

postdoctoral fellow postdoctoral fellow postdoctoral fellow of bioinformatics - University of Washington Medical Center Seattle, WA I am currently a postdoctoral researcher at the University of Washington Medical Center, focusing on Biomedical Informatics. With prior degrees in Biology and Computer Science, over eight years of experience as a data analyst, and eighteen years of experience as a software developer, I am seeking a position where I can utilize my skills in statistical analysis and software engineering to further research and application of Bioinformatics. Highlights of Qualifications: Mining of high-throughput gene expression data, including microarray and RNA-seq data, to identify pathway-based transcriptomic changes. Familiarity to statistical analysis of next-generation sequencing data. Tackling of statistical issues arising from high dimensionality, high data heterogeneity, and small sample sizes. Deep understanding and lab research experience in molecular biology, especially cancer biology. Machine learning prediction of patient outcomes using clinical and electronic health data. Extensive background in design and implementation of software applications by following the best practices of the IT industry. Proficiency in R, Python, MATLAB, SQL, Java, .Net, C++, JavaScript, JQuery, HTML5, etc. Considerable experience in relational databases design and management of data, including health care data. Development of research ideas through independent research and interpersonal discussions. Experience in Microsoft Azure cloud computing service. Working knowledge with AWS. Comfortable with high-paced settings and multi-tasking requirements. Highly motivated and detail oriented. Work Experience postdoctoral fellow Department of Anesthesiology & Pain Medicine, University of Washington Medical Center - Seattle, WA December 2018 to Present Key projects and accomplishments: Prediction for traumatic brain injury (TBI) patient outcomes to prevent secondary insults using a variety of machine learning techniques, including tree-based methods and deep learning. The prediction is done by classifying whether hypotension and/or hypocarbia would occur during surgery. (This project is funded by an NIH R21 grant) Translating biclusters into gene networks based on probabilistic graphical models. Biclusters identified by mining multiple gene expression datasets provide high-confidence information on inter-gene correlations, which can be used to build either directed or undirected acyclic graphs. The resulting graphs can

provide insights into how genes are regulated, and potentially aid in patient diagnosis and drug design.

Programming of a new Departmental Income Distribution Plan that involves sophisticated calculations and integration of different data sources. The plan is now in effect with an expected result to provide better incentive to the anaesthesia providers. I am honored to have received praises from the departmental management (please see Appendix B for details).

software engineer and data analyst  
Department of Surgery, University of Washington Medical Center - Seattle, WA  
November 2010 to November 2018

Key projects and accomplishments:

- Creating custom data reports, providing statistical analyses and visualization to support clinical research after integrating and querying diverse data sources that include electronic medical records, Amalga data warehouses, etc.
- Development of RevivePro (formerly EventDoc), a mobile documentation and cognitive aid system for in-hospital cardiac arrest events that captures care data, provides dynamic statistical summaries via user-friendly and novel visualization, and offers step-by-step cognitive aid. This software system has now been successfully commercialized ([www.formathealth.com](http://www.formathealth.com))
- Design and programming of a tablet displayed checklist application using a web-based framework to standardize operating room to post-anesthesia care unit (PACU) transfer of care through improved communications. The system operates by querying and updating real-time clinical data. Periodic reports are
- Design and programming of an aviation-style tablet-displayed crisis checklist application used in the operating rooms to enhance procedural compliance and improving clinical care as well as patient safety. The system is currently under evaluation by comparing with the traditional paper-based crisis checklists.

software and database developer  
Ultimate Solutions by Engineers Ltd - Toronto, ON  
December 2001 to December 2015

Key projects and accomplishments:

- Designing and developing IT solutions for mission-critical processes in real estate and banking industries (example clients: EXIT Realty International, Bank One, etc.)
- Design of large-scale relational databases to model complex business rules.
- Writing technical manuals and documentation.
- Interacting with clients, solving technical problems for the clients.

software developer  
IBM - Rochester, MN  
October 2001 to December 2001

Key projects and accomplishments:

- Evaluating a Java-based platform based on the IBM WebSphere application

server. Writing and publishing a technical manual. Education PhD in Biomedical Informatics University of Washington - Seattle, WA 2018 B.S. in Computer Science University of Toronto - Toronto, ON 2000 Molecular and Cell Biology University of Pennsylvania - Philadelphia, PA 1995 to 1997 M.S. in Plant Biology North Dakota State University - Fargo, ND 1995 Skills R, Python, MATLAB, SQL, Java, .Net, C++, JavaScript, JQuery, HTML5 (10+ years), Chemistry, Cell Culture Publications Randomised trial comparing the recording ability of a novel, electronic emergency documentation system with the AHA paper cardiac arrest record 2014 Grigg E, Palmer A, Grigg J, Oppenheimer P, Wu T, Roesler A, Nair B, Ross B. (2014) Randomised trial comparing the recording ability of a novel, electronic emergency documentation system with the AHA paper cardiac arrest record , Emerg. Med. J. 31:833-839 (Abstract) Design of EventDocTM: A Novel, Touch-Interface Documentation System for In-Hospital Emergencies 2015-03 Bala N, Oppenheimer P, Wu T, Ma K, Ehrmantraut RK, Ross BK, (Abstract) Design of EventDocTM: A Novel, Touch-Interface Documentation System for In-Hospital Emergencies , American College of Surgeons' 8th Annual Meeting of the Consortium of ACS-accredited Education Institutes (March 13-14, 2015, Chicago, IL) (Poster) A Tablet-based Informatics Tool for Safe Perioperative Transfer of Care 2017 Wu T, Nair B, Jelacic S, Bowdle A, Lang J. (2017) A Tablet-based Informatics Tool for Safe Perioperative Transfer of Care , UW Medicine Anesthesiology and Pain Medicine Tenth Annual Academic Evening (Poster) A Tablet-based Implementation of Emergency Checklists for Operating Rooms 2019 Wu T, Nair B, Jelacic S, Bowdle A. (2019) A Tablet-based Implementation of Emergency Checklists for Operating Rooms , UW Medicine Anesthesiology and Pain Medicine Twelfth Annual Academic Evening. Building iSeries Applications for WebSphere Advanced Edition 3.5 <https://www.redbooks.ibm.com/redbooks/pdfs/sg245691.pdf> 2001 Maatta B, Blight J, Marasco M, Nelson T, Panigrahi B, Wu J (my former name), Yang V. (2001) Building iSeries Applications for WebSphere Advanced Edition 3.5 (link) , published by IBM Corporation. Additional Information Appendix A: Description of my doctoral dissertation Title: Biclust-Based Identification of Gene Sets from Gene Expression Data through Multivariate Meta-Analysis (MVMA) Abstract: High-throughput technologies have led to production of massive amount of biological data. Much of

the data has been made publicly available but remains under-utilized. The current study aims to uncovering functional gene sets by mining cancer-related public gene expression data. The challenges of using public data include high dimensionality, considerable heterogeneity, and small sample sizes. The technique of biclustering is first employed to identify bicluster patterns from selected datasets. The individual biclusters are then integrated to combine the evidence of the embedded gene sets through multivariate meta-analysis (MVMA). Despite the widespread use of MVMA in clinical data, we show it is impractical to directly apply the traditional MVMA methods, whether based on the Bayesian or the frequentist framework, to analysis of high-dimensional and small sample-size data. To adapt MVMA to public expression data, a number of novel strategies were designed and evaluated, one of them being a sparse estimate of the weighted between-study covariance matrix. With this procedure, we are able to achieve favorable recall and precision in pattern recognition, while maintaining a high efficiency in computation time. The candidate gene sets that are statistically significant are validated using knowledge-based pathway analyses. The developed approach has led to a large number of gene sets uncovered that show promise of functional relevance for various cancer types. Furthermore, a statistic of the gene sets is found to be correlated with the levels of functional relevance, allowing screening of the candidate gene sets prior to the downstream analyses. The study has two key contributions: (1) it adapts the MVMA framework to analysis of high-dimensional and small sample-size public expression data to identify gene sets undergoing transcriptomic changes; (2) It discovers a statistic associated with candidate gene sets that is predictive of the levels of biological relevance. (A manuscript is currently being prepared for publication.)

Appendix B: Praises for my work in programming the Departmental Income Distribution Plan

I've incorporated your work. Thank you very, very much for the quick turnaround. You're a real superstar and please know I regularly sing your praises to senior leadership.

- Craig Brownson (Assoc. Director, Clinical Finance: Dept of Anesthesiology & Pain Medicine and Dept of Surgery, UW School of Medicine)

I agree wholeheartedly. Tim has been a godsend.

- George A. Rooke (medical director of UW Medicine's Pre-Anesthesia Clinic, and a UW professor of Anesthesiology and Pain Medicine)

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