Palash Sashittal

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Employment History

Aug. 2024 – to date	**Assistant Professor**, Department of Computer Science, Virginia Tech
Sep. 2021 – Aug. 2024	**Postdoctoral research associate**, Department of Computer Science, Princeton University
Aug. 2019 – Aug. 2021	**Graduate research assistant**, Department of Computer Science, University of Illinois at Urbana-Champaign
Aug. 2014 – Aug. 2019	**Graduate research assistant**, Department of Aerospace Engineering, University of Illinois at Urbana-Champaign

Education

2021	**Ph.D., University of Illinois at Urbana-Champaign** in Aerospace Engineering. Thesis: *Flow control and sensing using data-driven reduced-order modeling.*
	MSc., University of Illinois at Urbana-Champaign in Computer Science. Thesis: *Algorithms for infection and cancer genomics.*
2014	**B.Tech., Indian Institute of Technology Bombay** in Aerospace Engineering.

Awards

2023	**Mistletoe Research Fellowship** ($10,000 Unfettered Research Grant) Invited for the **Cornell Future Faculty Symposium** **Best paper award** at RECOMB-CCB conference.
2019	**Aerospace Graduate Student Travel Award**
2018	**IEEE CDC Student Travel Grant**. **Mavis Future Faculty Fellowship**, University of Illinois at Urbana-Champaign.
2016	**Center for Turbulence Research Summer Program Fellowship**, Stanford University.
2013	**Undergraduate Research Award**, Indian Institute of Technology Bombay.
2010	**Certificate of Merit by Central Board of Secondary Education**, given to the top 0.1% students in India. **Kishore Vaigyanik Protsahan Yojana (KVPY) Scholarship** (declined).

List of publications

Author order generally follows the convention in biology, where first author carried out majority of the work (joint first authorship is indicated by '∗'). Circled numbers indicate first author papers.

Journal Articles

①   ConDoR: Tumor phylogeny inference with a copy-number constrained mutation loss model
Palash Sashittal, Haochen Zhang, Christine Iacobuzio-Donahue and Ben Raphael
Genome Biology, 2023.

2 Startle: a star homoplasy approach for CRISPR-Cas9 lineage tracing
Palash Sashittal∗, Henri Schmidt∗, Michelle Chan and Ben Raphael
Cell Systems, 2023 (In Print).
Invited journal version of RECOMB 2023 conference paper.

3 A zero-agnostic model for copy number evolution in cancer
Henri Shcmidt, **Palash Sashittal** and Ben Raphael
PLOS Computational Biology, 2023.
Best paper award at RECOMB-CCB, 2023.

4 Application of high-throughput, high-depth, targeted single-nucleus DNA sequencing in pancreatic cancer
Haochen Zhang, Elias-Ramzey Karnoub, Shigeaki Umeda, Ronan Chaligné, Ignas Masilionis, Caitlin McIntyre, Akimasa Hayashi, **Palash Sashittal**, Amanda Zucker, Katelyn Mullen, Alvin Makohon-Moore, Christine Iacobuzio-Donahue
Nature Communications, 2023.

5 Modal analysis and interface tracking of multiphase flows using dynamic mode decomposition
Palash Sashittal, Robert Chiodi, Timothy B. Morgan, Olivier Desjardins, Theodore J. Heindel, Daniel J. Bodony
International Journal of Multiphase Flows, 2022.

6 Parsimonious clone tree integration in cancer
Palash Sashittal, Simone Zaccaria, and Mohammed El-Kebir
Algorithms for Molecular Biology, 2022.
Special issue for Workshop on Algorithms in Bioinformatics (WABI) 2021.

7 Accurate Identification of Transcription Regulatory Sequences and Genes in Coronaviruses
Chuanyi Zhang∗, **Palash Sashittal**∗, and Mohammed El-Kebir
Molecular Biology and Evolution, 2022.

8 Design of SARS-CoV-2 variant-specific PCR assays considering regional and temporal characteristics
Chamteut Oh∗, **Palash Sashittal**∗, Aijia Zhou, Leyi Wang, Mohammed El-Kebir, and Thanh H. Nguyen
Applied and Environmental Microbiology, 2022.

9 Jumper enables discontinuous transcript assembly in Coronaviruses
Palash Sashittal, Chuanyi Zhang, Jian Peng, and Mohammed El-Kebir
Nature Communications, 2021.

10 Data driven sensor placement for fluid flows
Palash Sashittal, and Daniel J. Bodony
Theoretical and Computational Fluid Dynamics, 2021.

11 doubletD: detecting doublets in single-cell DNA sequencing data
Leah Weber∗, **Palash Sashittal**∗, and Mohammed El-Kebir
Bioinformatics, 2021.
Special issue for Intelligent Systems for Molecular Biology (ISMB) 2021.

12 Sampling and summarizing transmission trees with multi-strain infections
Palash Sashittal, and Mohammed El-Kebir
Bioinformatics, 2020.
Special issue for Intelligent Systems for Molecular Biology (ISMB) 2020.

13 Reduced-order control using low-rank dynamic mode decomposition
Palash Sashittal, and Daniel J. Bodony
Theoretical and Computational Fluid Dynamics, 2019.

Conference Presentations

1 Startle: a star homoplasy approach for CRISPR-Cas9 lineage tracing
Palash Sashittal*, Henri Schmidt*, Michelle Chan, and Benjamin Raphael
27th Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2023.

2 A zero-agnostic model for copy number evolution in cancer
Henri Shcmidt, **Palash Sashittal** and Ben Raphael
15th RECOMB Satellite Workshop on Computational Cancer Biology, 2023.

3 CORSID enables de novo identification of transcription regulatory sequences and genes in Coronaviruses
Chuanyi Zhang*, **Palash Sashittal***, and Mohammed El-Kebir
26th Annual International Conference on Research in Computational Molecular Biology (RECOMB), 2022.

4 Parsimonious clone tree reconciliation in cancer
Palash Sashittal, Simone Zaccaria, and Mohammed El-Kebir
Workshop on Algorithms in Bioinformatics (WABI), 2021.

5 doubletD: detecting doublets in single-cell DNA sequencing data
Leah Weber*, **Palash Sashittal***, and Mohammed El-Kebir
Intelligent Systems for Molecular Biology (ISMB), 2021

6 Sampling and summarizing transmission trees with multi-strain infections
Palash Sashittal, and Mohammed El-Kebir
Intelligent Systems for Molecular Biology (ISMB), 2020.

7 SharpTNI: counting and sampling parsimonious transmission networks under a weak bottleneck
Palash Sashittal, and Mohammed El-Kebir
RECOMB Comparative Genomics (RECOMB-CG), 2019.

8 Low-rank dynamic mode decomposition using Riemannian manifold optimization
Palash Sashittal, and Daniel J. Bodony
IEEE conference on Decision and Control (IEEE CDC) 2018.

Software

Computational Biology

ConDoR ConDoR infers tumor phylogenies from targeted single-cell DNA sequencing data using SNVs as phylogenetic markers and partial information about CNAs in the form of clustering of cells with similar copy-number profiles.
https://github.com/raphael-group/ConDoR

Startle Startle computes parsimonious cell lineage trees from CRISPR-Cas9 based lineage tracing data using a specialized evolutionary model that captures the properties of CRISPR-Cas9 mutations.
https://github.com/raphael-group/startle

Lazac	Lazac employs a novel evolutionary model for copy number evolution to build tumor phylogenies from large-scale single-cell sequencing data. https://github.com/raphael-group/lazac-copy-number
CORSID	CORSID simultaneously identifies transcription regulatory sites (TRSs), the core sequence and gene locations given an unannotated coronavirus genome sequence. https://github.com/elkebir-group/CORSID
PRIMES	PRIMES enables the design of reliable PCR assays that can be used to track dominant SARS-CoV-2 variants in local sewage samples. https://github.com/elkebir-group/primer-analysis
Jumper	Jumper reconstructs RNA transcripts from RNA-seq data, specifically for transcriptomic analysis of viruses that exhibit subgenomic RNAs such as coronaviruses. https://github.com/elkebir-group/Jumper
Paction	Paction is a method to integrate SNV and CNA trees for the same tumor to generate a comprehensive phylogeny annotated with both SNV and CNA events. https://github.com/elkebir-group/paction
doubletD	doubletD is an efficient doublet detector designed for scDNA-seq data. Incorporating doubletD in scDNA-seq analysis pipelines leads to more accurate results. https://github.com/elkebir-group/doubletD
TiTUS	TiTUS is a tool that generates a set of feasbile transmission history for a given timed phylogeny that satisfies the direct transmission constraint while supporting a weak transmission bottleneck. https://github.com/elkebir-group/TiTUS
SharpTNI	SharpTNI counts and samples solutions from the space of most parsimonious transmission networks for an outbreak under a weak transmission bottleneck. https://github.com/elkebir-group/SharpTNI

Data-Driven Dynamical Modeling

lrDMD	Low-rank dynamic mode decomposition (lrDMD) solves for a rank-constrained linear representation of the dynamical system for given series of data snapshots. https://bitbucket.org/sashitt2/lrdmd
KF-DMD	A data-driven method for optimal sensor placement and parameter optimization using transfer operator based reduced order models. https://github.com/sashitt2/optimal_sensing

Teaching and Mentoring Experience

Postdoctoral Mentor	3 graduate and 2 undergraduate students
Graduate Mentor	1 graduate and 1 undergraduate student
Teaching Assistant	Computational Aerodynamics (Spring 2015) Viscous Flow and Heat Transfer (Fall 2016) Aerospace Flight Mechanics (Spring 2018) Incompressible Flows (Fall 2018)

Professional Activities

Outreach	Invited speaker at **Computer Science Youth of America** (CSYA) 2023
	Mentor of the winning team at **AAASE Summer Academy** 2023
	Volunteer at **Avanti Fellows** 2013-2014
Reviewer	Bioinformatics 2023
	International Journal of Multiphase Flows 2022
	PLOS Computational Biology 2021
	ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB) 2020, 2021, 2022
	Conference on Research in Computational Molecular Biology (RECOMB) 2020, 2021, 2022, 2023
	IEEE American Control Conference (ACC) 2019
Judge	UIUC Undergraduate Research Symposium 2018

References

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