

**BIOGRAPHICAL SKETCH**

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2. Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME Srinivasasainagendra, Vinodh		POSITION TITLE Statistician / Software Architect	
eRA COMMONS USER NAME (credential, e.g., agency login)			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
University of Alabama at Birmingham	M.S	07/2004	Computer and Information Sciences
University of Alabama at Birmingham	M.S	05/2003	Electrical Engineering
University of Madras, Chennai, India	B.S	05/1999	Electrical and Electronics Engineering

**A. Personal Statement**

I have close to 8+ years of experience in using information technology as a medium to communicate science, bring innovation and inspire others through outreach activities like mentoring, teaching and training. As a senior technical lead and IT solutions provider, I have architected and choreographed computing development of many scientific projects representing a broad spectrum of subject domains including biomedical science, healthcare, and engineering. My computing experience is highly diverse ranging from scientific computing to application computing to parallel computing using both traditional and modern computing frameworks, tools and programming languages. During my collaboration with the bioscience community, I have lead computing development, released numerous high-quality, and freely-available scientific software's , including but not limited to the **CressExpress** at <http://www.cressexpress.org> , a large scale coexpression analysis engine, **Exome Power Calculator** at <http://exomepower.ssg.uab.edu> , a tool for helping out experimental design and data analysis related to exome sequencing. **HDBSTAT!** at <http://www.ssg.uab.edu/hdbstat/>, a desktop application for microarray data analysis, **CCPMT** , a chip-to-chip probe matching tool for Microarrays. I have had opportunities to reach and connect many crucial components of projects through extended collaboration, innovation during training and exercising various strategies during the lifecycle of project management.

**B. Positions and Honors****Positions and Employment**

2002 - 2004	Programmer, Enabling Technology Lab, University of Alabama at Birmingham, Birmingham, AL
2004 - 2005	Programmer Analyst, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL
2005 - Present	Statistician / Software Architect, Section on Statistical Genetics, University of Alabama at Birmingham, Birmingham, AL

## Honors

- 2011 Recipient of UAB's Back of the Envelope Award to support intellectual creativity at the School of Public Health that can lead to the next generation of intellectual excellence and productivity
- 2010 UAB Employee of the Year, University of Alabama at Birmingham, Birmingham, AL
- 2009 UAB Employee of the Month, November, University of Alabama at Birmingham, Birmingham, AL
- 2007 Travel Award, BioMoby Informatics Workshop/Hackathon , J. Craig Venter Institute , Rockville, MD

## **C. Selected Peer-Reviewed Publications**

1. Trivedi P, Edwards JW, Wang J, Gadbury GL, **Srinivasasainagendra V**, Zakharkin SO, Kim K, Mehta T, Brand JP, Patki A, Page GP, Allison DB. HDBStat!: a platform-independent software suite for statistical analysis of high dimensional biology data. BMC Bioinformatics. 2005 Apr 6;6:86. [PMID: [15813968](#)]
2. Wei H, Persson S, Mehta T, **Srinivasasainagendra V**, Chen L, Page GP, Somerville C, Loraine A. Transcriptional coordination of the metabolic network in Arabidopsis. Plant Physiol. 2006 Oct;142(2):762-74. Epub 2006 Aug 18. [PMID: [16920875](#)]
3. Brand JP, Chen L, Cui X, Bartolucci AA, Page GP, Kim K, Barnes S, **Srinivasasainagendra V**, Beasley MT, Allison DB. An adaptive alpha spending algorithm improves the power of statistical inference in microarray data analysis. Bioinformatics. 2007 Apr 10;1(10):384-9. [PMID: [17597927](#)]
4. Ghanekar R, **Srinivasasainagendra V**, Page GP. Cross-Chip Probe Matching Tool: A Web-Based Tool for Linking Microarray Probes within and across Plant Species. Int J Plant Genomics. 2008;2008:451327. Epub 2008 Oct 21. [PMID: [18949054](#)]
5. **Srinivasasainagendra V**, Page GP, Mehta T, Coulibaly I, Loraine AE. CressExpress: a tool for large-scale mining of expression data from Arabidopsis. Plant Physiol. 2008 Jul;147(3):1004-16. Epub 2008 May 8. [PMID: [18467456](#)]
6. Inusah S, Sormani MP, Cofield SS, Aban IB, Musani SK, **Srinivasasainagendra V**, Cutter GR. Assessing changes in relapse rates in multiple sclerosis. Mult Scler. 2010 Dec;16(12):1414-21. Epub 2010 Sep 1. PMID: 20810517

## **D. Research Support**

### Funded Research

#### **Back of the Envelope (Srinivasasainagendra)**

**01/01/2012 – 12/31/2012**

#### *Research Reproducibility*

Reproducible research is important as a minimum standard, particularly for studies involving diverse collaborative network of knowledge, data and computer code. Although readymade infrastructure for reproducing research is limited, we can still demonstrate successful execution of future research inspections by aggregating some of the best practices of data management, software engineering and collaborative computing. In this effort, a computing toolkit comprising of a collection of workflows, tools and informatics frameworks will be showcased as a possible solution to accept the challenge of reproducible research in the

computer age. A data analysis case study involving information from diverse domains of bioscience - Bioinformatics, Genomics and Biostatistics - will be used to drive the proposed computing solution.

### **Ongoing Research Support (Relevant to the current application)**

#### **R00 RR024163 (Zhi)**

**07/15/2009-5/31/2012**

NCRR

Algorithms for protein structural classification and function prediction - A machine learning methods for protein evolutionary superfamily classification and function prediction by structure.

**Role:** Software Architect

#### **K01 DK080188-02 (Vaughan)**

Scientist Career Development Award (K01) Cluster Based Selection of Candidate Genes in Genome Wide Association Studies.

**Role:** Software Architect / Informatics Collaborator

#### **S10-005**

**06/30/2010-12/31/2011**

DHHS SRI

*Interrogation of Key Genomic Alterations in Glioblastoma Multiforme (GBM) for Identification of Molecular Pathways Critical to GBM Tumorigenesis and Progression*

This project is to profile global gene expression, SNP genotype, and kinase activities in the GBM xenograph lines and compare them with the primary tumors.

**Role:** Computing Team Collaborator

#### **NIH P30DK056336 (Allison)**

**06/01/2000 - 06/30/2012**

UAB NUTRITION OBESITY RESEARCH CENTER

This research center supports all aspects of research on nutrition with an emphasis on obesity.

**Role:** Computing Team Member

### **Completed Research Support (Not an exhaustive list)**

#### **Special ARRA Pilot/Feasibility Grant (Zhi)**

**06/01/2010 – 05/31/2011**

Nutrition & Obesity Research Center, University of Alabama at Birmingham

Differential gene expression of ribosomal proteins and its implication to obesity.

The goal of this pilot grant is to analyze RNA-Seq data for the discovery of aberrant gene expression patterns of ribosomal proteins and their pseudogenes and investigate their implications to obesity.

**Role:** Software Development Lead

#### **NSF 0501890 (Page)**

**09/01/2005 – 08/31/2009**

Functional Genomics of Woody Perennial Flowering

The goals are to discover the important differences and similarities among the factors that regulate flowering in annual and perennial plants. A research project has been developed to determine if the molecular basis of floral bud induction/initiation in response to environmental and physiological factors differs between Arabidopsis and Populus.

**Role:** Software Component Lead / Software Architect

#### **NIH U54CA100949(Barnes)**

**09/09/2003-08/31/2010**

Center for Gene-Nutrient Interaction (CNGI)

This Center will focus on the identification of genetic pathways that may distinguish cancer cells from normal cells, and the extent to which dietary polyphenols with documented chemopreventive activity modulate these pathways.

**Role:** Software Architect / Senior Software Developer

Program Director/Principal Investigator (Last, First, Middle):

**NSF 0217651 (Allison)**

10/01/2002 – 11/07/2006

Plant Genome Research Project

This research will contribute novel statistical techniques to the microarray field that are, in all cases, rigorously validated by either mathematical proofs or computer simulations.

**Role:** Senior Software Developer