<table>
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<tr>
<th>Technique</th>
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Case Study: Visualizing Sets of Evolutionary Trees (2002)  
Global Visualization and Alignments of Whole Bacterial Genomes (2003)  
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Global Visualization and Alignments of Whole Bacterial Genomes (2003)  
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 (2006)  
VitaPad: visualization tools for the analysis of pathway data (2005)  
Extending taxonomic visualisation to incorporate synonymy and structural markers (2005)  
Animated interval scatter-plot views for the exploratory analysis of large-scale microarray time-course data (2005)  
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)  
QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations (2008)  
Presenting and exploring biological pathways with PathVisio (2008)  
TreeMoz: a high-throughput phylogenomic approach to find and visualize phylogenetic mosaicism (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)  
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)  
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)  
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<td>Interactive microbial genome visualization with GView (2010)</td>
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<tr>
<td>Gremlin: An Interactive Visualization Model for Analyzing Genomic Rearrangements (2010)</td>
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<tr>
<td>MulteeSum: A Tool for Comparative Spatial and Temporal Gene Expression Data (2010)</td>
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<tr>
<td>Visual Integration of Quantitative Proteomic Data, Pathways, and Protein Interactions (2010)</td>
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<td>iHAT: Interactive Hierarchical Aggregation Table (2011)</td>
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<td>Visualization of Anisotropic Contact Potentials within Protein Structures (2011)</td>
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<td>MGV: a generic graph viewer for comparative omics data (2011)</td>
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<td>Automatic generation of protein structure cartoons with Pro-origami (2011)</td>
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<td>Cytoscape 2.8: new features for data integration and network visualization (2011)</td>
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<tr>
<td>RuleBender: Integrated Visualization for Biochemical Rule-Based Modeling (2011)</td>
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<tr>
<td>Visual Analysis of Next-Generation Sequencing Data to Detect Overlapping Genes in Bacterial Genomes (2011)</td>
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<td>Creating views on integrated multidomain data (2011)</td>
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<tr>
<td>Interactive, multiscale navigation of large and complicated biological networks (2011)</td>
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<tr>
<td>MDMAP: A System for Data-Driven Layout and Exploration of Molecular Dynamics Simulations (2011)</td>
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<td>Evaluating the VIPER Pedigree Visualisation: Detecting Inheritance Inconsistencies in Genotyped Pedigrees (2011)</td>
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<td>EVEVIs: A Multi-Scale Visualization System for Dense Evolutionary Data (2011)</td>
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<td>Metrics for Comparing Explicit Representations of Interconnected Biological Networks (2011)</td>
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<td>A Visual Analysis System for Metabolomics Data (2011)</td>
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<td>GenPlay, a multipurpose genome analyzer and browser (2011)</td>
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<td>Parallel Contour-Buildup Algorithm for the Molecular Surface (2011)</td>
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<td>TIALA – Time Series Alignment Analysis (2011)</td>
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<td>The Galaxy Track Browser: Transforming the Genome Browser from Visualization Tool to Analysis Tool (2011)</td>
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<td>Modeling and Visualization of Receptor Clustering on the Cellular Membrane (2011)</td>
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<tr>
<td>TVNViewer: An interactive visualization tool for exploring networks that change over time or space (2011)</td>
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<td>GenAMap: Visualization Strategies for Structured Association Mapping (2011)</td>
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<td>Visualizing Virus Population Variability From Next Generation Sequencing Data (2011)</td>
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<td>HITSEE: A Visualization Tool for Hit Selection and Analysis in High-Throughput Screening Experiments (2011)</td>
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<td>Sequence Surveyor: Leveraging Overview for Scalable Genomic Alignment Visualization (2011)</td>
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<td>Uncertainty-Aware Visual Analysis of Biochemical Reaction Networks (2012)</td>
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<td>ADViSe: Visualizing the dynamics of enzyme annotations in UniProt/Swiss-Prot (2012)</td>
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<td>Implicit Surfaces for Interactive Graph Based Cavity Analysis of Molecular Simulations (2012)</td>
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<tr>
<td>envRoute: Dynamic Path Extraction from Biological Pathway Maps for In-Depth Experimental Data Analysis (2012)</td>
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<td>Hive plots — rational approach to visualizing networks (2012)</td>
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<td>Guiding the interactive exploration of metabolic pathway interconnections (2012)</td>
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<td>Compressed Adjacency Matrices: Untangling Gene Regulatory Networks (2012)</td>
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<td>HumMod Browser: An Exploratory Visualization Tool for the Analysis of Whole-Body Physiology Simulation Data (2013)</td>
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<td>STAR: an integrated solution to management and visualization of sequencing data (2013)</td>
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<td>COMBat: Visualizing co-occurrence of annotation terms (2013)</td>
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<td>neuroMap – Interactive Graph-Visualization of the Fruit Fly’s Neural Circuit (2013)</td>
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<td>MoClo Planner: Interactive Visualization for Modular Cloning Bio-Design (2013)</td>
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<td>Leveraging Wall-sized High-Resolution Displays for Comparative Genomics Analyses of Copy Number Variation (2013)</td>
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<td>VisNEST – Interactive Analysis of Neural Activity Data (2013)</td>
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<td>PresentaBALL – a Powerful Package for Presentations and Lessons in Structural Biology (2013)</td>
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<tr>
<td>Large-scale multiple sequence alignment visualization through gradient vector flow analysis</td>
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<td>Entourage: Visualizing Relationships between Biological Pathways using Contextual Subsets</td>
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<td>Visual Cleaning of Genotype Data</td>
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<td>Exploring biological data: Mappings between ontology- and cluster-based representations</td>
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<td>LineUp: Visual Analysis of Multi-Attribute Rankings</td>
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<td>Variant View: Visualizing Sequence Variants in their Gene Context</td>
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<td>Genome-Wide Detection of sRNA Targets with rNAV</td>
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<td>From Biochemical Reaction Networks to 3D Dynamics in the Cell: the ZigCell3D Modeling, Simulation and Visualisation Framework</td>
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<td>Analyzing Chromatin Using Tiled Binned Scatterplot Matrices</td>
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<td>Visualization of gene expression information within the context of the mouse anatomy</td>
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<td>Helium: Visualization of Large Scale Plant Pedigrees</td>
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<td>Addressing the unmet need for visualizing conditional random fields in biological data</td>
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<td>ConTour: Data-Driven Exploration of Multi-Relational Datasets for Drug Discovery</td>
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<td>UpSet: Visualization of Intersecting Sets</td>
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<td>inPHAP: Interactive visualization of genotype and phased haplotype data</td>
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<td>Domino: Extracting, Comparing, and Manipulating Subsets across Multiple Tabular Datasets</td>
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<td>BiNA: a visual analytics tool for biological network data</td>
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<td>Rebuilding KEGG Maps: Algorithms and Benefits</td>
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<td>MCA: Multiresolution Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data</td>
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<td>MIMTool: A Tool for Drawing Molecular Interaction Maps</td>
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<td>eXamine: Exploring annotated modules in networks</td>
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<td>iGPS-e: A visual analytic system for integrative genomic based cancer patient stratification</td>
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<td>VisRseq: R-based visual framework for analysis of sequencing data</td>
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<td>GOplot: an R package for visualizing expression data with functional analysis</td>
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<td>Visual analysis of biological data-knowledge networks</td>
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<td>Integrated visual analysis of protein structures, sequences, and feature data</td>
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<td>VisExpress: Visual exploration of differential gene expression data</td>
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<td>Visual parameter optimisation for biomedical image processing</td>
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<td>Extended LineSets: A visualization technique for the interactive inspection of biological pathways</td>
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<td>VISIONET: Intuitive visualisation of overlapping transcription factor networks, with applications in cardiogenic gene discovery</td>
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<td>coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns</td>
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<td>cvnCurator: an interactive visualization and editing tool for somatic copy number variations</td>
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<td>XCluSim: A visual analytics tool for interactively comparing multiple clustering results of bioinformatics data</td>
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<td>miRTarVis: An interactive visual analysis tool for microRNA-mRNA expression profile data</td>
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<td>Pan-Tetris: an interactive visualisation for Pan-genomes</td>
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<td>GRAPHIE: graph based histology image explorer</td>
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<td>ReactionFlow: Visualizing Relationships between Proteins and Complexes in Biological Pathways</td>
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<td>PathwayMatrix: Visualizing binary relationships between proteins in biological pathways</td>
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<td>LayerCake: a tool for the visual comparison of viral deep sequencing data</td>
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<td>Epiviz: a view inside the design of an integrated visual analysis software for genomics</td>
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<td>BactoGeNIE: a large-scale comparative genome visualization for big displays</td>
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<td>J-Circos: an interactive Circos plotter</td>
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<td>Treelink: data integration, clustering and visualization of phylogenetic trees</td>
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<td>Vials: Visualizing Alternative Splicing of Genes</td>
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<td>CompNet: a GUI based tool for comparison of multiple biological interaction networks</td>
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<td>HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data</td>
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<td>Integrated Genome Browser: visual analytics platform for genomics</td>
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