notes (viewable via the Release Notes button) for issues and solutions pertaining to your installation***
- Surf to <http://www.cytoscape.org>, click on the Release Notes button, click on a User Manual link, and follow the instructions in the *Launching Cytoscape* section.

2. For Casual Cytoscape Users

If you're confident of your Cytoscape skills, please read the Power Users information (Section 3).

If you're Cytoscape skills are rusty, please continue with the New Users information (Section 1).

3. For Cytoscape Power Users

Is v3.x for Me?

The answer is most likely yes, provided you use the *apps* (formerly known as *plugins*) available for v3.x – apps are available from the new Cytoscape App Store, which you can browse directly (Section 6). Note that some v2.x apps have been incorporated directly into Cytoscape and need not be downloaded or installed. Consult the Apps Status table (Section 8) to see a list of these apps.

Note that v2.x plugins are not compatible with v3.x apps, and vice versa. If you rely on v2.x plugins that are not yet available for v3.x, you may need to remain with v2.x instead of upgrading to v3.x. Note, also, that the Cytoscape community is converting v2.x plugins to v3.x apps -- you might occasionally revisit the App Store to see if an app you need becomes available.

What's New in v3.x?

As described in the Welcome letter (above), v3.x incorporates a number of new features (Section 7) and productivity enhancing support offerings (Section 9), including the Cytoscape App Store (Section 6). The General Background section (Section 5) describes the rationale, advantages, and issues with v3.x.

Will Support for v2.x Continue?

Cytoscape v2.x will be supported by the Cytoscape community for now, but with fewer upgrades and support options over time.

Can I use v2.x and v3.x at the Same Time?

You can experiment with v3.x by installing it on your workstation – you can use both v2.x and v3.x on the same workstation.

How to Prepare for v3.x

1. If you have already installed a v3.1 beta version, *please uninstall it before proceeding*. The Cytoscape v3.0.x versions can coexist with v3.1, and do not need to be uninstalled.
2. Consult the Apps Status table (Section 8) to verify that the apps you need are available. Some apps have become part of the Cytoscape core, and you won't need to download them. Other apps are available in the Cytoscape App store (described in Section 6).
3. Browse the New Features table (Section 7) to see what we have added since v2.x.
4. Browse the Future Plans table (Section 10) and Support Offering table (Section 9) to see where the Cytoscape community is going.

How to Download and Install v3.x

- Surf to <http://www.cytoscape.org>, click on the Download Cytoscape button, and follow the prompts
- ***Be sure to consult with the Release Notes (viewable via the Release Notes button) for issues and solutions pertaining to your installation***
- Surf to <http://www.cytoscape.org>, click on the Release Notes button, click on a User Manual link, and follow the instructions in the *Launching Cytoscape* section.

4. For Cytoscape App Developers

Cytoscape manages graph storage and display, and contains a number of common analytic and visualization functions. App Developers may write *apps* (formerly known as *plugins*) to perform problem-specific analytics, graph layouts, or other visualizations.

Before starting app development, you should be familiar with overall Cytoscape usage and functionality – see the Power Users section (Section 3) to start working with v3.x if you have not already done so.

Note that v2.x plugins do not work with v3.x. In order to get the benefits of improved stability, the Cytoscape team found it necessary to change the relationship between plugins/apps and the Cytoscape core. Many plugins have been ported to v3.x (see Section 8). The porting exercise is substantial, and once a plugin is converted to an app, it will continue to work at least until v4.0 is released – there is no v4.0 planned at this time. For more on this topic, see:

http://wiki.cytoscape.org/Cytoscape_3/CoreDevelopment/Motivation

Should I Convert My v2.x Plugin to a v3.x App?

Yes! Cytoscape v2.x will be supported by the Cytoscape community for now, but with fewer upgrades and support options over time.

How Do I Get Started With App Development?

To get started with app development:

http://wiki.cytoscape.org/Cytoscape_3/AppDeveloper

To convert a v2.0 plugin to a v3.x app, refer to:

http://wiki.cytoscape.org/Cytoscape_3/AppDeveloper/PluginPortingGuide

For a broader view of the Cytoscape system (including the Core), refer to:

http://wiki.cytoscape.org/Cytoscape_3/CoreDevelopment

Are there App Samples?

Yes! See:

http://opentutorials.cgl.ucsf.edu/index.php/Tutorial:Creating_a_Simple_Cytoscape_3_App

Also note the App Cookbook:

http://wiki.cytoscape.org/Cytoscape_3/AppDeveloper/Cytoscape_3_App_Cookbook

5. General Background

The overall mission of Cytoscape is to be a freely available worldwide asset supporting network analysis and visualization for systems biology science.

The major focus of v3.x is the modularization and rationalization of code to solve stability issues in v2.x encountered as multiple developers pursued multiple agendas. Under v2.x, internal programmatic interfaces evolved from one release to the next, leading to the failure of working plugins over time and negative interactions between otherwise working plugins. Ultimately, this resulted in loss of programmer and user productivity, and undermined community confidence in Cytoscape.

v3.x addresses these issues by adopting modular coding practices promoted by the OSGi architectural framework¹. This enables both the Cytoscape core and externally developed apps (formerly called *plugins*) to evolve independently without compromising unrelated functionality. At the logical level, Cytoscape leverages OSGi precepts to produce v3.x APIs having cleaner and clearer demarcations between functional areas. At the deployment level, OSGi enables on-the-fly substitution of one processing element for another (e.g., apps) in order to tailor Cytoscape to meet user requirements at runtime without reinstalling or reconfiguring Cytoscape.

Creating v3.x occupied an international team of engineers for over a year, and represents a strong investment toward reducing future development and support costs, and increasing reliability and evolvability. With the completion of v3.x, we expect to leverage v3.x as a platform to satisfy the evolving needs of multiple stakeholder groups, and as a platform enabling research on leading edge analysis and visualization techniques. v3.x is the intended successor to v2.x, with development and support of v2.x expected to diminish and disappear over time in favor of v3.x.

We believe that users will benefit most directly from the v3.x by:

- experiencing fewer core and app bugs from one release to the next
- the availability of more and richer apps (due to developers spending less time tracking and fixing bugs)
- more core features with higher biological and logistical value (due to improved flexibility provided by interface-driven development)

During the creation of v3.x, a number of features were added, as listed in the New Feature Table below.

As a result, we incurred a number of current and future costs:

Cost	Reason	Time frame for addressing
Slower startup time	OSGi module inventorying	near-to-medium term
Loss of plugins	Lag in upgrading less popular plugins	as needed

¹ www.osgi.org – also used as the basic framework for Eclipse and numerous commercial products

6. The Cytoscape App Store

The Cytoscape App Store is new in v3.x and targets broad demographics through specific features:

Cytoscape User	Benefit
New or Casual	Find Cytoscape functionality easier via familiar paradigms of search and tag navigation
Power or Frequent	Find and install apps easier and provide crowdsourced rating and reviews
Plugin Developers	Have a dedicated presence for their work, including a direct line to their users and critical statistics to justify their development on the Cytoscape platform.

Furthermore, the App Store supports contests and social incentives that encourage critical technical and community development, including porting, analytics, rating/reviewing, and so on.

Note that the App Store supports only Cytoscape v3.x and does not contain plugins compatible with earlier Cytoscape versions. Likewise, plugins that work with earlier versions are not compatible with v3.x – Section 8 contains a list of apps available for v3.x.

To access the App Store, access Cytoscape’s new Apps menu and choose the App Manager menu item, or use your browser to surf directly:

<http://apps.cytoscape.org>

7. New Feature Table

Feature	Beneficiary	Manual Section
Welcome screen	New users (for solicitousness), casual and power users (for convenience)	5.1. Welcome Screen
New Style replaces VizMapper	All users	14. Styles
Export to cytoscape.js	Power users wanting to present networks on web pages	23. Cytoscape.js and Cytoscape
Merge columns	Users of attributes in multiple tables	17.2. Merging Tables
Command line interface	Power users creating repeatable workflows	24. Scripting
REST interface	Power users using other applications to communicate with Cytoscape	
New filter facility	All users	12. Finding and Filtering Nodes and Edges
Group annotations	Users with highly annotated networks	
Automatic citations	Users publishing Cytoscape analyses	5.3.8 Help
Improved PSICQUIC access	All users needing to download protein databases	

8. App Status Table

For the most up to date list of apps, see the App Store (described in Section 6). A URL for our development list is shown below, as a list of apps and their status at the time this letter was authored.

<https://docs.google.com/spreadsheet/cc?key=0ArzUWDuvdBn-dDI0R0kwOERjN1ZhCDZseC00dVZNNIE&authkey=CMGe99EM#gid=0>

Apps new since the v3.0.2 release are highlighted in yellow.

App	Capability	Status
addParentNeighbors	For a selected node in child network, adds neighboring nodes from a parent network .	
AdvancednetworkMerge	Merges multiple networks.	
AgilentLiteratureSearch	Mines scientific literatures to find ones related to search term and to create interaction network based on the search result.	Available in App Store
AllegroMCODE	Very fast clustering based on MCODE algorithm.	
APCluster	Uses affinity propagation described in Frey BJ and Duec D (2007) to perform clustering.	
APID2NET	Downloads PPI data from http://bioinfow.dep.usal.es/apid/ and performs various analyses including protein motif, GO, hub identification, etc. through the original GUI. Equipped with impressing "rainbow" coloring of nodes.	
BiLayout	Finds a bipartite network for two sets of user-selected nodes and performs layout.	
BiNGO	Calculates overrepresented GO terms in the network and display them as a network of significant GO terms.	Available in App Store
bioCycPlugin	Loads any pathway in bioCyc database. Original panel provides useful information for each node.	In Progress
BiogridPlugin	Loads Biogrid tab file onto Cytoscape.	
BiomartClient	Retrieves attributes associated with given gene or protein	
BioNetBuilder	Through the wizard, user can easily construct networks from public databases. User can also create interologs.	
BioQualiPlugin	Performs consistency check of regulatory network and expression data.	
Bisogenet	Retrieves interactions associated with input IDs. Sophisticated UI gives links to GO, KEGG, etc.	
BLAST2similarityGraph	Visualizes BLAST similarity as graph.	

bayelviraApp	Builds Bayesian networks using a file of patterns as input data using Naive Bayes, Semi Naive Bayes, Selective Naive Bayes, TAN, KDB and Class Tree Naïve algorithms.	Available in App Store
CABIN	Integrates interaction datasets from different resources to explore the integrated network and to perform confidence analysis for interactions. User can give weight to each interaction set which will be used for the level of confidence.	
CalculatenodeDegree	Simply calculates degree for selected single node.	
CentiScaPe	Calculates topological characteristic values (ex. Centralities) for each node.	Available in App Store
ChemViz	Visualizes chemical structure of each compound in chemical network with original interface.	
ClojureEngine	Provides Clojure API.	
ClueGO	Creates and visualizes a functionally organized GO term network or pathway from given interaction network.	Available in App Store
CluePedia	Pathway insights using integrated experimental and <i>in silico</i> data	Available in App Store
clusterExplorerPlugin	Explores a given similarity graph.	
clusterMaker	Clusters densely connected nodes and node attributes (i.e. expression data) in a given network. Results of these two types of clustering can be analysed in the integrated interface.	In Progress
ClusterONE	Finds overlapping protein complexes in a protein interaction network. Clusters are visualized by original interface with their p-values.	Available in App Store
ClusterViz	Clustering based on FAG-EC, EAGLE or MCODE. Found cluster can be subjected to GO enrichment analysis.	Available in App Store
commandTool	Provides simple command-line interface to Cytoscape.	
CommFinder	Clustering based on QCUT, HQCUT, MCL, MCODE.	
Commonattributes	Find attributes shared between selected nodes.	
CoNet	Clustering based on FAG-EC, EAGLE or MCODE. Found cluster can be subjected to GO enrichment analysis.	Available in App Store
ConsensusPathDBplugin	Retrieves interaction evidences for given pair of genes or proteins	

Cy3 Performance Reporter	Collects information about Cytoscape 3 performance	Available in App Store
CyAnimator	Creates animation based on added frames of network views.	
CyClus3D	Clusters a given network based on three-node motifs. Accepts multiple types of interactions. Cluster ID is given to edge attributes, "EdgeCluster".	
CyGoose	Provides Gaggle Boss, which routes data from one application to another.	
CyKEGGParser	Parses and increases accuracy and specificity of KEGG pathways.	Available in App Store
Cyni Toolbox	Network Inference Toolbox for inferences from bio-data.	Available in App Store
CyOog		
CyPath2	GUI client app for Pathway Commons 2 (BioPAX L3 pathway data) web service.	Available in App Store
CyTargetLinker	Extends biological networks with regulatory interactions.	Available in App Store
CyThesaurus-ID-Mapping	Performs ID mapping using BridgeDb and other public or custom database sources.	
CytoCluster	Analyze and visualize clusters from network.	Available in App Store
cytoHubba	Predicts and explores important nodes and subnetworks in a given network by several topological algorithms.	
CytoKegg	Identify Kegg pathways associated to specific expression profiles.	Available in App Store
CytoNCA	Providing calculation, evaluation and visualization analysis for several centralities of weighted and unweighted network.	Available in App Store
Cytoprophet		
CytoSaddleSum	Finds enriched function based on sum-of-weight scores.	
CytoscapeRPC	Allows user to query and modify networks through an XML-RPC connection.	
CytoSEED	Enables users to view, manipulate and analyze metabolic models created by the Model SEED. The reactions are organized into a set of maps based on each reaction's membership in KEGG pathways.	
CytoSQL	Retrieves attributes from SQL databases by invoking query command.	
DisGeNET	Queries and analyzes networks of diseases and their associated genes.	
DomainGraph	Visualizes domain-domain interactions which connect pairs of interacting proteins.	

DroID	Retrieves interactions associated with input IDs. Detailed information associated with interacting proteins can also be obtained.	
dynamicXpr	Dynamically change colors of nodes like a movie according to their expression level across many conditions.	
DynNetwork	Visualize dynamic networks.	Available in App Store
edgeLengthPlugin	Calculate edge length in the main network view window, and stores them as edge attributes "length".	
edgeLister	Records selected edges and provides some functionality for them (ex. hiding recorded edges)	
Enhanced Graphics	Passthrough mapper for charts and gradients.	Available in App Store
EnhancedSearch	Performs keyword search. Wildcards, logical operators, etc. are allowed.	Available as part of core
EnrichmentMap	Visualizes enrichment of specific functions (GO terms) by interactions between functions.	
eXamine	Set-oriented visual analysis approach for annotated modules that displays set membership as contours on top of a node-link layout.	Available in App Store
ExprEssence	Searches for differentially altered links in a given network using multiple set of expression data.	
ExpressionCorrelation	Makes a similarity network where nodes are genes, and edges denote highly correlated genes.	
FERN	Performs stochastic simulation of chemical reaction networks.	
FluxViz	Visualizes fluxes as visual effect to edges on Cytoscape network.	
FM3	Performs one of the fastest multilevel force directed Layouts called FM3 Layout introduced by Hachul S et al 2005.	
FunNetViz	Integrates and visualizes co-expression network with biological role of transcripts (e.g., GO terms). Centrality measures are equipped.	
Gasoline	Multiple local alignment of protein-protein interaction (PPI) networks.	Available in App Store
GeneMANIA	Generates interaction networks from public databases based on user's list of genes. Also provides annotation and putative function for those genes.	Available in App Store
GenomeSpace	Enables communication with GenomeSpace	Available in App Store

Genoscape		
GFD-Net	Analyze a gene network based on Gene Ontology (GO) and calculate a quantitative measure of its functional dissimilarity.	Available in App Store
GIANT	Network analysis according to the Guimerà-Amaral cartography	Available in App Store
GoogleChartFunctions	Creates image from attribute values (URL) using the Google Chart API.	
GPML-Plugin	Enables import of GPML file via import menu.	
GraphletCounter	Calculates "graphlet" (small connected non-isomorphic subgraph) degree distribution.	
GraphMLReader	Loads interactions or pathways in GraphML format.	Available as part of core
GroovyEngine	Provides scripting interface of Groovy.	
GroovyScriptingEngine	Provides scripting interface of Groovy.	
GroupTool	Enables user to defines groups of nodes. For each group, basic information such as number of nodes will be displayed on the panel.	In Progress
HiderSlider	Provides user sliders which can hide nodes whose continuous attribute is below threshold specied by sliders.	
HyperEdgeEditor	Enables one to create hyper-edge by Cytoscape editor.	
HyperModules	Uses local graph search heuristics to detect closely connected gene network regions in which gene mutations correlate with clinical features.	Available in App Store
IgraphPlugin	Brings some functionality of Igraph such as layouts into Cytoscape. Mac only.	
IntActWSCient	Retrieves interactions associated with input IDs.	Replaced by PSICQUIC
Interference	Evaluates the topological effects of single or multiple nodes removal from a network using the effect to Radiality, Closeness, Betweenness, Centroid Value and Eccentricity.	In Progress
iRefScape	Retrieves interactions associated with input IDs. Detailed information for each interaction as well as link to iRefIndex is provided.	
jActiveModules	Finds clusters where member nodes show significant changes in expression levels.	Available in App Store
JavaScriptEngine	Provides Java Script API.	Available as part of core
JEPETTO	Performs biological gene sets enrichment analysis based on interaction network and topological properties.	Available in App Store

KEGGscape		Available in App Store
KeyPathwayMiner	Detects highly-connected sub-networks where most genes show similar expression behavior.	Available in App Store
KGMLReader	Enables import of KEGG XML file via import menu.	
mcl-new	Clusters given network. Subnetwork is indicated by set of nodes, and they are shown by selecting subnetwork number.	
MCODE	Clusters a given network based on vertex weighting by local neighborhood density and outward traversal from a locally dense seed protein to isolate the dense regions.	Available in App Store
MetaNetter	Infers of metabolic networks based on high resolution metabolomic data.	
MetanodePlugin2	Enables user to define "meta-node", a group of nodes. Meta-nodes can have hierarchy.	Available as part of core
MetDisease	Annotates metabolic networks with MeSH disease terms and links to references.	Available in App Store
MetScape	Loads human or mouse metabolic network. Sophisticated GUI is provided which allows user to perform various tasks including gene expression analysis along the pathways.	Available in App Store
MiMlplugin	Retrieves interactions associated with input IDs. User can add own annotations to genes which can be viewed by different users.	In progress
MINE	Clusters a given network based on agglomerative clustering algorithm very similar to MCODE, but it uses a modified vertex weighting strategy and can factor in a measure of network modularity. Adjustment of only few parameters are necessary.	
MiSink	Provides network interface to MiSink-enabled Web sites, including DIP.	
MONET	Predicts gene regulatory network from biological annotations and expression data.	
Mosaic	Systematically partition the given graph, and layout and color nodes based on GO terms.	
NamedSelection	Assign name to selected nodes, and after unselection, enables user to re-select the nodes according to the name.	
NCBIClient	Imports various data from NCBI database.	
NCBIEntrezgeneUserInterface	Imports various data from NCBI database.	Available as part of core

NeighborHighlight	Highlights the current node and all its neighboring nodes and edges when the user hovers the mouse over it.	
NeMo	Identifies densely connected and biopartite network modules based on combination of a unique neighbour-sharing score with hierarchical agglomerative clustering.	
NetAtlas	Integrates gene expression data of multiple tissues (ex. from SymAtlas) into pre-loaded network. genes showing characteristic expression in specified tissues can be filtered and colored.	
NetCirChro	Visualizes interaction network on circular genome. Original GUI with some network analysis functions (shortest path, degree distribution, etc.) are equipped.	
NetMatch	Finds user defined network motifs in a given network. network motif can be created and edited using original GUI.	
NetworkAnalyzer	Computes basic properties of whole network (degree distribution, clustering coefficients, centrality, etc.)	Available as part of core
NetworkEvolution	Allows interactive comparative analysis of networks across different species.	
nodeCharts	Paints bar, line or pie graphs onto nodes.	
OmicsAnalyzer	Integrates omics data such as expression data, proteome data, etc. onto the network to visualize such data by graph on the network.	
OrthoNets	Enables simultaneous comparison of interaction network of two species. Protein domain information can be visualized.	
PathExplorer	Finds paths, filters them based on node and edge attributes and saves them.	Available in App Store
PanGIA	Performs integrated analysis and visualization of PPIs and genetic interactions to infer functional modules and interactions that connect these modules.	
Pathintegrator	Integrates pathways in which given proteins are associated.	
Pathway Scoring Application	Evaluates the biological activity of genes and processes in pathways	Available in App Store
PEPPER	Find meaningful pathways / complexes connecting a protein set members within a PPI-network using multi-objective optimization.	Available in App Store
PerturbationAnalyzer	Evaluates how perturbation of selected nodes affect other nodes in a given network based on level of each node (ex. protein abundances) and law of mass action.	

PhosphositePlus Web Service Client Module	Integrates phosphorylation-related information into the network.	
PhyloTree	Reads a file in phylogenetic tree format (Phylip or phyloXML) and visualizes it as a network.	
PICRClient		
PINA4MS	A visualization and analysis tool to study interactions between multiple sets of proteins.	Available in App Store
PiNGO	Finds candidate genes in a network that are associated with user-defined target GO terms.	
PinnacleZ	Searches for subnetworks which can discriminate given conditions according to PPI network and gene expression data obtained in given conditions	
PSICQUICUniversalClient	Retrieves interactions associated with input IDs from databases having PSICQUIC implementation	Available as part of core
PythonScriptingEngine	Provides Python API.	
Randomnetworks	Generates random network or randomizes already loaded network.	
RDFScsape	Allows to query, visualize and reason on ontologies represented in OWL or RDF within Cytoscape.	
Reactome FI Plugin	Accesses to Reactome Functional interaction (FI) network to perform pathway analyses such as identification of pathways enriched with proteins in given network.	Available in App Store
ReConn	Communicates with reactome server to load pathway data onto Cytoscape. Additional features such as integration of expression data are supported.	
RemainingDegreeDistribution	Calculates remaining degree (excess degree) distribution.	
ReOrientPlugin	Layouts node positions according to reference Cytoscape session file.	
RubyScriptingEngine	Provides Ruby Script API.	
ScriptEngineManager	Manages scripting engines for Cytoscape. Supports Ruby, JavaScript, Groovy, and Python.	Available as part of core
SemScape	Visualizes Semantic Data Landscapes	Available in App Store
SessionForWeb	Saves Cytoscape session in Web format.	
SFLDLoader	Represents structural protein families and their homologs by graph on Cytoscape.	
ShortestPath	Finds shortest pathway between two selected nodes.	

SimTrek	Assesses similarity of gene ontologies for given genes and their neighbours. All files must be installed in plugin folder.	
StringWSClient	Retrieves interactions associated with input protein name.	
structureViz	Enables user to traverse from biological networks to detailed view of their structures.	In Progress
Superpathways-Plugin	Downloads and integrates multiple pathways from Wikipathways.	
TransClust	Clusters a given similarity graph.	
Venn and Euler Diagrams	Provides a diagram view and a details view for comparing two or more Cytoscape groups at a time.	Available in App Store
VistaClaraPlugin	Provides effective visualization and analysis platform to analyse expression data on a given network.	
WikiPathways	WikiPathways web service client and GPML file format importer.	Available in App Store
WordCloud	Summarizes functions of interacting clusters as logos, where sizes of logo represents frequencies of these functions.	

9. Support Offering Table

Feature	Purpose	Beneficiary	URL
Cytoscape Google Groups Helpdesk Discuss	Community response on best effort basis	All users	mailto:cytoscape-helpdesk@googlegroups.com mailto:cytoscape-discuss@googlegroups.com
User Manual	Comprehensive manual	All users	http://wiki.cytoscape.org/Cytoscape_3/UserManual
Installation Guide	Cytoscape installation	New/Casual users	Section 3 of http://wiki.cytoscape.org/Cytoscape_3/UserManual
Tutorials	Streamlined productivity	All users	http://opentutorials.cgl.ucsf.edu/index.php/Portal:Cytoscape3
Presentation Slides on Web Site	Enable casual learning	All users	https://speakerdeck.com/cytoscape
Code Snippets	Commonly used App development code	App Developers	http://wiki.cytoscape.org/Cytoscape_3/AppDeveloper/Cytoscape_3_App_Cookbook

10. Future Plans Table

Feature	Purpose	Beneficiary	Timeframe
Movies	Clear and interactive engagement	New/Casual users	TBD
Additional Visualizations			TBD
Additional Analytics			TBD
Wallpaper Collection	Publicize good results associated with Cytoscape	All users, potential users, general public	TBD
Searchable Web Site	Fast access to manuals, tutorials, group transcripts, clinic transcripts	All users	TBD
Case Studies	Streamlined productivity	New/Casual Users	TBD
Cytoscape Clinics New/Casual User Power User App Developer	Chat rooms give instant response based on community availability	All users	TBD

Cytoscape v3.1 is the first feature-intensive release after the major refactoring represented by v3.0. We expect minor features and bug fixes to be released in v3.1.1, and we are planning another major feature release in v3.2. Though there is no time table yet for either.

11. Issues Addressed

The following issues were addressed in v3.1. Details for each issue can be found at Cytoscape's RedMine issue repository:

<http://code.cytoscape.org/redmine>

Issue	Description	Beneficiary
766	Need to think about "Tools" menu item. Likely confusion between Tools and Apps	All Users
1087	New edge drawn incorrectly if you zoom while placing edge	All Users
1251	Checking to save session before closing and opening another session	All Users
1383	Need more realistic tests for Session Integration Test	All Users
1419	Visual Style is not refreshing	All Users
1448	Toggling "Show All" under VizMapper -> Visual Mapping Browser causes z-order to change	All Users
1516	Newly-installed version of Cytoscape using old cached bundles	All Users
1524	Nested Network renderer doesn't compute bounds properly	Power Users
1540	Node disappears after adding its own network as a nested one	Power Users
1644	Handling of app dependencies in the App Manager	Developers
1645	Need way to specify order for Tunables	Developers
1700	Exported .cytable files can't be imported into a different session due to use of SUID as primary key	All Users
1707	Annotation selection not working right	All Users
1767	Need API to allow apps to clean up after being uninstalled	Developers
1795	VizMapper does not refresh after visual styles are applied	All Users
1796	Visual mappings not applied to view as attributes are specified in table view	All Users
1802	cannot save	All Users
1844	New table Merge Tool	Power Users
1846	IOException "resetting to invalid mark" when trying to find a CyNetworkReader for a FileInputStream	Developers
1867	App Manager does not retry accessing App Store if first connection failed	All Users
1869	Unloading a bundle that registers a layout doesn't unregister layouts	Developers
1872	Layout settings dialog does not respond to newly loaded layouts	All Users
1873	Export-->Network Menus are disabled if network view does not exist	All Users

1895	Cancel does not work for Session Loader	All Users
1898	Prompt to continue opening session appears *after* expanding .cys file	All Users
1902	Cleanup dependency version numbers in impl poms	Developers
1906	Update sample POM files to reflect release API	Developers
1908	Tunable dialog lost title if the params "ForceSetDirectly=true" is set	All Users
1909	NetworkAnalyzer UI doesn't fit in Results CytoPanel	All Users
1918	Samples are useless until we rename those	New Users
1919	Launching Cytoscape via scripts on Mac doesn't initialize menu properly	All Users
1928	Create new filter API and UI	Developers
1930	unable to scale nodes	All Users
1935	Filtering unusably slow with large networks (500K+ nodes/edges)	Power Users
1944	Select -> Nodes -> File ID list File, does not work	Power Users
1957	importing scientific notation values	All Users
1964	Edge color does not map	All Users
1968	Mac Pan/Add edge handle	All Users
1969	Feature: revamp the vizmapper GUI	All Users
1970	Pointless menu item	All Users
1977	Tool panel blocks Vizmapper	All Users
1983	Phantom node/edge selection while panning	All Users
1984	Panning de-selects nodes	All Users
1986	Installing apps via command line arguments (-b or -p) doesn't work...	Power Users
1998	Icon suggestion - Table settings	All Users
2008	Loading network from file	All Users
2009	MapTableToNetworkTablesTask should provide a way to map to columns other than SHARED_NAME	Developers
2011	Importing files	All Users
2016	getJMenu in CySwingApplication blindly appends gravity value to menu string, creates new menus if they don't exist	Developers
2022	cannot be saved	All Users
2026	Backport #2002	All Users
2027	Cannot load network in 3.0.1	All Users
2029	[VizMapper] ClassCastException when editing Discrete Mapping for visual property "Node Label"	All Users
2030	Edge label font size	All Users
2032	-h option doesn't properly display help screen	All Users
2034	Search should have an option to not be case sensitive	All Users
2036	Bugs in Group/Ungroup, collapse/expand, hide/unhide	All Users

2041	Tasks returned by createTaskIterator(File) in LoadTableFileTaskFactory abort with NPE	Developers
2044	edge font size	All Users
2047	NPE when setting Continuous Mapping to Node/Edge Label if current Network View is null	All Users
2051	Add a column when a local column already exists throws an exception, but getColumn does not see the local column	Developers
2052	[VizMapper] Discrete Mapping values set to wrong attribute	All Users
2054	Edge Label Transparency and Size (VizMapper)	All Users
2060	Typing error in LinkOut class	Developers
2063	Command line error loading table	Power Users
2068	Default node/edge labels do not work	All Users
2072	Update Karaf to 2.2.11	Developers
2079	[VizMapper] Ugly descriptions on discrete mapping's font chooser and editor is slow to open	All Users
2080	extend network error	All Users
2087	Edit -> Remove Duplicated Edges doesn't trigger screen update	All Users
2088	Gradient editor min/max change automatically	All Users
2089	App bundles that fail to load still show as installed	Developers
2090	Saving Continuous Mapping Values	All Users
2091	Installation problem	All Users
2092	Open/Save dialog boxes in Cytoscape lag on Mac Java 7	All Users
2093	Tunable ListMultipleSelection causes NPE if empty	Developers
2095	Network Merge	All Users
2096	Tunable changes have broken Layout Settings	All Users
2098	Font Face icons incorrectly aligned on Continuous-to-Discrete Mapping Editor	All Users
2099	"Undo: Hide Selected Nodes" does not work	All Users
2102	Vizmapper refresh	All Users
2109	ExportNetworkViewTaskFactory always uses SIF format when called with File, regardless of file extension	All Users
2112	Bad image export settings	All Users
2114	Bad csv table import settings	All Users
2119	installation warning	All Users
2121	XGMML: Wrong type on attribute	All Users
2126	BioPAX reader features/fixes	All Users
2137	Add SessionAboutToBeLoadedEvent as a CyEvent	Developers
2140	Update SynchronousTaskManager Javadoc to clarify function...	Developers
2141	Race condition at DestroyNetworkTask	All Users

2142	Acceptable values for ServiceProperties.PREFERRED_ACTION not documented	Developers
2144	Virtual columns are firing incorrect set events	All Users
2145	When new attributes are loaded, VizMapper does not refresh	All Users
2150	Visual Styles are completely lost when opening 2.x session	All Users
2155	inaccessible buttons	All Users
2157	Enhancement Request: API Access to Java Network View Area & JInternalFrames	Developers
2158	Enhancement Request: Add API For Choosing Control Panel Tab	Developers
2162	CyApplicationConfiguration.getAppConfigurationDirectoryLocation() Doesn't Work for Simple Apps	Developers
2165	Destroyed network view not removed immediately by NetworkViewManager	Developers
2166	The -v and --version command-line options cause invoke Karaf and cause Cytoscape to be run unnecessarily	Power Users
2169	bug in searching node name	All Users
2172	Need Cy3 Replacement for DingNetworkView.setGraphLOD()	Developers
2175	Need a way to enable REST from GUI	Power Users
2176	Need a way to select nodes based on selected rows	Power Users
2178	Node sorting by numbers	All Users
2180	cytoscape.sh syntax error	All Users
2182	Table browser context menu needs to be changed	All Users
2184	Ping Chianti for news on welcome screen	All Users
2186	Need to be able to quit Cytoscape without asking the user if they want to save the session	All Users
2190	Visual Style Discrete Edge Mappings Using EDGE_PAINT Don't Work	All Users
2191	Malfunctioning Edge paint	All Users
2195	Fix bug reporting on Mac	All Users
2197	"Grid Layout" task monitor is passed to a reader	Developers
2199	Right-click/Ctrl-click brings up context menu when zooming...	All Users
2202	Vizmapper: Color scheme reverts back to the default if NaN values	All Users
2206	Exception when changing layout parameters and executing the layout from settings dialog	All Users
2216	PSICQUIC Client creates less edges than actual number of records	All Users
2218	Need an event to notify when all apps successfully started	Developers

2221	Fix small PSICQUIC GUI Problems	Power Users
2222	Optimize PSICQUIC "get interactome" query	Power Users
2223	Fix Cancel function for PSICQUIC Client	All Users
2224	[Table Browser] ArrayIndexOutOfBoundsException after clicking the Function Builder button with no selected rows	All Users
2226	Fix cancel function for PSICQUIC Search	All Users
2227	File->Import->Ontology and Annotation does nothing	All Users
2235	Cy3 hangs during "Indexing Network Data" task	All Users
2236	[Table Browser] Popup menu shown when "Change Table Mode" button is disabled	All Users
2245	Improve organic network interface	All Users
2247	Changes to one edge bend apply to all in network with edge bend visual mapping	All Users
2250	PSICQUIC Expand Node feature should use new importer, not the MiCluster one	Power Users
2251	Legend labels are not alphabetically ordered	All Users
2257	[Table Browser] Selecting rows through the keyboard do not change node/edge selection	All Users
2259	Update Preset Visual Style for 3.1	All Users
2261	[Table Browser] Control-click deselects other selected rows on Mac	All Users
2262	VizMapper should treat NAN as empty value	All Users
2267	Cannot Unlock Node Width/Height	All Users
2268	Layout->Clear Edge Bends doesn't do anything	All Users
2269	Missing test cases for Cytoscape.js exporter	Power Users
2271	Provide more useful message for cancellation in PSICQUIC Client	Power Users
2272	Keep data source selection as a part of core property (for PSICQUIC)	Developers
2273	Race condition when columns deleted while BrowserTable is updating	All Users
2274	NetworkAnalyzer Help Does Not Point to Valid URLs	All Users
2279	New task monitor displays last task's message indefinitely	All Users
2280	Importing a Table from File Should Act	All Users
2281	LoadTableFileTaskFactory no longer merges table in 3.1	Power Users
2282	Merge data access rest service to rest-impl	Developers
2283	Importing a broken BioPAX does not provide correct user feedback	All Users
2285	Map Uniprot ID (or NCBI Gene ID) as String Column for PSICQUIC	Power Users
2286	Equations are not saved in the session	Power Users

2287	Trying to bend an individual edge results in all edges being bent.	All Users
2292	Change Table Mode button does not make sense for Network Table	All Users
2293	GenericReaderManager.getReader() / CopyInputStream.copyKBytes() IOException & Incorrect Reader Returned	Developers
2294	Race condition ends in deadlock when deleting network	All Users
2296	CyActions/TaskFactories without specified gravity appear on menu in indeterminate order	All Users
2298	Use scientific species name for buttons on Welcome Screen	All Users
2300	"Import Table from URL" examples aren't valid table files	New Users
2303	Equation cannot be restored from session file if it belongs to a shared table but references a local table's column	Power Users
2309	Splash screen overlays Windows Security Alert dialog	All Users
2310	JSON Exporter does not export edge color	Power Users
2311	JSON Exporter does not export edge arrow shape and color	Power Users
2312	Replace spaces in column name when exporting to Cytoscape.js Visual Style	Power Users
2313	Locked Visual Properties are not properly handled in Cytoscape.js exporter	Power Users
2314	filter-api needs to be locked down	Developers
2315	filter-api needs Javadoc	Developers
2316	Filters chapter in manual needs to be rewritten	All Users
2317	Clear Edge Bends Menu Sets Everything to Default Even When Default Has Bends	All Users
2318	After Clearing Edge Bends, Network Is No Longer Responsive to Changes to the Default	All Users
2319	Changes to the default edge bend do not have an effect after Layout->Bundle Edges->All Edges and Nodes is called	All Users
2320	UI still refers to "Visual Style", instead of just "Style"	All Users
2324	Decrease number of iterations for Edge Bundling	Power Users
2327	Size Visual Property does not work for Continuous Mapping	All Users
2329	Need to rework the View menu	All Users
2330	Update VizMapper GUI whenever new Bypass is created or when the default is cleared.	All Users
2331	When all edges are cleared, the default displayed in the VizMapper ought to display properly.	All Users
2335	JSON is the default format for Style export	Power Users

2336	When node width and height are locked, mappings does not work	All Users
2337	Add user/developer document for JSON exporter	Power Users
2338	Network Table should be exported as a part of JSON file.	Power Users
2339	The clear all edge bends menu item does not eliminate mappings.	All Users
2340	Clear All Edges From This Bend No Longer Working	All Users
2342	"Create View" menu item appears twice on Edit menu since Commands implementation	All Users
2343	News section of Welcome screen has light background on Linux	All Users
2344	export fails	All Users
2350	Remove D3.js JSON exporter code and create external App	Power Users
2353	Network View as Graphics... It is difficult to put dots in filenames	All Users
2358	Filters: Deactivating then reactivating "Apply automatically" checkbox prevents filter from being applied	All Users
2359	Deprecate some vizmap-gui-api interfaces and methods	Developers
2362	Command "command run commands" is unnecessarily redundant	Power Users
2363	File->Run doesn't work properly	All Users
2365	Deadlock in CyApplicationManager	All Users
2366	Cannot move node after clearing edge bends	All Users
2367	Remove unnecessary PSICQUIC columns	Power Users
2369	Edge bend editor overwrites current mappings if canceled	All Users
2370	Nightly builds failing regularly due to Sonar failure	Developers
2371	Bugs with task status bar clearing	All Users
2376	Custom value editor broken	Power Users
2379	Welcome Screen's news section should not use JLabel, use Editor Pane.	All Users
2384	BioPAX reader is not detected when importing a biopax network from URL	All Users
2386	Some options in Merge Tables shouldn't be available in some cases	Power Users
2387	BasicCyFileFilter: extensionsMatch(uri) and getExtension(name) bugs	All Users
2392	network import file command only imports networks from tables	Power Users
2395	REST server should return 4xx series status code for errors	Power Users
2397	Cannot get list of edges from REST	Power Users
2401	CSV table/network import doesn't parse quotes	All Users

2402	rest-impl doesn't load due to missing package org.cytoscape.rest.RESTResource	Developers
2403	AnnotationManager was never exposed	Developers
2405	Fit Label Width feature does not work in 3.1	All Users
2407	Reader manager returns wrong reader for URL import	All Users
2408	Tools menu order different from Cytoscape 3.0.x	All Users
2414	Ontology and Annotations not working again. Seems to be related to table import...	All Users
2423	CSV replaces commas with newlines	All Users
2424	File exported to incorrect location and incorrect name	All Users
2430	Update documentation for annotation-api to reflect correct package	Developers
2433	Need to replace fragile getExtension() methods	Developers
2435	Cannot read PSIMI XML v2.5.4	All Users
2441	tableimport failed to create a tmp file	All Users
2442	Loading large network from .cys file results in deadlock	Power Users
2444	BioPAX: ID_UNIPROT column displays not a primary ID	All Users
2445	File->Export->Table... is always disabled.	All Users
2450	Network Merge throws NPE when user specify List column as merge key	Power Users
2455	Some of the Link Out URLs are broken	Developers
2461	Cancel takes forever in Network Merge	All Users
2463	Reinstating modal task manager	Developers
2466	Clearing visual properties in DGraphView's setViewDefault degrades performance	All Users
2467	Need NCBI Gene Column for BioGRID Data Import	All Users
2469	Edge Color (unselected)	All Users
2471	Copy Style feature does only a shallow copy	All Users
2476	VisualStyle.apply(CyRow,View) is broken	Developers
2481	Undo Delete Nodes/Edges does not restore bypass values	All Users
2484	Key column drop down list does not update when changing table import type	Power Users
2485	Sample attribute data files should be renamed with proper extension	New Users
2486	Hang on MacOS 10.8.5 when opening a network	All Users
2488	Filters don't work on networks without a view	Power Users
2491	Selected network not set properly when sessions reload	All Users
2495	Add JSON format version number to exported JSON files (for cytoscape.js)	Power Users
2509	Off-by-one error during filter serialization	Power Users
2511	Mappings sometimes not applied when restoring session	All Users