

Sandeep K. Namilikonda

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OBJECTIVE: Seeking an internship/co-op to contribute my expertise in algorithm development and optimization towards developing world-class software solutions to real-world problems.

EDUCATION

- **Ph.D.**, Electrical and Computer Engineering
Michigan State University (MSU), MI
Completion: Dec '08
GPA: **3.75**
- **M.S.**, Computer Science and Engineering
University at Buffalo (UB), NY
Completion: Feb '03
GPA: **3.73**
- **B.Tech.**, Computer Science and Engineering,
Jawaharlal Nehru Technological University, Hyderabad, India
Completion: Jun '01

SELECTED PUBLICATIONS

- **S.K. Namilikonda** and N.R. Mahapatra, "User performance-constrained non-minimal cost-bounded search for high-performance discrete optimization", *in preparation*.
- **S.K. Namilikonda** and N.R. Mahapatra, "Instance-based learning approach to non-minimal cost-bounded search under constrained memory", *in preparation*.
- **S.K. Namilikonda** and N.R. Mahapatra, "Enhancing available-memory cost-bounded iterative-deepening search", *International Conference on Artificial Intelligence (ICAI-2008)*, Las Vegas, NV, Jul. 14-17, 2008.
- **S.K. Namilikonda** and N.R. Mahapatra, "Adaptive branch-and-bound for scalable, high-performance discrete optimization problems in computational biology", *Midwest Computational Structural Biology Workshop*, Augusta, MI, Apr. 30-May 01, 2005.
- **S.K. Namilikonda**, A.V. Sivalenka, and N.R. Mahapatra, "Scalable parallel branch-and-bound for protein structure prediction", *Proc. 2003 SIAM Conference on Computational Science and Engineering (CSE 2003)*, San Diego, CA, Feb. 10-13, 2003.
- N.R. Mahapatra and **S.K. Namilikonda**, "Comparison and analysis of limited-memory branch-and-bound algorithms", *Proc. 2002 IASTED Artificial Intelligence and Applications*, Malaga, Spain, Sep. 9-12, 2002.

PROFESSIONAL AFFILIATIONS AND AWARDS

- Member of Association for Advancement of Artificial intelligence (AAAI)
- Member of Association for Computing Machinery (ACM)
- **Academic Excellence Award**, Phi Beta Delta Chapter at Michigan State University, 2006
- **MSU Graduate School Research Fellowship**, Michigan State University, 2008

RESEARCH PROJECTS (SUBJECT AREA: HEURISTIC SEARCH IN AI, MACHINE LEARNING, CLASSIFICATION)

- A.** Development of a **self-learning framework** for **intelligent cost-bounded search** for solving **discrete optimization** problems under **available-memory** and **user QoS constraints**

Accomplishments:

1. **Developed** a discrete optimization problem modeler that can generate search spaces corresponding to problems of certain user-specified characteristics (e.g., size, branching factor, solution density, etc.)

2. **Designed** and **implemented** a new cost-bounded branch-and-bound heuristic search algorithm that adapts to the **memory available** during the search for optimal solution
 3. **Devised** and **automated** an innovative methodology of procuring knowledge about search space characteristics from already solved problem instances, storing it efficiently, and using it to guide the search on future instances
- B. A datamining** approach to empirical scoring function design to accurately **predict protein-ligand binding affinity**

Contribution:

1. **Suggested, implemented, and tested** a branch-and-bound-based feature subset selection algorithm to obtain optimal feature subset(s) with respect to residual sum of squares metric that improved the binding affinity prediction accuracy by 8%.
2. **Proposed** a hybrid clustering and classification approach for improved affinity prediction through specific scoring functions designed (*regression-based*) for automatically detected categories of protein-ligand complexes (*by clustering*) from the initial training set and applying them to any new test record.

Skills exercised: Problem solving and programming (MATLAB (statistical tool box) and PERL scripts for data preprocessing, automated feature extraction, training and testing scoring functions, C program and **R** statistical tool for feature subset selection)

RELEVANT COURSE WORK

- Design and analysis of sequential and parallel algorithms, algorithmic graph theory, data mining, computer and network security, complexity and computability theory

ACADEMIC PROJECTS

- Master's project: **Comparison and analysis of limited-memory branch-and-bound algorithms** (Presented at IASTED Artificial Intelligence Applications, Spain 2002)
- Senior design project: Developed a **discrete speech-command recognition software** in C and C++ based on back propagation neural network

TECHNICAL SKILLS

- Programming: C, C++, Python, FORTRAN
- Scripting: Perl, PHP
- Databases: MySQL
- Operating Systems: Linux, Solaris, Windows
- Other: HTML, CSS, Matlab, MS-Office, CVS, MPI

RELEVANT WORK EXPERIENCE

- **Software Analyst, Protein Structure Analysis and Design (PSA) Lab, Michigan State University**
Jan 05 – present

C. Development of Rigidity Optimized Conformational Kinetics (ROCK, v3.0) – a software that generates protein conformers by sampling flexible regions of an input protein, modeled as a 3D network of constraints of bonds and bond angles

Contribution:

1. **Analyzed** 12000+ lines of tersely commented FORTRAN code with unintuitive variable names and **documented** explanatory comments.
2. **Added** new constraints necessary to ensure correctness of protein conformers and **tested** and **debugged** the revised software.
3. **Manipulated** an already existing *intermolecular* collision resolution module written in C for another application to suit the *intra-molecular* collision removal in ROCK and then **integrated** the C module with FORTRAN code to facilitate efficient data sharing
4. **Added** a new module to perform protein main-chain termini conformation sampling

Skills exercised: FORTRAN and mixed-language programming, software testing, debugging, reuse and interoperability, documentation (release notes, manual), and version control (CVS)

- D.** Development of version 5.0 of ProFlex – a protein flexibility analysis tool kit with 20000+ lines of code written in C++, FORTRAN, and C

Contribution:

1. **Revamped** user interface in the interactive mode of the software by:
 - (a) consolidating multiple existent filter choices into fewer, more appropriate options
 - (b) handling some special cases of protein input files (for robustness)
 - (c) adding warning and error messages to aid user's understanding of the program run and documenting the messages and the user's choices of filters in logs for reference
2. **Added** new filters for bond inclusion to improve accuracy of flexibility analysis
3. **Identified** and **debugged** errors in output related to hydrogen bonds and **fixed** multiple out-of-bounds memory accesses
4. **Added** a new module that encodes flexibility information such that the protein's flexibility can be visualized in a molecular graphics package called Insight
5. **Debugged** and **revised** a module that outputs flexibility information as a postscript file

Skills exercised: C++ programming, software testing, debugging (exception handling), and documentation (release notes), user-interface design, and version control (CVS)

REFERENCES

- Dr. Leslie A. Kuhn, Professor, Dept. of Computer Science and Engg. and Biochemistry and Molecular Biology, Michigan State University, kuhn@msu.edu, 517-353 8745
- Dr. Nihar R. Mahapatra, Associate Professor, Electrical and Computer Engg. Dept., Michigan State University, nrm@egr.msu.edu, 517-432 4617