



December 7, 2004

Professor Bruce Weir,  
Chair, Bioinformatics Search Committee,  
Department of Statistics,  
Box 7566,  
North Carolina State University,  
Raleigh,  
NC 27695-7566

Dear Prof. Weir,

I am applying for the advertised **bioinformatics** faculty position at North Carolina State University. Currently, I am in my fifth tenure-track year as an Assistant Professor of Chemistry at California State Polytechnic University, Pomona. I accepted my current position because I believed it to be the appropriate balance of teaching and research. However, I am applying for this position because I recognize my need for a more challenging research environment. While I wish to continue to pursue my idealistic teaching goals, it is becoming increasingly clear that for my research to reach its full potential, a move to a more research oriented institution is necessary.

I received my Ph.D. from the University of Illinois at Urbana-Champaign under the guidance of Professor Shankar Subramaniam (now at the University of California, San Diego). Our work was at the interface of traditional computational biology and bioinformatic methods. Specifically, we focused on deciphering protein family sequence/structure/function relationships. This work resulted in four published journal article manuscripts. Our most important paper demonstrates how evolutionarily conserved electrostatic signatures maintain function across a variety of protein family and superfamily examples.

I accepted my current position at Cal Poly Pomona directly from graduate school. Despite a lack of formal postdoctoral training, I have developed a very active, externally funded research program. My current research still focuses on identifying new sequence/structure/function relationships. However, I am increasingly interested in application of these phenomena. For example, based on the evolutionary principles discovered during my graduate work, my lab has developed an accurate protein functional site prediction scheme based on *phylogenetic motifs*. I am also very interested in protein structure stability/flexibility relationships. In collaboration with Don Jacobs (Department of Physics and Astronomy, Cal State Northridge), we are developing a powerful Distance Constraint Model (DCM) that harmoniously calculates both thermodynamic stability and mechanical flexibility. The DCM is unique in its ability to calculate entropies in a computationally efficient, physical way. Future work will use the DCM to carefully balance stability and flexibility in protein design efforts. Five research manuscripts describing our current work have recently been accepted/published, one is in review, and two more will be submitted by the end of the calendar year. Results from my lab have also been presented at national and local meetings, where they have been well received – students from my lab have



won awards at the 2002 and 2004 annual meetings of the Protein Society and California State University Program for Educations and Research in Biotechnology, respectively.

My research is supported by a variety of extramural funding sources, including: the National Science Foundation, National Institutes of Health, the American Chemical Society-Petroleum Research Fund, and the California State Program for Education and Research in Biotechnology. We (myself and Don Jacobs) will re-submit our NIH-R01 proposal to fund continued DCM development in February. While not funded previously, we are encouraged by the positive comments from the reviewers. Recently, we also submitted an NIH-SCORE proposal to investigate Quantified Stability/Flexibility Relationships (QSFR) within protein families using the current model. I have also recently submitted an NSF-CAREER proposal to fund continued development of my phylogenetic motif functional site prediction approach.

I am also active in College- and University-level funding endeavors. In 2003, I was the main technical volume author for our multi-institution (Cal Poly Pomona, University of Maryland Biotechnology Institute, Michigan State University, and Battelle) response to the U.S. Army Broad Agency Announcement for a proposed \$36 million Institute for Collaborative Biotechnologies. Though not funded, learning the process of such large efforts was invaluable. In 2004, I was one of two original authors of our preliminary approach to the W.M. Keck Foundation for \$1.5 million to support the Cal Poly Pomona Center for Macromolecular Modeling & Materials Design (CM<sup>3</sup>D). The final version of the proposal will be presented to their Board of Directors in November, and according to them "it's exactly the type of proposal we fund".

In addition to scholastic research, I firmly believe in the importance of developing curricula to keep pace with biotechnology advances. Since arriving at Cal Poly Pomona, I have developed three completely new courses: *Bioinformatics*, *Macromolecular Modeling*, and a graduate *Protein Mass Spectrometry/Proteomics* course. (Course syllabi, notes, etc. can be viewed from the web at <http://www.csupomona.edu/~drlivesay/courses.html>.) Two of these courses are support courses for our new *Molecular Modeling and Simulation* degree. Future plans include both undergraduate and graduate degree programs in bioinformatics. I have also worked hard to change our scholastic culture at Cal Poly Pomona, which has resulted in the development of a state-of-the-art teaching/research computer lab, the CM<sup>3</sup>D, and creation of a new support position for these efforts.

Included are: my CV, research statement, and five recent reprints. I have requested recommendation letters be sent on my behalf. Thank you for your consideration.

Sincerely,

Dennis R. Livesay, Ph.D.