William J. Bruno

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Santa Fe, NM 87505 wbruno@gmail.com

Education

University of California at Berkeley
Ph.D. in Physics 1990
Thesis: "Vibrationally enhanced hydrogen tunneling in enzymatic reactions."
Advisor: William Bialek, Departments of Physics and Biophysics.
M.A. in Physics 1987

Massachusetts Institute of Technology
B.S. in Math 1985
B.S. in Physics Elected ΣΠΣ. Honors thesis advisor: Philip Morrison. 1985

Employment History

New Mexico Consortium, Los Alamos, NM 11/2014 –
Research Scientist, part-time
Collaboration with Los Alamos National Laboratory on NIH-funded project to study calcium ion channels through modeling and experiments.

SciTransTech, LLC, Santa Fe, NM 1/2016 –
Founder/Consultant
Consult on technical documents and perform site surveys to measure electromagnetic interference (EMI) and make mitigation recommendations.

Freelance tutor approved in 10 subjects on Wyzant.com 10/2013 –
Paid tutor of high school, college, and grad students in Kansas & New Mexico.
Wyzant rating of 4.8 stars out of 5.0 based on 26 students tutored to date.

Consultant, Lawrence, KS 9/2012–8/2014
Bioinformatics and technical consulting, including genomic data mining.
Primary customer: Gyrasol Technology LLC, Lawrence KS
under sub-contract, project for Mapp Biopharmaceutical, San Diego CA.

University of Kansas, Dept. of Physics & Astronomy 6/2012–7/2012
Lecturer, PHSX 115 (College Physics II, accelerated summer semester)

Los Alamos National Laboratory 1994–2000

Theoretical Biology and Biophysics Group Staff Scientist & 2002–4/2012

DNA Mining, Informatics Software LLC, Tesuque, NM 2000–2002
Founder and Chief Scientific Officer

Department of Energy 1992–1994
Distinguished Human Genome Postdoctoral Fellowship

Los Alamos National Laboratory 1990–1992
Postdoctoral Fellow

University of California at Berkeley 1985–1990
Research Assistant & Teaching Assistant, Dept. of Physics

Massachusetts Institute of Technology E.S.G. Program 1982–1985
Tutor and grader for students in independent study program.

Recent Presentations & Extramural Activities

University of Kansas Physics & Astronomy Dept. Colloquium: Oct. 1, 2012
"Cellphones and cancer: could conductive DNA play a role?"
Los Alamos Theoretical Biology & Biophysics Seminar: Aug. 3, 2011
"What do photon energies and densities tell us about cellphone safety"
Electric Power Research Institute (EPRI), Palo Alto, CA Jul. 12–13, 2011
Panelist, *International Expert Workshop on RF Fields Health Research*
University of Utah, Department of Electrical Engineering Seminar Apr. 8, 2011
"Biological Effects of Electromagnetic Fields" (host: Prof. Om Gandhi)
Biophysical Society Meeting Poster Mar. 5–9, 2011
"A predicted mechanism for biological effects of RF
electromagnetic fields: piezoelectric rectification," Abstract: *Biophys. J.* **100**(3) Suppl. 1: 623a
Los Alamos Theoretical Biology & Biophysics Seminar: Oct. 13, 2010
"'Frequentist' p-values from bootstrapped trees"
Princeton University Symposium in Honor of Bill Bialek, Nov. 6, 2010
"Animal Survival Skills and the Senses You Didn't Know You Had"

Previous Seminar & Lecture Venues

Society for Molecular Biology & Evolution • *Society of Systematic Biologists* • *Gordon Research Conferences* • *Mathematics & Molecular Biology* • *Critical Assessment of Structure Prediction (CASP)* • *Newton Institute* • *Santa Fe Institute* • *Aspen*

Center for Physics • U.C. Santa Cruz • Rensselaer Polytechnic Institute • Boston University • University of New Mexico • National Center for Genome Resources • NEC Research Institute • U.S. Defense Threat Reduction Agency • OpenEye Scientific Software • Aventis Pharmaceuticals (Bridgewater) • Structural Genomix

Reviewer

Proceedings of the National Academy of Sciences (USA) • Journal of the Royal Society of London B • PLoS Pathogens • Journal of Molecular Biology • BioMed Central Evolutionary Biology • Molecular Biology and Evolution • Bioinformatics • Journal of Molecular Evolution • Systematic Biology • IEEE Transactions on Computational Biology and Bioinformatics • Physica D • Applied Bioinformatics • Biological Procedures Online • Intelligent Systems for Molecular Biology (ISMB) • Pacific Symposium on Biocomputing (PSB)

Previous Extramural Committee Service

World Health Organization (WHO), Geneva 10/31–11/1, 2003
Temporary Advisor, Consultation on SARS Vaccine R&D

Albuquerque Technical Vocational Inst.'s Biotech Program Advisory Committee 2001

University of California System Industry-UC Cooperative Research Program 1998
Life Sciences Informatics Task Force & BioStar Grant Review Committee

Grants, Awards & Honors

DOE Computational Structural Biology Initiative Grant: 1996-2000
"Sequence-Structure Relationships: Quantifying Residue Fitness through Phylogenetic Analysis of Homologous Protein Sequences with Known Structure," P.I.
Los Alamos National Laboratory Distinguished Performance Award 1993

National Science Foundation Graduate Research Fellowship 1985-88

Apker Award Finalist, American Physical Society 1985

Putnam Exam Honorable Mention, Mathematical Association of America 1985

Peer-Reviewed Publications

Song, J. et al. "Development of Forensic Assay Signatures For Ebolaviruses" *J. of Forensic Sciences* 60(2):315–25 (2015).

Ullah, G., Bruno, W. J., & Pearson, J. E. "Simplification of reversible Markov chains by removal of states with low equilibrium occupancy." *J. Theor. Biology* 311:117–129 (2012).

Berendzen, J., Bruno, W., Cohn, J., Hengartner, N., Kuske, C., McMahon, B., Wolinsky, M. & Xie, G. "Rapid phylogenetic and functional classification of short genomic fragments with signature peptides." *BMC Research Notes,* 5(1), 460 (2012).

Srinivasan, T., Bruno, W. J., Wan, R., Yen, A., Duong, J., & Dean, D. "In Vitro Recombinants of Antibiotic-Resistant Chlamydia trachomatis Strains Have Statistically More Breakpoints than Clinical Recombinants for the Same Sequenced Loci and Exhibit Selection at Unexpected Loci." *Journal of Bacteriology,* 194(3): 617-626 (2012). Chicago

Dean, D., W. J. Bruno, R. Wan, J.P. Gomes, S. Devignot, T. Mehari, H.J.C. de Vries, S.A. Morre, G. Myers, T. D. Read et al. "Predicting phenotype and emerging strains among Chlamydia trachomatis infections." *Emerging Infectious Diseases* 15:1385-1394 (2009).

Berry, M. I., G. Athreya, M. Kothari, M. Daniels, W. J. Bruno, B. Korber, C. Kuiken, R. M. Rieiro, T. Leitner, "The evolutionary rate dynamically tracks changes in HIV-1 epidemics: Application of a simple method for optimizing the evolutionary rate in phylogenetic trees with longitudinal data." *Epidemics* 1:230-239 (2009).

Hraber, P. T., C. Kuiken, M. Waugh, S. Geer, W. J. Bruno & T. Leitner, "Classification of hepatitis C virus and human immunodeficiency virus-1 sequences with the branching index." *J. Gen. Virol.* 89:2098-2107 (2008).

Berry, I. M., R. Ribeiro, M. Kothari, G. Athreya, M. Daniels, H. Y. Lee, W. J. Bruno & T. Leitner, "Unequal evolutionary rates in the HIV-1 pandemic: The evolutionary rate of HIV-1 slows down when the epidemic rate increases." *J. Virol.* 81: 10625–10635 (2007).

Gomes, J.P., W. J. Bruno, A. Nunes, N. Santos, C. Florindo, M. J. Borrego & D. Dean, "Evolution of Chlamydia trachomatis diversity occurs by widespread interstrain recombination involving hotspots." *Genome Res.* 17: 50–60 (2007).

Bruno, W. J. & J. E. Pearson, "Transformations that preserve detailed balance in Markov models." *J. Comp. Biol.* 13: 9 (2006).

Yang, J., W. J. Bruno, W. S. Hlavacek & J. E. Pearson, "On Imposing Detailed Balance in Complex Reaction Mechanisms." *Biophys. J.* 91: 1136–41 (2006).

Hraber, P. T., W. Fischer, W. J. Bruno, T. Leitner & C. Kuiken, "Comparative analysis of hepatitis C virus phylogenies from coding and non-coding regions: the 5' untranslated region (UTR) fails to classify subtypes." *Virol J.* 3: 103–112 (2006).

Macken, C. A., R. J. Webby & W. J. Bruno, "Genotype turnover by reassortment of replication complex genes from avian Influenza A virus." *J. Gen. Virol.* 87: 2803–2815 (2006).

Gomes, J.P., A. Nunes, W. J. Bruno, M. J. Borrego, C. Florindo & D. Dean, "Polymorphisms in the nine polymorphic membrane proteins of Chlamydia trachomatis

across all serovars: Evidence for serovar Da recombination and correlation with tissue tropism." *J. Bact.*188: 275–286 (2006).

Bruno, W. J., J. Yang & J. E. Pearson, "Using independent open-to-closed transitions to simplify aggregated Markov models of ion channel gating kinetics." *Proc. Natl. Acad. Sci. (USA)* 102: 6326-31 (2005).

Joslyn, C. A. & W. J. Bruno, "Weighted Pseudo-Distances for Categorization in Semantic Hierarchies." *Conceptual Structures: Common Semantics for Sharing Knowledge, Lecture Notes in AI,*vol. 3596eds. F. Dau, M.-L. Mugnier & G. Stumme, 381–395 (2005).

Martin, J. et al. (121 authors), "The sequence and analysis of duplication-rich human chromosome 16." *Nature.* 432: 988–94 (2004).

Gomes, J. P., W. J. Bruno, M. J. Borrego & D. Dean, "Recombination in the genome of Chlamydia trachomatis involving the polymorphic membrane protein C gene relative to ompA and evidence for horizontal gene transfer." *J. Bacteriol.* 186: 4295–306 (2004).

Dutilh, B. E., M. A. Huynen, W. J. Bruno & B. Snel, "The consistent phylogenetic signal in genome trees revealed by reducing the impact of noise." *J. Mol. Evol.* 58: 527–539 (2004).

Holmes I. & W. J. Bruno, "Evolutionary HMMs: a Bayesian approach to multiple alignment." *Bioinformatics.* 17: 803-20 (2001).

Kishino, H., J. L. Thorne & W. J. Bruno, "Performance of a Divergence Time Estimation Method under a Probabilistic Model of Rate Evolution." *Mol. Biol. Evol.* 18: 352-361 (2001).

Holmes, I. & W. J. Bruno, "Finding regulatory elements using joint likelihoods for sequence and expression profile data." *Proc. Int. Conf. Intell. Syst. Mol. Biol. (ISMB)* 8: 202–210 (2000).

Pollock, D. D. & W. J. Bruno, "Assessing an unknown evolutionary process: effect of increasing site-specific knowledge through taxon addition." *Mol. Biol. Evol.* 17: 1854–1858 (2000).

Bruno, W. J., N. D. Socci, & A. L. Halpern, "Weighted Neighbor Joining: A Likelihood-Based Approach to Distance-Based Phylogeny Reconstruction." *Mol. Biol. Evol.* 17: 189–197 (2000).

Bruno, W. J. & A. L. Halpern, "Topological Bias and Inconsistency of Maximum Likelihood Using Wrong Models." *Mol. Biol. Evol.* 16: 564–566 (1999).

Koshi, J. M. & W. J. Bruno, "Major Structural Determinants of Transmembrane Proteins Identified by Principal Component Analysis." *Proteins* 34: 333–340 (1999).

Bruno, W. J., G.-C. Rota, & D. Torney, "Probability Set Functions." *Annals of Combinatorics,* 3: 13–25 (1999).

Bruno, W. J., F. Sun, & D. C. Torney, "Optimizing Non-Adaptive Group Tests for Objects with Heterogeneous Priors." *SIAM J. Appl. Math.* 58: 1043–1059 (1998).

Halpern, A. L. & W. J. Bruno, "Evolutionary Distances for Protein-Coding Sequences: Modeling Site-Specific Residue Frequencies." *Mol. Biol. Evol.* 15: 910–917 (1998).

Arvestad, L. & W. J. Bruno, "Estimation of Reversible Substitution Matrices from Multiple Pairs of Sequences." *J. Mol. Evol.* 45: 696–703 (1997).

Balding, D. J., W. J. Bruno, E. Knill, & D. C. Torney, "A Comparative Study of

Non-Adaptive Pooling Designs." in *Genetic Mapping and DNA Sequencing, IMA Volumes in Mathematics and its Applications, vol. 81*T. Speed and M. S. Waterman (eds.) 133–155. Springer-Verlag, Berlin (1996).

Bruno, W. J. "Modeling Residue Usage in Aligned Protein Sequences via Maximum Likelihood." *Mol. Biol. Evol.* 13: 1368–1374 (1996).

Bruno, W. J., E. Knill, D. J. Balding, D. C. Bruce, N. A. Doggett, W. W. Sawhill, R. L. Stallings, C. C. Whittaker & D. C. Torney, "Efficient Pooling Designs for Library Screening." *Genomics,* 26: 21–30 (1995).

Xie, G., R. Lobb, W. J. Bruno, D. C. Torney, & J. M. Gatewood, "Single-base Sequencing and Similarity Comparisons." *Genomics* 30: 445–449 (1995).

Doggett, N. A., L. A. Goodwin, J. G. Tesmer, L. J. Meincke, D. C. Bruce, L. M. Clark, M. R. Altherr, A. A. Ford, H. C. Chi, B. L. Marrone, J. L. Longmire, S. A. Lane, S. A. Whitmore, M. G. Lowenstein, R. D. Sutherland, M. O. Mundt, E. H. Knill, W. J. Bruno, et al., "An Integrated Physical Map of Human Chromosome 16." *Nature,* 377, Suppl. S: 335–366 (1995).

McCormick, M. K., A. Buckler, W. J. Bruno, E. Campbell, K. Shera, D. Torney, L. Deaven & R. Moyzis, "Construction and Characterization of a YAC Library with a Low Frequency of Chimeric Clones from Flow Sorted Human Chromosome 9." *Genomics* 18: 553–558 (1993).

Pearson, J., & W. J. Bruno, "Pattern Formation in an N+Q Component Reaction-Diffusion System." *CHAOS,* 2: 513–524 (1992).

Bruno, W. J. & W. Bialek, "Vibrationally Enhanced Tunneling as a Mechanism for Enzymatic Proton Transfer." *Biophys. J.* 63: 689–699 (1992).

Joseph, J. S., W. J. Bruno, & W. Bialek, "Bleaching of the Bacteriochlorophyll Monomer Band: Can Absorption Kinetics Distinguish Virtual from Two-Step Electron Transfer in Bacterial Photosynthesis?" *J. Phys. Chem.* 95: 6242–6247 (1991).

Bialek, W., W. J. Bruno, J. Joseph & J. N. Onuchic, "Quantum and Classical Dynamics in Biochemical Reactions." *Photosyn. Res.* 22: 15–27 (1989).

Sample, H. H., W. J. Bruno, S. B. Sample & E. K. Sichel, "Reverse-field reciprocity for conducting specimens in magnetic fields." *J. Appl. Phys.* 61: 1079-84 (1987).

Scientists Mentored, Hosted or Supervised

Subsequent positions

Lars Arvestad, Ph.D., hosted graduate student — Senior Scientist, KTH
Stockholm Bioinformatics Center
Senior Lecturer, Stockholm Univ., Dept. Comp. Biol.

Aaron L. Halpern, Ph.D., mentored postdoc — U. New Mexico faculty
Celera Genomics
J. Craig Venter Institute
The Center for Advancement of Genomics, MD
Complete Genomics, Mountain View, CA

Jeffrey Koshi, Ph.D., sponsored postdoc Cereon Genomics, Cambridge, MA
Monsanto Technology, St. Louis

Prof. David Pollock, sponsored postdoc Asst. Prof. Biology, Louisiana State Univ.
Assoc. Prof., U. Colorado Med. School

Prof. Ian Holmes, hosted postdoc Lecturer, Statistics, Oxford Univ.
Assoc. Professor, Bioenginering, U.C. Berkeley

Selected Software Packages Created

Weighbor: a fast, unbiased distance-based phylogeny reconstruction method. Implemented by Dr. Nick D. Socci who is now at Memorial Sloan-Kettering Cancer Center. Testing software by Dr. Aaron L. Halpern, who is now at Complete Genomics.

Rind: a rigorous alternative to sequence weights, using maximum likelihood on a tree to estimate site specific frequencies for large multiple alignments. Iteratively improves evolutionary model and tree.

CoRind: generalizes **Rind** to detect covariation of pairs of sites in an alignment. Can predict structural contact in many cases. Statistical interface by Dr. Aaron L. Halpern.

Setter: Tunable evolutionary model for blast nucleotide scoring matrices with graphical front-end for Blast. Implemented by Dr. Wim Hordijk.

Branch_boot: Computes rigorous p-values from phylogenetic bootstrap replicate trees.