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## 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 Microarrays, Next Generation Sequencing (NGS) and Proteomics (LC-MS/MS) data
- Development and validation of bioinformatics pipelines with real-world samples
- Technical assistance to other scientists in the group

### PROFESSIONAL EXPERIENCE

#### SCIENTIST, BIOINFORMATICS (09/2017 – till date)

Department of Human Genetics, Emory University, Atlanta, GA

##### Description:

Application of existing and novel algorithms to analyze WES, WGS, RNA-seq, 16S rRNA and proteomics (label free and TMT quantification) data from individuals living with

- Lesh-Nyhan disease (Rare genetic disease; Proteomics; Fibroblasts/iPSC/NPC)
- Neuromuscular disease (Variant effects on Splicing defects)
- Head & Neck Cancer (HPV+ vs HPV-, WES and RNA-seq)
- HIV-1 (Substance use; Microbiome/16S rRNA)
- 3q29 deletion (Genotyping and gene expression studies of NPC)

#### 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.

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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. Rectal microbiome composition correlates with humoral immunity to HIV-1 in vaccinated rhesus macaques. Elizaldi SR, Verma A, Rolston M, Dinasarapu AR et al. (2019). *mSphere* (accepted).
5. Impact of Th1 CD4 TFH skewing on antibody responses to an HIV-1 vaccine in Rhesus Macaques. Verma A, Schmidt B, Nguyen N, Elizaldi S, Walter K, Beck Z, Trinh H, Dinasarapu AR et al. (2019). *Journal of Virology* (accepted).
6. Modeling DYT1 Dystonia Using Induced Pluripotent Stem Cells. AR Dinasarapu, DJ Sutcliffe, ME Zwick, HA Jinnah (2018). *Annals Of Neurology* 84, S198-S199.
7. Disease Modeling of Lesch-Nyhan Disease Using Induced Pluripotent Stem Cells. D Sutcliffe, A Dinasarapu, M Zwick and H Jinnah (2018). In *Movement Disorders* (Vol. 33, pp. S351-S351). 111 RIVER ST, HOBOKEN 07030-5774, NJ USA: WILEY.
8. 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.
9. 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.
10. 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.
11. 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.
12. CMAP: Complement Map Database. K Yang, AR Dinasarapu, ES Reis, RA DeAngelis, D Ricklin, S Subramaniam, JD Lambris (2013) *Bioinformatics*, 29 (14), 1832-1833.
13. Signaling gateway molecule pages—a data model perspective. AR Dinasarapu, B Saunders, I Ozerlat, K Azam, S Subramaniam (2011). *Bioinformatics*, 27 (12), 1736-1738.
14. 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.
15. Comparative analysis of transcription start sites using mutual information. DA Reddy, CK Mitra (2006). *Genomics, proteomics & bioinformatics*, 4 (3), 189-195.
16. 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.

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Research Papers [under preparation]

17. Systems biology approach predicts immune-modulatory role of recreational marijuana use in HIV-infected young adults. Dinasarapu AR et al.
18. Induced pluripotent stem cells for Lesch-Nyhan disease. Sutcliffe DJ, Dinasarapu AR et. al.
19. 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.

## 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

### Immunology, Biochemistry/Molecular biology

- Working experience in gene cloning, protein expression and purification.

## COMPUTING SCRIPTS & TEACHING

R | Linux shell | Python  
Bioinformatics teaching

<https://bitbucket.org/adinasarapu>  
<https://adinasarapu.github.io/teaching/>