Manjusha Chintalapati

Website | manjushabiotech@gmail.com | +1 (510)-737-9930

An accomplished Human geneticist with a Ph.D. in Computer Science (Bioinformatics major) from the Max Planck Institute for Evolutionary Anthropology. Led projects in collaborative settings with diverse groups including scientists, decision makers and stakeholders. Actively led the UC Berkeley MCB school postdoctoral community as representative, organized scientific seminars, and mentored upcoming researchers. Seeking a challenging role to apply my technical skills and offer innovative solutions in a mission-oriented environment.

Areas of Expertise

- ***Computation Skills:*** Big data analysis and visualization; Method development; Pipeline/workflow creation and deployment; Machine Learning; Data management; AWS generative AI certified.
- ***Programming skills:*** R; Shell/Bash; AWK; Python; PERL; C++.
- **Statistical skills:** Quantitative methodology; Statistical inference; Time-series analysis; Preprocessing, dimensionality reduction & stratification; Supervised and unsupervised learning.
- ***Data Science:*** HPC clusters, Git-versioning, R Markdown, Jupyter notebooks, MS Excel, KNIME.
- ***Bioinformatics:*** Sequencing data analysis (WGS, Genotyping, long-read, short-read, ChIP arrays, RNAseq); Genome Assembly; Small- and large-scale genome variation detection; Meta-analysis; Comparative genomics.
- ***Genetics:*** Population genetic analysis; Method development; Mutation rate estimation; Selection inference; Disease & trait mapping; Phenotypic association; Structure identification; Admixture quantification; Phylogenetics; Evolution of Human genomes with comparative study with Neandertals and Denisovans.
- ***Interpersonal skills:*** Excellent scientific presenter; Multiple awards for scientific presentations; Proficient in English, Telugu, Hindi and Malayalam; Conversational German and Tamil.

Experience

Ancestry.com – *Researcher*   2023 - Present
- Developed methods infer population genetic parameters such as Recombination Rates using over 1 million genotyped customer data.
- Development and execution of new projects related to human ethnicity and demographic structure inference.
- Managed and deployed computational workflows for analyzing big data from consortia. Employed advanced statistical analysis, MVDA, supervised and unsupervised ML with reproducible codebases.
- Communicated complex analyses and findings through reports, effectively conveying actionable insights to stakeholders.
- Trained on ML and generative AI on AWS with successful certifications.

University of California, Berkeley – *Postdoctoral Scholar*   2019 - 2023
- Analysed 60 Early modern human genomes and 300 present day genomes to precisely infer the Neanderthal-Human gene flow timing. Identified key genes passed from Nenaderthals selected in humans play a role in functions such as immunity. Published this in Science as the First author.
- Developed a novel computational method DATES - combining Bayesian modeling and statistical inference using sparse markers from diverse datasets to discover events in human history.
- Efficiently processed sequencing data from over 5000 genomes with combinatorial techniques predicting unknown gene flow events between sub-populations.
- Analyzed Alzheimer's genetic datasets (LASI-DAD) to understand the effect size of GWAS sites, explainability in South Asians using Polygenic Risk Scores (PRS).
- Leveraged bioinformatics methods to build efficient workflows for multiple hominid and monkey species ensuring accuracy, completeness, and uniformity for mutation rate inference.

Max Planck Institute for Evolutionary Anthropology - *Ph.D. researcher*   2014 - 2018
- Processed and analyzed genetic data of modern humans and archaics (Neanderthal/Denisovans) and identified >300k Insertions & Deletions, correlated phenotypes such as menarche.
- Constructed a *denovo* assemblies of damaged ancient genomes by improving data quality through novel techniques and inferred large genomic changes (>10kb resolution).
- Published in high impact journals (Science & PNAS) on two 30X coverage Neanderthals.
- Analysed multiple gene CRISPR screen data computationally with over ~90% accuracy.

Tata Consultancy Services – *Software Programmer*   2012 - 2014
- Deployed cloud computing workflows increasing the efficiency by over 40%.
- Developed modules through bash workflows and C++ programming for telecom clients.

Education

University of Leipzig – **Ph.D. in Computer Science   Magna cum laude**   2014-2018

University of Hyderabad - **Masters in Bioinformatics** GPA: 4/4 (**University topper**) 2010-2012

Andhra University – **Bachelors in Biotechnology**   GPA: 4/4 (**Gold medalist**)   2006-2010

Professional Achievements and Certifications

- ❖ AWS generative AI certification from Amazon web services.
- ❖ Best talk and poster awards at UC Berkeley, CCB and GGDE seminars 2019-2023.
- ❖ Invited guest at BBC radio to discuss my work on "Neanderthal ancestry through time"
- ❖ Worked under supervision of Nobel laureate Svante Päboo, collaborated on projects with Nobel Laureate Thomas Lindhal and world renowned geneticist, Nick Patterson.
- ❖ GATE (Graduate Aptitude Test in Engineering) fellowship awardee (2010-2012).
- ❖ Summer research fellowship (SRFP) from the Indian Academy of Sciences (2009-2010).

Selected Publications

Total publications 10; citations till date 1439; i10-index 10

1. Iasi Leonardo*,**Chintalapati Manjusha***, et al., (2024). Neandertal ancestry through time: Insights from genomes of ancient and present-day humans. **Science**. DOI

2. Wei Zhao, ..., **Manjusha Chintalapati**, et al., (2023). Polygenic risk scores for Alzheimer's disease and general cognitive function are associated with measures of cognition in older South Asians from LASI-DAD. **Journal of Gerontology: Biological Sciences**. DOI

3. **Chintalapati Manjusha**, Nick Patterson and Priya Moorjani (2022). The spatiotemporal patterns of major human admixture events during the European Holocene. **eLife**. DOI

4. **Chintalapati Manjusha** and Priya Moorjani (2020). Evolution of mutation rate across primates. Current opinion in genetics & development. DOI

5. **Chintalapati, Manjusha**, Michael Dannemann, and Kay Prüfer. **2017**. Using the Neandertal Genome to Study the Evolution of Small Insertions and Deletions in Modern Humans. *BMC Evolutionary Biology*. DOI

6. Kay Prüfer, ..., **Manjusha Chintalapati**, ..., Svante Pääbo (2017). A high-coverage Neandertal genome from Vindija Cave in Croatia. **Science**. DOI

7. F Maffessoni,....**Manjusha Chintalapati**, ..., Svante Pääbo (2020). A high coverage Neandertal genome from Chagyrskaya cave. *Proceedings of the National Academy of Sciences*. DOI