Daniel Blankenberg

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EDUCATION

2010 - Present   Postdoctoral Research Associate
                   The Pennsylvania State University
                   University Park, PA

2004 - 2009   PhD Biochemistry, Microbiology and Molecular Biology
                   The Pennsylvania State University
                   University Park, PA
                   Thesis: Galaxy, a web-based platform for the integration of genome analysis.
                   Advisor: Anton Nekrutenko

2000 -2004   B.S. Biochemistry & Molecular Biology
                        Computer Science
                   Minor: Philosophy
                   Gettysburg College
                   Gettysburg, PA

PUBLICATIONS

Qu K, Garamszegi S, Wu F, Thorvaldsdottir H, Liefeld T, Ocana M, Borges-Rivera D, Pochet N, Robinson JT, Demchak B, Hull T, Ben-Artzi G, **Blankenberg D**, Barber GP, Lee BT, Kuhn RM, Nekrutenko A, Segal E, Ideker T, Reich M, Regev A, Chang HY, Mesirov JP. Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. *Nat Methods*. 2016 Jan 18.

Blankenberg D, Taylor J, Nekrutenko A. Online resources for genomic analysis using high-throughput sequencing. *Cold Spring Harb Protoc.* 2015 Feb 5;2015(4):pdb.top083667.

Blankenberg D, Johnson JE; Galaxy Team, Taylor J, Nekrutenko A. Wrangling Galaxy's reference data. *Bioinformatics*. 2014 Jul 1;30(13):1917-9.

Blankenberg D, Von Kuster G, Bouvier E, Baker D, Afgan E, Stoler N; Galaxy Team, Taylor J, Nekrutenko A. Dissemination of scientific software with Galaxy ToolShed. *Genome Biol.* 2014 Feb 20;15(2):403.

Rebolledo-Jaramillo B, Su MS, Stoler N, McElhoe JA, Dickins B, **Blankenberg D**, Korneliussen TS, Chiaromonte F, Nielsen R, Holland MM, Paul IM, Nekrutenko A, Makova KD. Maternal age effect and severe germ-line bottleneck in the inheritance of human mitochondrial DNA. *Proc Natl Acad Sci* U S A. 2014 Oct 28;111(43):15474-9.

Blankenberg D, Hillman-Jackson J. Analysis of next-generation sequencing data using Galaxy. *Methods Mol Biol*. 2014;1150:21-43.

Dickins B, Rebolledo-Jaramillo B, Su MS, Paul IM, **Blankenberg D**, Stoler N, Makova KD, Nekrutenko A. Controlling for contamination in re-sequencing studies with a reproducible web-based phylogenetic approach. *Biotechniques*. 2014 Mar 1;56(3):134-6, 138-41.

Minevich G, Park DS, **Blankenberg D**, Poole RJ, Hobert O. CloudMap: a cloud-based pipeline for analysis of mutant genome sequences. *Genetics*. 2012 Dec;192(4):1249-69.

Mouse ENCODE Consortium, Stamatoyannopoulos JA, Snyder M, Hardison R, Ren B, Gingeras T, Gilbert DM, Groudine M, Bender M, Kaul R, Canfield T, Giste E, Johnson A, Zhang M, Balasundaram G, Byron R, Roach V, Sabo PJ, Sandstrom R, Stehling AS, Thurman RE, Weissman SM, Cayting P, Hariharan M, Lian J, Cheng Y, Landt SG, Ma Z, Wold BJ, Dekker J, Crawford GE, Keller CA, Wu W, Morrissey C, Kumar SA, Mishra T, Jain D, Byrska-Bishop M, **Blankenberg D**, Lajoie1 BR, Jain G, Sanyal A, Chen KB, Denas O, Taylor J, Blobel GA, Weiss MJ, Pimkin M, Deng W, Marinov GK, Williams BA, Fisher-Aylor KI, Desalvo G, Kiralusha A, Trout D, Amrhein H, Mortazavi A, Edsall L, McCleary D, Kuan S, Shen Y, Yue F, Ye Z, Davis CA, Zaleski C, Jha S, Xue C, Dobin A, Lin W, Fastuca M, Wang H, Guigo R, Djebali S, Lagarde J, Ryba T, Sasaki T, Malladi VS, Cline MS, Kirkup VM, Learned K, Rosenbloom KR, Kent WJ, Feingold EA, Good PJ, Pazin M, Lowdon RF, Adams LB. An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biol*. 2012 Aug 13;13(8):418.

Hillman-Jackson J, Clements D, **Blankenberg D**, Taylor J, Nekrutenko A; Galaxy Team. Using Galaxy to perform large-scale interactive data analyses. *Curr Protoc Bioinformatics*. 2012 Jun;Chapter 10:Unit10.5.

Blankenberg D, Taylor J, Nekrutenko A; Galaxy Team. Making whole genome multiple alignments usable for biologists. *Bioinformatics*. 2011 Sep 1;27(17):2426-8.

Blankenberg D, Coraor N, Von Kuster G, Taylor J, Nekrutenko A; Galaxy Team. Integrating diverse databases into a unified analysis framework: a Galaxy approach. *Database (Oxford)*. 2011 Apr 29.

Blankenberg D, Gordon A, Von Kuster G, Coraor N, Taylor J, Nekrutenko A; Galaxy Team. Manipulation of FASTQ data with Galaxy. *Bioinformatics*. 2010 Jul 15;26(14):1783-5.

Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. Galaxy: a web-based genome analysis tool for experimentalists. *Curr Protoc Mol Biol.* 2010 Jan;Chapter 19:Unit 19.10.1-21.

Miller W, Rosenbloom K, Hardison RC, Hou M, Taylor J, Raney B, Burhans R, King DC, Baertsch R, **Blankenberg D**, Kosakovsky Pond SL, Nekrutenko A, Giardine B, Harris

RS, Tyekucheva S, Diekhans M, Pringle TH, Murphy WJ, Lesk A, Weinstock GM, Lindblad-Toh K, Gibbs RA, Lander ES, Siepel A, Haussler D, Kent WJ. 28-way vertebrate alignment and conservation track in the UCSC Genome Browser. *Genome Res.* 2007 Dec;17(12):1797-808.

Taylor J, Schenck I, **Blankenberg D**, Nekrutenko A. Using galaxy to perform large-scale interactive data analyses. *Curr Protoc Bioinformatics.* 2007 Sep;Chapter 10:Unit 10.5.

Sangar V, **Blankenberg D**, Altman N, Lesk AM. Quantitative sequence-function relationships in proteins based on gene ontology. *BMC Bioinformatics.* 2007 Aug 8;8:294.

Blankenberg D, Taylor J, Schenck I, He J, Zhang Y, Ghent M, Veeraraghavan N, Albert I, Miller W, Makova KD, Hardison RC, Nekrutenko A. A framework for collaborative analysis of ENCODE data: making large-scale analyses biologist-friendly. *Genome Res.* 2007 Jun;17(6):960-4.

Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, Zhang Y, **Blankenberg D**, Albert I, Taylor J, Miller W, Kent WJ, Nekrutenko A. Galaxy: a platform for interactive large-scale genome analysis. *Genome Res.* 2005 Oct;15(10):1451-5.

SELECTED ORAL PRESENTATIONS

Galaxy for the Analysis of Very Large Biomedical Data. Festival of Genomics. San Mateo, CA. November 2015.

Demystifying the Interoperability of Disparate Genomic Resources. Bioinformatics Open Source Conference (BOSC). Dublin, IE. July 2015.

Less Click, More Quick: Unattended Installation of Galaxy's Built-in Reference Data. 2015 Galaxy Community Conference. Norwich, UK. July 2015.

From the Ground to the Cloud in 25 minutes: Building a Customized Galaxy Analysis Server Using Only a Web Browser. Intelligent Systems for Molecular Biology (ISMB). Boston, MA. July 2014.

Enhancing the Galaxy Experience through Community Involvement. Bioinformatics Open Source Conference (BOSC). Boston, MA. July 2014.

More Options, Less Time: Streamlining Access to Reference Datasets. Galaxy Community Conference. Baltimore, MD. July 2014.

Galaxy: a Collaborative Web-based Workbench for the Analysis of Large-Scale Biomedical Data. Brain-CODE Workshop: Building Analytics for Integrated Neuroscience Data. Ontario Brain Institute. Toronto, ON. May 2014.

Introduction to Variant Analysis with Galaxy. Royal College of Pathologists of Australasia Genomic Bioinformatics Workshop. Sydney, Australia. October, 2013.

Managing Galaxy's Built-in Data. The 2013 Galaxy Community Conference. Oslo, Norway. July 2013.

Galaxy: open source NGS analyses. Keynote at Flemish Training Network Life Sciences Next Generation Sequencing workshop. KU Leuven, Belgium. September 2012.

Integrating Tools & Data Sources. The 2012 Galaxy Community Conference. Chicago, USA. July 2012.

Best practices for variant discovery through Galaxy: Oscillating evolution within dual coding genes. Genome Informatics 2011, Cold Spring Harbor, New York, United States. November 2011.

Galaxy for high-throughput NGS analysis. MipTec, Next Generation Sequencing for Research and Clinical Genomics User Group, Basel, Switzerland. September 2011.

NGS Best Practices through Galaxy: Cloud-based variant discovery with visual analytics. Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria. July 2011.

New Data Sources, New Tools. The 2011 Galaxy Community Conference. Lunteren, Netherlands. May 2011.

Galaxy Tools and Services for Enabling Next-Generation Sequencing Analysis. UCHC Stem Cell and Translational Genomics Cores Joint Training Symposium. Farmington, CT. January 2011.

Galaxy: Analyze, Visualize, Communicate. Plant and Animal Genome Conference (PAG XVIX). San Diego, CA. January 2011.

Galaxy: Making NGS Analyses Accessible for All. Short courses presented during: (1) BioIT World Europe. Hannover, Germany. October 2010. (2) NGx: Evolution of Next-Generation Sequencing. Providence, RI. September 2010.

Animal Genomics with Galaxy: Analyze, Publish, and Visualize. Plant and Animal Genome Conference (PAG XVIII). San Diego, CA. January 2010.

Making the analysis of multiple-species whole-genome alignments accessible to everyone. The Society for Molecular Biology and Evolution Annual Meeting. Halifax, Nova Scotia, Canada. June 2007.

Genome analysis in 15 minutes: clicking recipes for making sense of complex data with Galaxy. Genome Informatics Meeting. Hinxton, UK. September 2006.

Galaxy: A platform for interactive large-scale genome analysis. Evolution Meeting. Stony Brook, NY. June 2006.

A database of mouse Ka/Ks sliding window profiles. Northeast Ecology and Evolution Conference. University Park, PA. March 2005.