

Harish Chandran

CONTACT INFORMATION

D 330 Levine Science Research Center
Department of Computer Science
Duke University
Durham, NC 27708 USA

Voice: (919) 724-8205
Fax: (919) 660-6519
email: harish@cs.duke.edu
URL: www.cs.duke.edu/~harish

RESEARCH

Algorithms and Nanoscience

EDUCATION

Duke University, Durham, North Carolina, USA
Doctoral Candidate, Computer Science (expected graduation date: 2012)
Certificate in Nanoscience, Graduate Program in Nanoscience (expected graduation date: 2012)

Anna University, Chennai, Tamil Nadu, India
Bachelor of Engineering, Computer Science and Engineering (May 2007)

HONORS AND AWARDS

Nanoscience Fellowship, Duke University (Aug 2007 - May 2008)
Graduated First Class with Distinction, Anna University (May 2007)

RESEARCH EXPERIENCE

Waran Research Foundation, Chennai, Tamil Nadu India
Research Assistant (July 2005 - July 2007)
Microprocessor Design Automation, Brain Modeling, High Performance Computing, Benchmarking, VLSI Routing

LaBean-Reif Lab, Duke University, Durham, North Carolina USA
Lab Assistant (April 2008 - August 2008)
DNA Nanotech Techniques: DNA Purification, PAGE, Data Analysis

PUBLICATIONS

1. Microprocessor Design Automation: A DNA Based Evolutionary Approach, BICS 06
2. DNA Based Evolutionary Approach for Microprocessor Design Automation, ICANNGA 07
3. MMINi-DASS - Large-scale Brain Circuit Construction and Simulation for Interconnectivity Prediction, Neuroinformatics 08
4. The Tile Complexity of Linear Assemblies, submitted to STOC 09

PROJECTS

Computer Architecture - Dynamic Heterogeneous Core Scheduling

We investigated the benefits of a multicore processor design with cores of varied pipeline depth and frequency. Through intelligent speculative context swapping between cores, concurrent threads could be optimally allocated among the various heterogeneous cores based on their respective likelihood of branch misprediction. To test this, we considered a dynamic analysis method by which we heuristically determined when such swaps should occur. In order to evaluate our design, we compared our simulation results with those achieved by both an equivalent homogeneous multi-core processor and an idealized heterogeneous design using an oracle to make optimal swapping decisions.

Linear Programming - Geometric Duality and Linear Programming

We used geometric duality to convert a set of constraints C to a point set S in the dual space and then apply the idea of approximate point set of S . In particular we studied the following problem: Let for any set of constraints C and an objective function obj , $L(C, obj)$ represent the the maximal value of obj constrained by C . Then, for given set of constraints C with a non null feasible region, a parameter $\epsilon \in (0, 1)$ and any objective function obj is there a sparse set of constraints C' such that $L(C, obj) \leq L(C', obj) \leq (1 + \epsilon)L(C, obj)$.

Nanoscience - Biomolecular Detection using DNA Based Nanoparticle Arrays

Disease diagnosis often requires multiple time-consuming, labor-intensive methods. A quick and simple detection system for multiplexed analysis, using self-assembly of nanoparticle functionalized DNA tiles, was proposed. Two potential approaches to biomolecular detection were examined: SERS assays and a computational DNA tiling system. Spectra of the different systems and enhancements of nanoparticle arrays were determined analytically. It was found that both detection schemes exhibit promise, and further experimental exploration was recommended.

Computational Neuroscience - Project MMINiDASS

The MMINi-DASS aims at predicting the neuronal interconnectivity of various cortices of the human brain. We start out with a random interconnectivity of a cortex and then refine it iteratively based on actual fMRI imaging.

In each iteration, input stimuli are injected as spike trains into few neurons and the overall activity of the cortex is recorded based on the hemodynamic of the neurons. This simulated fMRI is then compared with the actual fMRI obtained for the same input. The difference between the two is reduced by altering the structure using Simulated Annealing.

Benchmarking - Project BENSIM

BENSIM is an effort to create a synthetic benchmark for use on supercomputing clusters. Key metrics determining the goodness of a system: power, performance and scalability, are determined when the cluster runs a synthetic mixture of algorithms created based on inputs from the user from a pre-existing bank of algorithms. A kernel extracts performance and power figures from the cluster-specific simulator based inputs and also calculates scalability by varying cluster size for the same benchmark.

Microprocessor Design Automation - DNA Evo Based Design Automation

This project aimed at developing a methodology to automate the design process of a microprocessor by using a DNA based evolutionary approach. Parameters that are defined a microprocessor are encoded onto DNA sequences which then undergo recombinations with other sequences along with mutations. These offsprings are then decoded into microprocessors and evaluated. Over a period of time a Gene-pool is built up from which processors according to user specifications can be evolved.

VLSI Routing - Channel Routing using PSO

The project aimed at using the methods of Particle Swarm Optimization for solving the channel routing problem in VLSI. Based on the requirements of the PSO algorithm, a set of parameters were identified, which affect the routing decisions. These parameters are used in turn, to develop the fitness functions, which are used to gauge the effectiveness of the solution produced. The project analyzed the results obtained from this algorithm for routing and provided insights that could result in further improvements with respect to algorithm fine tuning and parameters used.

PRESENTATIONS/ TALKS

Programmable Biomolecular Self-Assembly Pathways

Biomolecular Computation Journal Club, Duke University, Feb 2008

Hierarchical Self-assembly of DNA Into Symmetric Supramolecular Polyhedra

Biomolecular Computation Journal Club, Duke University, Oct 2008

Tile Complexity of Linear Assemblies

Biomolecular Computation Journal Club, Duke University, Nov 2008

PROFESSIONAL SERVICES

Organizing Committee

Secretary, Dhi Yantra 07, Workshop on Brain Modeling and Supercomputing, July 2007

COMPUTER SKILLS

Languages: C, C++ and Java(moderate)

Applications: GPLK, L^AT_EX, Photoshop, Dreamweaver, Access and Office Suite

Operating Systems: Linux, Windows 3.1-Vista

WORK EXPERIENCE

AIMS Education, Chennai, Tamil Nadu, India

Content Developer (May 2004 - May 2005)

Created educational content for grades eleven and twelve in forms of quizzes, examinations. Organized a city wide science talent test, attended by sixteen thousand students.

RELEVANT COURSEWORK

Graduate

Advanced Algorithms, Advanced Computer Architecture, Mathematical Methods in System Analysis, Randomized Algorithms, Artificial Intelligence, Linear & Integer Programming, Bio Nanotechnology, Foundations of Nanoscience.

Undergraduate

Algebra, Calculus, Probability and Queuing Theory, Numerical Methods, Discrete Mathematics, Theory of Computing, Compilers, Algorithms, Data Structures, Software Engineering, Object Oriented Analysis and Design, System Software, Computer Graphics, Artificial Intelligence, Operating Systems, Networks, Databases, Computer Architecture, Microprocessors, Digital Electronics, Electronic Circuits, Signal Processing, Physics, Semiconductors and Optoelectronics, Chemistry, Engineering Mechanics and relevant lab work for these.