DAMLA SENOL CALI

Staff Software Engineer, Hardware Acceleration

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RESEARCH INTERESTS

My main research is in bioinformatics and computer architecture. My research focuses on:

- Hardware Acceleration of Bioinformatics Applications
- Genome Analysis Tools
- Hardware/Software Co-Design
- Processing-in-Memory
- Memory Systems

EDUCATION

Carnegie Mellon University, Pittsburgh, PA *August 2021*

Ph.D. in Electrical and Computer Engineering

Advisors: Prof. Onur Mutlu, Prof. Saugata Ghose

Dissertation Title: *Accelerating Genome Sequence Analysis via Efficient Hardware-Algorithm Co-Design*

Carnegie Mellon University, Pittsburgh, PA *December 2019*

M.Sc. in Electrical and Computer Engineering

Advisors: Prof. Onur Mutlu, Prof. Saugata Ghose

Bilkent University, Ankara, Turkey *June 2015*

B.Sc. in Computer Engineering

WORK EXPERIENCE

Bionano Genomics, San Diego, CA, USA *October 2021 – Present*

Staff Software Engineer, Hardware Acceleration

Carnegie Mellon University, Pittsburgh, PA, USA *August 2015 – August 2021*

Graduate Research Assistant

Intel Labs, Portland, OR, USA *May 2020 – December 2020*

Research Intern

Carnegie Mellon University, Pittsburgh, PA, USA *January 2019 – May 2020*

Teaching Assistant (18-240: *Structure and Design of Digital Systems)*

Intel Labs, Santa Clara, CA, USA *May 2018 – August 2018*

Research Intern

Bilkent University, Ankara, Turkey *February 2013 – June 2015*

Undergraduate Research and Teaching Assistant

PEER-REVIEWED PUBLICATIONS

SeGraM: A Universal Hardware Accelerator for Genomic Sequence-to-Graph and Sequence-to-Sequence Mapping

Damla Senol Cali, Konstantinos Kanellopoulos, Joel Lindegger, Zulal Bingol, Gurpreet S. Kalsi, Ziyi Zuo, Can Firtina, Meryem Banu Cavlak, Jeremie S. Kim, Nika Mansouri Ghiasi, Gagandeep Singh, Juan Gomez-Luna, Nour Almadhoun Alserr, Mohammed Alser, Sreenivas Subramoney, Can Alkan, Saugata Ghose, and Onur Mutlu.

To appear in *Proceedings of the 49th International Symposium on Computer Architecture (ISCA), June 2022.*

GenStore: A High-Performance In-Storage Processing System for Genome Sequence Analysis

Nika Mansouri Ghiasi, Jisung Park, Harun Mustafa, Jeremie S. Kim, Ataberk Olgun, Arvid Gollwitzer, Damla Senol Cali, Can Firtina, Haiyu Mao, Nour Almadhoun Alserr, Rachata Ausavarungnirun, Nandita Vijaykumar, Mohammed Alser, and Onur Mutlu.

In *Proceedings of the 27th ACM International Conference on Architectural Support for Programming Languages and Operating Systems (ASPLOS), February 2022.*

FPGA-based Near-Memory Acceleration of Modern Data-Intensive Applications

Gagandeep Singh, Mohammed Alser, Damla Senol Cali, Dionysios Diamantopoulos, Juan Gomez-Luna, Henk Corporaal, and Onur Mutlu.

In *IEEE Micro,* July 2021.

GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis

Damla Senol Cali, Gurpreet S. Kalsi, Zulal Bingol, Can Firtina, Lavanya Subramanian, Jeremie S. Kim, Rachata Ausavarungnirun, Mohammed Alser, Juan Gomez-Luna, Amirali Boroumand, Anant Nori, Allison Scibisz, Sreenivas Subramoney, Can Alkan, Saugata Ghose, and Onur Mutlu.

In *Proceedings of the 53rd International Symposium on Microarchitecture (MICRO), October 2020.*

Accelerating Genome Analysis: A Primer on an Ongoing Journey

Mohammed Alser, Zulal Bingol, Damla Senol Cali, Jeremie S. Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

In *IEEE Micro,* September 2020.

Apollo: A Sequencing-Technology-Independent, Scalable, and Accurate Assembly Polishing Algorithm

Can Firtina, Jeremie S. Kim, Mohammed Alser, Damla Senol Cali, A. Ercument Cicek, Can Alkan, and Onur Mutlu.

In *Bioinformatics*, February 2020.

Demystifying Workload–DRAM Interactions: An Experimental Study

Saugata Ghose, Tianshi Li, Nastaran Hajinazar, Damla Senol Cali, and Onur Mutlu.

In *ACM SIGMETRICS*, June 2019.

GRIM-Filter: Fast Seed Location Filtering in DNA Read Mapping Using Processing-in-Memory Technologies

Jeremie S. Kim, Damla Senol Cali, Hongyi Xin, Donghyuk Lee, Saugata Ghose, Mohammed Alser, Hasan Hassan, Oguz Ergin, Can Alkan, and Onur Mutlu.

In *BMC Genomics*, May 2018.

Nanopore Sequencing Technology and Tools for Genome Assembly: Computational Analysis of the Current State, Bottlenecks and Future Directions

Damla Senol Cali, Jeremie Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

In *Briefings in Bioinformatics,* April 2018.

TECHNICAL REPORTS (OTHERWISE UNPUBLISHED)

FastRemap: A Tool for Quickly Remapping Reads between Genome Assemblies

Jeremie S. Kim, Can Firtina, Meryem Banu Cavlak, Damla Senol Cali, Can Alkan, and Onur Mutlu.

arXiv:2201.06255 [q-bio.GN], January 2022.

BLEND: A Fast, Memory-Efficient, and Accurate Mechanism to Find Fuzzy Seed Matches

Can Firtina, Jisung Park, Jeremie S. Kim, Mohammed Alser, Damla Senol Cali, Taha Shahroodi, Nika Mansouri-Ghiasi, Gagandeep Singh, Konstantinos Kanellopoulos, Can Alkan, and Onur Mutlu.

arXiv:2112.08687 [q-bio.GN], December 2021.

AirLift: A Fast and Comprehensive Technique for Remapping Alignments between Reference Genomes

Jeremie S. Kim, Can Firtina, Meryem Banu Cavlak, Damla Senol Cali, Nastaran Hajinazar, Mohammed Alser, Can Alkan, and Onur Mutlu.

arXiv:1912.08735 [q-bio.GN], February 2021.

PATENTS

Genome Sequence Alignment System and Method

Gurpreet S. Kalsi, Anant V. Nori, Christopher Justin Hughes, Sreenivas Subramoney, Damla Senol Cali.

Filed by *Intel Corporation.* US Patent 16729379, July 2021.

AWARDS

Top 10 Best Student Presenter Award, *TECHCON 2019*, Austin, TX, USA, September 2019.

BitMAC: An In-Memory Accelerator for Bitvector-Based Sequence Alignment of Both Short and Long Genomic Reads

Damla Senol Cali, Gurpreet S. Kalsi, Lavanya Subramanian, Can Firtina, Anant Nori, Jeremie S. Kim, Zulal Bingol, Rachata Ausavarungnirun, Mohammed Alser, Juan Gomez-Luna, Amirali Boroumand, Allison Scibisz, Can Alkan, Sreenivas Subramoney, Saugata Ghose, and Onur Mutlu.

Best Poster Award, *the Eighth RECOMB Satellite Workshop on Massively Parallel Sequencing* ***(RECOMB-Seq)*** *Poster Session*, Paris, France, April 2018.

Accelerating Approximate Pattern Matching with Processing-In-Memory (PIM) and Single-Instruction Multiple-Data (SIMD) Programming

Damla Senol Cali, Zulal Bingol, Jeremie S. Kim, Rachata Ausavarungnirun, Saugata Ghose, Can Alkan, and Onur Mutlu.

CONFERENCE & WORKSHOP PRESENTATIONS

"SeGraM: A Universal Hardware Accelerator for Genomic Sequence-to-Graph and Sequence-to-Sequence Mapping" or "GenGraph: A Hardware Acceleration Framework for Sequence-to-Graph Mapping"

- 49th International Symposium on Computer Architecture (ISCA), New York City, NY, USA, June 2022.
- TECHCON 2021, Virtual, September 2021.

"Accelerating Genome Sequence Analysis via Efficient Hardware-Algorithm Co-Design"

- 4th HPCA Workshop on Accelerator Architecture in Computational Biology and Bioinformatics (AACBB), New York City, NY, USA, June 2022.
- SAFARI Seminar Series, Virtual, November 2021.
- Bilkent University, Computer Engineering Seminar, Ankara, Turkey, December 2019.

"GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis" or "BitMAC: An In-Memory Accelerator for Bitvector-Based Sequence Alignment of Both Short and Long Genomic Reads" or "Accelerating Approximate Pattern Matching with Processing-In-Memory (PIM) and Single-Instruction Multiple-Data (SIMD) Programming"

- The 30th Conference on Intelligent Systems for Molecular Biology (ISMB) – High Throughput Sequencing Algorithms and Applications (HiTSeq), Madison, WI, USA, July 2022.
- The 26th Annual International Conference on Research in Computational Molecular Biology (RECOMB) Poster Session, San Diego, CA, USA, May 2022.
- 53rd International Symposium on Microarchitecture (MICRO), Virtual, October 2020.
- Semiconductor Research Corporation (SRC), Artificial Intelligence Hardware Annual Review, Virtual, September 2020.
- ARM Research Summit, Virtual, September 2020.
- Carnegie Mellon University, PDL Spring Visit Day Poster Session, Virtual, June 2020.
- Carnegie Mellon University, CALCM Seminar, Virtual, April 2020.
- Semiconductor Research Corporation (SRC), System Level Design Annual Review, Austin, TX, USA, September 2019.
- TECHCON 2019, Austin, TX, USA, September 2019.
- 8th RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq) Poster Session, Paris, France, April 2018.

"Nanopore Sequencing Technology and Tools for Genome Assembly: Computational Analysis of the Current State, Bottlenecks and Future Directions" or "Nanopore Sequencing Technology and Tools: Computational Analysis of the Current State, Bottlenecks and Future Directions"

- 2nd HPCA Workshop on Accelerator Architecture in Computational Biology and Bioinformatics (AACBB), Washington, DC, USA, February 2019.
- Intelligent Systems for Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB) Poster Session, Prague, Czech Republic, July 2017.
- Pacific Symposium on Biocomputing (PSB) Poster Session, Hawaii, USA, January 2017.

"Genome Read In-Memory (GRIM) Filter: Fast Location Filtering in DNA Read Mapping with Emerging Memory Technologies"

- 20th Annual International Conference on Research in Computational Molecular Biology (RECOMB) Poster Session, Santa Monica, CA, USA, April 2016.

SKILLS

- **Programming Languages:** C, C++, Python, SystemVerilog, Bash, Java, SQL, MATLAB.
- **Tools/Simulators:** perf, Intel VTune, Intel Quartus, Intel PCM, Synopsys VCS, Ramulator, Gem5.
- **Cloud Platforms:** AWS, Azure, Google Cloud.
- **Other:** Microsoft Office, LaTeX, GitHub, Bitbucket.
- **Languages:** English (Fluent), Turkish (Native Speaker).

MENTORING EXPERIENCE

- **CMU Undergraduate Research Students:** Allison Scibisz, Alisha Mayor, Ziyi Zuo.
- **ETH Zurich Undergraduate Research Students:** Linus Joos, Denis Buckingham, Rafael Wanner, Frederik Mohr.
- **ETH Zurich Master's Research Students:** Joel Lindegger.
- **ETH Zurich Research Interns:** Akanksha Baranwal**,** Meryem Banu Cavlak, Sam Cheung.

PROJECTS

iGarson, June 2015. **Most Usable Senior Project Award.**

iGarson is a mobile application to ease your restaurant experience with reservation, ordering, and table selection functions. It is developed for both iOS and Android mobile devices.

Transmission Patterns Discovery of Genome Structural Variations among Generations of a Family, May 2015**.**

Detecting structural variations of the whole genomes of 17 family members by using different sequencing-based computational tools and discovering the transmission patterns of these variations among these 3 generations of the family.

MEMBERSHIPS

Current:

- IEEE
- IEEE Women in Engineering
- IEEE Young Professionals
- IEEE Engineering in Medicine and Biology Society
    - Technical Committee on Biomedical & Health Informatics
- IEEE Computer Society
    - Technical Community on Computational Life Sciences
    - Technical Community on Computer Architecture
    - Technical Community on Microprogramming and Microarchitecture
- Carnegie Mellon University Alumni Association

- Bilkent University Alumni Association
- TED Ankara College Alumni Association

Past:

- The ACM Special Interest Group on Microarchitecture (ACM SIGMICRO)
- Semiconductor Research Corporation (SRC)
- International Society for Computational Biology (ISCB)
- Computer Architecture Lab at Carnegie Mellon (CALCM)
- Parallel Data Lab at Carnegie Mellon (PDL)