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

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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)																
ntegration 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)																$\overline{}$
springScape: visualisation of microarray and contextual bioinformatic data using spring embedding and an 'information landscape' (2006)																$\overline{}$
FreeQ-VISTA: an interactive tree visualization tool with functional annotation query capabilities (2007)																$\overline{}$
Exploring Multiple Trees through DAG Representations (2007)																$\overline{}$
GOlorize: a Cytoscape plug-in for network visualization with Gene Ontology-based layout and coloring (2007)																$\overline{}$
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)																$\overline{}$
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)																\rightarrow
Treevolution: visual analysis of phylogenetic trees (2009)																\rightarrow
Jsing 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)															-	\rightarrow
SpRay: A Visual Analytics Approach for Gene Expression Data (2009)															-	\rightarrow
GeneTerrain: Visual exploration of differential gene expression profiles organized in native biomolecular interaction networks (2010)																

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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)															П
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)															П
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)															\neg
VisNEST – Interactive Analysis of Neural Activity Data (2013)															
PresentaBALL – a Powerful Package for Presentations and Lessons in Structural Biology (2013)															

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Analyzing Drimonatin Using Titol Brinned Scatterpole Martines (2014) Genetic An Internative Web based Valual Exporation Framework to Support Validation of Gene Regulatory Networks (2014) Valualization of gene expression information within the context of the mouse analysing (2014) Addressing the rument exect for visualizing conditional random fields in biological data (2014) Addressing the rument exect for visualizing conditional random fields in biological data (2014) USSEN Valualization of Internating Sets (2014) INSENT Valualization of Internating Sets (2014) INSENT Valualization of Internating Sets (2014) INSENT Valualization and analysis of mapped sequences (2014) INSENT Valualization and analysis of mapped sequences (2014) INSENT Valualization and analysis of framped sequences (2014) INSENT Valualization and analysis of framped sequences (2014) INSENT Valualization of International Maps (2014) INSENT Valualization Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data (2014) INSENT Valualization Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data (2014) INSENT Valualization Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data (2014) INSENT Valualization Analysis of theorem Analysis of sequencing data (2015) Valual analysis of biological data knowledge personne based cancer patient stratification (2014) Valualization Analysis of theorem Valualization in interviews (2015) INSENT Valualization for between data (2015) Valualization of Analysis of Potentification (1998) (19	Genome-Wide Detection of sRNA Targets with rNAV (2013)																	
Genotes An Interactive Web based Visual Exploration Famework to Support Visitation of Game Regulatory Networks (2014)	From Biochemical Reaction Networks to 3D Dynamics in the Cell: the ZigCell3D Modeling, Simulation and Visualisation Framework (2013)																	
Genotes An Interactive Web based Visual Exploration Famework to Support Visitation of Game Regulatory Networks (2014)	Analyzing Chromatin Using Tiled Binned Scatterplot Matrices (2014)																	
Visualization of gene expression information within the content of the mouse anatomy (2014) Maddressing the unmel need for visualizing conditional random fields in biological data (2014) Conforu: Data-Chris Exploration of Multi-Relational Datasets for Drug Discovery (2014) USSET: Visualization of Intersecting Sets (2014) Intelligence in the Conforum Christopher and Pulsace Imployee data (2014) Read/Splorum - visualization of an analysis of mapped sequences (2014) Discovery - visualization of an analysis of mapped sequences (2014) Bill As a visual analysis to for biological network data (2014) Bill As a visual analysis to for biological network data (2014) Read/Splorum - visualization of an analysis of mapped sequences (2014) Bill As a visual analysis to for biological network data (2014) ROA: Multiresolution Correlation Analysis, a graphisal tool for subpopulation identification in single-cell gene expression data (2014) MCA: Multiresolution Correlation Analysis, a graphisal tool for subpopulation identification in single-cell gene expression data (2014) MCA: Multiresolution Correlation Analysis, a graphisal tool for subpopulation identification in single-cell gene expression data (2014) MCA: Multiresolution Correlation Analysis, a graphisal tool for subpopulation identification in single-cell gene expression data (2014) MCA: Multiresolution Correlation Analysis, a graphisal tool for subpopulation identification in single-cell gene expression data (2014) Wishall analysis of the subpopulation sequence (2014) Wishall analysis of the subpopulation sequence (2014) Wishall analysis of the subpopulation genetic sead cancer patient shealthcation (2014) Wishall analysis of the subpopulation genetic sead cancer patient shealthcation (2015) Wishall analysis of the subpopulation genetic sead cancer patient shealthcation (2015) Wishall analysis of the subpopulation genetic sead of the subpopulation (2015) Wishall analysis of the subpopulation of exploression (2015) Wishall analysis of the subpopulati																		
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