April 22, 2013

Welcome

Summary

- Cytoscape v3.0.1 is now available for immediate download.
- Relative to v3.0.0, it contains over 100 bug fixes.
- It is ready for use by all segments of the Cytoscape community.
- It continues v3.0.0's core feature set, specifically:
    - It is a major reorganization of Cytoscape 2.x's code and user interface.
    - 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.
- What to do next …

Dear Cytoscape User

We are proud and pleased to release Cytoscape v3.0.1. This new release contains many improvements on v3.0.0 (released Feb 1, 2013), all of which immediately benefit Cytoscape users, the most important part of the Cytoscape ecosystem.

> *If you are a <u>new</u> or <u>casual</u> Cytoscape user,* ***welcome aboard!*** *Feel free to either read on or jump to the end of this letter 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), 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 v3.0.1 (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, you can install v3.0.1 without uninstalling v3.0.0.

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 v3.0.0 beta version, *please uninstall it before proceeding.* The Cytoscape v3.0.0 release version can coexist with v3.0.1, and does 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 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 framework[1]. 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

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[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)	3.1.3. Launch the Application
Import network	Casual and power users (for ease of use)	7. Creating Networks
Edge bend visual property	Paper and presentation writers	12.4. Visual Attributes, Graph Attributes and Visual Mappers
Edge bundling	Users of high degree networks	11.3. Edge Bundling
Network annotations	Paper and presentation writers	
Grouping	Users of hierarchical networks	
Enhanced search	Users of highly populated networks	13.1. Enhanced Search
Show All in Table Browser	Users with highly annotated networks	7.2.3. Advanced Options
Multiple network management	All users	4.2. Network Management

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/ccc?key=0ArzUWDuvdBn-dDI0R0kwOERjN1ZhcDZseC00dVZNNlE&authkey=CMGe99EM#gid=0

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.	

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 calcuates 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**
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.	
commandTool	Provides simple command-line interface to Cytoscape.	
CommFinder	Clustering based on QCUT, HQCUT, MCL, MCODE.	
Commonattributes	Find attributes shared between selected nodes.	
ConsensusPathDBplugin	Retrieves interaction evidences for given pair of genes or proteins	
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.	

CyOog		
CyThesaurus-ID-Mapping	Performs ID mapping using BridgeDb and other public or custom database sources.	
cytoHubba	Predicts and explores important nodes and subnetworks in a given network by several topological algorithms.	
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 interactiong proteins can also be obtained.	
dynamicXpr	Dynamically change colors of nodes like a movie according to their expression level across many conditions.	
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)	
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.	
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.	
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**
Genoscape		
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.	
IgraphPlugin	Brings some functionality of Igraph such as layouts into Cytoscape. Mac only.	
IntActWSClient	**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**
KeyPathwayMiner	Detects highly-connected sub-networks where most genes show similar expression behavior.	
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**
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.	
MiMIplugin	Retrieves interactions associated with input IDs. User can add own annotations to genes which can be viewed by different users.	
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.	
PanGIA	**Performs integrated analysis and visualization of PPIs and genetic interactions to infer functional modules and interactions that connect these modules.**	**Available in App Store**
Pathintegrator	Integrates pathways in which given proteins are associated.	
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		
PiNGO	**Finds candidate genes in a network that are associated with user-defined target GO terms.**	**Available in App Store**
PinnacleZ	Searches for subnetworks which can discriminate givein 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 FIs	Accesses to Reactome Functional interaction (FI) network to perform pathway analyses such as identification of pathways enriched with proteins in given network.	
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**
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.	
VennDiagramgenerator	Generates a Venn/Euler Diagram of shared nodes for selected networks.	In Progress
VennDiagrams	Calculates overlap between multiple groups of interactions and creates Venn-diagram.	In Progress
VistaClaraPlugin	Provides effective visualization and analysis platform to analyse expression data on a given network.	
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

✵ = new feature

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 v3.0.0 was a major reorganization of the v2.x code, and the v3.0.1 release is oriented towards fixing the numerous small problems created or not solved by the reorganization. If we discover that v3.0.1 has any major problems needing immediate remediation, we plan to make a v3.0.2 release with just those problems solved – as of now, we don’t expect this to occur.

We will be shifting our focus to creating new features released as v3.1 sometime in the late fall of 2013.