Meghana Chitale

PhD candidate, Department of Computer Science, Purdue University, USA
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Education

PhD Computer Science
2006 - April 2012 expected, GPA 4.0 / 4.0, Purdue University, West Lafayette, Indiana, USA
MS Computer Science
2006 - 2008, GPA 3.8 / 4.0, Purdue University, West Lafayette, Indiana, USA
Bachelor of Computer Engineering
2000 - 2004, GPA 4.0 / 4.0, Pune University, Pune, India

Visa status Indian citizen on F1 visa (OPT unused)

Qualifications

- Extensive research background in the fields of data mining and computational biology
- Strong analytical skills and expertise in complex software development for bioinformatics
- Developed novel predictive models and algorithms for protein function prediction, analysis of functional ontologies, and missing enzyme prediction for metabolic pathways
- Involved in building and maintaining data analysis tools as well as statistically validating their performance
- Four years' experience in analyzing high throughput proteomics sequence data, biological network data and Gene Ontology based protein annotation data on Linux platform using Java and MySQL
- Two years' experience as a Software Engineer at Persistent Systems Private limited, India, working on data analysis projects in the Life Sciences area

Computer Science Graduate Coursework

- Operating Systems
- Algorithm Design
- Programming Languages
- Scientific Visualization
- Software Engineering
- Compiling and Programming Systems
- Data Mining
- Computational Biology Foundations of Machine Learning

Relevant Statistics Coursework

- Statistical Inference
- Statistical Programming
- Bayesian Applied Decision Theory
- Applied Regression Analysis
- Statistical Quality Control
- Design of Experiments

Work Experience

Graduate Research Assistant, Purdue University, Jun 2008 - Current

- Designed, implemented and analyzed a sequence homology based protein function prediction technique called Extended Similarity Group (ESG) method using Java and MySQL on Linux platform
- Worked on the development and analysis of functional similarity networks based on Protein Function Prediction (PFP) algorithm developed in Kihara Lab of Bioinformatics, Purdue University
- Designed a method to compute associations between pairs of protein function annotation terms in Gene Ontology vocabulary. Further analyzed the applicability of these associations to identify functionally coherent groups of proteins
- Identify missing enzymes in the metabolic pathways based on the functional annotations of neighboring enzymes using SVMs (Support Vector Machines) and Markov Random Fields (In progress)
- Participated in conception of new projects in lab and contributed ideas on existing research group projects
- Actively maintain and improve ESG & PFP protein function prediction web servers
- Managed and mentored more than five undergraduate students by assigning them bioinformatics based projects, delegating project tasks and monitoring their progress and results.

Graduate Teaching Assistant, Department of Computer Science, Purdue University, Aug 2006 - May 2008

- Conducted biweekly recitations for undergraduate 'Software Engineering' course involving student group projects with industrial partners like IBM, Cerner Corporation, HP, Yahoo!, and Caterpillar
- Mentored the students throughout the project development lifecycle and helped them understand the Software Engineering concepts with hands on experience.

Software Engineer, Persistent Systems Private limited, India, Jul 2004 - Jul 2006

- Extract-Transform-Load (ETL) tool development for Cancer Biomedical Information Grid at Washington University in St. Louis. Designed a module that parses gene annotation data from NCBI data sources, and loads the extracted data into a warehouse after converting it into a unified format. (Java and Oracle)
- Software development for the data collected by an instrument called 'ALP 5100 HT Expert' manufactured by Agilent Technologies, Germany. Contributed to the development of the analysis module, which allows users to construct and execute complex analysis rules to segregate the data samples. (C++)

Undergraduate part time intern, Computational Mathematical Laboratory (CML), Tata Institute of Fundamental Research (TIFR), Pune, India, Jul 2003 - Jun 2004

- Developed a specialized architecture for sparse matrix computation with processor-memory inter connections based on the projective geometry patterns (VHDL)
- Implemented a compiler to parallelize the input sparse matrix computations by processing the data flow graphs (C++)

Languages, Tools & Databases

Java, C, C++, SQL, Visual Basic, XML, HTML, VRML, ML, Perl, VHDL, Assembly Language of x86,MS Visual Studio, MS Project, Borland C++ IDE, Eclipse SDK, SAS, R, Cytoscape, MySQL and Oracle

Relevant Journal Publications

- ***Chitale, M.,*** Hawkins, T., Park, C., Kihara, D., ESG: Extended similarity group method for automated protein function prediction, Bioinformatics, 2009.
- Hawkins, T.*, ***Chitale, M.*,*** Kihara, D., Functional enrichment analyses and construction of functional similarity networks with high confidence function prediction by PFP, BMC Bioinformatics, 2010. (* equal contribution)
- ***Chitale, M.***, Palakodety, S., Kihara, D., Quantification of Protein Group Coherence and Pathway Assignment Using Functional Association, BMC Bioinformatics, 2011. (accepted)

Relevant Book Chapters

- ***Chitale, M.,*** Kihara, D., Hawkins, T., Automated prediction of protein function from sequence, A chapter in 'Prediction of Protein Structures, Functions and Interactions', John Wiley & Sons, Ltd, 2008.
- ***Chitale, M.,*** Kihara, D., Computational protein function prediction: framework and challenges. A chapter in 'Protein function prediction for omics era', Springer Verlag, 2011.

Relevant Conference Talks

- ESG: Extended similarity group method for automated protein function prediction. Selected to give 20 minutes talk at Automatic Function Prediction (AFP) meeting at ISMB (Intelligent Systems in Molecular Biology) Conference, Toronto, Canada, July 2008.
- Function Prediction for Systems Level: Functional Coherence of Protein Groups and Identification of Missing Genes. Selected to give 20 minutes talk at AFP at ISMB Conference, Vienna, Austria, July 2011.

Awards

- Bilsland Dissertation Fellowship, Purdue Graduate School (Summer and Fall 2011)
- Infosys gold medal student at Cummins College of Engineering, Pune, India (2004)
- Merit scholarship for 1st rank, Cummins College of Engineering, Pune University, India (2000-2004)