S Venkata Suresh Kumar, PhD

Chief Bioinformatics Officer, Navipointgenomics India

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|  | https://www.linkedin.com/in/svsk |
| @ kumars.sv@gmail.com  ℗ 91-9490823072 | https://www.github.com/svsuresh  https://ssvbio.github.io/ |

*Key words*

Chief bioinformatics officer, Team Manager, Clinical genomics, Bioinformatics, SDLC, Workflow development, Cardio vascular, Neuro and Onco informatics, Targeted panels, Biotechnology, Microbiome, Senior scientist

*Key skills*

Human, mouse and fungal genomics and transcriptomics, Microbiome analysis, Workflow creation, Business analysis, Product and service delivery, Bioinformatics SDLC, Team management

Products

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

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| R-shiny  apps | COVID-19 status across world (https://suressv.shinyapps.io/covid19\_19042020/) |
| COVID-19 status in India (https://suressv.shinyapps.io/india\_covid\_03052020/) |
| Basic volcano plot (https://suressv.shinyapps.io/expression\_plots/) |
| DNA and Peptide sequence simulator (https://suressv.shinyapps.io/aa\_nt\_seq\_simulation\_31052020/) |

*Industrial experience, post PhD*

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| November,  2019 - | Chief Bioinformatics Officer, Navipointgenomics India Private Limited, Hyderabad, India |
| Sep, 2018 –  Nov, 2019 | Bioinformatics manager, Bioserve Biotechnologies India Private limited (A Reprocell™ company), Hyderabad, India |
| June, 2016- Nov, 2016 | Team Manager, Cognizant Technology Solutions India Pvt Ltd, Mumbai, India |
| Oct, 2014-June, 2016 | Senior Scientist and Consultant, Virtue biologics, Hyderabad, India |
| June, 2013-Sep,2014 | Scientist II (functional lead), Genome Lifesciences, Chennai, India (Parent company: Genome International Corporation, WI, US) |
| July, 2011-May, 2013 | Bioinformatics analyst II, SemanticBits India private limited, Hyderabad, AP, India (Parent company: SemanticBits, Herndon, US) |
| Aug, 2008-June, 2010 | Sr. scientist II (bioinformatics), Strand Lifesciences private limited, Bangalore, KA, India |

Publications

* Parvez MK, Jagirdar RM, Purty RS, **Venkata SK**, Agrawal V, Kumar J and Tiwari N: COVID‑19 pandemic: Understanding the emergence, pathogenesis and containment
* (Review). World Acad Sci J 2: 18, 2020
* A unique microRNA profile in end-stage heart failure indicates alterations in specific cardiovascular signaling networks, Naga Prasad SV, Gupta MK, Duan ZH, **Surampudi VSK**, Liu CG, et al. (2017) A unique microRNA profile in end-stage heart failure indicates alterations in specific cardiovascular signaling networks. PLOS ONE 12(3): e0170456.
* Clinical genomicist workstation, **Surampudi S** *et al.*, AMIA Summits TranslSci Proc. 2013 Mar 18;2013:156-7 (not first author)
* 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

Research experience

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

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| Projects | MicroRNA (miRNA) signaling networks in end stage human heart failure |
| Signaling networks and pathways in end stage heart failure transgenic mouse models, using mouse genomic 3’-IVT 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 |

*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*

* Telugu vignana paritoshikam (1987- ‘89) (AndhraPradesh)
* Dept of Biotechnology (India) Fellowship (96-98) in MSc Biotechnology
* University 3rd (MSc Biotechnology, University of Calicut, Kerala)
* CSIR- JRF and GATE -98 fellowship for lifesciences qualified
* District 1st in Science fair 89, Kalyanadurgam, Anantapur
* District 1st in Science Quiz 89, Hindupur, Andhrapradesh, India
* College 3rd in Vivenkananda memorial Quiz, 1994, Nellore, Andhrapradesh, India
* State 3rd in Dwitiya (Sanskrit)
* Certificates in USO, APPLA, RRMI, TTD dharma prachara parishad

*Key skills*

***Bioinformatics*:**

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| Expertise in | Sequence analysis, Phylogenetics, Micro array data analysis - (SNP, 3’ IVT, Exon and miRNA), NGS data analysis (WGS, WES, Cancer exome/Panels, RNA-seq, Microbiome), GATK best practice workflows, Clinical variant classification, R-Shiny apps |
| Standards | HGVS, VCF, HL7 (CG template, Tier 1 and 2 pipelines), 21CFR 866.5950 |
| Products and tools | GenespringGX™, VectorNTI™, MacVector7™, Genesifter™, Ingenuity Pathway analysis™, Lucidyx™, Affymetrix genotype console*™*, IGV, Netaffx™, Samtools, BCFtools, BEDtools, SNPeff, ENSEMBL-VEP, Genome explorer™, GATK, PICARD tools, GEMINI, CLCbio, Designstudio™ (Globus genomics), Qiime 2, Megan v5, fast-GBS, TASSEL |
| Disease panels | Comprehensive cancer panel, Lung cancer panel, EOAD panel |
| NGS analysis | WGS, WES, Targeted panels, RNA-seq, 16s amplicon sequencing |
| Sequencers | Illumina™ Nextseq 550, Illumina™ HiSeq 2000, Ion-Torrent S5 |

***IT:***

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| OS | Windows, GNU-Linux (CentOS, RHEL, Ubuntu), OS X, FreeBSD |
| DB | Oracle 12g express, MS Access |
| Office | MS office, iWorks, Libre office |
| Cloud | Cloud (AWS) and cluster-based genomics application development |
| Project management | Informatics SDLC (Argo UML, Confluence, Trello, Balsamiq, JIRA-Zephyr, Testlink and JIRA) |
| Scripting/ Language | Bash, R, Python/biopython, AWK, SED, Markup (R, Git, Jekyll) |
| Documentation | RFQ and RFP documentation |
| Workflow management | Snakemake, Bpipe, Shell scripting |
| IDE | R-studio, Jupyter |
| Versioning | GIT |

*Other details*

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| 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)