Arun Kumar Boddapati

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Summary

Accomplished bioinformatics scientist with 8+ years of experience in multi-omics data analysis, computational immunology, and workflow development. Proven ability to lead cross-functional agile teams, develop scalable pipelines, and drive insights from genomics, transcriptomic and proteomic data. Strong record in mentoring, publishing high-impact research, and collaborating with stakeholder to deliver actionable solutions in infectious disease and vaccine research, epidemiological studies and bioinformatics with commitment to advancing translational science and precision medicine.

Professional Experience

Booz Allen Hamilton (Lead Scientist (Associate), CDC)

03/25 – Present

- **Project Management**: Develop and implement bioinformatics pipelines for pathogen surveillance, epidemiology and public health at CDC.
- **Stakeholder Collaboration**: Collaborate across cross-functional teams on (A)dvanced(M)olecular(D)etection-Platorm project to ensure efficient deployment of pathogen-related pipelines using NextFlow and AWS.

Leidos, Inc. (Bioinformatics Scientist (Senior), CDC)

06/22 – 01/25

- **Leadership and Project Management**: Directed development of the Nextflow pipeline Aquascope, improving CDC SARS-CoV-2 wastewater reporting.
- **Mpox Response**: Achieved a perfect score in WHO's global mock Mpox response and strategy evaluation, ranking among the top 8 of 80+ teams worldwide.
- **Research design and delivery**: Managed RNA-Seq, Metagenomics, and WGS projects, contributing to high-impact publications.
- **Team Management**: Mentored junior staff on Bulk-RNA sequencing projects, advanced bioinformatics tools (Nextflow, Singularity, HPC) and reproducible workflows.
- **Stakeholder Collaboration**: Partnered with cross-functional teams to align bioinformatics deliverables with business objectives of Scientific computing at CDC.

Emory National Primate Research Center (Sr. Bioinformatics Analyst)

01/22 – 06/22

- **Vaccine research**: Lead the Bioinformatics analysis of MVA/S vaccine research in non-human primates and published the findings in Immunity (**Impact factor: 43.47**).
- **Drug repurposing research**: Lead the Bioinformatics analysis of Baricitinib drug research in non-human primates and published the findings in Cell (**Impact factor: 66.54**)
- **Public Health Intervention**: Conducted Covid-19 wastewater analysis for Atlanta region.

- **Leadership and Collaboration**: Lead the Raw data processing and Quality Control of 5000 SARS-CoV2 infected patients (enrolled across the USA) leading to several high impact publications under IMPACC network.

Emory National Primate Research Center (Bioinformatics Analyst)
07/20 – 12/21

- **Pipeline Development**: Developed and deployed RNA and single-cell analysis pipelines in AWS, improving Genomics Core efficiency.
- **Scientific Research**: Analyzed single-cell data from Rhesus macaques, utilizing advanced immunophenotyping tools.

Leidos, Inc. (Bioinformatics Analyst II, NIH/NIAID)
05/18 – 06/20

- **Project management**: Developed a Whole Exome sequencing pipeline (WES-QC) for preliminary quality control of 3000 patient that reduced processing times by 80% with parallel computing on NIH's Biowulf cluster.
- **HIV, Malaria and autoimmunity research**: Led the single-cell bioinformatics analysis to uncover the common drivers of expansion and function in HIV, malaria and autoimmunity that results in a high-impact publication in Science Advances (Impact factor: 11.7)
- Managed 20+ multi-omics projects, delivering insights to guide high-impact research of which resulted in 6 high impact publications.

Indiana University (Graduate Research Assistant)
01/16 – 12/17

- **Algorithm development**: Developed mathematical model for structure prediction of RNA binding sites using CLIP-Seq data and presented the findings at RNARustBelt '17.
- **Epigenetics Research**: Studied m^6A post-transcriptional modifications on RNA-binding proteins and analyzed their impact in various TCGA cancers.

Education

- M.S. Bioinformatics, Indiana University (2015–2017)
- M.S. Biomedical Science, Symbiosis International University (2012–2014)
- B.Tech. Biotechnology, JNTU-H (2007–2011)

Certifications

- Microsoft Certified: Azure Fundamentals (08/2024)
- BCIL (Biotech Consortium India Limited) Certification (2015)

Key Skills & Tools

Category	Skills
Omics expertise	**Transcriptomics:** RNA-Seq, Single-Cell omics (10x, Cite-seq, Smart-seq) **Metagenomics:** 16s, Shotgun, Viral metagenomics **Proteomics:** Mass spec, Targeted protein panels (NULISA-Seq), **Immune repertoire:** T/B cell repertoire **Epitranscriptomics:** MeRIP-Seq (m6A, m5C methylation) and CLIP-Seq (RBPs) **Genomics:** WGS, WES, Variant calling (SNP & Indels only)
Omics Analysis tools	**RNA-Seq**: Deseq2, edgeR, Limma, Time-series, pathway enrichment, AUC analysis **scRNA-Seq**: Seurat, Monocle, FastMNN, singleR, Cellmarker, doublet finder **Proteomics**: DEP analysis, PPI network analysis and functional enrichment **Immune repertoire**: Immcantation package, MiXCR (RNA-Seq) **Epitranscriptomics:** Bedtools, homer, meme **Genomics:** GATK, SNPeff, VEP, de-novo assembly
Computational Tools	**Programming Languages & Frameworks**: R, Python, SQL, CSS, HTML, JavaScript(beginner) **Workflow Management**: Nextflow, Snakemake
HPC & Cloud Platforms	**Cloud Platforms**: AWS (EC2, S3), Azure Databricks **Containerization**: Singularity, Docker**,** Podman **HPC Scheduling**: SLURM, SunGridEngine(SGE)**,** PBS, AWS Batch, GPU computing
Visualization Tools	ggplot, plot.ly, quatro dashboards
Software Tools	CellRanger, CLCgenomics, Partek Flow, SeqGeq, BedTools, ONT-EPI2ME, Seqera Tower, DCIPHER, Palantir Foundry, Lucid Chart, Adobe Illustrator
Machine learning	RFs, Bootstrapping, LOOCV, CAE (Convolutional auto-encoders), Logistic regression.
Operating Systems	MacOS, Linux (CentOS & RHEL8), Windows
Version control	Github, Gitlab, BitBucket, CI/CD
Project management	Jira, kanban boards, confluence, MS (Planner, SharePoint, OneNote, Visio, PowerPoint, Excel), PowerBI, Tableau
Leadership skills	Stakeholder collaboration, Team management, Mentorship, Lead generation and Agile

Publications and Talks:

- Features of acute COVID-19 associated with post-acute sequelae of SARS-CoV-2 phenotypes: results from the IMPACC study. (Al Ozonoff et.al, IMPACC Network, 2024)

- Tau-typing: a Nextflow pipeline for finding the best phylogenetic markers in the genome for molecular typing of microbial species. (Matthew H Seabolt, 2023).
- Modulation of type I interferon responses potently inhibits SARS-CoV-2 replication and inflammation (EG Viox et al., 2023)
- Baricitinib treatment resolves lower-airway macrophage inflammation and neutrophil recruitment in SARS-CoV-2-infected rhesus macaques. (Timothy N. Hoang, 2021).
- Link to more publications: GoogleScholar