



Network Workbench Tool

User Manual, 1.0.0 beta

Getting Started

General Tutorial

Domain Specific: Information Science Tutorial

Domain Specific: Social Science Tutorial

Domain Specific: Scientometrics Tutorial

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Getting Started

1 Introduction

The Network Workbench (NWB) Tool (Herr II, Huang, Penumarthy, & Börner, 2007) is a network analysis, modeling, and visualization toolkit for physics, biomedical, and social science research. It is built on Cyberinfrastructure Shell (CIShell) (Cyberinfrastructure for Network Science Center, 2008), an open source software framework for the easy integration and utilization of datasets, algorithms, tools, and computing resources. CIShell is based on the OSGi R4 Specification and Equinox implementation (OSGi-Alliance, 2008).

The Network Workbench Community Wiki provides a one-stop online portal for researchers, educators, and practitioners interested in the study of networks. It is a place for users of the NWB Tool, CIShell, or any other CIShell based program to get, upload, and request algorithms and datasets to be used in their tool so that it truly meet their needs and the needs of the scientific community at large.

Users of the NWB Tool can

- Access major network datasets online or load their own networks.
- Perform network analysis with the most effective algorithms available.
- Generate, run, and validate network models.
- Use different visualizations to interactively explore and understand specific networks.
- Share datasets and algorithms across scientific boundaries.

In September 2008, the NWB Tool provides access to over 80 algorithms and 30 sample datasets for the study of networks. The loading, processing, and saving of seven file formats (NWB, GraphML, Pajek .net, Pajek .matrix, XGMML, TreeML, CSV) and an automatic conversion service among those formats are supported.

Additional algorithms and data formats can be integrated into the NWB Tool using wizard driven templates. Although the CIShell and the NWB Tool are developed in JAVA, algorithms developed in other programming languages such as FORTRAN, C, and C++ can be easily integrated. Among others, JUNG (O'Madadhain, Fisher, & Nelson, 2008) and Prefuse libraries (Heer, Card, & Landay, 2005) have been integrated into the NWB as plug-ins. NWB also supplies a plug-in that invokes the GnuPlot application (Williams & Kelley, 2008) for plotting data analysis results and the GUESS tool (Adar, 2007) for rendering network layouts. LaNet-vi (Alvarez-Hamelin, Dall'Asta, Barrat, & Vespignani, 2008) uses the k-core decomposition to visualize large scale complex networks in two dimensions.

2 Download and Install

The Network Workbench tool is a standalone desktop application that installs and runs on all common operating systems. NWB tool 0.7.0 and later versions require Java SE 5 (version 1.5.0) or later to be pre-installed on your local machine. You can check the version of your JAVA installation by running the command line:

```
java -version
```

If not already installed on your computer, download and install Java SE 5 or 6 from <http://www.java.com/en/download/index.jsp>.

To download NWB Tool, go to <http://nwb.slis.indiana.edu/download.html> and select your operating system from the pull down menu, see Figure 1.

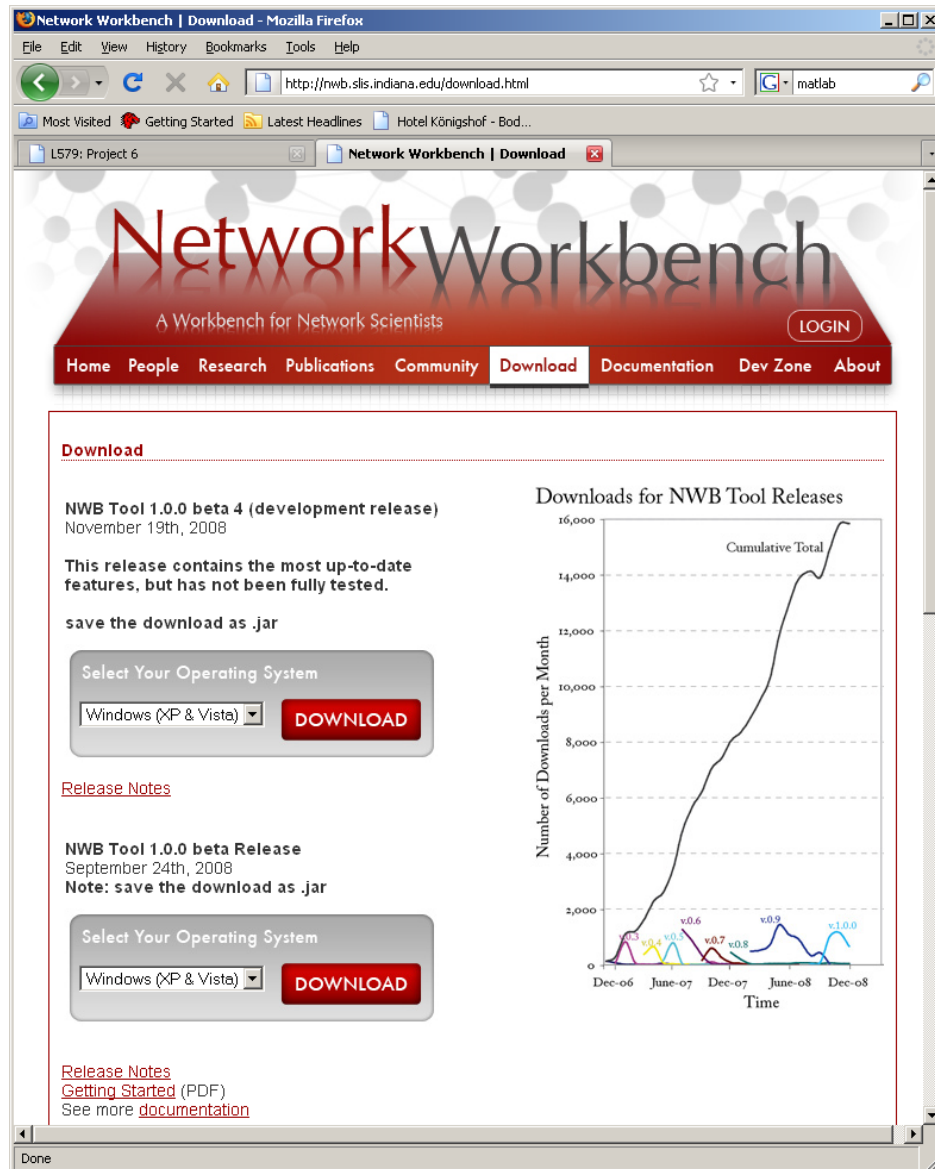


Figure 1: Select operating system and download NWB Tool

Save the jar file in a new empty **yournwbdirectory** directory, double click the jar file, or run the command line:
`java -jar nwb-installer_0.7.0.jar`



After the successful installation, two NWB icons will appear on the Desktop. To run NWB tool, double click the 'Network Workbench' icon.

To uninstall NWB tool, i.e., to delete all files in **yournwbdirectory**, double click the 'Uninstall NWB' icon.

3 User Interface

The general NWB Tool user interface is shown in Figure 2, see also (Herr II et al., 2007).

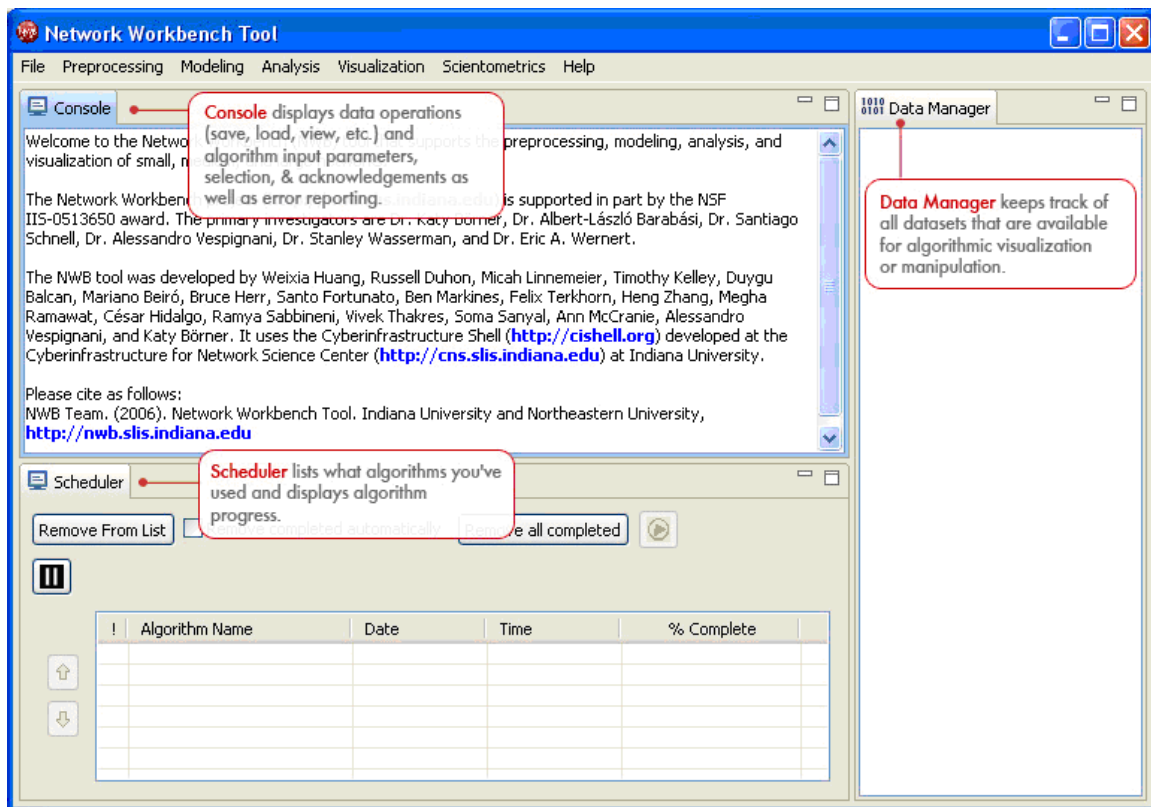









Figure 2: Network Workbench tool interface components

All operations such as loading, viewing, or saving datasets, running various algorithms, and algorithm parameters, etc. are logged sequentially in the Console window as well as in the log files. The Console window also displays the acknowledgement information about the original authors of the algorithm, the developers, the integrators, a reference paper, and the URL to the reference if available, together with an URL to the algorithm description in the NWB community wiki.

The Data Manager window displays all currently loaded and available datasets. The type of a loaded file is indicated by its icon:

-  Table—or csv file
-  Matrix—data (Pajek .mat)
-  Plot—plain text file that can be plotted using gnuplot
-  Text—other text file
-  GUESS—GUESS Visualizations
-  Tree—Tree Data Structure
-  Network—Network data, could be in-memory Graph/Network object or Network files saves as Graph/ML, XGMML, NWB, Pajek, .net or Edge list format

Derived datasets are indented under their parent datasets. That is, the children datasets are the results of applying certain algorithms to the parent dataset.

The scheduler lets users keep track of the progress of running algorithms. If an algorithm has implemented a ProgressTrackable interface, users can pause, resume or cancel that algorithm through the Scheduler while it is still running.

4 Workflow Design

Many if not all network studies require the application of more than one algorithm. A sequence of algorithm calls is also called a workflow. A common workflow comprises data loading/sampling/modeling, then preprocessing and analysis and finally visualization.

Figures 3 and 4 shows the menu items available in the v 1.0-beta release. There are domain specific plug-in sets, e.g., for scientometrics, see Domain Specific: Scientometrics, Figure 1. Algorithms that are not applicable to a currently loaded and selected dataset are grayed out.

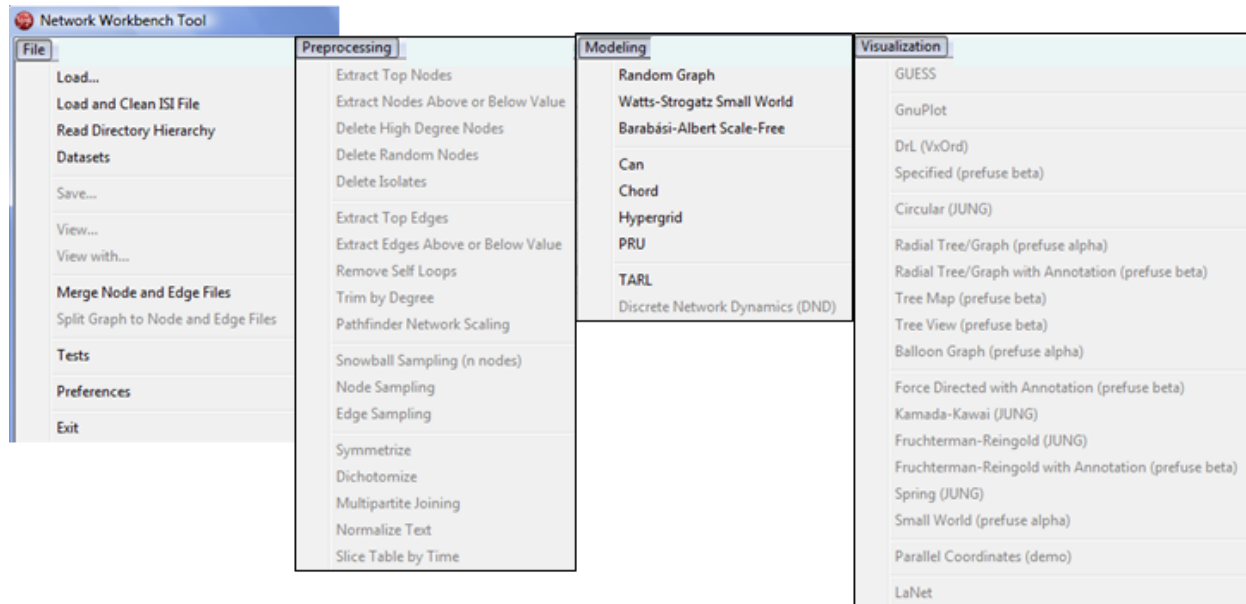


Figure 3: File, Preprocessing, Modeling, and Visualization menus

The Analysis menu has four submenus as shown in Figure 4. Weighted network analysis algorithms will be added shortly leading to two more submenus.

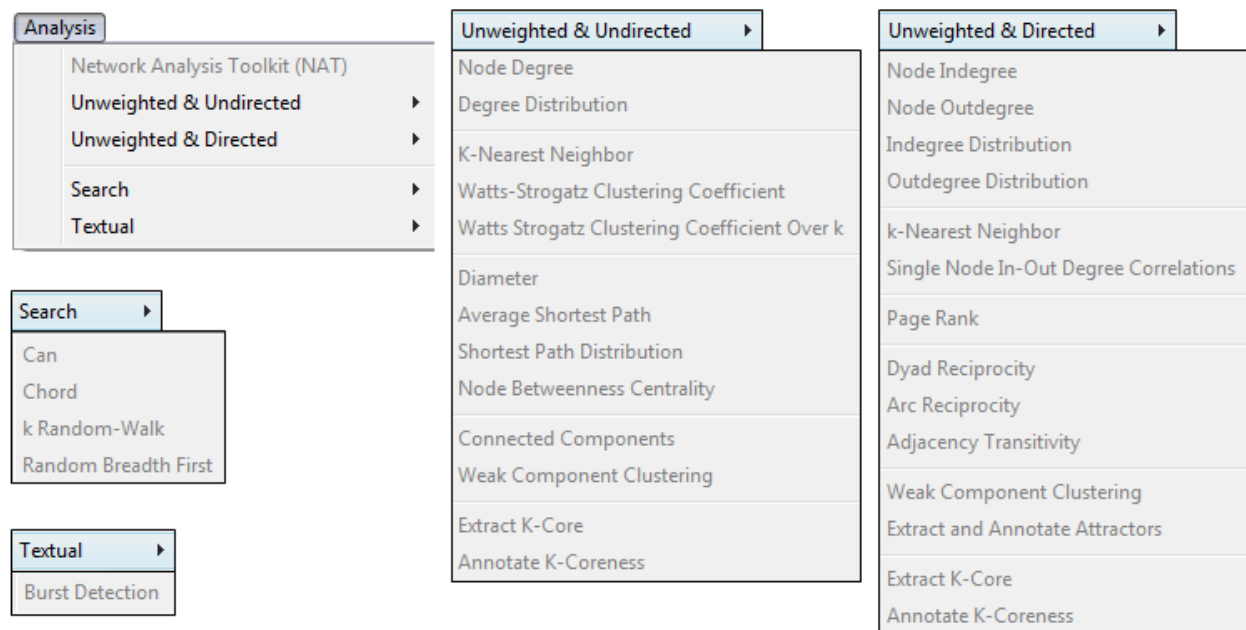


Figure 4: Analysis menu and submenus

Sample Datasets and Supported Data Formats

1 Sample Datasets

The ‘**yournwbdirectory*/sampledata*’ directory provides sample datasets from the biology, network, scientometrics, and social science research domains, see listing below.

/biology

FlyMINT.nwb
TF_DNA_regulonDB.nwb
WI5.nwb
WormMint.nwb
YeastMINT.nwb
humanprot.nwb

/biology/DND

colorectalCancerModel.csv
drosophila.csv
graduationUseCase.csv
samplePolynomialUseCase.csv
simpleDNDFunction.csv

* Used in DND model

/network

PSYCHCONSULT.nwb
convertGraph_v0.8.0.graphml
florentine.nwb
humanprot.nwb
kidscontest.net
netsci06-conference.net
seiyu.graphml.xml
terror.graphml.xml
terror.xgmml.xml
wikipedia-20080103-science.en.nwb

/scientometrics

/scientometrics/bibtex
bibsonomy.bib
barabasi.bib

/scientometrics/csv
barabasi.csv

/scientometrics/endnote
barabasi.enw

/scientometrics/isi
FourNetSciResearchers.isi
ThreeNetSciResearchers.isi
barabasi.isi
savedrecs-barabasi.isi
savedrecs-garfield.isi
savedrecs-vespignani.isi
savedrecs-wasserman.isi
test5papers.isi

/scientometrics/nsf
scientometrics/nsf/scipolicy.nsf

/scientometrics/scopus
barabasi.scopus

/sampledata/scientometrics/properties * Used to extract networks and merge data
bibtexCoAuthorship.properties
endnoteCoAuthorship.properties
isiCoAuthorship.properties
isiCoCitation.properties
isiPaperCitation.properties
mergeBibtexAuthors.properties
mergeEndnoteAuthors.properties
mergeIsiAuthors.properties

```

mergeNsfPis.properties
mergeScopusAuthors.properties
nsfCoPI.properties
scopusCoAuthorship.properties

/sampledata/scripts/GUESS          * Used to do color/size/shape code networks
co-author-nw.py
co-PI-nw.py
paper-citation-nw.py
reference-co-occurrence-nw.py

/socialscience
florentine.nwb
friendster.graphml.xml
friendster.xgmml.xml
terror.graphml.xml
terror.xgmml.xml

```

2 Data Formats

In September 2008, the NWB tool supports loading the following input file formats:

- GraphML (*.xml or *.graphml)
- XGMML (*.xml)
- Pajek .NET (*.net)
- Pajek .Matrix (*.mat)
- NWB (*.nwb)
- TreeML (*.xml)
- Edge list (*.edge)
- CSV (*.csv)
- ISI (*.isi)

and the following network file output formats:

- GraphML (*.xml or *.graphml)
- Pajek .MAT (*.mat)
- Pajek .NET (*.net)
- NWB (*.nwb)
- XGMML (*.xml)

These formats are documented at <https://nwb.slis.indiana.edu/community/?n=DataFormats.HomePage>.

Code Library

The NWB Tool is an ‘empty shell’ filled with plug-ins. Some plug-ins run the core architecture (see OSGi and CShell plug-ins); others convert loaded data into in-memory objects, or into formats the different algorithms can read behind the scenes. Most interesting for users are the algorithm plug-ins that can be divided into algorithms for preprocessing, analysis, modeling, and visualization purposes. Last but not least there are other supporting libraries and entire tools that are plugged-and-played.

1 OSGi Plugins

```

org.eclipse.core.commands_3.3.0.I20070605-0010.jar
org.eclipse.core.contenttype_3.2.100.v20070319.jar
org.eclipse.core.databinding_1.0.0.I20070606-0010.jar
org.eclipse.core.databinding.beans_1.0.0.I20070606-0010.jar
org.eclipse.core.expressions_3.3.0.v20070606-0010.jar
org.eclipse.core.jobs_3.3.0.v20070423.jar
org.eclipse.core.net_1.0.0.I20070531.jar
org.eclipse.core.runtime_3.3.100.v20070530.jar
org.eclipse.core.runtime.compatibility.auth_3.2.100.v20070502.jar
org.eclipse.equinox.app_1.0.1.R33x_v20070828.jar
org.eclipse.equinox.cm_3.2.0.v20070116.jar
org.eclipse.equinox.common_3.3.0.v20070426.jar

```


org.eclipse.equinox.ds_1.0.0.v20070226.jar
org.eclipse.equinox.event_1.0.100.v20070516.jar
org.eclipse.equinox.launcher_1.0.0.v20070606.jar
org.eclipse.equinox.launcher.gtk.linux.x86_1.0.0.v20070606
org.eclipse.equinox.log_1.0.100.v20070226.jar
org.eclipse.equinox.metatype_1.0.0.v20070226.jar
org.eclipse.equinox.preferences_3.2.101.R33x_v20080117.jar
org.eclipse.equinox.registry_3.3.1.R33x_v20070802.jar
org.eclipse.equinox.useradmin_1.0.0.v20070226.jar
org.eclipse.equinox.util_1.0.0.200803111100.jar
org.eclipse.help_3.3.0.v20070524.jar
org.eclipse.jface_3.3.0.I20070606-0010.jar
org.eclipse.jface.databinding_1.1.0.I20070606-0010.jar
org.eclipse.osgi_3.3.0.v20070530.jar
org.eclipse.osgi.services_3.1.200.v20070605.jar
org.eclipse.osgi.util_3.1.200.v20070605.jar
org.eclipse.rcp_3.2.0.v20070612.jar
org.eclipse.swt_3.3.0.v3346.jar
org.eclipse.swt.gtk.linux.x86_3.3.0.v3346.jar
org.eclipse.ui_3.3.0.I20070614-0800.jar
org.eclipse.ui.forms_3.3.0.v20070511.jar
org.eclipse.ui.workbench_3.3.0.I20070608-1100.jar
org.eclipse.update.configurator_3.2.100.v20070615.jar
org.eclipse.update.core_3.2.100.v20070615.jar
org.eclipse.update.core.linux_3.2.0.v20070615.jar
org.eclipse.update.ui_3.2.100.v20070615.jar

2 CShell Plugins

edu.iu.nwb.gui.brand_1.0.0.jar

org.cishell.framework_1.0.0.jar
org.cishell.reference_1.0.0.jar
org.cishell.reference.gui.datamanager_1.0.0.jar
org.cishell.reference.gui.guibuilder.swt_1.0.0.jar
org.cishell.reference.gui.log_1.0.0.jar
org.cishell.reference.gui.menumanager_1.0.0.jar
org.cishell.reference.gui.persistence_1.0.0.jar
org.cishell.reference.gui.prefs.swt_0.0.1.jar
org.cishell.reference.gui.scheduler_1.0.0.jar
org.cishell.reference.gui.workspace_1.0.0.jar
org.cishell.reference.prefs.admin_0.0.1.jar
org.cishell.reference.services_1.0.0.jar
org.cishell.service.autostart_1.0.0.jar
org.cishell.templates_1.0.0.jar
org.cishell.templates.jythonrunner_1.0.0
org.cishell.testing.convertertester.algorithm_0.0.1.jar
org.cishell.testing.convertertester.core.new_0.0.1.jar
org.cishell.tests.ProgressTrackableAlgorithm_1.0.0.jar

3 Converter Plugins

edu.iu.nwb.converter.edgelist_1.0.0.jar
edu.iu.nwb.converter.jungprefuse_1.0.0.jar
edu.iu.nwb.converter.jungprefusebeta_1.0.0.jar
edu.iu.nwb.converter.nwb_1.0.0.jar
edu.iu.nwb.converter.nwbgraphml_1.0.0.jar
edu.iu.nwb.converter.nwbpajeknet_1.0.0.jar
edu.iu.nwb.converter.pajekmat_1.0.0.jar
edu.iu.nwb.converter.pajekmatpajeknet_1.0.0.jar
edu.iu.nwb.converter.pajeknet_0.7.0.jar
edu.iu.nwb.converter.prefusebibtex_0.0.1.jar
edu.iu.nwb.converter.prefusecsv_0.7.0.jar
edu.iu.nwb.converter.prefusegraphml_0.7.0.jar
edu.iu.nwb.converter.prefuseisi_0.7.0.jar
edu.iu.nwb.converter.prefusensf_0.0.1.jar
edu.iu.nwb.converter.prefuserefer_0.0.1.jar
edu.iu.nwb.converter.prefusescopus_0.0.1.jar
edu.iu.nwb.converter.prefuseTreeBetaAlpha_1.0.0.jar
edu.iu.nwb.converter.prefusetreeml_1.0.0.jar
edu.iu.nwb.converter.prefusexgmm1_1.0.0.jar

edu.iu.nwb.converter.tablegraph_1.0.0.jar
edu.iu.nwb.converter.treegraph_1.0.0.jar

4 Algorithm Plugins

4.1 Preprocessing

edu.iu.nwb.composite.extractauthorpapernetwork_0.0.1.jar
edu.iu.nwb.composite.extractcowordfromtable_1.0.0.jar
edu.iu.nwb.composite.extractpapercitationnetwork_0.0.1.jar
edu.iu.nwb.composite.isiloadandclean_0.0.1.jar

edu.iu.nwb.preprocessing.bibcouplingsimilarity_0.9.0.jar
edu.iu.nwb.preprocessing.cocitationsimilarity_1.0.0.jar
edu.iu.nwb.preprocessing.csv_1.0.0.jar
edu.iu.nwb.preprocessing.duplicatenodedetector_1.0.0.jar
edu.iu.nwb.preprocessing.extractnodesandedges_0.0.1.jar
edu.iu.nwb.preprocessing.prefuse.beta.directoryhierarchyreader_1.0.0.jar
edu.iu.nwb.preprocessing.tablefilter_1.0.0.jar
edu.iu.nwb.preprocessing.text.normalization_1.0.0.jar
edu.iu.nwb.preprocessing.timeslice_1.0.0.jar
edu.iu.nwb.preprocessing.trimedges_1.0.0.jar

edu.iu.nwb.shared.isiutil_1.0.0.jar
edu.iu.nwb.tools.mergenodes_1.0.0.jar
edu.iu.nwb.util_1.0.0.jar

4.2 Analysis

edu.iu.nwb.analysis.averageshortestpath_1.0.0.jar
edu.iu.nwb.analysis.burst_1.0.0.jar
edu.iu.nwb.analysis.clustering_1.0.0.jar
edu.iu.nwb.analysis.clustering_vs_k_1.0.0.jar
edu.iu.nwb.analysis.connectedcomponents_1.0.0.jar
edu.iu.nwb.analysis.diameter_1.0.0.jar
edu.iu.nwb.analysis.dichotomize_1.0.0.jar
edu.iu.nwb.analysis.directedknn_1.0.0.jar
edu.iu.nwb.analysis.extractattractors_0.0.1.jar
edu.iu.nwb.analysis.extractcoauthorship_1.0.0.jar
edu.iu.nwb.analysis.extractdirectednetfromtable_1.0.0.jar
edu.iu.nwb.analysis.extractnetfromtable_1.0.0.jar
edu.iu.nwb.analysis.indegreedistribution_1.0.0.jar
edu.iu.nwb.analysis.indegreesequence_1.0.0.jar
edu.iu.nwb.analysis.isidupremover_0.0.1.jar
edu.iu.nwb.analysis.isolates_1.0.0.jar
edu.iu.nwb.analysis.kcore_1.0.0.jar
edu.iu.nwb.analysis.multipartitejoining_1.0.0.jar
edu.iu.nwb.analysis.onepointcorrelations_1.0.0.jar
edu.iu.nwb.analysis.outdegreedistribution_1.0.0.jar
edu.iu.nwb.analysis.outdegreesequence_1.0.0.jar
edu.iu.nwb.analysis.pagerank_1.0.0.jar
edu.iu.nwb.analysis.pathfindergraphnetworkscaling_1.0.0.jar
edu.iu.nwb.analysis.reciprocity.arc_1.0.0.jar
edu.iu.nwb.analysis.reciprocity.dyad_1.0.0.jar
edu.iu.nwb.analysis.sampling_1.0.0.jar
edu.iu.nwb.analysis.selfloops_1.0.0.jar
edu.iu.nwb.analysis.shortestpathdistr_1.0.0.jar
edu.iu.nwb.analysis.sitebetweenness_1.0.0.jar
edu.iu.nwb.analysis.symmetrize_1.0.0.jar
edu.iu.nwb.analysis.totaldegreedistribution_1.0.0.jar
edu.iu.nwb.analysis.totaldegreesequence_1.0.0.jar
edu.iu.nwb.analysis.transitivity.adjacency_1.0.0.jar
edu.iu.nwb.analysis.undirectedknn_1.0.0.jar
edu.iu.nwb.analysis.weakcomponentclustering_1.0.0.jar

edu.iu.iv.attacktolerance_1.0.0.jar
edu.iu.iv.errortolerance_1.0.0.jar
edu.iu.iv.search.p2p.bfs_1.0.0.jar
edu.iu.iv.search.p2p.randomwalk_1.0.0.jar

4.3 Modeling

```
edu.iu.nwb.modeling.barabasiAlbert_1.0.0.jar
edu.iu.nwb.modeling.discretenetworkdynamics_1.0.0.jar
edu.iu.nwb.modeling.erdosrandomgraph_1.0.0.jar
edu.iu.nwb.modeling.smallworld_1.0.0.jar
```

```
edu.iu.iv.modeling.p2p.can_1.0.0.jar
edu.iu.iv.modeling.p2p.chord_0.4.0.jar
edu.iu.iv.modeling.p2p.hypergrid_0.4.0.jar
edu.iu.iv.modeling.p2p.pru_0.4.0.jar
```

4.4 Visualization

```
edu.iu.nwb.visualization.balloongraph_1.0.0.jar
edu.iu.nwb.visualization.drl_1.0.0.jar
edu.iu.nwb.visualization.gnuplot_1.0.0.jar
edu.iu.nwb.visualization.guess_1.0.0.jar
edu.iu.nwb.visualization.jungnetworklayout_1.0.0.jar
edu.iu.nwb.visualization.prefuse.alpha.smallworld_1.0.0.jar
edu.iu.nwb.visualization.prefuse.beta_1.0.0.jar
edu.iu.nwb.visualization.radialgraph_1.0.0.jar
```

4.5 Tools

```
edu.iu.nwb.toolkit.networkanalysis_1.0.0.jar
nwb.visualization.lanet_1.0.0.jar
```

5 Supporting Libraries

```
cern.colt_1.2.0
com.ibm.icu_3.6.1.v20070417.jar
edu.uci.ics.jung_1.7.4
FreeHEP_VectorGraphics_1.0.0
javabib.orig_1.0.0.jar
joda_time_1.0.0
jythonlib_2.2.1
lucene_2.3.2
lucene_snowball_1.0.0
org.apache.commons.collections_3.1.0
org.mediavirus.parvis_0.4.0.jar
org.mediavirus.parvis.sampledata_1.0.0.jar
org.prefuse.lib_20060715.0.0
stax_1.0.0
uk.ac.shef.wit.simmetrics_1.0.0.jar
```

6 Integrated Tools

6.1 GUESS

GUESS is an exploratory data analysis and visualization tool for graphs and networks. The system contains a domain-specific embedded language called Gython (an extension of Python, or more specifically Jython) which supports the operators and syntactic sugar necessary for working on graph structures in an intuitive manner. An interactive interpreter binds the text that you type in the interpreter to the objects being visualized for more useful integration. GUESS also offers a visualization front end that supports the export of static images and dynamic movies. . For more information, see <https://nwb.slis.indiana.edu/community/?n=VisualizeData.GUESS>.

6.2 Gnuplot

Gnuplot is a portable command-line driven interactive data and function plotting utility for UNIX, IBM OS/2, MS Windows, DOS, Macintosh, VMS, Atari and many other platforms. For more information, see <http://www.gnuplot.info/>.

General Tutorial

1 Load, View, and Save Data

In the NWB tool, use 'File > Load File' to load one of the provided in sample datasets in '*yournwbdirectory*/sampledata' or any dataset of your own choosing, see section 2 on supported Data Formats and Figure 1.

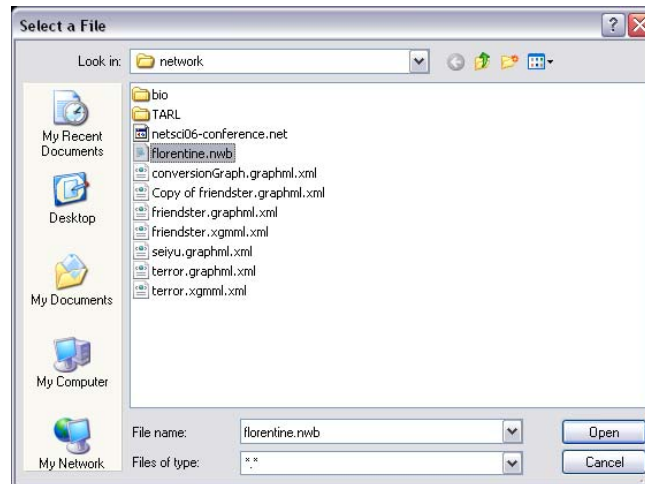


Figure 1: Select a file.

The result will be listed in the Data Manager window, see Figure 2.

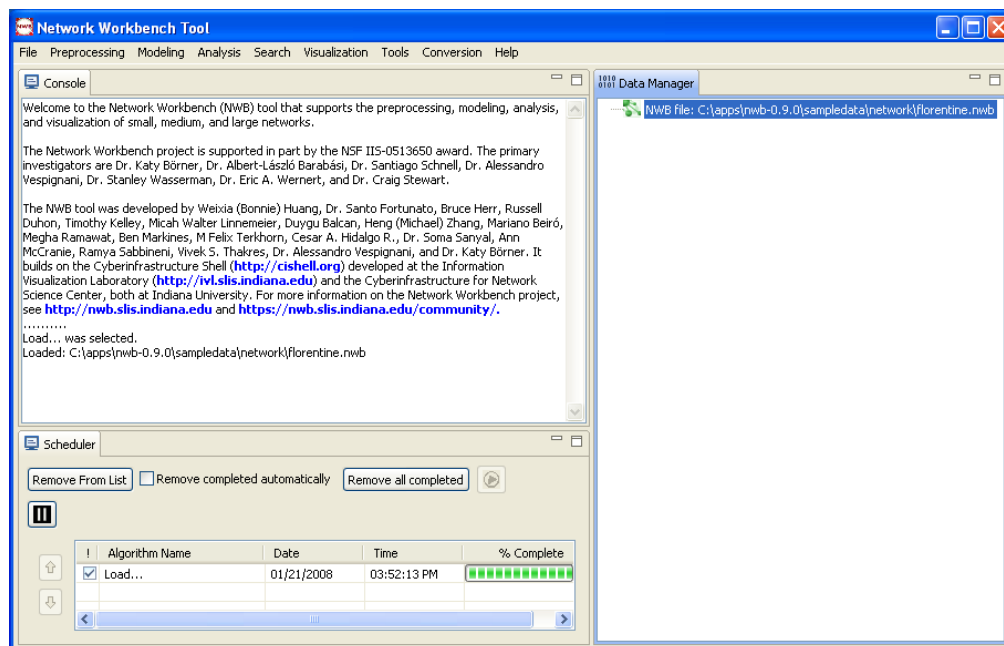


Figure2: Display of loaded network in the Data Manager window

Any file listed in the Data Manager can be saved, viewed, renamed, or discarded by right-clicking it and selecting the appropriate menu options. If 'File → View With...' was selected, the user can select among different application viewers, see Figure 7. Choosing 'Microsoft Office Excel...' for a tabular type file will open MS Excel with the table loaded.

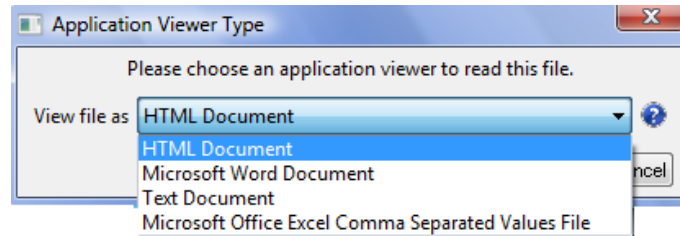


Figure 3: Select Application Viewer for selected file in Data Manager

The NWB tool can save a network using '*File* → *Save...*' which brings up the Output Data Type window, see Figure 3. Note that some data conversions are lossy, i.e., not all data is preserved, see also section on Sample Data and Supported Data Formats.

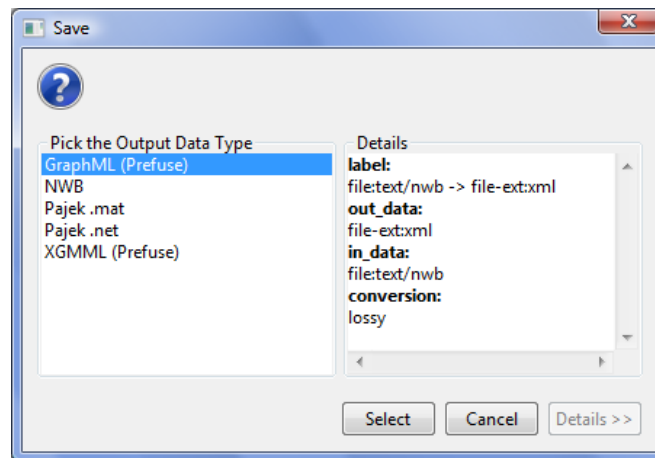
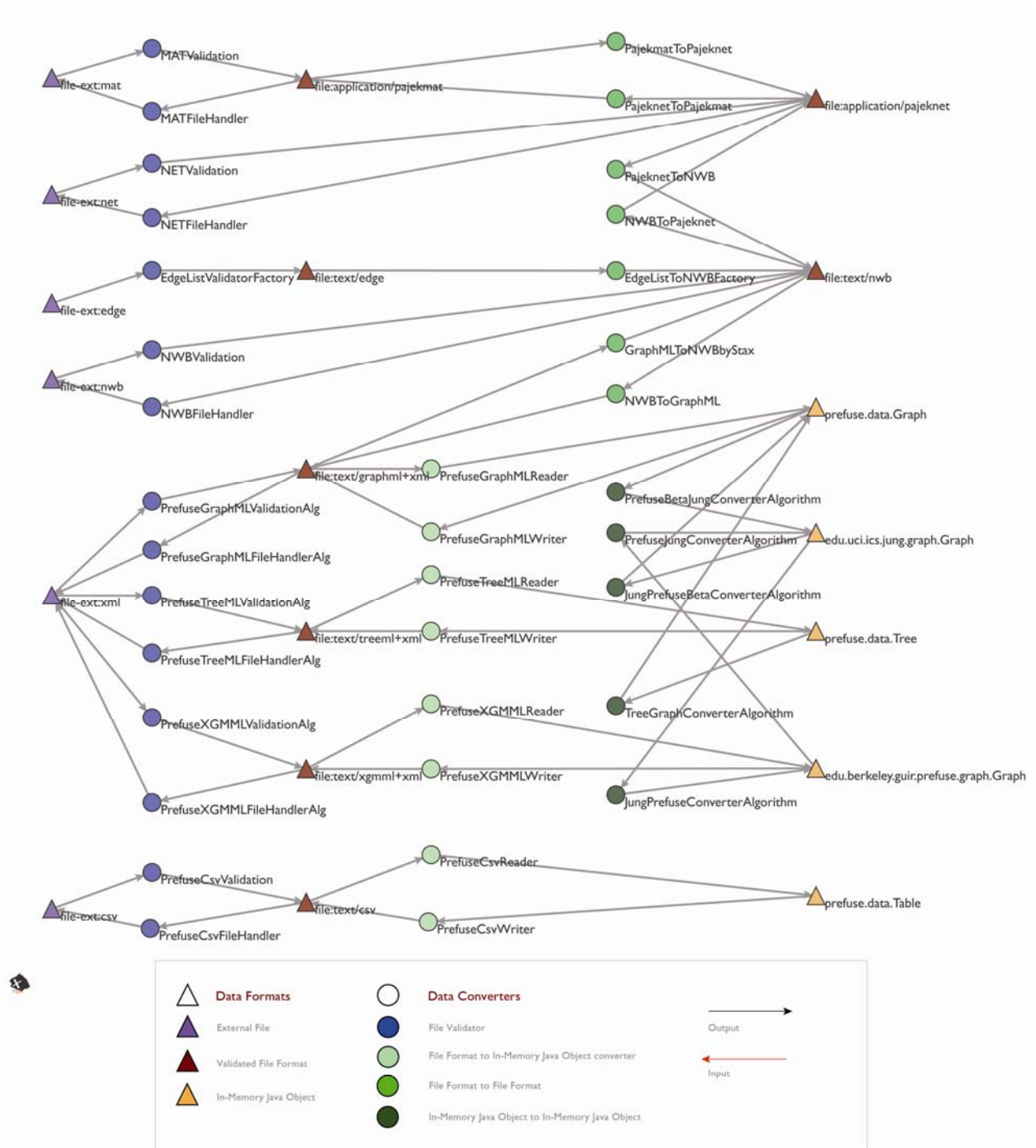


Figure 4: Output Data Type window

2 Data Conversion Service

More detailed explanation will be provided shortly.



CiShell & OSGI

<http://www.cishell.org/> <http://www.osgi.org/>

Figure 1: Converter graph

3 Compute Basic Network Statistics

It is often advantageous to know for a network

- Whether it is directed or undirected
- Number of nodes
- Number of isolated nodes
- A list of node attributes
- Number of edges
- Whether the network has self loops, if so, lists all self loops
- Whether the network has parallel edges, if so, lists all parallel edges
- A list of edge attributes
- Average degree
- Whether the graph is weakly connected
- Number of weakly connected components
- Number of nodes in the largest connected component
- Strong connectedness for directed networks
- Graph density

In the NWB tool, use ‘*Analysis > Network Analysis Toolkit (NAT)*’ to get basic properties, e.g., for the network of Florentine families available in ‘**yournwbdirectory*/sampledata/networks/florentine.nwb*’. *The result for this dataset is:*

```
This graph claims to be undirected.

Nodes: 16
Isolated nodes: 1
Node attributes present: label, wealth, totalties, priorates

Edges: 27
No self loops were discovered.
No parallel edges were discovered.
Edge attributes:
  Nonnumeric attributes:
      Example value
      marriag...    T
      busines...    F

  Did not detect any numeric attributes
  This network does not seem to be a valued network.

Average degree: 3.375
This graph is not weakly connected.
There are 2 weakly connected components. (1 isolates)
The largest connected component consists of 15 nodes.
Did not calculate strong connectedness because this graph was not directed.

Density (disregarding weights): 0.225
```

4 Tree Visualizations

Many network datasets come in tree format. Examples include family trees, organizational charts, classification hierarchies, and directory structures.

Mathematically, a tree graph is a set of straight line segments (edges) connected at their ends containing no closed loops (cycles). A tree graphs is also called a simple, undirected, connected, acyclic graph (or, equivalently, a connected forest). A tree with n nodes has $n-1$ graph edges. All trees are bipartite graphs.

Many trees have a root node and are called rooted trees. Trees without a root node are called free trees. Subsequently, we will only consider rooted trees. In rooted trees, all nodes except the root node have exactly one

parent node. Nodes which have no children are called leaf nodes. All other nodes are referred to as intermediate nodes.

This section introduces different algorithms to visualize tree data using tree views, tree maps, radial tree/graph, and balloon graph layouts.

4.1 Tree View Visualization

The tree view layout places the root node on the left of the canvas. First level nodes are placed on an imaginary vertical line to the right of it. Second level nodes are placed on an imaginary vertical line left of the first level nodes, etc.

In the NWB tool, select a tree dataset, e.g., generated using the Directory Hierarchy Reader, in the Data Manager window, then use '*Visualization → Tree View (prefuse beta)*' and a window similar to Figure 6 will appear displaying the Tree View visualization. If you press and hold the right or middle button of the mouse while moving it back and forth, you can zoom in and out on the Tree. By clicking a folder name such as "sampledata," all sub-folders and files inside the sampledata folder will display. Use the search box in the bottom right corner to enter a search terms and matching files will highlight.

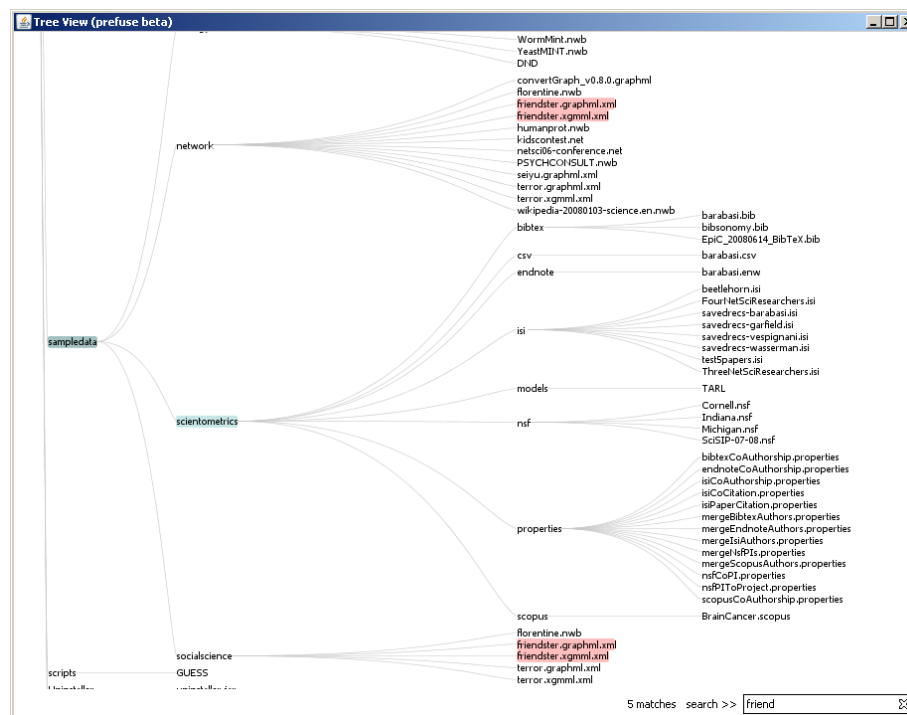


Figure 1: Tree View visualization with /sampledata directory expanded and florentine.nwb file highlighted

4.2 Tree Map Visualization

Tracing its ancestry to Venn diagrams, the Treemap algorithm was developed by Ben Shneiderman's group at the HCI Lab at the University of Maryland. It uses a space filling technique to map a tree structure (e.g., file directory) into nested rectangles with each rectangle representing a node.

A rectangular area is first allocated to hold the representation of the tree, and this area is then subdivided into a set of rectangles that represent the top level of the tree. This process continues recursively on the resulting rectangles to represent each lower level of the tree, with each level alternating between vertical and horizontal subdivisions.

The parent-child relationship is indicated by enclosing the child-rectangle by its parent-rectangle. That is, all descendents of a node are displayed as rectangles inside its rectangle. Associated with each node is a numeric value (e.g. size of a directory) and the size of a node's rectangle is proportional to its value. Shneiderman's 'Treemaps for space-constrained visualization of hierarchies' webpage (<http://www.cs.umd.edu/hcil/treemaps/>) provides the full story.

In the NWB tool, select a tree dataset, e.g., generated using the Directory Hierarchy Reader, in the Data Manager window, then run '*Visualization → Tree Map (prefuse beta)*'. A window similar to Figure 2 will appear displaying the Tree Map visualization. Use the search box in the bottom right corner to enter a search terms and matching files will highlight.



Figure 2: Tree Map visualization of complete /nwb directory hierarchy

4.3 Balloon Graph Visualization

A balloon graph places the focus node in the middle of the canvas and all its children in a circle around it. Children of children are again places in a circle around their parents, etc.

In the NWB tool, select a tree dataset, e.g., generated using the Directory Hierarchy Reader, and run '*Visualization → Balloon Graph (prefuse alpha)*'. A window similar to Figure 3 will appear displaying the Balloon Graph visualization. Double-click on a node to focus on it and observe the change of the layout. Like in all other Prefuse layouts, hold down left mouse button to pan and right button to pan.

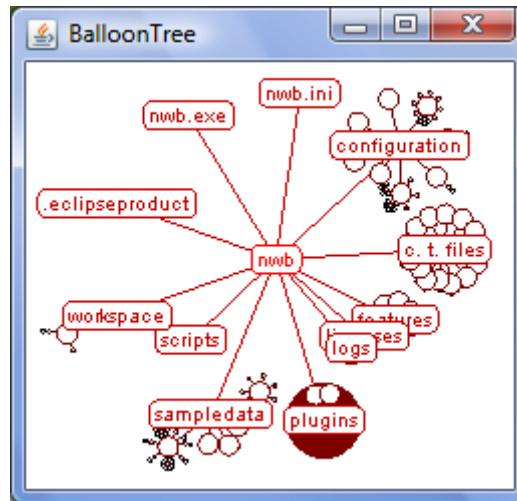


Figure 3: Balloon Graph Visualization of complete /nwb directory hierarchy

4.4 Radial Tree Visualization

Radial trees layout uses a focus + context (fisheye) technique for visualizing and manipulating very large trees. The focused node is placed in the center of the display and all other nodes are rendered on appropriate circular levels around that selected node. The further away a node is from the center, the smaller it is rendered. This way, potentially very large rooted or unrooted trees such controlled vocabularies, taxonomies, or classification hierarchies can be displayed. Users can focus on particular parts of those trees without losing context.

In the NWB tool, select a tree dataset, e.g., generated using the Directory Hierarchy Reader, first three levels, directories only. Run ‘*Visualization > Radial Tree/Graph (prefuse alpha)*’. A window similar to Figure 4 will appear displaying the Radial Tree/Graph visualization. Double-click on a node to focus on it and observe the change of the layout. Hovering over a node, e.g., the /nwb root directory, colors it red and all its neighbors blue. As in all other Prefuse layouts, hold down left mouse button to pan and right button to pan.

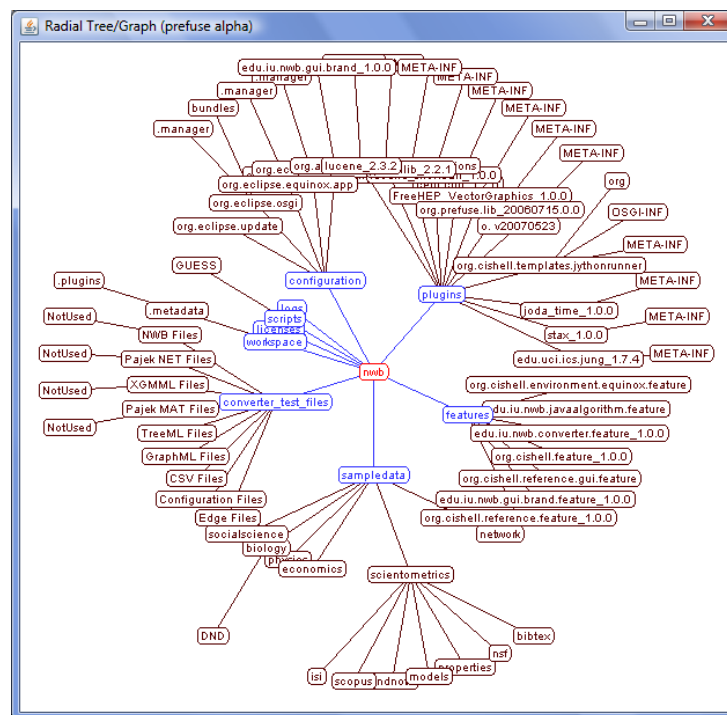


Figure 4: Radial Tree/Graph visualization of first three levels of /nwb directories

4.5 Radial Tree/Graph with Annotation

Highlight the same tree dataset and select '*Visualization → Radial Tree/Graph (prefuse beta)*' to set data mapping parameters such as node size, node color, node shape, ring color, edge size, and edge color. A legend will be generated automatically.

5 Graph Visualizations

Most visualization plug-ins provided in the NWB Tool are designed to layout graphs. Examples are the:

- JUNG based Circular layout, Kamada-Kawai, Fruchterman-Rheingold, and interactive Spring layout;
- prefuse based Specified, Radial Tree/Graph (with or without annotation), Force Directed with Annotation, and Fruchterman Rheingold with Annotation, and Small World layouts.
- GUESS tool supporting more customized visualizations and diverse output formats.
- DrL for visualizing very large networks – up to 1 million nodes.
- LaNet

5.1 JUNG-based Circular, Kamada-Kawai, Fruchterman-Rheingold, and Spring Layouts

Visualizations of the '**yournwbdirectory*/sampledata/networks/florentine.nwb*' network using Circular, Kamada-Kawai, Fruchterman-Rheingold, and Spring Layouts are given in Figure 5.

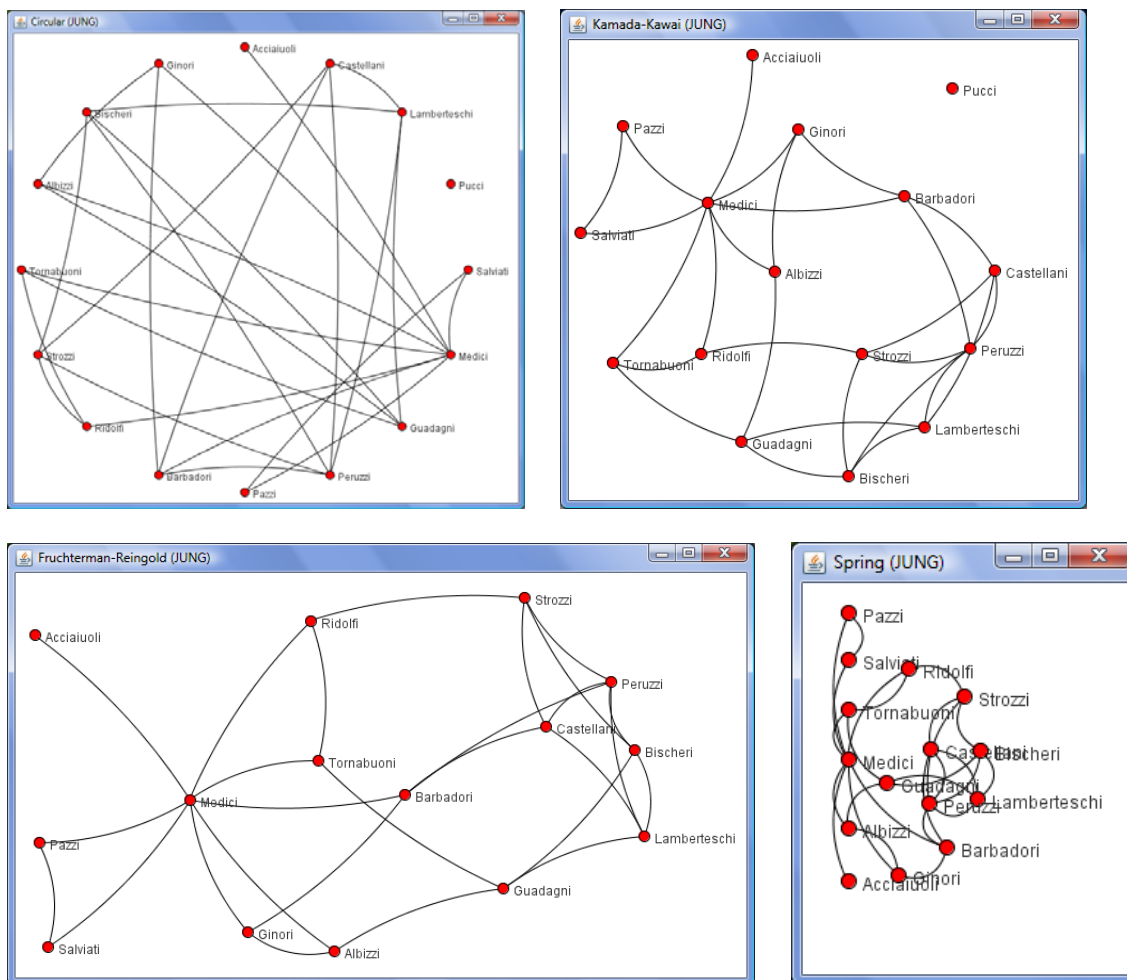


Figure 5: (Partial) Circular, Kamada-Kawai, Fruchterman-Rheingold, and Spring JUNG layouts

5.2 Prefuse-based Specified, Radial Tree/Graph, Force Directed, and Fruchterman-Rheingold, and Small World Layouts

Specified layout requires pre-computed x, y values for each node. Node positions can be computed, e.g., using ‘Visualization > DrL’

Visualizations of the ‘*yournwbdirectory*/sampledata/networks/florentine.nwb’ network using Radial Tree/Graph, Force Directed with Annotation, and Fruchterman Rheingold with Annotation, are given in Figure 6. Note that algorithms that do not read nwb format, e.g., Ballon Graph are grayed out and not selectable.

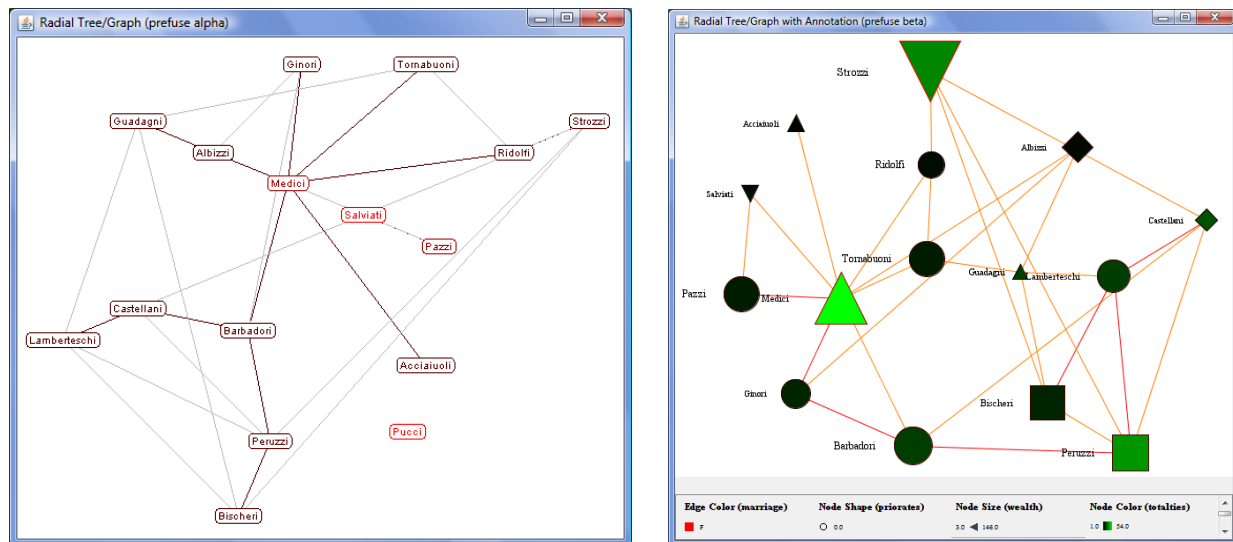


Figure 6: Radial Tree/Graph and Fruchterman-Rheingold with Annotation Prefuse layouts

The Fruchterman-Rheingold and the Force Directed with Annotation layout were run using the parameter values shown in Figure 7, left. The menu to the right of the Force Directed layout lets one increase the DefaultSpringLength to spread out nodes.

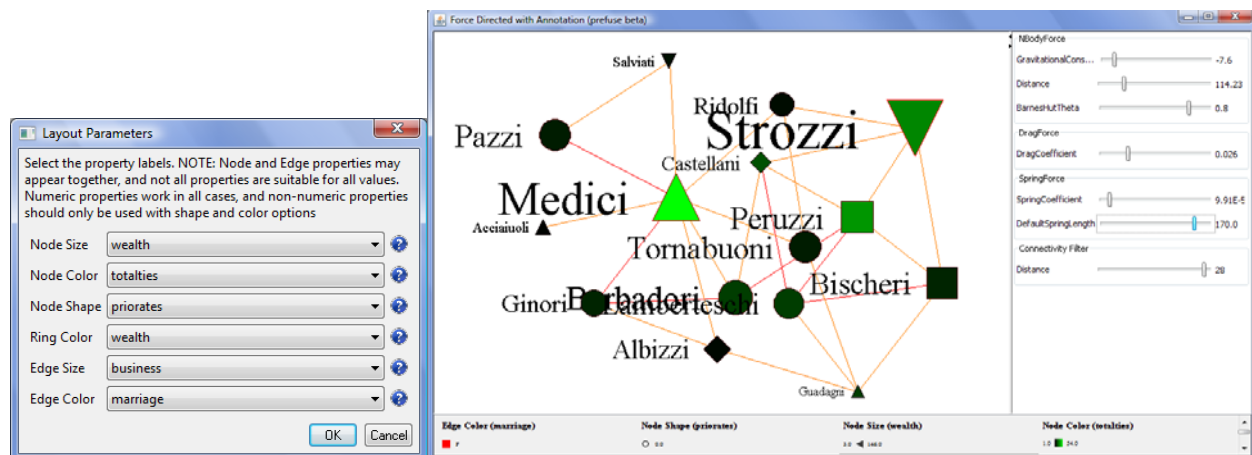


Figure 7: Force Directed with Annotation Prefuse layout

5.3 GUESS Visualizations

Here we use the sample dataset of ‘*yournwbdirectory*/sampledata/networks/florentine.nwb’ to demo how to visualize a network in GUESS. Feel free to compute an additional node attribute, “Betweenness Centrality” before

you visualize the network. Simply run ‘Analysis -> Unweighted & Undirected -> Node Betweenness Centrality’ with default parameters.

Select the network to be visualized and run ‘Visualization > GUESS’ to open GUESS with the file loaded. It might take some time for the network to load. The initial layout will be random. Wait until the random layout is completed and the network is centered.

GUESS has three windows called

1. Information window to examine node and edge attributes, see Figure 8, left
2. Visualization window to view and manipulate network, see Figure 8, right.
3. Interpreter/Graph Modifier Window to analyze/change network properties, below the Visualization window in Figure 8.

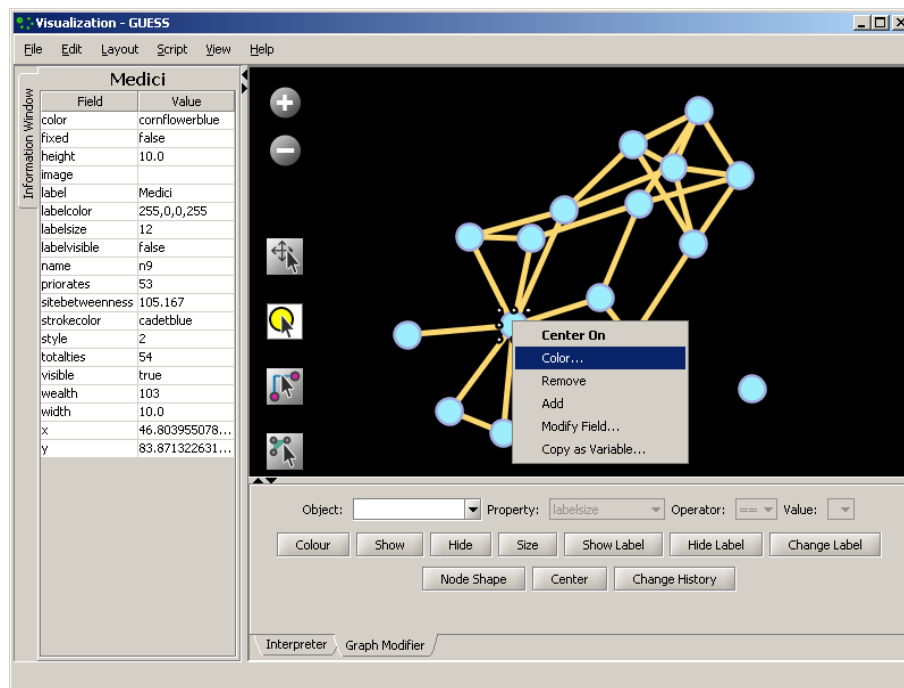


Figure 8: GUESS Information window, Visualization window and Interpreter/Graph Modifier window

5.3.1 Network Layout and Interaction


GUESS provides different layout algorithms under menu item ‘Layout’. Apply ‘Layout -> GEM’ to the Florentine network. Use ‘Layout -> Bin Pack’ to compact and center the network layout.

Using the mouse pointer, hover over a node or edge to see its properties in the Information window. Right click on a node to ‘center on’, ‘color’, ‘remove’, ‘Modify Field ...’ a node, see Figure 8.

Interact with the visualization as follows:

Pan – simply ‘grab’ the background by holding down the left mouse button and move it using the mouse.

Zoom – Using the scroll wheel on the mouse OR press the “+” and “-” buttons in the upper-left hand corner OR right-click and move the mouse left or right. Center graph by selecting ‘View -> Center’.

Select/move single nodes – Click  to select/move single nodes. Hold down ‘Shift’ to select multiple. Right click to modify Color, etc.

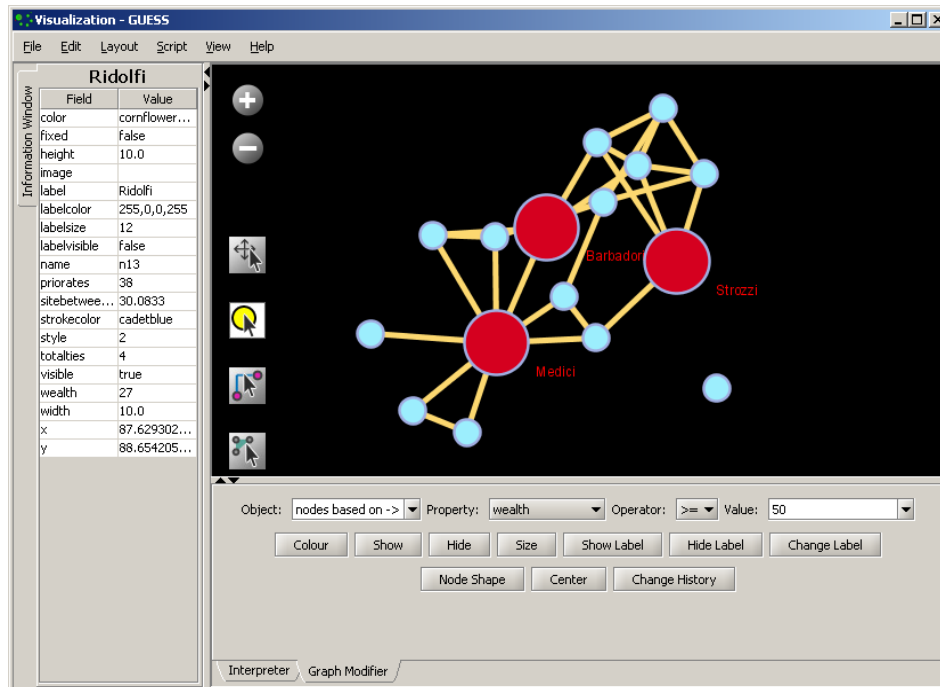


Figure 9: GUESS Graph Modifier

Use the Graph Modifier to change node attributes, e.g.,

- Select “all nodes” in the Object drop-down menu and click ‘Show Label’ button.
- Select “nodes based on ->” in the Object drop-down menu, then select “wealth” from the Property drop-down menu, “>=” from the Operator drop-down menu, and finally type “50” into the Value box. Then select a color/size/shape code, see Figure 9.

5.3.2 Interpreter

Use Jython, a combination of Java and Python, to write code that can be interpreted. Here we list some GUESS commands which can be used to modify the layout.

Coloring ALL Nodes *uniformly*

```
g.nodes.color =red           // circle filling
g.nodes.strokecolor =red     // circle ring
g.nodes.labelcolor =red      // circle label
colorize(numberofworks,gray,black)
for n in g.nodes:
    n.strokecolor = n.color
```

Size Code

```
g.nodes.size = 30
resizeLinear(numberofworks, .25, 8)
```

Label

```
for i in range(0, 50):           # make labels of most productive authors visible
    nodesbynumworks[i].labelvisible = true
```

Print

```
for i in range(0, 10):
    print str(nodesbydegree[i].label) + ": " + str(nodesbydegree[i].indegree)
```

Edges

```
g.edges.width=10
g.edges.color=gray
```

Figure 15 shows the network after coloring and resizing the nodes based on their betweenness using:

```
colorize(wealth, white, red)
resizeLinear(sitebetweenness, 5, 25)
```

Read <https://nwb.slis.indiana.edu/community/?n=VisualizeData.GUESS> on more information on how to use the interpreter.

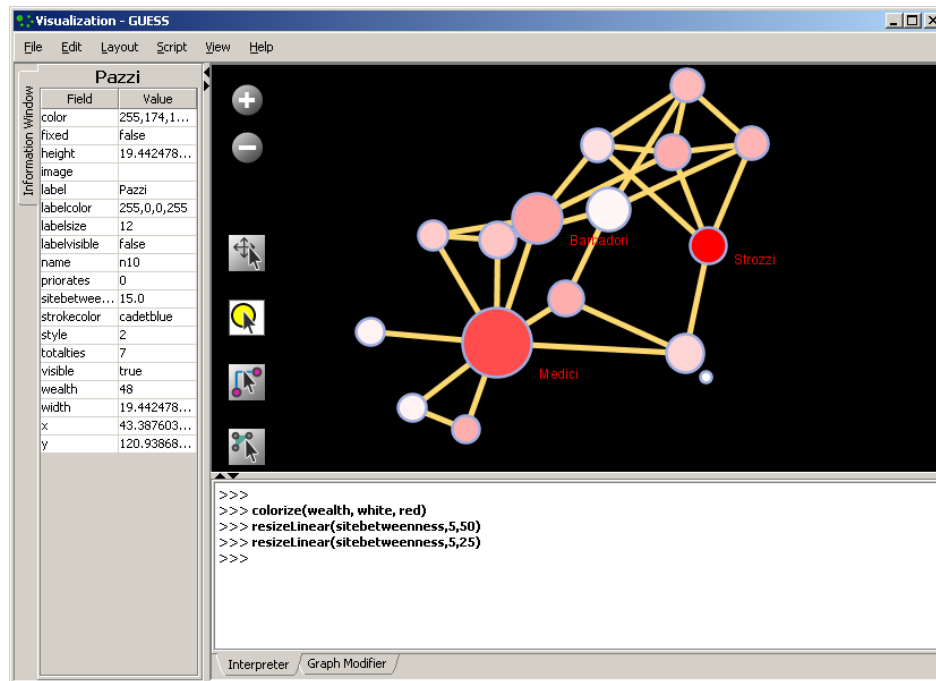


Figure 10: GUESS Interpreter

5.4 DrL Large Networks Layout

See <https://nwb.slis.indiana.edu/community/?n=VisualizeData.DrL>

5.5 LaNet

See <https://nwb.slis.indiana.edu/community/?n=VisualizeData.K-CoreDecomposition>

6 Saving Visualizations for Publication

Use 'File> Export Image' to export the current view or the complete network in diverse file formats such as jpg, png, raw, pdf, gif, etc.

Domain Specific: Information Science

1 Read and Display a File Hierarchy

It is interesting to see the structure of file directory hierarchies that can be thought of as a tree with a specific folder at its root and its subfolders and the files within them as its branches.

In the NWB tool, use 'File > Read Directory Hierarchy' to parse a file directory hierarchy recursively using parameters:

Root directory	Directory from where to start crawling subfolders and files
Levels to recurse	Number of levels of depth to recurse hierarchy
Recurse the entire tree	Check to resruece entire hierarchy
Read directories only	Check to disregard files

Change the default input by checking "Recurse the entire tree," and uncheck "Read directories only" (skips files), shown in Figure 1. After clicking the OK button a 'Directory Tree – Prefuse (Beta) Graph' shows up in the Data

Manager window. Select this dataset before selecting any other analysis or visualization, see General Tutorial, Section 4, for different tree visualizations.

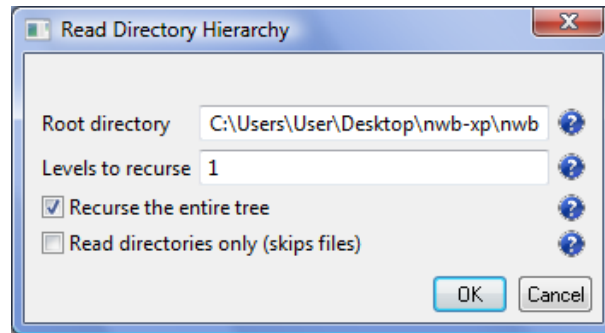


Figure 1: Directory Hierarchy Reader parameter settings window

2 Error and Attack Tolerance of Networks

Please see <http://iv.slis.indiana.edu/lm/lm-errorattack.html>

3 Studying Peer-to-Peer Networks

Please see <http://iv.slis.indiana.edu/lm/lm-p2p-search.html>

Domain Specific: Social Science

Tutorial originally prepared for Sunbelt 2008 by Ann McCranie, Department of Sociology, Indiana University, Bloomington, amccrani@indiana.edu.

For this example, we will use PSYCHCONSULT, an extract from the Staff Study of the Indianapolis Network Mental Health Study. This is a file in the Network Workbench (*.nwb) format, a basic edge-list format that can include node and edge attribute information in a text file. It is a directed (asymmetric) unvalued (unweighed) network that represents the consultation choices among the staff that work in a psychiatric hospital.

1 Load Data

Load the PSYCHCONSULT data after launching the NWB Tool with *File--> Load*.

Choose the PSYCHCONSULT data located in the *Sampledata/Networks* folder. This folder will be located in your NWB Installation Directory.

Once you have loaded this network, you will see it appear in the right-hand “Data Manager” window. You may right-click on this network and choose “View” to look at the contents. You may also open this file separately in a text editor to explore it or make changes. Please note that as you work, new files will be created in the Data Manager window. You may choose to save these files in various formats, and you will need to make sure that you have highlighted the network file that you wish to work in.

2 Basic Network Properties

As a matter of practice, you may want to learn a little about your network and confirm that it was read correctly into NWB. The Graph and Network Analysis Toolkit provides a quick overview of your network: *Analysis--> Network Analysis Toolkit*.

If you run this on the PSYCHCONSULT network, you will find that you have a directed network with 113 nodes and no isolated nodes. There are two node attributes present: the node label (which is, in this case, the job title of all of the employees) and the area (in this network, the unit in which the employee generally worked). You can also see

that you have 861 edges, no self-loops or parallel edges, and no edge attributes. A common edge attribute is weight (value), but this network is unweighted.

The network is weakly connected - each node is connected to another node in the main component with no isolates. It is not strongly connected, however, as some nodes are unreachable (they send, but do not receive ties). You will also see the network's density reported.

```
Network Analysis Toolkit (NAT) was selected.
Implementer(s): Timothy Kelley
Integrator(s): Timothy Kelley
Reference: Robert Sedgewick. Algorithms in Java, Third Edition, Part 5 - Graph
Algorithms. Addison-Wesley, 2002. ISBN 0-201-31663-3. Section 19.8, pp.205
Documentation:
https://nwb.slis.indiana.edu/community/?n=AnalyzeData.NetworkAnalysisToolkit
This graph claims to be directed.

Nodes: 113
Isolated nodes: 0
Node attributes present: label, area

Edges: 861
No self loops were discovered.
No parallel edges were discovered.
Edge attributes:
    Did not detect any nonnumeric attributes
    Numeric attributes:
        min    max    mean
weight      1      1      1

    This network seems to be valued.

Average total degree: 15.238938053097344
Average in degree: 7.619469026548669
Average out degree: 7.619469026548671
This graph is weakly connected.
There are 1 weakly connected components. (0 isolates)
The largest connected component consists of 113 nodes.
This graph is not strongly connected.
There are 13 strongly connected components.
The largest strongly connected component consists of 101 nodes.

Density (disregarding weights): 0.06803
Additional Densities by Numeric Attribute
densities (weighted against standard max)
weight: 0.06803
densities (weighted against observed max)
weight: 0.06803
```

If you should find isolates or self-loops in your data, they could pose problems for several algorithms that are currently implemented. NWB offers options for dealing with these issues: *Preprocessing --> Remove Self-Loops* and *Preprocessing--> Delete Isolates*.

These options will create a new network file in the Data Manager window. You can then select this network and save it with a new name.

3 Network Analysis

NWB implements a few basic algorithms that you can use with an unweighted and directed network like PSYCHCONSULT. Make sure your network is highlighted in the Data Manager window.

- In-degree and out-degree centrality can be calculated with *Analysis --> Unweighted & Directed --> Node Indegree*.

Note that this will actually create two files: a text file with a sequence of the in-degree centrality of the nodes and a new network file that has appended the in-degree as an integer attribute. Choose this network file, apply the *Node Outdegree* centrality algorithm from *Analysis--> Unweighted & Directed-->Node Outdegree* and you can create a new network with both measures as attributes.

- Reciprocity can be calculated with *Analysis --> Unweighted & Directed --> Dyad Reciprocity*. This will give you a network-level reciprocity measure. In this network, 17.5 percent of dyads are reciprocal.

4 Visualization

There are several visualization options under development in the NWB tool. To replicate the one shown at this poster presentation, you will need to use the GUESS package, which is an implementation of the open-source program developed by Eytan Adar. To learn more about this package, visit <http://graphexploration.cond.org/index.html> and be sure to look at the manual and wiki site.

With the original PSYCHCONSULT file you loaded into NWB highlighted (should be the top of the Data Manager) choose *Visualization --> GUESS*. For this relatively small network, the loading time will be a few seconds. You will see a second window appear with a network.

In this new window, choose *Layout --> Kamada-Kawai*.

You may choose to repeat this layout multiple times. The basic shape and layout of the network will remain the same, but you will notice the orientation changing. You can also drag and enlarge the window that the network is in. To see specific information about nodes or edges, choose *Display --> Information Window*.

As you pass your mouse over the edges and nodes in the network, you will see specific information about these nodes. In order to zoom into the network, right-click on the black space around the network and drag to the right. Drag left in order to zoom out. Dragging with the left mouse button will move the entire network. If you “lose” the network, choose *Display --> Center*.

Currently there are only a few menu-based interfaces for the rich options of GUESS. For instance, you can change the background color under *Display*. To take advantage of some of the other options of GUESS, you can actually type commands into the console (located in the bottom at >>>) or you can create a script file - a simple text file with the extension *.py

Either type the following commands into the console or create a .py file in a text editor. To run the script file, chose *File--> Run Script* and choose your newly created script file.

```
g.nodes.labelvisible=true
for node in g.nodes:
    node.x=node.x*10
    node.y=node.y*10
    colorize(label)
    (label=="psychiatrist").color=red
    (label=="med dir, inpt. unit").color=red
    (label=="nurse").color=blue
    clusts = groupBy(area)
    for c in clusts: createConvexHull(c,randomColor(50))
```

After you have entered these commands or run this script file, your network might disappear off-screen. Choose *Display--> Center* to return to the network.

These commands make the labels visible, change the sizes of the nodes and edges, colors the labels (the same color is assigned to nodes that have the same label of job type, thus psychiatrists and the medical director are red, while

nurses are colored blue). The script also creates “hulls,” or demarcations of areas of the network based on the attribute of area. You can experiment with the random colors assigned to the hulls by rerunning this script or line. To save your visualization, choose *File--> Export Image*.

Domain Specific: Scientometrics

1 Introduction

1.1 Available Datasets and Algorithms

Scientometrics specific sample datasets can be found in

```
/nwb/sampleddata/scientometrics/bibtex - personal bibliography files
/endnote - personal bibliography files
/isi - datasets downloaded from ISI/Thomson Scientific
/models - parameter and data files needed for TARL model
/nsf - datasets downloaded from the National Science Foundation
/properties - parameter files needed for network extraction
/scopus - datasets downloaded from Scopus
```

Relevant algorithm plugins are stored in the general

```
/nwb/plugins
```

Directory, see section Code Library. Each algorithm has the package name that best fits its function, e.g., preprocessing, analysis, visualization, etc. An example is

```
'edu.iu.nwb.preprocessing.cocitationsimilarity_1.0.0'.
```

In the NWB Tool, the scientometrics specific algorithms have been grouped under a special ‘Scientometrics’ menu item to ease usage, see Figure 1.

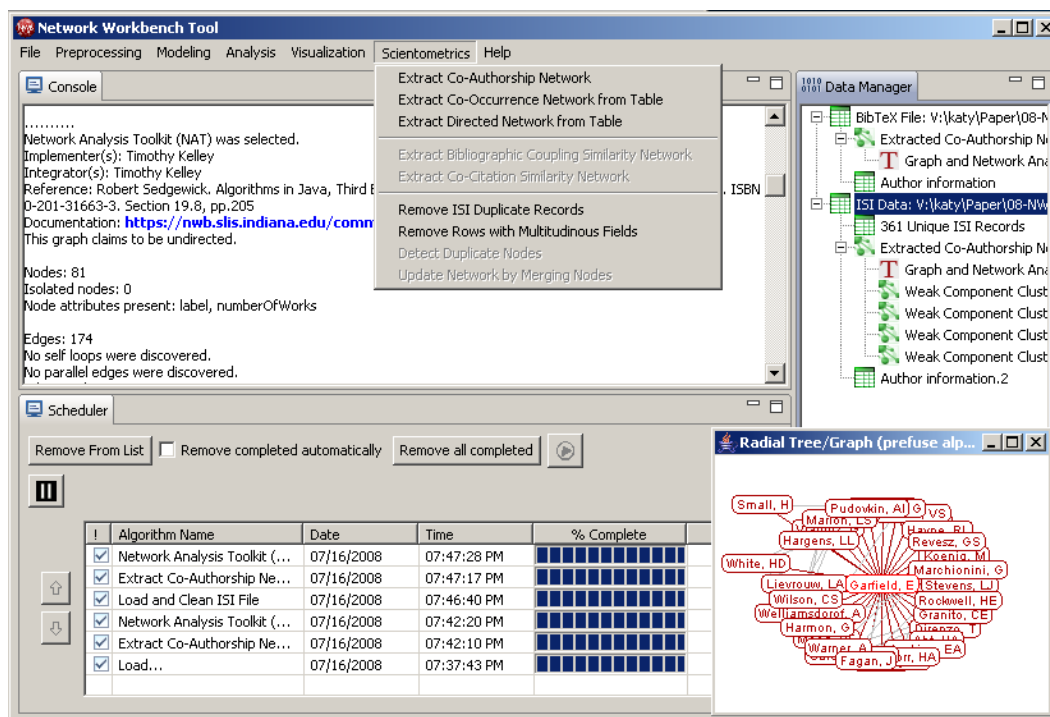


Figure 1: Scientometrics menu in the Network Workbench Tool

1.2 General Workflow

The general workflows of scientometric studies and specifically the mapping of science were detailed in (Börner, Chen, & Boyack, 2003). The general workflow of a scientometric study is given in Table 1. Major steps are (1) data extraction, (2) defining the unit of analysis, (3) selection of measures, (4) calculation of similarity between units, (5) ordination, or the assignment of coordinates to each unit, and (6) use of the resulting visualization for analysis and interpretation.

Table 1: General steps involved in a scientometric study, adopted from (Börner et al., 2003).

(1) Data Extraction	(2) Unit of Analysis	(3) Measures	Layout (often one code does both similarity and ordination steps)		(6) Display
			(4) Similarity	(5) Ordination	
Searches	Common Choices	Counts/ Frequencies	Scalar (unit by unit matrix)	Dimensionality Reduction	Interaction
<i>ISI</i>	<i>Paper</i>	<i>Attributes</i>	<i>Direct linkage</i>	<i>Eigenvector/Eigenvalue solutions</i>	<i>Browse</i>
<i>Scopus</i>	<i>Journal</i>	<i>(e.g. terms)</i>	<i>- Paper-citation</i>	<i>- Author-paper</i>	<i>Pan</i>
<i>Google Scholar</i>	<i>Institutional</i>	<i>Author citations</i>	<i>Co-occurrence</i>	<i>Factor Analysis (FA) and Principal Components Analysis (PCA)</i>	<i>Zoom</i>
<i>Medline</i>	<i>- Author</i>	<i>Co-citations</i>	<i>- Co-author</i>	<i>Multi-dimensional scaling (MDS)</i>	<i>Filter</i>
<i>Patents</i>	<i>- Lab/Center</i>	<i>By year</i>	<i>- Bibliographic coupling</i>	<i>Pathfinder Networks (PFNet)</i>	<i>Query</i>
<i>Grants</i>	<i>- Dep./School</i>		<i>- Co-word/co-term</i>	<i>Self-organizing maps (SOM)</i>	<i>Detail on demand</i>
	<i>- Institution</i>		<i>- Co-classification</i>	<i>Topics Model</i>	
Broadening		Thresholds	<i>Co-citation</i>		Analysis & Interpretation
<i>By citation</i>	<i>Geolocation</i>	<i>By counts</i>	<i>- Author co-citation (ACA)</i>		
<i>By terms</i>	<i>- County</i>		<i>- Document co-citation (DCA)</i>		
	<i>- State</i>		<i>Combined linkage</i>		
	<i>- Country</i>			Cluster Analysis	
	<i>- Continent</i>			Scalar	
	<i>Topical</i>		Vector (unit by attribute matrix)	<i>Triangulation</i>	
	<i>- Term</i>		<i>Vector space model (words/terms)</i>	<i>Force-directed placement (FDP)</i>	
	<i>- Keyword or ontologies, classifications, taxonomies, etc.</i>		<i>Latent Semantic Analysis (words/terms) including Singular Value Decomposition (SVD)</i>		
			Correlation (if desired)		
			<i>Pearson's R on any of above</i>		

1.2.1 Data Extraction

Data are either compiled by hand or downloaded in bulk from major databases. For details see section 1.

1.2.2 Units of Analysis

Major units of science studied in scientometrics are authors, papers, and journals as well as other institutional, geospatial, and topical units. Note that a laboratory and/or center can be interdisciplinary. A department/school is typically discipline specific.

Authors have an address with information on affiliation and geo-location. Most author consumed/produced records have a publication date, a publication type (e.g., journal paper, book, patents, grant, etc.), topics (e.g., keywords or classifications assigned by authors and/or publishers). Because authors and records are associated, the geo-location(s) and affiliation(s) of an author can be linked to the authors' papers. Similarly, the publication date, publication type and topic(s) can be associated with a paper's author(s).

1.2.3 Selection of Measures

Statistics such as the number of papers, grants, co-authorships, citation (over time) per author; bursts of activity (number of citations/patents/collaborators/funding, etc.); or changes of topics and geo-locations for authors and their institutions over time can be computed. Derived networks are examined to count the number of papers or co-authors per author, the number of citations per paper or journal, etc. but also to determine the strength or success of co-author/inventor/investigator relations, etc. The geospatial and topic distribution of funding input & research output; the structure and evolution of research topics; evolving research areas (e.g., based on young yet highly cited papers); or the diffusion of information, people, or money over geospatial and topic space can be studied.

1.2.4 Ordination

Ordination techniques such as triangulation or force directed placement take a set of documents, their similarities/distances, and parameters and generate a typically 2-dimensional layout that places similar documents closer together and dissimilar ones further apart.

Note that the table covers measures and algorithms commonly used in bibliometrics/scientometrics research yet few of the new temporal, geospatial, topical, and network based approaches in existence today.

1.2.5 Display

Analysis results can be communicated via text, tables, charts, maps that are printed on paper or explored online, to name just a few options.

Steps 3-5 will be discussed separately for

- Temporal analyses in section 2,
- Geospatial analyses in section 3,
- Topical analyses in section 4, and
- Network analyses in section 5.

2 Bibliographic Data Acquisition and Preparation

The NWB Tool reads publication data from Thomson Scientific/ISI or Scopus. Google Scholar data can be acquired using 3rd party tools such as *Publish or Perish* (Harzing, 2008) that retrieves papers from Google scholar for a specific data and supports the export into BibTex (bib), CSV (txt), or EndNote (enw) that can be read by NWB Tool. Personal references collected via reference management software such as EndNote (Thomson-Reuters, 2008a), Reference Manager (The-Thomson-Corporation, 2008), or the Bibtex format (Feder, 2006) can also be read, as can funding data downloaded from the National Science Foundation and other scholarly data available in plain comma-separated value files. Examples are given here.

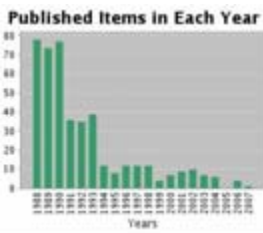
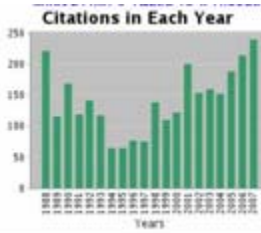
2.1 Publication Data: ISI, Scopus, and Google Scholar

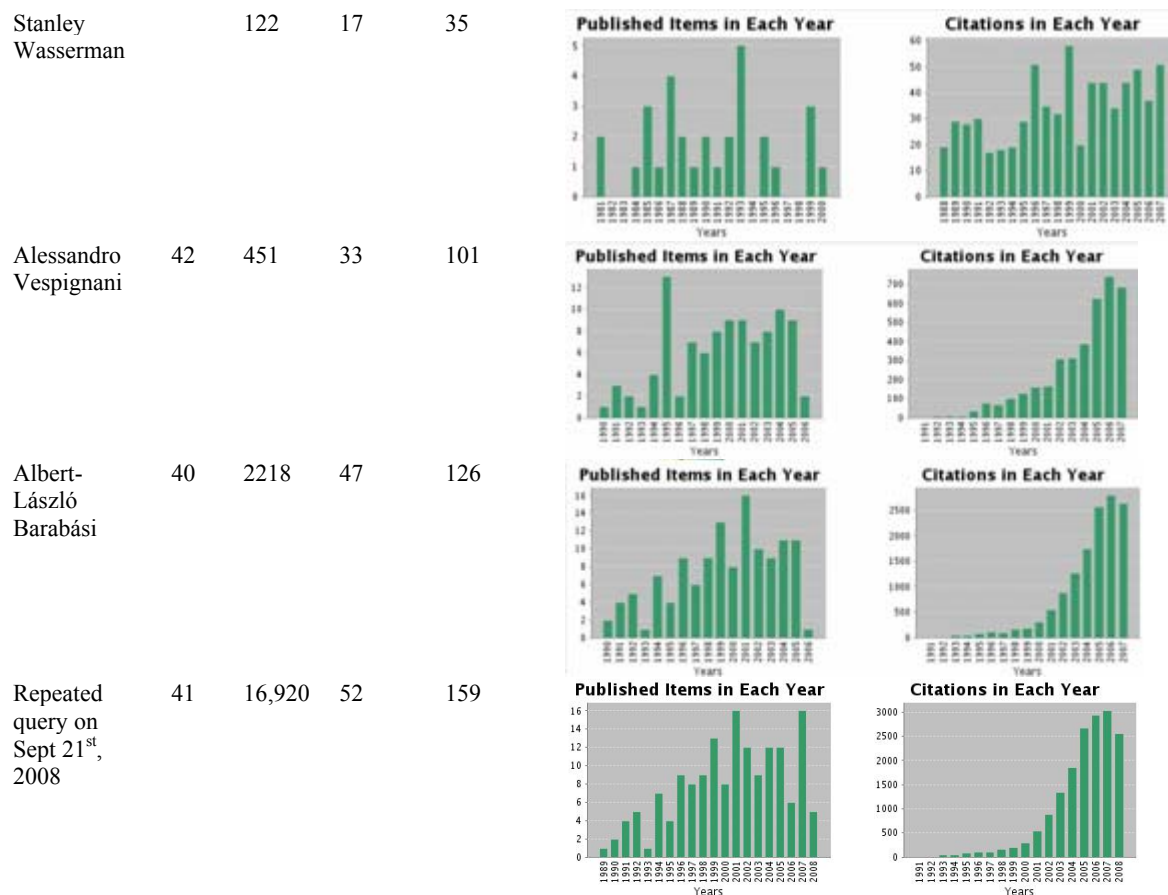
Today, most science studies use either Thomson Scientific's databases or Scopus as they each constitute a multi-disciplinary, objective, internally consistent database. Google Scholar constitutes a thirds choice. Please see comparison of three sources and discussion of coverage in section 2.1.4.

2.1.1 ISI Data

For the purposes of this tutorial we exemplarily downloaded publication records from four major network science researchers, three of whom are principal investigators of the Network Workbench project. Their names, ages (retrieved from Library of Congress), number of citations for highest cited paper, h-index (Bornmann, 2006), and number of papers and citations over time as calculated by the Web of Science by Thomson Scientific (Thomson-Reuters, 2008b) are given in Table 2. ISI formatted files of all papers including references were downloaded for all four researchers in December 2007. The superset of the four data files is called 'FourNetSciResearchers' in the remainder of this tutorial.

Table 2: Names, ages, number of citations for highest cited paper, h-index, and number of papers and citations over time as rendered in the Web of Science for four major network science researchers

Name	Age	Total # Cites	H-Index	Total # Papers	# Papers and Citations per Year for the last 20 Years	
Eugene Garfield	82	1525	31	672		



The table reveals that a high age, i.e., more time for publishing, typically results in more papers. The enormous differences in citation dynamics between physics and social sciences such as scientometrics or sociology are visible. Vespignani and Barabási are both physicists and their papers very rapidly acquire citation counts. Note that neither books nor Conference papers are captured in this dataset.

2.1.2 Scopus Data

The NWB Tool reads publication data from Scopus, documentation will be provided shortly.

2.1.3 Google Scholar

Google Scholar data can be acquired using *Publish or Perish* (Harzing, 2008) that can be freely downloaded from <http://www.harzing.com/pop.htm>. A query for papers by Albert-László Barabási run on Sept 21, 2008 results in 111 papers that have been cited 14,343 times, see Figure 2.

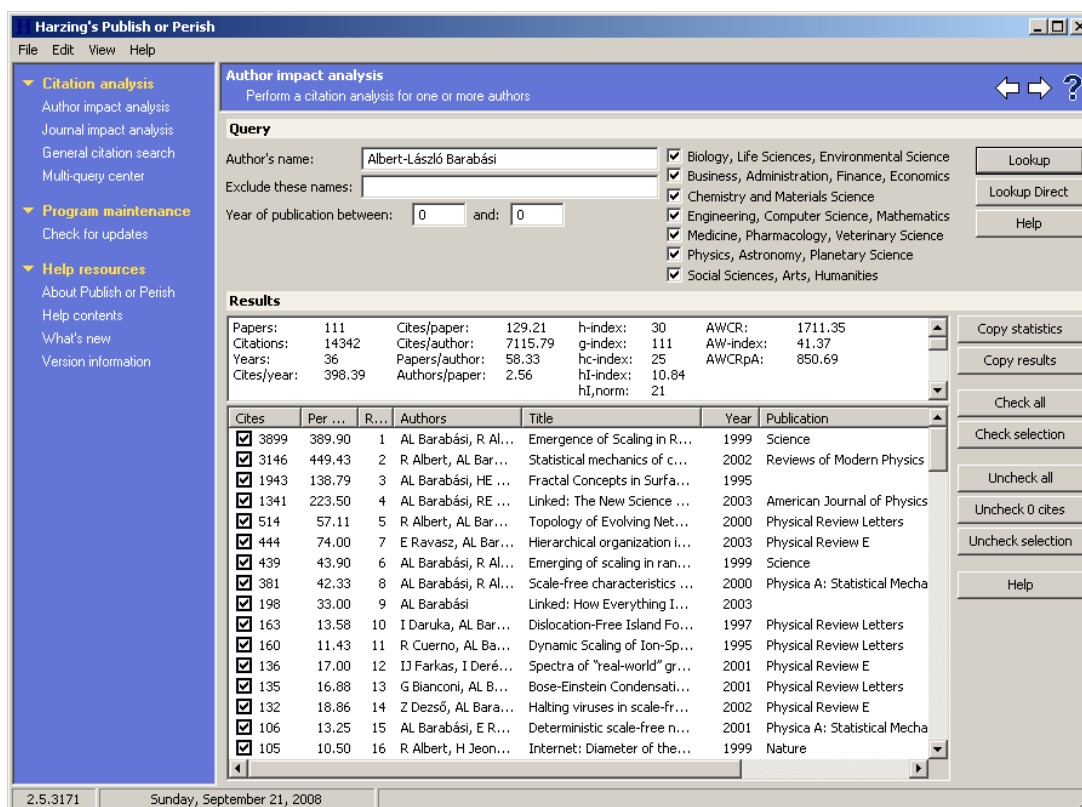


Figure 2: Publish or Perish interface with query result for Albert-László Barabási

To save records, select from menu 'File > Save as Bibtex' or 'File > Save as CSV' or File > Save as EndNote. All three file formats can be read by NWB Tool. The result in all three formats named 'barabasi.*' is also available in the respective subdirectories in '*yournwbdirectory*/sampledata/scientometrics' and will be used subsequently.

2.1.4 Comparison of ISI, Scopus, and Google Scholar

A number of recent studies have examined and compared the coverage of Thomson Scientific's Web of Science (WoS), Scopus, Ulrich's Directory, and Google Scholar (GS). It has been shown that the databases have a rather small overlap in records. The overlap between WoS and Scopus was only 58.2%. The overlap between GS and the union of WoS and Scopus was a mere 30.8%. While Scopus covers almost twice as many journals and conferences than WoS it covers fewer journals in the arts and humanities. A comprehensive analysis requires access to more than one database, see also (Bosman, Mourik, Rasch, Sieverts, & Verhoeff, 2006; de Moya-Anegón et al., 2007; Fingerman, 2006; Meho & Yang, 2007; Nisonger, 2004; Pauly & Stergiou, 2005).

In the NWB Tool, load

'*yournwbdirectory*/sampledata/scientometrics/isi/savedrecs-barabasi.isi'

'*yournwbdirectory*/sampledata/scientometrics/scopus/barabasi.scopus'

'*yournwbdirectory*/sampledata/scientometrics/bibtex/barabasi.bib // downloaded from Google Scholar

is also available in the respective subdirectories in '*yournwbdirectory*/sampledata/scientometrics'

It is interesting to compare the result set retrieved from ISI, Scopus, and Scholar Google.

2.2 Personal Bibliographies: EndNote and Bibtex

Personal references collected via reference management software such as EndNote (Thomson-Reuters, 2008a), Reference Manager (The-Thomson-Corporation, 2008) or the Bibtex format (Feder, 2006) can also be read. Sample datasets are included in /sampledata/bibtex/endnote

Simply load the file and a csv file with all unique files will appear in the Data Manager.

2.3 Funding: NSF Data

Funding data provided by the National Science Foundation (NSF) can be retrieved via the *Award Search* site (<http://www.nsf.gov/awardsearch/>). Search by PI name, institution, and many other fields, see Figure 3.

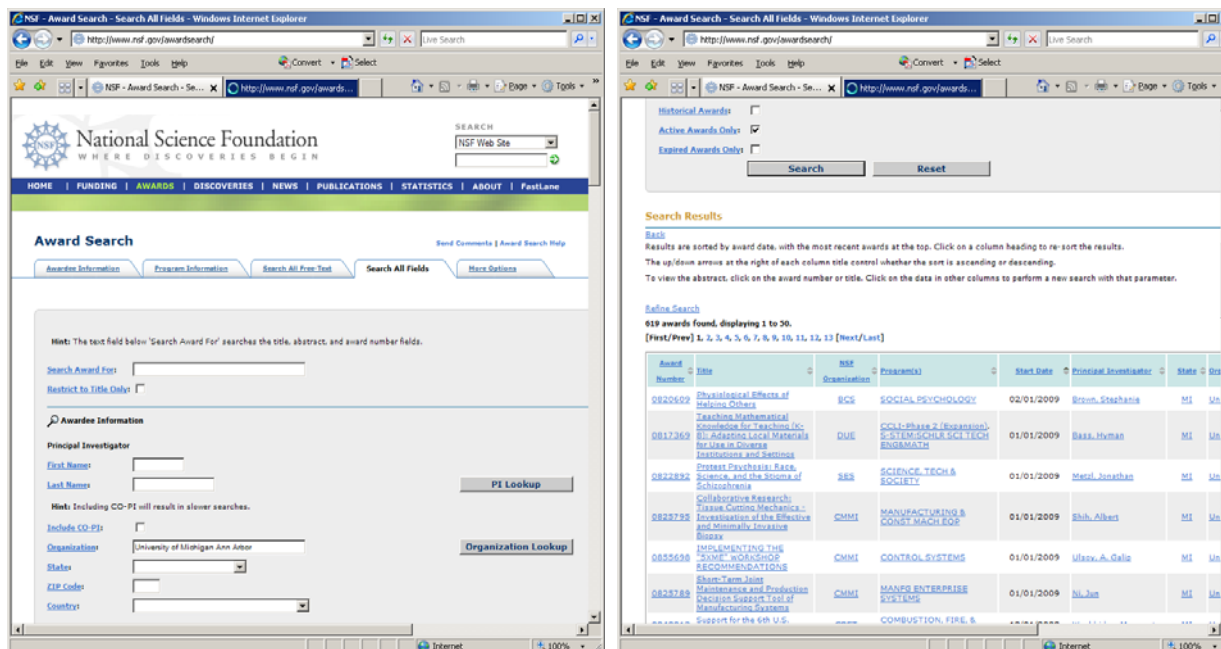


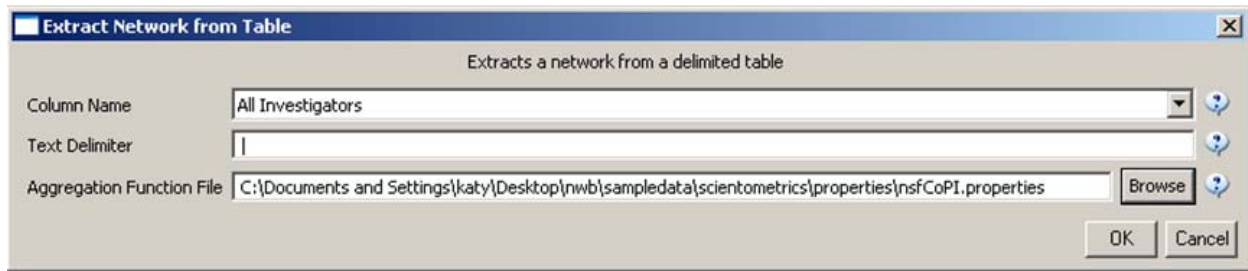
Figure 3: NSF Award Search site

To retrieve all projects funded under the new Science of Science and Innovation Policy (SciSIP) program, simply select the 'Program Information' tab, do an 'Element Code Lookup', enter '7626' into 'Element Code' field, and hit 'Search' button. On Sept 21st, 2008, exactly 50 awards were found. Award records can be downloaded in CSV, Excel or XML format. Save file in CSV format, and a sample csv file is available in '*yournwbdirectory*/sampledata/scientometrics/nsf/scipolicy.csv'. In the NWB Tool, load the file using 'File > Load File'. A table with all records will appear in the Data Manager. Right click and view file in 'Microsoft Office Excel'.

To show how to analyze and visualize funding data, we use the active NSF awards data from Indiana University (257 records), Cornell University (501 records) and University of Michigan Ann Arbor (619 records) which were downloaded on 11/07/2008. Save files as csv but rename into .nsf. Or simply use the files provided in '*yournwbdirectory*/sampledata/scientometrics/nsf/'.

2.3.1 Extracting Co-PI Networks

Load NSF data, selecting the loaded dataset in the Data Manager window, run '*Scientometrics > Extract Co-Occurrence Network*' using parameters:



Two derived files will appear in the Data Manager window: the co-PI network and a merge table. In the network, nodes represent investigators and edges denote their co-PI relationships. The merge table can be used to further clean PI names.

Choose the “Extracted Network on Column All Investigators” and run the ‘*Analysis > Network Analysis Toolkit (NAT)*’ which reveals the number of nodes and edges but also of isolate nodes that can be removed by running ‘*Preprocessing > Delete Isolates*’.

Select ‘*Visualization > GUESS*’ to visualize. Run ‘co-PI-nw.py’ script. Visualizations of co-PI network of three universities are given in Figure 4.

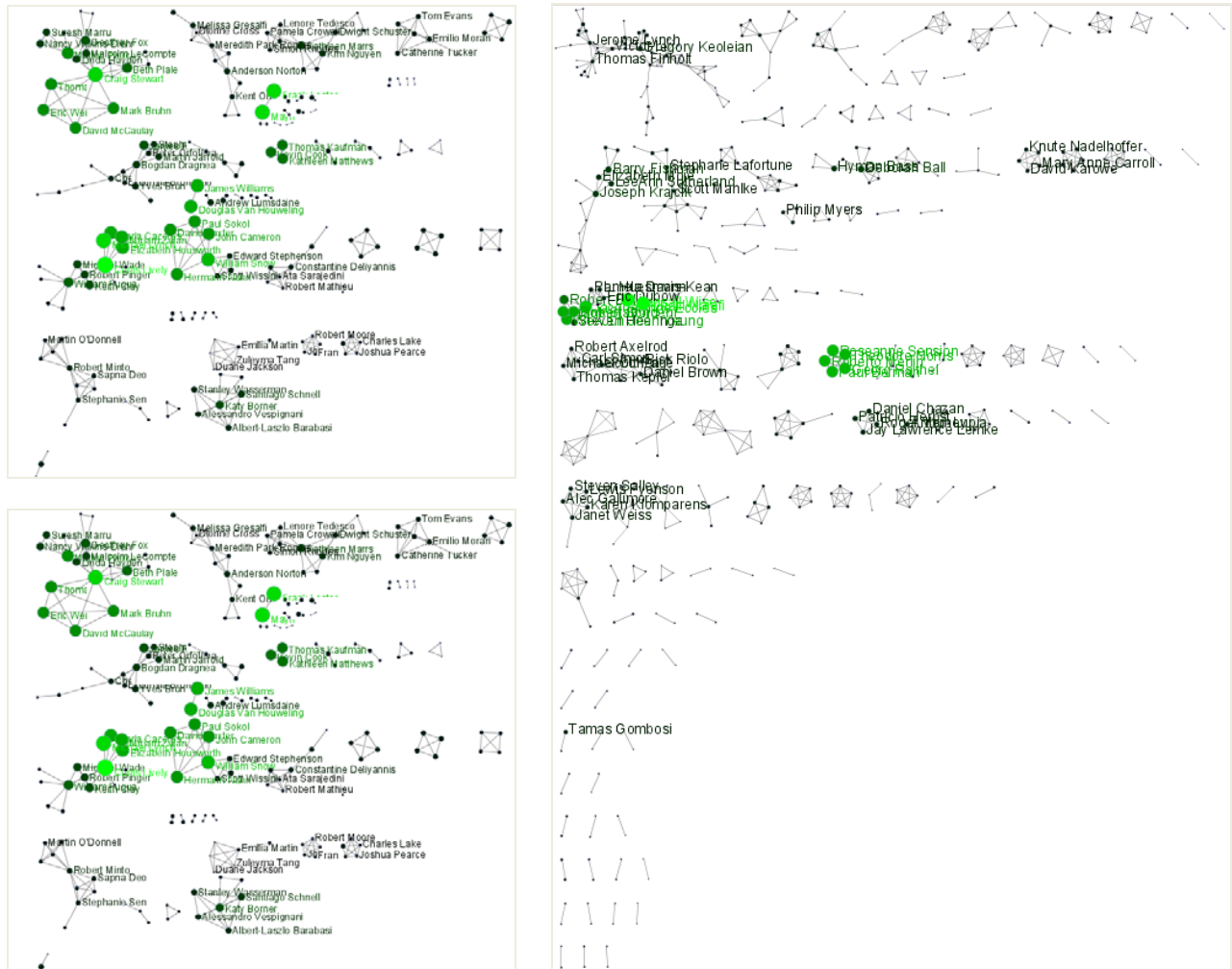
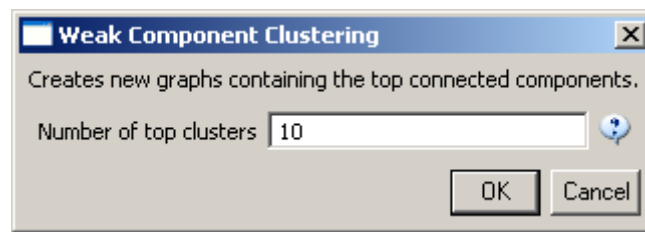


Figure 4: Co-PI network of Indiana University (top, left), Cornell University (bottom, left), and University of Michigan (right)

Select network after removing isolates and run 'Analysis > Unweighted and Undirected > Weak Component Clustering' with parameter



Indiana's largest component has 19 nodes, Cornell's has 67 nodes, Michigan's has 55 nodes. Visualize Cornell's network in GUESS using same .py script and save via 'File > Export Image' as jpg.



Figure 5: Largest component of Cornell University co-PI network. Node size and color encode the total award amount. The top-50 nodes with the highest total award amount are labeled.

2.4 Scholarly Database

Medline, U.S. patent, as well as funding data provided by the National Science Foundation and the National Institutes of Health can be downloaded from the Scholarly Database (SDB) at Indiana University. SDB supports keyword based cross-search of the different data types and data can be downloaded in bulk.

Register to get a free account or use 'Email: nwb@indiana.edu' and 'Password: nwb' to try out functionality.

Search the four databases separately or in combination for 'Creators' (authors, inventors, investigators) or terms occurring in 'Title', 'Abstract', or 'All Text' for all or specific years. If multiple terms are entered in a field, they are automatically combined using 'OR'. So, 'breast cancer' matches any record with 'breast' or 'cancer' in that field. You can put AND between terms to combine with 'AND'. Thus 'breast AND cancer' would only match records that contain both terms. Double quotation can be used to match compound terms, e.g., "breast cancer" retrieves records with the phrase "breast cancer", and not records where 'breast' and 'cancer' are both present, but not the exact phrase. The importance of a particular term in a query can be increased by putting a ^ and a number after the term. For instance, 'breast cancer^10' would increase the importance of matching the term 'cancer' by ten compared to matching the term 'breast'.

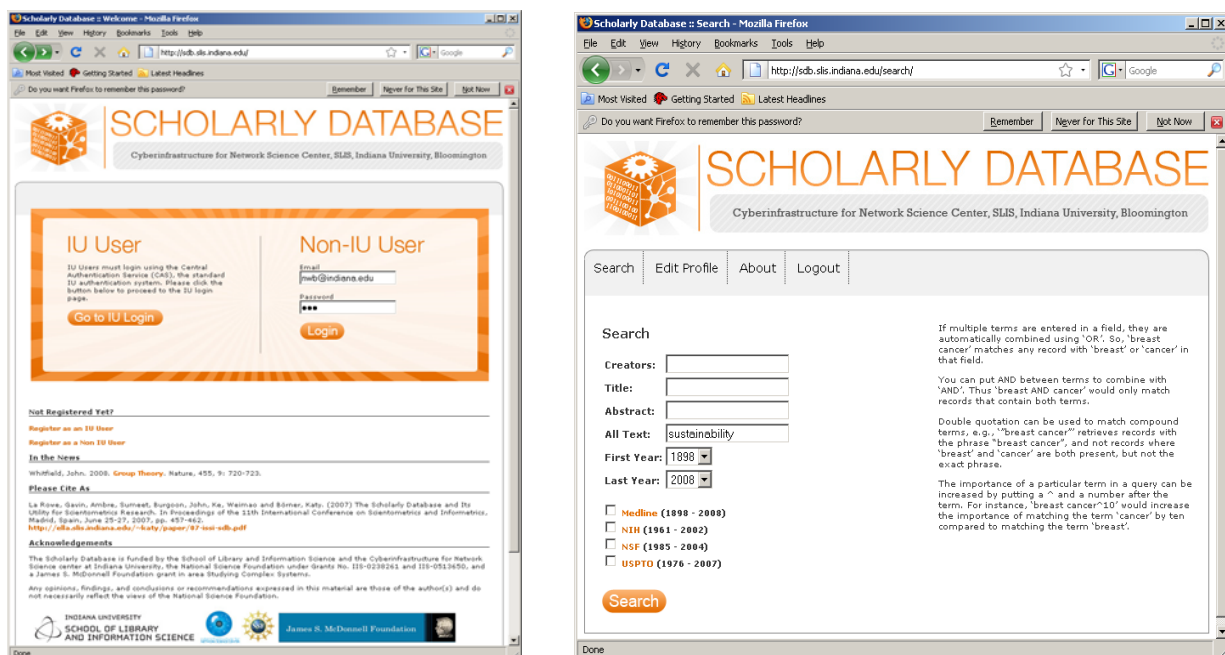


Figure 6: Scholarly Database home and search interface

Results are displayed in sets of 20 records, ordered by a Solr internal matching score. The first column represents the record source, the second the creators, third comes the year, then title and finally the matching score. Datasets can be downloaded as a dump for future analysis.

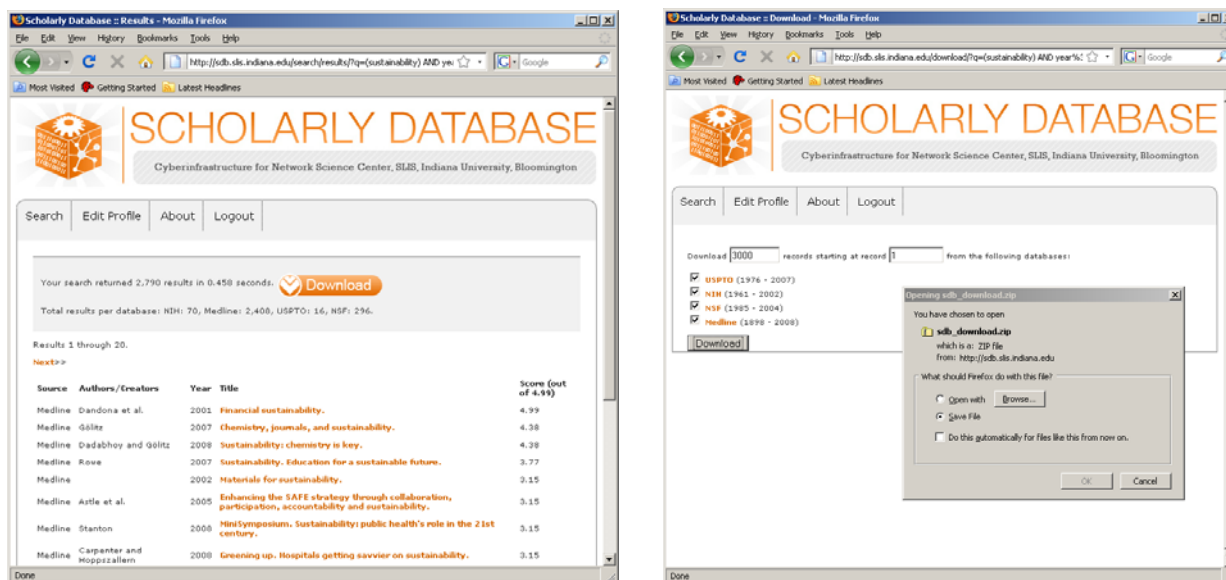
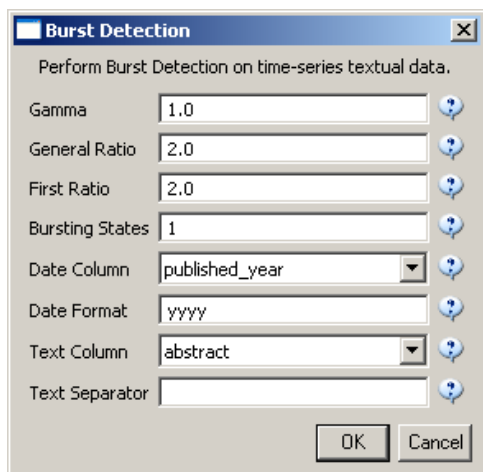


Figure 7: Scholarly Database search results and download interfaces

To run burst detection (see section 3.2) over Medline abstracts, simply download matching Medline records, load medline_medline_master.csv to NWB, run '*Preprocessing > Normalize Text*' with a space as 'New Separator' and select 'abstract'. Then Run '*Analysis > Textual > Burst Detection*' with parameters:



and space as a text separator. The result is a table that shows bursting words together with their length, weight, strength, start and end of burst.

3 Temporal Analysis

Science evolves over time. Attribute values of scholarly entities and their diverse aggregations increase and decrease at different rates and respond with different latency rates to internal and external events. Temporal analysis aims to identify the nature of phenomena represented by a sequence of observations such as patterns, trends, seasonality, outliers, and bursts of activity.

Data comes as a time series, i.e., a sequence of events/observations which are ordered in one dimension: time. Time series data can be continuous, i.e., there is an observation at every instant of time (see figure below), or discrete, i.e., observations exist for regularly or irregularly spaced intervals. Temporal aggregations, e.g., over journal volumes, years, decades, are common.

Temporal analysis frequently involves some form of filtering is applied to reduce noise and make patterns more salient. Smoothing (e.g., averaging using a smoothing window of a certain width) and curve approximation might be applied. The number of scholarly records over time is plotted to get a first idea of the temporal distribution of a dataset. It might be shown in total values or in % of total. Sometimes, it is interesting to know how long a scholarly entity was ‘active’, how ‘old’ it was in a certain year, what growth, latency to peak, or decay rate it has, what correlations with other time series exist, or what trends are observable. Data models such as the least squares model -- available in most statistical software packages – are applied to best fit a selected function to a data set and to determine if the trend is significant.

3.1 Charting Trends

Documentation coming soon.

3.2 Burst Detection

A scholarly dataset can be understood as a discrete time series: in other words, a sequence of events/ observations which are ordered in one dimension – time. Observations (here papers), exist for regularly spaced intervals, e.g., each month (volume) or year.

Kleinberg’s burst detection algorithm (Kleinberg, 2002) identifies sudden increases in the usage frequency of words. These words may connect to author names, journal names, country names, references, ISI keywords, or terms used in title and/or abstract of a paper. Rather than using plain frequencies of the occurrences of words, the algorithm employs a probabilistic automaton whose states correspond to the frequencies of individual words. State transitions correspond to points in time around which the frequency of the word changes significantly. The algorithm generates a ranked list of the word bursts in the document stream, together with the intervals of time in which they occurred. This can serve as a means of identifying topics, terms, or concepts important to the events being studied that increased in usage, were more active for a period of time, and then faded away.

In the NWB Tool, the algorithm can be found under ‘*Analysis > Textual > Burst Detection*’. As the algorithm itself is case sensitive, care must be taken if the user desires ‘KOREA’ and ‘korea’ and ‘Korea’ to be identified as the same word.

As the Garfield ISI data is very different in character from the rest, it is left out of the burst analysis done here. One particular difference is the absence of ISI keywords from most of the works in the Garfield dataset.

In the NWB tool, use ‘*File > Load and Clean ISI File*’ to load ThreeNetSciResearchers.isi, which is a file that contains all of Wasserman’s, Vespignani’s and Barabási’s ISI records and is provided as a sample dataset in ‘*yournwbdirectory*/sampledata/scientometrics/isi/ThreeNetSciResearchers.isi’. The result is two new tables in the Data Manager. The first is a table with all ISI records. The second is a derived (indented) table with unique ISI records named ‘*262 Unique ISI Records*’. In the latter file, ISI records with unique ID numbers (UT field) are merged, and only the record with the higher citation count (CT value) is kept. Select the ‘*262 Unique ISI Records*’ table and run ‘*Analysis > Textual > Burst Detection*’ using the parameters:

Gamma	1.0	# default setting
General Ratio	2.0	# default setting
First Ratio	2.0	# default setting
Bursting States	1	# default setting
Date Column	Select	"Publication Year" from the long listing
Date Format	Select	"yyyy"
Text Column	Select	"Authors"
Text Separator		

Note: Throughout the tutorial we will use ‘#’ to indicate comments or further instructions within parameter or code blocks. These do not need to be entered into the tool.

A third table (derived from ‘*262 Unique ISI Records*’) labeled ‘*Burst detection analysis ...*’ will appear in the Data Manager. On a PC running Windows, right click on this table and select view to see the data in Excel.

On a Mac or a Linux system, right click and save the file, then open using the spreadsheet program of your choice. The table has 6 columns. The first column lists bursting words, here author names, the length of the burst, the burst

weight, burst strength, together with the burst start and end year. Note that words can burst multiple times. If they do, then the burst ‘weight’ indicates how much support there is for the burst above the previous bursting level, while ‘strength’ indicates how much support there is for the burst over the non-bursting baseline. Since the burst detection algorithm was run with ‘bursting state = 1’, i.e., modeled only one burst per word, the burst weight is identical to the burst strength in this output.

To generate a visual depiction of the bursts in MS Excel perform the following steps:

1. Sort the data ascending by burst start year.
2. Add column headers for all years, i.e., enter first start year in G1, here 1980. Continue, e.g., using formulae ‘=G1+1’, until highest burst end year, here 2004 in cell AF1.
3. In the resulting word by burst year matrix, select the upper left blank cell (G2) and using ‘*Format > Conditional Formatting*’ color code the cells according to burst value. To color cells for years with a burst (total power) value of more or equal 10 red and cells with a higher value dark red use the following formulas and format patterns:

Condition 1 =AND(AND(G\$1>=\$E2,OR(G\$1<=\$F2,\$F2=" ")), \$D2>=10)
Condition 2 =AND(G\$1>=\$E2,OR(G\$1<=\$F2,\$F2=" "))

Apply the format to all cells in the word by year matrix. The result for the given example is shown in Figure 1.

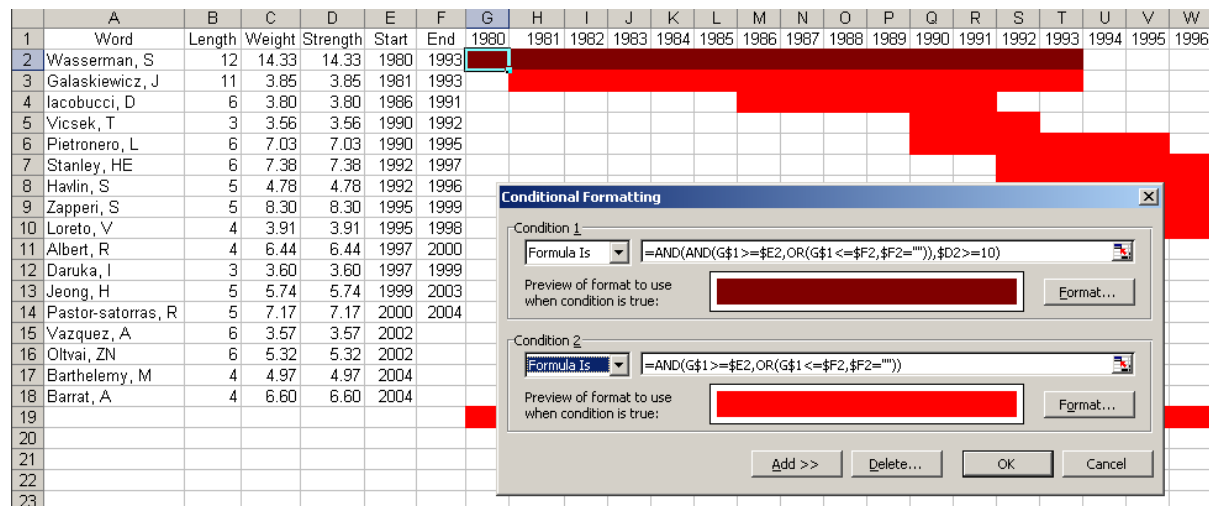


Figure 1: Visualizing burst results in MS Excel

Running burst detection on the combined Wasserman, Vespignani, and Barabási ISI file for authors, ISI keywords, and cited references results in Figure 3. To generate the latter two results, select Text Column ‘New ISI Keywords’ and ‘Cited References’ instead of ‘Authors’ in the burst parameters. The results reveal many of the trends one would expect to see among these major network science researchers. For instance, the ISI keywords burst with terms related to diffusion and growth in the early 90s, criticality and critical behavior in the late 90s, and finish with small-world networks, complex networks, and metabolic networks starting in the early 2000s and not being finished at the end of the dataset (as opposed to ending in 2005, the last year of the dataset but for three papers). Another pattern is that almost all of the authors with bursts in the dataset were graduate students of Wasserman, Vespignani, or Barabási during this period. One notable example of this is Reka Albert, who bursts from 1997 to 2000, corresponding to work on her Ph.D. with Barabasi.

The result can be visualized as a chart with word and time dimensions; see Figure 2. Bursts for each word are shown as horizontal red bars across the time dimension. Bursts with strength above 10 are colored a darker red. All bursts are shown for authors and keywords, but only words in the fifteen most powerful bursts are shown for cited references and terms in the abstract. For each type of word, words are sorted by the start of their first burst and the end of their last burst. In the burst for abstract terms, stop words are removed. This chart was made in MS Excel by following the steps enumerated to create Figure 1, with some minor modifications for display.

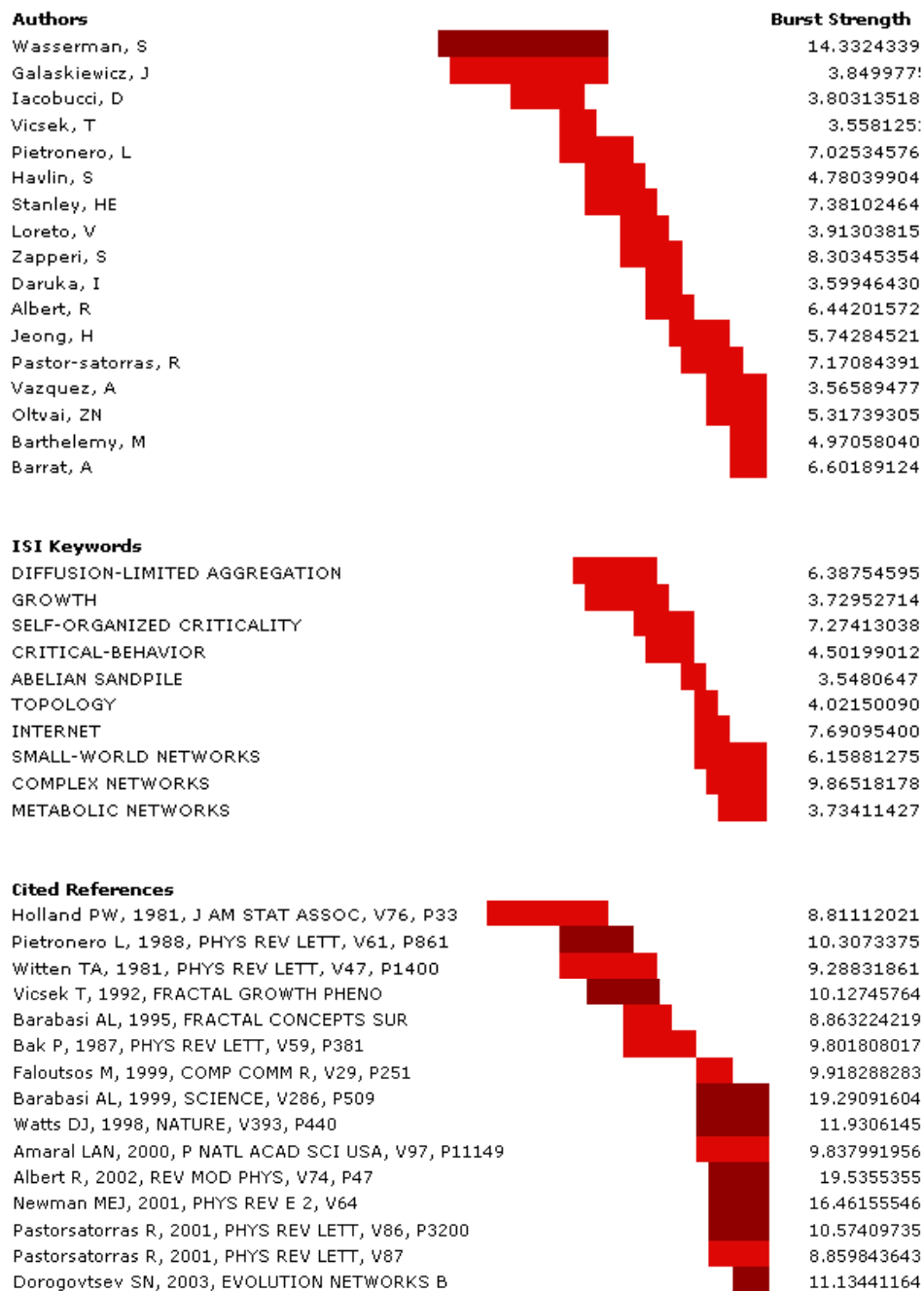


Figure 2: Visualization of bursts for author names, ISI keywords, and cited references

It is interesting to note in the cited reference bursts that many of the strongest bursts are the most recent. This confirms that many of the foundational techniques of network science have developed recently, particularly as the publications with very strong bursts include those by Barabasi and Albert on statistical mechanics of scale-free networks, Watts and Strogatz on small world networks, and Newman on random networks. It also reflects a change in dynamics, however, as the historically social-science-dominated-field of network science now sees major contributions by physicists.

4 Geospatial Analysis

Geospatial analysis has a long history in geography and cartography. Geospatial analysis aims to answer the question where something happens and with what impact on neighboring areas.

Geospatial analysis requires spatial attribute values such as geolocations for authors or their papers extracted from affiliation data or spatial positions of nodes generated from layout algorithms. Geospatial data can be continuous, i.e., each record has a specific position, or discrete, i.e., a position or area (shape file) exists for sets of records, e.g., number of papers per country.

Spatial aggregations, e.g., merging via zip codes, counties, states, countries, continents, are common.

Cartographic generalization refers to the process of abstraction such as (1) graphic generalization, i.e., the simplification, enlargement, displacement, merging, or selection of entities that does not affect their symbology and (2) conceptual symbolization: merging, selection, plus symbolization and enhancement of entities, e.g., representing high density areas by a new (city) symbol (Kraak & Ormeling, 1987).

Geometric Generalization aims to solve the conflict between the number of visualized features, the size of symbols, and the size of the display surface. Cartographers dealt with this conflict mostly intuitively until researcher's like Friedrich Töpfer attempted to find quantifiable expressions for it (Skupin, 2000; Tobler, 1973; Töpfer, 1974; Töpfer & Pillewizer, 1966).

5 Topical Analysis

The topic, also called semantic, coverage of a unit of science can be derived from text associated with it. For example, topic coverage and topical similarity of, e.g., authors or institutions, can be derived from units associated with them, e.g., papers, patents, or grants. Topical aggregations, e.g., over journal volumes, scientific disciplines, or institutions are common.

Topic analysis extracts the set of unique words or word profiles and their frequency from a text corpus. Stop words, such as 'the', 'of', etc., are removed. Stemming, i.e., the reduction of words such as 'scientific', 'science' to 'scien' can be applied (Porter, 1980).

Co-word analysis identifies the number of times two words are used in the title, keyword set, abstract and/or full text of, e.g., a paper. The space of co-occurring words can be mapped providing a unique view of the topic coverage of a dataset. Similarly, units of science can be grouped based on the number of words they share in common (Callon, Courtial, Turner, & Bauin, 1983; Callon, Law, & Rip, 1986).

Salton's term frequency inverse document frequency (TFIDF) is a statistical measure used to evaluate how important a word is to, e.g., paper, in a corpus. The importance increases proportionally to the number of times a word appears in the paper but is offset by the frequency of the word in the corpus (Salton & Yang, 1973).

Dimensionality reduction techniques such as self organizing maps (SOM) or the topics model, see Table 1, are commonly used to project high-dimensional information spaces, e.g., the matrix of all unique papers times their unique terms, into a low, typically 2-dimensional space.

See Section 6.2 Co-Occurrence Linkages for examples on how to use the NWB Tool for word co-occurrence analysis (Deerwester, Dumais, Furnas, Landauer, & Harshman, 1990; Griffiths & Steyvers, 2002; Kohonen, 1995; Kruskal, 1964; Landauer & Dumais, 1997; Landauer, Foltz, & Laham, 1998).

6 Network Analysis

The study of networks aims to increase our understanding of natural and manmade networks. It builds on social network analysis (Carrington, Scott, & Wasserman, 2005; Scott, 2000; Wasserman & Faust, 1994), physics (Barabási, 2002), information science (Börner, Sanyal, & Vespignani, 2007), bibliometrics (Borgman & Furner, 2002; Nicolaisen, 2007), scientometrics, webometrics (Narin & Moll, 1977; White & McCain, 1998), informetrics (Wilson, 2001), webometrics (Thelwall, Vaughan, & Björneborn, 2005), communication theory (Monge & Contractor, 2003), sociology of science (Lenoir, 2002), and several other disciplines.

Authors, institutions, countries as well as words, papers, journals, patents, funding, etc. are represented as nodes and their complex interrelations as edges. For example, author and paper nodes exist in a delicate ecology of evolving networks. Given a set of papers, diverse networks can be extracted. Typically, three types of linkages are distinguished: *direct linkages*, e.g., paper citation linkages; *co-occurrences*, e.g., of words, authors, references; and *co-citations*, e.g., of authors or papers. Linkages may be among units of the same type, e.g., co-authorship linkages, or between units of different types, e.g., authors produce papers. Units of the same type can be interlinked via different link types, e.g., papers can be linked based on co-word, direct, co-citation, or bibliographic coupling analysis. Linkages might be directed and/or weighted. Nodes and their linkages can be represented as adjacency matrix, edge list, and visually as structure plot or graph. Each non-symmetrical occurrence matrix, e.g., paper citations, has two associated (symmetrical) co-occurrence matrices, e.g., a bibliographic coupling and a co-citation matrix.

Figure 1 shows a sample dataset of five papers, A through E, published over three years together with their authors x, y, z, references (blue references are papers outside this set) and citations (green ones go to papers outside this set) as well as some commonly derived networks. The extraction and analysis of these and other scholarly networks is explained subsequently.

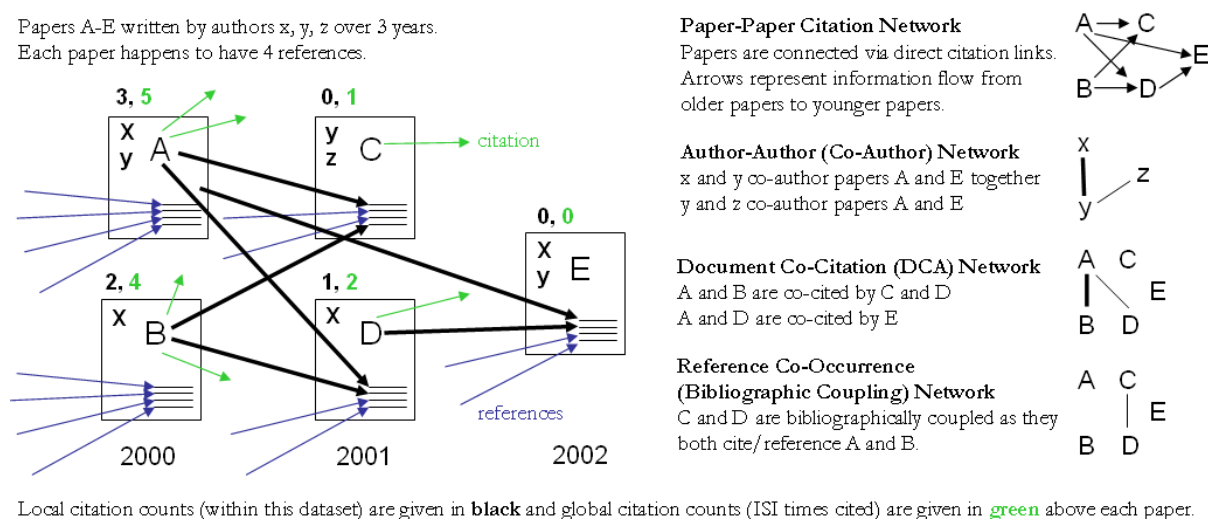


Figure 1: Sample paper network (left) and four different network types derived from it (right).

Diverse algorithms exist to calculate specific node, edge, and network properties, see (Börner, Sanyal et al., 2007). Node properties comprise degree centrality, betweenness centrality, or hub and authority scores. Edge properties included are durability, reciprocity, intensity ('weak' or 'strong'), density (how many potential edges in a network actually exist), reachability (how many steps it takes to go from one 'end' of a network to the other), centrality (whether a network has a 'center' point(s)), quality (reliability or certainty), and strength. Network properties refer to the number of nodes and edges, network density, average path length, clustering coefficient, and distributions from which general properties such as small world, scale-free, or hierarchical can be derived. Identifying major communities via community detection algorithms and calculating the 'backbone' of a network via Pathfinder network scaling or maximum flow algorithms helps to communicate and make sense of large scale networks.

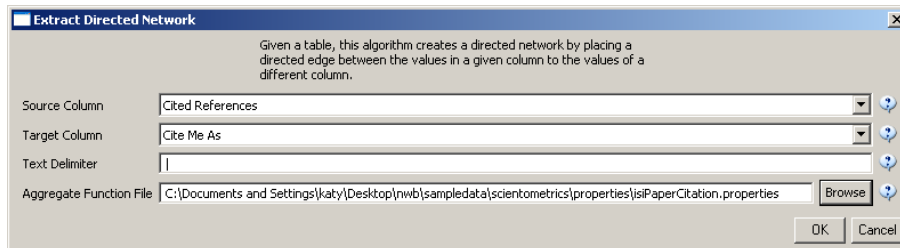
6.1 Direct Linkages

6.1.1 Paper-Paper (Citation) Network

Papers cite other papers via references forming an unweighted, directed paper citation graph. It is beneficial to indicate the direction of information flow, in order of publication, via arrows. References enable a search of the citation graph backwards in time. Citations to a paper support the forward traversal of the graph. Citing and being cited can be seen as roles a paper possesses (Nicolaisen, 2007).

In the NWB Tool, load the file *'*yournwbdirectory*/sampledata/scientometrics/isi/FourNetSciResearchers.isi'* using *'File > Load and Clean ISI File'*. A table of the records and a table of all records with unique ISI ids will appear in the Data Manager. In this file each original record now has a 'Cite Me As' attribute that is constructed from the 'first author, PY, J9, VL, BP' fields of its ISI record and will be used when matching paper and reference records.

To extract the paper citation network, select the *'361 Unique ISI Records'* table and run *'Scientometrics > Extract Directed Network'* using the parameters:



The result is a directed network of paper citations in the Data Manager. Each paper node has two citation counts. The local citation count (LCC) indicates how often a paper was cited by papers in the set. The global citation count (GCC) equals the times cited (TC) value in the original ISI file. Paper references have no GCC value, except for references that are also ISI records. Currently, the NWB Tool sets the GCC of references to -1 (except for references that are not also ISI records). This is useful to prune the network to contain only the original ISI records.

To view the complete network, select the network and run *'Visualization > GUESS'* and wait until the network is visible and centered. Layout the network, e.g., using the Generalized Expectation-Maximization (GEM) algorithm using *'GUESS: Layout > GEM'*. Pack the network via *'GUESS: Layout > Bin Pack'*. To change the background color use *'GUESS: Display > Background Color'*. To size and color code nodes, select the 'Interpreter' tab at the bottom, left-hand corner of the GUESS window, and enter the command lines:

```
> resizeLinear(globalcitationcount,1,50)
> colorize(globalcitationcount,gray,black)
> for e in g.edges:
...     e.color="127,193,65,255"           # enter a tab after the three dots
...                                     # hit Enter again
```

Note: The Interpreter tab will have *'>>>'* as a prompt for these commands. It is not necessary to type *'>'* at the beginning of the line. You should type each line individually and hit enter to submit the commands to the Interpreter. For more information, refer to the ***GUESS tutorial*.

This way, nodes are linearly size and color coded by their GCC, and edges are green as shown in Figure 2 (left). Any field within the network can be substituted to code the nodes. To view the available fields, open the Information Window (*'Display > Information Window'*) and mouse over a node, as in Figure 2 (right). Also note that each ISI paper record in the network has a dandelion shaped set of references.

The GUESS interface supports pan and zoom, node selection, and details on demand, see ***GUESS tutorial*. For example, the node that connects the Barabási-Vespignani network in the upper left to Garfield's network in the lower left is *Price, 1986, Little Science, Big Science*. The network on the right is centered on Wasserman's works.

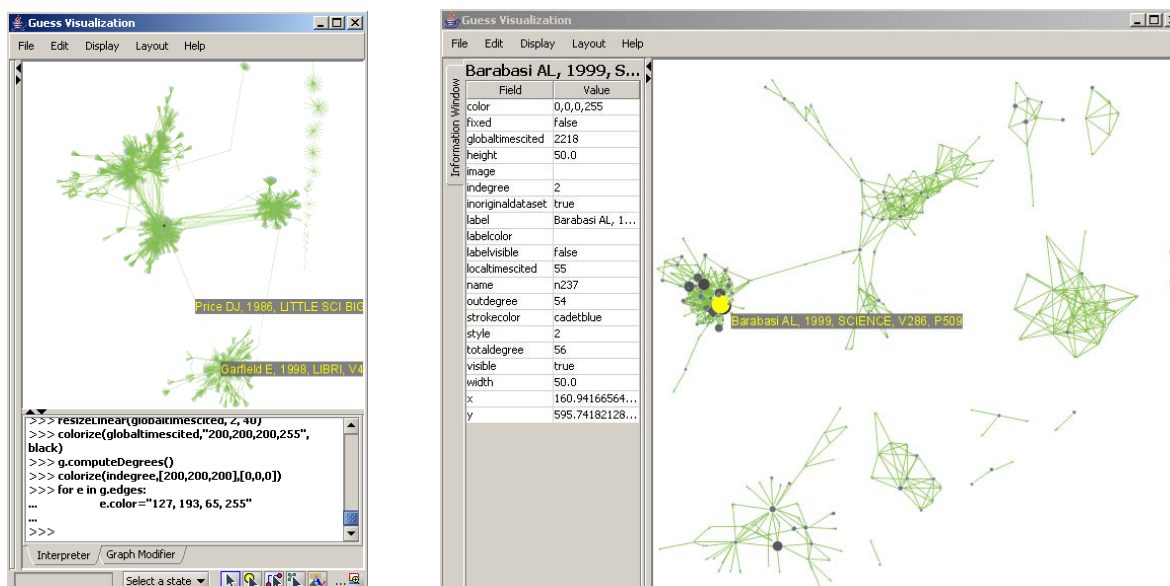


Figure 2: Directed, unweighted paper-paper citation network for ‘FourNetSciResearchers’ dataset with all papers and references in the GUESS user interface (left) and a pruned paper-paper citation network after removing all references and isolates (right)

The complete network can be reduced to papers that appeared in the original ISI file by deleting all nodes that have a GCC of -1. Simply run *‘Preprocessing > Extract Nodes Above or Below Value’* with parameter values:

```
Extract from this number      -1
Below?                        # leave unchecked
Numeric Attribute             globalCitationCount
```

The resulting network is unconnected, i.e., it has many subnetworks many of which have only one node. These single unconnected nodes, also called isolates, can be removed using *‘Preprocessing > Delete Isolates’*. Deleting isolates is a memory intensive procedure. If you experience problems at this step, you may wish to consult the tutorial entitled *‘Increasing Memory for NWB’*.

The ‘FourNetSciResearchers’ dataset has exactly 65 isolates. Removing those leaves 12 networks shown in Figure 2 (right) using the same color and size coding as in Figure 1 (left). Using *‘GUESS: Display > Information Window’* reveals detailed information for any node or edge. Here the node with the highest GCC value was selected.

Alternatively, nodes could have been color and/or size coded by their degree using, e.g.,

```
> g.computeDegrees()
> colorize(outdegree,gray,black)
```

Note that the *outdegree* corresponds to the LCC within the given network while the *indegree* reflects the number of references, helping to visually identify review papers.

The complete paper-paper-citation network can be split into its subnetworks using *‘Analysis > Unweighted & Directed > Weak Component Clustering’* with the default values. The largest component has 163 nodes, the second largest 45, the third 24, and the fourth and fifth have 12 and 11 nodes respectively. The largest component, also called giant component, is shown in Figure 3. The top 20 papers, by times cited in ISI, have been labeled using

```
> toptc = g.nodes[:]
> def bytc(n1, n2):
...     return cmp(n1.globalcitationcount, n2.globalcitationcount)
> toptc.sort(bytc)
> toptc.reverse()
> toptc
```

```
> for i in range(0, 20):
...     toptc[i].labelvisible = true
```

Alternatively, run ‘*GUESS: File > Run Script ...*’ and select
‘*yournwbdirectory*/sampledata/scientometrics/isi/paper-citation-nw.py’.

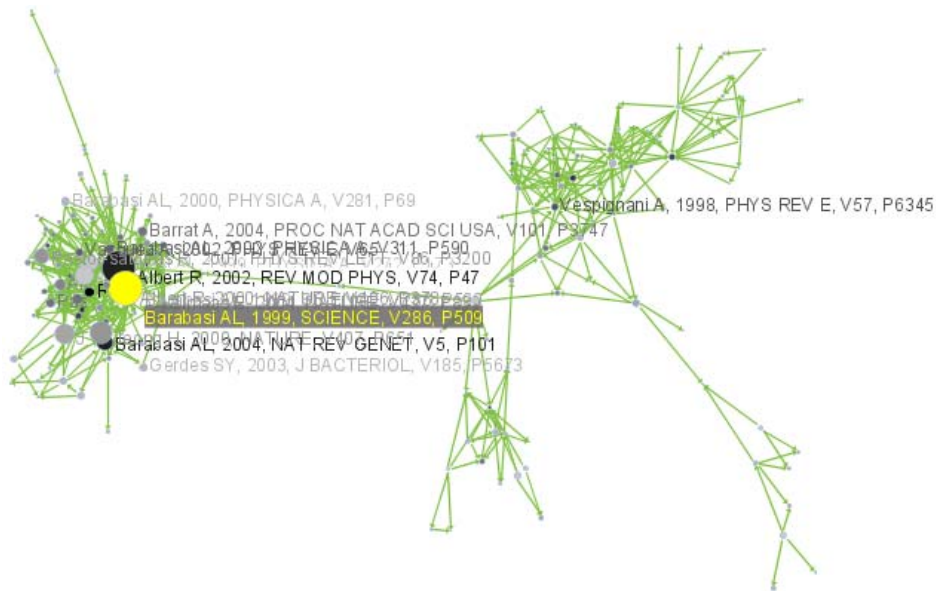


Figure 3: Giant components of the paper citation network

Compare the result with Figure 2 (right) and note that this network layout algorithm—and most others—are non-deterministic. That is, different runs lead to different layouts – observe the position of the highlighted node in both layouts. However, all layouts aim to group connected nodes into spatial proximity while avoiding overlaps of unconnected or sparsely connected subnetworks.

6.1.2 Author-Paper (Consumed/Produced) Network

There are active and passive units of science. Active units, e.g., authors, produce and consume passive units, e.g., papers, patents, datasets, software. The resulting networks have multiple types of nodes, e.g., authors and papers. Directed edges indicate the flow of resources from sources to sinks, e.g., from an author to a written/produced paper to the author who reads/consumes the paper.

Presently, NWB cannot derive this network type from ISI data: it can, however, simulate such a network using TARL—for more specific information, see the section *Modeling Scholarly Networks*.

6.2 Co-Occurrence Linkages

6.2.1 Author Co-Occurrence (Co-Author) Network

Having the names of two authors (or their institutions, countries) listed on one paper, patent, or grant is an empirical manifestation of scholarly collaboration. The more often two authors collaborate, the higher the weight of their joint co-author link. Weighted, undirected co-authorship networks appear to have a high correlation with social networks that are themselves impacted by geospatial proximity (Börner, Penumathy, Meiss, & Ke, 2006; Wellman, White, & Nazer, 2004).

To produce a co-authorship network in the NWB Tool, select the table of all 361 unique ISI records from the ‘*FourNetSciResearchers*’ dataset in the Data Manager window. Run ‘*Scientometrics > Extract Co-Author Network*’ using the parameter:

```
File Format      isi
```

The result is two derived files in the Data Manager window: the co-authorship network and a table with a listing of unique authors, also known as ‘merge table’. The merge table can be used to manually unify author names, e.g., “Albet, R” and “Albert, R” see example below.

In order to manually examine and if needed correct the list of unique authors, open the merge table, e.g., in a spreadsheet program. Sort by author names and identify names that refer to the same person. In order to merge two names, simply delete the asterisk (“*”) in the last column of the duplicate node’s row. In addition, copy the uniqueIndex of the name that should be kept and paste it into the cell of the name that should be deleted. Table 1 shows the result for merging “Albet, R” and “Albert, R” where “Albet, R” will be deleted yet all of the nodes linkages and citation counts will be added to “Albert, R”.

Table 1: Merging of author nodes using the merge table

label	timesCited	numberOfWorks	uniqueIndex	combineValues
Abt, HA	3	1	142	*
Alava, M	26	1	196	*
Albert, R	7741	17	60	*
Albet, R	16	1	60	

A merge table can be automatically generated by applying the Jaro distance metric (Jaro, 1989, 1995) available in the open source Similarity Measure Library (<http://sourceforge.net/projects/simmetrics/>) to identify potential duplicates. In the NWB Tool, simply select the co-author network and run ‘*Scientometrics > Detect Duplicate Nodes*’ using the parameters:

```
Attribute to compare on      label
Merge when this similar      0.95
Create notice when this similar 0.85
Number of shared first letter 2
```

The result is a merge table that has the very same format as Table 1, together with two textual log files. The log files describe which nodes will be merged or not merged in a more human-readable form. Specifically, the first log file provides information on which nodes will be merged (right click and select view to examine the file), while the second log file lists nodes which will not be merged, but are similar. Based on this information the automatically generated merge table can be further modified as needed.

In sum, unification of author names can be done manually or automatically independently or in conjunction. It is recommended to create the initial merge table automatically and to fine-tune it as needed. Note that the same procedure can be used to identify duplicate references – simply select a paper-citation network and run ‘*Scientometrics > Detect Duplicate Nodes*’ using the same parameters as above and a merge table for references will be created.

To merge identified duplicate nodes, select the merge table and the co-authorship network holding down the ‘Ctrl’ key. Run ‘*Scientometrics > Update Network by Merging Nodes*’. This will produce an updated network as well as a report describing which nodes were merged.

The updated co-author network can be visualized using ‘*Visualization > GUESS*’, see the above explanation on GUESS.

Figure 4 shows a layout of the combined ‘*FourNetSciResearchers*’ dataset after setting the background color to white and using the command lines:

```
> resizeLinear(numberofworks,1,50)
> colorize(numberofworks,gray,black)
> for n in g.nodes:
...     n.strokecolor = n.color          # border color same as its inside color
> resizeLinear(numberofcoauthoredworks, .25, 8)
> colorize(numberofcoauthoredworks, "127,193,65,255", black)
```



```

> nodesbynumworks = g.nodes[:] # make a copy of the list of all nodes
> def bynumworks(n1, n2):      # define a function for comparing nodes
...     return cmp(n1.numberofworks, n2.numberofworks)
> nodesbynumworks.sort(bynumworks) # sort list
> nodesbynumworks.reverse()       # reverse sorting, list starts with highest #
> for i in range(0, 50):         # make labels of most productive authors visible
...     nodesbynumworks[i].labelvisible = true

```

Alternatively, run ‘GUESS: File > Run Script ...’ and select ‘*yournwbdirectory*/sampledata/scientometrics/isi/co-author-nw.py’.

That is, author nodes are color and size coded by the number of papers per author. Edges are color and thickness coded by the number of times two authors wrote a paper together. The remaining commands identify the top-50 authors with the most papers and make their name labels visible.

GUESS supports the repositioning of selected nodes. Multiple nodes can be selected by holding down the ‘Shift’ key and dragging a box around specific nodes. The final network can be saved via ‘GUESS: File > Export Image’ and opened in a graphic design program to add a title and legend. The image below was created using Photoshop and label sizes were changed as well.

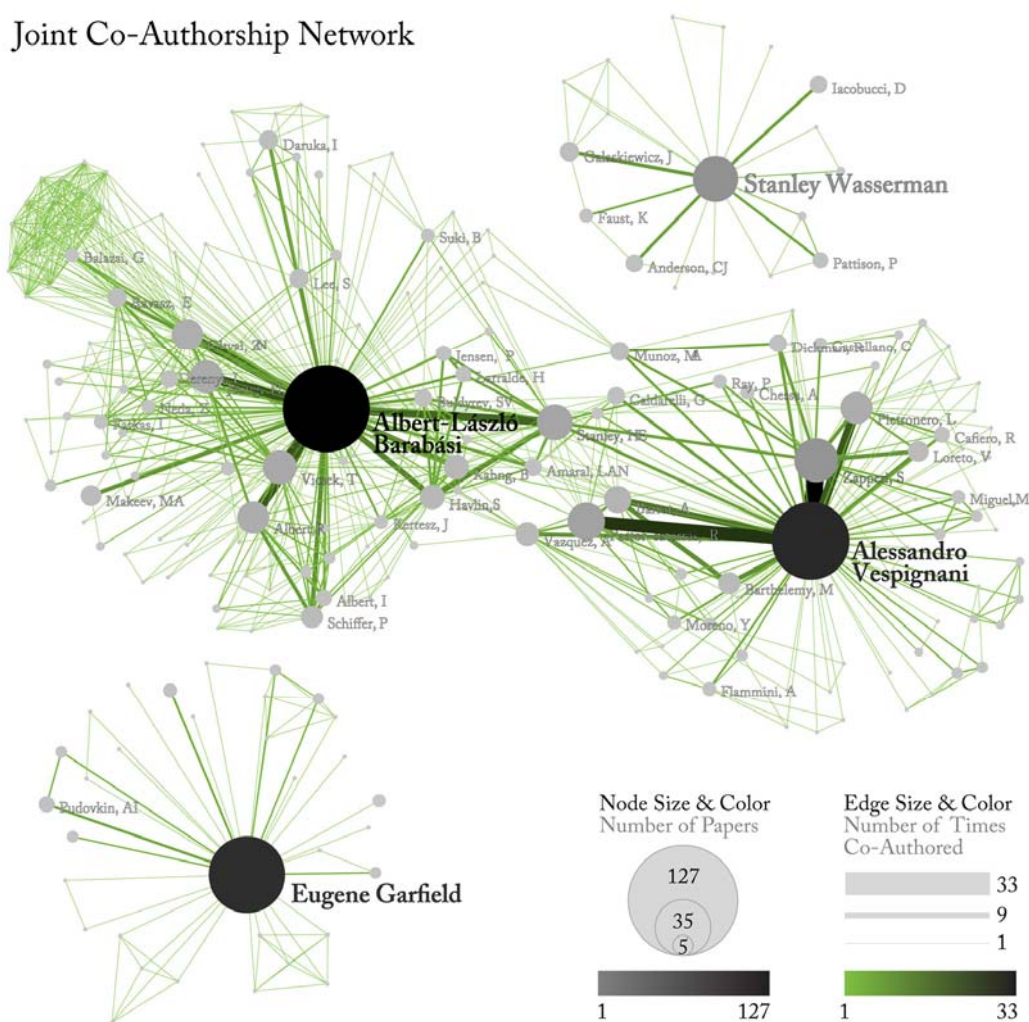


Figure 4: undirected, weighted co-author network for ‘FourNetSciResearchers’ dataset

6.2.2 Word Co-Occurrence Network

The topic similarity of basic and aggregate units of science can be calculated via an analysis of the co-occurrence of words in associated texts. Units that share more words in common are assumed to have higher topic overlap and are connected via linkages and/or placed in closer proximity. Word co-occurrence networks are weighted and undirected.

In the NWB Tool, select the table of 361 unique ISI records from the ‘*FourNetSciResearchers*’ dataset in the Data Manager. Run ‘*Preprocessing > Normalize Text*’ using parameters

New Separator		
Abstract		# Check this box

The performed text normalization utilizes the StandardAnalyzer provided by Lucene (http://lucene.apache.org/java/2_2_0/api/org/apache/lucene/analysis/standard/StandardAnalyzer.html). It separates text into word tokens, normalizes word tokens to lower case, removes ‘s’ from the end of words, removes dots from acronyms, and deletes stop words. Soon the Porter Stemmer Algorithm (<http://tartarus.org/~martin/PorterStemmer>) will become available as well.

The result is a derived table in which the text in the abstract column is normalized. Select this table and run ‘*Scientometrics > Extract Word Co-Occurrence Network*’ using parameters:

Node Identifier Column	Cite Me As
Text Source Column	Abstract
Text Delimiter	
Aggregate Function File	[None]

The outcome is a network in which nodes represent words and edges denote their joint appearance in a paper. Word co-occurrence networks are rather large and dense. Running the ‘*Analysis > Network Analysis Toolkit (NAT)*’ reveals that the network has 2,888 word nodes and 366,009 co-occurrence edges. There are 235 isolate nodes that can be removed running ‘*Preprocessing > Delete Isolates*’. Note that when isolates are removed, papers without abstracts are removed along with the keywords.

The result is one giant component with 2,653 nodes and 366,009 edges. To visualize this rather large network run ‘*Visualization > DrL (VxOrd)*’ with default values.

To keep only the strongest edges run ‘*Preprocessing > Extract Top Edges*’ using parameters

Top Edges	1000
-----------	------

and leave the others at their default values. Once edges have been removed, the network can be visualized by running ‘*Visualization > GUESS*’. In GUESS, run the following commands:

```
> for node in g.nodes:           # to position the nodes at the DrL calculated place
...     node.x = node.xpos * 40
...     node.y = node.ypos * 40
...
> resizeLinear(references, 2, 40)
> colorize(references,[200,200,200],[0,0,0])
> resizeLinear(weight, .1, 2)
> g.edges.color = "127,193,65,255"
```

and set the background color to white to re-create the visualization. The result should look something like the one in Figure 5.

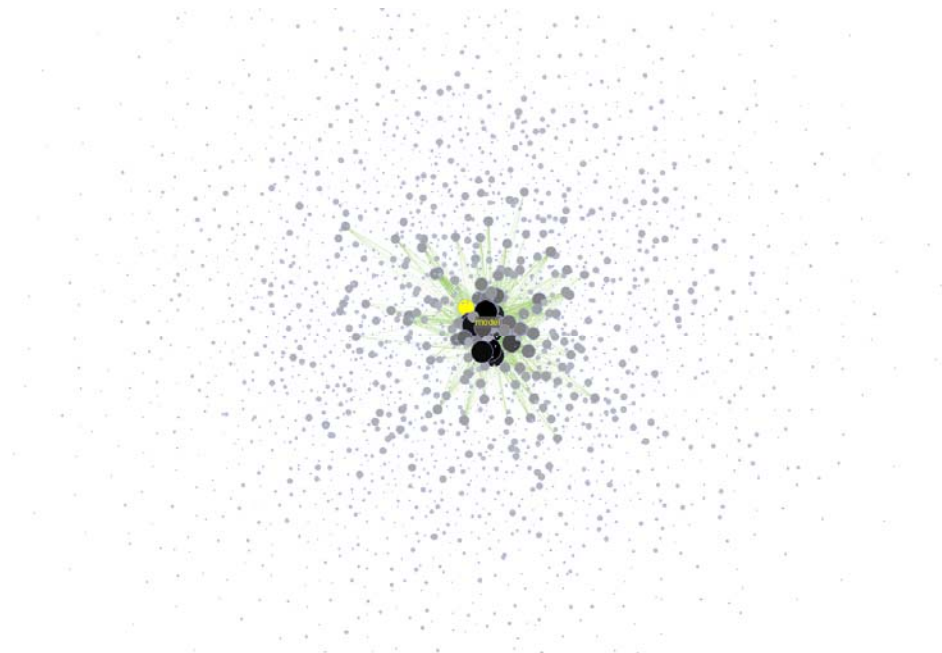


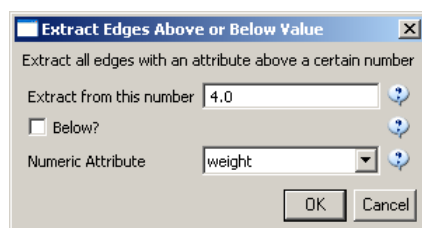
Figure 5: Undirected, weighted word co-occurrence network for 'FourNetSciResearchers' dataset

6.2.3 Cited Reference Co-Occurrence (Bibliographic Coupling) Network

Papers, patents or other scholarly records that share common references are said to be coupled bibliographically (Kessler, 1963), see Figure 4. The bibliographic coupling (BC) strength of two scholarly papers can be calculated by counting the number of times that they reference the same third work in their bibliographies. The coupling strength is assumed to reflect topic similarity. Co-occurrence networks are undirected and weighted.

In NWB Tool, a bibliographic coupling network is derived from a directed paper citation network; see section 'Paper-Paper (Citation) Networks'. Select the paper citation network of the 'FourNetSciResearchers' dataset in the Data Manager. Run '*Scientometrics* > *Extract Reference Co-Occurrence (Bibliographic Coupling) Network*' and the bibliographic coupling network becomes available in the Data Manager.

Running '*Analysis* > *Network Analysis Toolkit (NAT)*' reveals that the network has 5,335 nodes (5,007 of which are isolate nodes) and 6,206 edges. Edges with low weights can be eliminated by running '*Preprocessing* > *Extract Edges Above or Below Value*' with parameter values:



Isolate nodes can be removed running '*Preprocessing* > *Delete Isolates*'. The resulting network has 241 nodes and 1,508 edges in 12 weakly connected components. This network can be visualized in GUESS; see Figure x and the above explanation. Nodes and edges can be color and size coded, and the top-20 most cited papers can be labeled by entering the following lines in the GUESS Interpreter:

```
> resizeLinear(globalcitationcount,2,40)
> colorize(globalcitationcount,(200,200,200),(0,0,0))
> resizeLinear(weight,.25,8)
> colorize(weight,"127,193,65,255", black)
> for n in g.nodes:
```



```

...         n.strokecolor=n.color
> toptc = g.nodes[:]
> def bytc(n1, n2):
...     return cmp(n1.globalcitationcount, n2.globalcitationcount)
> toptc.sort(bytc)
> toptc.reverse()
> toptc
> for i in range(0, 20):
...     toptc[i].labelvisible = true

```

Alternatively, run ‘*GUESS: File > Run Script ...*’ and select ‘*yournwbdirectory*/sampledata/isi/reference-co-occurrence-nw.py’.

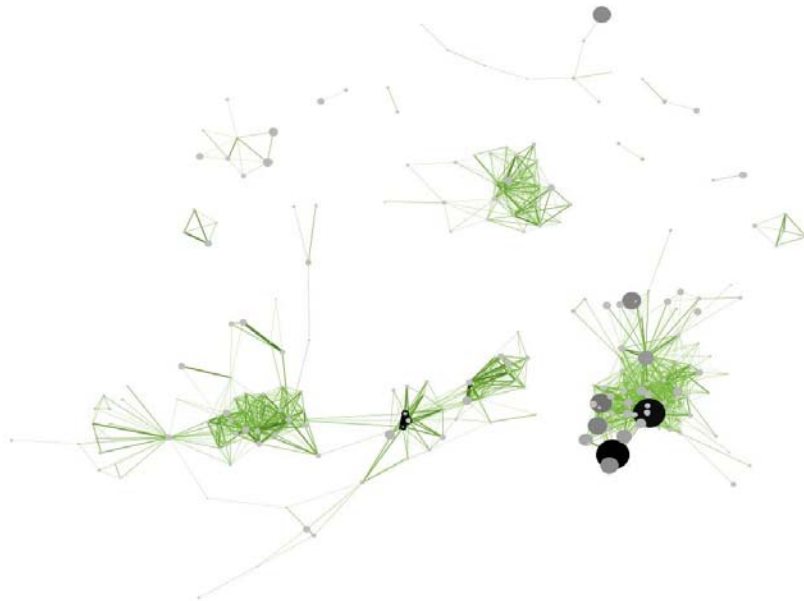


Figure 6: Reference Co-occurrence Network Layout for ‘FourNetSciResearchers’ dataset

6.3 Co-Citation Linkages

Two scholarly records are said to be *co-cited* if they jointly appear in the list of references of a third paper, see Figure 4. The more often two units are co-cited the higher their presumed similarity.

6.3.1 Document Co-Citation Network (DCA)

DCA was simultaneously and independently introduced by Small and Marshakova in 1973 (Marshakova, 1973.; Small, 1973; Small & Greenlee, 1986). It is the logical opposite of bibliographic coupling. The co-citation frequency equals the number of times two papers are cited together, i.e., they appear together in one reference list, see Figure 7.

In the NWB Tool, select the paper-citation network, see section ‘Paper-Paper (Citation) Linkages’ and run ‘*Scientometrics > Extract Document Co-Citation Network*’. The co-citation network will become available in the Data Manager. It has 5,335 nodes (213 of which are isolates) and 193,039 edges. Isolates can be removed running ‘*Preprocessing > Delete Isolates*’. The resulting network has 5122 nodes and 193,039 edges – and is too dense for display in GUESS. Edges with low weights can be eliminated by running ‘*Preprocessing > Extract Edges Above or Below Value*’ with parameter values:

Extract from this number	4	
Below?		# leave unchecked
Numeric Attribute	weight	

Here, only edges with a local co-citation count of five or higher are kept. The giant component in the resulting network has 265 nodes and 1,607 edges. All other components have only one or two nodes.

The giant component can be visualized in GUESS, see Figure 7 (right); see the above explanation, and use the same size and color coding and labeling as the bibliographic coupling network. Simply run ‘*GUESS: File > Run Script ...*’ and select ‘**yournwbdirectory*/sampledata/isi/reference-co-occurrence-nw.py*’.

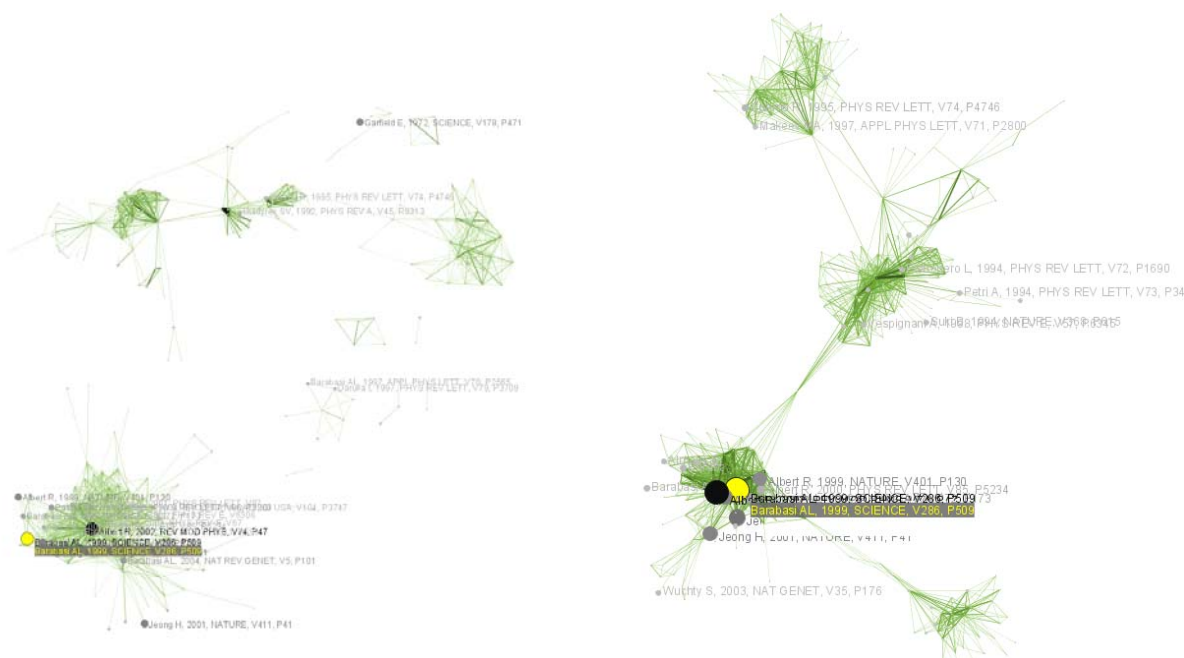


Figure 7: Undirected, weighted bibliographic coupling network (left) and undirected, weighted co-citation network (right) of ‘FourNetSciResearchers’ dataset, with isolate nodes removed.

6.3.2 Author Co-Citation Network (ACA)

Authors of works that are repeatedly juxtaposed in references-cited lists are assumed to be related. Clusters in ACA networks often reveal shared schools of thought or methodological approach, common subjects of study, collaborative and student-mentor relationships, ties of nationality, etc. Some regions of scholarship are densely crowded and interactive. Others are isolated and nearly vacant.

The NWB Tool will support this functionality in the near future.

7 Analyzing and Visualizing Large Networks

Most network analysis and visualization algorithms do not scale to millions of nodes. Even if a layout is produced it is often hard to interpret. Therefore, it is beneficial to employ algorithms that help identify the backbone, i.e., the major connections in a network, or identify communities.

7.1 Basic Network Properties

The ‘*Analysis > Network Analysis Toolkit (NAT)*’ (Cisco Systems, 2004) can be applied to any size network to compute basic network properties, see sample output for ‘FourNetSciResearchers’ dataset in Figure 1.

```
Nodes: 248
Isolated nodes: 1
Node attributes present: label, timesCited, numberOfWorks

Edges: 891
No self loops were discovered.
No parallel edges were discovered.
Edge attributes:
  Did not detect any nonnumeric attributes
  Numeric attributes:
```

	min	max	mean
number of works ...	1	33	1.76094

This network seems to be valued.

Average degree: 7.185483870967743
This graph is not weakly connected.
There are 4 weakly connected components. (1 isolates)
The largest connected component consists of 194 nodes.
Did not calculate strong connectedness because this graph was not directed.

Density (disregarding weights): 0.02909
Additional Densities by Numeric Attribute
densities (weighted against standard max)
numberOfCoAuthoredWorks: 0.05123
densities (weighted against observed max)
numberOfCoAuthoredWorks: 0.00155

Figure 1: Network Analysis Toolkit NAT result for ‘FourNetSciResearchers’ dataset

This is especially important if networks are large as the network properties suggest certain data reduction approaches. For example, if a network is unconnected, it might be beneficial to layout components separately – identify existing components using ‘*Analysis > Unweighted & Undirected > Connected Components*’. If a network is very dense, then backbone identification and community detection methods discussed below should be applied to identify major structures.

7.2 Backbone Identification

7.2.1 Pathfinder Network Scaling (PfNet)

is a structural modeling technique originally developed for the analysis of proximity data in psychology by Schvaneveldt, Durso & Dearholt (Schvaneveldt, Durso, & Dearholt, 1985) According to Chen (Chen, 1999), Pathfinder Network Scaling provides "a fuller representation of the salient semantic structures than minimal spanning trees, but also a more accurate representation of local structures than multidimensional scaling techniques."

The algorithm takes a proximity matrix as input and defines a network representation of the items while preserving only the most important links. It relies on the so-called triangle inequality to eliminate redundant or counter-intuitive links. Given two links or paths in a network that connect two nodes, the link/path is preserved that has a greater weight defined via the Minkowski metric. It is assumed that the link/path with the greater weight better captures the interrelationship between the two nodes and that the alternative link/path with less weight is redundant or even counter-intuitive and should be pruned from the network. Two parameters r and q influence the topology of a pathfinder network. The r -parameter influences the weight of a path based on the Minkowski metric. The q -parameter defines the number of links in alternative paths (=length of a path) up to which the triangle inequality must be maintained. A network of N nodes can have a maximum path length of $q=N-1$. With $q=N-1$ the triangle inequality is maintained throughout the entire network. For details on the method and its applications see (Schvaneveldt, 1990).

In the NWB Tool the algorithm can be found under ‘*Preprocessing > Pathfinder Network Scaling*’. Shown below is a visualization of the ‘FourNetSciResearchers’ dataset.

7.2.2 Main Path Analysis

is an alternative method from Hummon and Doreian that only works on directed acyclic graphs, such as ideal citation networks (real world citation networks can have loops, frequently due to citations into the future) (Hummon & Doreian, 1989). There are three variants, called node pair projection count (NPPC), search path link count (SPLC), and search path node pair (SPNP), all of which produce similar results. The SPLC method is frequently used due to lower computational requirements, and main path analysis using that method will be available in the NWB Tool shortly. All three methods work by counting how many times links are traversed based on various models of information flow through the network. The SPLC method counts how many times every edge is traversed over all possible search paths through the network from every origin node. A main path is found by traversing from a source (a node with no in-links) along each edge with the highest count until one or more sinks (nodes with no out-links)

are reached. In Hummon and Doreian, there is almost always a single main path that starts at the source having the highest count outwards on the first step (rarely there might be a tie, in which case there could be multiple main paths), but later research prefers the network of all main paths, which is more analogous to pathfinder network scaling (Verspagen 2007).

7.3 Community Detection

Diverse algorithms exist to identify sub-networks or communities in large scale networks. The simplest method is to extract individual connected components, which are any maximal set of nodes where every node can be reached from every other node. This Weak Component clustering is a useful technique from graph theory, because network algorithms generally work independently on each component (as no edges exist between components).

In the NWB Tool, running ‘*Analysis > Unweighted & Undirected > Weak Component Clustering*’ on the “FourNetSciResearchers” co-authorship network results in three unconnected components that can be visualized separately (see Garfield’s co-authorship network in Figure 2 and the complete co-authorship network in Figure 3).

In weighted networks, e.g., co-occurrence or co-citation networks (see section Co-occurrence Linkages) thresholds can be applied, e.g., all edges below a certain weight can be omitted, leading to a less dense, possibly unconnected network. As an example, we show the application of ‘*Preprocessing > Extract Edges Above or Below Value*’ to the “FourNetSciResearchers” for different thresholds in Figure 2. Higher thresholds result in fewer edges and more network components.

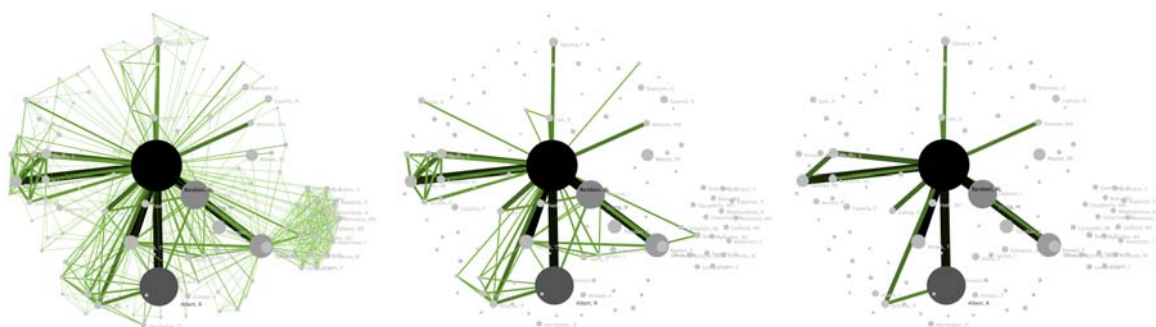


Figure 2: Layout of ‘FourNetSciResearchers’ dataset with no threshold (left), with three or more co-authorships (middle) and with 5 or more co-authorships (right)

7.3.1 Betweenness Centrality (BC)

refers to the number of times a path from any node in a network to any other node in this network goes through a specific node or edge (Freeman, 1977). A node or edge that interconnects two sub-networks has a high BC value and is also called a gatekeeper or weak link (Granovetter, 1973). The original algorithm is computationally very expensive and only applicable to networks of up to several hundred nodes. In 2001, Ulrik Brandes proposed a more efficient algorithm for betweenness that exploits the extreme sparseness of typical networks (Brandes, 2001). Other shortest-path based indices, like closeness or radiality, can be computed simultaneously within the same bounds (Anthonisse, 1971).

In the NWB Tool, application of ‘*Analysis > Unweighted & Undirected > Node Betweenness Centrality*’ to the ‘FourNetSciResearchers’ co-authorship network adds BC values to each node. The top-five nodes with the highest BC value are listed below.

BC Value	Name	ISI’s TC	# Papers
31515.5	Barabasi, AL	13496	127
19812.7	Vespignani, A	3811	101
3589.5	Garfield, E	2469	98
1531.35	Stanley, HE	994	22
1528.89	Vazquez, A	620	10

Figure 3 (left) shows a GUESS visualization, with nodes size coded and color coded according to their BC values, using the following GUESS interpreter commands:

```
> resizeLinear(sitebetweenness,2,40) # nodes
> colorize(sitebetweenness,[200,200,200],[0,0,0])
> colorize(numberofcoauthoredworks,[127,193,65],[0,0,0]) # edges
> resizeLinear(numberofcoauthoredworks,.5,8)
> gemLayout()
> binPackLayout()
```

The elimination of the top 5 nodes with the highest BC values leads to unconnected clusters of nodes (see Figure 3 (right)). Note how Garfield's network (top-right) disintegrates into many smaller subnetworks, while the joint Barabasi-Vespignani network exhibits a giant connected component even after the removal of the top-4 edges. The Wasserman network (bottom-right) is unaffected, since no nodes or edge have been removed.

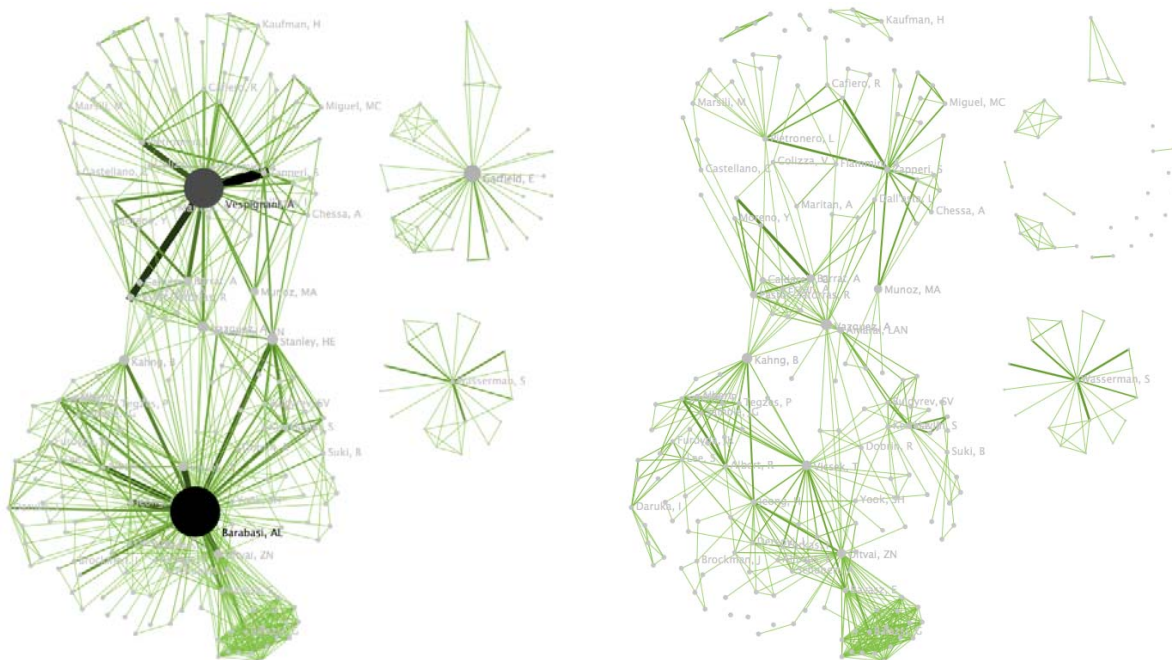


Figure 3: Layout of ‘FourNetSciResearchers’ dataset, with nodes size coded according to their BC value (left) and with the top 5 nodes with the highest BC values removed(right).

7.3.2 Other Community Detection Algorithms

The NWB team is currently working on integrating additional community detection algorithms into Network Workbench. We hope to include the following algorithms in the near future:

- Girvan and Newman 1999, which cuts edges in order of descending betweenness centrality to give clusters (Girvan & Newman, 2002),
- Blondel et al 2008, which agglomerates communities hierarchically based on improvements in modularity (Blondel, Guillaume, Lambiotte, & Lefebvre, 2008),
- Palla et. al 2005, also called CFinder which finds communities based on overlapping cliques (Palla, Derényi, Farkas, & Vicsek, 2005), and
- Reichardt and Bornholdt 2004, which models community structure as identical equilibrium spin states (Reichardt & Bornholdt, 2004)

7.4 Large Network Layout

The NWB Tool supports the layout of networks with up to 10 million nodes via DrL, formerly called VxOrd (Davidson, Wylie, & Boyack, 2001). For example, it is possible to select a co-citation network and run ‘Visualization > DrL (VxOrd)’ with parameters

```
Edge Cutting          0.8
Edge Weight Attribute weight
X Position Attribute  xpos
Y Position Attribute  ypos
```

The result is a *Laid Out Network* file that contains x, y positions for all nodes. The file can be visualized using ‘Visualization > Pre-defined Positions (*prefuse beta*)’ with parameters

```
x  xpos
y  ypos
```

or using GUESS. Note that only node positions are generated. Color and size coding of nodes and edges has to be done in a separate step.

9 Comparison with Other Tools

9.1 General Comparison

The NWB Tool has a number of unique features: It is open source, highly flexible, easily extendable, and scalable to very large networks. Table 1 provides an overview of existing tools used in scientometrics research, see also (Börner, Herr II, & Fekete, 2007; Fekete & Börner, 2004). The tools are sorted by the date of their creation. Domain refers to the field in which they were originally developed such as social science (SocSci), scientometrics (Scientom), biology (Bio), geography (Geo), and computer science (CS). Coverage aims to capture the general functionality and types of algorithms available, e.g., Analysis and Visualization (A+V), see also description column.

Table 1. Network analysis and visualization tools commonly used in scientometrics research.

Tool	Year	Domain	Coverage	Description	UI	Open Source	Operating System	References
S&T Dynamics Toolbox	1985	Scientom	Scientom.	Tools from Loet Leydesdorff for organization analysis, and visualization of scholarly data.	Command-line	No	Windows	(Leydesdorff, 2008)
In Flow	1987	SocSci	A + V	Social network analysis software for organizations with support for what-if analysis.	Graphical	No	Windows	(Krebs, 2008)
Pajek	1996	SocSci*	A + V	A network analysis and visualization program with many analysis algorithms, particularly for social network analysis.	Graphical	No	Windows	(Batagelj & Mrvar, 1998)
UCInet	2000	SocSci*	A + V	Social network analysis software particularly useful for exploratory analysis.	Graphical	No	Windows	(Borgatti, Everett, & Freeman, 2002)
Boost Graph Library	2000	CS	Analysis and Manipulation	Extremely efficient and flexible C++ library for extremely large networks.	Library	Yes	All Major	(Siek, Lee, & Lumsdaine, 2002)
Visone	2001	SocSci	A + V	Social network analysis tool for research and teaching, with a focus on innovative and advanced visual methods.	Graphical	No	All Major	(Brandes & Wagner, 2008)
GeoVISTA	2002	Geo	GeoVis	GIS software that can be used to lay out networks on geospatial substrates.	Graphical	Yes	All Major	(Takatsuka & Gahegan, 2002)
Cytoscape	2002	Bio*	Visualization	Network visualization and analysis tool focusing on biological networks, with	Graphical	Yes	All Major	(Cytoscape-Consortium, 2008)

				particularly nice visualizations.				
Tulip	2003	CS	Visualization	Graph visualization software for networks over 1,000,000 elements.	Graphical	Yes	All Major	(Auber, 2003)
iGraph	2003	CS	Analysis and Manipulation	A library for classic and cutting edge network analysis usable with many programming languages.	Library	Yes	All Major	(Csárdi & Nepusz, 2006)
CiteSpace	2004	Scientom	A + V	A tool to analyze and visualize scientific literature, particularly co-citation structures.	Graphical	Yes	All Major	(Chen, 2006)
HistCite	2004	Scientom	A + V	Analysis and visualization tool for data from the Web of Science.	Graphical	No	Windows	(Garfield, 2008)
R	2004	Statistics	A + V	A statistical computing language with many libraries for sophisticated network analyses.	Command-line	Yes	All Major	(Ihaka & Gentleman, 1996)
Prefuse	2005	Visualization	Visualization	A general visualization framework with many capabilities to support network visualization and analysis.	Library	Yes	All Major	(Heer et al., 2005)
GUESS	2007	Networks	Visualization	A tool for visual graph exploration that integrates a scripting environment.	Graphical	Yes	All Major	(Adar, 2007)
GraphViz	2004	Networks	Visualization	Flexible graph visualization software.	Graphical	Yes	All Major	(AT&T-Research-Group, 2008)
NWB Tool	2006	Bio, SocSci, Scientom	A + V	Network analysis & visualization tool conducive to new algorithms supportive of many data formats.	Graphical	Yes	All Major	(Huang, 2007.)
BibExcel	2006	Scientom	A + V	Transforms bibliographic data into forms usable in Excel, Pajek, NetDraw, and other programs.	Graphical	No	Windows	(Persson, 2008)
Publish or Perish	2007	Scientom	Data Collection and Analysis	Harvests and analyzes data from Google Scholar, focusing on measures of research impact.	Web-based	No	Windows, Linux	(Harzing, 2008)

Many of these tools are very specialized and capable. For instance, BibExcel and Publish or Perish are great tools for bibliometric data acquisition and analysis. HistCite and CiteSpace each support very specific insight needs – from studying the history of science to the identification of scientific research frontiers. The S&T Dynamics Toolbox provides many algorithms commonly used in scientometrics research and it provided bridges to more general tools. Pajek and UCINET are very versatile, powerful network analysis tools that are widely used in social network analysis. Cytoscape is excellent for working with biological data and visualizing networks.

The Network Workbench Tool has fewer analysis algorithms than Pajek and UCINET, and less flexible visualizations than Cytoscape. Network Workbench, however, makes it much easier for researchers and algorithm authors to integrate new and existing algorithms and tools that take in diverse data formats. The OSGi component architecture and CISHell algorithm architecture built on top of OSGi make this possible. Cytoscape is also adopting an architecture based on OSGi, though it will still have a specified internal data model and will not use CISHell in the core. Moving to OSGi will make it possible for the tools to share many algorithms, including adding Cytoscape's visualization capabilities to Network Workbench.

Many of these tools are also libraries. Unfortunately, it is often difficult to use multiple libraries, or sometimes any outside library, even in tools that allow the integration of outside code. Network Workbench, however, was built to integrate code from multiple libraries (including multiple versions of the same library). For instance, two different versions of Prefuse are currently in use, and many algorithms use JUNG (the Java Universal Network/Graph

Framework). We feel that the ability to adopt new and cutting edge libraries from diverse sources will help create a vibrant ecology of algorithms.

Although it is hard to discern trends for tools which come from such diverse backgrounds, it is clear that over time the visualization capabilities of scientometrics tools have become more and more sophisticated. Scientometrics tools have also in many cases become more user friendly, reducing the difficulty of common scientometrics tasks as well as allowing scientometrics functionality to be exposed to non-experts. Network Workbench embodies both of these trends, providing an environment for algorithms from a variety of sources to seamlessly interact in a user-friendly interface, as well as providing significant visualization functionality through the integrated GUESS tool.

9.2 HistCite by Eugene Garfield

Compiled by Angela Zoss

HistCite was developed by Eugene Garfield and his team to identify the key literature in a research field. As stated on the Web site, HistCite analyzes ISI data retrieved via a keyword based search or cited author search and identifies: important papers, most prolific and most cited authors and journals, other relevant papers, keywords that can be used to expand the collection. It can also be used to analyze publication productivity and citation rates of individuals, institutions, countries. By analyzing the result of an author search, highly cited articles, important co-author relationships, a time line of the authors' publications, and historiographs showing the key papers and timeline of a research field can be derived. A trial version of the tool is available at <http://www.histcite.com>. An interactive version of the "FourNetSciResearchers.isi" analysis result is at <http://ella.slis.indiana.edu/~katy/outgoing/combo>.

Subsequently, we compare paper-paper citation networks created by NWB Tool and HistCite for the "FourNetSciResearchers.isi" dataset.

HistCite identifies 360 nodes in this network, while NWB identifies 361 unique records. The discrepancy is the result of two records that have identical "Cite Me As" values: "ANDERSON CJ, 1993, J MATH PSYCHOL, V37, P299 0 0". NWB is able to distinguish these two records, which have unique ISI IDs but are both book reviews by the same reviewer on the same page in the same journal issue.

HistCite identifies 901 edges between the 360 papers. NWB Tool originally identified 5335 nodes and 9595 edges, as not only linkages between papers in the set but also linkages to references are extracted. The latter nodes can be excluded by removing nodes with a globalCitationCount value of -1 (see section Scientometrics section 6.1.1). The resulting network has 341 nodes and 738 edges (or 276 nodes and 738 edges after deleting isolates).

This network can be visualized in HistCite using *Tools > Graph Maker*. The Graph Maker inputs the nodes of the network, which are then laid out chronologically from the top of the screen to the bottom. The size of the nodes relates to the value of either the Local Citation Score (LCS) or the Global Citation Score (GCS), depending on the type of graph selected. The script examples from Scientometrics section 6.1.1 give suggestions on how to resize the nodes within *GUESS* to accomplish something similar with NWB.

The nodes included can be limited within the Graph Maker according to either their ranking in the sequence of LCS or GCS or their LCS/GCS values. In NWB, this corresponds to "Extract Top Nodes" or "Extract Nodes Above or Below Value". To see all nodes, set the limit to a number above the number of nodes and click on the "Make graph" button, see HistCite result in Figure 1.

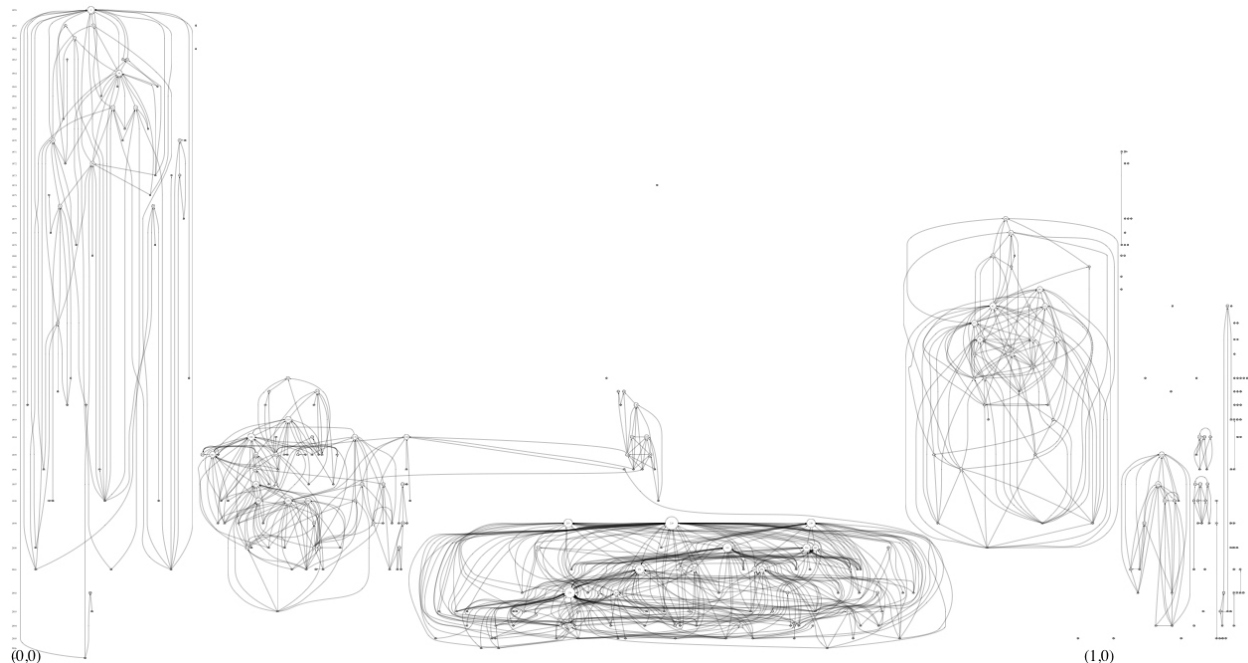


Figure1: Paper-citation graph of the FourNetSciResearcher network in HistCite

As can be seen, this graph includes several isolates, i.e., nodes that have no links to or from other nodes in the network (i.e., Local Cited References = 0 and Local Citation Score = 0). According to the textual summary of the dataset given by HistCite, there are 59 such isolates in this network. These nodes can be marked manually and deleted from the network for a cleaner version of this graph.

9.3 CiteSpace by Chaomei Chen

Compiled by Hanning Guo

CiteSpace II is a tool to visualize patterns and trends in scientific literature. The Java-based tool was developed by Dr. Chaomei Chen at Drexel University and can be downloaded from <http://cluster.cis.drexel.edu/~cchen/CiteSpace>.

For means of comparison, we apply CiteSpace to the FourNetSciResearcher dataset containing all of the ISI records of Garfield, Wasserman, Vespignani, and Barabási. Specifically, we derive the document co-citation, co-authorship, word co-occurrence networks, and burst detection.

9.3.1 Document Co-Citation Network

The document co-citation network for the FourNetSciResearcher dataset was derived using NWB Tool and CiteSpace, see Figure 2. In both cases the size of the nodes stand for betweenness centrality. Node color coding in NWB Tool was set to reflect betweenness centrality. CiteSpace color codes nodes based on ten 2-year time slices covering 1988-2007. Top 10% of most cited references are selected. 415 nodes and 7147 links are laid out in the network. An alternative, larger figure of a document co-citation network derived via NWB Tool is given in section 6.3.1 Document Co-Citation Network (DCA), Figure 7.

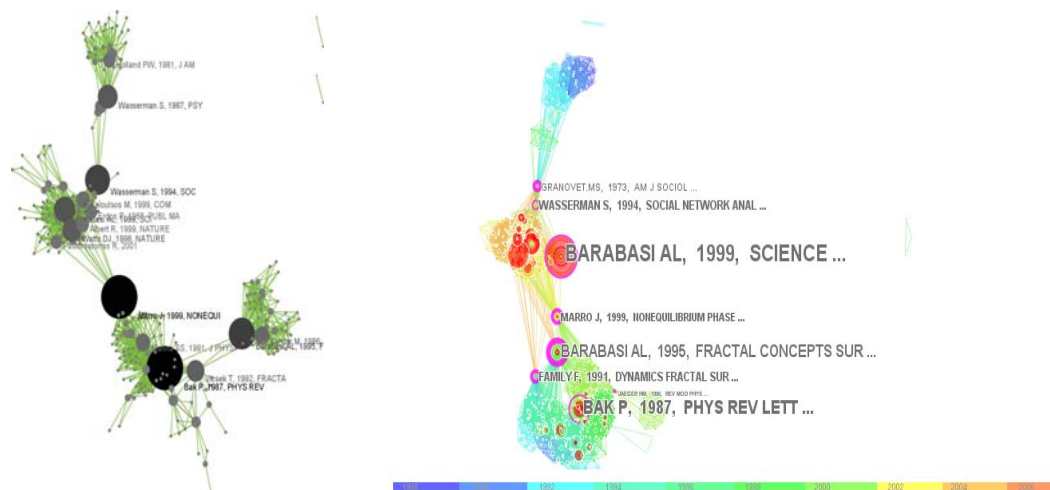


Figure 2: Document co-citation network of FourNetSciResearchers with NWB Tool (left) and using CiteSpace II (right)

9.3.2 Author Co-Occurrence (Co-Author) Network

Figure 3 shows the CiteSpace rendering of the co-authorship network for the FourNetSciResearchers dataset using five 4-year time slices covering 1988–2007. In this network, the **top100%** of most occurred authors from each slice are selected. There are 249 nodes and 907 links in it. Compare to NWB rendering in section ‘6.2.1 Author Co-Occurrence (Co-Author) Network’.

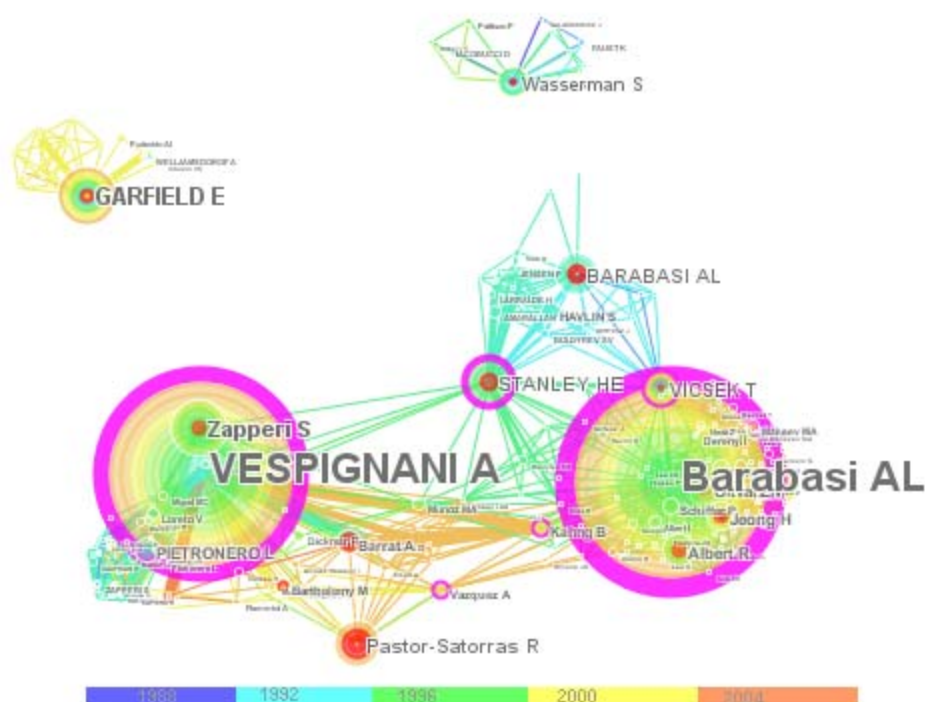


Figure 3: Co-authorship network of FourNetSciResearchers in CiteSpace II

9.3.3 Word Co-Occurrence Network

Figure 4 shows the CiteSpace rendering of the keywords (descriptors and identifiers) co-occurrence network for the FourNetSciResearchers dataset using ten 2-year time slices covering 1988–2007. The top 50% of the most often

occurring keywords from each slice are selected in the network which has 247 nodes and 830 links. Compare to NWB rendering in section ‘6.2.2 Word Co-Occurrence Network’.

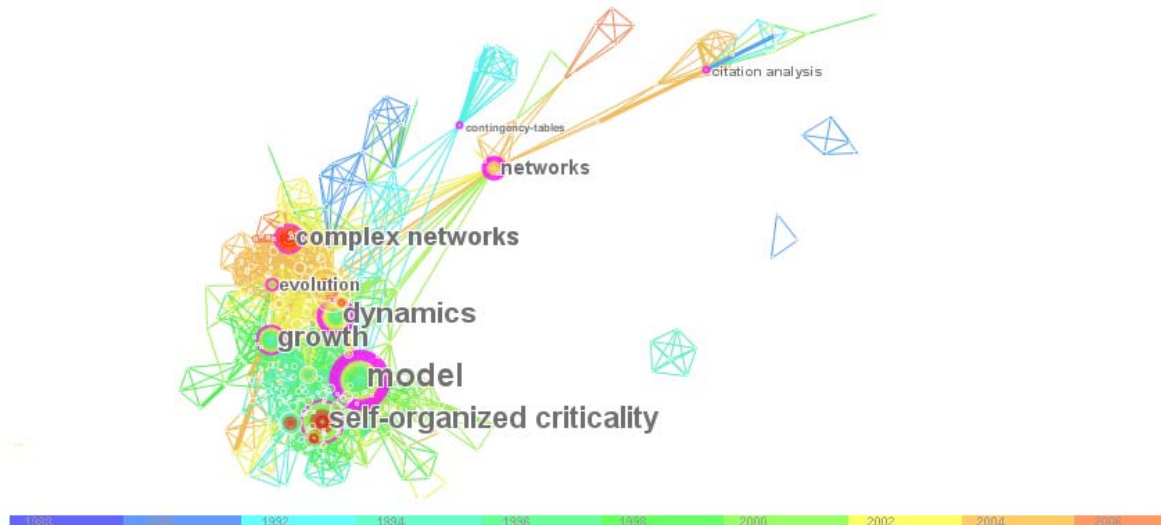


Figure 4: Keyword co-occurrence network of FourNetSciResearchers in CiteSpace II

9.3.4 Burst Detection

Burst detection using NWB Tool was discussed in section ‘3.2 Burst Detection’.

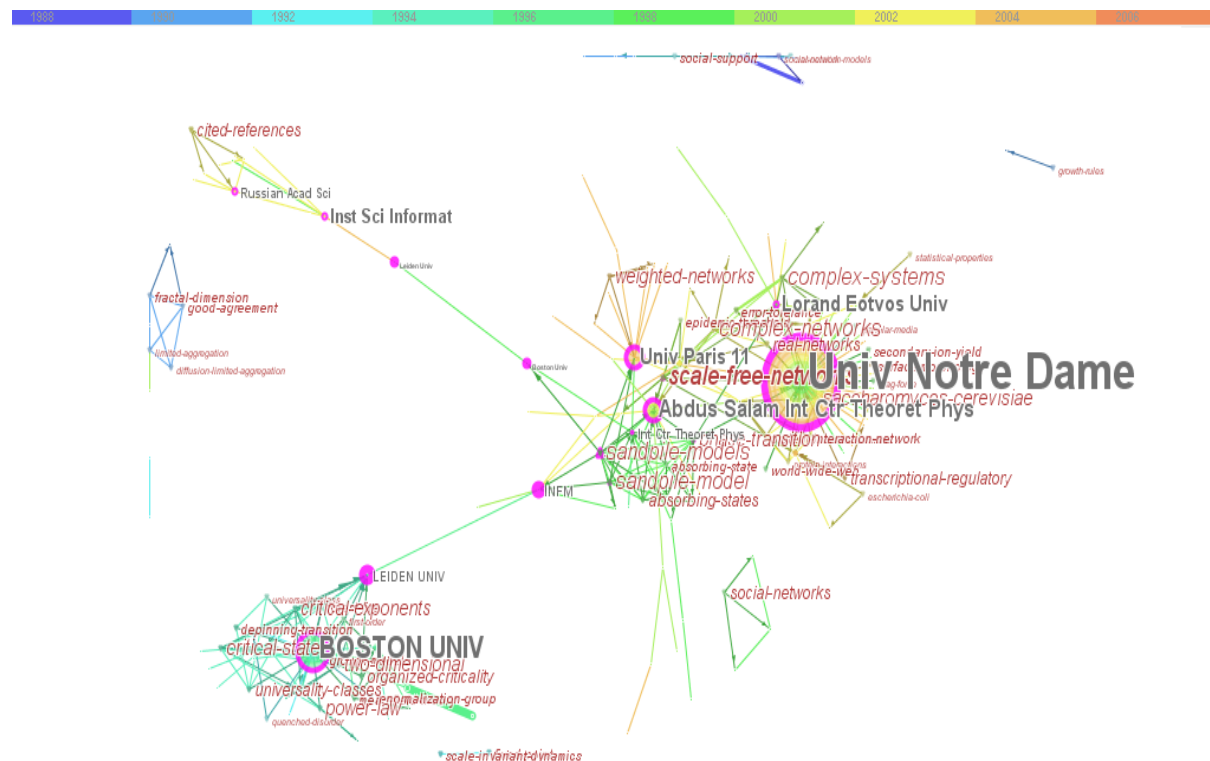


Figure 5: Network of co-author's institutions for “FourNetSciResearchers” with burst phrases in CiteSpace II

9.3.5 Comparison

Supported Data Formats

NWB Tool supports GraphML (*.xml or *.graphml), XGMML (*.xml), Pajek .NET (*.net), Pajek .Matrix (*.mat), NWB (*.nwb), TreeML (*.xml), Edge list (*.edge), CSV (*.csv), ISI (*.isi).

CiteSpace II can load ISI export format. It also offers converters from SDSS, NSF, Scopus, and Derwent to WOS (ISI), and **Medline**. See also Table 1.

Table 2: Network Workbench Tool vs. CiteSpace II

Function	NWB Tool	CiteSpace II
Data Extraction		
ISI	√	√
Scopus	√	√
Google Scholar	√	√
Medline	√	
NSF	√	√
Citeseer	√	√
Google Scholar	√	
Network Derivation		
Paper-Paper (Citation) Network	√	
Author-Paper (Consumed/Produced) Network	√	
Document Co-Citation Network	√	√
Author Co-citation Network		√
Journal Co-citation Network		√
Co-authorship Network	√	√
Network of Co-author's institutions		√
Network of Co-author's countries		√
Word Co-occurrence Network	√	√
Subject Categories Co-occurrence Network		√
Cited Reference Co-Occurrence (Bibliographic Coupling) Network	√	
Burst detection	√	√
Others		
Cluster View	√	√
Time Zone View		√
Time slicing		√
Pathfinder Network	√	√
Detect Duplicate Nodes	√	
Merge Duplicate Nodes	√	√
Betweenness Centrality	√	√
Extract K-core	√	
Geospatial Maps		√

Visualizations

CiteSpace II colors nodes and edges by time, e.g., In the co-citation network, papers by citation year, making it easy to observe the growth of a network over time, see the detailed explanation in Figure 6.

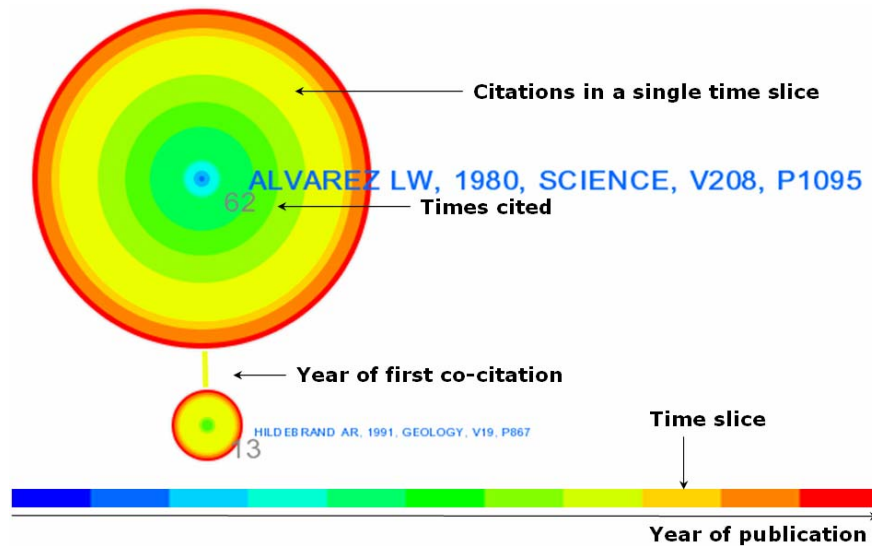


Figure 6: Sketch of the figure produced by Citespace II

CiteSpace II highlights high betweenness centrality (BC) nodes, also called pivotal points, by purple circle borders. This can be replicated in NWB Tool by coloring all nodes above a certain BC threshold value. However, Citespace II can also show the nodes with red colors whose citation has a sharp increase in certain time slice.

From Figure 15, we can see some remarkable nodes which colored with purple ring and red color. Take “BARABASI AL,1999,SCIENCE,V286,P5909” for example, it is the node which has purple ring and red color. Using the function of “Citation History” Citespace II provides, we can see the typical characteristic of this node, see Figure 7. It shows that the node not only has high betweenness, but also has the sharp increase on citation in certain time slices.

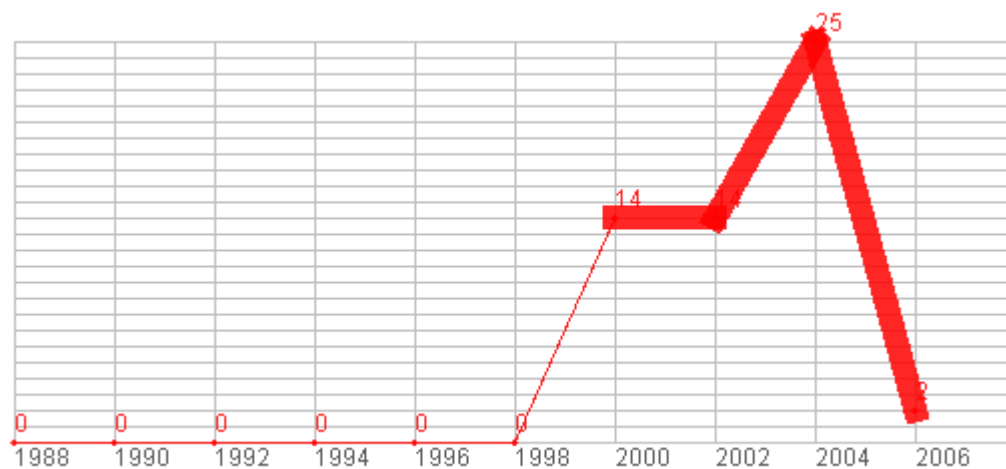


Figure 7: Citation History of Node “BARABASI AL,1999,SCIENCE,V286,P5909”

In the given example, co-authorship networks generated using NWB Tool appear to be easier to read while CiteSpace II renders word co-citation networks in a more legible way.

Citespace II also provide spectral clustering and expectation maximization clustering, see Figure 8.

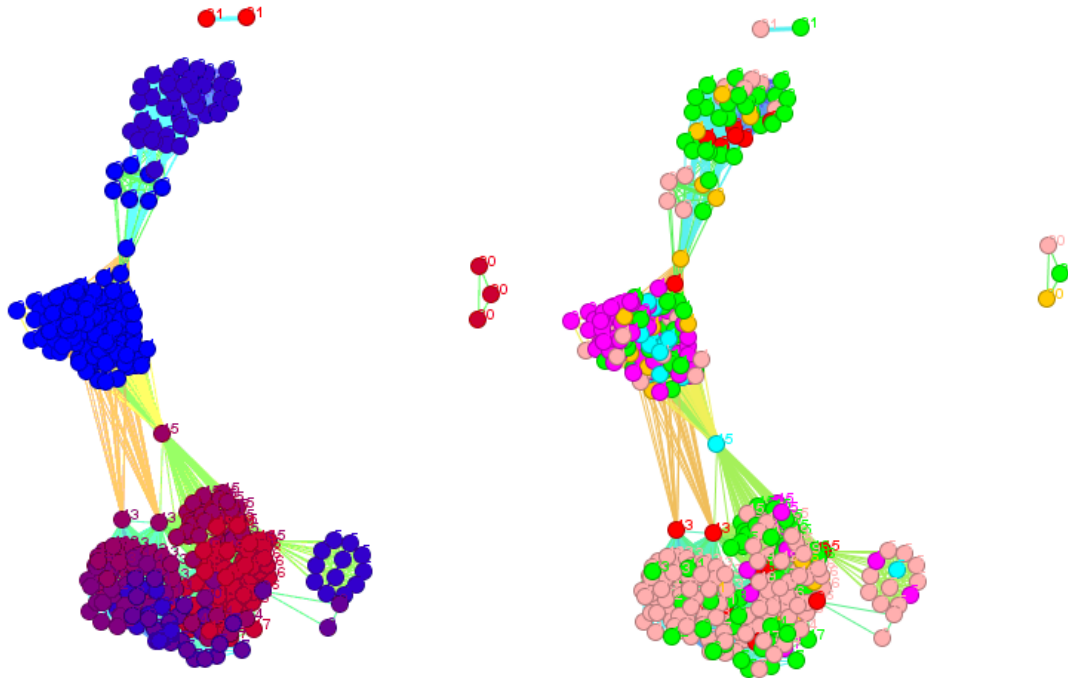


Figure 8: Spectral clustering (left) and expectation (right) maximization clustering of Document co-citation network of FourNetSciResearchers

Network Extraction

A comparison of networks that are extracted by NWB Tool and CiteSpace II can be found in Table 1.

As for word co-occurrence networks, NWB Tool can process the words from any data field but only from one field at a time. CiteSpace II can process words occurring in title, abstract, descriptors, and/or identifiers fields.

Burst Detection

Both tools support burst detection for time stamped author names, journal names, country names, references, ISI keywords, or terms used in title and/or abstract of a paper. NWB can detect different types of burst according to the need of research. CiteSpace II can detect burst phrases from noun phrases or plain text and visualize them. It notes that Noun Phrases are identified using part-of-speech tagging. Plain text terms are identified by sliding-window term selector.

9.4 Pajek by Vladimir Batagelj et al.

A comparison of NWB Tool with Pajek <http://pajek.imfm.si/doku.php> (supporting network analysis and visualization) is in preparation.

9.5 Software by Loet Leydesdorff

Loet Leydesdorff's software is a series of programs with different analysis functions. It contains the analysis of co-authorship network, word co-occurrence network, international collaboration network, institute collaboration network, etc. The results can be visualized by Pajek, Ucinet and NWB, etc. NWB is the program which specializes in the analysis of Scientometrics and visualizations. In this case, we simply compare the analysis functions between them. The data we use is from Network Work Bench sample data file which contains all of Eugene Garfield's, Wasserman's, Vespignani's and Barabási's ISI records for part 1-3. However, in part 4, we also use the NWB sample data of Brain Cancer from Scopus.

9.5.1 Co-authorship Network

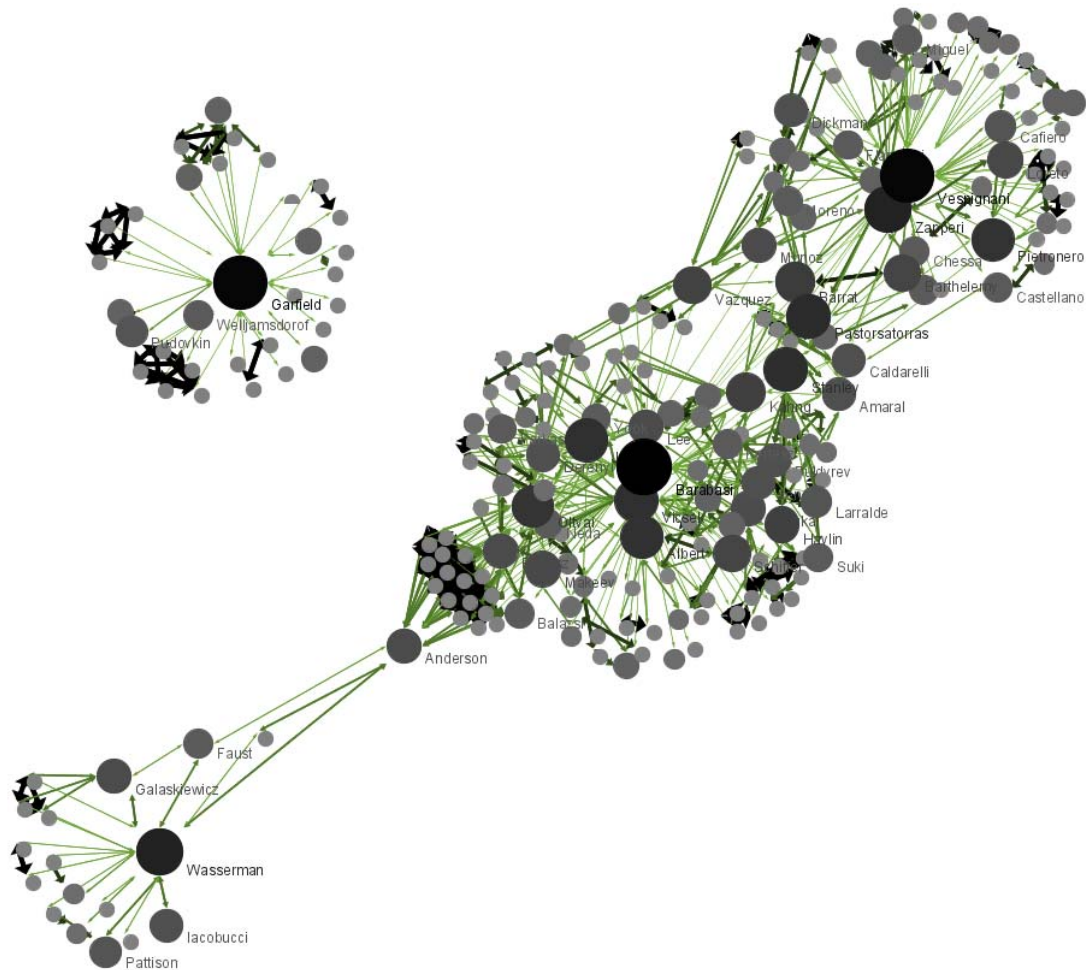


Figure 9: Co-author network for 'FourNetSciResearchers' with Loet's software

The figures indicate that the structures of the two networks which are derived by both two tools are similar. However, the network derived by Leydesdorff's software is directed. As we've seen in 6.2.1, NWB's co-authorship network is undirected. In addition, the former has four weakly connected component, the latter has two which caused by the linkage between Anderson and three authors in the component of Wasserman. See the detailed differences between two networks in Table 3.

Table 3. Comparison of Co-authorship network structure between two software

Attributes	Loet's software	NWB
Direction in the Graph	Directed	Undirected
Nodes	231	247
Edges	1708	891
Weakly connected component	2	3
Nodes in the largest connected component	198	194

9.5.2 Word Co-occurrence Network

Leydesdorff's software can perform the word co-occurrence analysis of title and full text while NWB can analyze title, abstract, keywords and so on.

Because the number of words that Leydesdorff's software can analyze is limited, we deleted the stop words such as a, an, and, with, 2001, by and so on with *stopword.exe* which Dr. Leydesdorff provides.

The word co-occurrence network produced by NWB has 908 nodes and 10694 edges. So we extract top 1000 edges by weight. However, NWB doesn't have the function of deleting stop words (coming soon). As a result, the main nodes in Figure 23 are the stop words which influence the result of the analysis.

Table 4 shows the differences of two networks of word co-occurrence.

Table 4. Comparison of Word Co-occurrence Network structure between the two software packages

Attributes	Leydesdorff's software	NWB
Direction in the Graph	Directed	Undirected
Nodes	295	908
Edges	4582	1000
Weakly connected component	1	3
Nodes in the largest connected component	295	903
Stop words' deleting	Yes	No

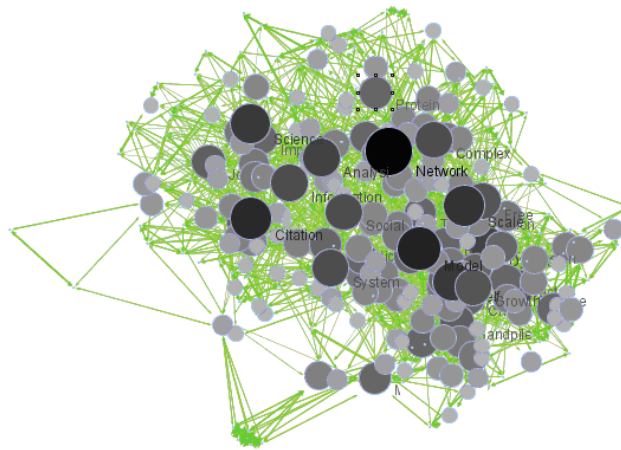


Figure 10: Word co-occurrence network with Leydesdorff's software

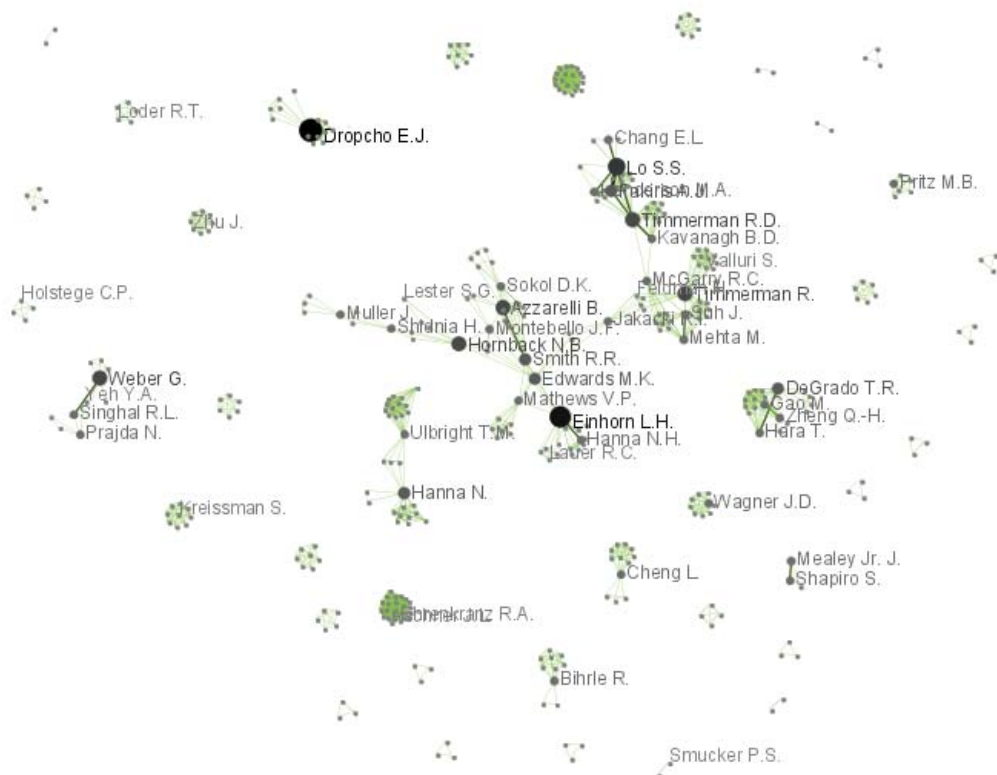


Figure 14: Co-authorship network with the data format from Scopus

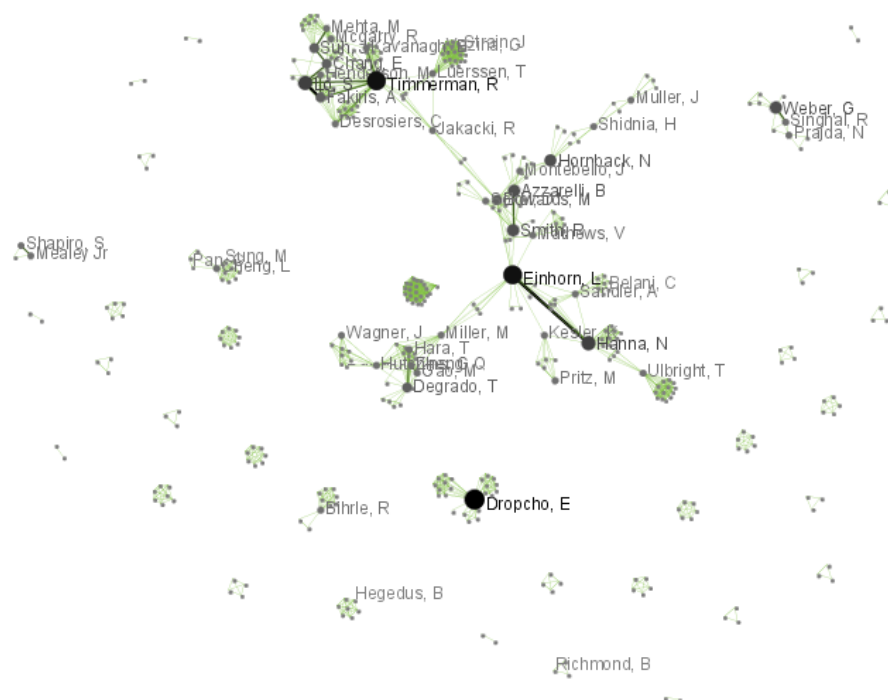


Figure 15: Co-authorship network with converted data format

9.5.5 Other Functionality

Except for the programs above, Leydesdorff's software also includes *Acc2ISI.exe* for the reverse route of turning databases (exported from MS Access) into the "tagged" format of the Web of Science, *IntColl.exe* for the analysis and visualization of international collaboration, *InstColl.exe* for the analysis and visualization of institutional collaboration, *GScholar.exe* for the organization of Google Scholar files into files for relational database management (MS Access, dBase) and *Google.exe* for the organization of Google files into files for relational database management (MS Access, dBase). Simultaneously, some of them are available for Chinese, Korean and Dutch data. NWB does not currently possess these functionalities.

NWB, however, can extract directed networks, paper citation networks, author paper networks, documentation co-citation networks, detect bursts, analyze time slices and so on.

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