S Venkata Suresh Kumar, PhD

@kumars.sv@gmail.com
℗ 91-9490823072
digibio.blogspot.com

https://www.linkedin.com/in/suresh-kumar-sv-00a602b3

Key words

Data science, Bioinformatics, Genomics, transcriptomics, Disease panels, Business analysis, R/BioC, Team management, Project management

Key skills

EDA, Data modeling, Python workflows, Translational and clinical genomics, RNAseq, Microarray, microRNA array, NGS pipeline, Product management, Team management, Business analysis.

Experience

June, 2016-Nov, 2016	Team Manager, Cognizant Technology Solutions India Pvt Ltd, Mumbai I worked as Team manager and involved analysis proteomic data markers for Alzheimer's disease using data from ADNI and AMPAD. Worked with proteostasis protein-protein networks.
Oct, 2014-June, 2016	Senior Scientist and Consultant, Virtue biologics, Hyderabad I worked as senior scientist and consultant director for a bioinformatics startup based in Hyderabad, Telangana. Microarray and qPCR data analysis pipelines were established. Bioinformatics infrastructure for workshops and academic training were set up. Workshops/ training programs on NGS (WES and RNA-seq) were conducted for PhD/MSc students employing R/bioconductor.
June, 2013-Sep,2014	Scientist II (functional lead), Genome Lifesciences, Chennai, India (Parent company: Genome International Corporation, WI,US) I worked as senior scientist cum functional lead for NGS clinical data analysis services and product development. Responsibilities involved NGS clinical data analysis for international clients, implementation of NGS data analysis pipelines for WES, WGS and RNA-seq, implementation of GATK best practices work flows, clinical annotation and classification of variants
July, 2011-May, 2013	Bioinformatics analyst II, SemanticBits Indiapvt ltd, Hyderabad, AP (Parent company: Semanticbits, Herndon, US) I worked as bioinformatics analyst for Clinical genomicist workstation™, now marketed by PierianDx, US. Responsibilities included bioinformatic analysis and clinical annotation ofhuman genomic variants for comprehensive cancer and EOAD panels using NGS clinical data.Reporting clinically significant variants forsingle, Tumor Vs normal, pedigree and Trios specimens as per HL-7 clinical genomics standards. I am also involved in business analysis of product development including functional requirement collection, documentation, functional testing and test cycle management.

Aug, 2008-June, 2010	Sr. scientist II (bioinformatics), Strand Lifesciencespvt ltd, Bangalore, KA I worked as senior scientist in implementing Affymetrix™ exon and SNP chip data analysis workflows for transcriptomic and genomic studies. I implemented genotyping algorithms, BRLMM, Segmentation algorithms such as GISTIC, CBS in GenespringGXcollaborating with developer team. Research activities involved omics data analysis from multiple cancer studies from GEO and EXPO

Products	Genome explorer™ & IGR™, GLC-GIC, Chennai, India Clinical genomicist work station™ , SB, Hyderabad GenespringGx™, Mass profiler Pro™, SLS, Bangalore

Research experience

2005-2008 1999-2005 1998	Post-doctoral fellow, Cleveland Clinic Foundation, Cleveland, USA PhD, IIT Bombay, Mumbai MSc Project, ICRISAT, Hyderabad, AP

Projects	MicroRNA (miRNA) signaling networks in end stage human heart failure Signaling networks and pathways in end stage transgenic mouse heart failure using microarrays Sequence analysis and phylogenetic studies of GPCRs Laccase purification, identification and characterization from *A.niger* Sequence, structure and phylogenetic analysis of fungal and plant laccases Identification of molecular markers in *C. graminicola*using RAPD, RFLP and AFLP

Publications
- Clinical genomicist workstation, Surampudi S *et al.,* AMIA Summits TranslSci Proc. 2013 Mar 18;2013:156-7
- A unique microRNA profile in end-stage heart failure indicates alterations in specific cardiovascular signalling networks, Venkata Suresh K. Surampudi *et al*., PLOS, 2016 (submitted).
- Isolation of genomic DNA from acetone-dried Aspergillus mycelia, Punekar, N. S., Suresh Kumar S.V., Jayashri, T.N., and R. Anuradha., Fungal Genet. Newsl. 2003, 50:15-16
- Combined sequence and structure analysis of the fungal laccase family, S V Suresh Kumar*et al*, Biotechnology and Bioengineering, 83 (4), 386 – 394

Abstract
- Too "DRY" GPCRs: sequence analysis of GPCRs. LRI annual symposium, 2005

Symposia
- NHLBI's PGA Symposium, "From Genome to Disease II: A Symposium of High Throughput Biology", Natcher Conference Center, National Institutes of Health Bethesda, Maryland, 2005.
- Lerner Research Institute 60th Anniversary Symposium, 2005

Teaching

- Teaching assistant, Bioschool, IITB, Mumbai (PG Course: Computers in Biology I & II, 1999-2000).
- Bioinformatics support, Continuing Education Program workshop (Bioinformatics),IITB, Mumbai(2001)
- Bioinformatics support, Bioinformatics workshop, CDAC, Pune (2001).
- Invited seminar on sequence, structure and functional analysis of proteins and genes, Advanced P G Diploma in bioinformatics, IICT, Hyderabad (2001)
- Guest faculty (bioinformatics), Diploma in Bioinformatics, SSI, Ghatkopar, Mumbai (2004).

Fellowships and academic achievements

- CSIR- JRF and GATE -98
- Dept of Biotechnology (India) Fellowship (96-98), Telugu vignanaparitoshikam (1987-'89)
- University 3rd (MSc, CEEB-Biotechnology)
- State 3rd in Dwiteeya (sanskrit)
- Certificates in USO, APPLA, RRMI, TTD dharma pracharaparishad

Key skills
Bioinformatics:

Expertise in	Sequence analysis, Phylogenetics, Micro array data analysis - (SNP, 3' IVT, Exon and miRNA), NGS data analysis (WES, Cancer exome, RNA-seq), GATK best practice work flow for WES and RNA-seq, Clinical variant db (Clinvar, HGMD, COSMIC), clinical variant classification
Standards	HGVS, VCF, HL7 (CG template, Tier 1 and 2 pipelines)
Tools	Genespring GX™, Vector NTI, Mac Vector 7™, R/Bioc, Gene sifter™, Ingenuity Pathway analysis™, Lucidyx™, Affymetrix genotype console™, IGV, Netaffx™, Samtools, VCFlib, BED tools, SNPeff, ENSEMBL-VEP, Genome explorer™, GATK, PICARD tools, BPIPE and GEMINI.
Disease panels	Comprehensive cancer, lung cancer, EOAD panel
NGS analysis	Targeted panels (cancer), WES, RNA-seq

IT:

OS	Windows, Linux (CentOS, RHEL, Ubuntu), OS X, FreeBSD
DB	Oracle 12g express, MS Access
Office	MS office, iWorks, Open and Libre office
Cloud/cluster	AWS-Starcluster architecture, openlava 2.x
Project management	Informatics SDLC (Argo UML, JIRA, Balsamiq, JIRA-Zephyr, Testlink and JIRA)
Scripting	Bash, Python/biopython
Documentation	RFQ and RFP documentation
Workflows	Snakemake, Bpipe, Shell scripting

Other details

Nationality	Indian
Marital status	Married

Languages	Telugu, Hindi and English

Declaration

I declare that the above information provided is true to the best of my knowledge.

(S V Suresh Kumar)