

Ravi Vijaya Satya

Contact Info

Address- 114 Long Acre Court Frederick MD 21702
Phone - 321-695-5181(cell)
E-mail- ravi.vijayasatya@gmail.com
Web - <http://www.cs.ucf.edu/~rvijaya>

Research Interests

- Haplotype Inference, block-partitioning and disease association
- Phylogenetics
- Motif Search, Probe Design, Sequence Alignment and other problems in Computational Biology
- Data Compression, Pattern Matching and Compressed Domain Pattern matching

Education

Ph.D. in Computer Science, August 2006

Title – “Algorithms for Haplotype Inference and Block Partitioning”

Advisor – Prof. Amar Mukherjee

University of Central Florida, Orlando, FL, USA

GPA – 3.8/4.0

M.S. in Computer Science, August 2001

University of Central Florida, Orlando, FL, USA

GPA – 3.75/4.0

B.Tech in Electronics and Communications Engineering, August 1999

Jawaharlal Nehru Technological University, Hyderabad, India

GPA – 3.2/4.0

Doctoral Dissertation

Title: “Algorithms for Haplotype Inference and Block Partitioning”

The central theme of the dissertation is the Haplotype Inference (HI) problem. The main focus is on developing efficient combinatorial algorithms for haplotype inference and block partitioning. One of the most important contributions of this dissertation work is the linear-time opph algorithm for perfect phylogeny haplotyping (PPH). Other results include efficient algorithms for near-perfect phylogeny haplotyping (NPPH) and incomplete perfect phylogeny haplotyping (IPPH). All of these algorithms were implemented, and were shown to be faster than existing methods.

Other Research Projects

- Worked on the Genographic Project as a summer intern at IBM Research.
- Research on finding Transcription Factor Binding Sites (TFBS). Developed and implemented a new algorithm for the monad pattern finding problem.
- Developed an automatic annotation tool for MuTAIL PCR sequences in the maize endosperm.
- Developed Codonopt, a codon optimization and motif-engineering tool for designing synthetic DNA vectors in C++, with a GUI developed using MFC
- Compressed domain pattern matching with an offline static dictionary-based LZW algorithm.

Experience

Postdoctoral Fellow

(Aug'06 – Present)
DOD Biotechnology High Performance
Computing Software Applications
Institute (BHSAI)
Ft. Detrick, MD

Research on designing microarray probes for pathogen identification. Development and maintenance of TOFI (Tool for Oligonucleotide Fingerprint Identification), a parallel software tool for designing probes for a given bacterial or viral genome.

Summer Intern

(May '05 – Aug '05)
IBM T.J. Watson Research Centre, NY
Manager: Ajay K. Royyuru

Worked on the Genographic Project (www.nationalgeographic.com/genographic). Worked on comparative analysis of different tree construction programs using publicly available mtDNA data.

Research Assistant

(Aug'02 – Present)
School of EECS, UCF
Advisor: Prof. Amar Mukherjee

Research in the areas of Bioinformatics, Data Compression and Pattern matching

Graduate Assistant

Jan '00 – Aug'03
Institute for Simulation and Training,
Orlando FL 32826
Manager: Dr. Guy A. Schiavone

Research on algorithms for multiprocessor task scheduling. Worked on parallel implementations of some optical systems on a Beowulf cluster using MPI.

Publications in Bioinformatics

Under Review

1. **Ravi Vijaya Satya** and Amar Mukherjee. The Undirected Incomplete Perfect Phylogeny Problem. CS-TR-05-11. Technical Report, December 12, 2005. School of Computer Science, University of Central Florida. Under review by IEEE transactions on Bioinformatics and computational biology.

Refereed Journal Publications

2. **Ravi Vijaya Satya**, Amar Mukherjee, Gabriela Alexe, Laxmi Parida and Gyan Bhanot. Constructing Near-Perfect Phylogenies with Multiple Homoplasy Events. ISMB 2006 (Special issue of *Bioinformatics*), 22 (14), pp e514-522. 2006.
3. **Ravi Vijaya Satya** and Amar Mukherjee. An Optimal Algorithm for Perfect Phylogeny Haplotyping. *Journal of Computational Biology*, 13(4), 897-928. 2006.

Refereed Conference Publications

4. **Ravi Vijaya Satya** and Amar Mukherjee. An Efficient Algorithm for Perfect Phylogeny Haplotyping. *Proceeding of CSB 2005*, Aug 8-11. 2005. Stanford, CA.
5. **Ravi Vijaya Satya** and Amar Mukherjee. New Algorithms for Finding Monad Patterns in DNA Sequences. *Proceedings of SPIRE 2004*, Oct 5-8, 2004 Padova, Italy.
6. **Ravi Vijaya Satya**, Amar Mukherjee and UdayKumar Ranga. A Pattern matching algorithm for codon optimization and CpG-motif engineering in DNA expression vectors. *Proceeding of CSB 2005*, Aug 11-14 2003, Stanford, CA.

Posters

- Gyan Bhanot, Gabriela Alexe, Daniel Platt, **Ravi Vijaya Satya**, Laxmi Parida, Saharon Rosset and Ajay Royyuru. Clustering, Patterns, Trees and Common Origins: An Analysis of Complete mtDNA Sequences. *Recomb 2006*.
- **Ravi Vijaya Satya** and Amar Mukherjee. Pruner: Algorithms for finding monad patterns in DNA sequences. *Proceeding of CSB 2004*, Aug 16-19. 2004. Stanford, CA.

Publications in Other Areas

Journal Publications

7. V. Shaoulov, **R. Vijaya Satya**, G. Schiavone, E. Clarkson, and J. Rolland. Model of Wide-angle Optical Field Propagation Using Scalar Diffraction Theory. *Optical Engineering*, 43(7), 1561-1567. 2004.
8. Donald A. Washburn, Lauriann M. Jones, **Ravi Vijaya Satya**, Clint A. Bowers, and Art Cortes. Olfactory Use in Virtual Environment Training. *Modeling and Simulation*, vol. 2, no. 3, 2003. pp. 19-25.

Conference Publications

9. Tao Tao, Amar Mukherjee and **Ravi Vijaya Satya**. A search-aware JPEG-LS Variation for Compressed Image Retrieval. *International Symposium on Intelligent Multimedia, Video & Speech Processing*. October 20-22, 2004
10. Nan Zhang, Tao Tao, **Ravi Vijaya Satya**, and Amar Mukherjee. Modified LZW algorithm for efficient compressed text retrieval. *International conference on information technology: coding and computing*, Las Vegas, Nevada. 2004.

Book Chapter

11. Amar Mukherjee, Nan Zhang, Tao Tao, **Ravi Vijaya Satya**, and Weifeng Sun. Search and retrieval of compressed text. In *Advances in Computers, Vol. 63*. Edited by Ali R. Hurson, Elsevier Academic Press, 2005.

Grant Proposal

Played a major role in the preparation of the NSF grant proposal titled – “Algorithms for Haplotype Inference and Block Partitioning”. My dissertation work forms the foundation for this proposal.

Teaching

- Participated in designing and organizing a graduate level introductory course in Bioinformatics
- Worked as a teaching assistant for many undergraduate courses.

Professional Organizations

- Member of IEEE & IEEE Computer Society