Vijender Singh PhD

Nationality: UK

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Summary: Bioinformatician with 15 years of experience in conducting and supervising research in academic settings and collaboration with industry partners. Skilled in bioinformatics data analysis of NGS based genomic research methods with strong focus on understanding molecular basis and identifying biomarkers for human pathologies (cancer, cardiac, renal, immune, bone and neural diseases). Collaborated/author on 28 publications and facilitated the successful funding of 15+ research grants. Experience in managing research core facility of a small team with strong focus on customer and stakeholder satisfaction.

Areas of Expertise

BIOINFORMATICS

RNA-seq (mRNA, miRNA, ncRNA)
ChIP-seq, ATACseq analysis
Epigenetics (WGBS, Infinium Arrays)
SingleCell Genomics (RNA, ATAC, CITE)
Genome/ Transcriptome assembly
Biomarker from liquid Biopsies (cfDNA)
Cancer Genomics (WGS, WXS)
Workflow development (Nextflow)

DATA ANALYTICS

Data munging
Exploratory Data Analysis
Data visualisation
Machine Learning
Docker/Singularity
Statistical analysis
Python /R / Linux/SQL
Cluster computing / AWS

MANAGEMENT

Project Management
Genomics project Consultant
Team Leadership/Coordination
Contract Research
Technical Support
Budget Management
Research and Analysis

Professional Experience

Lead Bioinformatics Consultant-CBC
(Oct 2020– Present)
Data Analysis (80%) : Management (20%)

Computational Biology Core,
UConn Health,
University of Connecticut
Storrs, USA

Experience:

- I developed workflows and provided hands-on data analysis of RNA-seq (mRNA, ncRNA, miRNA), ChIP-seq, ATAC-Seq, transcriptome and genome assembly, genome annotation, single-cell transcriptomics, CITE-Seq etc of clinical and non-clinical data

- In collaboration with Boston based startup, SeaLife, I created and managed AWS EC2 instance for genome assembly and variant analysis of shark genomes with Illumina and ONT long reads datasets. The findings were used to build a haplotype reference and a genotyping pipeline.

- During Covid pandemic, I developed the workflow for surveillance and analysis of SARS-CoV-2 virus from clinical and waste-water-treatment samples. This provided state health agencies a measure of the prevalence of different virus variants in the population.

- With members of the team, I lead the evaluation and introduction of commercial (GeneXplain, IPA, Geneious) and open-source bioinformatics solutions that were successfully integrated into the core's analysis workflows.

- I created protocols for the storage, retrieval, and sharing of clinical data that are in accordance with HIPAA regulations. I also developed short and long term data storage guidelines and portals for sharing the data with clients.

- I provided consultancy on experimental design and analysis methodology for grant applications which resulted in 12 successful grant applications translating into 30+ research publications.

- Currently I am redesigning the workflows with containers (Singularity/Docker) that will improve reproducibility, accuracy and runtime. This will also allow workflows to be flexible and can be deployed on any cloud platform.
- I developed a financial strategy to build cash flow to support core's activities by introducing fee-for-service model (https://bioinformatics.uconn.edu/cbc_rates/). During financial year 2022-2023 the core generated a revenue of ~$70,000.

Lead Bioinformatics Scientist
(Oct 2016 – Oct2020)
Data Analysis (90%) : Management (10%)

Computational Biology Core,
UConn Health,
University of Connecticut
Storrs, USA

Experience:

- I developed and implemented robust and scalable workflows for genomics data analysis. I provided hands on data analysis for several genomics projects. This includer RNAseq (mRNA), ChipSeq, biomarker development from liquid-biopsy samples (miRNA) for foot ulcers in diabetic patients, Whole genome bisulphite sequencing (WGBS) to identify epigenetic changes following PTSD, RADseq to understand population diversification in sharks.
- I performed GWAS analysis from LookAHEAD dataset to identify genomic variants associated with both elevated HDL-cholesterol (HDL-C) and myocardial infarction. I was able to identify SNPs in LAG3 gene that is known to associate with cholesterol levels and myocardial infarction.
- I established channels of communication between the core and clients (researchers) that allowed the continuous update on project progress and feedback. (Asana, Slack, google docs). This ensured real time data analysis consultation and support.
- I Managed a high-performance computing cluster (Linux OS) for advanced research analytics. I facilitated the maintenance and update of commonly used databases and software packages. I facilitated the maintenance and update of commonly used databases and software packages.
- Provided expert advice on study design to ensure that projects have sufficient power for downstream analysis.
- As a single member of the core facility, I focused on training researchers and to that end I developed tutorials in RNAseq analysis, ChIP-seq analysis, Genome size estimation, genome assembly, transcriptome assembly.
- I conducted bioinformatics training and data analysis workshops (RNA-seq, ChIP-seq, de-novo transcriptome assembly) for researchers. I also developed short training courses in computational languages (Linux, R, python and SQL) for researchers.
- Along with team members I actively provided bioinformatics support to over 100+ research laboratories across 6 university campuses.

Senior Research Associate (NGS Data Analyst)
May 2011 – Oct 2016

Division of Gene Regulation and Expression
University of Dundee
Dundee UK

Experience:

- In close collaboration with Dr. Wiechens I planned, coordinated and executed project "Understanding the role of chromatin remodeling ATPases SNF2H and SNF2L in nucleosomes positioning adjacent to CTCF and other transcription factors in HeLa cells" (2013-2016).
- I developed novel analysis methods for RNA-seq, ChIP-seq and ATAC-seq and implemented in ongoing projects.
- I initiated collaborations and coordinated research activities with national (Edinburgh University, Dundee University) and international teams (FMI Switzerland, CNRS France). The outcome of these collaborations are published in per reviewed journals.
- Presented research work at EMBO conference series on chromatin and epigenetics. Heidelberg, Germany (2015) and British Yeast Group Meeting 2013, Nottingham, UK (2013)
- Published 5 research articles in peer-reviewed international journals.

- Tutored and evaluated coursework of Bachelors' students (essay & article writing) (2013).
- Deputy Postdoc (research staff) representative with duties to attend the monthly divisional meetings and voice the issues of postdocs and research staff, organise seminars and presentations (2014-2016.

Postdoctoral Research Assistant
May 2007 – May 2011

Division of Gene Regulation and Expression
University of Dundee
Dundee UK

Experience:

- In close collaboration with other team members I managed and executed the research project "Understanding the role of ATP dependent chromatin remodelers in the organisation of chromatin" (2007-2011).
- I successfully developed an in-vivo assay for the functional characterisation of Chd1p a key chromatin remodelling enzyme.
- I developed methodology for in-vivo chemical mapping of nucleosomes that help us understand affects of histone modification on nucleosome positioning and remodelling.
- Published 5 research article in peer-reviewed international journals.
- Presented research work (Poster and Oral) at EMBO conference series on chromatin and epigenetics. Heidelberg, Germany (2011).
- Prepared and delivered lectures on molecular biology, PCR and sequencing methods (2009, 2010).

Education & Training

Certificate:
Supervised Machine Learning: Regression and Classification (Stanford University)
Statistics for Genomic Data Science (John Hopkins University)
Biostatistics for Health Professionals, University of Connecticut, 2018)(Audit).

PhD in Life sciences, Indian Institute of Science (IISc), India, 2007.

Master of Science in Chemistry, Bangalore University, India, 2000.

Bachelor of Science in Life Sciences, Rajasthan University, India, 1997.

'**Introduction to Project Management'** and '**Practical & Effective Project Managemen**t' University. of Dundee (Nov 2013);
Certificate course in '**Principles of Management**' , University of Dundee (Jan 2011);
Certificate course in '**Strategic Management**' , University of Dundee (Jun 2012) .

Grants (as CoPI)

CoPI: Institute for Systems Genomics Seed Grant, Identifying Novel miRNAs to Investigate as Diagnostic Biomarkers in Patients with Statin-Associated Muscle Symptoms. $12,399.81. PI: Amanda Zaleski

CoPI: National Science Foundation – Characterization of a novel, evolutionarily distinct chaperone for centromeric histone H3. PI: Barbara Malone.

CoPI: Research Enhancement Program: Assessing Structural Disorder as a New Key to Unlock Protein-Protein Interaction in Inflammatory Signaling. PI: Brian J. Aneskievich

Co-Mentor: NIH K01 career development Application: "Development of Exosome-Based Biomarkers to aid Treatment of Diabetic Foot Ulcers. PI: Roshanak Sharafieh

Awards and Activities

Best Poster Prize, EMBO Conference Series, Heidelberg, Germany (2011).
Awarded Research Fellowship during PhD from Indian Institute of Science.
Awarded NET-CSIR Junior Research fellowship, CSIR, HRD Ministry, India (1999).

STEMNET Ambassador: Actively participate in school visits to motivate students for STEM subjects (2014-2016).
Lead a team of 6 people at Biotechnology Young Entrepreneurs Scheme, the BBSRC exercise on developing a business plan and competed in B-Yes competition at Edinburgh (2009).
Code Club Coordinator at St. Josephs RC Primary School, Dundee; Organise, plan and manage resources for effective club activities (2014-2016).

Publications

Katrinli S, Smith AK., Drury SS, Covault J, Ford JD, **Singh V,** Reese B, Johnson A, Scranton V, Fall P, Briggs-Gowan M, Grasso DJ. Cumulative stress, PTSD, and emotion dysregulation during pregnancy and epigenetic age acceleration in Hispanic mothers and their newborn infants. *Epigenetics* (Accepted), 2023.

Wang Y, Malik S, Suh HW, Xiao Y, Deng Y, Fan R, Huttner A, Bindra RS, **Singh V**, Saltzman WM, Bahal R. Anti-seed PNAs targeting multiple oncomiRs for brain tumor therapy. Science Advances 2023 Feb 10;9(6)

Blümli S, Wiechens N, Wu MY, **Singh V**, Gierlinski M, Schweikert G, Gilbert N, Naughton C, Sundaramoorthy R, Varghese J, Gourlay R, Soares R, Clark D, Owen-Hughes T. Acute depletion of the ARID1A subunit of SWI/SNF complexes reveals distinct pathways for activation and repression of transcription. *Cell Rep*. 2021 Nov 2;37(5)

Gallagher AJ, Shipley ON, Reese B, Singh V. Complete mitochondrial genome of the Caribbean reef shark, Carcharhinus perezi (Carcharhinformes: Carcharhinidae). Mitochondrial DNA B Resour. 2021 Aug 19;6(9):2662-2664.

Sutter P., Karki S., Crawley I., **Singh V.,** Rowe D., Crocker SJ., Bernt K., Bayarsaihan D., and Guzzo RM. Mesenchyme-specific loss of Dot1L histone methyltransferase leads to skeletal dysplasia phenotype in mice. *Bone* 2021 Jan; 142:115677.

Rahmatpour N, Perera NV, **Singh V.**, Wegrzyn JL, Goffinet B. High gene space divergence contrasts with frozen vegetative architecture in the moss family Funariaceae. *Mol Phylogenet Evol*. 2021 Jan;154

Perry M, Sieberg CB, Young EE, Baumbauer K, **Singh V**, Wong C, Starkweather A. The Potential Role of Preoperative Pain, Catastrophizing, and Differential Gene Expression on Pain Outcomes after Pediatric Spinal Fusion. *Pain Manag Nurs*. 2021 Feb;22(1):44-49.

Knapp EM., Li W., **Singh V**., Sun J. Nuclear receptor Ftz-f1 promotes follicle maturation and ovulation partly via bHLH/PAS transcription factor Sim. *eLife* 2020; 9: e54568

Sharma T, Cotney J, **Singh V**, Sanjay A., Reichenberger EJ., Ueki Y., Maye P. Investigating global gene expression changes in a murine model of cherubism. *Bone*. 2020; 135:115315.

Boshans L., William Wood W., C. Factor C.D., **Singh V**., Jia Lu J., Zhao C., Mandoiu I., Lu R., Cassacia P., Tesar p., Nishiyama A. The chromatin environment around interneuron genes in NG2 cells and their direct reprogramming into GABAergic neuron-like cells. *Frontiers in Neuroscience* 2019; 13: 829.

Sundaramoorthy R, Hughes AL, **Singh V**, Wiechens N, Ryan DP, El-Mkami H,Petoukhov M, Svergun DI, Treutlein B, Quack S, Fischer M, Michaelis J, Böttcher B, Norman DG, Owen-Hughes T. Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. *Elife*. 2017 Mar 23;6.

Hauer MH, Seeber A, **Singh V**, Thierry R, Sack R, Amitai A, Kryzhanovska M, Eglinger J, Holcman D, Owen-Hughes T, Gasser SM. Histone degradation in response to DNA damage enhances chromatin dynamics and recombination rates. *Nat Struct Mol Biol.* 2017 Feb;24(2):99-107.

Dickerson D, Gierliński M, **Singh V**, Kitamura E, Ball G, Tanaka TU, Owen-Hughes T. High resolution imaging reveals heterogeneity in chromatin states between cells that is not inherited through cell division. *BMC Cell Biol*. 2016 Sep 8;17(1):33.

Schurch NJ, Schofield P, Gierliński M, Cole C, Sherstnev A, **Singh V**, Wrobel N, Gharbi K, Simpson GG, Owen-Hughes T, Blaxter M, Barton GJ. How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use? *RNA.* 2016 Jun;22(6):839-51.

Wiechens N*, **Singh V*,** Gkikopoulos T, Schofield P, Rocha S, Owen-Hughes T. The Chromatin Remodelling Enzymes SNF2H and SNF2L Position Nucleosomes adjacent to CTCF and Other Transcription Factors. *PLoS Genet*. 2016 Mar 28;12(3). * equal Contribution.

Gierliński M, Cole C, Schofield P, Schurch NJ, Sherstnev A, **Singh V**, Wrobel N, Gharbi K, Simpson G, Owen-Hughes T, Blaxter M, Barton GJ. Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. *Bioinformatics.* 2015 Nov 15;31(22):3625-30.

Allan J, Fraser RM, Owen-Hughes T, Docherty K, **Singh V**. A comparison of in vitro nucleosome positioning mapped with chicken, frog and a variety of yeast core histones. **J Mol Biol.** 2013 Nov 15;425(22):4206-22.

Singh V, Owen-Hughes T. Evolutionary insights into genome-wide nucleosome positioning. *Genome Biol*. 2012;13(9):170.

De Cian A, Praly E, Ding F, **Singh V**, Lavelle C, Le Cam E, Croquette V, Piétrement O, Bensimon D. ATP-independent cooperative binding of yeast Isw1a to bare and nucleosomal DNA. *PLoS One*. 2012;7(2):e31845.

Sen M, Shah B, Rakshit S, **Singh V**, Padmanabhan B, Ponnusamy M, Pari K, Vishwakarma R, Nandi D, Sadhale PP. UDP-glucose 4, 6-dehydratase activity plays an important role in maintaining cell wall integrity and virulence of Candida albicans. *PLoS Pathog*. 2011 Nov;7(11):

Gkikopoulos T, Schofield P, **Singh V**, Pinskaya M, Mellor J, Smolle M, Workman JL, Barton GJ, Owen-Hughes T. A role for Snf2-related nucleosome-spacing enzymes in genome-wide nucleosome organization. *Science*. 2011 Sep 23;333(6050):1758-60.

Ryan DP, Sundaramoorthy R, Martin D, **Singh V**, Owen-Hughes T. The DNA-binding domain of the Chd1 chromatin-remodelling enzyme contains SANT and SLIDE domains. *EMBO J.* 2011 May 27;30(13):2596-609.

Gkikopoulos T, **Singh V**, Tsui K, Awad S, Renshaw MJ, Scholfield P, Barton GJ, Nislow C, Tanaka TU, Owen-Hughes T. The SWI/SNF complex acts to constrain distribution of the centromeric histone variant Cse4. *EMBO J.* 2011 May 18;30(10):1919-27.

Bowman A, Ward R, Wiechens N, **Singh V**, El-Mkami H, Norman DG, Owen-Hughes T. The histone chaperones Nap1 and Vps75 bind histones H3 and H4 in a tetrameric conformation. *Mol Cell.* 2011 Feb 18;41(4):398-408.

Singh V, Satheesh SV, Raghavendra ML, Sadhale PP. The key enzyme in galactose metabolism, UDP-galactose-4-epimerase, affects cell-wall integrity and morphology in Candida albicans even in the absence of galactose. *Fungal Genet Biol*. 2007 Jun;44(6):563-74.

Singh V, Sinha I, Sadhale PP. Global analysis of altered gene expression during morphogenesis of Candida albicans in vitro. *Biochem Biophys Res Commun*. 2005 Sep 9;334(4):1149-58.

Singh SR, Rekha N, Pillai B, **Singh V**, Naorem A, Sampath V, Srinivasan N, Sadhale PP. Domainal organization of the lower eukaryotic homologs of the yeast RNA polymerase II core subunit Rpb7 reflects functional conservation. *Nucleic Acids Res. 2004* Jan 2;32(1):201.

Teaching & Training experience

Virtual Workshops
Instructor, RNA-Seq workshop (Model)	2016-2023
Instructor, RNA-Seq workshop Non-Model	2016-2023
Instructor, Variant Detection	2020-2023
Instructor, HPC-Linux intro workshop	2016-2023
Instructor, RAD-Seq Workshop	2020-2023
Instructor, Genome Assembly Workshop	2020-2023
Instructor, Genome Annotation Workshop	2020-2023
Instructor, Somatic Mutation detection in Cancer	2020-2023
Instructor, Single Cell Transcriptomics	2021-2023
Instructor, Single Cell CITE-Seq	2022-2023
Instructor, Structural Variants detection	2022-2023

UConn, Storrs, CT
Instructor, R - From basics to advance analytics	2019-2023
Guest Lecture, Bioinformatics of Pathway and Network Analysis (ANSC5619)	2016-2018
Guest Lecture, High performance computing in Bioinformatics (MCB 5430)	2018-2022

University of Dundee
Guest Lecture, Molecular Biology Techniques	2009, 2010
Co-Instructor, Proteomics and Transcriptomics Data interpretation	2013, 2014
Co-Instructor, Software Carpentry Bootcamp	2013

Indian Institute of Science, India
Instructor, Application of PCR and RT-PCR in clinical Diagnosis (Sir Dorabji Tata Centre for research in Tropical Diseases.)	2003
Instructor, Hands on Microarray Workshop and Data analysis,	2002