Ashok R. Dinasarapu

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SUMMARY

Highly motivated bioinformatics scientist with background in computing & biology, and currently responsible for

- Pre-process, analyze, and interpretation of high volumes of Next Generation Sequencing (**NGS**) and **Mass-Spectrometry** (MS) data
- Communicate findings to internal departments and key stakeholders
- Development and validation of bioinformatics pipelines with real-world samples
- Technical assistance to other scientists in the group
- Face-to-face customer interaction (pre-consultation meetings)

TECHNICAL SKILLS

Computing
- Proficiency in R, Python, Perl, Java and UNIX/Linux (Shell scripting)
- Experience with high-performance Linux clusters and Cloud computing

Bioinformatics
- NGS de-multiplexing, pre-/post-mapping quality control analysis
- Genome/transcriptome mapping and assembly
- **WGS/WES**: Variant calling, quality control and annotations
- **16s rRNA/ITS**: Microbiome diversity and taxonomic data analysis
- **RNA-seq**: Differential expression, alternative splicing and variant calling
- **ATAC-seq** to assess genome-wide chromatin accessibility
- 10X Genomics (scRNA-seq and scATAC-seq) pipelines
- **Mass spectroscopy** (**proteomics** and lipidomic) data analysis
- **SNP/Genotyping** arrays – Infinium array data analysis
- Network and clustering analysis.
- Pathway and Gene Set Enrichment analysis

Software and database development
- Experience in writing production level code.
- Java/J2EE, Java/Swing, JSP, Servlets, Spring MVC, Hibernate
- JDBC, MySQL and Tomcat
- GitHub, BitBucket, and Eclipse
- JavaScript, XML, RDF, and OWL

Immunology, Biochemistry/Molecular biology
- Working experience in gene cloning, protein expression and purification.

SCIENTIST, BIOINFORMATICS (09/2017 – till date)
Department of Human Genetics, Emory University, Atlanta, GA
Emory Integrated Computational Core (Team-lead), Emory University, Atlanta, GA

Description:
Application of existing and novel algorithms to analyze WES, WGS, RNA-seq and proteomic (label free and TMT quantification) data sets from individuals living with rare genetic diseases (Lesh-Nyhan disease (iPSC/NPC), Neuromuscular disease), Cancer (Head & Neck) or HIV-infected individuals. Genotyping and gene expression studies of NPC from subjects with 3q29 deletion.

SENIOR BIOINFORMATICS ANALYST (08/2016 - 09/2017)
Department of Human Genetics, Emory University, Atlanta, GA

Description:
Application of existing and novel algorithms to analyze NGS and microarray data sets and, communicate analysis results to industry clients and university collaborators, and clinicians.

SENIOR BIOINFORMATICS ANALYST (09/2015 - 08/2016)
Emory Vaccine Center, Emory University, Atlanta, GA

Description:
Integration of gene expression and immunological data of flu vaccination, with or without adjuvant at various time-points.

POSTDOCTORAL ASSOCIATE (11/2013 - 09/2015)
Dept., of Pathology, Immunology & Laboratory Medicine, University of Florida, Gainesville, FL

Description:
Performed integrative analysis of gene expression and immune/clinical data from substance use HIV-infected young adults.

POSTDOCTORAL FELLOW (03/2008 - 11/2013)
Dept., of Bioengineering, University of California San Diego, CA

Description:
Integrate transcriptomic and lipidomic data sets obtained from mouse macrophages stimulated with various ligands. Design and develop databases, applications and semantic data exchange formats to store and disseminate biological data.

EDUCATION

Ph.D	Biochemistry/Bioinformatics	University of Hyderabad, India	5/2003-5/2007
M.Tech	Biotechnology	Anna University, India	7/2000-1/2002

PUBLICATIONS

Book Chapters/Journal Reviews

1. Bioinformatics and systems biology of the lipidome. S Subramaniam, E Fahy, S Gupta, M Sud, RW Byrnes, D Cotter, AR Dinasarapu, MR Maurya (2011). *Chemical reviews,* 111 (10), 6452-6490.

2. Omics approaches to macrophage biology. S Gupta, AR Dinasarapu, MJ Gersten, MR Maurya, S Subramaniam. (2014). *Macrophages: Biology and Role in the Pathology of Diseases*, 587-615.

3. Biological data integration and dissemination on semantics web – a perspective. AR Dinasarapu**,** S Gupta (2015). *Journal of Bioinformatics and Intelligent control, 3 (4), 273-277*.

Journal Research Papers

4. Statistical insights into major human muscular diseases. S Gupta, SM Kim, Y Wang, AR Dinasarapu, S Subramaniam (2014). *Human molecular genetics*, 23(14): 3772-8.

5. A combined omics study on activated macrophages—enhanced role of STATs in apoptosis, immunity and lipid metabolism. AR Dinasarapu, S Gupta, MR Maurya, E Fahy, J Min, M Sud, MJ Gersten, CK Glass, S Subramaniam (2013). *Bioinformatics*, 29 (21), 2735-2743.

6. Analysis of inflammatory and lipid metabolic networks across RAW264. 7 and thioglycolate-elicited macrophages. MR Maurya, S Gupta, X Li, E Fahy, AR Dinasarapu, M Sud, HA Brown, CK Glass, RC Murphy, DW Russell, EA Dennis, S Subramaniam (2013). *Journal of lipid research*, 54 (9), 2525-2542.

7. MicroRNA 203 modulates glioma cell migration via Robo1/ERK/MMP-9 signaling. R Dontula, A Dinasarapu, C Chetty, P Pannuru, E Herbert, H Ozer, SS Lakka (2013) *Genes & cancer*, 4(7-8):285-96.

8. CMAP: Complement Map Database. K Yang, AR Dinasarapu, ES Reis, RA DeAngelis, D Ricklin, S Subramaniam, JD Lambris (2013) *Bioinformatics*, 29 (14), 1832-1833.

9. Signaling gateway molecule pages—a data model perspective. AR Dinasarapu, B Saunders, I Ozerlat, K Azam, S Subramaniam (2011). *Bioinformatics*, 27 (12), 1736-1738.

10. Comparative analysis of core promoter region: Information content from mono and dinucleotide substitution matrices. DA Reddy, B Prasad, CK Mitra (2006). *Computational biology and chemistry*, 30 (1), 58-62.

11. Comparative analysis of transcription start sites using mutual information. DA Reddy, CK Mitra (2006). *Genomics, proteomics & bioinformatics*, 4 (3), 189-195.

12. Functional classification of transcription factor binding sites: information content as a metric. DA Reddy, B Prasad, CK Mitra (2006). *Journal of Integrative Bioinformatics*, 3 (1), 20.

Research Papers [submitted/under preparation]

13. Systems biology approach predicts immune-modulatory role of recreational marijuana use in HIV-infected young adults. Dinasarapu AR et al.
14. Induced pluripotent stem cells for Lesch-Nyhan disease. Sutcliffe DJ, Dinasarapu AR et. al.
15. Landscape of genetic alterations in oropharyngeal squamous cell carcinoma based on RNA-seq and WES analysis of FFPE samples. Saba Nabil, Dinasarapu AR et al.
16. Adjuvant-dependent Modulation of CD4 T Follicular Helper Cells Impacts Longevity and Functional Quality of Antibody Responses to a subtype C HIV-1 Envelope Vaccine in Rhesus Macaques. Verma A, Schmidt B, Nguyen N, Elizaldi S, Walter K, Beck Z, Trinh H, Dinasarapu AR et al.
17. Rectal microbiome composition correlates with humoral immunity to HIV-1 vaccination in rhesus macaques. Elizaldi SR, Verma A, Rolston M, Dinasarapu AR et al.

COMPUTING SCRIPTS

R | Linux shell | Python   https://bitbucket.org/adinasarapu
Bioinformatics teaching   https://adinasarapu.github.io/teaching/