NAGA SAI KAVYA VADDADI

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Research Interests

Computational Genomics, Computational Pangenomics, AI for Healthcare, Precision Medicine.

Education

Ph.D. in Computer Science (CGPA: 3.904/4.0) **Aug 2021 - Present**
Advisor: Dr. Ben Langmead, **Johns Hopkins University (JHU), Baltimore, MD, USA.**

- **Relevant Courses**: Computational Genomics, Computing for Applied Mathematics, Sketching & Indexing, ML:DL, Applied Comparative Genomics, Intro. Computational Immunogenomics

MS & B.Tech. (Hons) (Dual degree in Computer Science) (CGPA: 8.2/10) **Aug 2016**
International Institute of Information Technology (IIIT), Hyderabad, India.

- **Relevant Courses**: Artificial Intelligence, Optimization Methods, Data Mining, Algorithms, Statistical methods in AI, Software Engineering
- **Thesis**: Coverage Patterns-based Allocation Approaches for Display Advertising. [Thesis]

Research Experience

Research Assistant at Langmead Lab @ JHU, MD, USA **Aug 2021 - Present**
Project: *Personalized-genome analysis for understanding Human Genome Variation*
My research advances personalized-genome analysis through the use of large reference panels and diverse computational techniques to reduce reference bias for improved genome analysis:
(i)Personalized genome analysis

- Considered the fundamental problem of utilizing scalable bias-free genotyping methods.
- Construct personalized reference genome using extensive referenc panels data.
- Develop imputation-driven personalized downstream analysis of alignment and variant calling.

Researcher at TCS Research - Life Sciences, Hyderabad, India **Aug 2016 - Aug 2021**
Project: *Pan-genome analysis for understanding Human Genome Variation*
Mentors: *Dr. Naveen Sivadasan & Dr. Rajgopal Srinivasan.*
Genome variation graphs represent the genomic diversities of a pangenome collection. My research involves working on developing computational algorithms for pangenome analysis. The projects where I contributed profoundly are:
(i) Sequence Alignment on Directed Graphs Developed a novel dynamic programming formulation that allows gapped alignment directly on the graphs.
(ii) Read Mapping on Genome Variation Graphs Developed space-efficient index using novel approaches of graph winnowing, path sampling, and graph embedding.
(iii) Visualization of SARS-COV2 Genome Atlas Developed Bag-of-Words model-based fast visualization methods to inspect similarity and temporal evolution of evolving collection of SARS-COV2 Genome Sequences.

Papers

Mun, Taher, **Naga Sai Kavya Vaddadi**, and Ben Langmead. *Pangenomic Genotyping with the Marker Array.* Workshop on Algorithms in Bioinformatics **WABI 2022**. [Paper]

Kavya, Vaddadi, Rajgopal Srinivasan, and Naveen Sivadasan. *Read Mapping on Genome Variation Graphs.* Workshop on Algorithms in Bioinformatics **WABI 2019**. [Paper]

Kavya, Vaddadi, and P.K. Reddy. *Coverage patterns-based approach to allocate advertisement slots for display advertising.* International Conference on Web Engineering **ICWE 2016**. [Paper]

Journals

Mun, Taher, **Naga Sai Kavya Vaddadi**, and Ben Langmead. *Pangenomic Genotyping with the Marker Array.* Algorithms for Molecular Biology. 2023 **Algorithms Mol. Biol. 2023**. [Journal]

Kavya, Vaddadi, Kshitij Tayal, Rajgopal Srinivasan, and Naveen Sivadasan. *Sequence Alignment on Directed Graphs.* Journal of Computational Biology **JCB 2019**. [Journal]

Talk & Posters

Kavya, Vaddadi, Taher Mun, and Benjamin Langmead. *Minimizing Reference Bias: The Impute-First Approach for Personalized Genome Analysis.* **ACM BCB 2023**. [Abstract][Poster]

Kavya, Vaddadi, et al. *Visualization of SARS-CoV-2 Genome Atlas.* In Proceedings of the ISMB 2021. [Talk] [Abstract]

Kavya, Vaddadi, Rajgopal Srinivasan, and Naveen Sivadasan. *Read Mapping on Genome Variation Graphs.* Conference on Intelligent Systems for Molecular Biology **ISMB 2019**. [Slides] [Poster]

Kavya, Vaddadi, Kshitij Tayal, Rajgopal Srinivasan, and Naveen Sivadasan. *Sequence Alignment on Directed Graphs.* Conference on Research in Computational Molecular Biology **RECOMB 2017**. [Poster][Best Poster Award]

Kavya, Vaddadi, and P.K. Reddy. *An Approach to Allocate Advertisement Slots for Banner Advertising.* IKDD Conference on Data Science **IKDD CODS 2016**. [Short Paper][Poster]

Patents Issued

METHOD AND SYSTEM FOR MAPPING READ SEQUENCES USING A PANGENOME REFERENCE. Application No: EP3938932B1; Inventors: **Naga Sai Kavya Vaddadi**, Naveen Sivadasan, Rajgopal Srinivasan; Applicant: TCS Ltd. [Patent]

Teaching Experience

Graduate TA: *Text to Speech Conversion* (IIIT, Hyderabad) **Spring, 2015**
Conducted discussion sessions to help students with the introductory topics. Graded assignments, class-works and answer scripts for the final evaluation.

Graduate TA: *Data Warehousing & Data Mining* (IIIT, Hyderabad) **Spring, 2014**
Allocated relevant Kaggle challenges as student projects and assisted in hands-on learning. Evaluated viva & course projects, assignments and answer scripts throughout the curriculum.

Technical Skills

- **Programming:** C/C++, Java, Python, R, Bash
- **Frameworks:** PyTorch, Tensorflow, scikit-learn, WDL
- **Misc:** AWS, LaTeX, Vim, GitHub, Linux

Achievements

Dean's List - Academic Award 2015
— Received for outstanding academic excellence (top 5%) during Masters at IIIT Hyderabad.
Best Poster Award - RECOMB 2017
— Received for our work titled *Sequence Alignment on Directed Graphs.*
Tata Citation Award 2019 & 2020
— Received consecutively for notable contribution (top-tier publications) to Life Sciences R&D.
IP Creation Award 2020
— Received in appreciation of notable contribution (patent creation) to Life Sciences R&D.

References

Dr. Ben Langmead (Associate Professor, Johns Hopkins University, Baltimore, MD, USA.)
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Dr. Rajgopal Srinivasan (Chief Scientist, TCS Research, Hyderabad, India)
✉:rajgopal.srinivasan@tcs.com

Dr. Naveen Sivadasan (Senior Scientist, TCS Research, Hyderabad, India)
✉:naveen.sivadasan@tcs.com