

# Can Firtina

+41 76 453 34 24    canfirtina@gmail.com    <https://canfirtina.com>

## RESEARCH INTERESTS

---

I specialize in the intersection of bioinformatics and computer architecture. My key expertise and research areas include:

- **Sequence Analysis:** Designing fast and accurate algorithms for sequence analysis (e.g., read mapping and *de novo* assembly) to improve the speed and accuracy of bioinformatics workflows.
- **Real-time and Raw Nanopore Signal Analysis:** Developing algorithms and systems for the rapid and accurate real-time analysis of raw nanopore sequencing data (i.e., raw electrical signals). Designing systems for portable and on-site sequence analysis using resource-constrained devices.
- **Hardware-Software Co-Design for Bioinformatics:** Integrating computing architectures and algorithms tailored for bioinformatics applications using emerging technologies and computing paradigms (e.g., memory- and storage-centric designs) alongside commodity hardware (e.g., GPUs, FPGAs), ensuring high performance and accuracy.
- **Error Correction:** Designing architectures and algorithms to correct errors in sequencing data by using AI/ML approaches.
- **Computational Tools for Genome Editing:** Designing and optimizing algorithms, tools, and pipelines to perform accurate and fast genome editing experiments.

## EDUCATION

---

- |                       |  |
|-----------------------|--|
| Sep. 2018 - Present   | ETH Zurich, Zurich, Switzerland<br>Ph.D. in Electrical and Computer Engineering (D-ITET)<br>Advisor: <a href="#">Prof. Onur Mutlu</a><br>Thesis: “Enabling Fast, Accurate, and Efficient Real-Time Genome Analysis via New Algorithms and Techniques”<br>Thesis Committee: <a href="#">Prof. Reetuparna Das</a> , <a href="#">Dr. Hasindu Gamaarachchi</a> , <a href="#">Prof. Benjamin Langmead</a> , <a href="#">Prof. Heng Li</a> |
| Sep. 2015 - Jan. 2018 | Bilkent University, Ankara, Turkey<br>M.Sc. in Computer Engineering<br>Advisor: <a href="#">Prof. Can Alkan</a><br>Thesis: “Assessment and Correction of Errors in DNA Sequencing Technologies”  |
| Sep. 2011 - Jun. 2015 | Bilkent University, Ankara, Turkey<br>B.Sc. (High Honors) in Computer Engineering  |

## RESEARCH EXPERIENCE

---

- |                |   |
|----------------|---|
| 2018 - Present | Graduate Research Assistant, <a href="#">SAFARI Research Group</a> , ETH Zurich, Switzerland                                |
| 2015 - 2017    | Graduate Research Assistant, <a href="#">Alkan Lab</a> , Bilkent University, Turkey   |
| 2015           | Undergraduate Research Assistant, Supervisor: <a href="#">Levent Onural</a> , Bilkent University, Turkey                    |
| 2015           | Undergraduate Research Assistant, Supervisor: <a href="#">Fatos Yarman Vural</a> , Middle East Technical University, Turkey |

- 2014** Undergraduate Research Intern, Supervisor: [Levent Burak Kara](#), Carnegie Mellon University, PA, USA
- 2013 - 2015** Undergraduate Research Assistant, Supervisor: [Oznur Tastan](#), Bilkent University, Turkey

## TEACHING EXPERIENCE

---

- Sep. 2023 - Present** Lecturer, ETH Zurich
- Genome Sequencing on Mobile Devices  
Fall 2024: [\[Course Page\]](#), [\[Course Catalogue\]](#)  
Spring 2024: [\[Course Page\]](#), [\[Course Catalogue\]](#), [\[YouTube Playlist\]](#)  
Fall 2023: [\[Course Page\]](#), [\[Course Catalogue\]](#), [\[YouTube Playlist\]](#)
  - Accelerating Genome Analysis with FPGAs, GPUs, and New Execution Paradigms  
Fall 2024: [\[Course Page\]](#), [\[Course Catalogue\]](#)  
Spring 2024: [\[Course Page\]](#), [\[Course Catalogue\]](#), [\[YouTube Playlist\]](#)  
Fall 2023: [\[Course Page\]](#), [\[Course Catalogue\]](#), [\[YouTube Playlist\]](#)
- Sep. 2018 - Present** Teaching Assistant, ETH Zurich
- [Digital Design and Computer Architecture](#) (Spring 2019 - )
  - [Computer Architecture](#) (Fall 2018 - )
  - [Seminar in Computer Architecture](#) (Spring 2018 - )
  - [Genome Sequencing on Mobile Devices](#) (Spring 2020 - Spring 2023)
  - [Accelerating Genome Analysis with FPGAs, GPUs, and New Execution Paradigms](#) (Spring 2020 - Spring 2023)
  - Information Systems for Engineers (Fall 2018)
- Fall 2015 - Fall 2017** Teaching Assistant, Bilkent University
- Automata Theory and Formal Languages (Fall 2015 - Fall 2017)

## HONORS AND AWARDS

---

- 2017** Best Teaching Assistant Award  
Computer Engineering Department, Bilkent University
- 2015** Second Place in Software Development Contest on Scientific Solutions  
The Scientific and Technological Research Council of Turkey
- 2015** First Place in Senior Design Project  
Computer Engineering Department, Bilkent University
- 2012 - 2015** High Honors Scholarship  
Computer Engineering Department, Bilkent University

## THESIS PUBLICATIONS

---

1. **Can Firtina**, Maximilian Mordig, Harun Mustafa, Joël Lindegger, Sayan Goswami, Stefano Mercogliano, Yan Zhu, Andre Kahles, and Onur Mutlu, “Rawsamble: Overlapping and Assembling Raw Nanopore Signals using a Hash-based Seeding Mechanism,” Accepted Talk in [ISMB \(HiTSeq\)](#), Montreal, QC, Canada, July 2024.
2. **Can Firtina**, Melina Soysal, Joel Lindegger, and Onur Mutlu, “[RawHash2: Mapping Raw Nanopore Signals Using Hash-Based Seeding and Adaptive Quantization](#),” *Bioinformatics*, July 2024.

3. **Can Firtina**, Nika Mansouri Ghiasi, Joel Lindegger, Gagandeep Singh, Meryem Banu Cavlak, Haiyu Mao, and Onur Mutlu, “[RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes](#),” in Proceedings of ISMB/ECCB, Lyon, France, July 2023.
4. **Can Firtina**, Jisung Park, Mohammed Alser, Jeremie S Kim, Damla Senol Cali, Taha Shahroodi, Nika Mansouri Ghiasi, Gagandeep Singh, Konstantinos Kanellopoulos, Can Alkan, and Onur Mutlu, “[BLEND: a fast, memory-efficient and accurate mechanism to find fuzzy seed matches in genome analysis](#),” *NAR Genomics and Bioinformatics*, March 2023.

## **FIRST AND CO-FIRST AUTHOR PUBLICATIONS**

---

1. **Can Firtina**, Maximilian Mordig, Harun Mustafa, Joël Lindegger, Sayan Goswami, Stefano Mercogliano, Yan Zhu, Andre Kahles, and Onur Mutlu, “[Rawsamble: Overlapping and Assembling Raw Nanopore Signals using a Hash-based Seeding Mechanism](#),” Accepted Talk in **ISMB (HiTSeq)**, Montreal, QC, Canada, Jul 2024.
2. Jeremie S. Kim, **Can Firtina**, Meryem Banu Cavlak, Damla Senol Cali, Nastaran Hajinazar, Mohammed Alser, Can Alkan, and Onur Mutlu, “[AirLift: A Fast and Comprehensive Technique for Remapping Alignments between Reference Genomes](#),” *IEEE/ACM TCBB*, Aug 2024.
3. **Can Firtina**, Melina Soysal, Joel Lindegger, and Onur Mutlu, “[RawHash2: Mapping Raw Nanopore Signals Using Hash-Based Seeding and Adaptive Quantization](#),” *Bioinformatics*, Jul 2024.
4. **Can Firtina**, Kamlesh Pillai, Gurpreet S. Kalsi, Bharathwaj Suresh, Damla Senol Cali, Jeremie Kim, Taha Shahroodi, Meryem Banu Cavlak, Joel Lindegger, Mohammed Alser, Juan Gómez Luna, Sreenivas Subramoney, and Onur Mutlu, “[ApHMM: Accelerating Profile Hidden Markov Models for Fast and Energy-Efficient Genome Analysis](#),” *ACM TACO*, Feb 2024.
5. **Can Firtina**, Nika Mansouri Ghiasi, Joel Lindegger, Gagandeep Singh, Meryem Banu Cavlak, Haiyu Mao, and Onur Mutlu, “[RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes](#),” in Proceedings of ISMB/ECCB, Lyon, France, Jul 2023.
6. Onur Mutlu, and **Can Firtina**, “[Accelerating Genome Analysis via Algorithm-Architecture Co-Design](#),” in the 60th Design Automation Conference (DAC), San Francisco, CA, USA, Jul 2023.
7. **Can Firtina**, Jisung Park, Mohammed Alser, Jeremie S Kim, Damla Senol Cali, Taha Shahroodi, Nika Mansouri Ghiasi, Gagandeep Singh, Konstantinos Kanellopoulos, Can Alkan, and Onur Mutlu, “[BLEND: a fast, memory-efficient and accurate mechanism to find fuzzy seed matches in genome analysis](#),” *NAR Genomics and Bioinformatics*, Mar 2023.
8. **Can Firtina**, Jeremie S. Kim, Mohammed Alser, Damla Senol Cali, A. Ercument Cicek, Can Alkan, and Onur Mutlu, “[Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm](#),” *Bioinformatics*, Jun 2020.
9. **Can Firtina**, Ziv Bar-Joseph, Can Alkan, and A. Ercument Cicek, “[Hercules: a profile HMM-based hybrid error correction algorithm for long reads](#),” *Nucleic Acids Research*, Nov 2018.
10. **Can Firtina**, and Can Alkan, “[On genomic repeats and reproducibility](#),” *Bioinformatics*, Aug 2016.

## **CO-SUPERVISED PUBLICATIONS**

---

1. Meryem Banu Cavlak, Gagandeep Singh, Mohammed Alser, **Can Firtina**, Joel Lindegger, Mohammad Sadrosadati, Nika Mansouri Ghiasi, Can Alkan, and Onur Mutlu, “[TargetCall: Eliminating the Wasted Computation in Basecalling via Pre-Basecalling Filtering](#),” *Frontiers in Genetics*, Sep 2024.
2. Joël Lindegger, **Can Firtina**, Nika Mansouri Ghiasi, Mohammad Sadrosadati, Mohammed Alser, and Onur Mutlu, “[RawAlign: Accurate, Fast, and Scalable Raw Nanopore Signal Mapping via Combining Seeding and Alignment](#),” *arXiv*, Oct 2023. [Under Submission]

## **OTHER CO-AUTHORED PUBLICATIONS**

---

1. Nika Mansouri Ghiasi, Mohammad Sadrosadati, Harun Mustafa, Arvid Gollwitzer, **Can Firtina**, Julien Eudine, Haiyu Mao, Joël Lindegger, Meryem Banu Cavlak, Mohammed Alser, Jisung Park, and Onur Mutlu, “[MegIS: High-Performance, Energy-Efficient, and Low-Cost Metagenomic Analysis with In-Storage Processing](#),” in *ISCA*, Jul 2024.
2. Mohammed Alser, Brendan Lawlor, Richard J. Abdill, Sharon Waymost, Ram Ayyala, Neha Rajkumar, Nathan LaPierre, Jaqueline Brito, André M. Ribeiro-dos-Santos, Nour Almadhoun, Varuni Sarwal, **Can Firtina**, Tomasz Osinski, Eleazar Eskin, Qiyang Hu, Derek Strong, Byoung-Do (B.D) Kim, Malak S. Abedalthagafi, Onur Mutlu, and Serghei Mangul, “[Packaging and containerization of computational methods](#),” *Nature Protocols*, Apr 2024.
3. Gagandeep Singh, Mohammed Alser, Kristof Denolf, **Can Firtina**, Alireza Khodamoradi, Meryem Banu Cavlak, Henk Corporaal, and Onur Mutlu, “[RUBICON: a framework for designing efficient deep learning-based genomic basecallers](#),” *Genome Biology*, Feb 2024.
4. Arvid E. Gollwitzer, Mohammed Alser, Joel Bergholdt, Joel Lindegger, Maximilian-David Rumpf, **Can Firtina**, Serghei Mangul, and Onur Mutlu, “[MetaFast: Enabling Fast Metagenomic Classification via Seed Counting and Edit Distance Approximation](#),” *arXiv*, Nov 2023. [Under Submission]
5. Maximilian-David Rumpf, Mohammed Alser, Arvid E. Gollwitzer, Joel Lindegger, Nour Almadhoun, **Can Firtina**, Serghei Mangul, and Onur Mutlu, “[SequenceLab: A Comprehensive Benchmark of Computational Methods for Comparing Genomic Sequences](#),” *arXiv*, Oct 2023. [Under Submission]
6. Taha Shahroodi, Gagandeep Singh, Mahdi Zahedi, Haiyu Mao, Joel Lindegger, **Can Firtina**, Stephan Wong, Onur Mutlu, and Said Hamdioui, “[Swordfish: A Framework for Evaluating Deep Neural Network-Based Basecalling Using Computation-In-Memory with Non-Ideal Memristors](#),” in *MICRO*, Oct 2023.
7. Konstantinos Kanellopoulos, Rahul Bera, Kosta Stojiljkovic, F. Nisa Bostanci, **Can Firtina**, Rachata Ausavarungnirun, Rakesh Kumar, Nastaran Hajinazar, Mohammad Sadrosadati, Nandita Vijaykumar, and Onur Mutlu, “[Utopia: Fast and Efficient Address Translation via Hybrid Restrictive & Flexible Virtual-to-Physical Address Mappings](#),” in *MICRO*, Oct 2023.
8. Haiyu Mao, Mohammed Alser, Mohammad Sadrosadati, **Can Firtina**, Akanksha Baranwal, Damla Senol Cali, Aditya Manglik, Nour Almadhoun Alserr, and Onur Mutlu, “[GenPIP: In-Memory Acceleration of Genome Analysis via Tight Integration of Basecalling and Read Mapping](#),” in *MICRO*, Oct 2022.
9. Jeremie S Kim, **Can Firtina**, Meryem Banu Cavlak, Damla Senol Cali, Can Alkan, and Onur Mutlu, “[FastRemap: a tool for quickly remapping reads between genome assemblies](#),” *Bioinformatics*, Sep 2022.
10. Mohammed Alser, Joel Lindegger, **Can Firtina**, Nour Almadhoun, Haiyu Mao, Gagandeep Singh, Juan Gomez-Luna, and Onur Mutlu, “[From molecules to genomic variations: Accelerating genome analysis via intelligent algorithms and architectures](#),” *CSBJ*, Aug 2022.
11. Taha Shahroodi, Mahdi Zahedi, **Can Firtina**, Mohammed Alser, Stephan Wong, Onur Mutlu, and Said Hamdioui, “[Demeter: A Fast and Energy-Efficient Food Profiler Using Hyperdimensional Computing in Memory](#),” *IEEE Access*, Aug 2022.
12. Damla Senol Cali, Konstantinos Kanellopoulos, Joël Lindegger, Zülal Bingöl, Gurpreet S. Kalsi, Ziyi Zuo, **Can Firtina**, Meryem Banu Cavlak, Jeremie Kim, Nika Mansouri Ghiasi, Gagandeep Singh, Juan Gómez-Luna, Nour Almadhoun Alserr, Mohammed Alser, Sreenivas Subramoney, Can Alkan, Saugata Ghose, and Onur Mutlu, “[SeGraM: A Universal Hardware Accelerator for Genomic Sequence-to-Graph and Sequence-to-Sequence Mapping](#),” in *ISCA*, Jun 2022.
13. Nika Mansouri Ghiasi, Jisung Park, Harun Mustafa, Jeremie Kim, Ataberk Olgun, Arvid Gollwitzer, Damla Senol Cali, **Can Firtina**, Haiyu Mao, Nour Almadhoun Alserr, Rachata Ausavarungnirun,

- Nandita Vijaykumar, Mohammed Alser, and Onur Mutlu, “GenStore: A High-Performance in-Storage Processing System for Genome Sequence Analysis,” in *ASPLOS*, Mar 2022.
14. Levent Onural, Mustafa Çelebi Pınar, and **Can Firtina**, “Modeling Economic Activities and Random Catastrophic Failures of Financial Networks via Gibbs Random Fields,” *Computational Economics*, Aug 2021.
  15. Damla Senol Cali, Gurpreet S. Kalsi, Zülal Bingöl, **Can Firtina**, Lavanya Subramanian, Jeremie S. Kim, Rachata Ausavarungnirun, Mohammed Alser, Juan Gómez-Luna, Amirali Boroumand, Anant Norion, Allison Scibisz, Sreenivas Subramoney, Can Alkan, Saugata Ghose, and Onur Mutlu, “GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis,” in *MICRO*, Oct 2020.
  16. Burçak Otlı, **Can Firtina**, Sündüz Keleş, and Ozgur Tastan, “GLANET: genomic loci annotation and enrichment tool,” *Bioinformatics*, Sep 2017.

## CONFERENCE AND WORKSHOP TALKS

---

1. **Rawsample: Overlapping and Assembling Raw Nanopore Signals using a Hash-based Seeding Mechanism**  
[32nd Annual Conference on Intelligent Systems for Molecular Biology \(ISMB\)](#), Montreal, QC, Canada. July 14 2024.  
[Slides [pdf/ppt](#)]
2. **ApHMM: Accelerating Profile Hidden Markov Models for Fast and Energy-Efficient Genome Analysis**  
[High Performance, Edge And Cloud computing \(HiPEAC\) 2024](#), Munich, Germany. January 17 2024.  
[Video] [Slides [pdf/ppt](#)]
3. **RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes**  
[31st Annual Conference on Intelligent Systems for Molecular Biology \(ISMB\) and the 22nd European Conference on Computational Biology \(ECCB\)](#), Lyon, France. July 25 2023.  
[Video] [Slides [pdf/ppt](#)]
4. **RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes**  
[The 5th Workshop on Accelerator Architecture in Computational Biology and Bioinformatics \(AACBB\)](#), Orlando, Florida, USA. June 18 2023.  
[Video]
5. **BLEND: A fast, memory-efficient and accurate mechanism to find fuzzy seed matches in genome analysis**  
[27th Annual International Conference on Research in Computational Molecular Biology \(RECOMB\)](#), Istanbul, Turkey. April 19 2023.  
[Video] [Slides [pdf/ppt](#)]
6. **AirLift: A Fast and Comprehensive Technique for Remapping Alignments between Reference Genomes**  
[The 21st Asia Pacific Bioinformatics Conference \(APBC\)](#), Changsha, China. April 16 2023.  
[Video] [Slides [pdf/ppt](#)]
7. **Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm**  
ExaBiome/PASSION/SAFARI Workshop on Architectures and HPC for Genomics, Virtual. May 26

2021.

[Video] [Slides [pdf](#)/[ppt](#)]

## INVITED TALKS AND LECTURES

---

- 1. Enabling Fast, Accurate, and Efficient Real-Time Genomic Sequence Analysis via New Algorithms and Architectures**  
Invited Talk, [AMD](#), Virtual, September 13 2024.  
[Slides [pdf](#)/[ppt](#)]
- 2. Enabling Fast, Accurate, and Efficient Real-Time Genomic Sequence Analysis via New Algorithms and Architectures**  
Invited Talk, [Huawei Research Center Zurich](#), Zurich, Switzerland. May 17 2024.  
[Slides [pdf](#)/[ppt](#)]
- 3. Real-time Sequence Analysis from Raw Nanopore Electrical Signals with Accurate Hash-based Search Mechanisms**  
Invited Talk, [The Broad Institute of MIT and Harvard](#), hosted by [Victoria Popic, Ph.D.](#), Cambridge, MA, USA. May 10 2024.  
[Slides [pdf](#)/[ppt](#)]
- 4. Real-time Analysis of Genomic Sequences from Nanopore Electrical Signals by Fast and Accurate Hash-based Search**  
Invited Talk, [The Jackson Laboratory \(JAX\)](#), hosted by [Joshy George, Ph.D.](#), Farmington, CT, USA. May 6 2024.  
[Slides [pdf](#)/[ppt](#)]
- 5. Real-time Analysis of Genomic Sequences from Nanopore Electrical Signals by Fast and Accurate Hash-based Search**  
Invited Talk, [Tufts University - Department of Computer Science](#), hosted by [Prof. Lenore J. Cowen](#), Medford, MA, USA. May 3 2024.  
[Video] [Slides [pdf](#)/[ppt](#)]
- 6. Introduction to Real-Time Raw Nanopore Signal Analysis: RawHash and RawHash2**  
Invited Lecture, [BIO310 - Introduction to Bioinformatics](#), taught by [Oznur Tastan](#), Sabanci University, Istanbul, Turkey. March 18 2024.  
[Video] [Slides [pdf](#)/[ppt](#)]
- 7. RawHash and RawHash2: Enabling Fast and Accurate Real-time Analysis of Raw Nanopore Signals for Large Genomes using a Hash-based Seeding Mechanism**  
Invited Talk, [Leibniz Institute for Immunotherapy \(LIT\)](#), hosted by [Prof. Birte Kehr](#), Regensburg, Germany. January 17 2024.  
[Slides [pdf](#)/[ppt](#)]
- 8. Enabling Fast, Accurate and Efficient Real-Time Genome Analysis via New Algorithms and Architectures**  
Invited Talk, [Technical University of Munich \(TUM\) - School of Computation, Information and Technology \(CIT\)](#), hosted by [Prof. Ulf Schlichtmann](#), Munich, Germany. January 16 2024.  
[Slides [pdf](#)/[ppt](#)]
- 9. Enabling Fast, Accurate and Efficient Real-Time Genome Analysis via New Algorithms and Architectures**  
Invited Talk, [Huawei Munich Research Center](#), Munich, Germany. January 15 2024.  
[Slides [pdf](#)/[ppt](#)]
- 10. Enabling Accurate, Fast, and Memory-Efficient Genome Analysis via Efficient and Intelligent Algorithms**



Invited Talk, [Department of Electrical Engineering and Computer Sciences](#), hosted by Giulia Guidi, UC Berkeley, Berkeley, CA, United States. May 27 2022.

[\[Video\]](#) [\[Slides pdf/ppt\]](#)

#### 11. **Enabling Accurate, Fast, and Memory-Efficient Genome Analysis via Efficient and Intelligent Algorithms**

Invited Seminar Talk, [BIN590 Graduate Seminar in Bioinformatics](#), Graduate School of Informatics, Middle East Technical University, Virtual. January 10 2022.

[\[Video\]](#) [\[Slides pdf/ppt\]](#)

### OPEN SOURCE TOOLS

---

- **RawHash, RawHash2 and Rawsamble:** <https://github.com/CMU-SAFARI/RawHash>
- **BLEND:** <https://github.com/CMU-SAFARI/BLEND>
- **ApHMM-GPU:** <https://github.com/CMU-SAFARI/ApHMM-GPU>
- **AirLift:** <https://github.com/CMU-SAFARI/AirLift>
- **Apollo:** <https://github.com/CMU-SAFARI/Apollo>
- **Hercules:** <https://github.com/BilkentCompGen/hercules>
- **On Genomic Repeats and Reproducibility:** <https://github.com/calkan/reproducibility>

### STUDENT MENTORSHIP

---

- **ETH Zurich Ph.D. and M.Sc. Students**

Joël Lindegger (2023 - 2024), Taha Shahroodi (2023), Meryem Banu Cavlak (2022 - 2024), Melina Soysal (2023)

- **ETH Zurich B.Sc. Students**

Ulysse McConnell (2024), Furkan Eris (2024), Marie-Louise Dugua (2023 - 2024), Yan Zhu (2023 - 2024), Markus Lacher (2023), Özcan Mulaimi (2023), Nicolas Nanzer (2023), Lars Kröger (2023), Nicolas Lehmann (2022), Sebastian Waszkis (2022), Patrick Zimmermann (2022), David Schober (2021), Simone Brunner (2021), Jiacheng Ma (2019), Peter Resutik (2018 - 2019), Batuhan Tomekce (2018 - 2019), Ege Karaismailoglu (2018 - 2019), Burak Kaya (2018 - 2019)

### SERVICE

---

- Technical Reviewer for Conferences: RECOMB, RECOMB-Seq, MICRO, ISCA, HPCA, ASPLOS, PACT, FAST, DSN, ISCAS, ISPASS, USENIX ATC
- Technical Reviewer for Journals: Bioinformatics, BMC Bioinformatics, IEEE Micro, IEEE TC
- Organization Lead:
  - [BIO-Arch: Workshop on Hardware Acceleration of Bioinformatics Workloads](#), jointly held with [RECOMB 2023](#).
  - [Panel on Hardware Acceleration of Bioinformatics Workloads](#), at [RECOMB 2023](#).
  - [ExaBiome/PASSION/SAFARI Workshop on Architectures and HPC for Genomics](#), co-organized with [Giulia Guidi](#).
- Volunteer in Conference Organizations: [RECOMB 2023](#)
- IT Infrastructure Co-Lead, SAFARI Research Group, ETH Zurich, 2018 - 2021.
- IT Infrastructure Lead, Alkan Lab, Bilkent University, 2016 - 2017.

### COLLABORATORS

---

- Onur Mutlu (ETH Zurich)

- Can Alkan (Bilkent University)
- Damla Senol Cali (Bionano Genomics)
- Jeremie S. Kim (Apple)
- Juan Gomez-Luna (NVIDIA)
- Mohammad Sadrosadati (ETH Zurich)
- Nika Mansouri Ghiasi (ETH Zurich)
- Gagandeep Singh (AMD)
- Haiyu Mao (ETH Zurich)
- Taha Shahroodi (TU Delft)
- Andre Kahles (ETH Zurich)
- Harun Mustafa (ETH Zurich)
- Giulia Guidi (Cornell University)
- Sreenivas Subramoney (Intel Labs)
- Gurpreet S. Kalsi (Intel Labs)
- Jisung Park (POSTECH)
- Saugata Ghose (University of Illinois Urbana-Champaign)
- Serghei Mangul (USC)
- A. Ercument Cicek (Bilkent University)
- Oznur Tastan (Sabanci University)
- Levent Onural (Bilkent University)
- Ziv Bar-Joseph (Carnegie Mellon University)

## **REFERENCES**

---

Available upon request.