Avinash R

MPhil, Bioinformatics

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Summary

Enthusiastic Bioinformatician eager to contribute to team success through hard work, attention to details and 5+ Years of Industrial Experience in Genomics research. Motivated to learn, grow and excel in Science. Actively looking for a suitable position to contribute my knowledge of Bioinformatics in research.

Work History

- ✓ **QA Engineer (Bioinformatics)**, **November 2021 to February 2023**
  Pieriandx/Velsera Pvt, Ltd., Pune, Maharashtra, India

  - Review technical design documents, requirements documents, and specifications to provide timely and insightful feedback.

  - Assess requirements in collaboration with teams (such as SMEs, developers and product managers).

  - Create detailed, comprehensive, and well-structured test plans and test cases.

  - Estimate, prioritize, plan, and coordinate testing activities.

  - Design and execute automation scripts using open-source tools.

  - Identify, record, document thoroughly and track bugs.

  - Perform thorough regression testing when bugs are resolved.

  - Investigate the causes of non-conforming software and train users to implement solutions.

  - Track quality assurance metrics, like defect densities and open defect counts.

  - Develop and apply testing processes for new and existing products to meet client needs.

  - Create QSI and SDLC documents and getting them reviewed by peers and QMS.

- ✓ **<u>Senior Scientific Analyst</u>, July 2020 to May 2021**

  Genotypic Technologies Pvt, Ltd., Bengaluru, Karnataka, India

  - Analyzing Next Generation Sequencing Data of Transcriptome, miRNA, Degradome, Metagenomics, Whole Genome and Methyl-Seq.

  - Exploring new tools and improving analysis pipelines for breaking down and analyzing complex data.

  - Evaluated potential subject participants to assess suitability for planned studies.

  - Collaborated with Scientist to identify relevant.

- ✓ **<u>Junior Scientific Analyst</u>, January 2019 to June 2020**

  Genotypic Technologies Pvt, Ltd., Bengaluru, Karnataka, India

  - Analyzed Next Generation Sequencing Data of Transcriptome, miRNA, Degradome and Metagenomics.

  - Built and improved analysis pipelines for breaking down and analyzing complex data.

  - Worked with Linux, Perl and R to manage project requirements.

  - Performed statistical, qualitative, and quantitative analysis.

- ✓ **<u>Bioinformatics Analyst</u>, October 2017 to December 2018**

  Arraygen Technologies Pvt. Ltd., Pune, Maharashtra, India

  - Taught NGS data Analysis to the clients on information compiled from public resources and research materials.

  - Handled projects on Transcriptome, small RNA, Metagenomics and R for the Clients.

Publication

Deshpande SS, Nemani H, Arumugam G, **Ravichandran A**, Balasinor NH. High-fat diet-induced and genetically inherited obesity differentially alters DNA methylation profile in the germline of adult male rats. Clin Epigenetics. 2020 Nov 19;12(1):179. doi: 10.1186/s13148-020-00974-7. PMID: 33213487; PMCID: PMC7678167.

Education

- ✓ **Masters in Philosophy Bioinformatics - August 2017**
  Department Of Bioinformatics, Alagappa University, Karaikudi

  - Thesis: **Discovery of potent inhibitors of Dengue Envelope protein through E-Pharmacophore Screening and Drug Repurposing Approach**

  - Graduated with 7.66 CGPA

- ✓ **Master of Science Bioinformatics - August 2013**
  Centre For Bioinformatics, Pondicherry University, Puducherry

  - Thesis: **Molecular Evolutionary study of KISS1 in Mammals**

  - Graduated with 5.8 CGPA

- ✓ **Bachelor of Science Bioinformatics - April 2011**
  Achariya Arts and Science College, Puducherry

  - Graduated with 67.3%

- ✓ **Higher Secondary - April 2008**
  Vaillankani Matric. Higher Secondary School, Puducherry

  - With 53.5%

- ✓ **High School / SSLC -March 2006**
  Govt. High School, Thattanchavady, Puducherry

  - With 65.8%

Areas of Interest

- Next Generation Sequencing Analysis

Practical Experiences

- Drug designing

- Next Generation Sequence Analysis – RNA-Seq, miRNA-Seq, Methyl-Seq, Chip-Seq, Metagenomics, Microarray, WGS.

Software and Tools

- Phylogenetic Tools: MEGA, CLUSTALW, Philip.

- Databases: UCSC Genome Broswer, NCBI, Uniprot, KEGG, JGI

- NGS:

    - RNA-Seq: FastQC, Cutadapt, Bowtie, Cufflinks, Samtools, Tophat, HISAT2, String Tie, Aspli, Astalavista, BWA, DESeq

    - Methyl-Seq: Homer, bismark, Methylkit

    - Chip-Seq: Chipseeker.

    - Metagenomics: Qiime , Centrifuge, Blast+

    - MicroArray: Affy, DAVID, G:Profiler

    - WGS: MaSurca, Spades, MiniMap, BWA

- Docker

- AWS

Programming Languages

- Perl
- R
- Python

Skills

- R and Perl proficiency
- Python scripting
- Shell scripting
- Linux expertise
- MS Office

- Code troubleshooting
- Data collection and analysis
- Software and system modification
- Communications
- Work independently

Declaration

I hereby declare that the above information is correct to the best of my knowledge.

Avinash R