J. Perry Evans

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Career Summary

In my current role at the Children's Hospital of Philadelphia, I provide computational support for research as part of the bioinformatics core. My projects have included an analysis of germline pediatric variants, characterization of cysteine posttranslational modifications, operations research for blood transfusions, and an omics study of mitotic exit.

Education

2005–2010 **PhD in Genomics and Computational Biology**, *University of Pennsylvania*, Philadelphia, PA.

2001–2005 **BS in Computer Science**, *Rose–Hulman Institute of Technology*, Terre Haute, IN.

Experience

2013–Current **Bioinformatics Scientist**, *Department of Biomedical and Health Informatics*, Children's Hospital of Philadelphia, Philadelphia, PA.

I provide computational consultation and support in collaborations with hospital investigators

- Analysis of variants predisposing to pediatric cancer using 600 whole genomes
- Structural and functional analysis of cysteine modifications
- ChIP-Seq and RNA-Seq analysis for post mitotic reboot
- Calling and analysis of variants from ENCODE ChIP-Seq data
- Analysis of PRO-seq data
- Variant prioritization for cancer and epilepsy patients

2010–2013 **Postdoctoral Fellow**, *Yale Center for Medical Informatics, Yale University*, New Haven, CT.

Worked closely with melanoma biologists to analyze exome sequence data from over 200 paired normal and tumor samples to discover new genes important for melanoma

- Developed a pipeline to call novel somatic single nucleotide variations (SNVs) from exome sequences
- Integrated public resources such as TCGA, COSMIC, and 1000 Genomes to evaluate SNV function
- Developed a new method to identify common focal copy number variations (CNVs) across tumors
- Developed novel tools to identify genes with a significant number of nonsynonymous mutations
- Integrated expression, CNVs, SNVs, and indels to arrive at list of genes important for melanoma

2012–2013 **Consultant**, *FXI R&D*, Aston, PA.

Developed a database and website for FXI, a polyurethane foam company

- Developed an automated web-crawler to gather data and store it in a MySQL database
- Built an interactive website for researchers to retrieve, monitor, and plot data
- Guided an intern through Access Database construction and its interface with Excel

2006–2010 **Research Assistant**, *Computer and Information Science Department, University of Pennsylvania*, Philadelphia, PA.

Conducted dissertation research on biological networks under the direction of Lyle Ungar

- Developed a new approach to align biological networks
- Developed a method to predict virus-host protein interactions based on protein and network motifs

2007–2010 **Research Assistant**, *Center for Integrated Bioinformatics at Drexel University*, Philadelphia, PA.

Assisted professor Aydin Tozeren in running the bioinformatics lab at Drexel

- Helped write the narrative and preliminary studies section for multiple NIH grants
- Facilitated communication between labs at Drexel, UPenn, and George Washington University
- Helped administrate computational resources, including a 56 node IBM Bladecenter

2008–2010 **Teaching Assistant**, *School of Biomedical Engineering, Drexel University*, Philadelphia, PA.
Aided professor Aydin Tozeren in teaching his Quantitative Systems Biology graduate class
- Gave lectures describing the methodology behind my research
- Guided students through computational labs I designed
- Mentored students as they completed their final projects

August, 2008 **Instructor**, *Greater Philadelphia Bioinformatics Alliance*, Philadelphia, PA.
Organized and taught a two week online introduction to Biopython
- Developed course curriculum to cover sequence annotation, motif discovery, and database integration
- Guided students through the development of Python scripts for bioinformatics analyses
- Answered questions via email and graded assignments

Technical Skills

Extremely Proficient With

languages Python, R/Bioconductor, JavaScript D3, Bash Scripting

technologies Linux, OS X, MySQL, Git, Snakemake, LaTeX, Sun Grid Engine

datatypes Next-gen sequencing (WXS, WGS, ChIP-Seq, RNA-Seq), Protein/gene networks, Protein sequence and structure data

mathematics Development and application of statistical and machine learning methods to problems in bioinformatics/comp bio, structural biology, systems biology, biostatistics, epidemiology, genetics

Have Experience With

languages Java, Go, PHP, JavaScript, Matlab, HTML, CSS, Ruby, C, C++, C#, Scheme

technologies Windows, TORQUE batch queuing system, JSON, Subversion

datatypes CaptureC, Peptide counts, DNase hypersensitivity

Publications

S. C. Hsu, T. G. Gilgenast, C. R. Bartman, C. R. Edwards, A. J. Stonestrom, P. Huang, D. J. Emerson, **Perry Evans**, M. T. Werner, C. A. Keller, *et al.*, "The bet protein brd2 cooperates with ctcf to enforce transcriptional and architectural boundaries," *Molecular Cell*, vol. 66, no. 1, pp. 102–116, 2017.

C. C.-S. Hsiung, C. R. Bartman, P. Huang, P. Ginart, A. J. Stonestrom, C. A. Keller, C. Face, K. S. Jahn, **Perry Evans**, L. Sankaranarayanan, *et al.*, "A hyperactive transcriptional state marks genome reactivation at the mitosis–g1 transition," *Genes & development*, vol. 30, no. 12, pp. 1423–1439, 2016.

D. Cohen, H. Hartung, **Perry Evans**, D. F. Friedman, and S. T. Chou, "Red blood cell alloimmunization in transfused patients with bone marrow failure syndromes," *Transfusion*, vol. 56, no. 6, pp. 1314–1319, 2016.

M. Krauthammer, Y. Kong, A. Bacchiocchi, **P. Evans**, N. Pornputtapong, C. Wu, J. McCusker, S. Ma, E. Cheng, R. Straub, *et al.*, "Exome sequencing identifies recurrent mutations in nf1 and rasopathy genes in sun-exposed melanomas.," *Nature genetics*, 2015.

N. S. Gould, **P. Evans**, P. Martínez-Acedo, S. M. Marino, V. N. Gladyshev, K. S. Carroll, and H. Ischiropoulos, "Site-specific proteomic mapping identifies selectively modified regulatory cysteine residues in functionally distinct protein networks," *Chemistry & biology*, vol. 22, no. 7, pp. 965–975, 2015.

K. Raju, P. Doulias, **P. Evans**, E. Krizman, J. Jackson, O. Horyn, Y. Daikhin, I. Nissim, M. Yudkoff, I. Nissim, *et al.*, "Regulation of brain glutamate metabolism by nitric oxide and S-nitrosylation," *Science Signaling*, vol. 8, no. 384, pp. ra68–ra68, 2015.

A. J. Stonestrom, S. C. Hsu, K. S. Jahn, P. Huang, C. A. Keller, B. M. Giardine, S. Kadauke, A. E. Campbell, **P. Evans**, R. C. Hardison, *et al.*, "Functions of bet proteins in erythroid gene expression," *Blood*, pp. blood–2014, 2015.

P. Evans, Y. Kong, and M. Krauthammer, "Computational analysis in cancer exome sequencing," in *Cancer Genomics and Proteomics* (N. Wajapeyee, ed.), Springer New York, 2014.

J. Choi, S. Landrette, T. Wang, **P. Evans**, A. Bacchiocchi, R. Bjornson, E. Cheng, A. Stiegler, *et al.*, "Identification of PLX4032-resistance mechanisms and implications for novel RAF inhibitors," *Pigment cell & melanoma research*, vol. 27, no. 2, pp. 253–262, 2014.

M. Johnson, **P. Evans**, M. Sarmady, K. Hankenson, A. Wells, and S. Grant, "A number of novel loci are implicated for height and bone density determination through integration of esr1 dna occupancy and snp association data.," in *Journal of Bone and Mineral Research*, vol. 29, pp. S74–S74, 2014.

P. Evans, S. Avey, Y. Kong, and M. Krauthammer, "Adjusting for background mutation frequency biases improves the identification of cancer driver genes," *IEEE transactions on Nanobioscience*, 2013.

R. Mukherjee, **P. Evans**, L. Singh, and S. Hannenhalli, "Correlated evolution of positions within mammalian cis elements," *PLoS ONE*, vol. 8, p. e55521, 2013.

P. Evans and M. Krauthammer, "Estimating a gene's mutation burden by the number of synonymous base substitutions," in *Proceedings of the 2012 IEEE International Conference on Bioinformatics and Biomedicine*, IEEE Computer Society, 2012.

M. Krauthammer, Y. Kong, B. Ha, **P. Evans**, A. Bacchiocchi, J. McCusker, E. Cheng, M. Davis, G. Goh, M. Choi, *et al.*, "Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma," *Nature Genetics*, vol. 44, no. 9, pp. 1006–1014, 2012.

P. Evans and M. Krauthammer, "Exploring the use of social media to measure journal article impact," in *Proceedings of the American Medical Informatics Association (AMIA) Annual Symposium*, 2011.

P. Evans, A. Sacan, L. Ungar, and A. Tozeren, "Sequence alignment reveals possible MAPK docking motifs on HIV proteins," *PLoS ONE*, vol. 5, p. e8942, 2010.

P. Evans, W. Dampier, L. Ungar, and A. Tozeren, "Prediction of HIV-1 virus-host protein interactions using virus and host sequence motifs," *BMC Medical Genomics*, vol. 2, p. 27, 2009.

W. Dampier, **P. Evans**, L. Ungar, and A. Tozeren, "Host sequence motifs shared by HIV predict response to antiretroviral therapy," *BMC Medical Genomics*, vol. 2, p. 47, 2009.

P. Evans, T. Sandler, and L. Ungar, "Protein-protein interaction network alignment by quantitative simulation," in *Proceedings of the 2008 IEEE International Conference on Bioinformatics and Biomedicine*, pp. 325–328, IEEE Computer Society, 2008.

P. Evans, G. Donahue, and S. Hannenhalli, "Conservation patterns in cis-elements reveal compensatory mutations," *4th RECOMB Comparative Genomics Satellite Workshop*, vol. 4205, pp. 186–199, 2006.

Talks and Posters

April, 2017 **A guide to filtering TARGET Complete Genomics germline variants**, *American Association for Cancer Research Annual Meeting*, Washington, DC.
My poster described a decision tree for classifying false positive variant calls in Complete Genomics data.

October, 2012 **Estimating a gene's mutation burden by the number of synonymous base substitutions**, *IEEE International Conference on Bioinformatics and Biomedicine*, Philadelphia, PA.
My talk compared methods for determining genes with significant nonsynonymous mutation burden based on the ratio of nonsynonymous to synonymous mutation frequencies.

June, 2012 **Evaluating melanoma whole exome sequences suggests new gene drivers**, *National Library of Medicine Informatics Training Conference 2012*, Madison, WI.
My poster outlined novel methods for determining genes with significant mutation burden by examining the ratio of nonsynonymous to synonymous mutation frequencies.

October, 2011 **Exploring the use of social media to measure journal article impact**, *American Medical Informatics Association Annual Symposium*, Washington DC.
My talk demonstrated that high impact journal articles are cited in Wikipedia pages, while low impact journal articles are not. I suggested that monitoring Wikipedia science updates would help one keep up with the latest science advances.

March, 2010 **Modularity in protein interaction network hubs predicts viral host–pathogen interactions**, *Keystone Symposia, Biomolecular Interaction Networks: Function and Disease*, Quèbec City, QC, Canada.
My poster demonstrated that human hub proteins interacting with HIV and HCV have a preference between intra/intermodular hubs.

November, 2009 **MAPK docking motifs on HIV proteins**, *Greater Philadelphia Bioinformatics Alliance Annual Research Retreat*, Philadelphia, PA.
My talk showed that standard MAPK docking motifs are missing from 4 of 5 HIV proteins phosphorylated by ERK1/2, and suggested evidence for alternative docking sites.

November, 2008 **Protein–protein interaction network alignment by quantitative simulation**, *IEEE International Conference on Bioinformatics and Biomedicine*, Philadelphia, PA.
My talk focused on the application of the quantitative simulation algorithm to the alignment of fly and yeast protein networks.

September, 2006 **Conservation patterns in *cis*–elements reveal co–evolution**, *RECOMB Comparative Genomics International Workshop*, Montrèal, QC, Canada.
My talk covered a project in which I utilized phylogenetic trees made using five mammalian species to present evidence for dependencies between positions in JASPAR transcription factor binding sites.

Awards

June, 2012 **Best Poster: Evaluating melanoma whole exome sequences suggests new gene drivers**, *National Library of Medicine Informatics Training Conference 2012.*
Awards were chosen by vote of the conference attendees each day.

2010–2013 **NLM Postdoctoral Fellow**, *National Library of Medicine Training Grant in Biomedical Informatics.*
Grant awarded by Yale University.

2007–2010 **NIH Training Grant**, *National Human Genome Research Institute Training Grant in Computational Genomics.*
Grant awarded by the University of Pennsylvania.