

Career Objective – To combine my quantitative skills, biological and computer science knowledge in order to make an impact in big data industries whether it be medicine, marketing, or finance.

Education

Northeastern University, Boston, MA

Sept. 2003 – May 2008

Bachelor of Science in Computer Science and Biology

GPA: 3.61/4.00, Dean's Scholarship recipient, Outstanding Co-op Student Award, Compass Award, Computing Research Association Outstanding Undergraduate Honorable Mention, Member of UPE Computer Science Honors Society, Leader of CISters – NU Women's Computing Group

Work Experience

Computational Analyst/Science Manager – **Gene Network Sciences – Cambridge, MA** March 2008 - Present

- Utilize high performance Bayesian network reconstruction and simulation algorithms to build quantitative and predictive integrative genomics models in metabolic disease, inflammation and cancer.
- Manipulate and simulate predictive models to allow new target and biomarker identification for personalized medicine and enable drug-repositioning efforts.
- Successfully increased revenue generation by writing research grants and project proposals to top pharmaceutical companies. Following revenue sources secured:
 - \$750,000 NCI grant for a 6-month project to identify mechanisms of action of several cancer drugs
 - \$500,000 collaboration to identify biomarkers and potential drug targets for Diabetes
 - \$200,000 collaboration with Harvard Medical School to identify biomarkers for Asthma
- Act as Lead Science Manager assisting the Executive Vice President by visiting client sites, discussing ideal experimental designs and securing project deals.
- Designed a pipeline to streamline the pre-processing of genetic data from quality control to imputation.
- Collaborate with top-level scientists to review analysis plans, innovate new ones and interpret statistical results.
- Analyzed and predicted which factors would shift and maximize market success for a particular consumer product based on survey data.

Bioinformatics Analyst – **Dana-Farber Cancer Institute – Cancer Biology Dept., Boston, MA** 2007 – 2008

- Designed and maintained a Rich Internet Application (eNotebook – publication pending), which enables scientists to describe, track and analyze their experiments by enhancing the data capture process.
- Enabled machine-learning and expert human analysis of protein identification, modification and interaction. Developed a protein-protein interactor component, which is linked to a local instance of the Human Protein Reference Database (HPRD)
- Implemented encryption, authorization, and authentication security mechanisms for eNotebook using PHP
- Maintained an Oracle 10g database linked to a custom automated data analysis pipeline, which monitors .RAW files being acquired from several mass spectrometers. Incorporated scriptable analysis tools into our proteomics pipeline

Bioinformatician – **Children's Hospital Informatics Program, Boston, MA**

2006 – 2007

- Analyzed genetic data involving Huntington's disease and Asthmatic patients using methods such as Principal Components Analysis, Hierarchical Clustering, t-tests, SAM (Significance Analysis of Microarrays), and various filtering/normalization procedures
- Applied Gene Set Enrichment Analysis (GSEA) to a time series of mouse cerebellum developmental data to discover metabolic pathways that are regulated during specific stages of brain development
- Utilized GSEA to identify underlying mechanisms common to both human medulloblastoma and specific stages of cerebellar development
- Attended the 2006 NIH Roadmap Biomedical Computing Conference in Bethesda, MD to present results obtained from analyzing Huntington's disease samples

- Derived algorithms to analyze complex diseases such as Autism and Asthma using linkage peak data in conjunction with GSEA
- Participated in the the Harvard-MIT Division of Health Sciences and Technology Summer Scholars program, which teaches undergrads about the latest tools and techniques for bioinformatics research

Application Analyst - Harvard Partners Center for Genetics and Genomics, Cambridge, MA 2005 –2006

- Provided analytical, user adoption, and QA support throughout software development life cycle for the following projects: Variant Database, DNA Microarray & Research Sequencing, GIGPAD Performed usability assessment on DNA Microarray Laboratory Information Management Systems (LIMS) and Variant Database
- Created user documentation for the following systems: Variant Database, GIGPAD, FIND (Freezer-Management System)
- Defined requirements for variant nomenclature to enable structured reporting of point mutations to the electronic medical record (EMR)
- Co-designed baseline aCGH (array comparative genome hybridization) structured report format
- Participated in baseline XML object model design for messaging genetic variant results to enterprise systems

Professor's Assistant/Researcher - Northeastern University – Boston, MA 2004 – 2005

- Researched tools to be used in the development of an online portfolio system for students
- Co-authored “Calculator Problem and the Design Recipe,” published in ACM SIGPLAN Notices, Volume 40, Issue 3 (March 2005)
- Presented student poster and co-led workshop entitled “*Focus on the Design of Classes in OO Programming Courses*” at the Consortium for Computing Sciences in Colleges - Northeastern Region 2005.
- Analyzed diagrams from open access biology publications on BioMed Central for parsing/NLP research

Publications:

- Cashorali T, McDonagh P, Runge K, Miller R, DeCaprio D, Church B, Seymour A, Khalil I, Laramie J. Using Bayesian Networks to Discover Combinations of Genetic Loci and Clinical Covariates Associated with Disease. BMC Syst. Biol. [Under Review].
- Xing H, McDonagh P, Bienkowska J, Cashorali T, Khalil I, Carulli J. Causal Modeling Using Network Ensemble Simulations of Genetic and Gene Expression Data Predicts Genes Involved in Rheumatoid Arthritis. PLoS Comp. Biol. [Under Review].
- Lee J-M, Ivanova EV, Seong IS, Cashorali T, Kohane I, et al. (2007) Unbiased Gene Expression Analysis Implicates the huntingtin Polyglutamine Tract in Extra-mitochondrial Energy Metabolism. PLoS Genet 3(8): e135. doi:10.1371/journal.pgen.0030135.
- Parikh JR, Askenazi M, Ficarro SB, Cashorali T, Webber JT, Blank NC, Zhang Y, Marto JA. multiplierz: an extensible API based desktop environment for proteomics data analysis. BMC Bioinformatics. 2009 Oct 29;10:364.
- Viera K. Proulx , Tanya Cashorali, Calculator problem and the design recipe, ACM SIGPLAN Notices, v.40 n.3, March 2005 [doi>10.1145/1057474.1057478]

Computer and Scientific Skills

Languages: R, Perl, Java, PHP, SQL, C++, C, Adobe Flex, ActionScript, Python, JavaScript, HTML, CSS

Systems: Windows (All), Unix, Linux

IDEs: Eclipse, Adobe Flex Builder, Macromedia Flash, Borland Builder

Technologies: Oracle, PostGres, GIS, MySQL/psql, Apache HTTP Server, Tomcat, OpenSSL, CVS;Subversion

Office Applications: Microsoft Office (Excel, Powerpoint, Word), Adobe Photoshop & Illustrator

Scientific Applications: LIMS (Laboratory Information Management Systems), Bioconductor, TIGR MeV,

Mascot

Clinical Applications: Tamtron PowerPath (diagnostic reporting system)

Functional Skills: communication (verbal, written and graphical), able to work independently and in cross-functional team environment, prolific results-driven work style, multi-tasking and task management, social media and mobile marketing, SEO, web design

References Furnished Upon Request