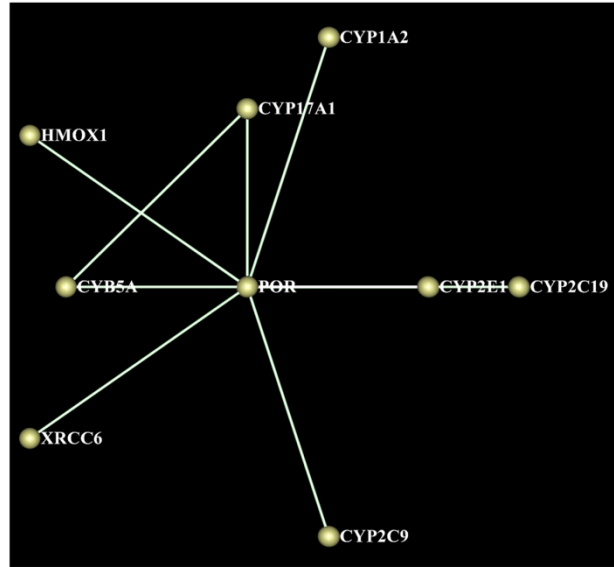
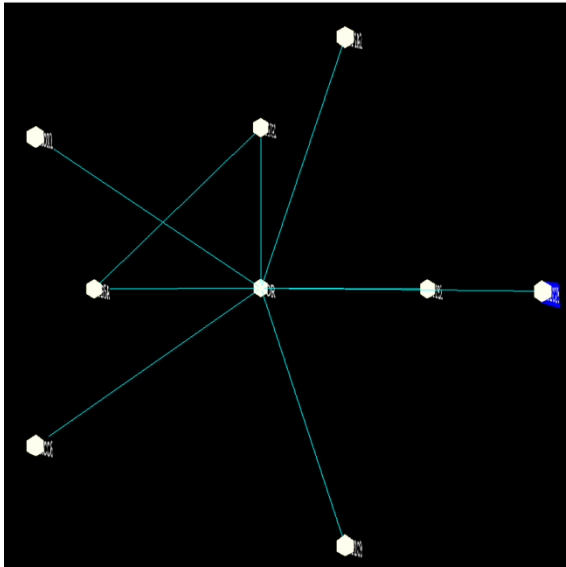
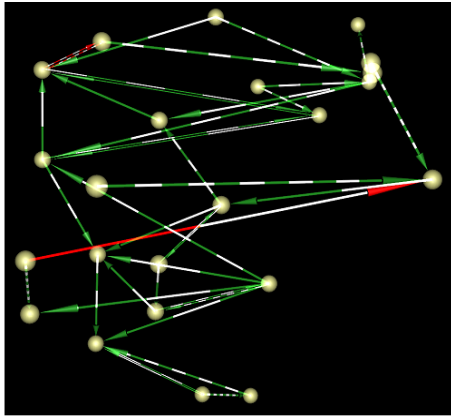


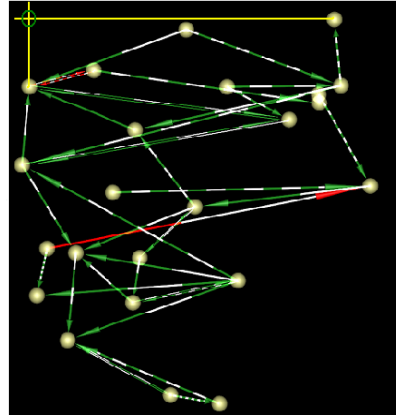
Supplementary Figures and Tables



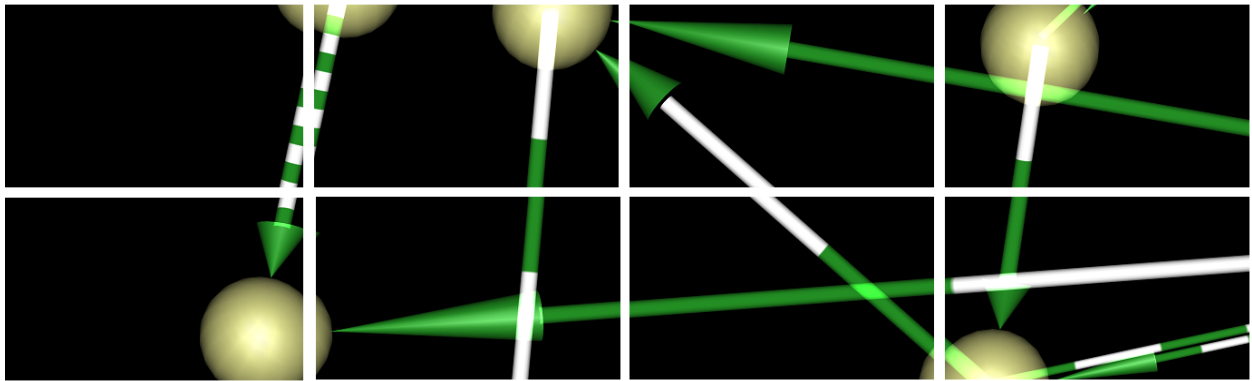
Supplementary Figure 1. Labels created with VRUI versus iCAVE. Left: VRUI intern method; Right: texture mapping.



Low resolution starting image



Projected image



Examples of sub images, taken during snapshot creation

Supplementary Figure 2. High-resolution image creation steps. Upper left image is a low-resolution snapshot created with common tools (800*600). This picture was projected into 2D screen plane (upper-right) and upper-left corner location was recorded as shown in upper right. 170 sub-images were taken to create a 18490*17560 resolution image (only 8 are shown in the bottom panels).

Supplementary Table 1. iCAVE currently provides a limited database within the COMBO repository for quick queries. Because of iCAVE's modular structure, users (who have some programming experience) can populate COMBO with additional databases.

COMBO Database	Version	# of entities (genes, drugs, diseases)	# of interactions
Protein-protein interaction			
HPRD Human Protein Reference (http://www.hprd.org)	07/2010	19,651 (genes)	39,240
intAct Molecular interaction (http://www.ebi.ac.uk/intact)	03/2012	29,665 (genes)	116,522 (mapped)
Disease-associated gene variant databases			
GWAS (http://genome.gov/gwastudies)	05/2012	5,234 (diseases)	11,199
Drug-target databases			
STITCH (http://stitch.embl.de)	V3	2,467 (drugs) 19,686 (genes)	39,117
DRUGBANK (http://drugbank.ca)	06/2012	1,578 (drugs)	4,235
Pathway databases			
SuperPathway (Personal communication with Josh Stuart, UCSD)	11/2011	20,076 (proteins) 8,897 (complexes) 1,866 (families) 491 (abstracts) 122 (RNAs) 15 (miRNAs)	8,345 (directed interactions)

Supplementary Table 2. iCAVE user-interactive menu options.

Show Netview Info	display clicked 3D coordinates
Show General Measurements	calculate network topological properties (e.g. hubs, centrality)
Show Labels	display node names
Show Single Nodes	display nodes with no interactions
Show Neighbors List	highlight all interacting neighbors of selected node
Show Additional Information	display the name of selected component of interest, and its membership in a family or a complex (if available)
Show GWAS Information	display GWAS information if provided
Reset Options	Choose from: Reset navigation; Network
Move Methods	Choose from: Move Nodes; Layers; Clusters
Allow Deleting Nodes	Allow deleting of selected nodes
Allow Deleting Edges	Allow deleting of selected edges
Rotate Model	set the rotation rate along X/Y/Z axis
Adjust Colors	Adjust node or edge color
Adjust Label Size	Use pop-up slider to change label size
Adjust Circos Size	Use pop-up slider to change hemisphere size
Layout Algorithms	Choose from: Force Directed; Weighted Force Directed; Hemisphere; Semantic Levels; LinLog; Hybrid Force Directed
Clustering Algorithms	Choose from: Betweenness Centrality; LinLog; MCL
Network Algorithms	Choose from: Bundle Edges; 3D to 2D projections; Save Snapshot; Select Nodes; Deselect Nodes; Separate Small Network; Create 3D Circos; Separate different categories
Save Layout	save current network layout in sql database format (.db)
Save Zoom As Movie	Generate movie of current network layout