

Manjusha Chintalapati

Computational Biologist with over a decade of Bioinformatics and programming experience. I'm passionate about scientific problem solving, motivated by a rigorous work ethic and enjoy scientific communication.

<https://manjushachintalapati.github.io/>
m_chintalapati@berkeley.edu | +1 (510)-737-9930

Areas of Expertise

- **Bioinformatics:** NGS data analysis (WGS, Genotyping, long-read, short-read, ChIP arrays), Genome Assembly, Genome Browser, small- and large-scale genome variation detection, Meta-analysis.
- **Computation Skills:** Big data analysis and visualization, Method development, Pipeline development and deployment, Statistical testing, Machine Learning, Workflow management.
- **Genetics:** Population genetic analysis, Mutation detection, Selection analysis, Disease & trait mapping, Genetic structure analysis, Analysis of complex populations, Admixture mapping, Demographic inference, Archaic/Ancient genome analysis, Evolutionary genetics.
- **Programming skills:** R, Shell/Bash, AWK, Python, PERL, C++.
- **Data Science:** Linux/Unix/Windows OS, HPC clusters, Git versioning, R markdown, Jupyter notebooks.

Experience

University of California, Berkeley – Postdoctoral Researcher Jan. 2019 - Jan. 2023

- Developed a statistical genetics method for dating admixture using genomic data (applicable to sparse/low quality data) and uncovered major demographic events timings in the European Holocene.
- Developed a bioinformatics pipeline for standardized estimation of mutation rates in primate lineages.
- Analysis of Longitudinal Aging Study of India - Diagnostic Assessment of Dementia (LASI-DAD) for Alzheimer's disease and general cognitive function using European GWAS.
- Worked with large genome datasets (1000G, HGP, SGDP, UCSC genomes, UK Biobank etc).
- Collaborative project – Genetic structure and genome variation in Hummingbirds.
- Mentored an undergrad and a graduate student.
- Organized summer lab discussions for basic training, science communication and brainstorming.
- Organized scientific presentations for the Center for Theoretical and Evolutionary Genetics (CTEG).
- Representative for the postdoc community in the Molecular and Cell Biology department.

Max Planck Institute for Evolutionary Anthropology - Ph.D. Candidate March 2014 - Dec. 2018

- Analysis of small indels in humans using comparative approach using the Altai Neanderthal genome.
- *denovo* assembly of the Altai Neanderthal genome and inference of genome variation.
- Developed a method for large genomic rearrangement detection.
- Bioinformatic analysis of multiple gene CRISPR edited data.
- Worked on two consortium projects – high coverage Neanderthal genomes from Vindija cave located in Croatia and Chagyrskaya cave located in Russia.
- Collaborative project - Comparative genome analysis of Lacertid lizards for structural variation detection and genetic inference.

Tata Consultancy Services – Software Programmer May 2012 - Feb. 2014

- Shell scripting for testing modules and programmed in C++ for client-based needs.
- Worked on initial cloud computing deployment project.

Education

University of Hyderabad- M. Tech Bioinformatics	GPA: 9.73 (University topper)	2010-2012
Andhra University – B. Tech in Biotechnology	GPA: 90% (Gold medalist)	2006-2010

Professional Achievements

Topper of the cohort in Masters (Bioinformatics) at the University of Hyderabad (2010-2012).

GATE (Graduate Aptitude Test in Engineering) Fellowship awardee (2010-2012).

Summer research fellowship (**SRFP**) from the Indian Academy of Sciences (2009-2010).

Gold medalist for the best academic performance for Bachelor's in Biotechnology (2006-2010).

Publications

1. Wei Zhao, ..., **Manjusha Chintalapati**, ..., Sharon L. R. Kardia (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.org/10.1093/gerona/glad057
2. **Chintalapati Manjusha**, Nick Patterson and Priya Moorjani (2022). The spatiotemporal patterns of major **human admixture** events during the European Holocene. eLife. doi.org/10.7554/eLife.77625
3. Fabrizio Mafessoni, Steffi Grote, ..., **Manjusha Chintalapati**, ..., Svante Pääbo. (2020). A high-coverage Neandertal genome from Chagyrskaya Cave. PNAS. doi.org/10.1073/pnas.2004944117
4. **Chintalapati Manjusha** and Moorjani Priya (2020). Evolution of the Mutation rate across primates. Current Opinion in Genetics & Development. doi.org/10.1016/j.gde.2020.05.028
5. Stephan Riesenberger, **Manjusha Chintalapati**, .., Svante Pääbo (2019). Simultaneous precise editing of multiple genes in human cells. Nucleic Acids Res. doi.org/10.1093/nar/gkz669
6. Sree Rohit Raj Kolora, ..., **Manjusha Chintalapati**, ..., Martin Schlegel. (2018). Divergent evolution in the genomes of the closely related lacertids, *Lacerta viridis* and *L. bilineata* and implications for speciation. Giga science. [doi:10.1093/gigascience/giy160](https://doi.org/10.1093/gigascience/giy160)
7. **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.org/10.1186/s12862-017-1018-8
8. Kay Prüfer, ..., **Manjusha Chintalapati**, ..., Svante Pääbo (2017). A high-coverage Neandertal genome from Vindija Cave in Croatia. Science. doi.org/10.1126/Science.Aao1887

Selected Scholarly Presentations

1. **Best poster awards** at Center for Computational Biology retreats, UC Berkeley, CA, USA (2020 and 2021).
2. Talk at Molecular and Cell Biology retreat, UC Berkeley, CA, USA (2020).
3. Talk at the Human Evolution conference held at Wellcome Genome Campus, Hinxton, UK (2019).
4. **Best talk award** at Center for Computational Biology retreat, University of Berkeley, CA, USA (2019).
5. Talk at Bay Area Populations genetics meeting, Stanford, CA, USA (2019).
6. Talk at the Genome Informatics CSHL, Cold Spring Harbor Laboratories, New York, USA. (2017).
7. Poster at International Society for molecular bio systems (ISMB), Orlando, Florida, USA. (2016).