Sree Krishna CHANUMOLU

Date of Birth: 30th May 1984
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EDUCATIONAL BACKGROUND

Degree	University/Institute	Specialization	Period
B.TECH	Jaypee University of Information Technology, India	Bioinformatics	2002-2006
M.TECH	Jaypee University of Information Technology, India	Biotechnology with specialization in Bioinformatics	2006-2007
PhD	Jaypee University of Information Technology, India	Bioinformatics	2007-2013
Visiting Research Faculty	University of Nebraska at Omaha, USA	Bioinformatics	2013-2014
Asst. Professor	Jaypee University of Information Technology, India	Bioinformatics	2014-2015
Post-Doctoral Research Associate	University of Nebraska-Lincoln	Bioinformatics	2016-Present

Current Projects as Postdoc at University of Nebraska Lincoln:

1. Identifying multi species probiotics (MSPs) and next generation probiotics (NGPs) using novel computational techniques and determining diagnostics markers to segregate pathogens and probiotics. This project involves development of algorithms and computational applications using genomic, proteomic, metabolomic data and Perl/Python programing languages.
2. Applying Bayesian network-based approaches to identify genome-level gene interaction networks also called atlases. Construction of interaction atlases in pancreatic cancer.

Previous Projects:

1. Determination of the role of TGF-β in cleft palate formation.
2. Role of early dietary habits in infant's growth and development using micro-array data analysis of piglets
3. Role of the Simvastatin drug in triggering genes involved in periodontal bone regeneration
4. Identification of missing links in the metabolic network of medicinally important plants to enhance the production of secondary metabolites for their medicinal value (using case study *Picrorhiza kurroa* next generation sequence data)

5. Deciphering the role of simple sequence repeats (SSRs) in the structural and functional plasticity of bacterial pathogens using developed case-specific computational analysis applications.
6. **UniDrugTarget**: a computational application for identification of unique target sites in pathogenic bacteria.

Technical Experience:

- Programming in C, C++, Perl, JAVA, R, Python, Android, and MATLAB, Scripting languages (Server/Client-side languages such as ASP, PHP, CGI-Perl, J2EE, HTML, etc.)
- Development of simulation programs to mimic biological reaction environment
- Development of web/standalone applications and integration with databases
- Machine learning/Computational algorithms/Data mining application development and their implementation to analyze biological data
- Programs development to solve problems in computational biology, genomics and proteomics
- Next generation sequencing and Microarray data analysis
- Genomic, Proteomic, and Biological Network analysis

Courses Studied:

Statistics, Data Mining, Algorithms, Data Structures, Database Management System, Object Oriented Programming, Machine Learning, Scripting Languages, Systems Biology, Biochemistry, Microbiology, Tissue Culture, Genetics, Pharmacogenomics, Developmental Biology, Molecular biology, Drug Designing, Chemoinformatics, Recombinant DNA Technology, Fermentation, Programming Languages (Perl, C, C++, JAVA, MATLAB, Scripting languages), etc.

Conferences Attended:

1. INCOB, International conference of Bioinformatics, New Delhi, 2006
2. International conference on Molecular Medicine, IIT Madras, 2009
3. University of Nebraska Lincoln Plant Science Retreat, Lincoln/Nebraska City, 2018

Honors/Awards:

GATE qualified in Life Sciences, 2007

Best poster award: Won best poster award at International conference on Molecular medicine for the presentation 'Computational Identification of Therapeutic Drug Targets in Bacterial Pathogens' held in IIT Madras, January 2009.

Co-Principle-Investigator (2010-2014) for Bioinformatics section of a DBT funded program support at the Jaypee University of Information Technology.

Principle-Investigator (2014-2015) for Bioinformatics section of a DBT funded program support at the Jaypee University of Information Technology. **Project**:

Identification of intermediate metabolites for linking missing links in the biosynthetic pathways of desired chemical constituents in target plant species.

TEACHING EXPERIENCE AT JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY (8 YEARS)
Lectures:

Systems Biology (2008, 2009: Jan-May)

Scripting Languages for Bioinformatics (2008, 2009, and 2010: July-Dec)

Advanced Algorithms in Bioinformatics (2009, 2010, and 2013: Jan-May)

Bio-Programming (2008-2012: Jan-May)

Linux Programing (2014: July-Dec)

Introduction to Computational Biology (2014: July-Dec,)

Introduction to Biological Databases (2014: July-Dec)

Programming Languages for Bioinformatics (2015: Jan-May)

Next Generation Sequencing (2015: Jan-May)

Practicals:

Computational Biology (2006-2011: July-Dec)

Object Oriented Programming (2007-2008: Jan-May)

Drug Designing Techniques (2007-2009: Jan-May)

Machine Learning for Bioinformatics (2007-2011: Jan-May)

Scripting Languages for Bioinformatics (2008-2010: July-Dec)

Biological databases (2009-2010: Jan-May)

Fundamentals of Algorithms (2008-2009: July-Dec)
Advanced Algorithms in Bioinformatics (2009, 2010, 2013: Jan-May)

Workshops Attended (Resource Person/Judge)

S. No.	Organization	Topic	Dates
1	CSK HPKV,Palampur, (H.P.)	DBT sponsored workshop on Hands-on Training on Role of Computers in Bioinformatics	March, 2007
2	CSK HPKV,Palampur, (H.P.)	DBT sponsored workshop Application of Bioinformatics Tools in Genome Analysis	March, 2008
3	Himachal Pradesh University, Shimla, (H.P.)	Functional and Structural Proteomics : An *In Silico* approach	Oct, 2009
4	Jaypee University of Information Technology, Waknaghat (H.P)	Data Mining for Bioinformatics and its Industrial Applications (DMBIA)	Jan, 2010

5	Himachal Pradesh University, Shimla, (H.P.)	DBT sponsored workshop on Genome analysis: Gene prediction and annotation	Sep, 2011
6	University of Nebraska-Lincoln, Nebraska, USA	Plant Science Retreat	Oct, 2018

PUBLICATIONS:

1. Metabolic pathway analysis and location of drug target sites Marla S, **Chanumolu S**, Sharma R. BIOBYTES. 2009 March

2. **Chanumolu SK**, Rout C, Chauhan RS. UniDrug-target: a computational tool to identify unique drug targets in pathogenic bacteria. PloS one. 2012; 7(3):e32833.

3. Jaiswal V, **Chanumolu SK**, Gupta A, Chauhan RS, Rout C. Jenner-predict server: prediction of protein vaccine candidates (PVCs) in bacteria based on host-pathogen interactions. BMC bioinformatics. 2013; 14:211.

4. Jaiswal V, **Chanumolu SK**, Sharma P, Chauhan RS, Rout C. EpiCombFlu: exploring known influenza epitopes and their combination to design a universal influenza vaccine. Bioinformatics (Oxford, England). 2013; 29(15):1904-7.

5. Chauhan RS, **Chanumolu SK**, Rout C, Shrivastava R. Can mycobacterial genomics generate novel targets as speed-breakers against the race for drug resistance. Current pharmaceutical design. 2014; 20(27):4319-45.

6. Sood A, Jaiswal V, **Chanumolu SK**, Malhotra N, Pal T, Chauhan RS. Mining whole genomes and transcriptomes of Jatropha (Jatropha curcas) and Castor bean (Ricinus communis) for NBS-LRR genes and defense response associated transcription factors. Molecular biology reports. 2014; 41(11):7683-95.

7. Vashisht I, Mishra P, Pal T, **Chanumolu S**, Singh TR, Chauhan RS. Erratum to: Mining NGS transcriptomes for miRNAs and dissecting their role in regulating growth, development, and secondary metabolites production in different organs of a medicinal herb, Picrorhiza kurroa. Planta. 2015; 241(5):1269-70.

8. Vashisht I, Mishra P, Pal T, **Chanumolu S**, Singh TR, Chauhan RS. Mining NGS transcriptomes for miRNAs and dissecting their role in regulating growth, development, and secondary metabolites production in different organs of a medicinal herb, Picrorhiza kurroa. Planta. 2015; 241(5):1255-68.

9. Pal T, Malhotra N, **Chanumolu SK**, Chauhan RS. Next-generation sequencing (NGS) transcriptomes reveal association of multiple genes and pathways contributing to secondary metabolites accumulation in tuberous roots of Aconitum heterophyllum Wall. Planta. 2015; 242(1):239-58.

10. Liu J, **Chanumolu S**, Z K, Albahrani M, Akhtam A, Jia Z, Wang X, Wang D, Otu H, Reinhardt R, Nawshad A. Identification of genes differentially expressed in simvastatin-induced alveolar bone formation JBMR plus. 2018 November 16.

11. Gonzalez-Munoz E, Arboleda-Estudillo Y, **Chanumolu SK**, Otu HH, Cibelli JB. Zebrafish macroH2A variants have distinct embryo localization and function. Sci Rep. 2019 Jun 14;9(1):8632. doi: 10.1038/s41598-019-45058-6.

12. **Chanumolu SK**, Albahrani M, Otu HH. FQStat: a parallel architecture for very high-speed assessment of sequencing quality metrics. BMC Bioinformatics. 2019 Aug 15;20(1):424. doi: 10.1186/s12859-019-3015-y.

CONFERENCE PAPERS:
1. Marla S**, Chanumolu SK**, Khurana S, Singh VK (2006). A Medical Tool for Diagnosis of Viral Diseases**.** Proc. Of second national Conference on Computational Techniques in Engineering, 2006, Sirsa, Haryana, India.

2. Singh VK**, Chanumolu SK**., Marla S (2006). In-silico identification of Regulatory elements of flowering plants. Proc. of second national Conference on Bioinformatics Computing, Feb.19, 2006, CDLU, Sirsa, Haryana, India.

3. **Chanumolu SK**., Sharma RY, Marla S (2006). A Biocircuit to Model Glycolytic pathway in human cancer cells. Bioinformatics, Accepted for publication in International Conference on Biocomputation (INCOB2006), Asia Pacific Bioinformatics Group, New Delhi, Dec., 18-20, 2006**.**

4. **Chanumolu SK**, Rout C, Chauhan RS (2009) Computational Identification of Therapeutic Drug Targets in Bacterial Pathogens. International conference on Molecular medicine, IIT Madras, Chennai (Tamil Nadu), January 19-21,2009.

5 . Pal T**, Chanumolu SK**, Jaiswal V, Chauhan RS (2013). Computational Pipeline for Analysis of NGS Transcriptome Data Sets in Medicinal Herbs. 7th Annual Convention of ABAP & International Conference on Plant Biotechnology, Molecular Medicine & Human Health, University of Delhi South Campus, October 18-20, 2013.

6. Vashisht I, **Chanumolu SK**, Pal T, Mishra P, Singh TR, Chauhan RS (2013) Deciphering the Role of miRNAs in Regulating Growth, Development and Secondary Metabolites Production in an Endangered Medicinal Herb, *Picrorhiza kurroa.*7th Annual

7. Pal T, Jaiswal V, **Chanumolu SK**, Chauhan RS (2014) Computational mining of Aconitum heterophyllum transcriptomes for transcription factors controlling atisine biosynthesis. National Symposium on Advances in Biotechnology for Crop Improvement, Eternal University, Baru Sahib (H.P.), July 12, 2014.