

Palash Sashittal

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Employment History

Sep. 2021 – to date	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: <i>Flow control and sensing using data-driven reduced-order modeling.</i>
	MSc., University of Illinois at Urbana-Champaign in Computer Science. Thesis: <i>Algorithms for infection and cancer genomics.</i>
2014	B.Tech., Indian Institute of Technology Bombay in Aerospace Engineering.

Prizes and Awards

2023	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.

Under Review

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

- 2 Startle: a star homoplasy approach for CRISPR-Cas9 lineage tracing
Palash Sashittal*, Henri Schmidt*, Michelle Chan and Ben Raphael
under review for *Cell Systems*, 2023.
Invited journal version of RECOMB 2023 conference paper.
- 3 A zero-agnostic model for copy number evolution in cancer
Henri Schmidt, **Palash Sashittal** and Ben Raphael
under review for *PLOS Computational Biology*, 2023.
Best paper award at RECOMB-CCB, 2023.

Journal Articles

- 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 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.
- 8 Jumper enables discontinuous transcript assembly in Coronaviruses
Palash Sashittal, Chuanyi Zhang, Jian Peng, and Mohammed El-Kebir
Nature Communications, 2021.
- 9 Data driven sensor placement for fluid flows
Palash Sashittal, and Daniel J. Bodony
Theoretical and Computational Fluid Dynamics, 2021.
- 10 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.
- 11 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.

- 12 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 Schmidt, **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/constrained-Dollo>

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 feasible 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 and Mentoring Experience (continued)

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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