JEREMY LEIPZIG, PHD

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Research Focus

I am interested in developing bioinformatics tools and platforms to conduct reproducible research. My career has been focused on enabling biologists to visualize, explore, and publish their data. I have helped four diagnostic, therapeutic and SaaS startups define their bioinformatic product strategy.

Experience

Product Manager
TileDB - 08/22 - present

Manage the population genomics product line, including product development, sales demos, customer support, and marketing. Develop analysis workflows for biopharma and hospital partners.

Content Lead
Truwl - 09/20 – 7/22

Onboarding tools, workflows, and high-impact analyses into the Truwl platform. Developed benchmarking product and customer acquisition strategies.

Bioinformatics Engineer
Panorama Medicine - 09/17-11/19

Develop cloud-based pipelines and analysis for drug repositioning efforts. Lead for data mining and competitive intelligence research. First employee.

Senior Bioinformatics Scientist
CytoVas LLC 06/17-08/18

Scaled up flow cytometry workflows for lab developed tests. Developed novel statistical analyses to measure subpopulations of cells and extracellular vesicles in a number of clinical trials and experimental assays. CytoVas closed its doors in 2018.

Senior Data Integration Analyst
GRIN Informatics Lead
Center for Biomedical Informatics - Bioinformatics Core
Children's Hospital of Philadelphia (CHOP) — 11/10-06/17

Developed tools for mitochondrial and exome variant analysis, ChIP-Seq and RNA-Seq reproducible reports. Performed studies of miRNA differential expression and cleavage in retinoblastoma. Designed and implemented sequence manifest validation for Pediatric Cardiac Genetic Consortium exome data hub repository. Developed fork of SnpEff to use HGVS nomenclature. Developed myBiC, a portal for bioinformatics report deliverables used by the core. Lead CHOP team to build GRIN epilepsy analysis portal and Jupyter notebook based platform for variant discovery.

Senior Research Associate
DuPont Crop Genetics — 07/07 - 11/10
Developed bioinformatics tools for transcriptome assembly analysis, miRNA target scanning, and gene annotation. Developed LIMS systems for high throughput mutagenesis screens.

Bioinformatics Programmer
Univ. of Penn. Dept. of Microbiology, Bushman Lab — 11/04-07/07
Developed bioinformatics pipeline to perform annotation and statistical analysis of HIV integration sites, microbial diversity, and viral resistance mutations.

Web Developer
Dept. of Electrical Engineering, NC State Univ. — 01/03-11/04
Developed various applications to manage student, employee, and equipment records.

Consultant
The Trout Group — 8/00-12/01
Developed scientific presentations used in investor road shows for The Trout Group's biotechnology client, Enchira.

Research Technician
UNC School of Medicine Dept. of Psychiatry - Duncan Lab — 8/97-8/99
Responsible for all techniquesi nvolved in 2-deoxyglucose autoradiography studies of ketamine-induced psychotomimetic effects in rodents.

Summer Intern
Glaxo-Wellcome, Inc. — 5/95-8/95, 5/94-8/94, 5/93-8/93
Rotations in Regulatory Affairs, Research Computing, and Purchasing. Duties included database management, pharmacoeconomic research, and technical troubleshooting.

Education

Wake Forest University – Bachelor of Science in Biology 1997
North Carolina State University – Master of Computer Science 2003
Drexel University - PhD Information Science 2021

Publications (h-index 30)

Leipzig, J., Nüst, D., Hoyt, C.T., Ram, K., and Greenberg, J. The role of metadata in reproducible computational research. Cell Patterns 2021, 100322.

Elhamod, M., Diamond, K.M., Maga, A.M., Bakis, Y. Bart H.L, Mabee PM, Wasila Dahdul, W, **Leipzig J.**, Greenberg, Avants B, Karpatne A. Hierarchy-guided neural network for species classification. Methods Ecol. Evol. 2021.

Leipzig, J., Bakis, Y., Wang, X., Elhamod, M., Diamond, K., Dahdul, W., Karpatne, A., Maga, M., Mabee, P., Bart, H.L., et al. (2021). Biodiversity Image Quality Metadata Augments Convolutional Neural Network Classification of Fish Species. Research Conference on Metadata and Semantics Research 2020, 3-12

Raman, P.; Zimmerman, S.; Rathi, K. S.; de Torrenté, L.; Sarmady, M.; Wu, C.; **Leipzig, J.**; Taylor, D. M.; Tozeren, A.; Mar, J. C. A Comparison of Survival Analysis Methods for Cancer Gene Expression RNA-Sequencing Data. Cancer Genet. 2019, 235-236, 1–12.

McManus, M. J.; Picard, M.; Chen, H.-W.; De Haas, H. J.; Potluri, P.; **Leipzig, J.**; Towheed, A.; Angelin, A.; Sengupta, P.; Morrow, R. M.; Kauffman, B. A.; Vermulst, M.; Narula, J.; Wallace, D. C. Mitochondrial DNA Variation Dictates Expressivity and Progression of Nuclear DNA Mutations Causing Cardiomyopathy. Cell Metab. 2019, 29 (1), 78–90.e5.

Leipzig, J. Computational Pipelines and Workflows in Bioinformatics. In Reference Module in Life Sciences; Elsevier, 2018.

Sonney, S.; **Leipzig, J.**; Lott, M. T.; Zhang, S.; Procaccio, V.; Wallace, D. C.; Sondheimer, N. Predicting the Pathogenicity of Novel Variants in Mitochondrial tRNA with MitoTIP. PLoS Comput. Biol. 2017, 13 (12), e1005867.

Chalkia, D.; Singh, L. N.; **Leipzig, J.**; Lvova, M.; Derbeneva, O.; Lakatos, A.; Hadley, D.; Hakonarson, H.; Wallace, D. C. Association Between Mitochondrial DNA Haplogroup Variation and Autism Spectrum Disorders. JAMA Psychiatry 2017 DOI: 10.1001/jamapsychiatry.2017.2604.

Leipzig, J. (2017). A review of bioinformatic pipeline frameworks. Briefings in Bioinformatics. 2016 10.1093/bib/bbw020

Navarro-Gomez D, **Leipzig J,** Shen L, Lott M, Stassen AP, Wallace DC, Wiggs JL, Falk MJ, van Oven M, Gai X.
Phy-Mer: a novel alignment-free and reference-independent mitochondrial haplogroup classifier.
Bioinformatics. 2014 Dec 12. 10.1093/bioinformatics/btu825

Falk MJ, Shen L, Gonzalez M, **Leipzig J**, Lott MT, Stassen AP, Diroma MA, Navarro-

Gomez D, Yeske P, Bai R, Boles RG, Brilhante V, Ralph D, DaRe JT, Shelton R, Terry SF, Zhang Z, Copeland WC, van Oven M, Prokisch H, Wallace DC, Attimonelli M, Krotoski D, Zuchner S, Gai X.
Mitochondrial Disease Sequence Data Resource (MSeqDR): A global grass-roots consortium to facilitate deposition,curation, annotation, and integrated analysis of genomic data for the mitochondrial disease clinical and research communities.
Mol Genet Metab. 2014 Dec 4. pii: S1096-7192(14)00377-1.

Glessner JT, Bick AG, Ito K, Homsy JG, Rodriguez-Murillo L, Fromer M, Mazaika E, Vardarajan B, Italia M, **Leipzig J**, DePalma SR, Golhar R, Sanders SJ, Yamrom B, Ronemus M, Iossifov I, Willsey AJ, State MW, Kaltman JR, White PS, Shen Y, Warburton D, Brueckner M, Seidman C, Goldmuntz E, Gelb BD, Lifton R, Seidman J, Hakonarson H, Chung WK.
Increased frequency of de novo copy number variants in congenital heart disease by integrative analysis of single nucleotide polymorphism array and exome sequence data.
Circ Res. 2014 Oct 24;115(10):884-96.

Lott MT, **Leipzig JN**, Derbeneva O, Xie HM, Chalkia D, Sarmady M, Procaccio V, Wallace DC.
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Curr Protoc Bioinformatics. 2013 Dec 12;1(123):1.23.1-1.23.26

Zaidi, S., Choi, M., Wakimoto, H., Ma, L., Jiang, J., Overton, J. D., et al.
De novo mutations in histone-modifying genes in congenital heart disease.
Nature 498, 220–223

Zhang Z, **Leipzig J**, Sasson A, Perin JC, Xie M, Sarmady M, Warren P, White P.
Digest of high-throughput sequencing in a reproducible report.
BMC Bioinformatics. 2013, 14(Suppl 11):S3.

Barrantes I, **Leipzig J**, Marwan W.
A next-generation sequencing approach to study the transcriptomic changes during the differentiation of physarum at the single-cell level.
Gene Regul Syst Bio. 2012;6:127-37.

Shi L, Perin JC, **Leipzig J**, Zhang Z, Sullivan KE. Genome-wide analysis of interferon regulatory factor I binding in primary human monocytes. Gene. 2011 Nov 1;487(1).

Leipzig J, Li Xiao-Yi.
Data Mashups in R.
O'Reilly. 2009. (Reissued in 2011)

Wang GP, Garrigue A, Ciuffi A, Ronen K, **Leipzig J**, Berry C, Lagresle-Peyrou C, Benjelloun F, Hacein-Bey-Abina S, Fischer A, Cavazzana-Calvo M, Bushman FD.
DNA barcoding and pyrosequencing to analyze adverse events in therapeutic gene transfer.
Nucleic Acids Res. 2008 May;36(9):e49.

Meekings KN, **Leipzig J**, Bushman FD, Taylor GP, Bangham CR.
HTLV-1 integration into transcriptionally active genomic regions is associated with proviral expression and with HAM/TSP.
PLoS Pathog. 2008 Mar 21;4(3):e1000027.

Hoffmann C, Minkah N, **Leipzig J**, Wang G, Arens MQ, Tebas P, Bushman FD.
DNA bar coding and pyrosequencing to identify rare HIV drug resistance mutations.
Nucleic Acids Res. 2007;35(13):e91.

Wang GP, Ciuffi A, **Leipzig J**, Berry CC, Bushman FD.
HIV integration site selection: analysis by massively parallel pyrosequencing reveals association with epigenetic modifications.
Genome Res. 2007 Aug;17(8):1186-94.

Berry C, Hannenhalli S, **Leipzig J**, Bushman FD.
Selection of target sites for mobile DNA integration in the human genome.
PLoS Comput Biol. 2006 Nov 24;2(11):e157.

Lewinski MK, Yamashita M, Emerman M, Ciuffi A, Marshall H, Crawford G, Collins F, Shinn P, **Leipzig J**, Hannenhalli S, Berry CC, Ecker JR, Bushman FD.
Retroviral DNA integration: viral and cellular determinants of target-site selection.
PLoS Pathog. 2006 Jun;2(6):e60.

Barr SD, Ciuffi A, **Leipzig J**, Shinn P, Ecker JR, Bushman FD.
HIV integration site selection: targeting in macrophages and the effects of different routes of viral entry.
Mol Ther. 2006 Aug;14(2):218-25.

Ciuffi A, Mitchell RS, Hoffmann C, **Leipzig J**, Shinn P, Ecker JR, Bushman FD.
Integration site selection by HIV-based vectors in dividing and growth-arrested IMR-90 lung fibroblasts.
Mol Ther. 2006 Feb;13(2):366-73.

Ciuffi A, Llano M, Poeschla E, Hoffmann C, **Leipzig J**, Shinn P, Ecker J, Bushman F.
A role for LEDGF/p75 in targeting HIV DNA integration.
Nat Med. 2005 Dec;11(12):1287-9.

Bushman F, Lewinski M, Ciuffi A, Barr S, **Leipzig J**, Hannenhalli S, Hoffmann C.
Genome-wide analysis of retroviral DNA integration.
Nat Rev Microbiol. 2005 Nov;3(11):848-58.

Barr SD, **Leipzig J**, Shinn P, Ecker JR, Bushman FD.
Integration targeting by avian sarcoma-leukosis virus and human immunodeficiency virus in the chicken genome.
J Virol. 2005 Sep;79(18):12035-44.

Leipzig J, Pevzner P, Heber S. The Alternative Splicing Gallery (ASG): bridging the gap between genome and transcriptome.
Nucl. Acids. Res. 2004 32: 3977-3983.

Leipzig J, Nielsen D, and Heber, S.
The Splicing Graph - A Tool for Visualising Gene Structure and Alternative Splicing.
Future Drug Discovery 2004 Mar.

Duncan GE, Miyamoto S, **Leipzig JN**, Lieberman JA.
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J Pharmacol Exp Ther. 2000 Apr;293(1):8-14.

Miyamoto S, **Leipzig JN**, Lieberman JA, Duncan GE.
Effects of ketamine, MK-801, and amphetamine on regional brain 2-deoxyglucose uptake in freely moving mice.
Neuropsychopharmacology. 2000 Apr;22(4):400-12.

Duncan GE, Miyamoto S, **Leipzig JN**, Lieberman JA.
Comparison of brain metabolic activity patterns induced by ketamine, MK-801 and amphetamine in rats: support for NMDA receptor involvement in responses to subanesthetic dose of ketamine.
Brain Res. 1999 Oct 2;843(1-2):171-83.

Duncan GE, **Leipzig JN**, Mailman RB, Lieberman JA.
Differential effects of clozapine and haloperidol on ketamine-induced brain metabolic activation.
Brain Res. 1998 Nov 23;812(1-2):65-75.

Presentations and Posters

Drexel-CODATA FAIR-RRDM Workshop 2019 (Philadelphia)

CYTO2018 (Prague)

2016 MidAtlantic Bioinformatics Conference (Philadelphia)

Regional Translational Research in Mitochondria, Aging, and Disease Symposium October 2013 (Philadelphia)

IEEE BIBM 2012 (Philadelphia)

ASHG 2012 (San Francisco)

RECOMB 2004 (San Diego)

Rocky Mountain Regional Bioinformatics Meeting 2003 (Aspen)

Social Media

biostars.org - Bioinformatics Q&A Site. Top-20 ranking.
jermdemo.blogspot.com - Over 70,000 pageviews.

Teaching

Adjunct Instructor

Drexel University College of Computing and Informatics
Spring Quarter 2018
Taught INFO103 Introduction to Data Science

Instructor & Teaching Assistant

Programming for Biology 2007-2010
Cold Spring Harbor Laboratory

Professional Associations

PhillyR Founder & Organizer
PhillyR is aimed at sharing knowledge and experience among users of the R statistical programming environment.

Software

myBiC

Django application that manages user authentication and presentation of bioinformatics deliverables.

Mitomaster

Web application that allows clinicians to quickly investigate mitochondrial mutations in sequenced or genotyped samples.

blast-wrapper

Node.js web-service wrapper for fetching pairwise BLAST or BLAST+ alignments against a fixed reference.

Standard Velvet Assembly Report

Scripts and Sweave report to analyze effect of altering Velvet assembly parameters on sequence assemblies.

miRNA TargetScan

Search input sequences for targets of known miRNAs using plant miRNA binding heuristics.

DRMViewer

Suite of tools to view and perform statistical analysis on drug resistant mutations in pyrosequenced HIV samples.

InSiPiD - Integration Site Pipeline and Database

Set of tools and interfaces to manage processing, reconciliation, annotation, and analysis, and display of viral integration site data.

ASG - Alternative Splicing Gallery

Web-based visualization tool for the analysis of alternative splicing events.

Technical Skills

Languages and frameworks:

R, Python, Perl, Java, Groovy, Scala, Javascript & JQuery, C++, C, PHP, Snakemake, WDL, Nextflow, CWL

Expert knowledge:

Bioinformatics algorithms, alignment & annotation pipelines, LIMS web interfaces, flow cytometry analysis, reproducible research principles, software development methodologies, pipeline frameworks, containerization, dependency management, AWS & GCP cloud infrastructure

Certifications

Sun Certified Java Programmer (SCJP) - Java 2 Platform 1.4 Candidate ID SR1768642