

Robert Kincaid

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Education

1982 Ph.D. Theoretical Chemistry, Cornell University, Ithaca NY
1976 B.S. Chemistry, Texas Christian University, Fort Worth TX

Programming Languages

Java, C#, C, C++, Objective-C, Fortran, Basic, Perl

Development Platforms

Microsoft Windows: .NET, WPF, MFC
Apple MacOS: XCode, Cocoa Touch, iPhone SDK
Databases: Oracle, Sybase, Microsoft SQL Server

Professional Affiliations

Senior Member of the Association for Computing Machinery
IEEE & IEEE Computer Society
International Society for Computational Biology
Sigma Xi
Program Committee 2011 IEEE InfoVis & IEEE BioVis
Co-chair for Student Volunteers, 2004 IEEE Visualization
Paper Reviewer for:
IEEE Transactions on Visualization and Computer Graphics
IEEE BioVis Symposium
IEEE Visualization Conference
IEEE Information Visualization Conference
IEEE Symposium on Visual Analytics Science and Technology
Eurographics/ IEEE-VGTC Symposium on Visualization
ACM Symposium on Applied Computing
Proteomics

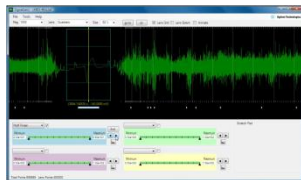
Experience

Agilent Technologies April 2000 - present

Senior Research Scientist

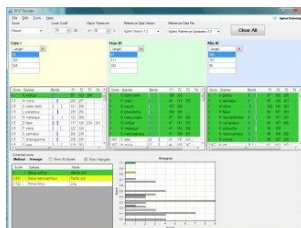
Computational Biology and Computer Science
Agilent Laboratories / Molecular Technologies Lab.

Main research interests are Information Visualization that supports interactive and visually-oriented data mining across widely disparate data (either separately, or in joint analyses; particularly how gene expression and proteomic data can be combined with other measurements and attributes including mass spectrometry results, phenotypes, clinical observations, etc. Recent publicly disclosed research projects include:



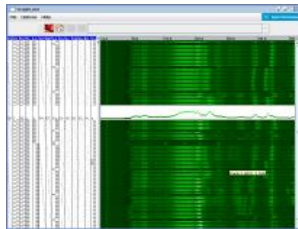
Signal Lens

Signal Lens: A Focus+Context approach for analyzing large time series of electronic signals. SignalLens enables a very compact visualization which supports ad hoc visual data mining of long electronic time series. A brief video demo was presented by Agilent CTO Darlene Solomon at the IEEE MTT-S International Microwave Symposium in 2009. This work was presented at the 2010 IEEE Information Visualization Conference and received a "Paper Honorable Mention" award.



RFLP Decoder

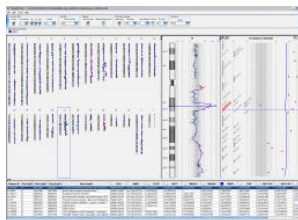
RFLP Decoder: This software was developed to support authenticating fish species; a problem important to the food industry and critical to complying with new regulations to protect endangered fish species from being overfished. This is now part of an Agilent product (Agilent DNA Fish ID Solution) and was published in the Journal of Visual Experiments. There you can see a complete demo of the lab protocol as well as the software.



Line Graph Explorer

Line Graph Explorer: A scalable Focus+Context visualization designed specifically for large collections of line graphs. Published at AVI '06, Venice Italy.

VistaChrom: A visual environment for analyzing CGH data. This was transferred as part of a new microarray-based CGH platform and is now known commercially as CGH Analytics. See the recent publication in "Information Visualization" for details. Published in Information Visualization.



VistaChrom

Mass Hunter/Profiler: A visual environment for analyzing proteomic and metabolomic biomarkers based using Mass Spectrometry. This software was announced and demonstrated at ASMS 2005 and will be released later in 2005.

VistaClara: An exploratory heat map style visualization of gene expression data that combines additional meta-data to assist in finding meaningful patterns in the data. Published in SAC 2004 Proceedings.



VistaClara

Biomolecule Naming Service: A novel LDAP-based lookup service for programmatically resolving biomolecule names and identifiers. This was released as an open source project (<http://openbns.sourceforge.net>).

ALFA – Contributed the original object model design used to construct the ALFA object model and related architectures. See the papers co-authored with Aditya Vailaya for more detail about the ALFA architecture.

**June 1997 -
April 2000**

Technical Lead, Bioinformatics - Bioscience Products/Chemical Applications Group

Responsible for the design and implementation of the data storage subsystem for a next generation Microarray system.

Responsible for design and development of Microarray probe design software.

Led design of the COM/ActiveX-based component architecture of new system architecture.

Led integration with third party software from Rosetta Inpharmatics including design of XML DTD's to enable data exchange between both systems.

Responsible for specifying, installing and maintaining an HP NetServer running NT Server, MS SQL Server, Sybase 11 and Oracle 8. This system operates as the central data storage system for the new Micro-Array system.

Engineering lead responsible for supporting the 241 N- And C-Terminal Protein Sequencer.

Other Work

First Floor

Senior MS-Windows Developer.

1996 - 1997

Responsible for graphical user interfaces (design and implementation). Designed and developed a notification add-on for the SmartBookmarks/InfoPilot line which interfaces to FirstFloor ActiveX/OLE automation interfaces as well as MAPI. Developed Java applets to provide CDF navigation capabilities to Netscape Netcaster Channels.

Oracle	Senior Software Engineer Distributed Solutions Group, Workgroup Solutions Division.
Spring 1996	Delivered ocx-based components for database import/export/load as part of a remote database administration console (Enterprise Manager). This relied on an OLE2.0 distributed computing model. Developed prototype for web software management utilizing Java with CORBA and CORBA-like ORB's. This development included rich sophisticated UI comparable to traditional standalone MFC-based applications, but was completely platform independent and accessible via Web browsers.
Xerox	Principal Software Scientist
1993-1995	<p>1995 - Implemented Windows, Macintosh and Motif-based file upload functionality to World Wide Web servers. This involved direct low-level connectivity to remote Web servers including proxy services via the Windows Sockets API, Unix sockets and MacTCP. This file upload functionality was officially adopted in HTML 3.0. This is in support of a new Web-based service that also requires a sophisticated database back-end to maintain and handle customer job requests.</p> <p>1994 - Responsible for overall software architecture of a new Microsoft At Work-based multi-function fax device. Specifically responsible for implementing the low level printer driver (DMA-based) as well as a "paper user interface" (i.e. Optical Mark Recognition) based on PARC developed "DataGlyph" technology.</p> <p>1993 - Responsible for developing and prototyping new product concepts based on PARC technology, as well as providing overall technical leadership to the Tools and Utilities line of business. Developed new collaborative network-based applications based on PARC research in work group collaboration. Implemented and prototyped next generation of UI products from XSoft including TabWorks (currently bundled on most Compaq computers).</p>
1991-1992	Lead developer and team leader of Rooms for Windows, the first highly successful and visible Windows-based product from the XSoft division of Xerox. Significant contributions were made to the actual development as well as a broad range of technical program management roles.
1990-1991	Manager of "Operating Environments and Toolkit Support" responsible for coupling Xerox proprietary environment with SunOS and X11 via interoperability tools and environments.
1988-1990	Team leader and key contributor to the X-Environment Window project (X server provided within the ViewPoint/GlobalView environment). Personally implemented direct low-level modifications to Sun Microsystems' X11/NeWS server code. Significant contributor to the Companion 386 project (PC/Viewpoint interoperability via a tethered PC environment). Involved heavy use of DOS and assembler development, including DOS device driver development.
1985-1987	Lead developer and Team Leader of a large engineering group responsible for developing a C-based PC word processor (Writer II).
Good Software Dallas Texas 1984-1985	Development of C-based PC word processor
PharmAssist Arlington Texas 1983-1984	Development of UCSD Pascal-based in-store pharmacy automation system.

Publications

Ankit Singh, Alex Endert, Lauren Bradel, Christopher Andrews, Chris North, Robert Kincaid, **Using Large Displays for Live Visual History of Cyber-security Analytic Process** (VizSec 2011) accepted.

Steffen Mueller, Harini Ravi, Natalia Novoradovskaya, Robert Kincaid and Yang-Lee Chee **Enhanced fish species identification by PCR-RFLP using the 2100 Bioanalyzer system**, *International Food Research Journal* **18**, 3 (2011) 1154-1158

Robert Kincaid, **SignalLens: Focus+Context Applied to Electronic Time Series**, *IEEE Trans. Vis. Comput. Graph.* (InfoVis 2010) **16**, 6 (2010) 900-907

Formosa R, Ravi H, Happe S, Huffman D, Novoradovskaya N, Kincaid R, Garrett S. **DNA-based Fish Species Identification Protocol**. *JoVE* **38** (2010)
<http://www.jove.com/index/details.stp?id=1871>, doi: 10.3791/1871

R. Kincaid, K. Dejgaard, **MassVis: Visual Analysis of Protein Complexes Using Mass Spectrometry**, IEEE Symposium on Visual Analytics Science and Technology (VAST '09), Atlantic City NJ, October 11-12 2009.

A. Barsky, T. Munzner, J. Gardy, R. Kincaid, **Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context**, *IEEE Trans. Vis. Comput. Graph.* (InfoVis '08) **15**, 6 (2008) 1253-1260.

R. Kincaid, A. Kuchinsky, M. Creech, **VistaClara: an expression browser plug-in for Cytoscape**, *Bioinformatics* **24**, 18 (2008) 2112.

O. Mueller, E. Chang, D. Deng, T. Franz, D. Jing, R. Kincaid, Y. Konigshofer, M. Kratzmeier, M. McNulty, H. Qian, J. Schneider, H. Schulte, U. Seedorf, X. D. Tian, M. Van Cleve, D. Yang, G. Assmann, **PROCAM Study: risk prediction for myocardial infarction using microfluidic high-density lipoprotein (HDL) sub-fractionation is independent of HDL cholesterol**, *Clin. Chem. Lab. Med.* **46**, 4 (2008) 490-498.

Lam, T. Munzner, R. Kincaid, **Overview Use in Multiple Visual Information Resolution Interfaces**, *IEEE Trans. Vis. Comput. Graph.* (InfoVis '07) **13**, 6 (2007) 1278-1285.

R. Kincaid, H. Lam, **Line Graph Explorer: Scalable Display of Line Graphs Using Focus+Context**, Proc. of the Workshop on Advanced Visual Interfaces (AVI'06), ACM Press, Venice, Italy (2006) 404-411.

D. X. Deng, A. Tsalenko, A. Vailaya, A. Ben-Dor, R. Kundu, I. Estay, R. Tabibiazar, R. Kincaid, Z. Yakhini, L. Bruhn, T. Quertermous, **Differences in vascular bed disease susceptibility reflect differences in gene expression response to atherogenic stimuli**, *Circulation Research* **98**, 2 (2006) 200.

R. Kincaid, A. Ben-Dor, Z. Yakhini, **Exploratory visualization of array-based comparative genomic hybridization**, *Information Visualization* **4**, 3 (2005) 176.

J. Y. King, R. Ferrara, R. Tabibiazar, J. M. Spin, M. M. Chen, A. Kuchinsky, A. Vailaya, R. Kincaid, A. Tsalenko, D. X.-F. Deng, A. Connolly, P. Zhang, E. Yang, C. Watt, Z. Yakhini, A. Ben-Dor, A. Adler, L. Bruhn, P. Tsao, T. Quertermous, E. A. Ashley, **Pathway analysis of coronary atherosclerosis**, *Physiol. Genomics* (2005) 00101.2005.

A. Vailaya, P. Blugas, R. Kincaid, A. Kuchinsky, M. Creech, A. Adler, **An architecture for biological information extraction and representation**, *Bioinformatics* **21**, 4 (2005) 430.

M. T. Barrett, A. Scheffer, A. Ben-Dor, N. Sampas, D. Lipson, R. Kincaid, P. Tsang, B. Curry, K. Baird, P. S. Meltzer, Z. Yakhini, L. Bruhn, S. Laderman, **Comparative genomic hybridization using oligonucleotide microarrays and total genomic DNA**, *Proceedings of the National Academy of Sciences of the United States of America* **101**, 51 (2004) 17765.

R. Kincaid, **VistaClara: an interactive visualization for exploratory analysis of DNA microarrays**, Proceedings of the 2004 ACM symposium on Applied computing, ACM Press, Nicosia, Cyprus 2004.

A. Vailaya, P. Bluvas, R. Kincaid, A. Kuchinsky, M. Creech, A. Adler, **An architecture for biological information extraction and representation**, Proceedings of the 2004 ACM symposium on Applied computing, ACM Press, Nicosia, Cyprus 2004.

G. Delenstarr, H. Cattell, C. Chen, A. N. Dorsel, R. H. Kincaid, K. Nguyen, N. M. Sampas, S. Schidel, K. W. Shannon, A. Tu, P. K. Wolber, **Estimation of the confidence limits of oligonucleotide-array-based measurements of differential expression**, *Microarrays: Optical Technologies and Informatics*, SPIE, 2001.

D. A. Huckaby, R. Pitis, R. H. Kincaid, C. Hamilton, **Inclusion--exclusion calculation of the dipole--dipole energy of hexagonal ice and of cubic ice**, *The Journal of Chemical Physics* **98**, 10 (1993) 8105.

R. H. Kincaid, D. A. Huckaby, **Harmonic surface entropy of noble gas crystals: Cell cluster method**, *The Journal of Chemical Physics* **78**, 5 (1983) 2598.

R. H. Kincaid, D. A. Huckaby, **Cell cluster calculations of the surface entropy of harmonic fcc crystals**, *The Journal of Chemical Physics* **76**, 7 (1982) 3836.

R. H. Kincaid, H. A. Scheraga, **Acceleration of convergence in Monte Carlo simulations of aqueous solutions using the Metropolis algorithm. Hydrophobic hydration of methane**, *Journal of Computational Chemistry* **3** (1982) 525.

R. H. Kincaid, H. A. Scheraga, **Revised empirical potential for conformational, intermolecular, and solvation studies. 6. Testing of parameters by application to liquid ammonia**, *Journal of Physical Chemistry* **86** (1982) 838.

R. H. Kincaid, H. A. Scheraga, **Revised empirical potential for conformational, intermolecular, and solvation studies. 7. Testing of parameters by application to liquid methane**, *Journal of Physical Chemistry* **86** (1982) 838.

R. L. Kincaid, D. A. Huckaby, **Two methods for calculating the effect of vacancy defects on the free energy of harmonic solids**, *The Journal of Chemical Physics* **65**, 6 (1976) 2353.

Issued Patents	Pat. No.	Title
	7,930,108	Exploratory Visualization of Protein Complexes by Molecular Weight
	7,894,998	Method for identifying suitable nucleic acid probe sequences for use in nucleic acid arrays
	7,879,541	Apparatus and methods of detecting features on a microarray
	7,825,929	Systems, tools and methods for focus and context viewing of large collections of graphs
	7,750,908	Focus plus context viewing and manipulation of large collections of graphs
	7,588,889	Chemical arrays and methods of using the same
	7,519,605	Systems, methods and computer readable media for performing a domain-specific metasearch, and visualizing search results therefrom
	7,344,831	Methods for controlling cross-hybridization in analysis of nucleic acid sequences
	7,224,362	Systems and methods for providing visualization and network diagrams
	7,155,453	Biotechnology information naming system
	6,251,588	Method for evaluating oligonucleotide probe sequences
	6,461,816	Methods for controlling cross-hybridization in analysis of nucleic acid sequences
	6,920,448	Domain specific knowledge-based metasearch system and methods of using
	6,950,756	Rearrangement of microarray scan images to form virtual arrays

Published Patent Filings	Filing No.	Title
	20100191790	System and Method for Correlation Scoring of Signals
	20100188406	Systems and Methods for Focus Plus Context Viewing of Dense, Ordered Line Graphs
	20100128988	Cellular- or Sub-Cellular-Based Visualization Information Using Virtual Stains
	20090192719	Exploratory visualization of protein complexes by molecular weight
	20090147005	Methods, systems and computer readable media facilitating visualization of higher dimensional datasets in a two-dimensional format
	20070031883	Analyzing CGH data to identify aberrations
	20060263789	Unique identifiers for indicating properties associated with entities to which they are attached, and methods for using
	20060084067	Method and system for analysis of array-based, comparative-hybridization data
	20060028471	Focus plus context viewing and manipulation of large collections of graphs
	20050278321	Systems, methods and computer readable media for performing a domain-specific metasearch, and visualizing search results therefrom
	20050244885	Array based methods for synthesizing nucleic acid mixtures
	20050216459	Methods and systems, for ontological integration of disparate biological data
	20050206644	Systems, tools and methods for focus and context viewing of large collections of graphs
	20050197784	Methods and systems for analyzing term frequency in tabular data
	20050148004	Chemical arrays and methods of using the same
	20050136427	Methods for controlling cross-hybridization in analysis of nucleic acid sequences
	20050112689	Systems and methods for statistically analyzing apparent CGH data anomalies and plotting same
	20050039123	Method and system for importing, creating and/or manipulating biological diagrams
	20050027729	System and methods for visualizing and manipulating multiple data values with graphical views of biological relationships
	20050027461	Methods for evaluating oligonucleotide probe sequences
	20050026306	Method and system for generating virtual-microarrays
	20040241730	Visualizing expression data on chromosomal graphic schemes
	20040153251	Rearrangement of microarray scan images to form virtual arrays
	20040150644	Systems and methods for providing visualization and network diagrams
	20040061702	Methods and system for simultaneous visualization and manipulation of multiple data types
	20040027350	Methods and system for simultaneous visualization and manipulation of multiple data types
	20040024532	Method of identifying trends, correlations, and similarities among diverse biological data sets and systems for facilitating identification
	20040002070	Method for identifying suitable nucleic acid probe sequences for use in nucleic acid arrays
	20030220910	Biotechnology information naming system
	20030218634	System and methods for visualizing diverse biological relationships
	20030186310	Apparatus and methods of detecting features on a microarray
	20030162183	Array design system and method
	20030124588	Methods for controlling cross-hybridization in analysis of nucleic acid sequences
	20030054346	Methods for evaluating oligonucleotide probe sequences
	20020169764	Domain specific knowledge-based metasearch system and methods of using