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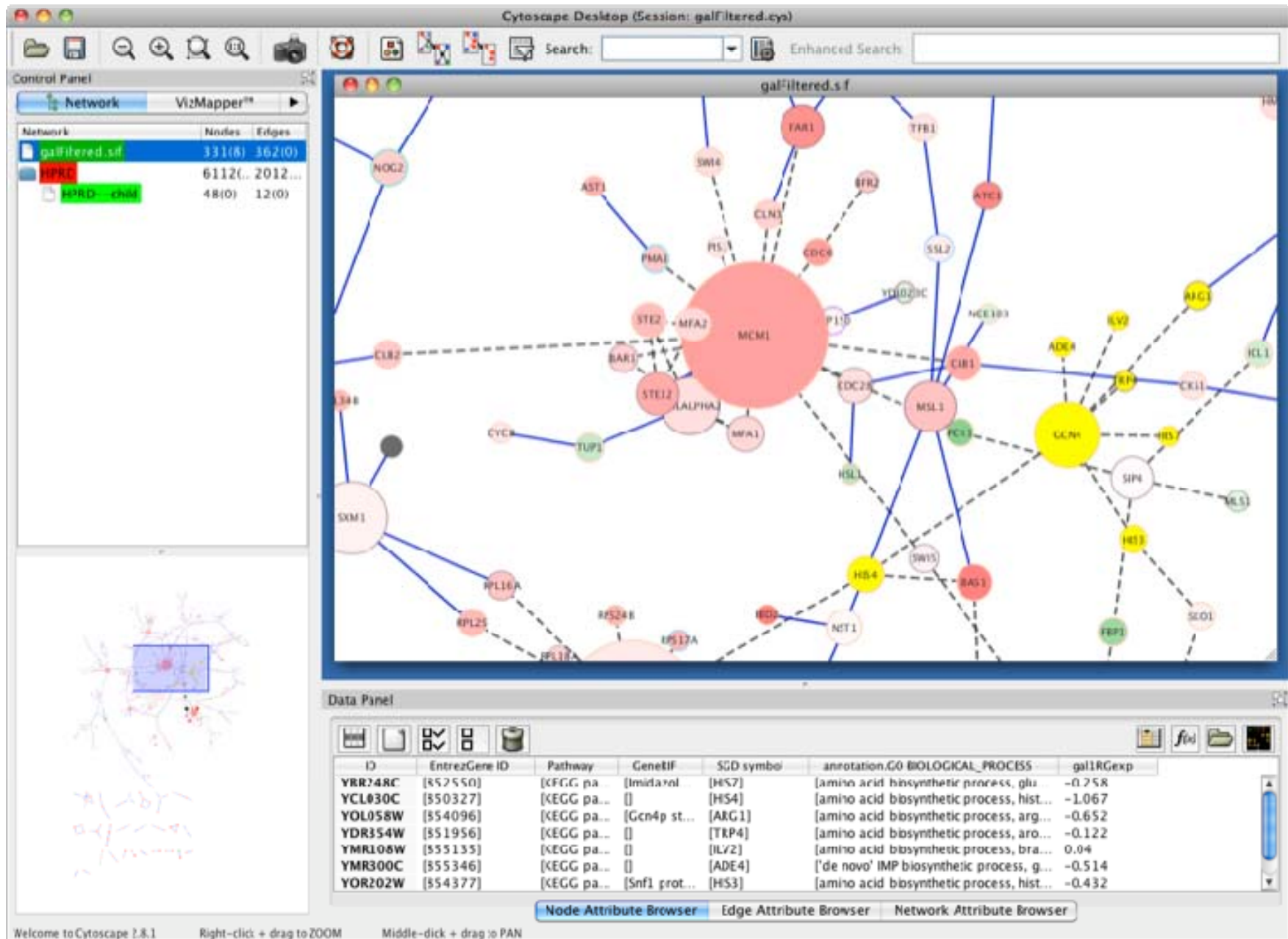
COMBINE 2012
Toronto, Aug 17, 2012

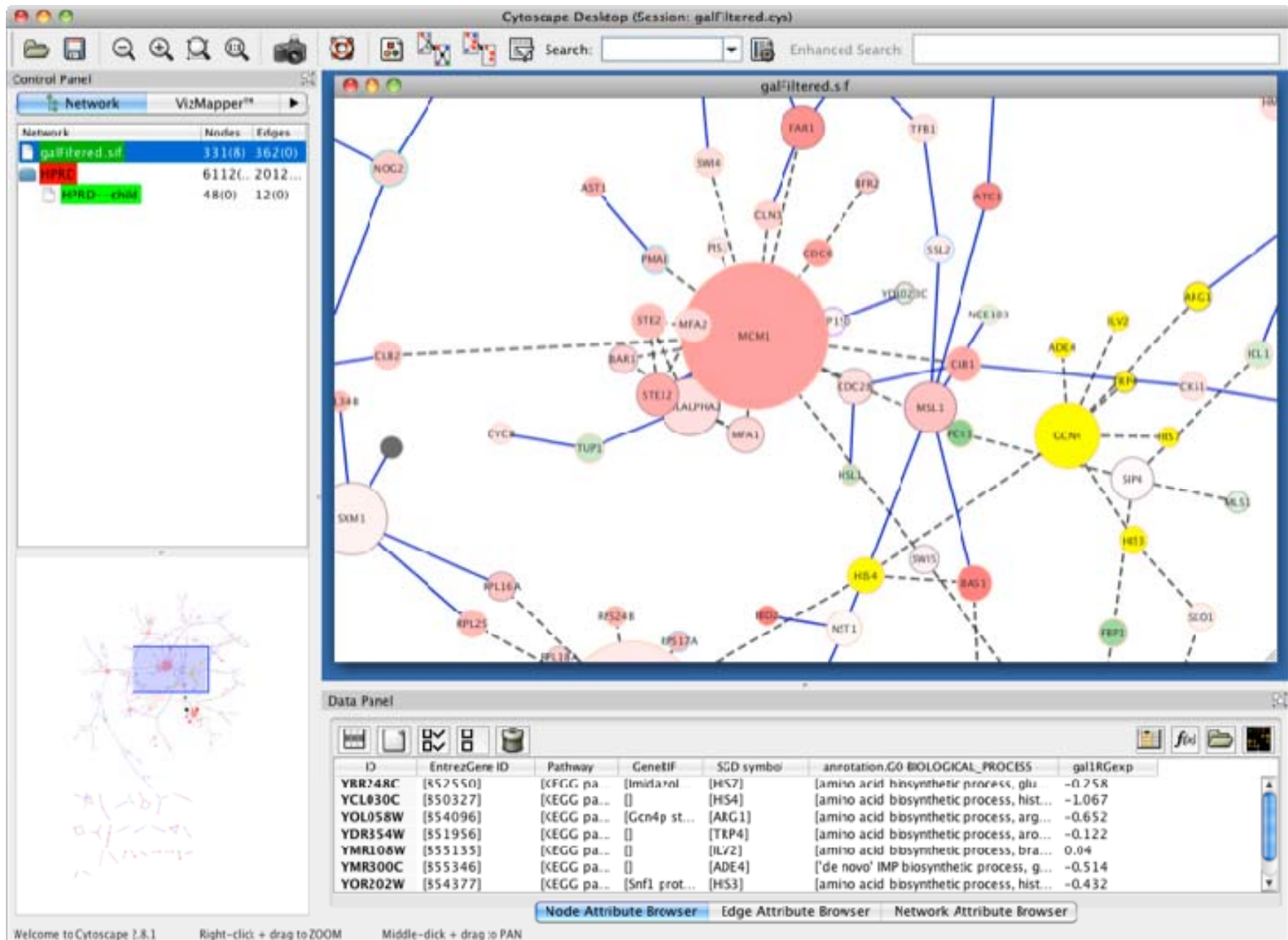


Cytoscape 3

- Complete re-architecture: OSGi – everything is an app
- Enables future features:
 - ↕ More stable and powerful APIs
 - ↕ Scripting, macros, recordable history, better undo/redo
 - ↕ Command line mode, good for use on compute clusters
 - ↕ Interactive control from other scripting languages e.g. R
- Fixing bugs and porting plugins
- 3.0 developer beta now available
 - ↕ Mirror functionality in 2.8

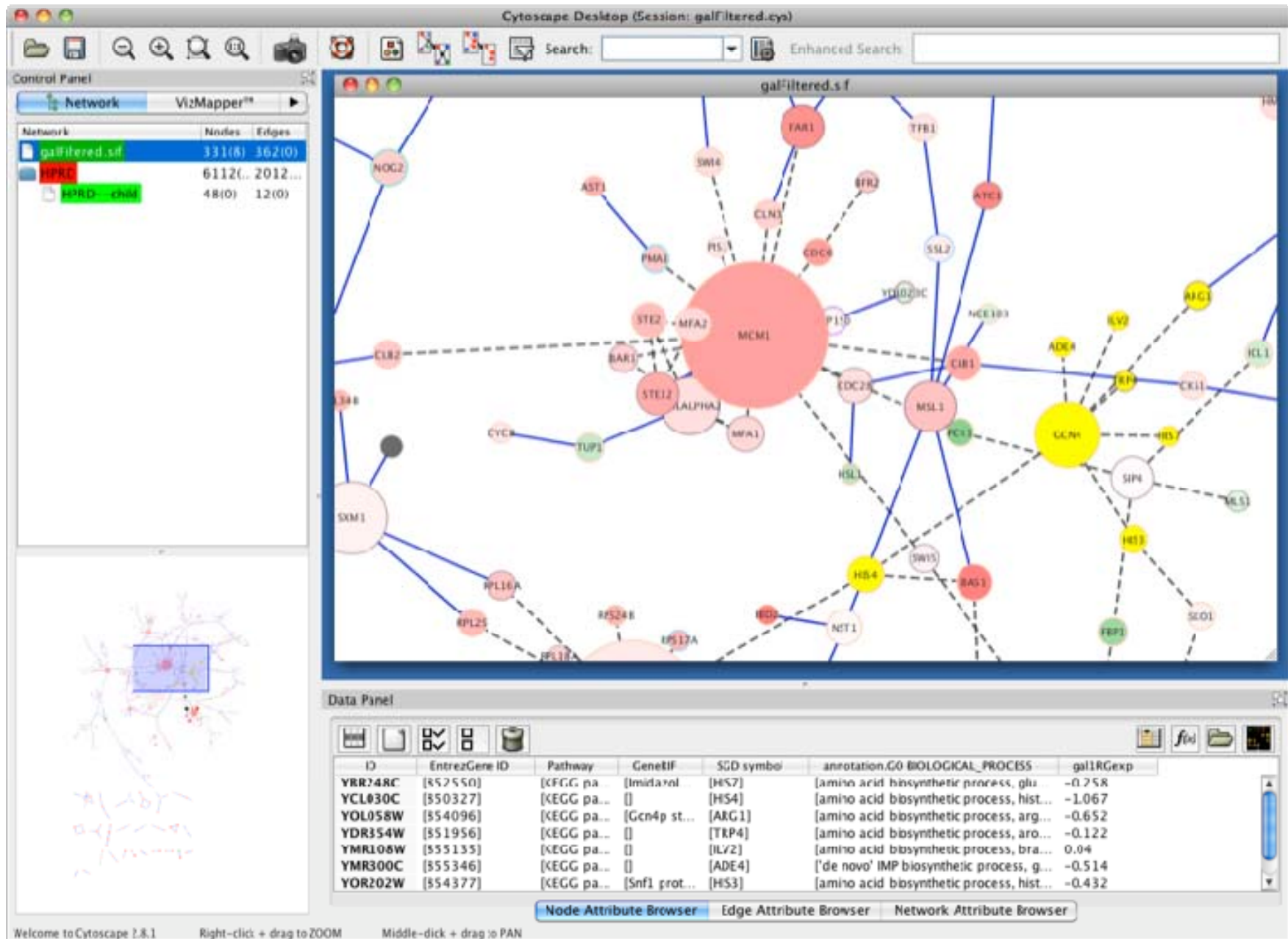
Desktop Application written in Java

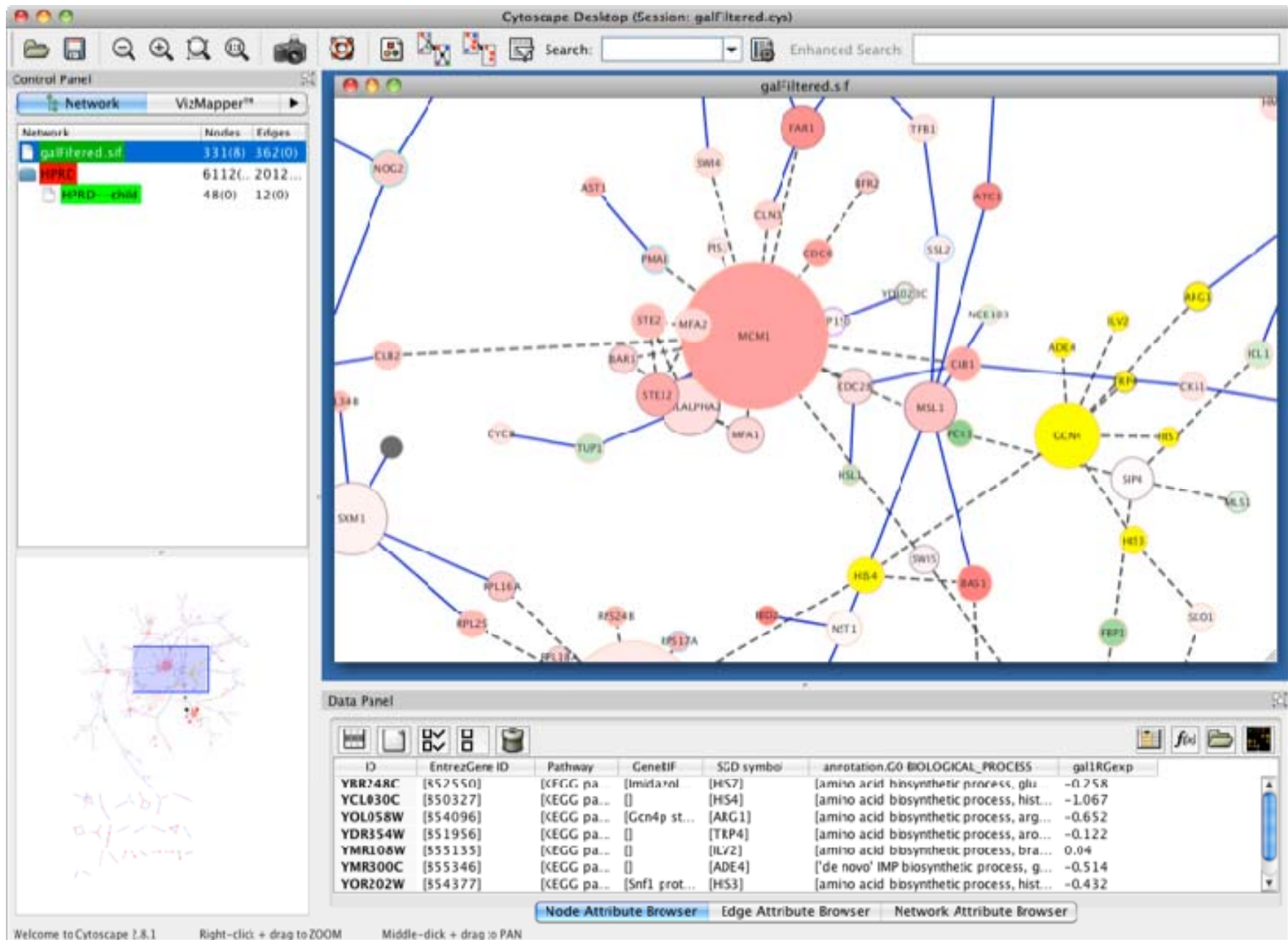




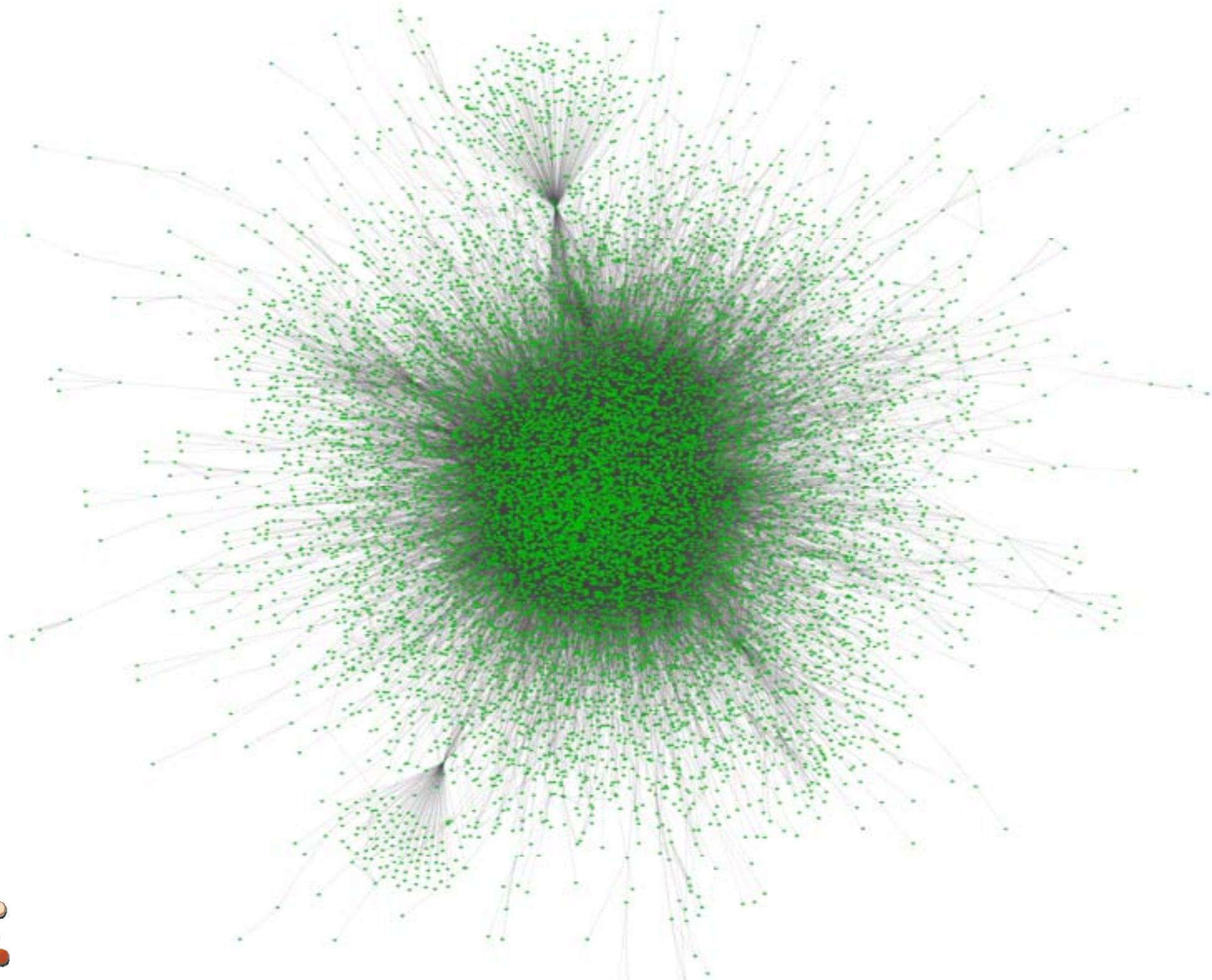
Biological Network Visualization + Analysis

Free Software - LGPL





~5000 downloads per month



Cytoscape's most important feature?



Our ~~Plugin~~ App Architecture



Apps allow for customization

Primary analysis mechanism

Builds a community of stakeholders



AllegroMCODE APCluster APID2NET BioQualiPlugin BLAST2SimilarityGraph BNMatch
CABIN CalculateNodeDegree CentiScaPe ChemViz clusterExplorerPlugin clusterMaker
ClusterONE ClusterViz COMA CommFinder CyClus3D CyOog cytoHubba Cytomcl
DualLayout dynamicXpr EnhancedSearch EnrichmentMap ExprEssence GraMoFoNe
GraphletCounter HiderSlider jActiveModules mcl-new MCODE MINE NeMo NetAtlas
NetCirChro netMatch NetworkAnalyzer NetworkEvolution OmicsAnalyzer OmicsViz
OrthoNets PanGIA PerturbationAnalyzer PinnacleZ RandomNetworks RDFScsape
Reactome Fls RemainingDegreeDistribution ReOrientPlugin ShortestPath Plugin
SimTrek structureViz TransClust VennDiagramGenerator VistaClaraPlugin WordCloud
BiNoM bioCycPlugin BiogridPlugin BiomartClient BioNetBuilder BisoGenet
ConsensusPathDBplugin CoryneRegNetLoader CyThesaurus-ID-Mapping CytoSQL
DroID Genoscape GPML-Plugin GraphMLReader IntActWSCClient iRefScape
KGMLReader MetScape MiMlplugin NCBIClient NCBIEntrezGeneUserInterface
Pathintegrator PhosphositePlus Web Service Client Module PICRClient
PSICQUICUniversalClient ReConn SessionForWeb SFLDLoader StringWSCClient
Superpathways-Plugin 3DScape AgilentLiteratureSearch Cytoprophet DisGeNET
DomainGraph ExpressionCorrelation GeneMANIA MetaNetter MONET BiNGO
BubbleRouter ClueGO CommonAttributes DisplayNetworkFromFlatFile FluxViz
FunNetViz HyperEdgeEditor PiNGO CyGoose CytoscapeRPC GroovyScriptingEngine
JavaScriptEngine MiSink PythonScriptingEngine RubyScriptingEngine
ScriptEngineManager addParentNeighbors AdvancedNetworkMerge batchTool BiLayout
commandTool coreCommands CyAnimator edgeLengthPlugin edgeLister EpiTrace
FERN FM3 GoogleChartFunctions GroupTool MetaNodePlugin2 MultilevelLayoutPlugin
NamedSelection NatureProtocolsWorkflow NeighborHighlight NetLink nodeCharts
PhyloTree VennDiagrams



AllegroMCODE APCluster APID2NET BioQualiPlugin BLAST2SimilarityGraph BNMatch
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AllegroMCODE APCluster APID2NET **BioQualiPlugin** **BLAST2SimilarityGraph** **BNMatch**
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So what's the problem?



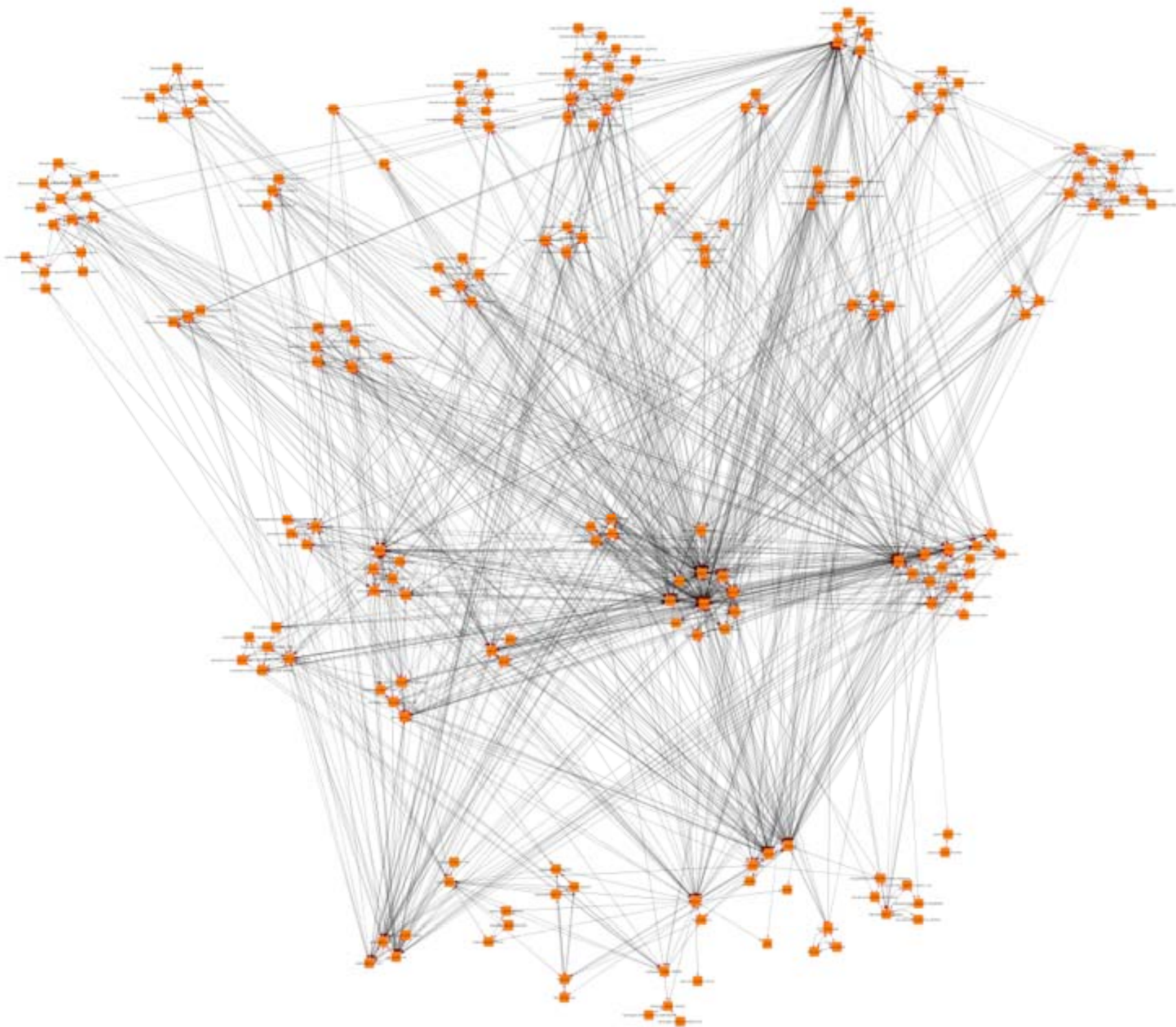




Photo credit: Taekwonweirdo
Photo credit: Dean247

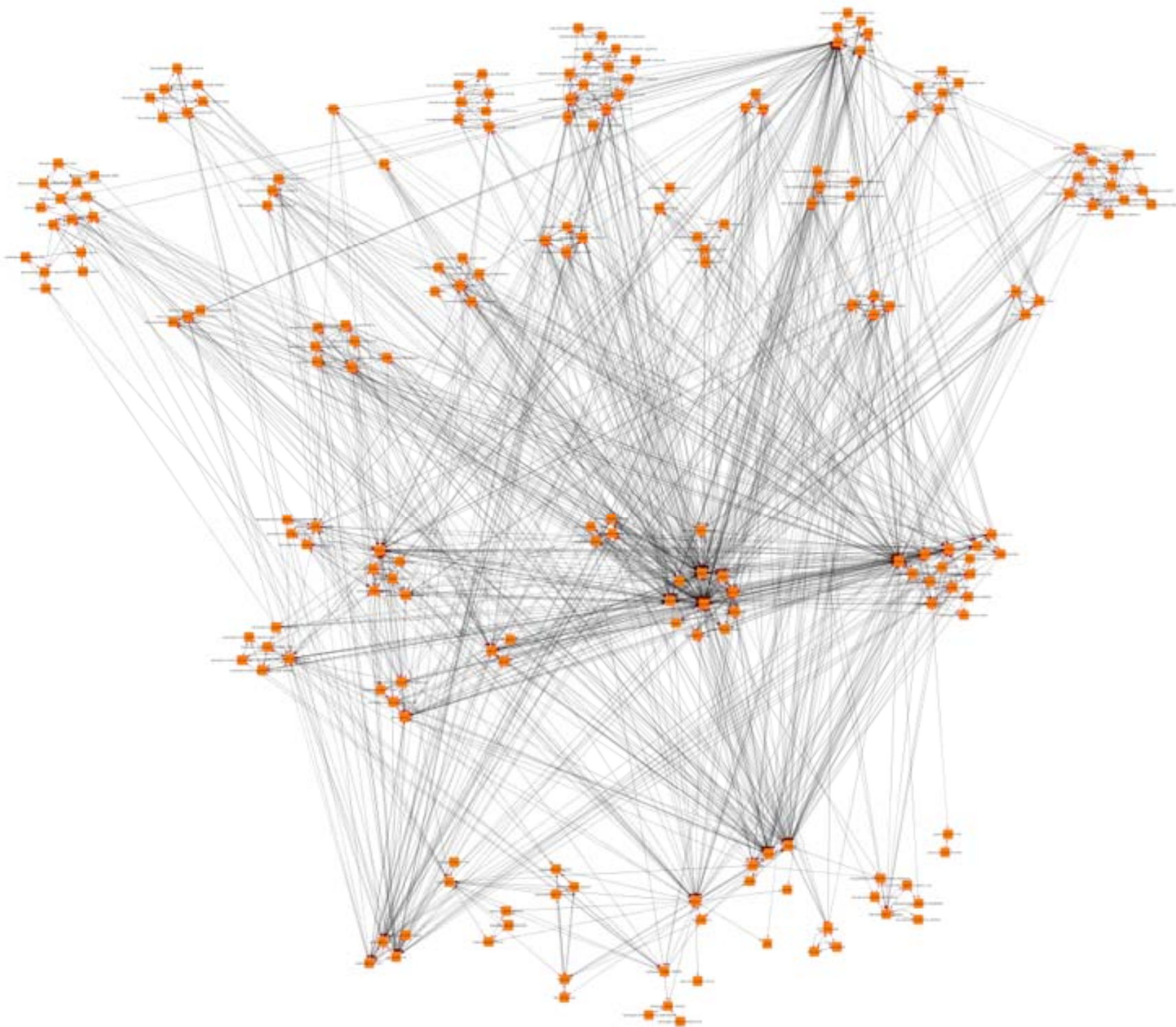
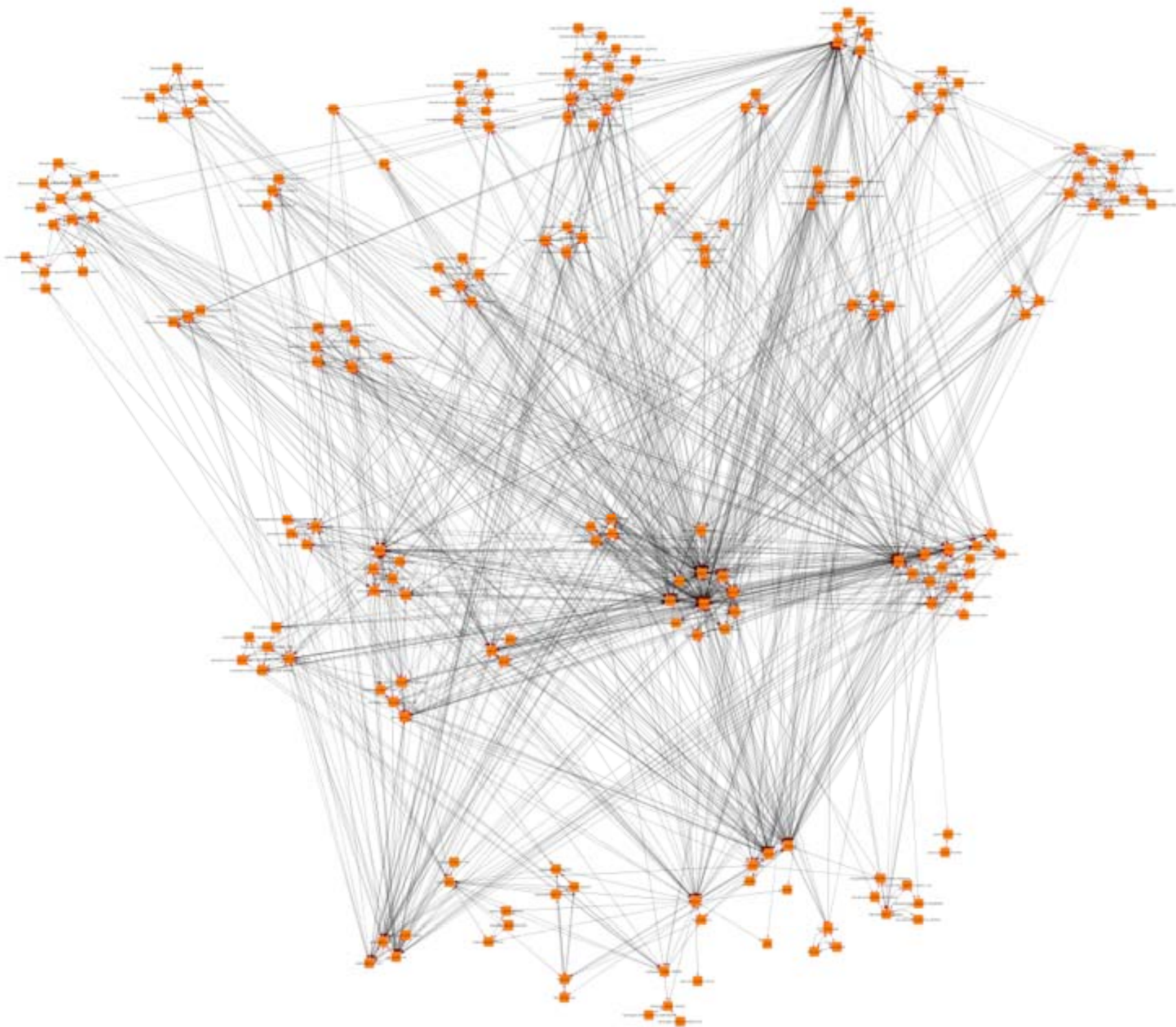




Photo credit: Taekwonweirdo



!!! A tangled mess of inter-dependencies

!!! Every public class is part of the API

!!! Backwards compatibility is impossible

!!! Poor deprecation and versioning strategy



Is that all?



!!! Apps can't use conflicting libraries

!!! Apps can't publish their own APIs



*Hurts core developers,
app writers,
and users!*



How do we fix this?



1. OSGi
2. Semantic Versioning
3. Maven



Cytoscape 3.0



Cytoscape 3.0 Milestone 5
is available here:

[*http://cytoscape.org*](http://cytoscape.org)



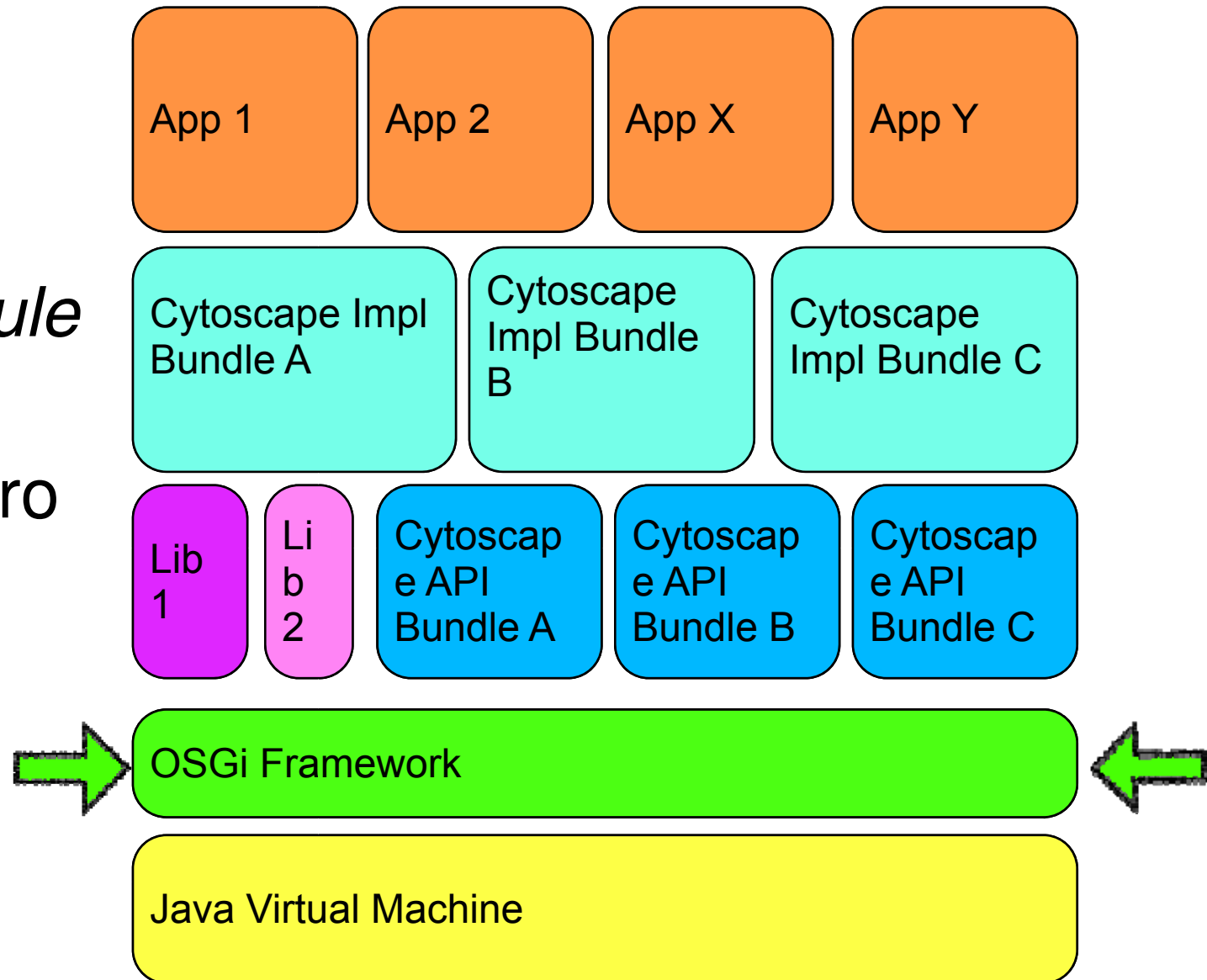
Cytoscape Application Stack

- OSGi

↕ provides
runtime
container

↕ *defines module
boundaries*

↕ provides micro
service
architecture



How does OSGi accomplish this?



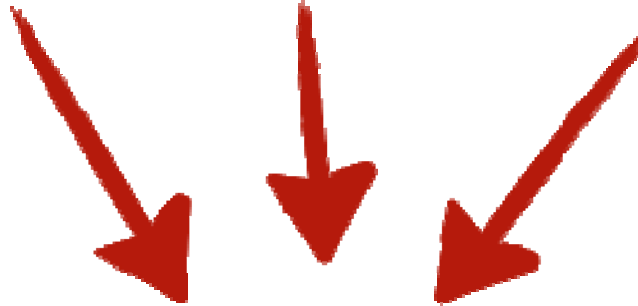
Module = Jar + Metadata



Module X

Module Y

Module Z

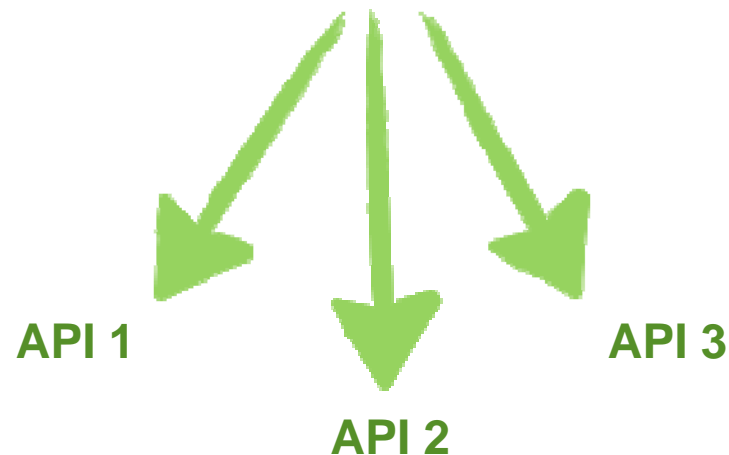


Defines what can depend on the module.

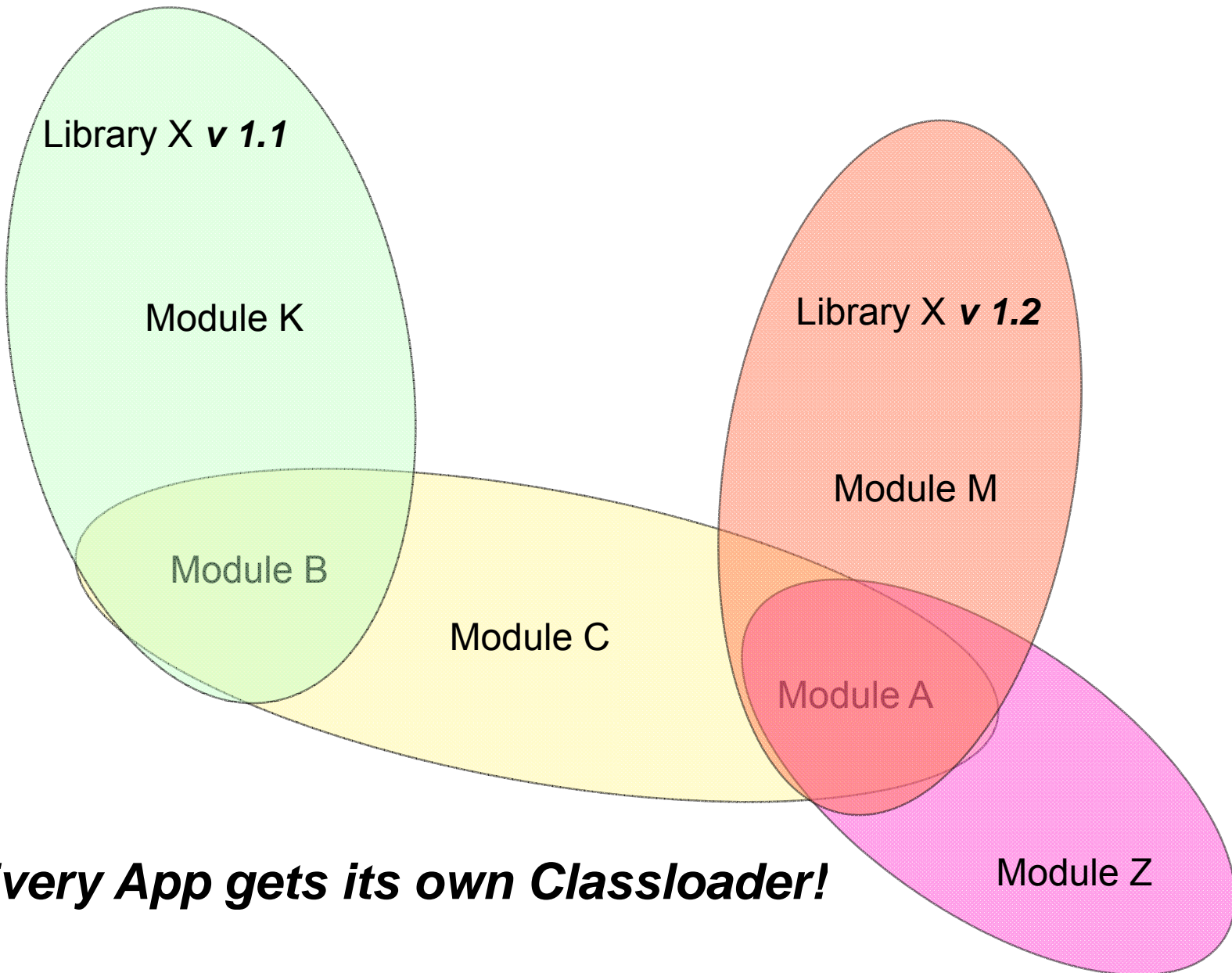
`Export-Packages: org.cytocape.model`

Defines what the module can depend on.

`Import-Packages: org.cytoscape.events`



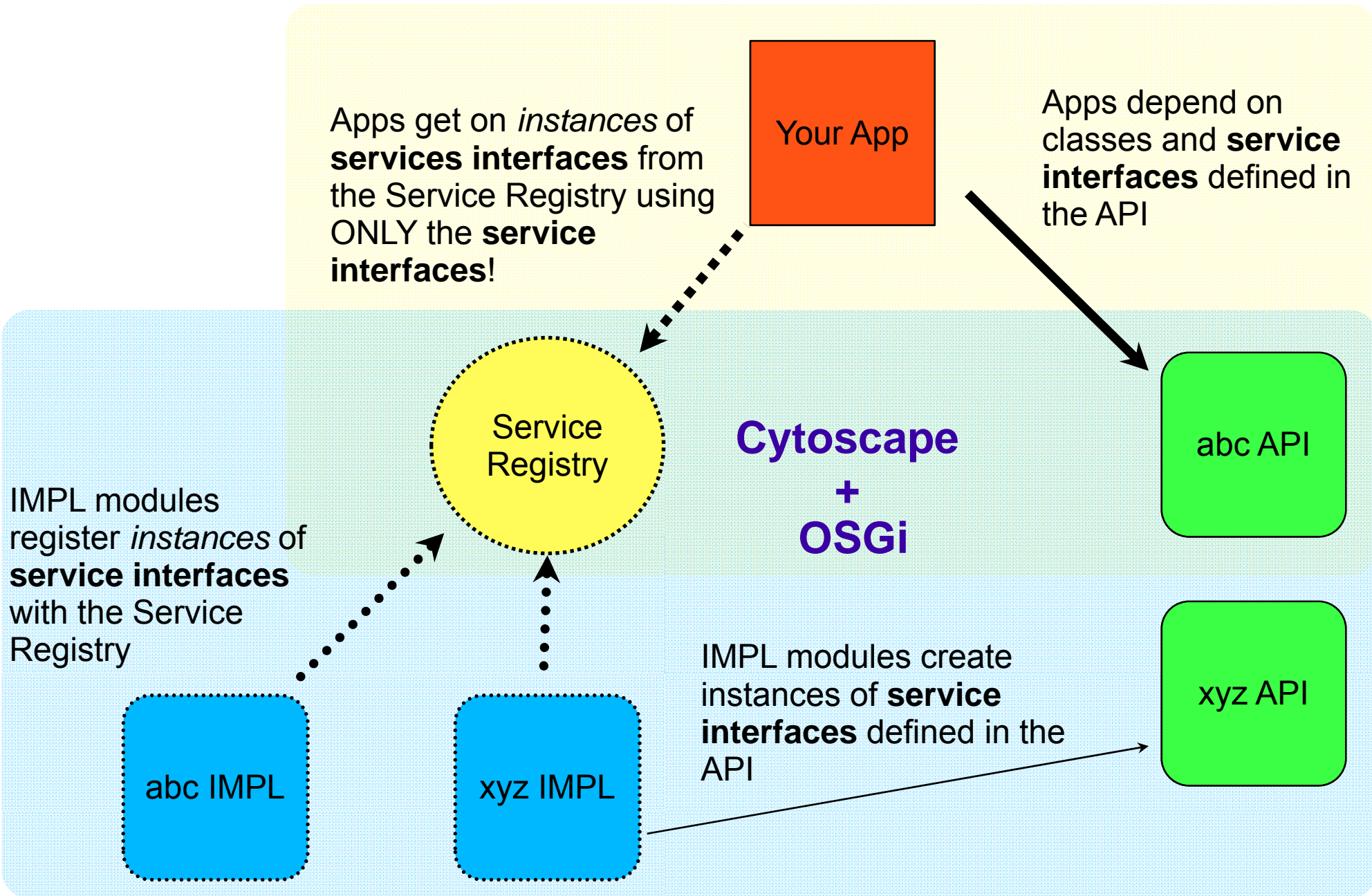
Independence



Every App gets its own Classloader!



μServices



OSGi *enables* Modularity

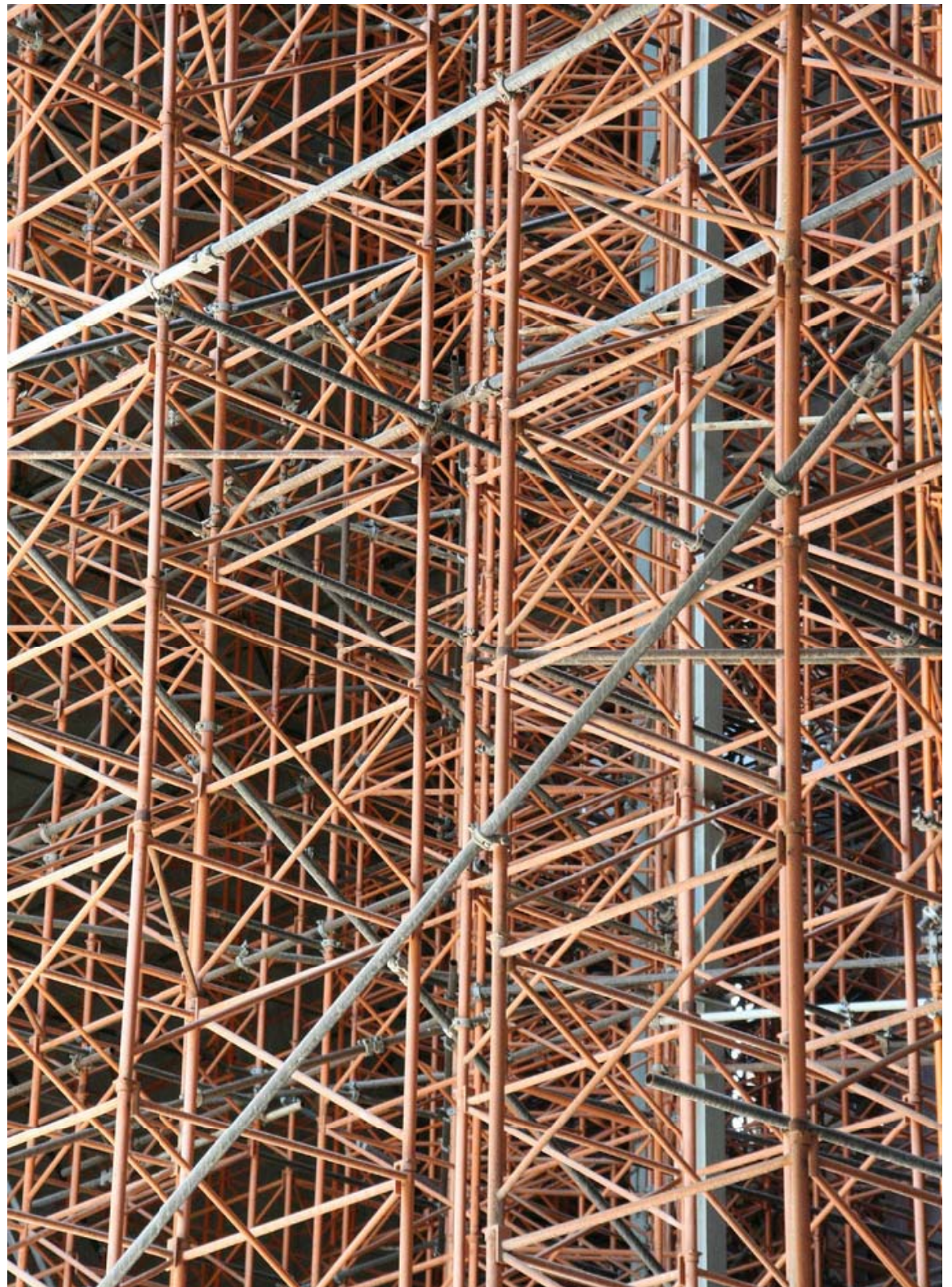


Photo credit: Maurice Koop



OSGi *enforces* Modularity



Semantic Versioning:

Version numbers have meaning!



VERSION: *major.minor.patch*

patch - backwards compatible bug fixes

minor - backwards compatible new features

major - backwards ***INcompatible*** changes



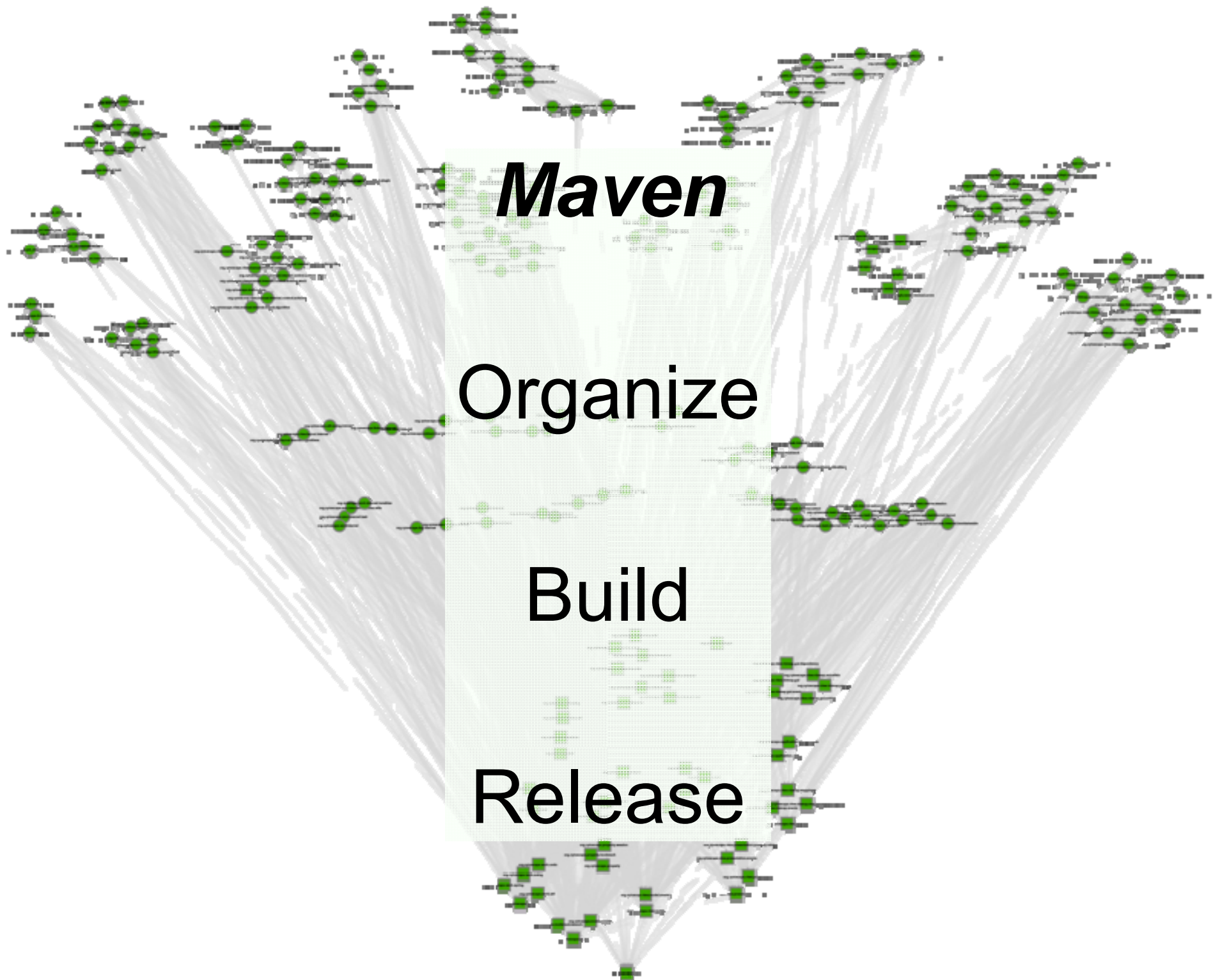
Because versions have a functional meaning, we can reason about ranges

[3.1,4)

***As long as we version honestly,
your app will always work!***

(At least until the next major version update)





1. OSGi

- To enable/enforce modularity

2. Semantic Versioning

- To define how and when changes happen

3. Maven

- To organize, build, and release



- ✓ 1. Clearly define API
- ✓ 2. Enforce separation of API and implementation
- ✓ 3. Clearly define what can change and when
- ✓ 4. Sensible dependencies
- ✓ 5. Make writing and maintaining plugins easy



For more information visit:

<http://cytoscape.org>



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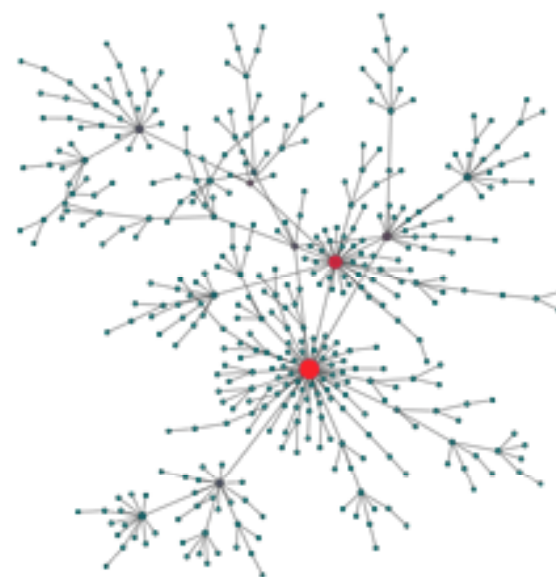


NATIONAL RESOURCE FOR NETWORK BIOLOGY

Mission Statement

The aim of the National Resource for Network Biology (NRNB) is to provide a freely available, open-source suite of software technology that broadly enables network-based visualization, analysis, and biomedical discovery for NIH-funded researchers. This software is enabling researchers to assemble large-scale biological data into models of networks and pathways and to use these networks to better understand how biological systems operate under normal conditions and how they fail in disease.

The National Resource for Network Biology is an NIH National Center for Research Resources (**NCRR**) Biomedical Technology Research Center (**BTRC**), organized around the following key components: Technology Research and Development, Driving Biomedical Projects, Outreach, Training and Dissemination of Tools. NRNB is funded by RR031228.



What is Network Biology?

Collaborate with NRNB

[View ongoing collaborations](#)

Annual Report