

CMSC 829C: Algorithms, AI, and Hardware for Biological Data

Lecture 1: Introduction and Course Logistics

Fall 2026

September 1, 2026

Can Firtina | canfirtina@gmail.com | cs.umd.edu/~firtina

Assistant Professor of Computer Science at UMD



Brief Self Introduction

- **Can Firtina**

- Assistant Professor of Computer Science at UMD since Sept 2025
- STORM Group at UMD: storm.cs.umd.edu
- Personal website: cfirtina.com | Contact: canfirtina@gmail.com
- PhD in CS from ETH Zurich in 2025
- MSc and BSc in Computer Engineering from Bilkent University

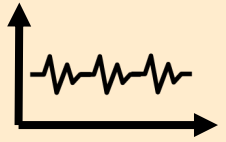
- **Research Interests:** Bioinformatics & Computer Architecture

- Designing algorithmic, machine learning, and hardware solutions for genomics
- Real-time, portable, energy-efficient genome analysis

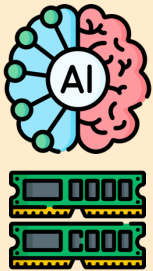


STORM Research Group

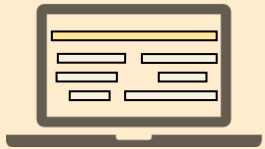
Research Directions



Real-Time and Portable
Genomic Signal Analysis



Data-centric and
AI-Driven Solutions to Analyze
Genomic Data



Accurate and Fast
Algorithms Scalable to
Large Volumes of
Genomic Data



Goal

Enable fundamentally
better integration of
biological data analysis in
our **everyday lives**



Agenda

- The need to co-design algorithms, ML and hardware
- Course information and logistics

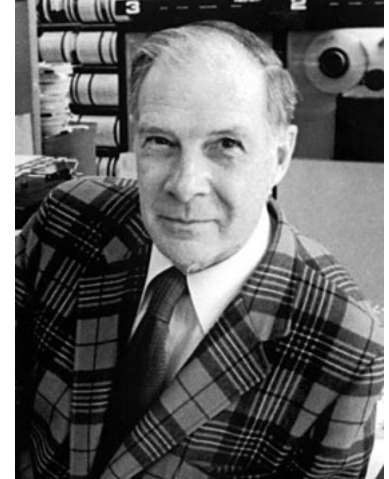
Agenda

- **The need to co-design algorithms, ML and hardware**
- Course information and logistics

The Goal of Computing: Beyond Numbers

"The purpose of computing is insight, not numbers"

Richard Hamming



Recommended: You and Your Research

- Richard Hamming,
["You and Your Research"](#)
Bell Communications Research Colloquium Seminar, 1986.
[\[Lecture Video\]](#) [\[Podcast\]](#)

Richard Hamming

``You and Your Research''

Transcription of the
Bell Communications Research Colloquium Seminar
7 March 1986

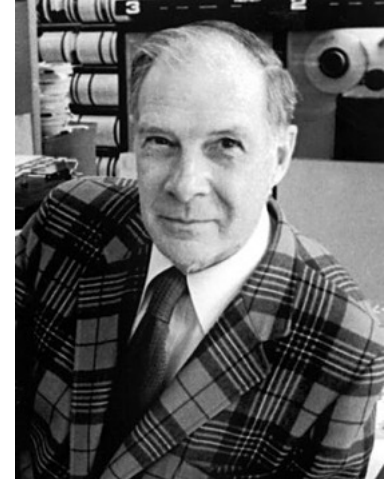
Some More Materials to Internalize

- Bill Dally,
["Moving the needle: Effective Computer Architecture Research in Academe and Industry"](#)
ISCA, 2010.
[\[Alternative Talk Video\]](#)
- Michael Stonebraker,
["Make it Happen"](#)
ACM Turing Award Lecture, 2014.
- Martin A. Schwartz,
["The importance of stupidity in scientific research"](#)
Journal of Cell Science, 2008.

The Goal of Computing: Beyond Numbers

"The purpose of computing is insight, not numbers"

Richard Hamming



Analyzing Genomes Reveals Key Insights



Personalized Medicine



Genome Editing

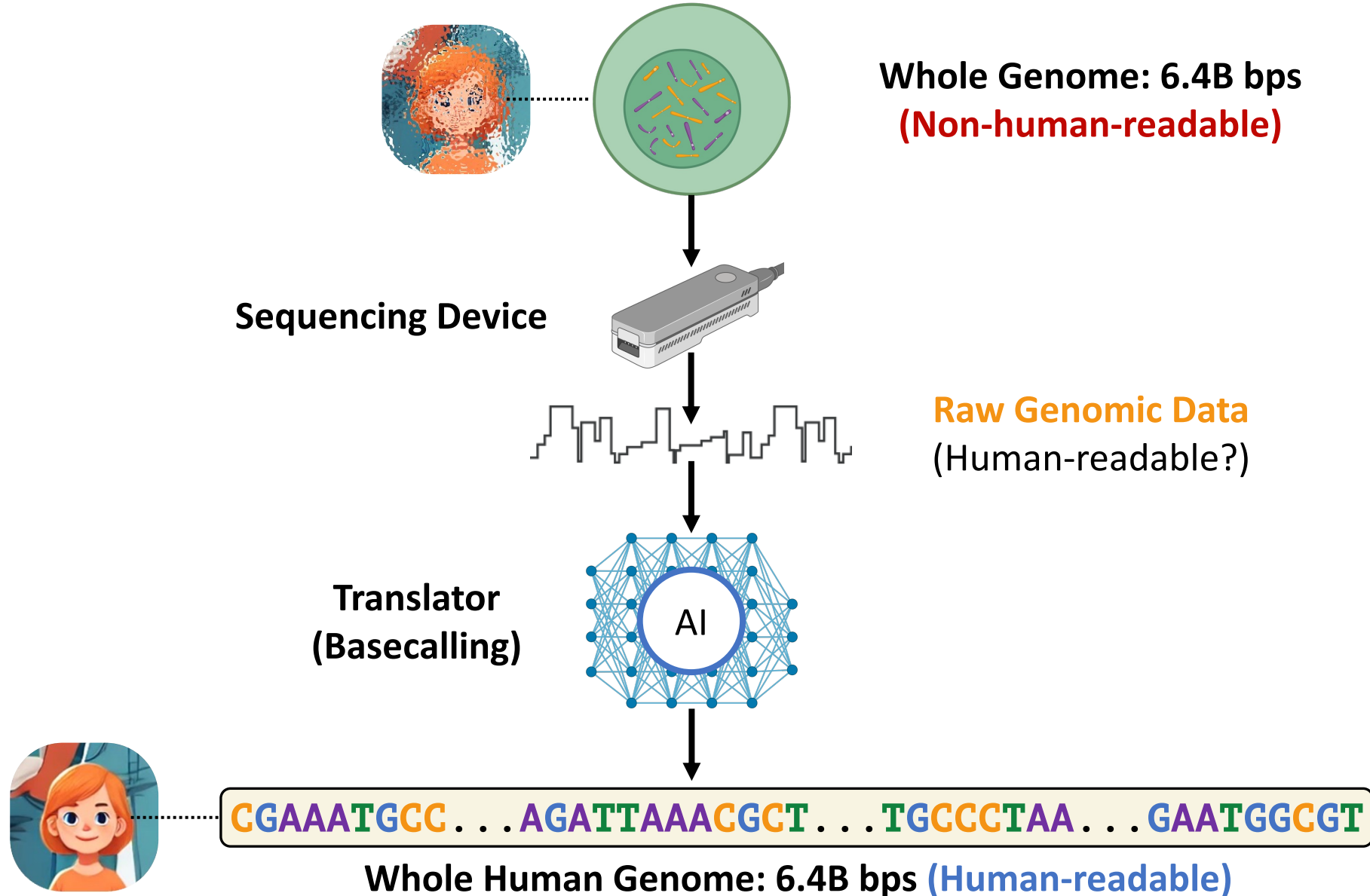


Detecting **pathogens**
in the environment

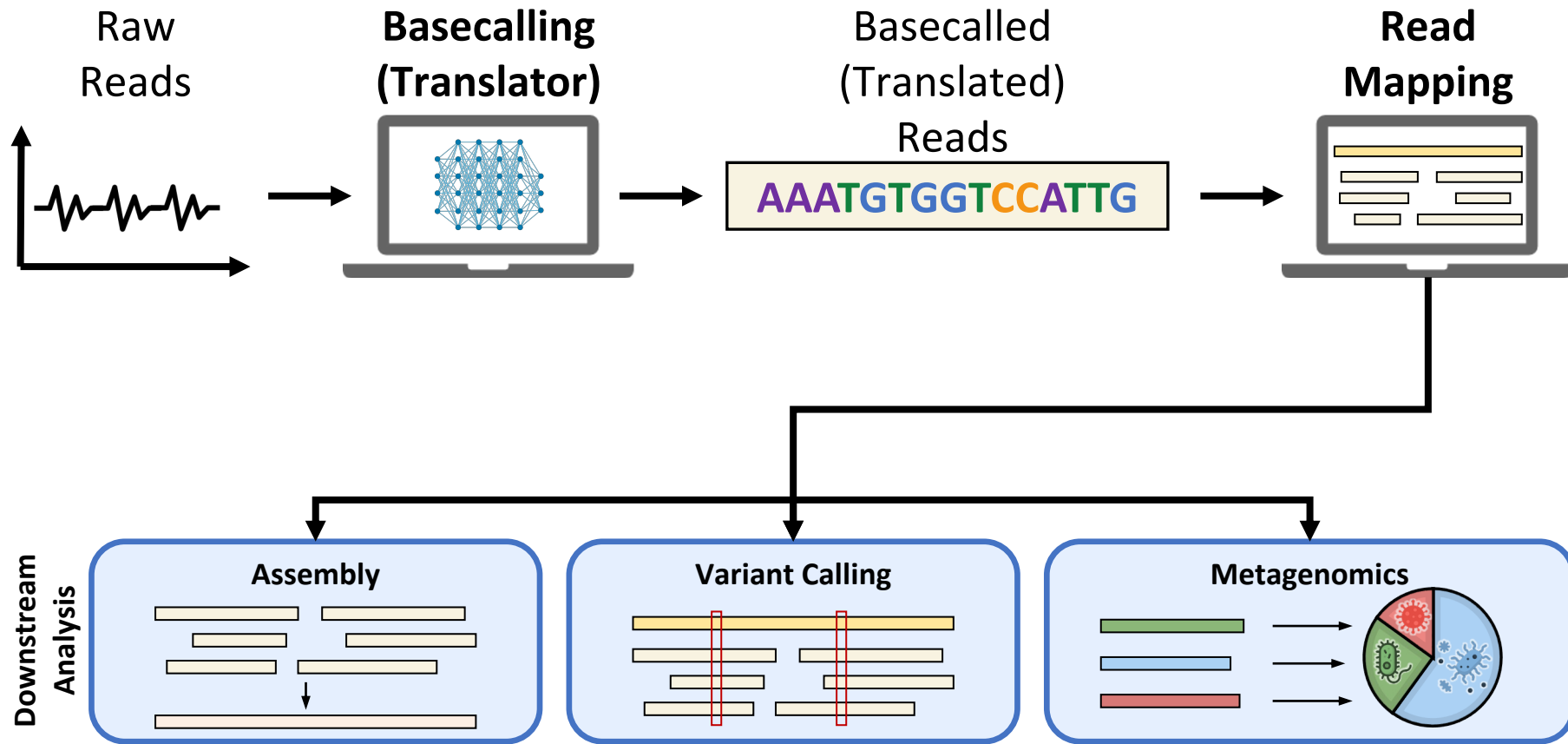


Rapid surveillance of
disease outbreaks

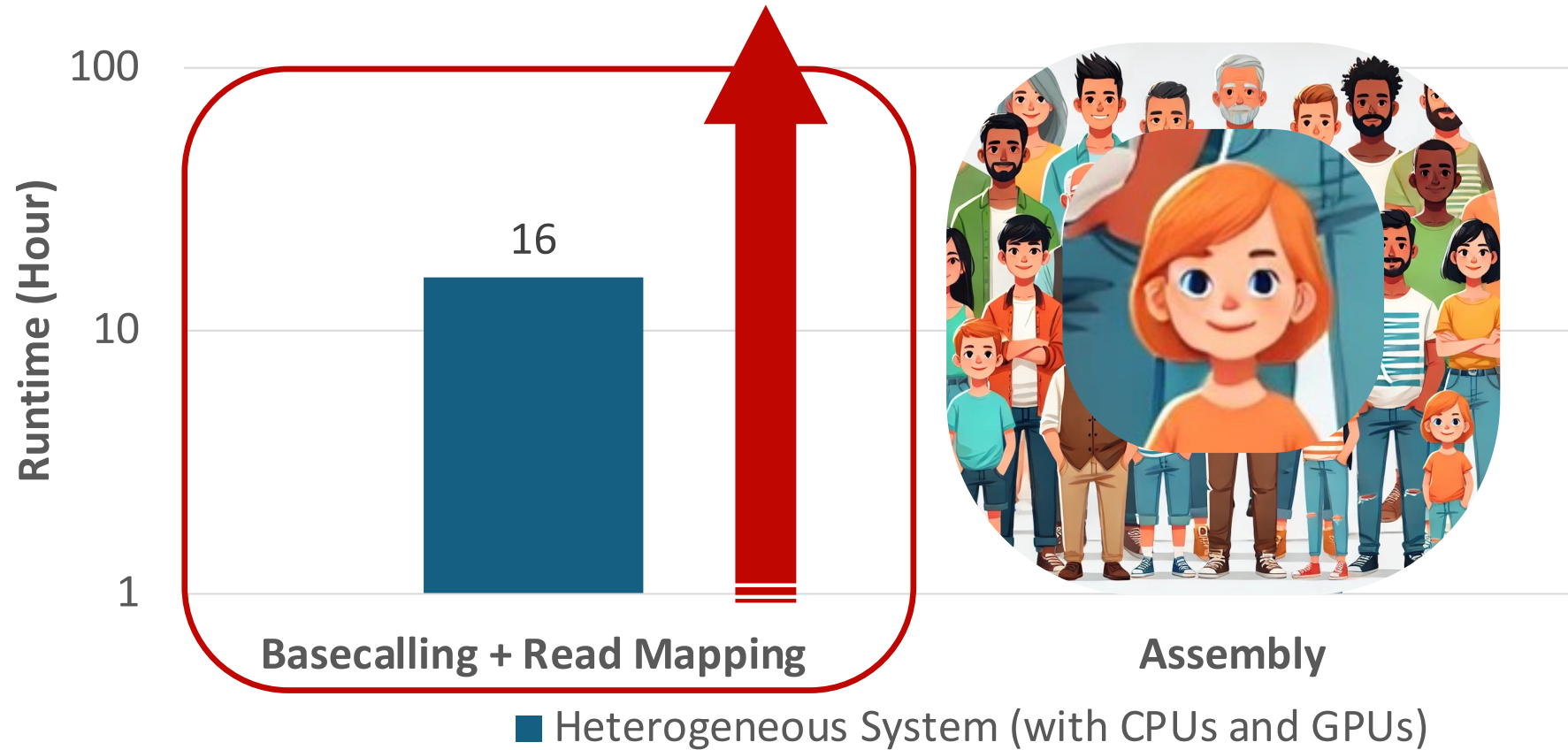
Generating the Entire Genomic Sequence



A Common Genome Analysis Pipeline

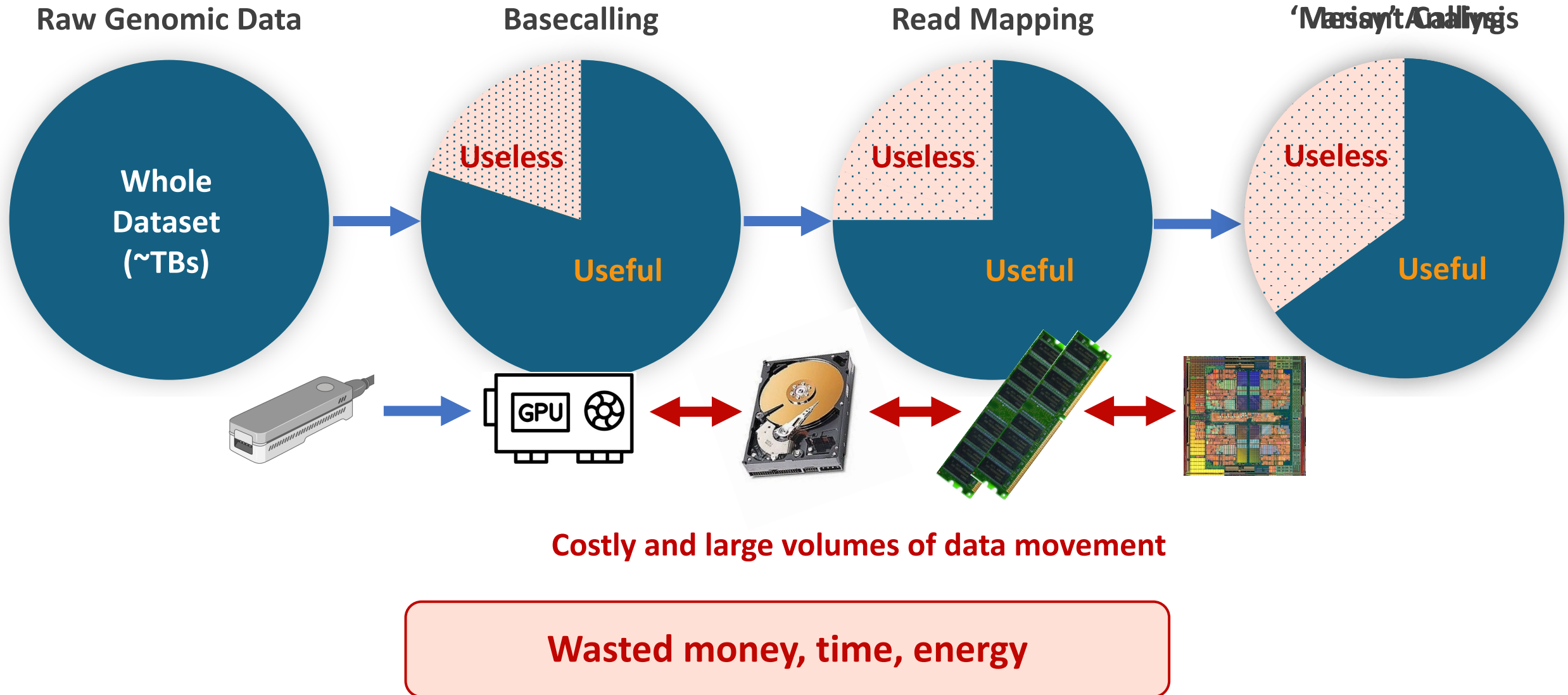


A Pipeline That is Computationally Costly



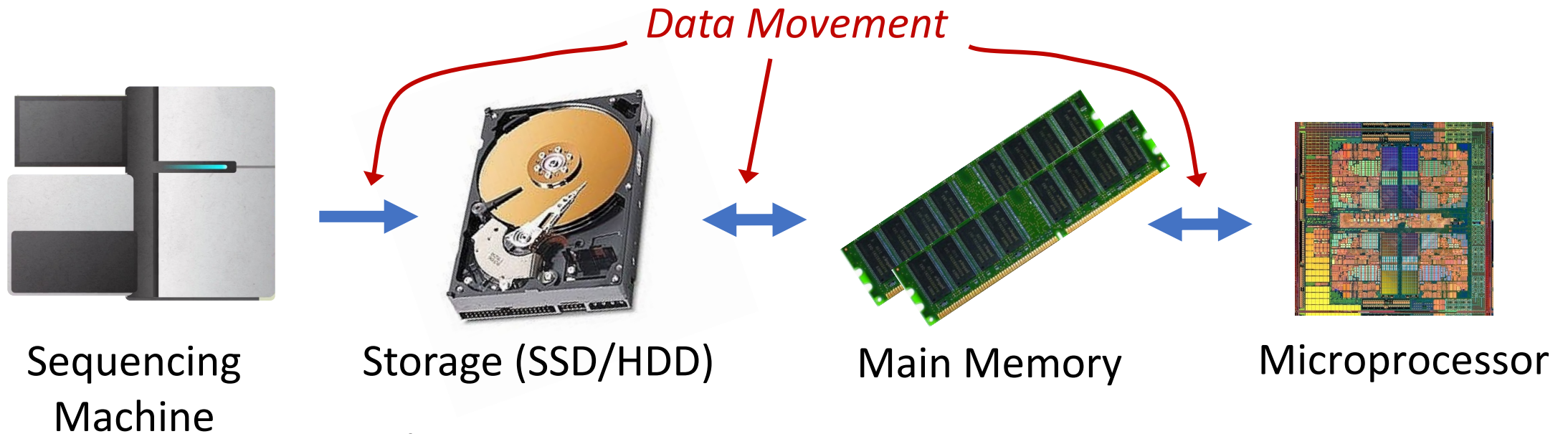
Significant computational overhead

A Pipeline That Wastes Resources



Data Movement Dominates Performance

- **Data movement** dominates performance and is a **major system energy bottleneck** (accounting for 40% - 62%)

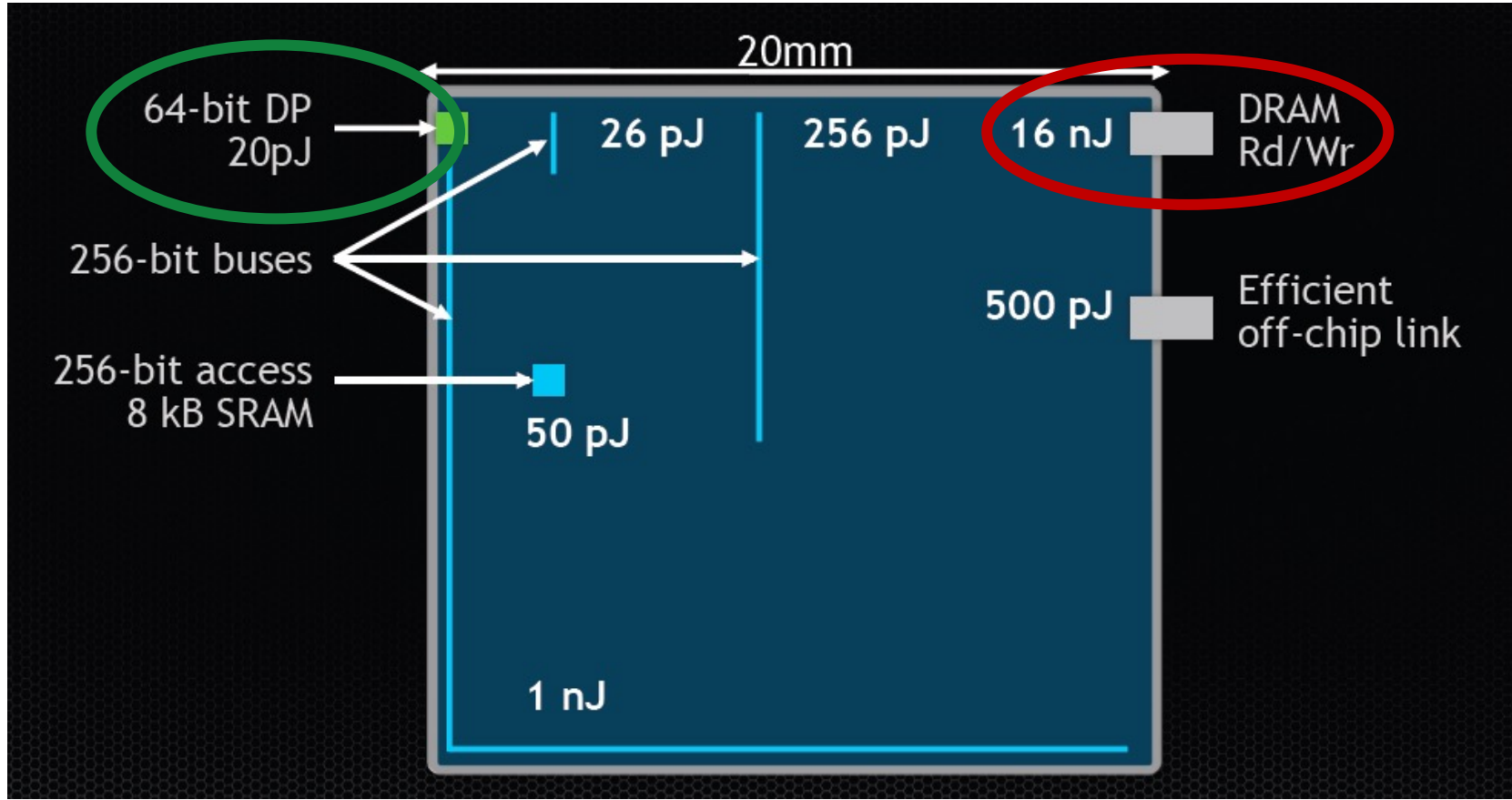


Single **memory** request **consumes >160× - 800× more energy** compared to performing an **addition operation**

- Boroumand et al., "Google Workloads for Consumer Devices: Mitigating Data Movement Bottlenecks," ASPLOS 2018
- Kestor et al., "Quantifying the Energy Cost of Data Movement in Scientific Applications," IISWC 2013
- Pandiyan and Wu, "Quantifying the energy cost of data movement for emerging smart phone workloads on mobile platforms," IISWC 2014

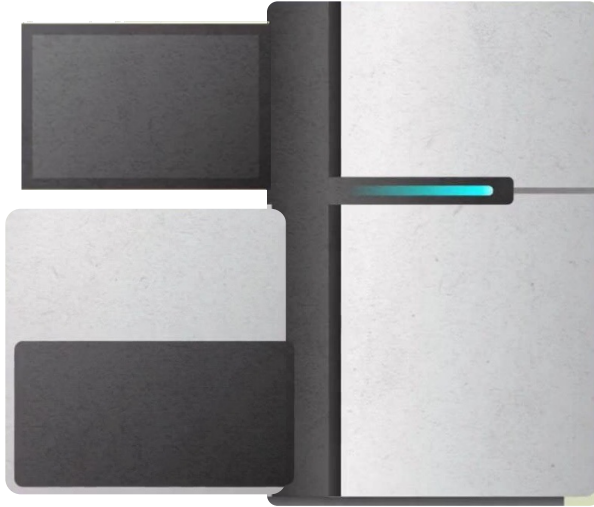
Communication Dominates Arithmetic

- Single **memory** request **consumes >160× - 800× more energy** compared to performing an **addition operation**



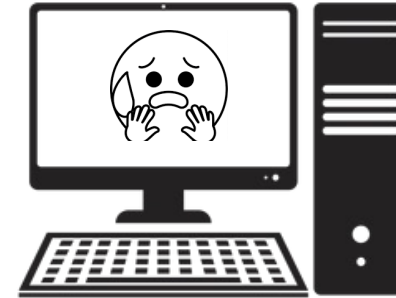
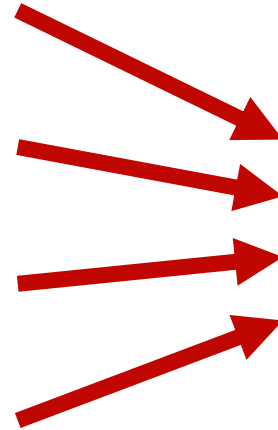
William Dally, HiPEAC 2015

Problems with Data Analysis Today



Special-Purpose Machine
for **Data Generation**

FAST



General-Purpose Machine
for **Data Analysis**

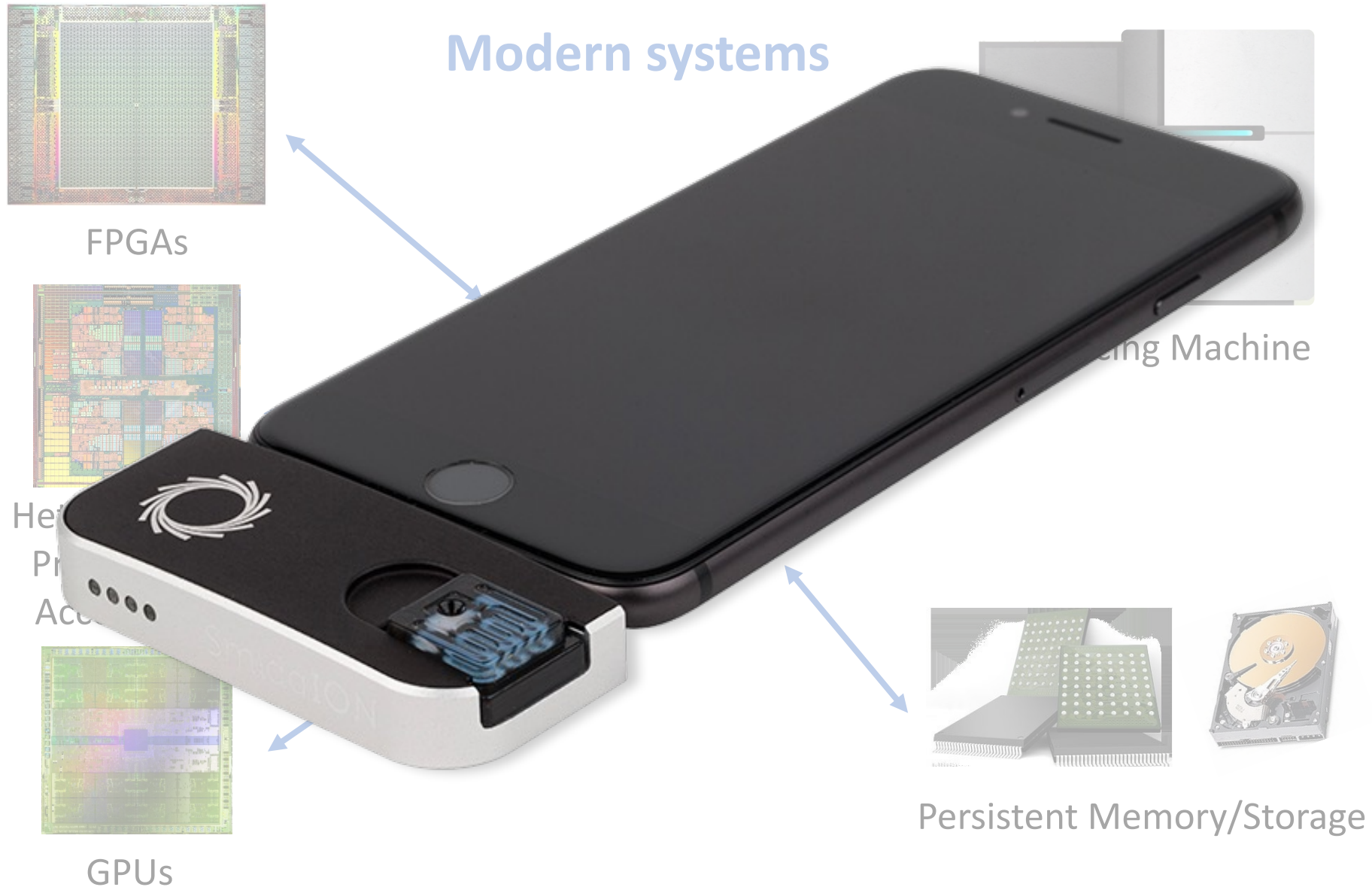
SLOW

Processing capabilities oblivious to data analysis requirements

Large amounts of data movement

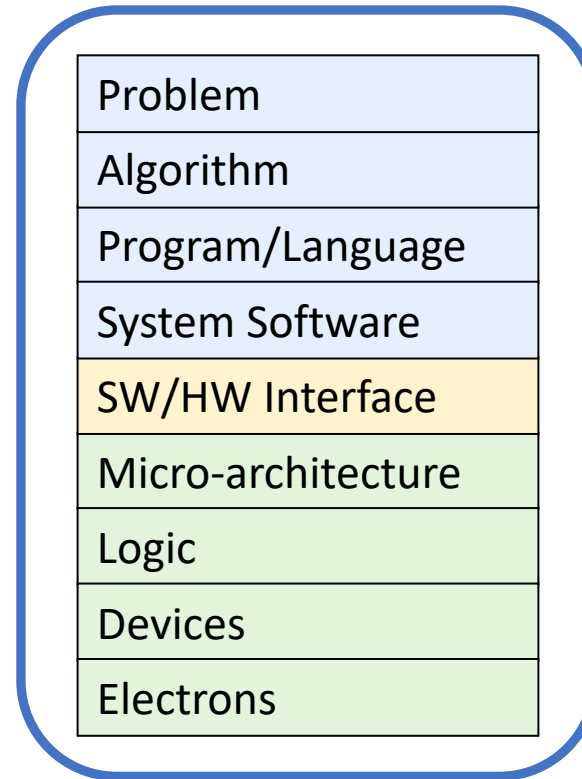
**We need to co-design
algorithms and architecture
to handle data well**

Pushing Towards New Architectures



Algorithm-Architecture Co-design is Critical

**Computer Architecture
(expanded view)**



Why Do We Need This Course?

- To give you the perspective:

**We need to co-design
algorithms and architecture
to handle data well**

- Learn how to critically analyze and present research papers
- To inform you on computational challenges and solutions in bioinformatics

**Applications are
Limitless (Almost)**

Genome Editing

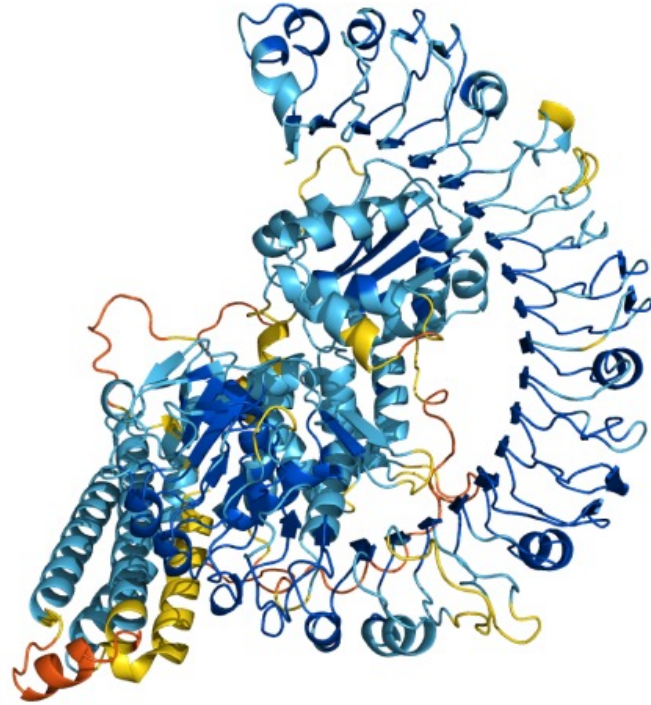


The Nobel Prize in Chemistry 2020

awarded "for the development of a
method of genome editing"



Protein Structure Prediction



Large Scale Analysis



Democratizing Genome Analysis

Sequencing the genome of the freshwater angelfish

By Indeever Madireddy

Backed by Clive, Zach Mueller, Venky, Charlie Kinsella, Srisail, Johan Sosa, David Lang, and Cindy Wu



BioCurious San Jose, California Biology Computer Science DOI: 10.18258/27105

\$1,036

Raised of \$900 Goal

115%

Funded on 10/12/22

Successfully Funded

? How does this work?

First Ever Whole Genome Sequencing and De Novo Assembly of the Freshwater Angelfish, *Pterophyllum scalare*

Indeever Madireddy

BioCurious, Santa Clara, CA, USA

BASIS Independent Silicon Valley, San Jose, CA, USA

Correspondence to: Indeever Madireddy indeever@gmail.com



Indeever Madireddy

@indeever_m



Wow. I didn't realize this fun project of mine would gain so much traction! I did in fact use my dead pet fish for this research. Even though my fish isn't alive, I'm glad a piece of it is still living on forever! @nanopore

Democratizing Genome Analysis



Seth Howes ✓
@SethSHowes



I sequenced my genome at home, on my kitchen table.

I wrote up exactly how I did it - the equipment, protocol, theory, and cost:



Seth Howes ✓ @SethSHowes · Apr 22



My first sequencing run produced terrible data, in part because I used DNA from cheek cells.

So this time, I'm using blood.

For nanopore sequencing, DNA input quality matters a lot. You want a tight distribution of long fragments, because that's how you maximise yield from the

[How I sequenced my genome at home](#)

From iwantosequencemygenomeathome.com

4:34 AM · Apr 19, 2026 · **1.2M** Views



107



858



4.6K



7.3K



Relevant ▾

[View quotes >](#)

<https://x.com/SethSHowes/status/2045782975380406623>

Rapid Surveillance of Disease Outbreaks

Real-time, portable genome sequencing for Ebola surveillance

Figure 1: Deployment of the portable genome surveillance system in Guinea.



University spinout's portable DNA sequencer has proved invaluable in tracking the global spread of coronavirus



Subscribe Sign In



Cheap & Fast SARS-CoV-2 Testing

nature biomedical engineering

[Explore content](#) ▾ [About the journal](#) ▾ [Publish with us](#) ▾

[nature](#) > [nature biomedical engineering](#) > [articles](#) > [article](#)

Article | [Published: 01 July 2021](#)

Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples

[Joshua S. Bloom](#) ✉, [Laila Sathe](#), [...] [Valerie A. Arboleda](#) ✉

[Nature Biomedical Engineering](#) **5**, 657–665 (2021) | [Cite this article](#)

4675 Accesses | **110** Altmetric | [Metrics](#)

In-Field Portable Analysis



Challenging Environment in Outer Space



DNA is a Valuable Asset to Protect

Worried about the 23andMe hack? Here's what you can do.

A bad actor offered to sell information on 23andMe's users, calling out Jewish people specifically



By [Tatum Hunter](#)

Updated October 13, 2023 at 3:18 p.m. EDT | Published October 12, 2023 at 7:00 a.m. EDT



(Illustration by The Washington Post;)

Listen 4 min Share Comment Save

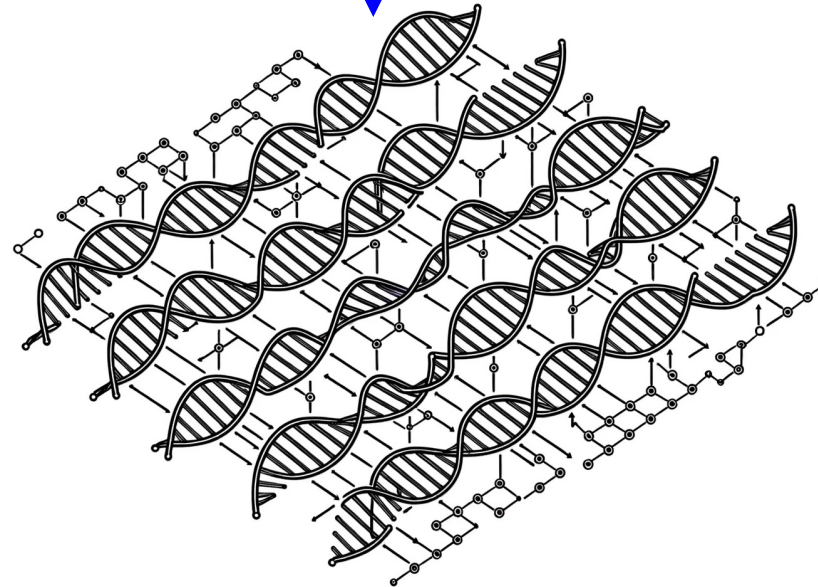
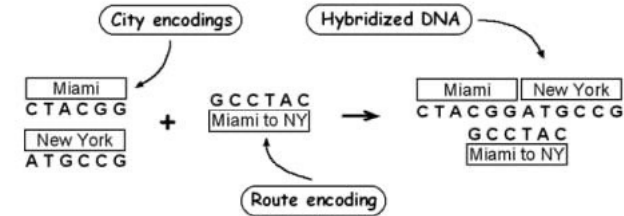
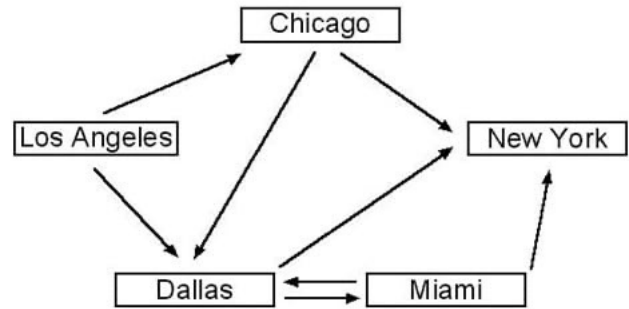
Fourteen million people have shared their genetic information with 23andMe in hopes of learning more about their heritage. After [a hack](#) that appeared to target people with Jewish ancestry, some might be wondering how to cut ties with the company.

<https://www.washingtonpost.com/technology/2023/10/12/23andme-hack-data-breach/>

New Personalized Shopping Paradigm



DNA Computing

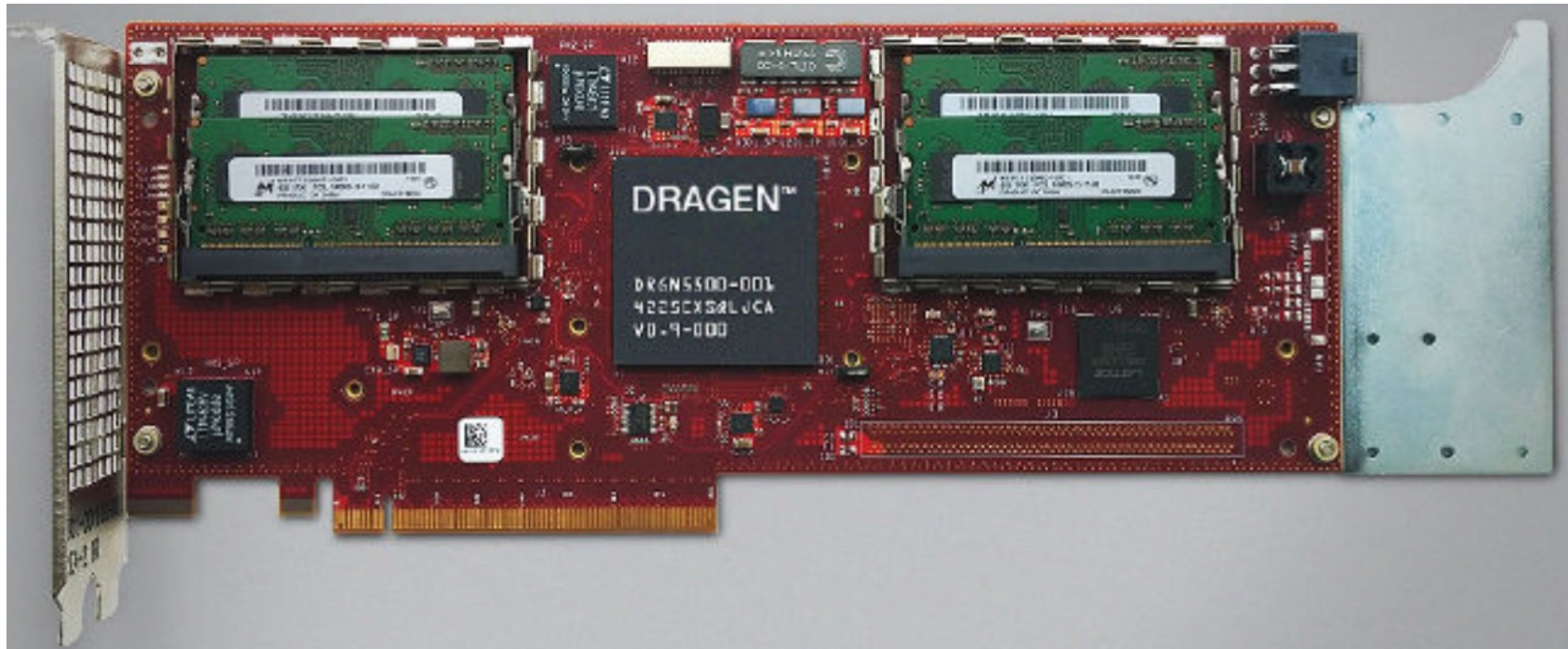


Massive parallelism to solve
(hard) problems!

Things are Happening in Industry

Illumina DRAGEN Platform

- Processes whole genome at 40x coverage in ~30 minutes with hardware support for data compression
- **FPGA Board** integrated within Illumina sequencers



Nova/NextSeq with Analysis Capability



Scale your studies with ease

Process high-throughput data quickly with **hardware acceleration**

Process high-throughput data quickly with **hardware acceleration**. With four field-programmable gate arrays (FPGAs) onboard you have the most powerful DRAGEN analysis ever, enabling you to process NovaSeq X System data easily. Perform up to four simultaneous applications per flow cell in a single run.

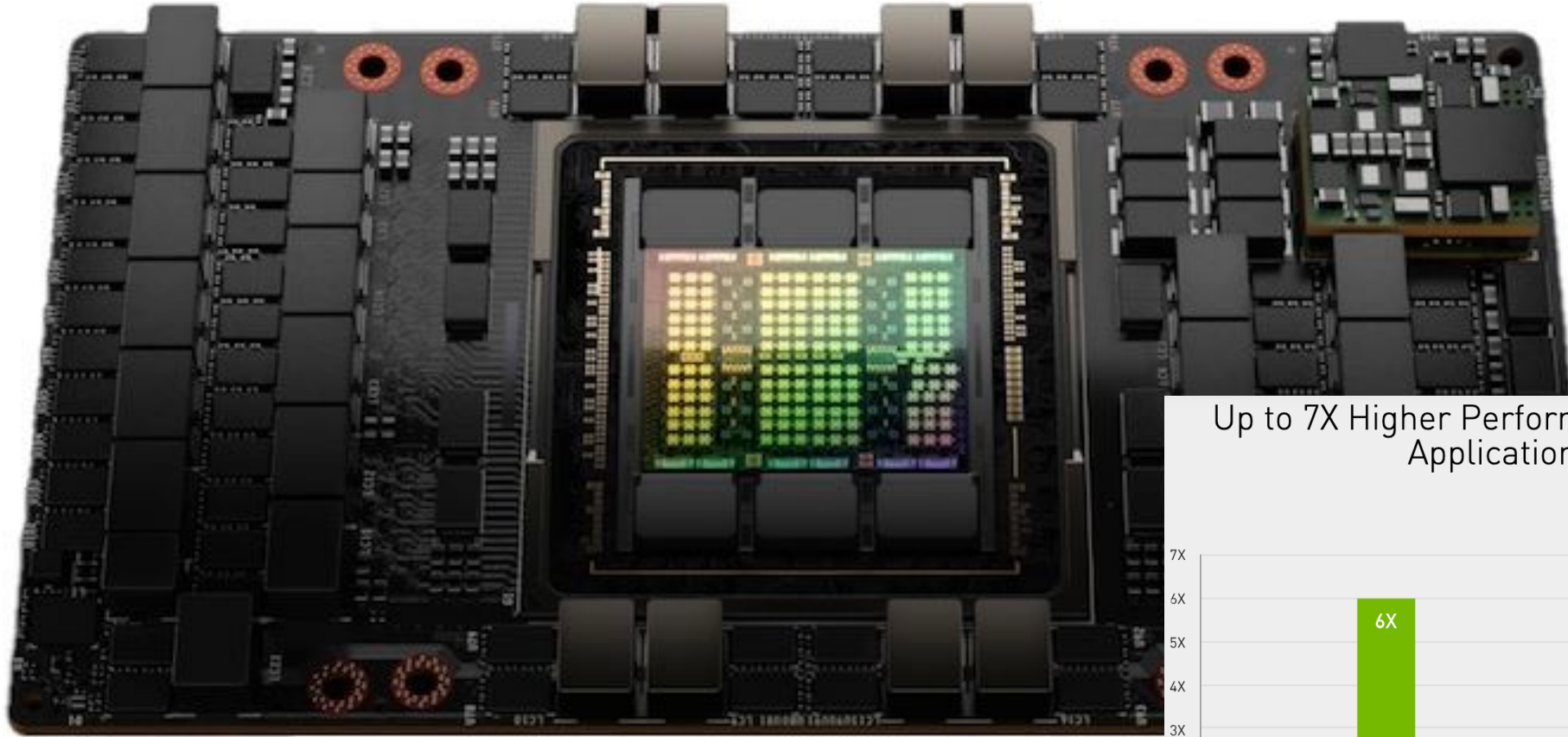
Reduce data footprint, manage and store data easily with lower costs and lower energy consumption, with built-in compression that reduces FASTQ file sizes by up to 80%.²

Stream data directly to Illumina Connected Analytics or BaseSpace Sequence Hub on the cloud for scalable data management, analysis, and aggregation.

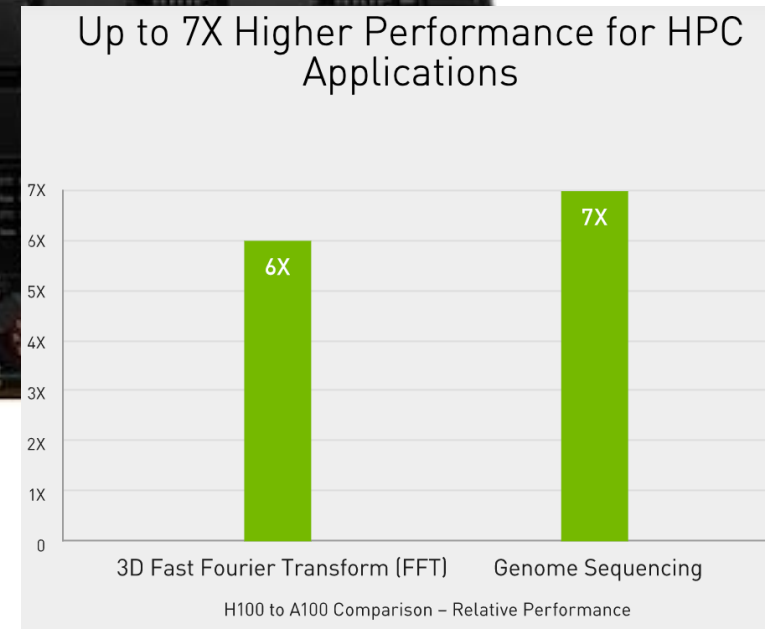
<https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/dragen-bio-it-data-sheet-m-gl-00680/dragen-bio-it-data-sheet-m-gl-00680.pdf>

<https://emea.illumina.com/systems/sequencing-platforms/novaseq-x-plus/products-services/software.html>

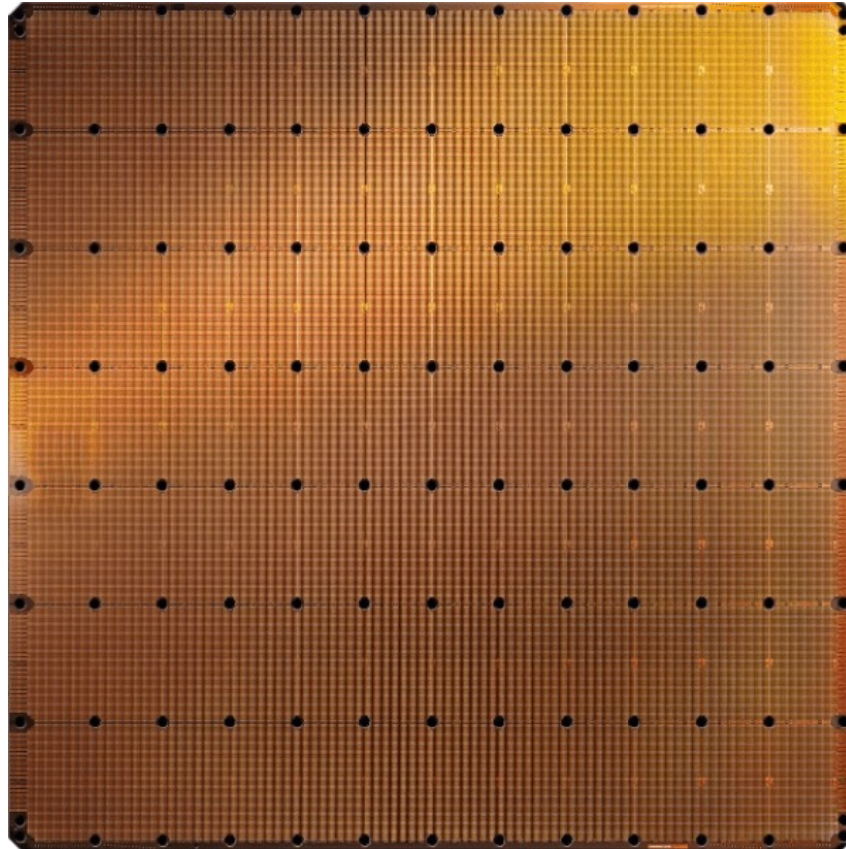
NVIDIA H100 (2022)



NVIDIA is claiming a **7x improvement** in dynamic programming algorithm (**DPX instructions**) performance on a single H100 versus naïve execution on an A100.



Cerebras's Wafer Scale Engine (2024)



Cerebras WSE-3

~4 Trillion transistors

46,225 mm²

- The largest ML accelerator chip (2024)
- 900,000 cores

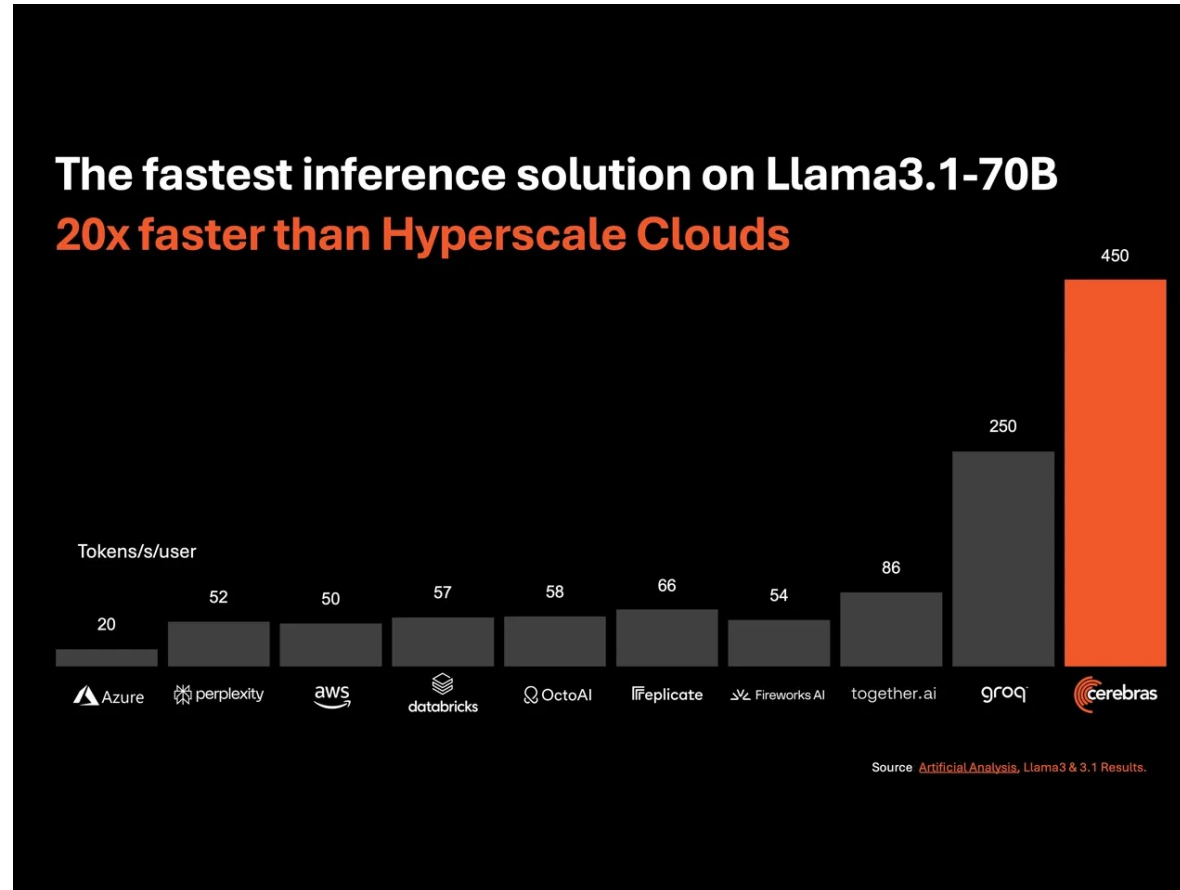


NVIDIA H100 GPU

80 Billion transistors

814 mm²

Cerebras's Wafer Scale Engine (2024)

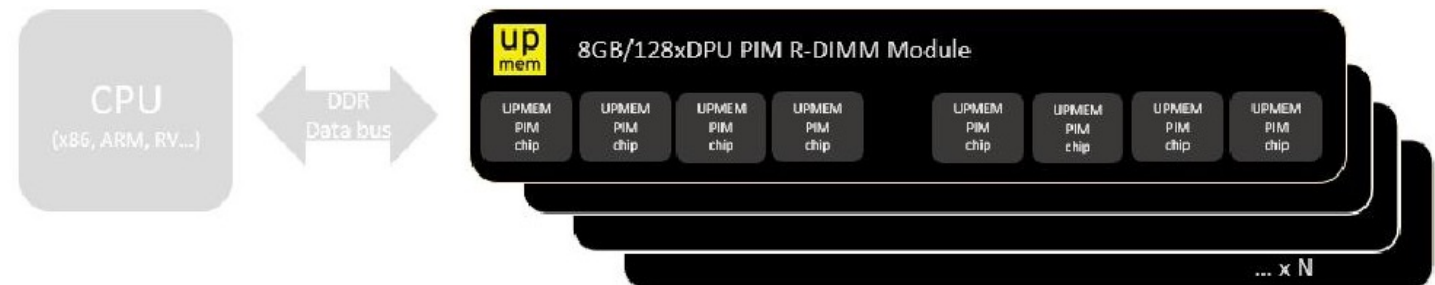
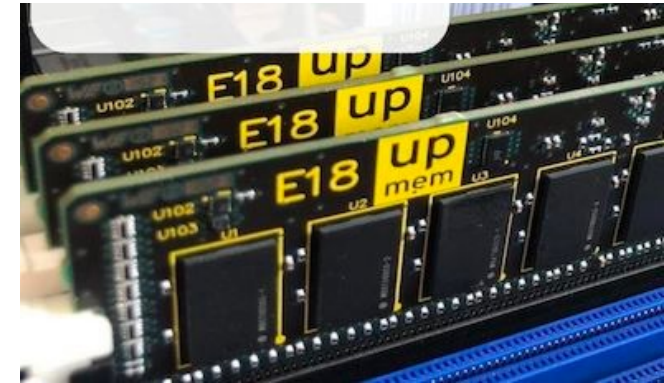


<https://cerebras.ai/blog/cerebras-cs3>

<https://cerebras.ai/press-release/cerebras-launches-the-worlds-fastest-ai-inference>

UPMEM Processing-in-DRAM Engine (2019)

- Processing in DRAM Engine
- Includes **standard DIMM modules**, with a **large number of DPU processors** combined with DRAM chips.
- Replaces **standard DIMMs**
 - DDR4 R-DIMM modules
 - 8GB+128 DPUs (16 PIM chips)
 - Standard 2x-nm DRAM process
 - **Large amounts of** compute & memory bandwidth



GPU Acceleration of Bioinformatics Workloads



Gagandeep Singh
3mo · Edited

AMD just dropped a big one for the bioinformatics community!

Minimap2 DNA/RNA aligner accelerated on AMD Instinct™ GPUs

- ✓ Drop-in compatible with familiar minimap2 workflows
- ✓ Modular pipeline with seeding, chaining, and alignment stages
- ✓ Built to engage the community early and shape the roadmap together

Sign up for free early access: <https://lnkd.in/eq3un7gc>

Huge thanks to our early collaborators for their support and feedback: [Mohammed Alser](#), [Hasindu Gamaarachchi](#), [Igor Sfiligoi](#), [Can Firtina](#), [Satish Narayanasamy](#)

Stay tuned. Lots more coming from AMD in Healthcare & Life Sciences.

[Vikas C Sajjan Soumitra Chatterjee](#) [Anik Chaudhuri](#) [Prateek Chokse](#) [Quim Aguado](#)
[Vish Vadlamani](#) [Phani Vaddadi](#) [Kristof Denolf](#) [Mike Schulte](#) [Aleks Shar](#), MBA 🇮🇳 🇮🇳
[Sriranjani \(Gina\) Sitaraman](#), Ph.D. [Beatrice Branchini](#)



Breaking Barriers in Genomics: Slorado Brings Open-Source Genomic Basecalling to AMD GPUs

Nov 24, 2025



Shop Drivers Support Search Sign In

Healthcare and Life Sciences

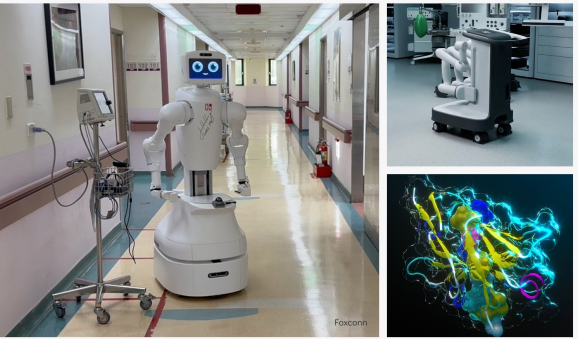
Industries / Healthcare and Life Sciences

AI for Healthcare and Life Sciences

Open source tools, pretrained models, and GPU-accelerated pipelines for drug discovery, healthcare robotics, medical imaging, genomics, and digital health.

[Download the State of AI Report](#)

[NVIDIA Guide to Healthcare and Life Sciences](#)



Recommended: Accelerating Genome Analysis [DAC '23]

- **Invited: Accelerating Genome Analysis via Algorithm-Architecture Co-Design**

Onur Mutlu, Can Firtina

[Proceedings of the 60th Design Automation Conference \(DAC 2023\)](#), San Francisco, CA, USA, July 2023.

[\[PDF\]](#) [\[Link\]](#)

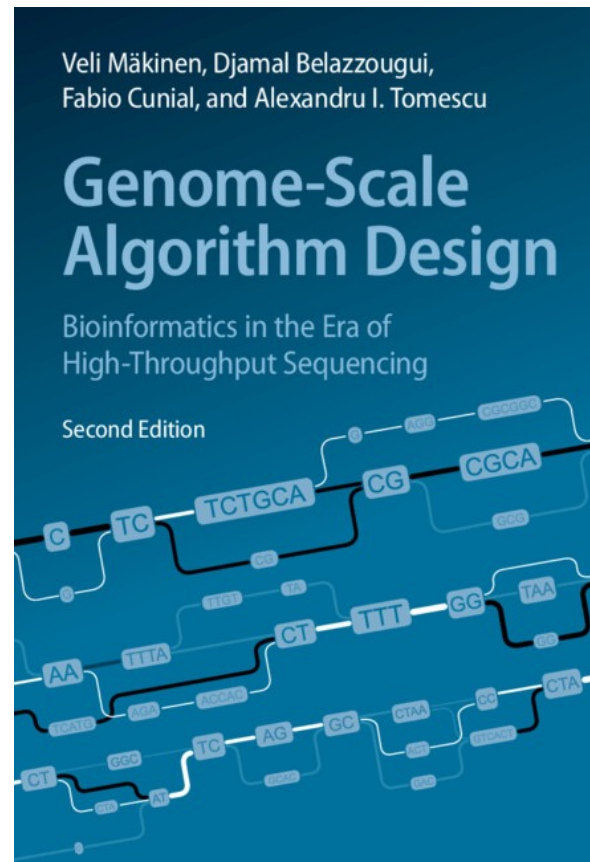
Invited: Accelerating Genome Analysis via Algorithm-Architecture Co-Design

Onur Mutlu Can Firtina

ETH Zürich

Recommended Textbook for Algorithm Design

- Veli Mäkinen, Djamel Belazzougui, Fabio Cunial, and Alexandru I. Tomescu.
"Genome-Scale Algorithm Design: Bioinformatics in the Era of High-Throughput Sequencing," Cambridge University Press, 2023.



Enabling New Directions in Genome Analysis **via New Algorithms**

New Frontiers: Raw Signal Analysis [ISMB '23]

- **RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes**

Can Firtina, Nika Mansouri Ghiasi, Joel Lindegger, Gagandeep Singh, Meryem Banu Cavlak, Haiyu Mao, Onur Mutlu

[Proceedings of the 31st Annual Conference on Intelligent Systems for Molecular Biology and the 22nd European Conference on Computational Biology \(ISMB/ECCB 2023\)](#), Lyon, France, July 2023.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Conference talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

Preprint (bioRxiv) [\[Link\]](#) [\[PDF\]](#)

Social media thread [\[Twitter \(X\)\]](#)

Bioinformatics, 2023, **39**, i297–i307
<https://doi.org/10.1093/bioinformatics/btad272>
ISMB/ECCB 2023

OXFORD

RawHash: enabling fast and accurate real-time analysis of raw nanopore signals for large genomes

Can Firtina ^{1,*}, Nika Mansouri Ghiasi ¹, Joel Lindegger ¹, Gagandeep Singh ¹,
Meryem Banu Cavlak ¹, Haiyu Mao ¹, Onur Mutlu ^{1,*}

¹Department of Information Technology and Electrical Engineering, ETH Zurich, 8092 Zurich, Switzerland

*Corresponding author. Department of Information Technology and Electrical Engineering, ETH Zurich, Gloriastrasse 35, 8092 Zurich, Switzerland.
E-mail: firtinac@ethz.ch (C.F.), omutlu@ethz.ch (O.M.)

Real-Time Raw Signal Analysis [Bioinformatics '24]

- **RawHash2: Mapping Raw Nanopore Signals Using Hash-Based Seeding and Adaptive Quantization**

Can Firtina, Melina Soysal, Joël Lindegger, Onur Mutlu

[Bioinformatics](#), July 2024.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Bioinformatics, 2024, **40(8)**, btac478
<https://doi.org/10.1093/bioinformatics/btac478>
Advance Access Publication Date: 30 July 2024
Applications Note



Sequence analysis

RawHash2: mapping raw nanopore signals using hash-based seeding and adaptive quantization

Can Firtina ^{1,*}, Melina Soysal ¹, Joël Lindegger ¹, Onur Mutlu ^{1,*}

¹Department of Information Technology and Electrical Engineering, ETH Zurich, Zurich 8092, Switzerland

*Corresponding authors. Department of Information Technology and Electrical Engineering, ETH Zurich, Zurich 8092, Switzerland.
E-mail: firtinac@ethz.ch (C.F.); omutlu@ethz.ch (O.M.)

New Directions: Assembling Raw Signals

- **Rawsample: Overlapping Raw Nanopore Signals using a Hash-based Seeding Mechanism**
Can Firtina, Maximilian Mordig, Harun Mustafa, Sayan Goswami, Nika Mansouri Ghiasi, Stefano Mercogliano, Furkan Eris, Joel Lindegger, Andre Kahles, Onur Mutlu
[Bioinformatics](#), February 2026.
[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)
ISMB 2024 Talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)
CSHL 2024 (Biological Data Science) Talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)
Social media thread [\[Twitter \(X\)\]](#) [\[LinkedIn\]](#)

Bioinformatics, 2026, 42(3), btag087
<https://doi.org/10.1093/bioinformatics/btag087>
Published: 26 February 2026
Original Paper | Sequence Analysis

OXFORD

Rawsample: overlapping raw nanopore signals using a hash-based seeding mechanism

Can Firtina^{1,2,*}, Maximilian Mordig^{3,4}, Harun Mustafa^{3,5,6}, Sayan Goswami³,
Nika Mansouri Ghiasi¹, Stefano Mercogliano¹, Furkan Eris¹, Joel Lindegger¹, André Kahles^{3,5,6,*},
Onur Mutlu^{1,*}

¹Department of Information Technology and Electrical Engineering, ETH Zurich, Zurich, 8092, Switzerland

²Department of Computer Science, University of Maryland, MD 20742, United States

³Department of Computer Science, ETH Zurich, Zurich, 8092, Switzerland

⁴Max Planck Institute for Intelligent Systems, Tübingen, 72076, Germany

⁵University Hospital Zurich, Zurich, 8091, Switzerland

⁶Swiss Institute of Bioinformatics, Zurich, 8057, Switzerland

*Corresponding authors. Can Firtina, Department of Computer Science, University of Maryland, MD 20742, United States. E-mail: firtina@umd.edu; André Kahles, Department of Computer Science, ETH Zurich, Zurich, 8092, Switzerland. E-mail: andre.kahles@inf.ethz.ch; Onur Mutlu, Department of Information Technology and Electrical Engineering, ETH Zurich, Zurich, 8092, Switzerland. E-mail: omutlu@ethz.ch.
Associate Editor: Inanc Birol

Quickly Aligning Raw Signals [IEEE Access '24]

- **RawAlign: Accurate, Fast, and Scalable Raw Nanopore Signal Mapping via Combining Seeding and Alignment**

Joël Lindegger, Can Firtina, Nika Mansouri Ghiasi, Mohammad Sadrosadati, Mohammed Alser, Onur Mutlu
[IEEE Access](#), December 2024.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

RawAlign: Accurate, Fast, and Scalable Raw Nanopore Signal Mapping via Combining Seeding and Alignment

**JOËL LINDEGGER^{ID}, CAN FIRTINA^{ID}, NIKA MANSOURI GHIASI, MOHAMMAD SADROSADATI^{ID},
MOHAMMED ALSER^{ID}, AND ONUR MUTLU^{ID}, (Fellow, IEEE)**

Department of Information Technology and Electrical Engineering, ETH Zürich, 8092 Zürich, Switzerland

Corresponding authors: Joël Lindegger (jmlindegger@gmail.com), Can Firtina (firtinac@ethz.ch), and Onur Mutlu (omutlu@ethz.ch)

This work was supported in part by the Semiconductor Research Corporation (SRC), in part by the ETH Future Computing Laboratory, in part by European Union's Horizon Programme for Research and Innovation under Grant 101047160-BioPIM, and in part by the Swiss National Science Foundation (SNSF) under Grant 200021_213084.

In-Storage Raw Signal Analysis [ICS '25]

- **MARS: Processing-In-Memory Acceleration of Raw Signal Genome Analysis Inside the Storage Subsystem**

Melina Soysal, Konstantina Koliogeorgi, [Can Firtina](#), Nika Mansouri Ghiasi, Rakesh Nadig, Haiyu Mao, Geraldo Francisco Oliveira Junior, Yu Liang, Klea Zambaku, Mohammad Sadrosadati, Onur Mutlu

[Proceedings of the 39th International Conference on Supercomputing \(ICS 2025\)](#), Salt Lake City, Utah, USA, June 2025.

[\[PDF\]](#) [\[DOI\]](#)

Conference talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

MARS: Processing-In-Memory Acceleration of Raw Signal Genome Analysis Inside the Storage Subsystem

Melina Soysal[†] Konstantina Koliogeorgi[†] Can Firtina[†] Nika Mansouri Ghiasi[†]
Rakesh Nadig[†] Haiyu Mayo^{*} Geraldo F. Oliveira[†]
Yu Liang[†] Klea Zambaku[†] Mohammad Sadrosadati[†] Onur Mutlu[†]

[†] *ETH Zürich*

^{*} *King's College London*

Correcting Raw Signals [arXiv '26 & ISMB'26]

- **CRANE: Correcting Errors in Raw Nanopore Signals Using Hidden Markov Models**
Simon Ambrozak, Ulysse McConnell, Bhargav Srinivasan, Burak Ozkan, Ernest Zhang, Can Firtina
[arXiv](#), March 2026.
[\[PDF\]](#) [\[Code\]](#) [\[Link\]](#)
ISMB 2026 (HiTSeq) Talk [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

CRANE: Correcting Errors in Raw Nanopore Signals Using Hidden Markov Models

Simon Ambrozak¹ Ulysse McConnell^{1,2} Bhargav Srinivasan¹
Burak Ozkan^{1,3} Ernest Zhang¹ Can Firtina¹
¹*University of Maryland* ²*ETH Zurich* ³*Bilkent University*

Benchmarking Raw Signal Analysis [ACM-BCB '25]

- **RawBench: A Comprehensive Benchmarking Framework for Raw Nanopore Signal Analysis Techniques**

Furkan Eris, Ulysse McConnell, Can Firtina, Onur Mutlu

[Proceedings of the 16th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics \(ACM-BCB 2025\)](#), Philadelphia, PA, USA, October 2025.

[\[PDF\]](#) [\[DOI\]](#)

Conference talk [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

RawBench: A Comprehensive Benchmarking Framework for Raw Nanopore Signal Analysis Techniques

Furkan Eris
ETH Zurich
Zurich, Switzerland
furkan6olm@gmail.com

Can Firtina*
University of Maryland, College Park
MD, USA
firtina@umd.edu

Ulysse McConnell
ETH Zurich
Zurich, Switzerland
umcconnell@student.ethz.ch

Onur Mutlu*
ETH Zurich
Zurich, Switzerland
omutlu@gmail.com

Tolerating Noise in String Matching [NARGAB '23]

- **BLEND: a fast, memory-efficient and accurate mechanism to find fuzzy seed matches in genome analysis**

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

[NAR Genomics and Bioinformatics \(NARGAB\)](#), March 2023.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Preprint (bioRxiv) [\[Link\]](#) [\[PDF\]](#)

RECOMB 2023 Talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

Social media thread [\[Twitter \(X\), publication\]](#) [\[Twitter \(X\), preprint\]](#)



Volume 5, Issue 1
March 2023

JOURNAL ARTICLE

BLEND: a fast, memory-efficient and accurate mechanism to find fuzzy seed matches in genome analysis

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

NAR Genomics and Bioinformatics, Volume 5, Issue 1, March 2023, lqad004,

Mitigating Useless Computations [IEEE/ACM TCBB '24]

- **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, Onur Mutlu
[IEEE/ACM Transactions on Computational Biology and Bioinformatics \(TCBB\)](#), August 2024.
[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)
APBC 2023 Talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

IEEE/ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS, VOL. 23, NO. 2, MARCH/APRIL 2026

589

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 , *Fellow, IEEE*

Mitigating Useless Computations [Bioinformatics '22]

- **FastRemap: a tool for quickly remapping reads between genome assemblies**

Jeremie S. Kim, [Can Firtina](#), Meryem Banu Cavlak, Damla Senol Cali, Can Alkan, Onur Mutlu
[Bioinformatics](#), September 2022.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Bioinformatics, 38(19), 2022, 4633–4635

<https://doi.org/10.1093/bioinformatics/btac554>

Advance Access Publication Date: 17 August 2022

Applications Note



Genome analysis

FastRemap: a tool for quickly remapping reads between genome assemblies

Jeremie S. Kim ^{1,*}, **Can Firtina** ¹, **Meryem Banu Cavlak**¹, **Damla Senol Cali** ²,
Can Alkan ³ and **Onur Mutlu** ^{1,3}

¹Department of Computer Engineering, ETH Zurich, D-ITET, Zurich 8006, Switzerland, ²Department of Computer Engineering, Bionano Genomics, San Diego, CA 92121, USA and ³Department of Computer Engineering, Bilkent University, Ankara 06800, Turkey

Utilizing AI/ML in
Genome Analysis
**via New Algorithms and
Architectures**

Error Correction using ML [Bioinformatics '20]

- **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](#), [Onur Mutlu](#)
[Bioinformatics](#), June 2020.

[\[PDF\]](#) [\[Code\]](#) [\[Link\]](#)

Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm

FREE

[Can Firtina](#), [Jeremie S Kim](#), [Mohammed Alser](#), [Damla Senol Cali](#), [A Ercument Cicek](#),
[Can Alkan](#) ✉, [Onur Mutlu](#) ✉

Bioinformatics, Volume 36, Issue 12, 15 June 2020, Pages 3669–3679,
<https://doi.org/10.1093/bioinformatics/btaa179>

Published: 13 March 2020 **Article history** ▼

Accelerating ML & Genome Graphs [ACM TACO '24]

- **ApHMM: Accelerating Profile Hidden Markov Models for Fast and Energy-efficient Genome Analysis**

[Can Firtina](#), [Kamlesh Pillai](#), [Gurpreet S. Kalsi](#), [Bharathwaj Suresh](#), [Damla Senol Cali](#), [Jeremie S. Kim](#), [Taha Shahroodi](#), [Meryem Banu Cavlak](#), [Joël Lindegger](#), [Mohammed Alser](#), [Juan Gómez Luna](#), [Sreenivas Subramoney](#), [Onur Mutlu](#)

[ACM Transactions on Architecture and Code Optimization \(TACO\)](#), February 2024.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

HiPEAC 2024 Talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

RESEARCH-ARTICLE | **OPEN ACCESS** |  



ApHMM: Accelerating Profile Hidden Markov Models for Fast and Energy-efficient Genome Analysis

Authors:  [Can Firtina](#),  [Kamlesh Pillai](#),  [Gurpreet S. Kalsi](#),  [Bharathwaj Suresh](#),  [Damla Senol Cali](#),  [Jeremie S. Kim](#), 
[Taha Shahroodi](#),  [Meryem Banu Cavlak](#),  [Joël Lindegger](#),  [Mohammed Alser](#),  [Juan Gómez Luna](#),  [Sreenivas Subramoney](#),
 [Onur Mutlu](#) ([Less](#)) | [Authors Info & Claims](#)

[ACM Transactions on Architecture and Code Optimization, Volume 21, Issue 1](#) • Article No.: 19, Pages 1 - 29

<https://doi.org/10.1145/3632950>

Translating Raw Signals using ML [Genome Biology '24]

- **RUBICON: a framework for designing efficient deep learning-based genomic basecallers**

Gagandeep Singh, Mohammed Alser, Kristof Denolf, [Can Firtina](#), Alireza Khodamoradi, Meryem Banu Cavlak, Henk Corporaal, Onur Mutlu

[Genome Biology](#), February 2024.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Method | [Open access](#) | Published: 16 February 2024

RUBICON: a framework for designing efficient deep learning-based genomic basecallers

[Gagandeep Singh](#), [Mohammed Alser](#), [Kristof Denolf](#), [Can Firtina](#) ✉, [Alireza Khodamoradi](#), [Meryem Banu Cavlak](#), [Henk Corporaal](#) & [Onur Mutlu](#) ✉

[Genome Biology](#) **25**, Article number: 49 (2024) | [Cite this article](#)

Eliminating Useless Basecalling [Frontiers In Genetics '24]

- **TargetCall: Eliminating the Wasted Computation in Basecalling via Pre-Basecalling Filtering**
Meryem Banu Cavlak, Gagandeep Singh, Mohammed Alser, Can Firtina, Joel Lindegger, Mohammad Sadrosadati, Nika Mansouri Ghiasi, Can Alkan, Onur Mutlu
[Frontiers in Genetics](#), September 2024.
[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

TargetCall: eliminating the wasted computation in basecalling via pre-basecalling filtering

Meryem Banu Cavlak^{1*}, Gagandeep Singh¹, Mohammed Alser¹,
Can Firtina^{1*}, Joël Lindegger¹, Mohammad Sadrosadati¹,
Nika Mansouri Ghiasi¹, Can Alkan² and Onur Mutlu^{1*}

¹SAFARI Research Group, Department of Information Technology and Electrical Engineering, ETH Zurich, Zurich, Switzerland, ²Department of Computer Engineering, Bilkent University, Ankara, Türkiye

Basecalling using PIM [MICRO '23]

- **Swordfish: A Framework for Evaluating Deep Neural Network-Based Basecalling Using Computation-In-Memory with Non-Ideal Memristors**

Taha Shahroodi, Gagandeep Singh, Mahdi Zahedi, Haiyu Mao, Joel Lindegger, Can Firtina, Stephan Wong, Onur Mutlu, Said Hamdioui

[Proceedings of the 56th International Symposium on Microarchitecture \(MICRO 2023\)](#), Toronto, ON, Canada, November 2023.

[\[PDF\]](#) [\[DOI\]](#)

Conference talk [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

Swordfish: A Framework for Evaluating Deep Neural Network-based Basecalling using Computation-In-Memory with Non-Ideal Memristors

Taha Shahroodi¹ Gagandeep Singh^{2,3} Mahdi Zahedi¹ Haiyu Mao³ Joel Lindegger³ Can Firtina³
Stephan Wong¹ Onur Mutlu³ Said Hamdioui¹

¹TU Delft ²AMD Research ³ETH Zürich

DNN Hardware Acceleration

DNN execution is dominated by:

Vector-Matrix
Multiplication (VMM)

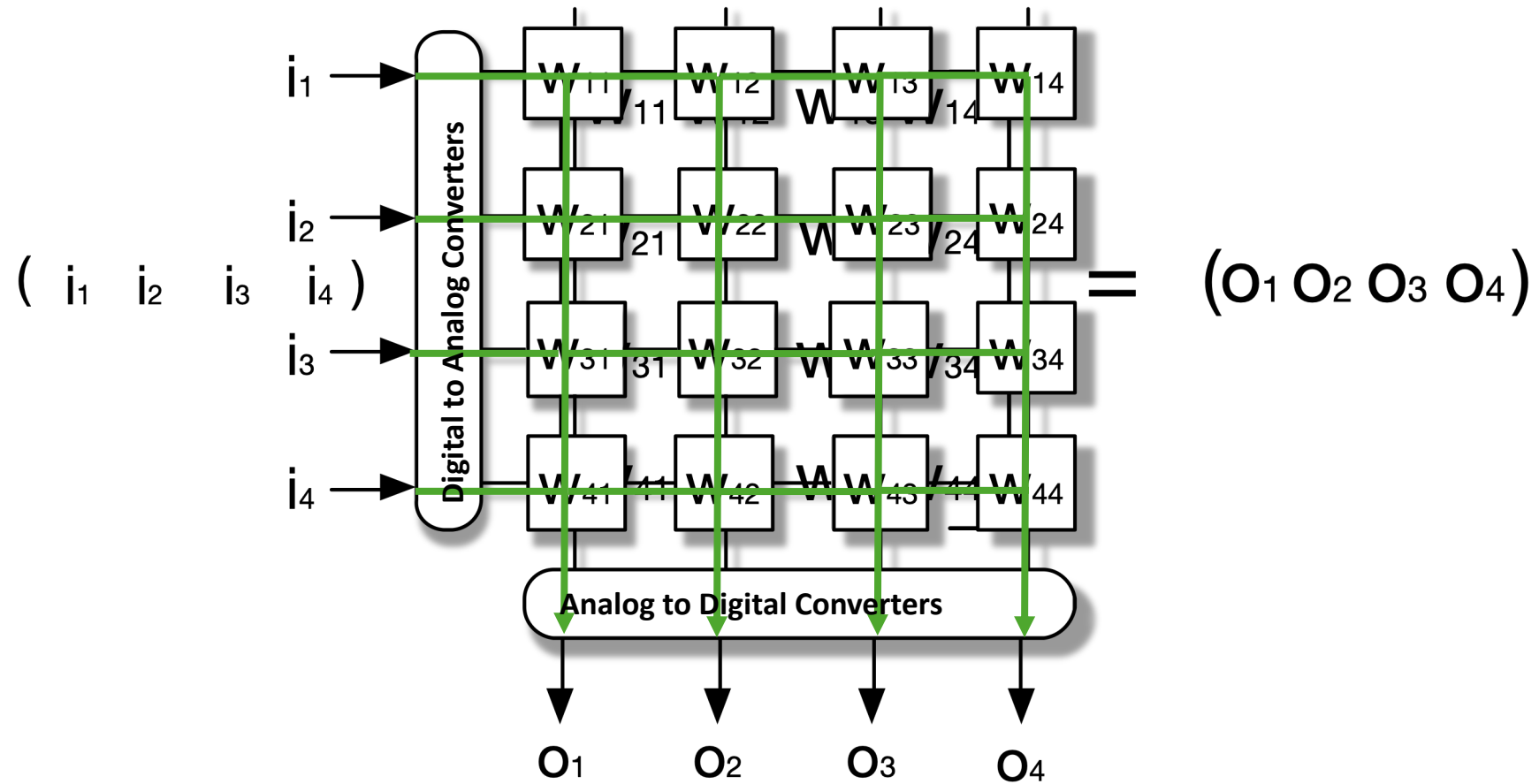
Data movement
between memory and
accelerator

Memristor-based PIM for DNN Acceleration

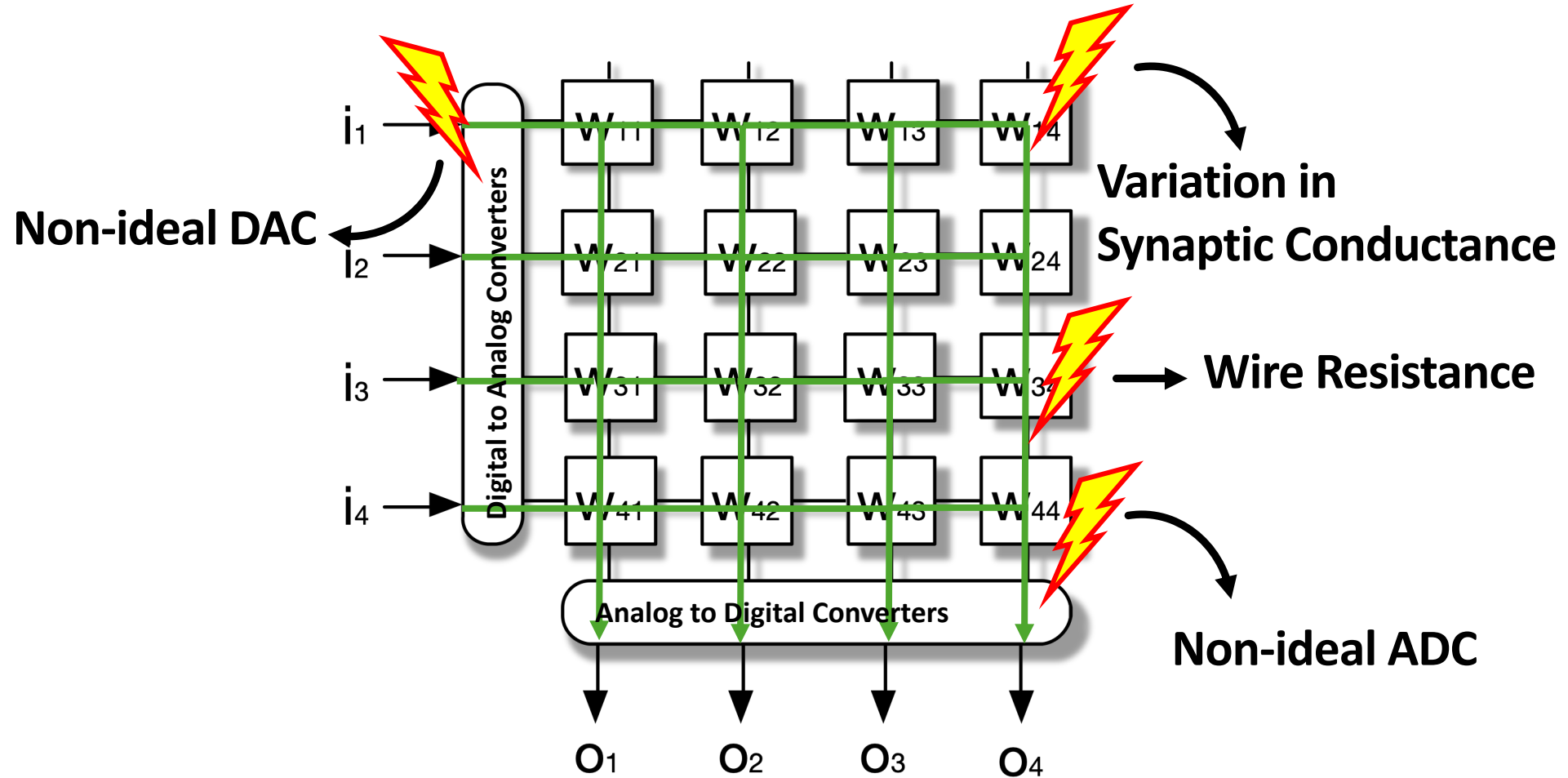
Memristor-based
crossbars support VMM

Processing in Memory
(PIM) minimizes data
movement

VMM in Memristor-based Crossbars

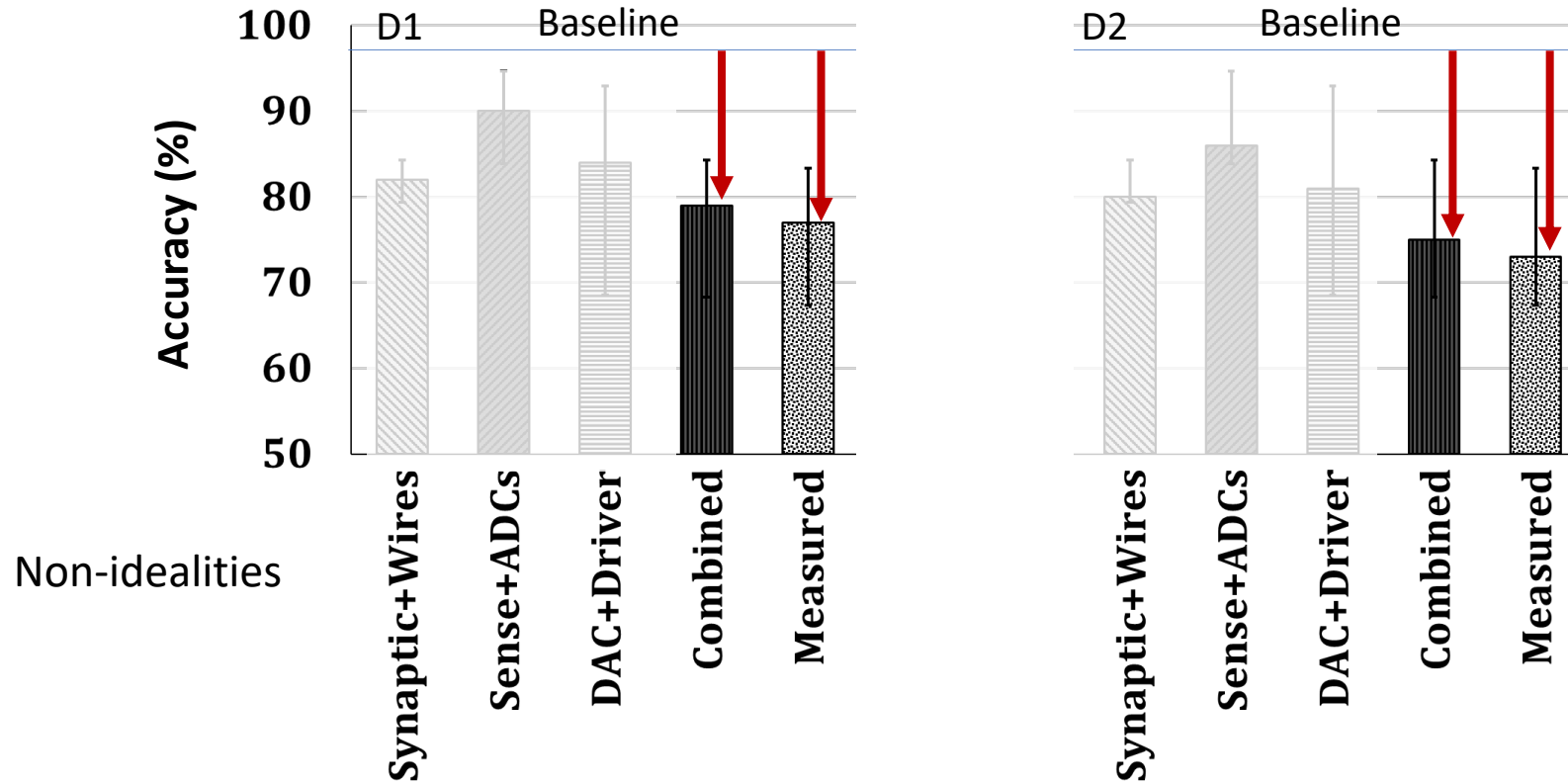


Non-idealities in Memristor-based Crossbars



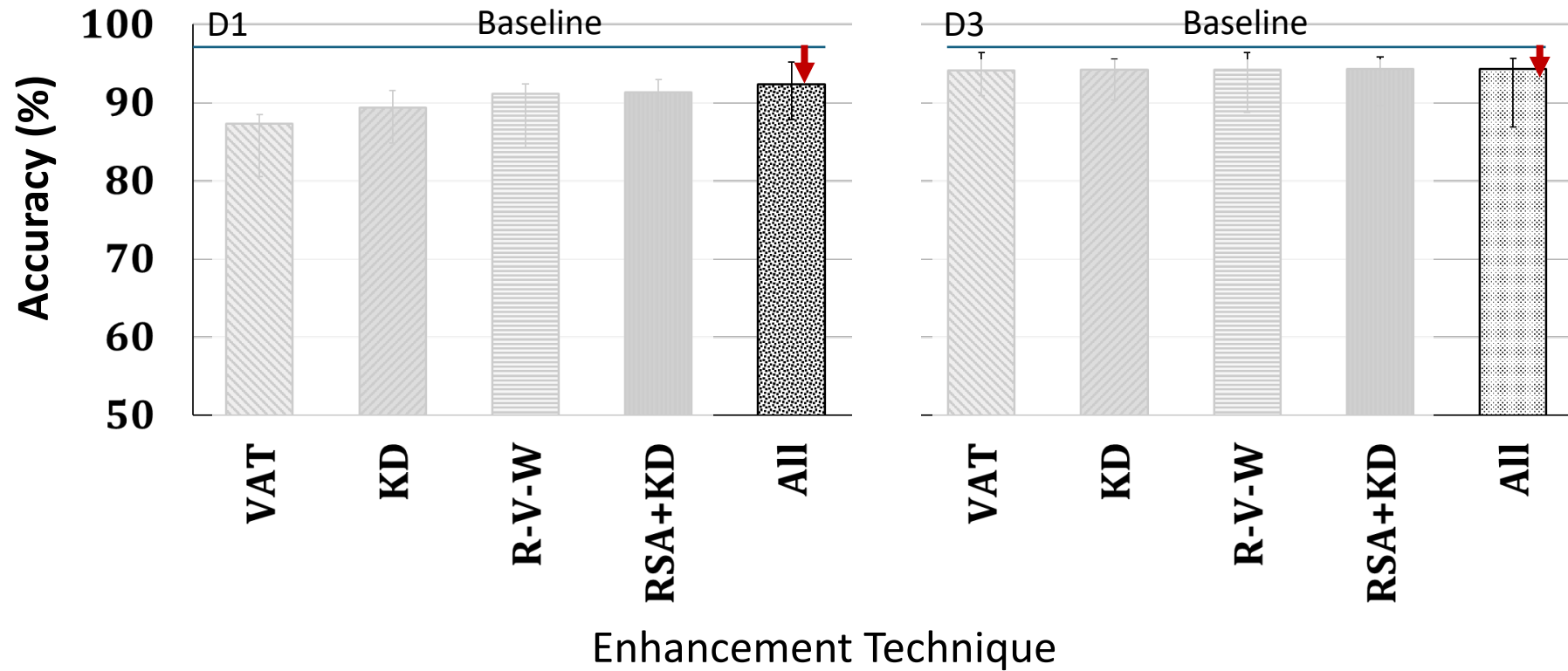
Subpar utilization of trained models **due to non-idealities**

Accuracy: All Non-idealities without Mitigation



Combined non-idealities leads to significant accuracy loss (>18%)

Accuracy: Enhancement Techniques on All Non-idealities



Accuracy loss drops to 6% from 18% after handling all non-idealities

ML-based Genome Analysis via PIM [MICRO '22]

- **GenPIP: In-Memory Acceleration of Genome Analysis via Tight Integration of Basecalling and Read Mapping**

Haiyu Mao, Mohammed Alser, Mohammad Sadrosadati, Can Firtina, Akanksha Baranwal, Damla Senol Cali, Aditya Manglik, Nour Almadhoun Alserr, Onur Mutlu

[Proceedings of the 55th International Symposium on Microarchitecture \(MICRO 2022\)](#), Chicago, IL, USA, October 2022.

[\[PDF\]](#) [\[Link\]](#)

Conference talk [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

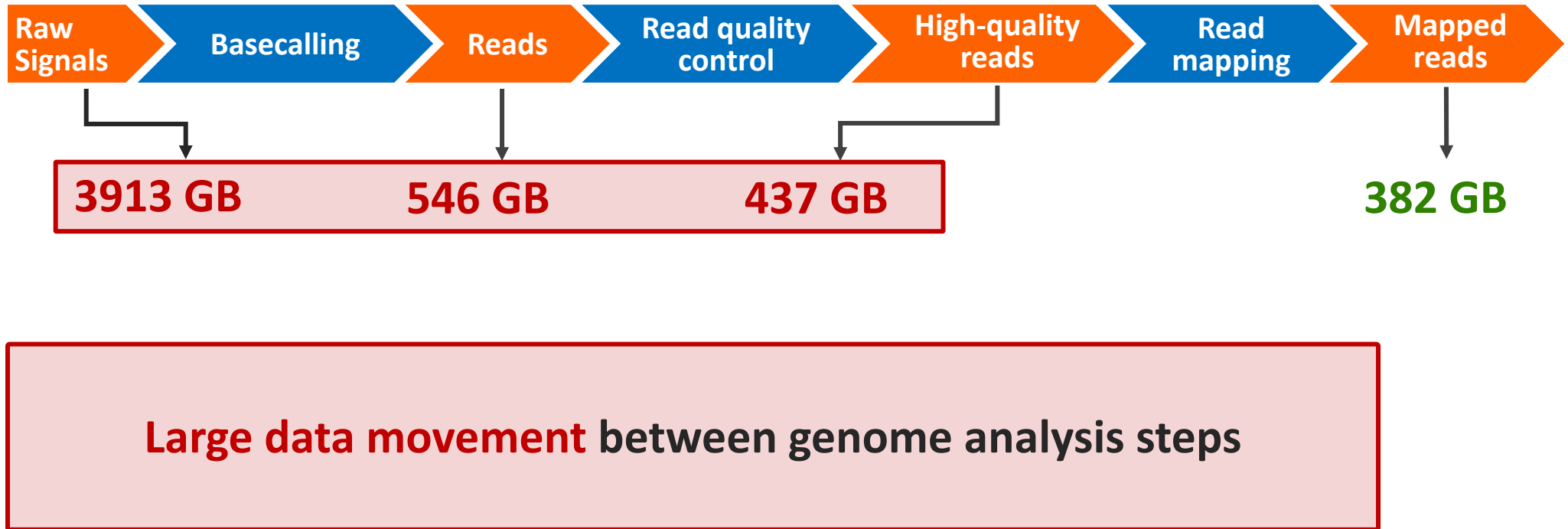
GenPIP: In-Memory Acceleration of Genome Analysis via Tight Integration of Basecalling and Read Mapping

Haiyu Mao¹ Mohammed Alser¹ Mohammad Sadrosadati¹ Can Firtina¹ Akanksha Baranwal¹
Damla Senol Cali² Aditya Manglik¹ Nour Almadhoun Alserr¹ Onur Mutlu¹

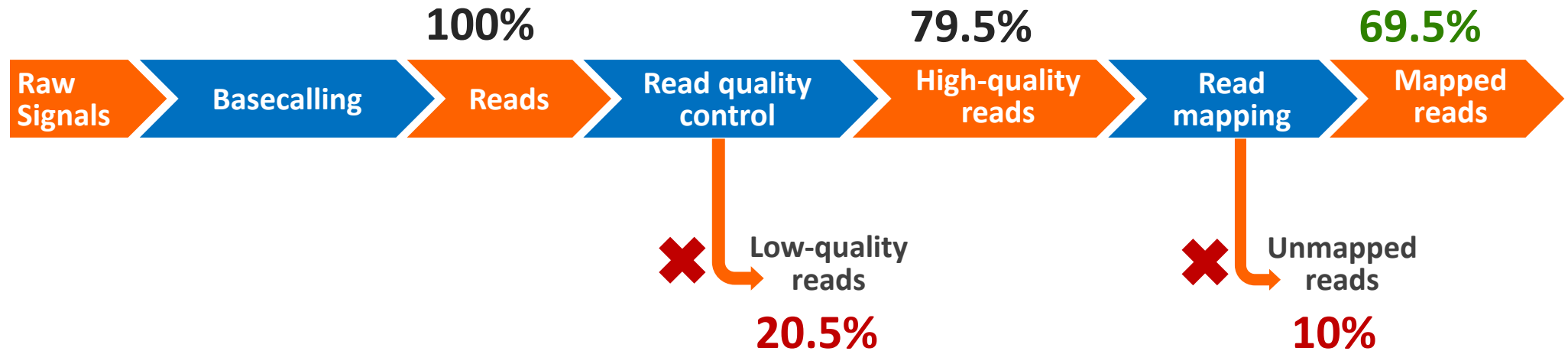
¹*ETH Zürich*

²*Bionano Genomics*

Problem 1: Large Data Movement



Problem 2: Wasted Computation



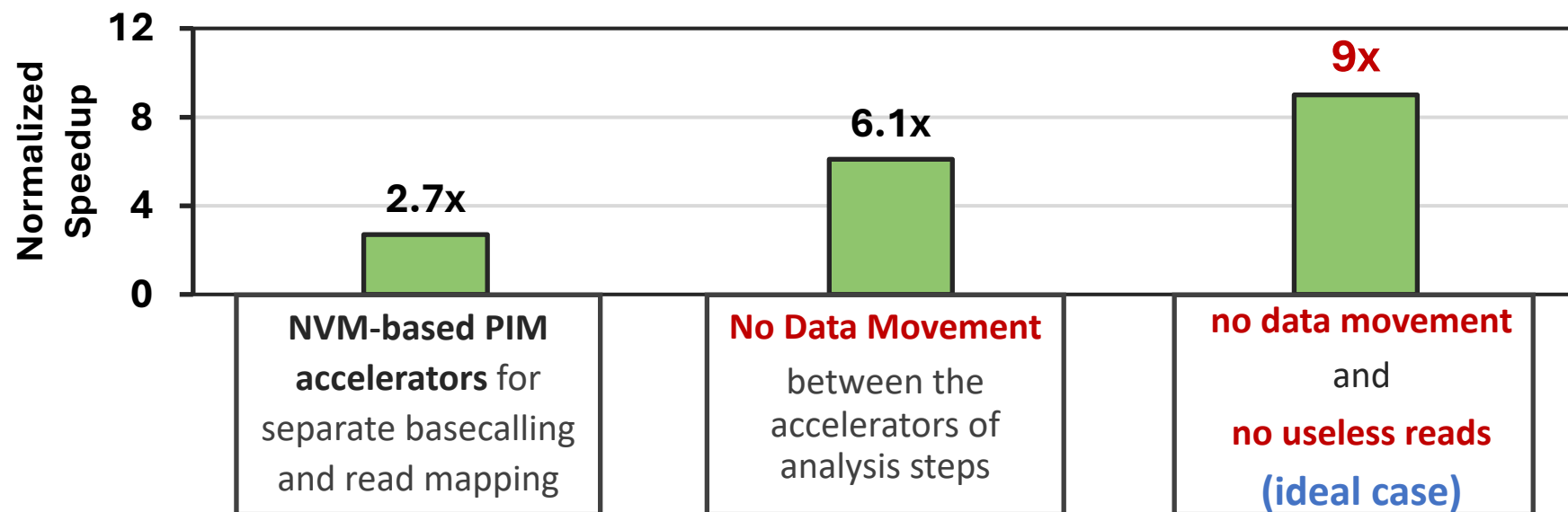
A considerable amount of computation on **useless data** due to

- Low-quality reads
- Unmapped reads

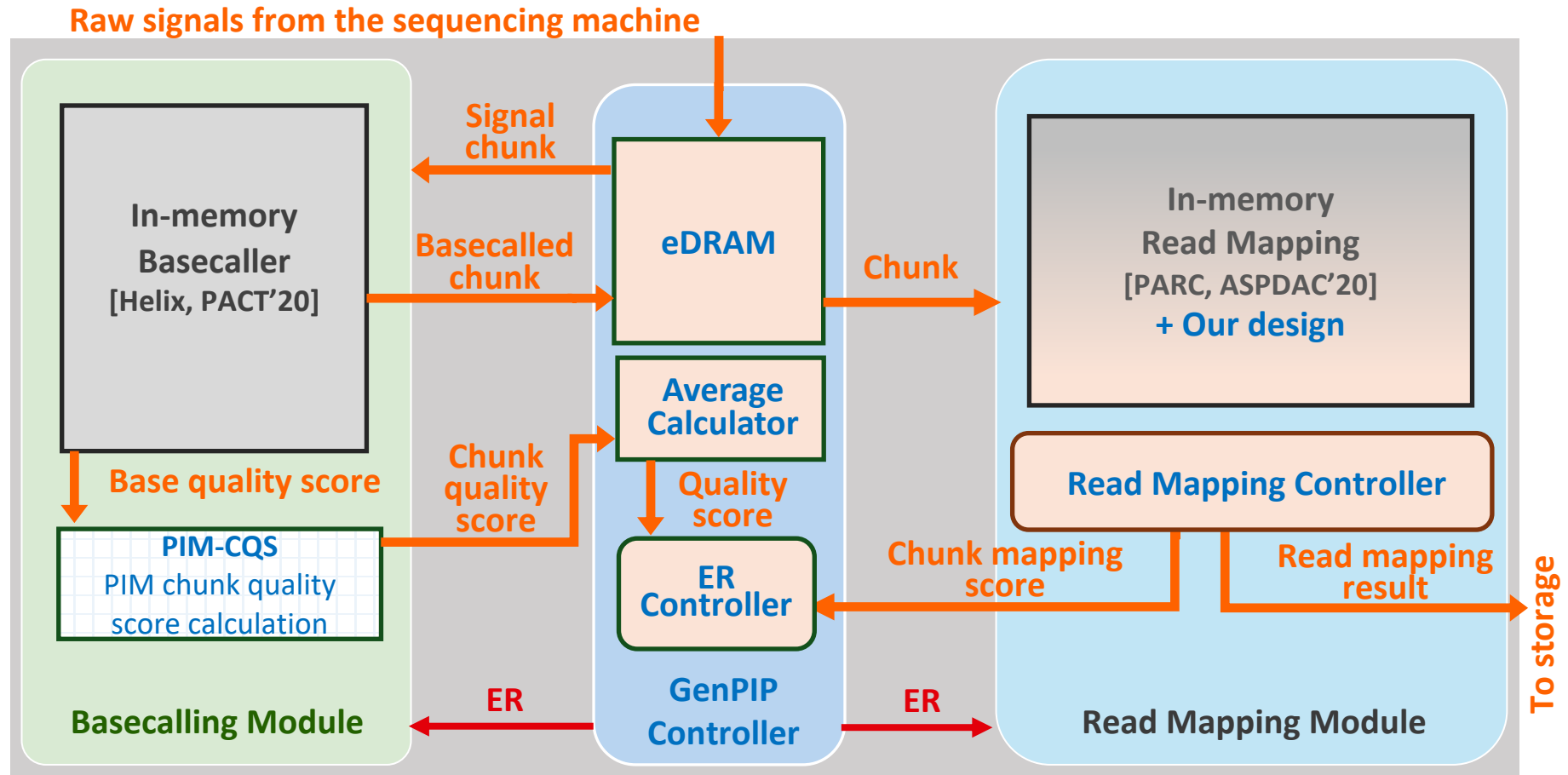
Goal and Opportunities

Goal: Efficiently accelerate the entire genome analysis pipeline while **minimizing data movement and useless computation**

We perform a study to quantify potential performance benefits



GenPIP Overview



Fast, Accurate, and Efficient
Genome Analysis
**via Algorithm-Architecture
Co-design**

Accelerating String Matching [MICRO '20]

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

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, Onur Mutlu

[Proceedings of the 53rd International Symposium on Microarchitecture \(MICRO 2020\)](#), Virtual, October 2020.

[\[PDF\]](#) [\[Code\]](#) [\[Link\]](#)

Conference talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

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

Damla Senol Cali[†]✕ Gurpreet S. Kalsi[✕] Zülal Bingöl[▽] 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^{*†} Onur Mutlu^{◇†▽}

[†]*Carnegie Mellon University* [✕]*Processor Architecture Research Lab, Intel Labs* [▽]*Bilkent University* [◇]*ETH Zürich*

[‡]*Facebook* [⊙]*King Mongkut's University of Technology North Bangkok* ^{*}*University of Illinois at Urbana-Champaign*

Accelerating Genome Graphs [ISCA '22]

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

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, Onur Mutlu
[Proceedings of the 49th Annual International Symposium on Computer Architecture \(ISCA 2022\)](#), New York City, NY, USA, June 2022.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Conference talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

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

Damla Senol Cali¹ Konstantinos Kanellopoulos² Joël Lindegger² Zülal Bingöl³
Gurpreet S. Kalsi⁴ Ziyi Zuo⁵ Can Firtina² Meryem Banu Cavlak² Jeremie Kim²
Nika Mansouri Ghiasi² Gagandeep Singh² Juan Gómez-Luna² Nour Almadhoun Alserr²
Mohammed Alser² Sreenivas Subramoney⁴ Can Alkan³ Saugata Ghose⁶ Onur Mutlu²

¹Bionano Genomics ²ETH Zürich ³Bilkent University ⁴Intel Labs

⁵Carnegie Mellon University ⁶University of Illinois Urbana-Champaign

In-Storage Filtering for Genomics [ASPLOS '22]

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

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, Onur Mutlu

[Proceedings of the 27th International Conference on Architectural Support for Programming Languages and Operating Systems \(ASPLOS 2022\)](#), Lausanne, Switzerland, February 2022.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Conference talk [\[Video\]](#) [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

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

Nika Mansouri Ghiasi¹ Jisung Park¹ Harun Mustafa¹ Jeremie Kim¹ Ataberk Olgun¹
Arvid Gollwitzer¹ Damla Senol Cali² Can Firtina¹ Haiyu Mao¹ Nour Almadhoun Alserr¹
Rachata Ausavarungnirun³ Nandita Vijaykumar⁴ Mohammed Alser¹ Onur Mutlu¹

¹ETH Zürich ²Bionano Genomics ³KMUTNB ⁴University of Toronto

In-Storage Decompression for Genomics [HPCA '26]

- **SAGe: A Lightweight Algorithm-Architecture Co-Design for Mitigating the Data Preparation Bottleneck in Large-Scale Genome Sequence Analysis**

Nika Mansouri Ghiasi, Talu Güloglu, Harun Mustafa, Can Firtina, Konstantina Koliogeorgi, Konstantinos Kanellopoulos, Haiyu Mao, Rakesh Nadig, Mohammad Sadrosadati, Jisung Park, Onur Mutlu

[Proceedings of the 32nd International Symposium on High-Performance Computer Architecture \(HPCA 2026\)](#),

Sydney, Australia, January 2026.

[\[PDF\]](#) [\[Link\]](#)

SAGe: A Lightweight Algorithm-Architecture Co-Design for Mitigating the Data Preparation Bottleneck in Large-Scale Genome Sequence Analysis

Nika Mansouri Ghiasi¹ Talu Güloglu¹ Harun Mustafa¹ Can Firtina^{1,2}
Konstantina Koliogeorgi¹ Konstantinos Kanellopoulos¹ Haiyu Mao³ Rakesh Nadig¹
Mohammad Sadrosadati¹ Jisung Park⁴ Onur Mutlu¹

¹ETH Zürich ²University of Maryland ³King's College London ⁴POSTECH

In-Storage Metagenomics [ISCA '24]

- **MegIS: High-Performance, Energy-Efficient, and Low-Cost Metagenomic Analysis with In-Storage Processing**

Nika Mansouri Ghiasi, Mohammad Sadrosadati, Harun Mustafa, Arvid Gollwitzer, Can Firtina, Julien Eudine, Haiyu Mao, Joël Lindegger, Meryem Banu Cavlak, Mohammed Alser, Jisung Park, Onur Mutlu
[Proceedings of the 51st Annual International Symposium on Computer Architecture \(ISCA 2024\)](#), Buenos Aires, Argentina, July 2024.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Conference talk [\[Slides \(pptx\)\]](#) [\[Slides \(pdf\)\]](#)

MegIS: High-Performance, Energy-Efficient, and Low-Cost Metagenomic Analysis with In-Storage Processing

Nika Mansouri Ghiasi¹ Mohammad Sadrosadati¹ Harun Mustafa¹ Arvid Gollwitzer¹
Can Firtina¹ Julien Eudine¹ Haiyu Mao¹ Joël Lindegger¹ Meryem Banu Cavlak¹
Mohammed Alser¹ Jisung Park² Onur Mutlu¹

¹ETH Zürich ²POSTECH

Recommended: Accelerating Genome Analysis [DAC '23]

- **Invited: Accelerating Genome Analysis via Algorithm-Architecture Co-Design**

Onur Mutlu, Can Firtina

[Proceedings of the 60th Design Automation Conference \(DAC 2023\)](#), San Francisco, CA, USA, July 2023.

[\[PDF\]](#) [\[Link\]](#)

Invited: Accelerating Genome Analysis via Algorithm-Architecture Co-Design

Onur Mutlu Can Firtina

ETH Zürich

Recommended: Genome Analysis Steps [CSBJ '22]

- **From molecules to genomic variations: Accelerating genome analysis via intelligent algorithms and architectures**

Mohammed Alser, Joel Lindegger, Can Firtina, Nour Almadhoun, Haiyu Mao, Gagandeep Singh, Juan Gomez-Luna, Onur Mutlu

[Computational and Structural Biotechnology Journal \(CSBJ\)](#), August 2022.

[\[PDF\]](#) [\[Code\]](#) [\[DOI\]](#)

Review

From molecules to genomic variations: Accelerating genome analysis via intelligent algorithms and architectures



Mohammed Alser^{*}, Joel Lindegger, Can Firtina, Nour Almadhoun, Haiyu Mao, Gagandeep Singh, Juan Gomez-Luna, Onur Mutlu^{*}

ETH Zurich, Gloriastrasse 35, 8092 Zürich, Switzerland

Agenda

- **The need to co-design algorithms, ML and hardware**
- Course information and logistics

Agenda

- The need to co-design algorithms, ML and hardware
- **Course information and logistics**

Sanity Check

- Make sure you are here for
CMSC 829C: Algorithms, AI, and Hardware for Biological Data

CMSC829C **Advanced Topics in Bioinformatics and Computational Biology; Algorithms, AI, and Hardware for Biological Data**

► [Syllabus Repository \(1\)](#)



Credits: 3

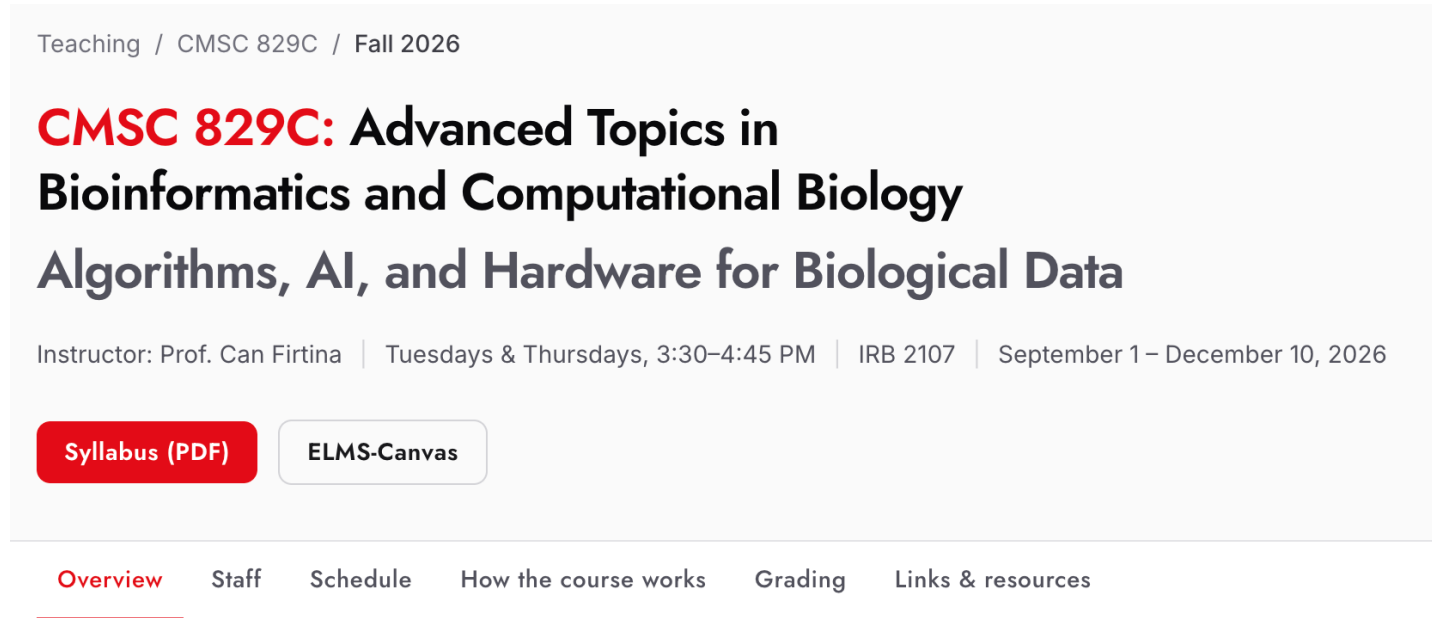
Grading Method: Regular

Must be in the Computer Science Master's or Doctoral programs, or permission of instructor.

Computational methods and hardware systems play an important role in biological research, enabling the analysis of large, complex datasets of biological data such as DNA, RNA, and proteins. This course covers cutting-edge and fundamental research papers on algorithms, AI methods, and hardware accelerators for bioinformatics. Papers are selected from diverse areas including genomics, transcriptomics, proteomics, protein structure prediction, and emerging computing paradigms. This is a seminar-style course intended for graduate students and advanced undergraduates with a strong research interest in bioinformatics. No prior knowledge of biology is required.

Course Website

- Slides, syllabus, other required materials will be publicly released at
 - <https://storm.cs.umd.edu/teaching/cmssc829c/fall2026/>

A screenshot of a course website for CMSC 829C. The page has a light gray background. At the top, it says "Teaching / CMSC 829C / Fall 2026". Below that is the course title "CMSC 829C: Advanced Topics in Bioinformatics and Computational Biology Algorithms, AI, and Hardware for Biological Data" in bold black text. Under the title, it lists the instructor "Prof. Can Firtina", the schedule "Tuesdays & Thursdays, 3:30–4:45 PM", the location "IRB 2107", and the dates "September 1 – December 10, 2026". There are two buttons: a red one labeled "Syllabus (PDF)" and a white one with a gray border labeled "ELMS-Canvas". At the bottom, there is a navigation bar with links: "Overview" (underlined in red), "Staff", "Schedule", "How the course works", "Grading", and "Links & resources".

Teaching / CMSC 829C / Fall 2026

**CMSC 829C: Advanced Topics in
Bioinformatics and Computational Biology**
Algorithms, AI, and Hardware for Biological Data

Instructor: Prof. Can Firtina | Tuesdays & Thursdays, 3:30–4:45 PM | IRB 2107 | September 1 – December 10, 2026

[Syllabus \(PDF\)](#) [ELMS-Canvas](#)

[Overview](#) [Staff](#) [Schedule](#) [How the course works](#) [Grading](#) [Links & resources](#)

- Canvas for discussion and assignments at
 - <https://umd.instructure.com/courses/1408667>

Course Structure

- 2 x 75-minute **lectures** or **paper presentation sessions** per week
 - TuTh 3:30pm – 4:45pm in IRB 2107
 - Office Hours: TuTh 4:45pm - 5:30pm (after class)
 - My office: IRB 3236
- **Lectures (first few weeks):** To provide the necessary background
 - How to review, analyze, and present research papers
 - Fundamentals of bioinformatics
 - Algorithmic, machine learning, and hardware solutions
- **Paper presentation sessions**

Who Is This Course For?

- **No prior background in biology is required**
 - The first few weeks cover the fundamentals you need
- Intended primarily for **graduate students**
 - Interested in algorithms, machine learning, hardware, or bioinformatics
- Advanced **undergraduates** with a strong research interest are welcome
 - Follow the university's guidelines for undergraduates taking graduate courses
 - Send me an email with your CV if you would like to enroll

Paper Presentation Sessions

- You will choose the papers you want to present
 - Paper list will be released soon
 - Typically 1 or 2 papers per student
- Presenter's role (lead)
 - Meet with your mentor (me) at least 1 week before your session
 - Read the paper and bring a draft of your slides to get feedback
 - Submit your final slides at least 24 hours before class
 - In-class: present, analyze, lead the discussion (~40 + ~30 min)
- Participants' role
 - Read the paper before each class and submit your questions
 - Engage in discussions

Assignments

- Submitting your questions before each presentation session
 - Due 11:59 PM the day before each presentation session
 - Questions should enable a nice discussion in class
 - Try to avoid obvious questions (e.g., "what if we try dataset X?")
 - We will ask some (or all) of these questions to the presenter
- Paper review towards the end of the semester
 - Use your analysis and review skills to write a structured review, the way real conference and journal reviews are written
 - You will review the same assigned paper (will be announced later)
 - Due Thursday, December 10 – we discuss the reviews together in the last class

Grading

- Please make sure you are here to learn and get a new perspective
- Leading paper presentations: 35%
 - Before-class preparedness: 10%
 - Paper presentation without the analysis part: 15%
 - Analysis and discussion leadership: 10%
- Participation: 20%
 - Engaging with questions asked by other students
 - Helping to drive the discussions related to the questions you submitted
- Submitting questions: 25%
 - Your 5 lowest scores are dropped (busy weeks, absences)
- Writing a paper review: 20%

Key Dates to Remember

- **Every presentation session** (when you are not presenting)
 - Discussion questions due 11:59 PM the day before
- **Your presentation session**
 - Mentor meeting with draft slides: at least 1 week before your session
 - Final slides: at least 24 hours before class
- **End of the term**
 - Paper review due Thursday, December 10 (we discuss reviews in the last class)
- Check the course website and ELMS-Canvas regularly – turn on notifications!

Questions?

Next Lecture

- **Lecture 2: Moving the Needle – A Bioinformatics Perspective**
 - Thursday, September 3, 3:30pm – 4:45pm, IRB 2107
 - Key aspects in research and how to present with these aspects in mind
- **Before next class**
 - Read the syllabus on the course website
 - Log in to ELMS-Canvas and turn on notifications
 - Email me if you have questions about enrollment or the course

CMSC 829C: Algorithms, AI, and Hardware for Biological Data

Lecture 1: Introduction and Course Logistics

Fall 2026

September 1, 2026

Can Firtina | canfirtina@gmail.com | cs.umd.edu/~firtina

Assistant Professor of Computer Science at UMD

