

Dick Kreisberg
Data Visualization & Interactive Analytics

Contact Information

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Research Interests

- Exploration of Large-scale and Complex Data
- Interactive Data Visualization
- Visual Perception and Cognition
- Machine Learning
- Collaborative, Distributed Research
- Computational Systems Biology, Genomics, Bioinformatics
- On-Demand, Steerable Computation

Education

M.S. in Electrical Engineering (May 2003)
University of Washington, Seattle, WA

B.S. in Computer Engineering (May 2001)
University of Oklahoma, Norman, OK

Research Experience

- *Institute for Systems Biology*, Seattle, Washington (2013 - present), (Senior Software Engineer)
- *Institute for Systems Biology*, Seattle, Washington (2009 - 2013), (Software Engineer)
- *Fisheries Acoustics Lab*, School of Aquatic and Fishery Sciences, *University of Washington*, Seattle, Washington (2005 - 2009), (Research Engineer)
- Department of Electrical Engineering, *The University of Washington*, Seattle, Washington (2003-2005), (Researcher)

Publications

Journals

2013

Lin, Jake, et al. "POMO-Plotting Omics analysis results for Multiple Organisms." *BMC genomics* 14.1 (2013): 918

M. Heinäniemi, M. Nykter, R. Kramer, A. Wienecke-Baldacchino, L. Sinkkonen, J. X. Zhou, R. Kreisberg, S. A. Kauffman, S. Huang, I. Shmulevich, "Gene-pair expression signatures reveal lineage control," *Nature Methods* (April 21), 2013. [doi: 10.1038/nmeth.2445]

2012

R. Bressler, J. Lin, A. Eakin, T. Robinson, R. Kreisberg, H. Rovira, T. Knijnenburg, J. Boyle, I. Shmulevich, "Fastbreak: a tool for analysis and visualization of structural variations in genomic data," *EURASIP Journal on Bioinformatics and Systems Biology*, Vol. 2012(1), No. 15, 2012.

The Cancer Genome Atlas Network, "Comprehensive Molecular Portraits of Human Breast Tumors," *Nature*, Vol. 490, No. 7418, pp. 61–70, 2012.

The Cancer Genome Atlas Network, "Comprehensive Molecular Characterization of Human Colon and Rectal Cancer," *Nature*, Vol. 487, No. 7407, pp. 330-337, 2012.

Farrah, T., Deutsch, E. W., Kreisberg, R., Sun, Z., Campbell, D. S., Mendoza, L., Kusebauch, U., Brusniak, M.-Y., Hüttenhain, R., Schiess, R., Selevsek, N., Aebersold, R. and Moritz, R. L. "PASSEL: The PeptideAtlas SRMexperiment library," *Proteomics*, 12: 1170–1175, 2012

Boyle, John, et al. "Methods for visual mining of genomic and proteomic data atlases." *BMC bioinformatics* 13.1 (2012): 58.

2011

Jennifer J Smith, Leslie R Miller, Richard Kreisberg, Laura Vazquez, Yakun Wan & John D Aitchison, "Environment-responsive transcription factors bind subtelomeric elements and regulate gene silencing," *Molecular Systems Biology* 7 Article number: 455

Barbee, David H., et al. "Interfacing a scientific echosounder with a cabled ocean observatory." *The Journal of the Acoustical Society of America* 129 (2011): 2400.

2009

Horne, John K., et al. "Swimbladders under pressure: anatomical and acoustic responses by walleye pollock." *ICES Journal of Marine Science: Journal du Conseil* 66.6 (2009): 1162-1168.

Talks

- 1st Annual TCGA Symposium, "Visualization Techniques for Cancer Research," National Harbor, MD, Nov, 2011
- Systems Bioinformatics Workshop, "Interactive Data Visualization for the Web," Seattle, WA, Sep, 2012
- 2nd Annual TCGA Symposium, "Regulome Explorer Workshop," Crystal City, VA, Nov, 2012
- Understanding Cancer Genomics Through Information Visualization, University of Tokyo, Institute for Medical Science. "Visualizing Multivariate Analysis of Cancer Data", Feb 2013

- Understanding Cancer Genomics Through Information Visualization, University of Tokyo, Institute for Medical Science. "Regulome Explorer Workshop and an Introduction to D3.js", Feb 2013
- Research in Progress, Institute for Systems Biology, "Data Stratification with Visual Analytics", December, 2013

Open Source Projects

- *Inspectra*, github.com/rbkreisberg/Inspectra, Interactive comparison of multiple networks via intuitive layout and clustering.
- *Regulome Explorer*, regulome-explorer.googlecode.com, [ithub.com/cancerregulome/RegulomeExplorer](https://github.com/cancerregulome/RegulomeExplorer), Interactive Exploratory interface for association-based analysis. Cancer Regulome Explorer hosts data from The Cancer Genome Atlas
- *Circvis*, visquick.googlecode.com, A of dynamically configurable, interactive circular layout visualization for exploring multi-dimensional genomic datasets. Based on *Circos*.
- *Visquick*, visquick.googlecode.com, github.com/Visquick, A suite of interactive visualizations used in multiple applications
- *Carve.js* – github.com/rbkreisberg/carve - A flexible 2.5 dimension visual tool for exploring intricate relationships in high-dimensional datasets.
- *Transcription Regulation and Epigenetic Landscape Explorer*, trel.systemsbiology.net, A web application built around a set of interactive heatmaps. Used to explore the results of the *Nature Methods* paper: "Gene-pair expression signatures reveal lineage control."
- *ChromaVis* – A plot for displaying and comparing multiple protein mass spectrometry datasets.

Other

Google IO 2012 Keynote for Google Compute Engine focused on the use of Random Forest and *Circvis*. A custom version of *Circvis* was created for this demonstration.