

ACADEMIC Timeline

Postdoctoral Research Associate:

Nov 2016-Date

Current Research: I am part of four different projects all involving transcriptome analysis using RNA-Seq data.

Project 1: Transcriptome analysis to understand transgressive segregation and dehydration tolerance in rice.

Project 2: Transcriptome analysis to understand Salinity and dehydration tolerance in the cultivated tetraploid *Gossypium* (Cotton) germplasm.

Project 3: Analysis of QTL x QTL interactions to understand drought tolerance in rice.

Project 4: Food Safety: Transcriptome analysis of Shiga toxin-producing *E.Coli* O157:H7 in response to gaseous chlorine dioxide treatment.

Department of Plant and Soil Science, Texas Tech University, Lubbock, TX, USA

PhD: Computational Structural Biology. 2011-16
Thesis submitted: 19th Dec 2016
PhD degree awarded: 27th Jun 2017

Thesis title: "Structural analysis of proteins and their interactions".

Computational Structural Biology Lab, Advanced Technology Development Center, Indian Institute of Technology Kharagpur. (Premiere Institute in India)

M.Tech: Biotechnology and Biochemical Engineering **8.52 CGPA** 2009-11

Project Title: "Structural analysis of antigen-antibody interactions".

EX (Excellent) grade in research project.

Department of Biotechnology, Indian Institute of Technology Kharagpur. (Premiere Institute).

B.Tech: Biotechnology **First class with Distinction (72 %)** 2004-08

Project Title: "Structure based drug design by virtual screening method-Tuberculosis".

Board of Intermediate Education **First division (71.3 %)** 2002-04

Board of Secondary Education **First division (66.3 %)** 2000-01

PUBLICATIONS

- 1) **Karampudi, N. B. R.**, & Bahadur, R. P. (2015). Layers: A molecular surface peeling algorithm and its applications to analyze protein structures. *Nature Scientific Reports*, 5, 16141. <http://doi.org/10.1038/srep16141>.
- 2) Barik, A., Nithin, C., **Karampudi, N. B. R.**, Mukherjee, S., & Bahadur, R. P. (2015). Probing binding hot spots at protein-RNA recognition sites. *Nucleic Acids Research*. <http://doi.org/10.1093/nar/gkv876>.
- 3) **Karampudi, N. B. R.**, & Bahadur, R. P. (2016). Influence of polymorphic conformations of DSS1 on its binding with BRCA2. (Submitted to *Nature Scientific Reports*; Awaiting revision)

- 4) **Karampudi, N.B.R.**, & Bahadur, R.P. (2016). PeBLES: Prediction of B-cell epitope using molecular layers. [arXiv:1611.09648](https://arxiv.org/abs/1611.09648).
- 5) **Three manuscripts under preparation.**

Key Skills

- 1) Algorithm design, development and automation of workflow pipelines.
- 2) Transcriptome (RNA-Seq) analysis and Reference guided de-novo genome assembly.
- 3) Molecular dynamics simulations of biomolecules.
- 4) Machine learning and development of Classifiers/Prediction models.
- 5) Development and deployment Web-applications and Web-servers.
- 6) Working with extremely large datasets.

ACHIEVEMENTS

- ✓ Adaptation of propensity normalization and development of methodology for critical analysis of the transcriptome data (Manuscript under preparation).
- ✓ A novel algorithm named “Layers” (Karampudi & Bahadur, Nature Sci. Rep. 2015, 5, 16141) was developed to understand the protein folding in new perspective besides multiple applications in the structural analysis of proteins.
- ✓ Developed and deployed a webserver (www.csb.iitkgp.ernet.in) and multiple web applications namely “MolLayers” and “HotSPRing” (Barik et al., NAR, 2015).
- ✓ PeBLES: Deep Learning based B-Cell structural epitope prediction model with 89% prediction accuracy.
- ✓ Two Random Forest based classifiers, one of which is to classify and predict the hot-spot residues in protein-RNA interfaces with a prediction accuracy of 80% (Barik et al., NAR, 2015).

TECHNICAL SKILLS

Operating Systems : Linux, Unix and Windows.

Programming :

C, Python: Core, Numpy, PyOpengl, Pandas, PyQt4 and more, Functional and Object oriented programming, Version control using Mercurial/git, Hadoop/Spark.

Machine Learning :

Deep Learning, Support Vector Machines, Random Forests.

Molecular Dynamics simulations : ACEMD, VMD, NAMD, Gromacs, Amber.

Parallelization and scale up : OpenMP/MPI, NVIDIA-CUDA.

Webservers and web applications : **LAMP / LEMP** (Linux, Apache/Nginx, MySQL, PHP / Django) webserver development and deployment in Linux/Unix (**RED-HAT, DEBIAN, BSD**) based Operating Systems. **CSS (cascading style sheets)**

User Interface Development : Python and PyQt.

Graphics (3D) : Blender, PyOpenGL/opengl.

Genome Analysis

:

RNASeq transcriptome analysis, Reference genome based assemblies using Trinity, velvet, oases, barracuda, bowtie2, samtools, gmap and more.

Softwares and Modules

:

Bioedit, ORF (Open Reading Frame) finder, Map Viewer, Genscan, Genemark, Primer3, ProtParam, ProtScale, SignalP, NetOGly, NetNGlyc, NetPhos2.0, Sulphinator, Hyperchem, Arguslab, Spdbv, QSAR, Naccess, Hbplus, Discovery Studio.

Exposure to Wet-lab analytical techniques

My research expertise is in computational analytical techniques, however by the virtue of my undergrad and postgrad studies in Biotechnology major, I have firsthand experience with the following wet-lab tools and techniques.

Microbiological Methods

: Handling and culture of different bacterial and fungal strains, Transformation, Antibiotic sensitivity assay (MIC).

Microscopy

: Bright field, Phase contrast, Confocal, Fluorescence. Worked with Olympus-IMT-2 inverted microscope

Molecular Biology

: Isolation of DNA/RNA, Gel electrophoresis of nucleic acids, Gene Cloning, Construction of cDNA/genomic DNA libraries screening, PCR, RT-PCR.

Protein Methods

: Estimation of proteins and carbohydrates, Native and SDS-PolyAcrylamide Gel Electrophoresis, Precipitation, Purification of proteins using various chromatographic techniques and Enzyme assays, Chromatography and Spectrophotometry.

Animal Cell Culture/Immunology

: Handling and passaging of mammalian cell lines, Raising polyclonal antibodies and their purification by affinity methods, Western blot, ELISA, Fluorescence-activated cell sorter.

Plant tissue culture

: Callus culture, Somatic embryogenesis, Micro-propagation, Production of plant metabolites by Air Lift Bioreactor, their isolation, purification, biochemical characterization by GC-MS and Agrobacterium mediated transformation.

TEACHING AND ADVISING EXPERIENCE

IIT Kharagpur: Contributed in devising course work for the subject Computational Structural Biology.

IIT Kharagpur: Assistant Head Tutor “Computational Structural Biology” course for **two semesters** for a mixed group comprising Undergraduates, postgraduates and PhD scholars.

IIT Kharagpur: Mentored four projects for Undergraduate and Postgraduate students.

The ICFAI University, Jaipur: 6 Months as Faculty Member.

Teaching experience summing up to **14 months** in all, excluding the projects I have mentored for Undergraduate and postgraduate students.

International Conferences

- 1) Karampudi, N.B.R., Das, S.B., Bahadur, R.P. (2017). Influence of polymorphic conformations of DSS1 on its binding with BRCA2. *Springer*; European biophysics journal with biophysics letters, 46, S219-S219.
- 2) Presented a poster titled “Uncovering distinctive spatio-temporal transcriptome signatures across genotypes, stress regimes, and developmental stages in rice: Assumptions and strategies” in PAG 2018 held in San Diego, California, USA.
- 3) Co-authored a poster titled “A case study on novel dehydration stress tolerance mechanism in transgressive recombinant inbred lines of IR29xPokkali: Phenotypic and transcriptomic analysis.” in PAG 2018 held in San Diego, California, USA.
- 4) Co-authored a poster titled “Biological and physiological implications of qDTY_{12.1} and qDTY_{4.1} introgression to basal growth and developmental processes in Rice cultivar IR64 as inferred from transcriptome signatures.” in PAG 2018 held in San Diego, California, USA.
- 5) Co-presented a poster titled “Understanding the molecular basis of transgressive phenotypes in rice. A case study on novel dehydration stress tolerance mechanisms in recombinant inbred lines derived from dehydration-sensitive parents” in PAG 2017 held in San Diego, California, USA.

International Workshops

- 1) Attended “4th workshop on Advanced Techniques for Scientific Programming and Management of Open Source Software Packages”. ICTP, Trieste, Italy.
- 2) Attended “Deal.II Users and Developers Training”, ICTP, Trieste, Italy.

National level Workshops and short-term courses

- 1) Attended short-term course on Machine Learning and Complex Networks, organized by Department of Computer Science and Engineering, IIT Kharagpur, West Bengal.
- 2) Attended workshop on “Applications of Support Vector Machines in Biological science” held at Department of Microbiology, Vidyasagar University, West Bengal.
- 3) Participated in 57th Indian Pharmaceutical Congress.
- 4) Participated in National workshop on “Molecular Techniques” organized by ISTE chapter of DVR & Dr. HS MIC College of Technology.
- 5) Participated in National Seminar on “Recent Trends in Immunology” seminar conducted by ISTE chapter of DVR & Dr. HS MIC College of Technology.
- 6) Participated in National Seminar on “Microbial Biotechnology” seminar conducted by ISTE chapter of DVR & Dr. HS MIC College of Technology.
- 7) Participated in National Conference on “Recent Trends in Pharmaceutical Sciences”.

Awards and Honors

- 1) Recognition received from Texas Tech University for distinguished academic achievement. 2017.
- 2) Received scholarship from Ministry of Human Resource Development (MHRD) of India, for a period of two years during M.Tech. 2009-2011.
- 3) Receiving scholarship from Ministry of Human Resource Development (MHRD) of India for a period of five years during PhD. 2011-2016.
- 4) Two International Workshops fully funded by International Center for Theoretical Physics (ICTP), Trieste, Italy.

PERSONAL INFORMATION

First Name : Naga Bhushana Rao
Last Name : Karampudi
Gender : Male
Marital status : Married
Languages : English, Hindi, Telugu