

# 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-Platform 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<sup>6</sup>A 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
<b>Omics expertise</b>	<b>Transcriptomics:</b> RNA-Seq, Single-Cell omics (10x, Cite-seq, Smart-seq) <b>Metagenomics:</b> 16s, Shotgun, Viral metagenomics <b>Proteomics:</b> Mass spec, Targeted protein panels (NULISA-Seq), <b>Immune repertoire:</b> T/B cell repertoire <b>Epitranscriptomics:</b> MeRIP-Seq (m6A, m5C methylation) and CLIP-Seq (RBPs) <b>Genomics:</b> WGS, WES, Variant calling (SNP & Indels only)
<b>Omics Analysis tools</b>	<b>RNA-Seq:</b> Deseq2, edgeR, Limma, Time-series, pathway enrichment, AUC analysis <b>scRNA-Seq:</b> Seurat, Monocle, FastMNN, singleR, Cellmarker, doublet finder <b>Proteomics:</b> DEP analysis, PPI network analysis and functional enrichment <b>Immune repertoire:</b> Immcantation package, MiXCR (RNA-Seq) <b>Epitranscriptomics:</b> Bedtools, homer, meme <b>Genomics:</b> GATK, SNPeff, VEP, de-novo assembly
<b>Computational Tools</b>	<b>Programming Languages &amp; Frameworks:</b> R, Python, SQL, CSS, HTML, JavaScript(beginner) <b>Workflow Management:</b> Nextflow, Snakemake
<b>HPC &amp; Cloud Platforms</b>	<b>Cloud Platforms:</b> AWS (EC2, S3), Azure Databricks <b>Containerization:</b> Singularity, Docker, Podman <b>HPC Scheduling:</b> SLURM, SunGridEngine(SGE), PBS, AWS Batch, GPU computing
<b>Visualization Tools</b>	ggplot, plot.ly, quatro dashboards
<b>Software Tools</b>	CellRanger, CLCgenomics, Partek Flow, SeqGeq, BedTools, ONT-EPI2ME, Seqera Tower, DCIPHER, Palantir Foundry, Lucid Chart, Adobe Illustrator
<b>Machine learning</b>	RFs, Bootstrapping, LOOCV, CAE (Convolutional auto-encoders), Logistic regression.
<b>Operating Systems</b>	MacOS, Linux (CentOS & RHEL8), Windows
<b>Version control</b>	Github, Gitlab, BitBucket, CI/CD
<b>Project management</b>	Jira, kanban boards, confluence, MS (Planner, SharePoint, OneNote, Visio, PowerPoint, Excel), PowerBI, Tableau
<b>Leadership skills</b>	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](#)