XUEOIN PANG

Relocating to Fort Washington, PA | Do NOT need work authorization sponsorship | 608-628-0319 | xpang3@wisc.edu

PROFILE

Dedicated professional with a M.S. in Computer Science and a Ph.D. in Pharmaceutical Science paired with five years of experience in programming, machine learning, data mining, and computer modeling. Solid knowledge of supervised/unsupervised machine learning, natural language processing, statistical analysis, data storage, and database system structure. Proven successes in solving problems and applying experience and knowledge to tasks.

EDUCATION

UNIVERSITY OF WISCONSIN-MADISON

Ph.D. in Pharmaceutical Science, GPA: 3.9/4.0 Anticipated: May 2017

Thesis: "Fast and Automated: Employing Machine Learning Algorithms to Analyze Neuropeptide Sequence and Structure in Mass Spectrometry"

• 2014 Paul and Kathryn Pisarzewicz Scholarship

M.S. in Computer Science, GPA: 3.8/4.0

Dec. 2016

Relevant Graduate Coursework: Machine Learning, Artificial Intelligence, Database Management, Advanced Database Management, Big Data, Operating Systems, Distributed Systems, Network, Data Structure, Algorithms

2016 officer in the Association for Computing Machinery (SACM) student chapter.

COMPUTER SKILLS

Programming: Python/iPython, SQL, Java, Scala, R, C/C++, MATLAB, HTML, JavaScript

Platform: MySQL, ScikitLearn, Weka, Eclipse, Github, Linux, LaTeXCloud Computing: MapReduce, Hadoop, GraphX, SPARK, Tez, Hive, MLlib, Storm

Modeling/Simulation: Molecular Dynamics, Monte Carlo, Docking, homology modeling, distributed computing

PROJECT EXPERIENCE

Performed Natural Language Processing on Twitter via Unsupervised Learning (M.S.) | 2016

Environment: Java, Scala, JSON, Hadoop, Spark & Storm Data Analytics Stacks

- Deployed Hadoop, Spark and Storm on a self-built virtual machine cluster
- Streamed 5 million tweets and summarized top 10 common words in a high-throughput manner for every 30 seconds
- . Built TF-IDF vectors and clustered with k-means clustering algorithm to identify trending topics in Twitter
- . Identified most popular words and frequency of appearance using GraphX

Created a Simplified Operating System within Systems Development Life Cycle Framework (M.S.) | 2014-2016 Environment: C & C++

- . Built command line interpreter that parses/executes user commands
- . Constructed dynamic memory allocator for user-level processes
- . Created multi-threaded concurrency control via spinlock
- . Developed HTTP based multi-threaded web server with FIFO, SFF, and SFF-BS scheduling policies
- . Built an AFS-like distributed file system with crash recovery

Designed Data Mining Pipeline to Automate Product Matching in Amazon and Wal-Mart (M.S.) | 2016

Environment: Python, SQL, JSON, Natural Language Toolkit, and Scikit-learn

- · Performed natural language processing on product information, transformed and stored in JSON format
- . Made predictions on 200K pairs of unlabeled products based on 20K pairs of labeled product data
- Predicted entity matching with classifiers: decision tree, random forest, logistic regression, SVM, and naïve Bayes
- . Achieved 96% precision and 90% recall by applying ensemble method and heuristic rules

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Predicted Protein Mass Spectrometry Signal-Structure Relationship *via* Supervised Learning (Ph.D.) | 2016

Environment: Java, R, and Weka

- . Crawled, indexed, and unified protein structural data from online protein databank
- . Generated feature vectors from protein structures and calculated protein collision cross-section
- . Predicted protein mobility signal out of reduced structural features via LASSO regression
- . Improved prediction accuracy via support vector regression algorithm

Developed Statistical Analysis Tools for Ion Mobility Measurements (Ph.D.) | 2014-2016

Environment: Java

- . Designed tools to automatically identify target signal distribution from a noisy and wide spectrum
- . Identified structure-mobility relation *via* nonlinear regression
- Modeled dynamic motion of ions and predicted their confirmation distribution
- . Clustered ion structures via K-Nearest Neighbors algorithm and derived their collision cross-section distributions

Diagnosed Lymphatic Diseases from Medical Images by Tree Augmented Naïve Bayes (M.S.) | 2014-2015 Environment: Java

- . Implemented expectation-maximization (EM) algorithm to impute missing data
- . Constructed a Bayes network, mapping symptoms to disease via Chow-Liu algorithm and Prim's algorithm
- . Determined lymphatic disease probability with trained Bayes network of symptoms

Improved Performance of a Medical Database Management System (M.S.) | 2013

Environment: SQL and C++

- . Implemented clock algorithm for buffer management
- . Built file manager for heap files and created B+ tree index to organize medical data
- . Developed front-end utilities for SQL, DDL, and DML

SELECTED PUBLICATIONS

- **Pang, X.**; Jia, C.; Chen, Z.; Li, L. Structural characterization of monomers and oligomers of D-amino acid containing peptides using T-wave ion mobility separations, *Journal of the American Society for Mass Spectrometry*. 2016, in press
- Lietz, C.; Chen, Z.; Son, C.; Pang, X.; Cui, Q.; Li, L. Intrinsic structural preferences of the L7P Neuropeptide Y signal peptide revealed by ion mobility-mass spectrometry, *Analyst*. 2016, 141, 4863
- Pang, X.; Han, K.; Cui., Q. A simple but effective modeling strategy for structural properties of non-heme Fe(II) sites in proteins: Test of force field models and application to proteins in the AlkB family, *Journal of Computational Chemistry*. 2013, 34, 1620 (cover article)
- Pang, X.; Yang, M.; Han, K. Antagonist Binding and Antagonism Induced Conformational Dynamics of GPCR A2AAR, Proteins. 2013, 81, 1399-410

SELECTED CONFERENCE TALKS

- Pang, X. "Structural Characterization of Monomers and Oligomers of D-amino Acid Containing Peptides (DAACPs) Using T-Wave and Nonlinear Ion Mobility Separations" Presented at American Society for Mass Spectrometry National Conference, San Antonio, TX. June 2016
- Pang, X. "Structural analysis of monomeric and dimeric neuropeptide Y (NPY) with IM-MS, MD simulations and HDX-MS"

 Presented at American Society for Mass Spectrometry National Conference, St Louis, MO. June 2015