SHASHANK PRAKASH KATIYAR

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I recently moved to Los Angeles, California, and obtained a work permit (EAD card on J2 visa type), after working as a Global Scientific Consultant and **Senior Research Scientist** in Eone Diagnomics Genome Center (EDGC), South Korea. I joined EDGC in 2017 after completing my Ph.D. from the Indian Institute of Technology, Delhi. Being a startup Korean healthcare company, there was ample exposure to cutting-edge technologies. Grasping the opportunities at EDGC, I got involved in the planning and development of (bioinformatics aspects) Next-Generation Sequencing (NGS) and liquid biopsy projects of the R&D department. My job profile at EDGC involved the development of pipelines (WGS, WES, targeted panels), data analysis, development of algorithms & tools, maintenance of the code, and guidance to newcomers. Over three years at EDGC, I have acquired skills that are essential for both the precise planning as well execution of the projects and have gained experience to work under strict deadlines with an ever-changing work environment and teamwork.

I would like to emphasize some of the major highlights of my work experiences here.

•I was involved in the development of custom targeted panels for the liquid biopsy monitoring service, in which I designed and developed a patient-specific SNV marker selection algorithm, primer identification algorithm for the target markers, and pipeline to analyze patient-specific custom targeted panel data.

•A more recent and major EDGC project was to develop cancer detection panels of various cancer types using machine learning algorithms on the NGS-based epigenetic data. I was tasked with the design and development of the NGS-based epigenetic data analysis, statistical modeling to identify the cancer-specific markers, and implementation of machine learning algorithms to identify cancer patient samples.

•An important requirement for an R&D team of a company is to have independent in-house tools. I have experience in developing NGS analysis-related in-house tools such as sequence data preprocessing, PCR duplicate removal and error correction, in-house variant caller, variant annotator, and SNV classifier, etc.

•I also have extensive experience in writing research articles, gained during routine project-related white paper production as well as a part of my Ph.D. training.

I have the experience to adapt and survive well in diverse cultural backgrounds, gained during doctoral degree from India, training in Japan, and as the Research Scientist position in South Korea. I am very well exposed to both the academic and corporate environment, where the corporate environment taught me to think, implement and deliver high-quality results in a fast-paced environment. Also, having been involved in various collaborative projects during my doctoral and job career, I understand the importance and dynamics of teamwork.

Yours Sincerely,

Shashank Prakash Katiyar, Ph.D.

PROFESSIONAL SUMMARY

- **More than three and half years of working experience as a Senior Research Scientist (Bioinformatics)** in *Next-generation sequencing (NGS)* technology:
  - *WGS*, *WES*, *targeted panel*, and *methylation-related* pipeline design, development, implementation, and maintenance.
  - *Variant calling*, *copy number variation*, and various sequencing-related downstream and statistical data analysis.
  - Bioinformatics algorithms and computational analytics tools development.
  - Successful implementation of statistical analysis and machine learning algorithms for the completion of projects.
  - Experienced with bioinformatics databases and tools.
  - Proven coding expertise in *Python, Perl,* and shell scripting, for bioinformatics analysis.
- **Ph.D.:** Experience in *computational drug discovery*, *proteins structures prediction*, and *molecular dynamics simulation*.
- **Motivated and goal-oriented:** Demonstrated abilities to work in fast-paced, dynamic, and collaborative projects. Ability to complete the objectives, write and publish the findings.
- **A skilled communicator and active listener:** Successful completion of projects **in collaboration** with various *national* and *international* research groups.
- **A published writer and skilled presenter:** Published the research work in **more than 10** *peer-reviewed international journals* and **orally presented** work in *International conferences*.

SKILLS AND EXPERTISE

OS, Programming, and Tools	*Sequence/Data analysis Tools*
- Python, Shell, Perl - Linux/UNIX, Windows OS, Linux based server - Google and AWS cloud - Git and GitHub for code management - Asana for project and work management	- Self-developed sequenced read pre-preprocessing tool - BWA sequence alignment tool - UMI-tools and self-developed PCR duplicate removal (error correction) tool - Variant-callers; GATK, VarDict, Strelka, and in house developed tool - Variant annotator and classifiers - Primer identification; primer3, primer-blast, ThermonucleotideBLAST - Differential expression analysis: DESeq2, combat and statistical modeling - Other tools: FastQC, Cutadapt, BBMap, Samtools, sambamba, bedtools

EXPERIENCE

1. ***Global scientific consultant (Eone Diagnomics Genome Center, South Korea; R&D Bioinformatics Team) (May 2021 – August 2021)***
   - Consultancy for epigentitic analysis related projects (breast, lung, and colon cancer).
   - Article writting

2. ***Senior research scientist (Eone Diagnomics Genome Center, South Korea; R&D Bioinformatics Team) (August 2017 – April 2021)***

- **Contributed to the development of *methylation*-based multi-cancer screening panel using liquid biopsy *(in process for Korean Food and Drug Administration (KFDA) approval)*** :
  - Designed the algorithm, developed methods, tools, and the pipeline for the identification of *methylation cancer markers* for a panel that uses *restriction enzyme digestion and NGS technologies*.
  - Used *python* for the pipeline development, tool development, and statistical analysis.
  - Used *statistical methods* for identifying *differentially methylated markers* and *machine learning* algorithms for the *classification* of the samples.

- **Contributed to the development of *SNP based* cancer screening and monitoring service using liquid biopsy:**
  o Developed methods, tools, and pipeline for the *screening of the somatic mutation* cancer markers
  o Identification of *primers for the patient-specific targeted panel* for the screened cancer markers
  o Developed a pipeline for the *monitoring* of the patient, using the screened cancer markers.

- **NGS related methods and tools development:**
  o Developed WGS and WES somatic variant calling pipeline.
  o Copy number variations calling using WGS pipeline.
- Developed tools to *pre-process fastq*, *PCR duplicate removal* & *error correction*, and various *add-ons* for bioinformatics related works.
- Produced, enhanced, corrected, and maintained the *documentation*, *results, white papers, and research articles*.

3. ***Ph.D. and Senior Research Fellow** (Indian Institute of Technology Delhi, India) (2011 - 2017):*
- **Accomplishments:**
  o Successfully revealed and resolved the molecular mechanism of small molecules of interest, using computational methods.
  o Studied the permeability of withanolides using Molecular Dynamics Simulations.
  o Successful identification of an active anti-leishmanial natural compound.
  o Independent development of scripts in *Perl/Python* and standalone *GUI software in JAVA* to simplify the complex steps of Molecular dynamics simulations using AMBER software; scripts and software were adequately *documented* and made available to the public.
  o Achieved Ph.D. objectives within the proposed timeline.
- **Experience gained:**
  o Development of *pipeline*, *automated scripts (Perl/Python)*, and *parallelization* (SSH, MPI, NFS & ROCKs Linux) for *sequence analysis*, *modeling of biological molecules*, and studying the dynamics using *computer simulations*.
  o Development of GUI software in JAVA and scripts in Perl/Python.
  o Experience in Perl, Python, SSH, HPC, storage maintenance, database, and web servers.
  o Fundamentals and applications of statistics in biology and real life.
  o Team leadership and management during the completion of lab projects with colleagues as a team.
  o Communication and execution of projects with other research groups in collaboration.
  o International exposure with foreign work style, ethics, and cultures.

EDUCATION

Degree	Field	Institution	Year
Ph.D.	Computational Biology	Indian Institute of Technology Delhi, India	July 2012-April 2017
Post M.Sc Diploma	Molecular Diagnostics	Alagappa University, Tamil Nadu, India	July 2010-June 2011
M.Sc.	Bioinformatics	Pondicherry University, Pondicherry, India	July 2008-June 2010
B.Sc.	Biology & Chemistry	MJP Rohilkhand University, UP, India	July 2004-June 2007

OTHER HIGHLIGHTS

o Presented work as poster publications in international conferences.
o Oral presentations in *international conferences* and international seminar series (DAILAB-CAFE PLUS).
o Selected as one of the few participants among Asian countries for *one week workshop (AIST International Imaging Workshop)* in the *National Institute of Advanced Industrial Science and Technology (AIST), Japan.*

o   Awarded *three months of training* in *AIST, Japan* under the DAILAB-STAR program.

PUBLICATIONS

Next generation sequencing related

1) *Machine learning assisted Breast cancer detection from genome-wide hypomethylation analysis of SacII digested ctDNA.* **Under preparation to be submitted at Genome Research.**

2) *DeepClean: Correcting sequencing errors using Unique Molecular Barcode based deduplication method.* **(Abstract #PgmNr 1667). Presented at the Annual Meeting of The American Society of Human Genetics, 2019, Houston, USA.**

3) *Noninvasive Prenatal Testing for Fetal Chromosomal Abnormalities Using Massively Parallel Sequencing: Clinical Experience from 7910 Korean Pregnancies.* **Scientific Research Publishing (2018)**

Published Peer-reviewed scientific articles (14 Publications: *Google Scholar*):

1) *Molecular dynamics simulations and experimental studies reveal differential permeability of withaferin-A and withanone across the model cell membrane.* **Scientific Reports (2021)**

2) *Wild type p53 function in p53 Y220C mutant harboring cells by treatment with Ashwagandha derived anticancer withanolides: bioinformatics and experimental evidence.* **Journal of Experimental & Clinical Cancer Research (2019)**

3) *2, 3-Dihydro-3β-methoxy Withaferin-A Lacks Anti-Metastasis Potency: Bioinformatics and Experimental Evidences.* **Scientific Reports (2019)**

4) *Withaferin-A kills cancer cells with and without telomerase: Chemical, computational and experimental evidences.* **Cancer Death & Disease (2017)**

5) *Mixed inhibition of cPEPCK by genistein using an extended binding site located adjacent to its catalytic cleft.* **PLoS One (2015)**

6) *Computational structure-based de novo design of hypothetical inhibitors against the anti-Inflammatory target COX-2.* **PLoS One (2015)**

7) *Targeting mortalin by Embelin causes activation of tumor suppressor p53 and deactivation of metastatic signaling in human breast cancer cells.* **PLoS One (2015)**

8) *Probing molecular mechanism of hypericin-induced parasitic death: an insight into role of spermidine beyond redox metabolism of Leishmania.* **Antimicrobial Agents and Chemotherapy (2014)**

9) *Withanone-rich combination of Ashwagandha withanolides restricts metastasis and angiogenesis through hnRNP-K.* **Molecular Cancer Therapeutics (2014)**

10) *Molecular interactions of Bcl-2 and Bcl-xL with mortalin: identification and functional characterization.* **Bioscience Reports (2013)**

11) *Blocking Protein Kinase C signaling pathway: mechanistic insights into the anti-leishmanial activity of prospective herbal drugs from Withania somnifera.* **BMC Genomics (2012)**

12) *Mechanistic insights into the dual inhibition strategy for checking Leishmaniasis.* **J. Biomolecular Structure and Dynamics (2012)**

13) *A Leishmaniasis study: structure-based screening and molecular dynamics mechanistic analysis for discovering potent inhibitors of spermidine synthase.* **Biochimica et Biophysica Acta - BBA: Proteins and Proteomics (2012)**

14) *Role of aromatic stack pairing at the catalytic site of gelonin protein.* **Biochem Biophys Res Commun (2011)**

Book Chapters

1) Computational methods to understand the anti-cancer mechanism of withanolides. Invited chapter for *Springer* book on "Science of Ashwagandha: Preventive and Therapeutic Potentials" **(2017)**

REFERENCES

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