

# Palash Sashittal

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## Employment History

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| Sep. 2021 – to date   | <b>Postdoctoral research associate</b> , Department of Computer Science, Princeton University                        |
| Aug. 2019 – Aug. 2021 | <b>Graduate research assistant</b> , Department of Computer Science, University of Illinois at Urbana-Champaign      |
| Aug. 2014 – Aug. 2019 | <b>Graduate research assistant</b> , Department of Aerospace Engineering, University of Illinois at Urbana-Champaign |

## Education

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

## Awards

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| 2023 | Invited for the <b>Cornell Future Faculty Symposium</b><br><b>Best paper award</b> at RECOMB-CCB conference.   |
| 2019 | <b>Aerospace Graduate Student Travel Award</b>   |
| 2018 | <b>IEEE CDC Student Travel Grant</b> .<br><b>Mavis Future Faculty Fellowship</b> , University of Illinois at Urbana-Champaign.   |
| 2016 | <b>Center for Turbulence Research Summer Program Fellowship</b> , Stanford University.   |
| 2013 | <b>Undergraduate Research Award</b> , Indian Institute of Technology Bombay.   |
| 2010 | <b>Certificate of Merit by Central Board of Secondary Education</b> , given to the top 0.1% students in India.<br><b>Kishore Vaigyanik Protsahan Yojana (KVPY) Scholarship</b> (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 (In Print).
- 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 Shmidt, **Palash Sashittal** and Ben Raphael  
*PLOS Computational Biology*, 2023 (In Print).  
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  
*27<sup>th</sup> 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  
*15<sup>th</sup> 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  
*26<sup>th</sup> 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

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|----------------|--|
| <b>ConDoR</b>  | 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.<br><a href="https://github.com/raphael-group/ConDoR">https://github.com/raphael-group/ConDoR</a> |
| <b>Startle</b> | 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.<br><a href="https://github.com/raphael-group/startle">https://github.com/raphael-group/startle</a>                              |
| <b>Lazac</b>   | Lazac employs a novel evolutionary model for copy number evolution to build tumor phylogenies from large-scale single-cell sequencing data.<br><a href="https://github.com/raphael-group/lazac-copy-number">https://github.com/raphael-group/lazac-copy-number</a>   |

|                 |   |
|-----------------|---|
| <b>CORSID</b>   | CORSID simultaneously identifies transcription regulatory sites (TRSs), the core sequence and gene locations given an unannotated coronavirus genome sequence.<br><a href="https://github.com/elkebir-group/CORSID">https://github.com/elkebir-group/CORSID</a>                                     |
| <b>PRIMES</b>   | PRIMES enables the design of reliable PCR assays that can be used to track dominant SARS-CoV-2 variants in local sewage samples.<br><a href="https://github.com/elkebir-group/primer-analysis">https://github.com/elkebir-group/primer-analysis</a>   |
| <b>Jumper</b>   | Jumper reconstructs RNA transcripts from RNA-seq data, specifically for transcriptomic analysis of viruses that exhibit subgenomic RNAs such as coronaviruses.<br><a href="https://github.com/elkebir-group/Jumper">https://github.com/elkebir-group/Jumper</a>                                     |
| <b>Paction</b>  | 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.<br><a href="https://github.com/elkebir-group/paction">https://github.com/elkebir-group/paction</a>  |
| <b>doubletD</b> | doubletD is an efficient doublet detector designed for scDNA-seq data. Incorporating doubletD in scDNA-seq analysis pipelines leads to more accurate results.<br><a href="https://github.com/elkebir-group/doubletD">https://github.com/elkebir-group/doubletD</a>                                  |
| <b>TiTUS</b>    | 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.<br><a href="https://github.com/elkebir-group/TiTUS">https://github.com/elkebir-group/TiTUS</a> |
| <b>SharpTNI</b> | SharpTNI counts and samples solutions from the space of most parsimonious transmission networks for an outbreak under a weak transmission bottleneck.<br><a href="https://github.com/elkebir-group/SharpTNI">https://github.com/elkebir-group/SharpTNI</a>  |

## Data-Driven Dynamical Modeling

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

## Teaching and Mentoring Experience

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

## Professional Activities

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

## References

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