

Biostatistician/Experienced Bioinformatics Developer/Trained in Computer Science/Trained in Genetics

OBJECTIVE

Full time position as biostatistician or bioinformatics developer.

Specific interests include statistical modeling and data analysis, database design, and programming.

EDUCATION

Master of Arts in Biostatistics, May 2004,
University of California, Berkeley

Two Years of undergraduate Computer Science Classes,
California Polytechnic University, San Luis Obispo

Bachelor of Science in Genetics,
University of California, Davis, June 2000

Bioinformatics courses,
Stanford, Continuing education

PROFILE

Extensive microarray data analysis.

Experience working with nation's leading-edge pathogen bioinformatics group under Tom Slezak. Met strict deadlines to **design and implement novel bioinformatics infrastructure** that has been used to design pathogen detection signatures now in daily use for homeland defense and public health.

Experience using **multidisciplinary background** in computer science, genetics, and biostatistics to facilitate communication between colleagues of different backgrounds.

Experience designing and implementing **statistical data analysis studies** at Lawrence Livermore National Laboratory.

Experience presenting complicated ideas through teaching work.

US Citizen with Q Security Clearance

COMPUTER SKILLS

Experience with UNIX, Sweave, Bioconductor, and BLAST.

Programming Languages: Python, SAS, Splunk, LaTeX, R, Java, Perl, C,
HTML/XHTML, DHTML, CSS, JavaScript, SQL, STATA

Design work: Detection algorithms for DNA microarrays, Scalable infrastructure for bioinformatics systems, statistical studies.

PROFESSIONAL EXPERIENCE

Full time employee at Lawrence Livermore National Laboratory (June 2004 to present)

Performed viral genome complexity analysis in relation to microarray probe design.

Designed and implemented machine learning algorithms for pathogen detection and virulence gene detection.

Analysis of gene expression and DNA detection microarray data.

Designed and conducted experiments testing microarray probe design parameters and hybridization affinity.

Resulted in array probe success rate exceeding 99.4%.

Team lead for bioinformatics infrastructure setup group.

Primary statistician for the Lawrence Livermore Microarray Center.

Created graphical data visualization images for team projects.

Experienced at analyzing time course and cross sectional data.

Summer Scholar at Lawrence Livermore National Laboratory (Summers 2000-2003)

Worked closely with computer scientists to design and implement working prototype of pathogen DNA signature development system referenced in publication below.

Designed and implemented statistical data analysis infrastructure, including a database, analysis techniques, and analysis code, for project that analyzed how much whole genome sequencing is required for high-quality pathogen DNA signatures.

Graduate Student Instructor in Biostatistics

(Fall 2002, Spring 2003)

Worked twenty hours per week as a full time graduate student, teaching discussions, holding office hours, attending meetings, grading papers, and attending lectures for Introduction to Probability and Statistics in Biology and Public Health I and II.

PUBLICATIONS

1. Malfatti, M.A., Dingley, K.H., Nowell-Kadlubar, S., Esther U.A., Mulakken, N, Nelson, D., Lang, N.P., Felton, J.S., Turtletaub, K.W., (2006) The Urinary Metabolite Profile of the Dietary Carcinogen 2-Amino-1Methy-6-Phenylimidazo[4, 5-b] Pyridine Is Predictive of Colon DNA Adducts after a Low-Dose Exposure in Humans. *Cancer Research* 66(21):10541-7.
2. Gardner, S.N., Lam, M.W., Mulakken, N.J., Torres, C.L., Smith, J.R., Slezak, T.R. 2004. Sequencing needs for viral diagnostics. *Journal of Clinical Microbiology*.
3. Slezak T, Kuczmarowski T, Ott L, Torres C, Medeiros D, Smith J, Truitt B, Mulakken N, Lam M, Vitalis E, Zemla A, Zhou CE, Gardner S (2003) *Comparative genomics tools applied to bioterrorism defense*, *Briefings in Bioinformatics* 4(2):133-49.

HONORS AND AWARDS

Fall 2006 Excellence in Publication award, LLNL

Fall 2003 Fellowship Grant, UC Berkeley

RELEVANT COURSE WORK

Statistics Classes

- Linear Models
- Longitudinal Data Analysis
- Categorical Data Analysis
- Survival Analysis (spring 2004)
- SAS (spring 2004)
- Computational Techniques in Biostatistics
- Advanced Introduction to Probability and Statistics I
- Advanced Introduction to Probability and Statistics II
- Statistics Using Splus

Bioinformatics/Computer Science Classes

- Representations and Algorithms in Computational Biology
- Computations Structural Biology: Protein Simulation, Function, and Prediction.
- Operating Systems
- Design and Analysis of Algorithms
- Software Engineering
- Object Oriented Analysis and Design using UML
- Theory of Computing
- Distributed Computing
- Fundamentals of Computer Science II and III

Biology Classes

- Advanced Eukaryotic Genetics
- General Bacteriology
- Molecular Genetics
- Genes and Gene Expression
- Regulation of Cell Function
- Structure and Function of Biomolecules
- Bioenergetics and Metabolism