John C. Obenauer, Ph.D.

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SUMMARY

Biochemistry expert (Ph.D., Brandeis University)
Strong publication record (16 publications, including *Science* and *Nature*)
Computational Biology/Bioinformatics scientist (13 years experience at MIT, St. Jude, and freelancing)
Experienced programmer (23 years experience, mostly using Perl, C, and PHP/MySQL)
Wide range of research areas (cancer biology, infectious diseases, genomics, proteomics)
Managerial experience (supervised staff of 11 in a bioinformatics core facility)
Excellent teaching and presentation skills (several public talks per year)

EDUCATION

Ph.D. in Biochemistry, Brandeis University, Waltham, MA, May 2001
Graduate courses in Physics, SUNY Buffalo, NY, September 1991 to May 1992
B.A. in Liberal Studies, St. John's College, Annapolis, MD, May 1990

SKILLS

Programming: C, Perl, R, PHP, Javascript, Ajax, MySQL, LAMP web applications.

Teaching: Math, physics, biochemistry, proteomics, and computing courses at high school, college, graduate, and adult education levels.

RESEARCH EXPERIENCE

Co-founder, CEO, and Research Scientist, Digital Genomics LLC, September 2013 to present. Analyze expression arrays, genotyping arrays, and next-generation sequencing experiments for clients.

1) Detected differentially expressed genes in Affymetrix microarray experiments.
2) Analyzed ChIP-seq data to detect peaks and novel binding motifs.
3) Analyzed Affymetrix CytoScan HD arrays, DMET Plus arrays, SNP 6.0 arrays, and Ion Torrent next-generation sequencing data.
4) Developed tools for detecting clinically relevant mutations in SNP array data and in next-generation sequencing data.
5) Provided bioinformatics training.

Bioinformatics Research Scientist, St. Jude Children's Research Hospital, August 2012 to August 2013. Analyze genome sequencing and genotyping data sets as a member of Jinghui Zhang's research laboratory in Computational Biology. Projects included:

1) Detecting influenza mutations involved in adaptation from birds to mammals;
2) Identifying DNA copy number variants involved in brain tumors and solid tumors;
3) Developing methods to detect sample contamination in multiplexed sequencing experiments;
4) Adapting human structure variant detection methods to work in other organisms.

Bioinformatics Group Leader, St. Jude Children's Research Hospital, April 2006 to August 2012. Provide bioinformatics services to hospital faculty and manage a staff of 11 scientists and programmers. Assign research projects, assist staff with analysis methods, plan group budget, recruit new staff, review manuscripts, give public presentations, serve on advisory committees, and analyze data. Major projects included:

1) Detecting peaks and affected genes in chromatin immunoprecipitation sequencing (ChIP-seq) experiments in mice;
2) Providing method development and analysis assistance to the Pediatric Cancer Genome Project;
3) Mapping genomes for human cell lines and finding their sequence differences;
4) Profiling miRNA expression from high-throughput sequencing data;
5) Identifying human transmissibility markers in avian influenza viruses;
6) Developing algorithms for assigning genotypes and proteotypes to large sets of aligned sequences;
7) Making databases for investigators to store and analyze research results on acute myeloid leukemia, intrinsically unstructured proteins, and T cell receptor sequences, and for the Bioinformatics group to record our projects;
8) Arranging joint workshops with the Biostatistics department to share expertise;
9) Attending annual meetings of the American Association for Cancer Research to update cancer biology knowledge;
10) Strategic planning for the Bioinformatics group and the Information Sciences department.

Associate Research Scientist, St. Jude Children's Research Hospital, June 2003 to March 2006. Assisted faculty members with research needs in bioinformatics. Major tasks included:

1) Assembling data from public sources for a gene annotation database;
2) Developing a parallel-processing version of the protein interaction prediction program Scansite and making it web-accessible;
3) Developing a program to convert LC/MS data to a 2D graphical image for peak processing by commercial software;
4) Identifying genes likely to be translationally regulated by microRNAs;
5) Examining promoter regions of genes for SNPs that could disrupt transcription factor binding sites;
6) Reorganizing all data collected and stored by St. Jude's core facilities to group them by principal investigator;
7) Building a database and novel data analysis tools to study DNA and protein sequences for an influenza genome sequencing project.

Research scientist, Massachusetts Institute of Technology, Center for Cancer Research, June 2001 to May 2003. Wrote bioinformatics software and provided bioinformatics support for affiliated departments. Major projects included:

1) Developed software called Scansite for predicting phosphoprotein interactions important in cancer biology using data derived from oriented peptide library experiments;
2) Installed and maintained the Scansite server hardware and software (Red Hat Linux 7.3 on a Dell PowerEdge 8450 8-CPU server);
3) Collaborated with the Sharp laboratory to create bioinformatics software for predicting microRNA binding sites on gene transcripts;
4) Assisted in the selection and setup of computational tools for analyzing DNA microarray data for the MIT BioMicro Center.

Graduate research assistant, Biochemistry Department, Brandeis University, August 1996 to May 2001. Studied structural features of electron transfer proteins by multidimensional nuclear magnetic resonance (NMR). Specific tasks included:

1) Synthesizing the gene for adrenodoxin, a 13 kDa iron-sulfur protein, using molecular biology techniques;
2) Teaching rotation students and other lab members how to make mutations and purify proteins;
3) Growing and purifying uniformly ^{15}N-labeled adrenodoxin, as well as its bacterial homologs putidaredoxin and terpredoxin, for heteronuclear 2D NMR studies;
4) Growing and purifying uniformly ^{13}C,^{15}N-labeled adrenodoxin for 3D NMR sequential assignment experiments;
5) Measuring the magnetic susceptibilities of all three proteins in their oxidized forms using residual dipolar couplings at multiple magnetic fields;
6) Developing a semi-automated batch curve fitting tool using Visual Basic for Applications, Microsoft Excel and Mathcad;
7) Writing programs for text processing of NMR chemical shift lists using Perl;
8) Making a toolbar for Microsoft Word with buttons to convert DNA sequences to protein sequences, display the strand complementary to a DNA template, and calculate molecular weights;
9) Designing and maintaining the lab web page from 1997 to 2000.

Research associate, Marketing and Planning Systems (MaPS), Waltham, MA, May 1995 to August 1996. Made custom spreadsheet applications to analyze market research data for Fortune 500 companies (AT&T, American Express, Walt Disney, UPS) using Microsoft Excel and Visual Basic for Applications. Developed software for automating the creation of structural-equations-based satisfaction model spreadsheets using Visual Basic for Applications.

Analyst, National Highway Traffic Safety Administration, Bethesda, MD, October 1994 to April 1995. Analyzed hospital data for several government agency studies using the SAS statistics language. Developed a program that automatically identified inconsistencies in hospital records based on invalid combinations of form data, and another that identified perpetrator-caused or weapons-related accidents in hospital records based on keywords in text entries. This work was contracted by I-Net, Inc.

Physicist, Naval Research Laboratory, Washington, DC, May 1990 to August 1991 and May 1992 to August 1993. Calibrated detectors for the OSSE experiment on NASA's Compton Gamma Ray Observatory satellite and screened the results to improve data quality. Used pre-flight data collected from radioactive sources to measure the linearity, resolution, and efficiency of the crystalline gamma ray detectors. After the satellite was launched and data started being transmitted, worked on removing background noise, interfering sources, and experimental artifacts from the data stream. This work was contracted by Sachs-Freeman Associates, Inc.

TEACHING EXPERIENCE

Teaching parallel programming for St. Jude Children's Research Hospital, Memphis, TN, in April 2005 and June 2006. The class title was “Introduction to MPI Programming.”

Teaching advanced undergraduate seminar for the Massachusetts Institute of Technology, Cambridge, MA, September 2002 to December 2002 (part-time). The class title was "Current Methods in Proteomics and Bioinformatics." I focused on DNA microarrays, two-dimensional gel electrophoresis, isotope-coded affinity tag mass spectrometry, structure determination and modeling, and sequence analysis.

Teaching adult education computer classes for Brookline Adult & Community Education Program, Brookline, MA, June 2000 to February 2001 (part-time). Class titles included "PC Overview: Microsoft Windows, Microsoft Office, and the Internet," "Upgrading Your PC," and "Introduction to the Linux Operating System."

Teaching assistant for Physical Chemistry of Macromolecules, Brandeis University, Waltham, MA, January 1998 to May 1998 (part-time). I taught physical and mathematical techniques for studying proteins and DNA, including linked equilibria, single-molecule experiments, energetics of charges in membranes, structures of DNA and proteins, experimental protein folding, X-ray crystallography, and nuclear magnetic resonance.

Teaching math and physics at Emerson Preparatory School, Washington, DC, September 1992 to January 1993 (part-time), and September 1993 to January 1994 (full-time). I taught Algebra II for the part-time semester and Physics and Calculus for the full-time semester.

Teaching assistant for Physics Laboratory, State University of New York, Buffalo, NY, September 1991 to May 1992. I taught common experiments in classical mechanics and electromagnetism while taking graduate courses in physics.

INVITED PRESENTATIONS

1. February 23, 2009, University of Nebraska at Kearney, graduate student seminar series. "The genetics of leukemia relapse."
2. September 25, 2008, International Electronics and Electrical Engineering event, St. Jude Children's Research Hospital, Memphis, TN. "Data analysis of next generation sequencing experiments."

PUBLICATIONS

1. Koçer ZA, **Obenauer J**, Zaraket H, Zhang J, Rehg JE, Russell CJ, Webster RG. Fecal influenza in mammals: selection of novel variants. *J Virol* 2013 Aug 21. [Epub ahead of print]
2. Zhang J, Ding L, Holmfeldt L, Wu G, Heatley SL, Payne-Turner D, Easton J, Chen X, Wang J, Rusch M, Lu C, Chen SC, Wei L, Collins-Underwood JR, Ma J, Roberts KG, Pounds SB, Ulyanov A, Becksfort J, Gupta P, Huether R, Kriwacki RW, Parker M, McGoldrick DJ, Zhao D, Alford D, Espy S, Bobba KC, Song G, Pei D, Cheng C, Roberts S, Barbato MI, Campana D, Coustan-Smith E, Shurtleff SA, Raimondi SC, Kleppe M, Cools J, Shimano KA, Hermiston ML, Doulatov S, Eppert K, Laurenti E, Notta F, Dick JE, Basso G, Hunger SP, Loh ML, Devidas M, Wood B, Winter S, Dunsmore KP, Fulton RS, Fulton LL, Hong X, Harris CC, Dooling DJ, Ochoa K, Johnson KJ, **Obenauer JC**, Evans WE, Pui CH, Naeve CW, Ley TJ, Mardis ER, Wilson RK, Downing JR, Mullighan CG. The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. *Nature*, 481:157-63, 2012.
3. Wang J, Mullighan CG, Easton J, Roberts S, Heatley SL, Ma J, Rusch MC, Chen K, Harris CC, Ding L, Holmfeldt L, Payne-Turner D, Fan X, Wei L, Zhao D, **Obenauer JC**, Naeve C, Mardis ER, Wilson RK, Downing JR, Zhang J. CREST maps somatic structural variation in cancer genomes with base-pair resolution. *Nat Methods*, 8:652-4, 2011.
4. Liu X, Nguyen P, Liu W, Cheng C, Steeves M, **Obenauer JC**, Ma J, Geiger TL. T cell receptor CDR3 sequence but not recognition characteristics distinguish autoreactive effector and Foxp3(+)

regulatory T cells. *Immunity* 31:909-920, 2009.

5. Galea CA, High AA, **Obenauer JC**, Mishra A, Park CG, Punta M, Schlessinger A, Ma J, Rost B, Slaughter CA, Kriwacki RW. Large-scale analysis of thermostable, mammalian proteins provides insights into the intrinsically disordered proteome. *J Proteome Res* 8:211-226, 2009.
6. Hargrove PW, Kepes S, Hanawa H, **Obenauer JC**, Pei D, Cheng C, Gray JT, Neale G, Persons DA. Globin lentiviral vector insertions can perturb the expression of endogenous genes in beta-thalassemic hematopoietic cells. *Mol Ther* 16:525-533, 2008.
7. Krauss S, Obert CA, Franks J, Walker D, Jones K, Seiler P, Niles L, Pryor SP, **Obenauer JC**, Naeve CW, Widjaja L, Webby RJ, Webster RG. Influenza in migratory birds and evidence of limited intercontinental virus exchange. *PLoS Pathog* 3:e167, 2007.
8. Finkelstein DB, Mukatira S, Mehta PK, **Obenauer JC**, Su X, Webster RG, Naeve CW. Persistent host markers in pandemic and H5N1 influenza viruses. *J Virol* 81:10292-10299, 2007.
9. Pottier N, Cheok MH, Yang W, Assem M, Tracey L, **Obenauer JC**, Panetta JC, Relling MV, Evans WE. Expression of SMARCB1 modulates steroid sensitivity in human lymphoblastoid cells: identification of a promoter SNP that alters PARP1 binding and SMARCB1 expression. *Hum Mol Genet* 16:2261-2271, 2007.
10. Galea CA, Pagala VR, **Obenauer JC**, Park CG, Slaughter CA, Kriwacki RW. Proteomic studies of the intrinsically unstructured mammalian proteome. *J Proteome Res* 5:2839-2848, 2006.
11. **Obenauer JC**, Denson J, Mehta PK, Su X, Mukatira S, Finkelstein DB, Xu X, Wang J, Ma J, Fan Y, Rakestraw KM, Webster RG, Hoffmann E, Krauss S, Zheng J, Zhang Z, Naeve CW. Large-scale sequence analysis of avian influenza isolates. *Science* 311:1576-1580, 2006.
12. Wadkins RM, Hyatt JL, Wei X, Yoon KJ, Wierdl M, Edwards CC, Morton CL, **Obenauer JC**, Damodaran K, Beroza P, Danks MK, Potter PM. Identification and characterization of novel benzil (diphenylethane-1,2-dione) analogues as inhibitors of mammalian carboxylesterases. *J Med Chem* 48:2906-2915, 2005.
13. Mansfield JH, Harfe BD, Nissen R, **Obenauer J**, Srineel J, Chaudhuri A, Farzan-Kashani R, Zuker M, Pasquinelli AE, Ruvkun G, Sharp PA, Tabin CJ, McManus MT. MicroRNA-responsive 'sensor' transgenes uncover Hox-like and other developmentally regulated patterns of vertebrate microRNA expression. *Nat Genet* 36:1079-1083, 2004.
14. **Obenauer JC**, Yaffe MB. Computational prediction of protein-protein interactions. *Methods Mol Biol* 261:445-468, 2004.
15. **Obenauer JC**, Cantley LC, Yaffe MB. Scansite 2.0: Proteome-wide prediction of cell signaling interactions using short sequence motifs. *Nucleic Acids Res* 31:3635-3641, 2003.
16. Kostic M, Pochapsky SS, **Obenauer J**, Mo H, Pagani GM, Pejchal R, Pochapsky TC. Comparison of functional domains in vertebrate-type ferredoxins. *Biochemistry* 41:5978-5989, 2002.