DAMLA SENOL CALL

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RESEARCH INTERESTS

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

EDUCATION

Carnegie Mellon University, Pittsburgh, PA

Ph.D. in Electrical and Computer Engineering

August 2021 (expected)

Advisors: Prof. Onur Mutlu, Prof. Saugata Ghose

Carnegie Mellon University, Pittsburgh, PA

M.S. in Electrical and Computer Engineering

December 2019

Advisors: Prof. Onur Mutlu, Prof. Saugata Ghose

Bilkent University, Ankara, Turkey

B.S. in Computer Engineering

June 2015

WORK EXPERIENCE

Carnegie Mellon University, Pittsburgh, PA, USA

Graduate Research and Teaching Assistant, August 2015 - Present

Intel Labs, Portland, OR, USA

Research Intern, May 2020 - December 2020

Intel Labs, Santa Clara, CA, USA

Research Intern, May 2018 - August 2018

Bilkent University, Ankara, Turkey

Undergraduate Research and Teaching Assistant, February 2013 - June 2015

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

<u>Damla Senol Cali</u>, 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

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

PEER-REVIEWED PUBLICATIONS

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

<u>Damla Senol Cali,</u> 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, <u>Damla Senol Cali</u>, Jeremie S. Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

In IEEE Micro, 2020.

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

Can Firtina, Jeremie S. Kim, Mohammed Alser, <u>Damla Senol Cali</u>, 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, <u>Damla Senol Cali</u>, 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, <u>Damla Senol Cali</u>, 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

<u>Damla Senol Cali</u>, Jeremie Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

In Briefings in Bioinformatics, April 2018.

CONFERENCE PRESENTATIONS

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

<u>Damla Senol Cali</u>, 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.

Presented at ARM Research Summit, September 2020.

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

<u>Damla Senol Cali</u>, 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.

Presented at TECHCON 2019, Austin, TX, USA, September 2019.

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

<u>Damla Senol Cali</u>, Jeremie S. Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

Presented at the 2nd HPCA Workshop on Accelerator Architecture in Computational Biology and Bioinformatics (AACBB), Washington, DC, USA, February 2019.

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

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

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

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

<u>Damla Senol</u>, Jeremie Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

Presented at Intelligent Systems for Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB) Poster Session, Prague, Czech Republic, July 2017.

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

<u>Damla Senol</u>, Jeremie Kim, Saugata Ghose, Can Alkan, and Onur Mutlu.

Presented at *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

Jeremie Kim, <u>Damla Senol</u>, Hongyi Xin, Donghyuk Lee, Mohammed Alser, Hasan Hassan, Oguz Ergin, Can Alkan, and Onur Mutlu.

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

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.

CERTIFICATIONS

IB Bilingual Diploma, Certificate of Achievement, August 2010.

MEMBERSHIPS

- ♦ IEEE and IEEE Computer Society
- ♦ IEEE Women in Engineering
- ♦ IEEE Engineering in Medicine and Biology Society
- ◆ Semiconductor Research Corporation (SRC)
- ♦ International Society for Computational Biology (ISCB)
- ♦ Computer Architecture Lab at Carnegie Mellon (CALCM)
- ♦ Parallel Data Lab at Carnegie Mellon (PDL)
- ♦ Bilkent University Alumni Association
- ♦ TED Ankara College Alumni Association