Jon Lapham, PhD

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Currently employed as the bioinformatics and IT manager for Extracta, a small Brazilian biotechnology company specializing in small-molecule drug discovery. Successfully integrated a high-throughput screening system with a computer database and automated analysis system, including hit prioritization. Would like to return to the North America to work for a creative and energetic company working in either a computational biology or IT department in a research and development environment. 10 years experience in both doctorate and post-doctorate biochemical research, studies involved modeling experimental data, statistics, and computer simulations. 12 years experience in IT with an emphasis in computer programming and database administration.

Computer Skills

OS (Platform): SunOS/Solaris (SPARC), Linux (x86), IRIX (MIPS), Windows

Programming Languages: Perl, SQL, C/C++, FORTRAN, Bash (want to learn Java, Python, etc)

Software: Web services (Apache, ModPerl), Database (PostgreSQL, MySQL), Security (IPTable firewall, encryption certs), Email (Sendmail, Procmail), Math and Statistics (XMGrace, ODRPACK), Chemistry (Gaussian, XPLOR, CNS, Felix), Biology (MSI Insight)

IT experience: 12 years experience as system administrator. 5 years experience as head of IT at a 40 person company.

Authored software (documentation or examples available at http://www.JandR.org):

Cyclize predicts DNA cyclization rates via Monte Carlo simulation, written in C and Perl. Online documentation: http://www.jandr.org/jpl_files/cyclize_html/

YARM simulates NMR relaxation rates given a structural and dynamic model for DNA/RNA, written in C and Perl. Online documentation: http://www.jandr.org/jpl_files/yarm_html/

PhotoLyzer a web application for viewing digital photos, written in Perl. Online documentation: http://www.jandr.org/photolyzer/

RecipeLyzer a web application for organizing recipes, written in Perl uses a database backend. Online: http://www.jandr.org/recipelyzer/

WebFit a web application for performing regression analysis (fitting a mathematical model) to arbitrary data.

Extracta's Biodiversity Database is a web-based database which processes, analyzes and stores the results of the high throughput screening of natural product drug candidates against human disease targets.

Science Skills

Computer simulations: *ab initio* (Gaussian), Monte Carlo methods.

Statistical Methods: Speak statistics fluently, ie: Chi-Squared, Confidence Intervals, F-test, etc.

High-throughput screening (techniques, methodology, equipment multiprobe, platemate, etc)

Synthesis, isotopic enrichment (13C, 15N), purification and sequencing of DNA and RNA

Radioactive and biotin labeling of nucleic acids

Protein over-expression and purification

Nuclear Magnetic Resonance: structure and dynamics of nucleic acids, worked with both Bruker

and Varian high field magnet systems.

Experience in a wide variety of analytical methods: HPLC (Varian and Waters), LCMS (Waters), Capillary Electrophoresis, Gel Electrophoresis.

Education

YALE UNIVERSITY, New Haven, CT, USA
   PhD: Chemistry, May 1998, MS: Chemistry, May 1993
FLORIDA STATE UNIVERSITY, Tallahassee, FL, USA
   BS: Chemistry, May 1991

Professional Experience

EXTRACTA MOLÉCULAS NATURAIS SA, Rio de Janeiro, Brazil
   Information Technologies Manager, July 1999 – present
   Managed interaction between biology and chemistry departments with IT. Developed database applications to integrate scientific equipment data with data processing applications. Wrote all principal IT and science computer applications used in the company. System administrator for 40 computers in a mixed UNIX/Windows environment.

UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, Dept Biophysics, Rio de Janeiro, Brazil
   Postdoctoral assistant research, January 1999 – March 2000.
   Advisor: Professor Jerson Lima de Silva
   Research area: Theoretical simulations of NMR relaxation phenomena. System administrator for a lab of 10 UNIX computers.

YALE UNIVERSITY, New Haven, CT, USA
   Graduate assistant research, 1992 – 1998 Advisor: Professor Donald M. Crothers
   Research area: Structural and dynamic studies of nucleic acids by nuclear magnetic relaxation.
   Teaching Assistant, Advanced Physical Chemistry, September 1994 – May 1995
   Advisor: Professor Peter Moore

FLORIDA STATE UNIVERSITY, Tallahassee, FL, USA
   Undergraduate assistant research, 1990 – 1991, Advisor: Prof. William Cooper
   Research Area: Environmental chemistry, specifically, analysis of solid state NMR results from river sediment samples.

Personal Information

Citizenship: USA
Languages: English and Portuguese

Publications

BARTOSCHEK S, BUURMAN G, GEIERSTANGER BH, LAPHAM J, AND GRIESINGER C. 2003. Measurement and ab initio calculation of CSA/dipole-dipole cross-correlated relaxation provide insight into the mechanism of a H2 forming dehydrogenase. *Journal of the American Chemical Society* **125 (44)**: 13308 9.

Lapham J and Kover R; 2001. Develoment of an Integrated System to Manage a Natural Product Lead Discovery Program; *Society for Biomolecular Screening – 7th Annual Conference and Exhibition*, Baltimore, USA

Roychoudhury M, Sitlani A, Lapham J, Crothers DM. 2000. Global structure and mechanical properties of a 10-bp nucleosome positioning motif. *Proceedings of the National Academy of Sciences: USA* **97**:13608 13.

Lapham J, Crothers DM. 2000. Site specific cleavage of transcript RNA. *Methods in Enzymology*. **317**:132 139.

Dhavan G., Lapham J, Crothers, DM. 1999. Imino proton spectroscopy and exchange kinetics of the Integration Host Factor DNA binding site. Journal of Molecular Biology. 288:659 671.

Lapham J. 1998. 1) NMR studies of the spliced leader RNA from Crithidia fasciculata and Leptomonas collosoma. 2) Hydrodynamic properties of nucleic acids by NMR. Yale University. Ph.D. Thesis.

Lapham J, Rife J, Moore PB, Crothers DM. 1997. Measurement of diffusion constants for nucleic acids by NMR. *Journal Biomolecular NMR* **10**:255 262.

Lapham J, Yu Y T, Shu M D, Steitz JA, Crothers DM. 1997. The position of site directed cleavage of RNA using RNase H and 2 O methyl oligonucleotides is dependent on the enzyme source. *RNA* **3**:950 951.

Xu J, Lapham J, Crothers DM. 1996. Determining RNA Solution Structure by Segmental Isotopic Labeling and NMR:Applications to Caenorhabditis elegans Spliced Leader RNA *1. Proceedings of the National Academy of Sciences: USA* **93**:44 48.

Lapham J, Crothers DM. 1996. RNase H Cleavage for Processing of in vitro Transcribed RNA for NMR Studies and RNA Ligation. *RNA* **2**:289 296.