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Educational qualification:

PhD	Bioinformatics and Computational Biology	Iowa State University	2012- present date
Master of Science	Biological Sciences	National University of Singapore, Singapore	2006-2009
Bachelor of Technology	Biotechnology	PSG College of Technology, Coimbatore, India	2001-2005

Current Position: Working as a Graduate Research Assistant with Dr. William Beavis at Iowa State University for my PhD dissertation in Bioinformatics and Computational Biology.

Master of Science Thesis Topic - "Dissecting gene regulatory networks in vertebrate development using genomic and proteomic approaches"

Thesis Advisor- Dr. Thomas Lufkin, Genome Institute of Singapore, Singapore

Scholarships:

- Iowa State University BCB Graduate Program (Aug-2012 – July 2013)
- National University of Singapore Research Scholarship (2006-2009)

Research Experience:

January, 2014 – present date: Graduate Research Assistant with Dr. William Beavis, Agronomy & Bioinformatics and Computational Biology Program, Iowa State University

- 1) **Prediction Tools and Selection Methods for Genetic Gain in Simulated SoyNAM Populations (Dissertation):** The project aims to investigate approaches to improve genetic gain by improving genomic prediction models and parent selection methods.
- 2) **Testing Goff's hypothesis to explain heterosis in maize using computational tools:** Goff's hypothesis posits that heterotic hybrids have allelic variants that produce more stable protein isoforms compared to inbreds. Computational verification of Goff's hypothesis involves identification of alternatively spliced variants that are differentially expressed between the heterotic hybrids and inbreds. It also involves computational prediction of protein structure encoded by the identified alternatively spliced variants. We have identified a list of differentially expressed alternatively spliced variants that can be modelled for differential protein stability. However, the lack of good computational tools to estimate change in protein stability due to alternative splicing remains a challenge to take the analysis further.
- 3) Management of SoyNAM database for the use of nine soybean research groups in the Midwest. (Not in operation, since December-2015)
- 4) GFS-Sprague Population Genetics Group website management.

• **August, 2012 – November, 2013: Graduate Research Assistant – Bioinformatics and Computational Biology Program, Iowa State University**

Rotations done during the first year of the graduate program:

- 1) Dr. Jernigan's lab that focuses on Computational Modelling of Protein Dynamics: Worked on a project that aimed to analyze the changes in the dynamics of Fructose Bisphosphate Aldolase (FBA) enzymes as they form functional oligomers. The dynamics of the different oligomers were studied for the enzyme from three different organisms, each of them belonging to a different class of FBA. It was interesting to compare the dynamics for these FBA enzymes which have different structures but same function. Even the mechanism of action of FBA is different in Class 1 and Class2 FBA. The dynamics was modelled by Anisotropy Network Modelling. During my rotation, we were able to define the problem and perform preliminary analysis of the dynamics of FBA from three different classes
- 2) Dr. Eric Henderson that focuses on DNA nano-biotechnology: During this lab rotation, designed and synthesized triangular and circular nanostructures by two different methods. One involving M13 scaffold and the other involving scaples. The structures were viewed under an Atomic Force Microscope (AFM). With this we were able to compare the yield of DNA nanostructures obtained by these two methods.
- 3) Dr. Vasant Honavar group that focuses on applying machine learning methods to biological problems: Worked on a project that compared the performance of two different programs

that implemented two different algorithms (PINALOG and MGK Aligner) for the alignment of Protein-Protein Interaction Networks.

- 4) Dr. Michael Cho's lab that works on Molecular Immunology: Worked on a project to analyse the antibody-ome for studying affinity maturation of antibodies against HIV-1 antigen.
- 5) Lab project with Dr. Ling Li (BCB Lab - Graduate Students organised group for Bioinformatics consulting): The aim of the project was to dissect the network of regulatory genes that work with QQS (an orphan protein) in starch metabolism. For this project, I analysed RNAseq data from Arabidopsis Starch metabolic mutants and found differentially expressed genes using GSNAP, HtSeq-Count and Edge R packages. The analysis was done on lightning3 cluster under the guidance of Dr. Andrew Severin in ISU computing group.

2. Nov-2011 – Jul-2012: Research Technician – Health Sciences Center, Kuwait University

- 1) Worked as a Gene Expression Microarray data analyst in a project that aimed to study biomarkers for various cancers.
- 2) The job also involved performing electrophoresis-on a chip (Agilent Bioanalyser) runs and Affymetrix gene chips for researchers. It also involved creating inventory list and conducting practical workshop for researchers on the use of several analytical instruments available in the facility and assisting in the general management of the facility.

3. 2006- 2009 – Graduate Student, Genome Institute of Singapore / National University of Singapore, Singapore

- 1) **Dissecting gene regulatory networks in cell type specification:** Was involved in a project that aims to study the gene regulatory network involved in the chondrogenic specification pathway in developing mouse embryos by using a combination of transgenic methods, fluorescence activated cell sorting and whole-genome microarray technology.
- 2) **Identification of cis-regulatory elements for *dlx5a/dlx6a* in zebrafish:** Was involved in a project that aims to identify enhancers for the *dlx5a/dlx6a* genes and other developmental control genes using a combination of comparative genomics and *in vivo* transgenic reporter assay in developing zebrafish embryos.
- 3) Worked on a project that aims to generate mouse embryonic stem cell lines expressing epitope tagged transcription factors for Tandem Affinity Purification-Mass Spectrometry (TAP-MS) based proteomic study of protein interaction network for pluripotency.

Publications:

- 1) Xavier, Alencar, Diego Jarquin, Reka Howard, **Vishnu Ramasubramanian**, James E. Specht, George L. Graef, William D. Beavis, *et al.* "Genome-Wide Analysis of Grain Yield Stability and Environmental Interactions in a Multiparental Soybean Population." *G3: Genes/Genomes/Genetics* (2017).

Teaching experience: Have taught introductory laboratory courses in Molecular Genetics and Forensic Science for 5 semesters as a part-time teaching assistant at the National University of Singapore.

Technical skills: Basic molecular biology skills like PCR, Molecular Cloning, etc., Western Blotting, Southern Blotting, Microarrays, Cell Culture, Handling zebrafish embryos & microinjection, Basic Light and Fluorescence Microscopy, Genomic data analysis, Data management.

Computer proficiency:

- 1) Knowledge of Perl, R/Bioconductor, C, Java, Python
- 2) OS- Linux, Windows
- 3) Software: Beadstudio, Genespring, Vector NTi
- 4) SQL-server, HTML/CSS

Relevant Extracurricular activities:

- 1) Member and Ex-Treasurer of Philosophy and Religious Studies Student Organization at Iowa State University from 2013-2016.

Hobbies: Reading books on Popular Science, Philosophy and Psychology. Watching nature, society and universe is another favourite hobby.

Contact information of Referees:

- 1) Dr. William Beavis.
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- 2) Dr. Thomas Lufkin,
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- 3) Dr. V. Ramamurthy,
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- 4) Trish Stauble,
Program Administrator for the Bioinformatics and Computational Biology Program,
Iowa State University,
Ames, Iowa, United States