BioVis Explorer (http://biovis.lnu.se) — survey summary (as of June 1, 2017)

Technique																			
Visualizing large hierarchical clusters in hyperbolic space (2000)		■		■				■			■	■		■					
BioLayout - an automatic graph layout algorithm for similarity visualization (2001)		■						■			■								
Visualizing Biosequence data using Texture Mapping (2002)				■				■			■				■				
Patika: an integrated visual environment for collaborative construction and analysis of cellular pathways (2002)		■					■	■			■	■							
Case Study: Visualizing Sets of Evolutionary Trees (2002)			■		■			■			■			■	■	■			
Global Visualization and Alignments of Whole Bacterial Genomes (2003)				■				■			■				■				
A fast layout algorithm for protein interaction networks (2003)		■						■			■								
Coordinated Graph and Scatter-Plot Views for the Visual Exploration of Microarray Time-Series Data (2003)	■				■				■		■	■	■	■					
GeneVis: Simulation and Visualization of Genetic Networks (2003)		■			■			■			■				■				
An Interactive Visualisation for Investigating DNA Sequence Information (2004)				■		■		■			■		■	■					■
Visualizations for taxonomic and phylogenetic trees (2004)				■				■			■	■							
Integration of metabolic networks and gene expression in virtual reality (2005)	■	■						■	■		■		■			■			
A system for visualizing and analyzing near-optimal protein sequence alignments (2005)				■		■		■			■		■	■					
Exploratory visualization of array-based comparative genomic hybridization (2005)	■					■	■	■	■		■	■							
ProViz: protein interaction visualization and exploration (2005)		■						■			■			■	■				
VitaPad: visualization tools for the analysis of pathway data (2005)		■						■			■			■					
Extending taxonomic visualisation to incorporate synonymy and structural markers (2005)			■					■			■			■	■				
A Framework for Visualization of Microarray Data and Integrated Meta Information (2005)	■					■		■	■		■								■
Animated interval scatter-plot views for the exploratory analysis of large-scale microarray time-course data (2005)	■				■				■		■		■	■					
Paloverde: an OpenGL 3D phylogeny browser (2006)			■								■						■		
springScape: visualisation of microarray and contextual bioinformatic data using spring embedding and an ‘information landscape’ (2006)	■		■		■			■	■		■								
TreeQ-VISTA: an interactive tree visualization tool with functional annotation query capabilities (2007)			■					■			■	■	■	■		■			
Exploring Multiple Trees through DAG Representations (2007)			■					■			■	■		■					
GOlorize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring (2007)		■						■			■								
Cerebral: a Cytoscape plugin for layout of and interaction with biological networks using subcellular localization annotation (2007)		■					■	■			■					■			
QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations (2008)	■			■		■		■		■	■	■							
Presenting and exploring biological pathways with PathVisio (2008)		■					■	■			■								
Dynamic Visualization of Coexpression in Systems Genetics Data (2008)		■						■			■	■	■	■		■			
TreeMos: a high-throughput phylogenomic approach to find and visualize phylogenetic mosaicism (2008)				■				■			■			■		■			
VistaClara: an expression browser plug-in for Cytoscape (2008)	■				■		■		■		■	■	■	■	■				
NetworkBLAST: comparative analysis of protein networks (2008)		■													■				
PhyloWidget: web-based visualizations for the tree of life (2008)			■					■			■			■					
Interactive visualization software for exploring phylogenetic trees and clades (2008)			■					■		■	■		■	■	■	■			■
Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context (2008)	■	■			■			■	■		■		■	■	■				
Caleydo: Connecting Pathways and Gene Expression (2009)	■	■						■	■		■	■	■	■		■			
Treevolution: visual analysis of phylogenetic trees (2009)			■					■			■					■			
Using Projection and 2D Plots to Visually Reveal Genetic Mechanisms of Complex Human Disorders (2009)	■								■		■		■						
ABySS-Explorer: Visualizing Genome Sequence Assemblies (2009)				■				■			■								
MizBee: A Multiscale Synteny Browser (2009)				■	■			■			■		■	■	■				
AssociationViewer: a scalable and integrated software tool for visualization of large-scale variation data in genomic context (2009)				■				■			■	■	■	■					
PhyloDet: a scalable visualization tool for mapping multiple traits to large evolutionary trees (2009)			■			■		■			■								
Circos: An information aesthetic for comparative genomics (2009)		■		■		■		■	■		■								
MassVis: Visual Analysis of Protein Complexes Using Mass Spectrometry (2009)	■								■		■	■	■	■	■				
GeneShelf: A Web-based Visual Interface for Large Gene Expression Time-Series Data Repositories (2009)	■	■			■			■	■	■	■		■	■	■				
BioCichlid: central dogma-based 3D visualization system of time-course microarray data on a hierarchical biological network (2009)	■	■			■						■								
A novel method for large tree visualization (2009)			■					■			■	■				■			
SpRay: A Visual Analytics Approach for Gene Expression Data (2009)	■								■		■		■	■					
GeneTerrain: Visual exploration of differential gene expression profiles organized in native biomolecular interaction networks (2010)	■	■						■	■		■			■					

Technique																			
Interactive microbial genome visualization with GView (2010)				■		■		■			■			■					
Gremlin: An Interactive Visualization Model for Analyzing Genomic Rearrangements (2010)				■		■		■		■	■			■	■				
MulteeSum: A Tool for Comparative Spatial and Temporal Gene Expression Data (2010)	■			■	■		■	■	■		■		■	■	■				
Visual Integration of Quantitative Proteomic Data, Pathways, and Protein Interactions (2010)	■	■						■	■		■	■	■	■		■			
iHAT: interactive Hierarchical Aggregation Table (2011)			■	■		■		■	■		■		■		■				
Visualization of Anisotropic Contact Potentials within Protein Structures (2011)			■				■				■				■	■			
MGV: a generic graph viewer for comparative omics data (2011)	■	■			■		■	■	■	■	■		■	■	■	■			
Automatic generation of protein structure cartoons with Pro-origami (2011)				■		■					■								
Cytoscape 2.8: new features for data integration and network visualization (2011)		■			■	■			■		■	■	■	■					■
RuleBender: Integrated Visualization for Biochemical Rule-Based Modeling (2011)		■					■				■		■	■	■				
Visual Analysis of Next-Generation Sequencing Data to Detect Overlapping Genes in Bacterial Genomes (2011)				■		■					■		■	■					■
Creating views on integrated multidomain data (2011)	■	■			■		■	■	■		■	■	■	■					■
Interactive, multiscale navigation of large and complicated biological networks (2011)		■						■			■		■	■		■			
MDMap: A System for Data-Driven Layout and Exploration of Molecular Dynamics Simulations (2011)		■			■						■	■	■			■			■
Evaluating the VIPER Pedigree Visualisation: Detecting Inheritance Inconsistencies in Genotyped Pedigrees (2011)	■		■	■		■			■		■		■	■	■				
EVEVis: A Multi-Scale Visualization System for Dense Evolutionary Data (2011)	■	■	■		■		■		■		■		■	■		■			
Metrics for Comparing Explicit Representations of Interconnected Biological Networks (2011)		■					■								■				
A Visual Analysis System for Metabolomics Data (2011)	■						■				■		■	■	■				■
GenPlay, a multipurpose genome analyzer and browser (2011)				■		■		■	■		■	■	■		■	■			
Parallel Contour-Buildup Algorithm for the Molecular Surface (2011)		■			■		■				■								
TIALA – Time Series Alignment Analysis (2011)				■	■						■			■	■				■
The Galaxy Track Browser: Transforming the Genome Browser from Visualization Tool to Analysis Tool (2011)				■		■					■		■		■			■	■
Modeling and Visualization of Receptor Clustering on the Cellular Membrane (2011)		■			■		■				■					■			
TVNViewer: An interactive visualization tool for exploring networks that change over time or space (2011)		■			■			■			■				■				
GenAMap: Visualization Strategies for Structured Association Mapping (2011)	■					■			■		■	■	■	■	■	■			■
Visualizing Virus Population Variability From Next Generation Sequencing Data (2011)				■		■					■		■	■	■				■
HiTSEE: A Visualization Tool for Hit Selection and Analysis in High-Throughput Screening Experiments (2011)	■								■		■	■		■					■
Sequence Surveyor: Leveraging Overview for Scalable Genomic Alignment Visualization (2011)				■				■			■				■	■			
Uncertainty-Aware Visual Analysis of Biochemical Reaction Networks (2012)		■								■	■		■	■	■				
ADVISe: Visualizing the dynamics of enzyme annotations in UniProt/Swiss-Prot (2012)	■		■			■		■			■		■	■			■		
Gene-RiViT: A visualization tool for comparative analysis of gene neighborhoods in prokaryotes (2012)				■				■			■			■	■				
Implicit Surfaces for Interactive Graph Based Cavity Analysis of Molecular Simulations (2012)		■			■		■				■		■	■	■				
enRoute: Dynamic Path Extraction from Biological Pathway Maps for In-Depth Experimental Data Analysis (2012)	■	■									■	■	■	■	■				
Heterogeneity-based Guidance for Exploring Multiscale Data in Systems Biology (2012)		■			■						■								■
Dynamic Channels in Biomolecular Systems: Path Analysis and Visualization (2012)		■					■				■			■					
Hive plots — rational approach to visualizing networks (2012)		■				■		■	■		■				■				
Guiding the interactive exploration of metabolic pathway interconnections (2012)		■						■			■		■	■					■
Towards Real-Time Visualization of Detailed Neural Tissue Models: View Frustum Culling for Parallel Rendering (2012)		■			■						■								
Compressed Adjacency Matrices: Untangling Gene Regulatory Networks (2012)		■						■			■		■	■		■			
MaTSE: The Microarray Time-Series Explorer (2012)				■	■						■		■		■	■			
HumMod Browser: An Exploratory Visualization Tool for the Analysis of Whole-Body Physiology Simulation Data (2013)	■				■			■			■		■	■	■				■
STAR: an integrated solution to management and visualization of sequencing data (2013)				■		■		■			■	■	■		■				
COMBat: Visualizing co-occurrence of annotation terms (2013)	■		■			■		■			■		■	■	■		■		
neuroMap – Interactive Graph-Visualization of the Fruit Fly's Neural Circuit (2013)	■						■				■		■	■					
MoClo Planner: Interactive Visualization for Modular Cloning Bio-Design (2013)	■			■				■			■		■	■					
The Molecular Control Toolkit: Controlling 3D Molecular Graphics via Gesture and Voice (2013)		■					■				■			■					
Leveraging Wall-sized High-Resolution Displays for Comparative Genomics Analyses of Copy Number Variation (2013)				■				■			■			■	■				
VisNEST – Interactive Analysis of Neural Activity Data (2013)	■						■				■			■	■				
PresentaBALL – a Powerful Package for Presentations and Lessons in Structural Biology (2013)		■					■				■		■	■					

Technique																			
Large-scale multiple sequence alignment visualization through gradient vector flow analysis (2013)				■		■		■			■				■				
Entourage: Visualizing Relationships between Biological Pathways using Contextual Subsets (2013)	■	■						■	■		■	■		■	■				
Visual Cleaning of Genotype Data (2013)	■			■				■			■		■	■					■
Exploring biological data: Mappings between ontology- and cluster-based representations (2013)		■	■			■		■			■		■	■					
LineUp: Visual Analysis of Multi-Attribute Rankings (2013)	■					■		■	■	■	■	■	■	■	■	■			
Variant View: Visualizing Sequence Variants in their Gene Context (2013)				■				■			■			■	■				
Genome-Wide Detection of sRNA Targets with rNAV (2013)				■				■			■	■	■	■	■				
From Biochemical Reaction Networks to 3D Dynamics in the Cell: the ZigCell3D Modeling, Simulation and Visualisation Framework (2013)		■			■		■				■		■	■	■	■			
Analyzing Chromatin Using Tiled Binned Scatterplot Matrices (2014)	■			■				■	■		■				■				
Genotet: An Interactive Web-based Visual Exploration Framework to Support Validation of Gene Regulatory Networks (2014)	■	■						■	■		■			■		■			
Visualization of gene expression information within the context of the mouse anatomy (2014)	■		■	■	■	■		■			■	■		■	■				
Helium: Visualization of Large Scale Plant Pedigrees (2014)		■	■	■		■	■	■	■		■	■	■	■				■	
Addressing the unmet need for visualizing conditional random fields in biological data (2014)		■		■		■		■	■		■		■	■	■				
ConTour: Data-Driven Exploration of Multi-Relational Datasets for Drug Discovery (2014)	■	■							■		■		■		■				
UpSet: Visualization of Intersecting Sets (2014)	■							■	■		■	■	■	■		■			
inPHAP: Interactive visualization of genotype and phased haplotype data (2014)				■		■		■			■	■	■	■	■			■	■
ReadXplorer – visualization and analysis of mapped sequences (2014)				■		■			■		■	■	■		■				
Domino: Extracting, Comparing, and Manipulating Subsets across Multiple Tabular Datasets (2014)	■							■	■		■	■	■	■		■			
BiNA: a visual analytics tool for biological network data (2014)	■	■			■			■	■	■	■		■	■	■				
Rebuilding KEGG Maps: Algorithms and Benefits (2014)		■					■				■								
MCA: Multiresolution Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data (2014)				■				■	■		■				■				
MIMTool: A Tool for Drawing Molecular Interaction Maps (2014)		■					■	■			■			■				■	
eXamine: Exploring annotated modules in networks (2014)		■	■	■			■	■			■		■	■			■		
iGPSe: A visual analytic system for integrative genomic based cancer patient stratification (2014)	■			■	■	■		■	■		■	■	■	■	■	■			■
VisRseq: R-based visual framework for analysis of sequencing data (2015)	■			■		■		■	■		■		■	■		■			
GOplot: an R package for visually combining expression data with functional analysis (2015)	■		■			■		■	■		■		■						
Visual analysis of biological data-knowledge networks (2015)		■						■	■		■		■	■	■		■		
Integrated visual analysis of protein structures, sequences, and feature data (2015)		■		■		■	■	■			■	■		■	■	■		■	
VisExpress: Visual exploration of differential gene expression data (2015)	■		■	■		■		■	■		■	■	■	■	■	■			
Visual parameter optimisation for biomedical image processing (2015)	■	■						■	■		■		■	■	■		■	■	
Extended LineSets: A visualization technique for the interactive inspection of biological pathways (2015)		■	■				■	■			■	■	■	■	■				■
VISIONET: intuitive visualisation of overlapping transcription factor networks, with applications in cardiogenic gene discovery (2015)		■						■	■		■		■	■					
coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns (2015)	■							■	■		■			■	■		■		
cnvCurator: an interactive visualization and editing tool for somatic copy number variations (2015)				■		■		■			■			■					
XCluSim: A visual analytics tool for interactively comparing multiple clustering results of bioinformatics data (2015)	■							■	■		■		■	■	■	■			
miRTarVis: An interactive visual analysis tool for microRNA-mRNA expression profile data (2015)	■	■				■		■	■		■	■	■	■				■	
Pan-Tetris: an interactive visualisation for Pan-genomes (2015)	■			■		■		■			■			■				■	
GRAPHIE: graph based histology image explorer (2015)		■						■	■		■	■	■	■	■	■	■	■	■
ReactionFlow: Visualizing Relationships between Proteins and Complexes in Biological Pathways (2015)		■					■	■			■	■	■	■		■			
PathwayMatrix: Visualizing binary relationships between proteins in biological pathways (2015)		■					■	■			■		■	■		■			
LayerCake: a tool for the visual comparison of viral deep sequencing data (2015)				■		■				■	■		■	■	■		■		
Epiviz: a view inside the design of an integrated visual analysis software for genomics (2015)				■				■			■		■	■	■	■		■	
BactoGeNIE: a large-scale comparative genome visualization for big displays (2015)				■		■		■			■		■	■	■	■			
J-Circos: an interactive Circos plotter (2015)				■		■		■	■		■			■	■				
Treelink: data integration, clustering and visualization of phylogenetic trees (2015)				■			■	■			■	■		■	■	■	■		
Vials: Visualizing Alternative Splicing of Genes (2016)		■		■		■		■	■		■			■	■				
CompNet: a GUI based tool for comparison of multiple biological interaction networks (2016)		■						■			■			■	■	■			
HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data (2016)				■		■			■		■				■				
Integrated Genome Browser: visual analytics platform for genomics (2016)				■		■					■	■		■	■		■	■	