

# SHRUTII SARDA

Current address: 4410 Oglethorpe St, Apt 211, Hyattsville, Maryland - 20781

Email: shrutiisarda@gmail.com

Phone: +1 513 549 9542

## ACADEMIC QUALIFICATIONS

Since Aug'12      **Ph.D. in Computational Biology @ University of Maryland, College Park**      **CGPA: 3.88/4.0**

- Recipient of the Flagship Fellowship Award: Conferred upon 8-10 exceptional graduate school applicants across all departments of the University of Maryland Flagship campus. It includes an enhancement package of \$40,000 over the base stipend, for the entire duration of the programme.
- Recipient of the Dean's Fellowship Award: Financial award of \$10,000 for the first semester of the programme.

Aug'10–May'12      **M.S. in BioInformatics @ Georgia Institute of Technology, Atlanta**      **CGPA: 3.92/4.0**

- Scored highest grades in Programming for Bioinformatics, Algorithms in Bioinformatics and Computational Biology, Modeling and Dynamics, CS in Bioinformatics, Database Systems, Computational Genomics and Molecular Evolution.

Aug'06–May'10      **B. Tech (Honors) in Biotechnology @ SRM University, India**      **CGPA: 9.34/10.0**

- Graduated with scholarship of Rs. 30000/- for consistent academic excellence. Placed in First class with Distinction.
- Achieved highest grades and topped in Bioinformatics, Biostatistics, Calculus I & II, Programming in C & C++, FORTRAN Programming, and Genetic Engineering amongst others.
- Made it to the **Dean's List** of Toppers at SASTRA University and received scholarship of Rs. 12000/-

## OTHER ACADEMIC AWARDS

- Won the **1<sup>st</sup> place** in **Math Olympiad contest** consecutively during the years 2003-04
- Ranked **1<sup>st</sup>** in a **National Level Hindi Literature Competition** held by "**Hindi Vikaas Kendra**", Chennai in 2004
- Won the "**General Proficiency**" award 5 times during schooling; given to the top three students of a batch every year at Chettinad Vidyashram, Chennai

## PUBLICATIONS AND PRESENTATIONS

- Sarda S, Hannenhalli S (2014) *Next-Generation Sequencing and Epigenomics Research: A Hammer in Search of Nails*. Genomics and Informatics (in press)
- Sarda S, Zeng J, Hunt BG, Yi SV (2012) *The evolution of invertebrate gene body methylation*. Mol Biol Evol 29:1907–1916
- Jordan IK, Conley AB, Antonov IV, Arthur RA, Cook ED, Cooper GP, Jones BL, Knipe KM, Lee KJ, Liu X, Mitchell GJ, Pande PR, Petit RA, Qin S, Rajan VN, Sarda S, Sebastian A, Tang S, Thapliyal R, Varghese NJ, Ye T, Katz LS, Wang X, Rowe L, Frace M, Mayer LW (2011) *Genome sequences for five strains of the emerging pathogen Haemophilus haemolyticus*. J. Bacteriol. 193:5879–5880
- *Conservation and Divergence of Gene-Body Methylation in Invertebrate Genomes*; poster presented at the 8<sup>th</sup> International Conference on Bioinformatics, joint venture of Oak Ridge National Laboratory, Emory and Georgia Tech in Nov 2011
- "*In silico* models of specific drugs against causative agents of Whipple's Disease", presented at the National Conference on Recent trends in Environmental Biotechnology, SRM University in Oct 2009
- "*Use of Bioinformatics tools in Molecular parasitology and its applications in drug designing*", presented at the National Level Technical Symposium on "Emerging Innovations in Biotechnology", at Bharatidasan College of E&T, Trichy
- Won 2<sup>nd</sup> place for a Presentation on the topic: "*Systems Modeling of Cancer*"- organized during a Student Development Program on "*Computational Systems Biology*" at MVIT, Bangalore

## RESEARCH PROJECTS AND INTERNSHIPS

- Currently working as a **GRADUATE RESEARCH ASSISTANT** at UMaryland, College Park      *Jan '13 – present*  
On the **Evolution of Transcriptional Regulation in Diverse Yeast species – Hannenhalli Lab**      *July '13 - present*
- Worked as a **GRADUATE RESEARCH ASSISTANT** at Georgia Institute of Technology      *Aug '10 – May '12*  
On the **Evolution of Developmental GRNs and Genomic Hourglass – Yi Lab**      *Aug '11 – May '12*
  - Testing hypotheses resulting from a computational model that mimics the evolution of developmental GRNs (generated by C. Dovrolis, Professor, CS Dept., Georgia Tech); statistically analyzing the developmental progressions of gene expression data.
- On the **Evolution of Gene-Body Methylation in Diverse Animals - Yi Lab**      *Aug '10 – Dec '11*
  - Deducing correlation between experimentally determined and computationally predicted DNA methylation levels; intra & inter-specific variation of methylation status; relationship between sequence evolution & DNA methylation within species.
- Completed a **summer internship** in R&D at **Dow AgroSciences, Indianapolis**      *May '11 – Aug '11*
  - Performed extensive computational analysis of gene-rich regions in the maize genome for efficient multi-gene construct design.
  - Filed an **IDM (Invention Disclosure Memorandum)** to register novel findings, during the course of research at the company.

- Actively contributed to the **OPEN SOURCE DRUG DISCOVERY** programme - a venture by the **CSIR** (Council of Scientific and Industrial Research) Team India Consortium, by working in the *Mycobacterium tuberculosis* *HRv37* Pathway Annotation division and **created an interactive map of the organism** to be used further for system's analysis.  
**Was awarded the title of "Best Fresh Annotator" for Phase I of the program**
- A final year undergraduate project on the **Comparison of results obtained from in-house Qualitative HIV DNA PCR;**
  - Using 50,100 and 200 µl of blood from new-born babies
  - By employing GAG and ENV primers
- Researched the metabolic pathways of *Tropheryma whipplei*, the causative agent of **Whipple's Disease**, and successfully designed *in silico* molecular simulations of modified inhibitors with improved specificity against primary pathogenic proteins.
- Data analysis of **hypothetical proteins** to aid **construction of a database of those that can act as transporter molecules in Homo sapiens**. (Synthetic constructs are also tagged)
- Acquired hands-on experience in Bioinformatics during internship at Neozene Biosciences Pvt. Ltd., and successfully completed their certificate program in **Molecular Tools and Softwares**

## OTHER CLASS PROJECTS

- A pipeline to analyze the **sequential and spatial distribution** of amino acids around **P-Tyr** to extract distinguishing **signature patterns** in the **3D conformation** of phosphorylated and non-phosphorylated protein sites.
- ChIP-Seq mapping/analysis pipeline:** A tool (Perl based) that takes you from **mapping** short reads to effectively **processing** them and generating wiggle tracks for **viewing** on a browser.
- Wrote a **critical review/synthesis paper** on **Genome fluidity and HGT in the prokaryotic family Pasteurellaceae**.
- Worked on a **computational genomics pipeline** that involved assembly, gene prediction, annotation and comparative genomic studies; developed for analyzing raw genome sequence data of **5 novel strains** of *H. haemolyticus* (**provided by the CDC, Atlanta**)
- Bioinformatics Algorithms:** Coded the **Global and Local Alignment** methods (with anchoring), dynamic motif finding using **Gibb's sampling**, phylogenetic tree building (using **UPGMA, Neighbor joining and maximum parsimony methods**), in addition to a simplified version of the **GeneMark** gene prediction software.
- Developed a **PHP based web application**, for an **Emergency Response Management System**, driven by a **backend created on MySQL**; both modules as a part of a term project.

## LEADERSHIP AND RESPONSIBILITIES

- Served as **Head of Organizing Committee** during the **National level Technical Fest–Aaruush07** hosted by SRM University
- Served as the **Event Manager** of **BIOMODELING** during the **National Conference on Environmental Biotechnology** held at SRM University

## SKILLS AND OTHER INTERESTS

- Programming Languages : PERL, awk, Python, C, VisualBasic, FORTRAN, MATLAB, R (Statistical Computing)
- Scripting and Markup Languages : Shell Scripting (Linux), HTML, PHP
- Database : MySQL, PostgreSQL, NoSQL
- Web User Interface : GMOD (GBrowse)
- Molecular modeling and simulation software : MODELLER9v7, ArgusLab, AUTODOCK4.0, SPDBViewer, Accelrys Discovery Studio 1.5, Cell Designer 4.0, Hex, MATLAB (SysBio)
- NGS and phylogenetic analysis software/packages : TopHat, Cufflinks, JMP Genomics, ERANGE, BWA, MEGA, BLAST+, HMMER, Bioconductor, MrBayes, PhyML, PAUP
- Animation tools in Web Designing : Macromedia Dreamweaver, Flash and ULEAD 3D
- Experience in working with **BiS-Seq, RNA-Seq, Hi-C, DNase-Seq, ChIP-Seq, ChIP-on-Chip** and microarray data.
- Interested in fields that broadly include concepts of **Transcriptional Regulation and Evolution, Epigenomics, Machine Learning, Systems Biology and Next-Generation Sequencing Technology**