Ghanshyam Chandra

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EDUCATION

Indian Institute of Science   Bangalore, India
PhD in Computational and Data Sciences   *Oct 2020 – Present*

National Institute of Technology   Raipur, India
Bachelor of Technology (Hons) in Mechanical Engineering   *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 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

- Integer programming framework for pangenome-based genome inference.
  Ghanshyam Chandra, Md Helal Hossen, Stephan Scholz, Alexander T Dilthey, Daniel Gibney, Chirag
  Jain. (under review) doi.org/10.1101/2024.10.27.620212

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)