

POINTS OF VIEW

Visualizing biological data

Data visualization is increasingly important, but it requires clear objectives and improved implementation.

Researchers today have access to an unprecedented amount of data. The challenge is to benefit from this abundance without being overwhelmed. Data visualization for efficient exploration and effective communication is integral to scientific progress. For visualization to continue to be an important tool for discovery, its practitioners need to be present as members of research teams.

One of the goals of data visualization is to enable people to explore and explain data through interactive software that takes advantage of human beings' ability to recognize patterns. Its success depends on the development of methods and techniques to transform information into a visual form for comprehension. It is a process that synthesizes skills from engineering, statistics and graphic design along with a number of other disciplines.

In recent years we have witnessed a growing appetite for the visual display of information. The ease of generating sophisticated computer graphics has encouraged the use of visualization. However, the value and utility of this popular form of communication remains unclear. We can easily be fooled into believing that we absorb more than we do when looking at large, colorful displays of information.

Data visualization, when applied to scientific research, has to be more than just the graphical display of information. Clear objectives are needed to drive design so we can assess the utility and practicality of visualizations. What is it that the researchers want to and need to see in the data? Which computational approaches and visual encodings will best bring out the trends? It is essential for the visualization practitioners to work side by side with the researchers to ensure that design decisions are continually refined to meet research objectives.

Unfortunately, there are few models for highly integrative teams consisting of visualization experts and biological researchers. The existence of distinct professional meetings and publication venues may be partially responsible for the barrier to working together. For example, the major professional meetings in information visualization such as Visualizing Biological Data (VIZBI) and BioVis (part of the Institute of Electrical and Electronics Engineers' VisWeek) attract few biologists. As a consequence, advances in visualization are not adequately described and shared with the biological community.

Identifying shared funding sources will certainly help to unite the professions under a common set of responsibilities and deliverables. Unfortunately, it is uncommon to hear stories in which agencies supporting scientific research have been successfully convinced to fund visualization efforts. Without the tight working relationships of an integrated team, we give up the ability to



Figure 1 | Visualization of whole-genome rearrangement. Representative Circos plots¹ of whole-genome sequence data from two different tumors showing gene duplications and chromosome rearrangements. The outer ring depicts chromosomes arranged end to end. The inner ring displays copy-number data in green and interchromosomal translocations in purple. Reprinted from ref. 2 with permission from Elsevier.

rapidly turn sketches into software prototypes at a pace relevant to the research; as data types and research questions evolve, there is a constant need to refine and adapt visualizations. One funding mechanism that has enabled an integrated focus on visualization in the context of biological research is supplemental support associated with awarded grants. The primary objective of such work is to extend the utility and accessibility of the research findings.

It is useful to recognize that not every biological question will benefit from visualization, and graphical approaches should therefore be reserved for projects for which they will produce the greatest impact. Many data challenges can be addressed perfectly with computation alone. For a subset of research questions, however, visualizations can offer specific advantages over computation. In instances when we do not yet know the regularities in the data, visualization provides a powerful approach to explore the data for patterns. Visualization can also be useful for projects in which it complements algorithmic approaches. In genomics, for example, automated processes can reliably find sites where rearrangement occurs, but visualization is then needed to provide a mental image so that the detail of structural variation can be fully appreciated and understood (Fig. 1).

Data visualization represents a powerful aid to understanding data because well-designed graphical depictions of information can replace arduous cognitive assessment with simple perceptual inferences. For this reason, visualization can have a significant impact in biology, especially in the age of big data. For the last two and a half years, I have covered visual strategies for depicting scientific data. Although Points of View will go on hiatus after this month, these columns represent part of Nature Publishing Group's commitment to meeting visual communication challenges of scientific data.

Bang Wong

1. Kryszewski, M. et al. *Genome Res.* **18**, 1639–1645 (2008).
2. Delielinski, M. et al. *Cell* **250**, 1107–1120 (2012).

Bang Wong is the creative director of the Broad Institute of the Massachusetts Institute of Technology & Harvard and an adjunct assistant professor in the Department of Art as Applied to Medicine at The Johns Hopkins University School of Medicine.

Visualizing Biological Information

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Visualizing Biological Information Clifford A. Pickover, 1995 Biological data of all kinds is proliferating at an incredible rate. If humans attempt to read such data in the form of numbers and letters they will take in the information at a snail's pace. If the information is rendered graphically however, human analysts can assimilate it and gain insight at a much faster rate. The emphasis of this book is on the graphic representation of information containing sequences such as DNA and amino acid sequences in order to help the human analyst find interesting and biologically relevant patterns. The editor's goal is to make this voyage through molecular biology, genetics, and computer graphics as accessible to a broad audience as possible with the inclusion of glossaries at the end of most chapters and program outlines where applicable. The book will be of most interest to biologists and computer scientists and the various large reference lists should be of interest to beginners and advanced students of biology, graphic art, and computer science. Contributors have sought to find pattern and meaning in the cacophony of genetic and protein sequence data using unusual computer graphics and musical techniques. *Data Analysis and Visualization in Genomics and Proteomics* Francisco Azuaje, Joaquin Dopazo, 2005-06-24 *Data Analysis and Visualization in Genomics and Proteomics* is the first book addressing integrative data analysis and visualization in this field. It addresses important techniques for the interpretation of data originating from multiple sources encoded in different formats or protocols and processed by multiple systems. One of the first systematic overviews of the problem of biological data integration using computational approaches. This book provides scientists and students with the basis for the development and application of integrative computational methods to analyse biological data on a systemic scale. Places emphasis on the processing of multiple data and knowledge resources and the combination of different models and systems.

Interactive Visualization and Plotting with Julia Diego Javier Zea, 2022-08-29 Represent and analyze data using Plots to find actionable insights using Julia programming. Key Features: Learn to use static and interactive plots to explore data with Julia. Become well versed with the various plotting attributes needed to customize your plots. Create insightful and appealing plots using data interactions, animations, layouts, and themes. Book Description: The Julia programming language offers a fresh perspective into the data visualization field. *Interactive Visualization and Plotting with Julia* begins by introducing the Julia language and the Plots package. The book then gives a quick overview of the Julia plotting ecosystem to help you choose the best library for your task. In particular, you will discover the many ways to create interactive visualizations with its packages. You'll also leverage Pluto notebooks to gain interactivity and use them intensively through this book. You'll find out how to create animations, a handy skill for communication and teaching. Then the book shows how to solve data analysis problems using DataFrames and various plotting packages based on the grammar of graphics. Furthermore, you'll discover how to create the most common statistical plots for data exploration. Also, you'll learn to visualize geographically distributed data, graphs, and networks, and biological data. Lastly, this book will go deeper into plot customizations with Plots Makie and Gadfly.

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Visual Informatics: Sustaining Research and Innovations Halimah Badioze Zaman, Peter Robinson, Maria Petrou, Patrick Olivier, Timothy K. Shih, Sergio Velastin, Ingela Nyström, 2011-10-28 The two volume set LNCS 7066 and LNCS 7067 constitutes the proceedings of the Second International Visual Informatics Conference IVIC 2011 held in Selangor Malaysia during November 9 11 2011 The 71 revised papers presented were carefully reviewed and selected for inclusion in these proceedings They are organized in topical sections named computer vision and simulation virtual image processing and engineering visual computing and visualisation and social computing In addition the first volume contains two keynote speeches in full paper length and one keynote abstract

Visualizing Biological Information Clifford A Pickover, 1995-12-15 Biological data of all kinds is proliferating at an incredible rate If humans attempt to read such data in the form of numbers and letters they will take in the information at a snail s pace If the information is rendered graphically however human analysts can assimilate it and gain insight at a much faster rate The emphasis of this book is on the graphic representation of information containing sequences such as DNA and amino acid sequences in order to help the human analyst find interesting and biologically relevant patterns The editor s goal is to make this voyage through molecular biology genetics and computer graphics as accessible to a broad audience as possible with the inclusion of glossaries at the end of most chapters and program outlines where applicable The book will be of most interest to biologists and computer scientists and the various large reference lists should be of interest to beginners and advanced students of biology graphic art and computer science Contributors have sought to find pattern and meaning in the cacophony of genetic and protein sequence data using unusual computer graphics and musical techniques

Graph Drawing Ioannis G. Tollis, Maurizio Patrignani, 2009-02-13 This book constitutes the proceedings of the 16th International Symposium on Graph Drawing GD 2008 held in Heraklion Crete Greece during September 21 24 2008 The 31 long papers

and 8 short papers presented together with 10 posters and two invited papers were carefully reviewed and selected from 83 submissions. The volume also includes a report on the Graph Drawing Contest which was held during the conference. An important aspect of the conference is bridging the gap between theoretical advances and implemented solutions of geometric representation of graphs and networks. It is motivated by those applications where it is crucial to visualize structural information as graphs.

Educational Screen, 1930 Cadernos de Computação, 2000 **Bioinformatics** Jonathan M. Keith, 2008-05-22. In Bioinformatics leading researchers provide a selection of the most useful and widely applicable methods able to be applied as is or with minor variations to many specific problems. Volume II Structure Function and Applications contains methods pertinent to the prediction of protein and RNA structures and the analysis and classification of structures, methods for inferring the function of previously identified genomic elements, chiefly protein coding genes, medical applications in diagnostics and drug discovery, and meta methods for developers of bioinformatics algorithms. Over 80 authors from around the globe have contributed to the two volumes.

Visual Education, 1920 Conference Proceedings, 2001 *Proceedings of the ... IEEE Conference on Visualization*, 1990 *IBM Journal of Research and Development*, 2006 *Interactive Visualization and Model-based Analysis of Genomics Data* Nameeta Yogeshkumar Shah, 2006

Study and Analysis of Knowledgebase of Molecular Systems and to Develop Model for Prediction of Molecular Structure Binod Kumar, 2019-12-16. Doctoral Thesis Dissertation from the year 2010 in the subject Computer Science Miscellaneous Saurashtra University Computer Science Dept course PhD language English abstract. This research work aims to analyze experimental data about biochemical properties and their corresponding kinetics. In this research, the attempt has been made to analyze protein and DNA structure using tools such as DAMBE and Jemboss. Some Molecular Visualization or Analysis tools are already developed that reads analyses and crosscorrelates experimental information which is useful for chemist, Organist, Chemist, Biochemist, and Druggist. In this research, using ACD/ChemSketch, compounds are stored in databases and SMILE code (Simplified Molecular Input Line Specification) is generated. A SMILE defines the molecules in the form of alphanumeric chains. In this research work, chemical shift of every carbon atom of the molecule has been displayed by using NMR Prediction. Under this research, CML codes of molecules have been developed and that codes have been used for molecular information like symmetry and atom and bond attributes. Here, multiple observations of the same molecule like conformational analysis and NMR prediction have been performed. Using Pubchem/NCBI additional miscellaneous information such as bioactivity analysis by structure activity similarity and revised compound selection after addition of similar compounds have been analyzed. Under the research work, geometric optimization of molecules, chemical structure visualization, and calculation of electronic absorption spectra of chemical structure have been performed using ArgusLab tool. In this research, Single Entry Point Calculation, Molecular Orbital calculation on grids for plotting HOMO and LUMO, and ESP Mapped Density calculations have been also performed. Under the research work of different types of

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The Application of Spatial Data Analysis and Visualization in the Development of Landscape Indicators to Assess Stream Conditions Aileen R. Buckley,1997 [The Cumulative Book Index](#) ,1996 A world list of books in the English language

Educational Screen and Audiovisual Guide ,1925 **Visual Education** University of Oklahoma. University Extension Division. Dept. of Visual Education,1921 *Visualization of Temporal and Spatial Data for Civilian and Defense Applications* Glenn O. Allgood,Nickolas Lea Faust,2001

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