

# Robert Kincaid

## Address

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## Phone

650 224 1289

## Technical Skills

Proficient: Java, C#, C++, C, Fortran, SQL, Apache Spark, HTML, Tibco Spotfire  
Familiarity: Scala, Python, R, Perl, Hadoop, JavaScript, CSS  
Special expertise: Information Visualization, Visual Analytics, Human Computer Interaction, algorithm development, bioinformatics, computational biology, genomics and proteomics data analysis

## Professional Affiliations and Activities

Senior Member of the Association for Computing Machinery  
Senior Member of IEEE & Member of IEEE Computer Society  
Member of International Society for Computational Biology  
Member of Sigma Xi  
Poster co-chair, 2012-2013 IEEE BioVis, Industry Liaison, 2011, 2014 IEEE BioVis Program Committee 2011-2014 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  
EuroVis/IEEE-VGTC Symposium on Visualization  
ACM Symposium on Applied Computing  
Proteomics, Bioinformatics, Pacific Symposium on Biocomputing  
BMC Bioinformatics

## Education

1982 Ph.D. Theoretical Chemistry, Cornell University, Ithaca NY  
1979 M.S. Theoretical Chemistry, Cornell University, Ithaca NY  
1976 B.S. Chemistry, Texas Christian University, Fort Worth TX

## Experience

### Agilent Laboratories 2013-present

#### Research Manager, Big Data Applications in Life Science

Agilent Laboratories, Santa Clara CA  
Performing hands-on research and software development to explore how big data technologies such as Hadoop, Apache Spark, Amazon Web Services, etc. can be leveraged to increase the scalability of life science data analysis. This also includes architectures for scalable interactive visualization of big data problems. Duties include hands on investigation and research as well as developing several proof-of-concept demonstrations. This position also requires project coordination, alignment with product divisions, people management as well as hiring responsibilities to bring needed expertise into the project.

**Agilent Laboratories  
2000-2013**

**Senior Research Scientist Computational Biology and Computer Science**

Agilent Laboratories / Molecular Technologies Lab, Palo Alto & Santa Clara CA  
Conducted on-going applied research in the visualization and visual analytics of various forms of life science data. This work resulted in several significant transfers including VistaChrom which became a commercial release as CGH Analytics and led to Agilent's ongoing and still successful commercial platforms for CGH and DNA Copy Number analysis. Google Scholar reports over 2000 scientific publications that have cited this software in their analysis. Other projects have varied from genomics to mass spec proteomics and even fish species identification for food testing. Another recent significant transfer was the development of critical visualization components for the Agilent Masshunter IMS Browser. This analytical tool is used to perform novel analyses of Ion Mobility Mass Spectrometry data. See the attached list of publications for more details about the various published research conducted during this time. Note that this body of body of visualization work was instrumental in significantly raising the awareness within Agilent of the importance of well-designed, well-founded visualization of biological data.

**Hewlett-Packard &  
Agilent  
Technologies  
1997-2000**

**Technical Lead, Bioinformatics**

Bioscience Products/Chemical Applications Group, Palo Alto CA  
Designed and implemented a database architecture for storage of microarray data, developed software for microarray probe and array design and worked with Rosetta Informatics to help development Object Management Group approved XML standards for gene expression data (GEML). GEML was eventually incorporated as part of MAGE-ML. Much of this early microarray work is reflected in the various microarray patents listed below.

**First Floor  
1996-1997**

**Senior Software Engineer**

Mountain View CA  
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  
1996**

**Senior Software Engineer**

Distributed Solutions Group, Redwood Shores CA  
Delivered ocx-based components for database import/export/load as part of a remote database administration console (Enterprise Manager).

**Xerox  
1985-1995**

**Principal Software Scientist**

Lewisville TX, Sunnyvale CA, Palo Alto CA  
Helped develop numerous office automation tools for the Office Products and XSoft divisions of Xerox. Development components of a PC-based word processor, integrated X-Windows capabilities into GlobalView and led the team that produced Rooms for Windows. This was the first transfer of Xerox Parc technology into a consumer-level product.

## Publications

C. Grote, E. Segreto, J. Okerlund, R. Kincaid, O. Shaer, **Eugenie: Multi-Touch and Tangible Interaction for Bio-Design**, Conference on Tangible, Embedded and Embodied Interaction (TEI'15).

C. Grote, E. Segreto, J. Okerlund, R. Kincaid, O. Shaer, **Eugenie: Gestural and Tangible Interaction with Active Tokens for Bio-Design**, Extended Abstract, ACM UIST 2014.

Orit Shaer, Consuelo Valdes, Sirui Liu, Kara Lu, Casey Grote, Veronica Lin, Linda Ding, Nicole Francisco, Kimberly Chang, Wendy Xu, Nahum Seifelasie, Robert Kincaid, **Designing Reality-Based Interfaces for Experiential Bio-Design**, Personal and Ubiquitous Computing (Special Edition on Educational Interfaces, Software, and Technology) 2014, **18**: p. 1515-1532.

Melanie Tory, Robert Kincaid, **Comparing Physical, Overlay, and Touch Screen Parameter Controls**, ACM Interactive Tabletops and Surfaces 2013 Conference (ITS), 2013.

Orit Shaer, Consuelo Valdes, Sirui Liu, Kara Lu, Traci Haddock, Swapnil Bhatia, Douglas Densmore, Robert Kincaid, **MoClo Planner: Interactive Visualization for Modular Cloning Bio-Design**, Accepted IEEE Symposium on Biological Data Visualization (BioVis), 2013.

Wendy Xu, Kimberly Chang, Nicole Francisco, Consuelo Valdes, Robert Kincaid, and Orit Shaer, **From Wet Lab Bench to Tangible Virtual Experiment: SynFlo**. ACM International Conference on Tangible, Embedded and Embodied Interaction (TEI'13).

Sirui Liu, Kara Lu, Nahum Seifelasie, Casey Grote, Nicole Francisco, Veronica Lin, Linda Ding, Consuelo Valdes, Robert Kincaid, and Orit Shaer, **MoClo planner: supporting innovation in bio-design through multi-touch interaction**. ACM international conference on Interactive tabletops and surfaces (ITS '12) 307-310.

Kimberly Chang, Wendy Xu, Nicole Francisco, Consuelo Valdes, Robert Kincaid, and Orit Shaer, **SynFlo: an interactive installation introducing synthetic biology concepts**, ACM international conference on Interactive tabletops and surfaces (ITS '12) 303-306.

Robert Kincaid, **Tactile Guides for Touch Screen Controls** (BCS HCI 2012) 339-344.

Ankit Singh, Alex Endert, Lauren Bradel, Christopher Andrews, Chris North and Robert Kincaid, **Using Large Displays for Live Visual History of Cyber-security Analytic Process**, in International Symposium on Visualization for Cyber Security (VizSec)2011: Carnegie Mellon University.

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, 2011. **18**(3): p. 1154-1158.

R. Kincaid, **SignalLens: Focus plus Context Applied to Electronic Time Series**. IEEE Transactions on Visualization and Computer Graphics, 2010. **16**(6): p. 900-907.

R Formosa, H Ravi, S Happe, D Huffman, N Novoradovskaya, R Kincaid and S Garrett, **DNA-based Fish Species Identification Protocol**. Journal of Visualized Experiments, 2010(38).

R Kincaid and K Dejgaard. **MassVis: Visual analysis of protein complexes using mass spectrometry**. in IEEE Symposium on Visual Analytics Science and Technology. 2009. IEEE.

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 and G. Assmann, **PROCAM Study: risk prediction for myocardial infarction using microfluidic high-density lipoprotein (HDL) sub-fractionation is independent of HDL cholesterol**. *Clinical Chemistry and Laboratory Medicine*, 2008. **46**(4): p. 490-498.

R. Kincaid, A. Kuchinsky and M. Creech, **VistaClara: An expression browser plug-in for Cytoscape**. *Bioinformatics*, 2008. **24**(18): p. 2112-2114.

A. Barsky, T. Munzner, J. Gardy and R. Kincaid, **Cerebral: Visualizing Multiple Experimental Conditions on a Graph with Biological Context**. *IEEE Transactions on Visualization and Computer Graphics*, 2008. **14**(6): p. 1253-1260.

H. Lam, T. Munzner and R. Kincaid, **Overview use in multiple visual information resolution interfaces**. *IEEE Transactions on Visualization and Computer Graphics*, 2007. **13**(6): p. 1278-1285.

D. X. F. Deng, A. Tsalenko, A. Vailaya, A. Ben-Dor, R. Kundu, I. Estay, R. Tabibiazar, R. Kincaid, Z. Yakhini, L. Bruhn and T. Quertermous, **Differences in vascular bed disease susceptibility reflect differences in gene expression response to atherogenic stimuli**. *Circulation Research*, 2006. **98**(2): p. 200-208.

A. Vailaya, A. Kuchinsky, R. Kincaid, A. Adler, R. Tabibiazar, R. Wagner and T. Quertermous. **Ontology-based statistical analysis of microarray data**. in 8th Annual Bio-Ontologies Meeting. 2005.

A. Vailaya, P. Bluvas, R. Kincaid, A. Kuchinsky, M. Creech and A. Adler, **An architecture for biological information extraction and representation**. *Bioinformatics*, 2005. **21**(4): p. 430-438.

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 and E. A. Ashley, **Pathway analysis of coronary atherosclerosis**. *Physiological Genomics*, 2005. **23**(1): p. 103-118.

R Kincaid, A Ben-Dor and Z Yakhini, **Exploratory visualization of array-based comparative genomic hybridization**. *Information Visualization*, 2005. **4**(3): p. 176-190.

Aditya Vailaya, Peter Bluvas, Robert Kincaid, Allan Kuchinsky, Michael Creech and Annette Adler, **An architecture for biological information extraction and representation**, in *Proceedings of the 2004 ACM Symposium on Applied Computing*, 2004, ACM: Nicosia, Cyprus. p. 103-110.

R Kincaid. **VistaClara: an interactive visualization for exploratory analysis of DNA microarrays**. in *ACM Symposium on Applied Computing*. 2004. ACM.

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 and 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*, 2004. **101**(51): p. 17765-17770.

G Delenstarr, H Cattell, C Chen, AN Dorsel, RH Kincaid, K Nguyen, NM Sampas, S Schidel, KW Shannon and A Tu. **Estimation of the confidence limits of oligonucleotide-array-based measurements of differential expression.** in SPIE. 2001.

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

RH Kincaid and DA Huckaby, **Harmonic surface entropy of noble gas crystals: Cell cluster method.** The Journal of Chemical Physics, 1983. **78**: p. 2598.

RH Kincaid and HA Scheraga, **Revised empirical potential for conformational, intermolecular, and solvation studies. 7. Testing of parameters by application to liquid methane.** The Journal of Physical Chemistry, 1982. **86**(5): p. 838-841.

RH Kincaid and HA Scheraga, **Revised empirical potential for conformational, intermolecular, and solvation studies. 6. Testing of parameters by application to liquid ammonia.** The Journal of Physical Chemistry, 1982. **86**(5): p. 833-838.

RH Kincaid and HA Scheraga, **Acceleration of convergence in Monte Carlo simulations of aqueous solutions using the metropolis algorithm. Hydrophobic hydration of methane.** Journal of Computational Chemistry, 1982. **3**(4): p. 525-547.

RH Kincaid and DA Huckaby, **Cell cluster calculations of the surface entropy of harmonic fcc crystals.** The Journal of Chemical Physics, 1982. **76**: p. 3836.

RL Kincaid and DA Huckaby, **Two methods for calculating the effect of vacancy defects on the free energy of harmonic solids.** The Journal of Chemical Physics, 1976. **65**: p. 2353.

## Patents

Pat. No.	Title
8,340,389	Cellular- or Sub-Cellular-Based Visualization Information Using Virtual Stains
8,131,471	Methods and system for simultaneous visualization and manipulation of multiple data types
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
6,950,756	Rearrangement of microarray scan images to form virtual arrays
6,920,448	Domain specific knowledge-based metasearch system and methods of using
6,461,816	Methods for controlling cross-hybridization in analysis of nucleic acid sequences
6,251,588	Method for evaluating oligonucleotide probe sequences