

# Manjusha Chintalapati

<https://manjushachintalapati.github.io/>

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Highly skilled and accomplished Data Scientist with a Ph.D. in Informatics from the Max Planck Institute for Evolutionary Anthropology. Experienced in leading research projects in a collaborative setting across diverse groups including researchers and decision makers. Recently managed initiatives as a postdoc representative, departmental organizer and research mentor at UC Berkeley bringing organizational changes to benefit the university community. Seeking a challenging role to apply technical skills through critical thinking, perform data analysis and offer solutions in a collaborative and innovative environment.

## Areas of Expertise

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- **Computation Skills:** Big data analysis and visualization; Method development; Pipeline/workflow creation and deployment; Machine Learning; Data management.
- **Programming skills:** R; Shell/Bash; AWK; Python; PERL; C++.
- **Statistical skills:** Quantitative methodology; Statistical inference through frequentist and Bayesian approaches; Correlation and association tests; Time-series data analysis; Data normalization; Outlier detection, clustering, dimensionality reduction & stratification; Supervised and unsupervised learning.
- **Data Science:** Linux/Mac/Windows OS, 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.
- **Genetics:** Population genetic analysis; Mutation detection; Selection analysis; Disease & trait mapping; Genetic structure analysis; Admixture and demographic inference; Evolutionary genetics.
- **Interpersonal skills:** Excellent scientific presenter, Multiple awards for oral and poster presentations, Proficient in English, Telugu, Hindi, Malayalam and conversational German and Tamil.

## Experience

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### University of California, Berkeley – Postdoctoral Researcher

Jan. 2019 - Jan. 2023

- Developed a computational method using Bayesian modeling and statistical inference using genetic markers from diverse datasets and inferred event timelines across human history.
- Successfully leveraged advanced bioinformatics methods to analyze sequencing datasets ensuring accuracy, completeness, and uniformity of data for inferring of mutation rates.
- Expertise in advanced statistical analysis, MVDA, supervised and unsupervised machine learning techniques for gaining insights from big data.
- Skilled in developing predictive and statistical models, clustering approaches and simulations.
- Efficient in communicating complex analyses and findings through clear visualizations and reports, effectively conveying actionable insights to stakeholders.
- Collaborated with cross-functional teams including mathematicians, computer scientists and biologists to transform big data into critical information for improved biological mechanistic understanding.
- Developed computational tools with reproducible code promoting scientific integrity through open science.

- Efficiently processed data from over 5000 genomes (over 100Tb) with millions of combinations for effective inference on interactions between sub-groups.
- Outreach activities
  - Mentored younger scientists in the lab and served as advisor for grad students.
  - Organized lab discussions for undergraduate and graduate training, science communication and brainstorming to provide inclusive environment.
  - Organized scientific seminars for the Center for Theoretical and Evolutionary Genetics (CTEG).
  - Representative for the postdoctoral community for the Molecular and Cell Biology department.

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

- Proficient in querying and analyzing genetic data of humans and archaics.
- Excellent critical thinking and problem-solving abilities- constructed a *denovo* assembly of an ancient genome using low quality data and inferred of structural changes.
- Tackled complex bioinformatics problems by developing efficient genomic change detection methods.
- Computational analysis of multiple gene CRISPR edited screen data.
- Worked on highly collaborative consortium projects with international scientists on diverse systems.

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

- Shell scripting for testing modules and programmed in C++ for telecommunications clients.
- Worked on cloud computing deployment.

## Education

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University of Leipzig – <b>Ph.D. Informatics</b>	Magna cum laude	2014 - 2018
University of Hyderabad- <b>M.Tech Bioinformatics</b>	GPA: 9.73 (University topper)	2010 - 2012
Andhra University – <b>B.Tech in Biotechnology</b>	GPA: 90% (Gold medalist)	2006 - 2010

## Professional Achievements

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**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).

## Selected Scholarly Presentations

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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).

## Selected Publications

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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](https://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](https://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](https://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](https://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](https://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](https://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](https://doi.org/10.1126/Science.Aao1887)