

EDUCATION

Indian Institute of Science

PhD in Computational and Data Sciences

Bangalore, India

Oct 2020 – Present

National Institute of Technology

Bachelor of Technology (Hons) in Mechanical Engineering

Raipur, India

July 2016 – July 2020

HONORS AND AWARDS

- **Winner:** National HPC Hackathon 2021. (Awarded AWS credits worth 10K USD)
Organised by Intel India and AWS in association with Govt. of India.
- **Empower Program:** Awarded research funding from Kotak-IISc AI ML Center.

FELLOWSHIPS

- **Intel India Research Fellowship 2023-24**
- **RECOMB 2023 Travel Fellowship**

JOURNAL PUBLICATIONS

- **Genome Research 2024**
Haplotype-aware Sequence Alignment to Pangenome Graphs.
Ghanshyam Chandra, Daniel Gibney and Chirag Jain. *Genome Research*.
doi.org/10.1101/2023.11.15.566493 (in press, RECOMB'24 extended version)
- **AMB 2024**
Co-linear Chaining on Pangenome Graphs.
Jyotshna Rajput, **Ghanshyam Chandra** and Chirag Jain. *Algorithms for Molecular Biology*.
doi.org/10.1186/s13015-024-00250-w (Invited paper, WABI'23 extended version)
- **JCB 2023**
Gap-Sensitive Co-Linear Chaining Algorithms for Acyclic Pangenome Graphs.
Ghanshyam Chandra and Chirag Jain. *Journal of Computational Biology*.
doi.org/10.1089/cmb.2023.0186 (Invited paper, RECOMB'23 extended version)

REFEREED CONFERENCE PUBLICATIONS

- **RECOMB 2025**
Integer programming framework for pangenome-based genome inference.
Ghanshyam Chandra, Md Helal Hossen, Stephan Scholz, Alexander T Dilthey, Daniel Gibney and Chirag Jain. *International Conference on Research in Computational Molecular Biology*. (acceptance rate: 16%) doi.org/10.1101/2024.10.27.620212
- **RECOMB 2024**
Haplotype-aware Sequence-to-Graph Alignment.
Ghanshyam Chandra, Daniel Gibney and Chirag Jain. *International Conference on Research in Computational Molecular Biology*. (acceptance rate: 16%) doi.org/10.1101/2023.11.15.566493
- **WABI 2023**
Co-linear Chaining on Pangenome Graphs.
Jyotshna Rajput, **Ghanshyam Chandra** and Chirag Jain. *23rd International Workshop on Algorithms in Bioinformatics (WABI 2023)*. doi.org/10.4230/LIPIcs.WABI.2023.12

- **RECOMB 2023**

Sequence to Graph Alignment Using Gap-Sensitive Co-linear Chaining.

Ghanshyam Chandra and Chirag Jain. International Conference on Research in Computational Molecular Biology. (acceptance rate: 20%) doi.org/10.1007/978-3-031-29119-7_4

PREPRINTS

- Accelerating whole-genome alignment in the age of complete genome assemblies.
Ghanshyam Chandra, Md Vasimuddin, Sanchit Misra and Chirag Jain. (under review)
doi.org/10.1101/2024.11.25.6253281

TEACHING AND MENTORING

- Teaching assistant for DS295: Parallel Programming (DS295) 2024

TALKS

- Scalable Algorithms for Genome Inference and Pattern Matching on Pangenome Graphs.
Parallel Computing Lab, Intel Labs Bangalore 2024, Bangalore, India.
- Haplotype-aware Sequence-to-Graph Alignment.
RECOMB 2024, MIT, USA.
- Accelerating Whole-Genome Alignment using Parallel Chaining Algorithm.
RECOMB-Seq 2024, MIT, USA.
- Scalable Algorithms for Genome-aware Sequence-to-Graph Alignment.
EECS Symposium 2024, IISc Bangalore, India.
- Why Use Human Genome Graphs as a Reference? Insights into Scalable Genome Graph Algorithms.
IEEE IISc CS&CIS/HKN Mu Xi Deep Tech Outreach Seminar Series 2024, Bangalore, India.
- Sequence to Graph Alignment using Gap-Sensitive Co-linear Chaining.
RECOMB 2023, Istanbul, Turkey.
- A Scalable Algorithm for Sequence to Graph Alignment.
EECS Symposium 2023, IISc Bangalore, India.

POSTER PRESENTATION

- Minichain: A New Method for Pangenome Graph Construction.
Ghanshyam Chandra and Chirag Jain. RECOMB Satellite Conference on Biological Sequence Analysis.
RECOMB-Seq 2023, Istanbul, Turkey.
- Scaling Sequence to DAG Alignment with Parameterized Gap-Sensitive Co-linear Chaining Algorithms.
Ghanshyam Chandra and Chirag Jain. IEEE International Conference on High Performance Computing, Data, and Analytics. HiPC 2022, Bangalore, India.

SKILLS

- **Languages:** C, C++, Python, CUDA, JavaScript, HTML
- **ML Frameworks:** PyTorch, ScikitLearn
- **Parallel Computing Frameworks:** OpenMP, OpenACC, MPI
- **Optimization Frameworks:** Gurobi Optimizer

SOFTWARE DEVELOPED

- **Minichain:** Genome-aware long reads or phased contigs aligner to acyclic pangenome graphs.
- **PanAligner:** Long reads aligner to cyclic pangenome graphs.
- **mm2-plus:** Fast long-read and whole-genome aligner.
- **PHI:** Scalable tool for pangenome-based haplotype imputation.

MEDIA COVERAGE

- New algorithms advance genomic equity and personalised medicine.
Covered by: *Times of India*, *Indian Institute of Science* [\[Link\]](#)

ACADEMIC SERVICE

- **PC member & Reviewer:** AccMLBio (ICML 2024)