

Technology Dictates Algorithms: Developments in Read Mapping

Mohammed Alser

 @mealser

ISMB 2022

Mohammed Alser



- Lecturer and Senior Researcher, [SAFARI Research Group, ETH Zürich](#), since Sept. 2018.
- PhD from Bilkent University (Turkey) 2018, worked at UCLA, TU Dresden, and PETRONAS.
- [Received the IEEE Turkey Doctoral Dissertation Award](#) and a number of international prestigious awards.
-  <https://twitter.com/mealser>
- My main research is in **bioinformatics, computational genomics, metagenomics**, and computer architecture.
- I am especially excited about **building** new data structures, algorithms, and architectures that **make intelligent genome analysis a reality**.

How to Analyze a Genome?

NO

machine gives the **complete sequence** of genome as output



>CCTCCTCAGTGCCACCCAGCCCCTGGCAGCTCCAAACAGGGCTTTAAGCTTAAACACCCTGTCCTGCCCTGGAGTGAGGTGTCAAG
GACCTAAACTAAAAAAAAAGAAAAAGAAAAGAATTAAAATTAAGTAATTCTTGAAAAAAACTAATTCTAAGCTTCTT
CATGTCAAGGACCTAATGTGCTAACAGCACTTTGACCATTATTTGGATCTGAAAGAAATCAAGAATAATGAAGGACTTGATACATTG
GAAGAGGAGAGTCAGGACCTACAGAAAAAAAAAGAAAAAGAAAAGA**A**TTAAAATTAAGTAATTCTTGAAAAAA
ACTAATTCTAAGCTTCTT**C**ATGTCAAGGACCTAATGTCTGTGCAGGTCTTGCATTCCCTGTCAAAAGAAAAAGAATTAAAATT
AAGTAATTCTTGAAAAAAACTAATTCTAAGCTTCTTCATGTCAAGGACCTAATGTCAGGCCAAGAGTTGCAAAAAAAAAAGAAAAAA
GAAAAGAAAAAGAATTAAAATT**A**GTATTCTTGAAAAAAACTAATTCTAAGCTTCTTCATGTCAAGGACCTAATGTAGCCAGAATGG
TTGTGGATGGGAGCCTGTGGACCGACCAGGTAGCTCTTTCCACACTGTAGTCTCAAAGCTTCTCATGTGGTTCTGAGTGAAA
AAAAAAAGAAAAAGAAAAGAAAAAGAATTAAAATTAAAGTAATTCTTGAAAAAAACTAATTCTAAGCTT**TT**CATGTCAAGGACC
TAATGTAGCTACTGAACGTTATCTAGGGGAAAGATTGAAGGGGAGCTAAGGTCAACACACCACCTCCAGAAAGCTTCTTC.....

Genome Analysis



NO machine can read the
entire content of a genome



Why?!

```
>CCTGACCATGGAAGACTAAAGTGAAGCTTCAAGCTTTAGGGAGCTAACACACCCAGAAAGCTTCA.....  
CAAGTTCTTCATTGAAAAATTTCTTAAGCTTCAAGCTTTAGGGAGCTAACACACCCAGAAAGCTTCA.....  
AAAAAATTTCTTAAGCTTCAAGCTTTAGGGAGCTAACACACCCAGAAAGCTTCA.....  
ATGGAAAGCTTCAAGCTTTAGGGAGCTAACACACCCAGAAAGCTTCA.....  
GAAAATTTCTTAAGCTTCAAGCTTTAGGGAGCTAACACACCCAGAAAGCTTCA.....
```

Intelligent Genome Analysis

 arXiv > q-bio > arXiv:2205.07957

Quantitative Biology > Genomics

[Submitted on 16 May 2022]

Going From Molecules to Genomic Variations to Scientific Discovery: Intelligent Algorithms and Architectures for Intelligent Genome Analysis

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

<https://arxiv.org/abs/2205.07957>

High-Throughput Sequencers



Illumina MiSeq



Illumina NovaSeq 6000



Pacific
Biosciences
Sequel II



Pacific Biosciences RS II

Oxford
Nanopore
PromethION



Oxford Nanopore MinION

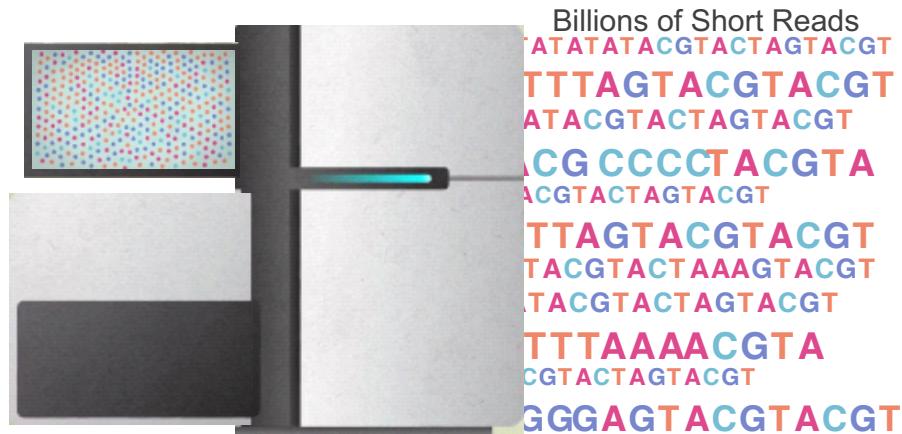


Oxford
Nanopore
SmidgION

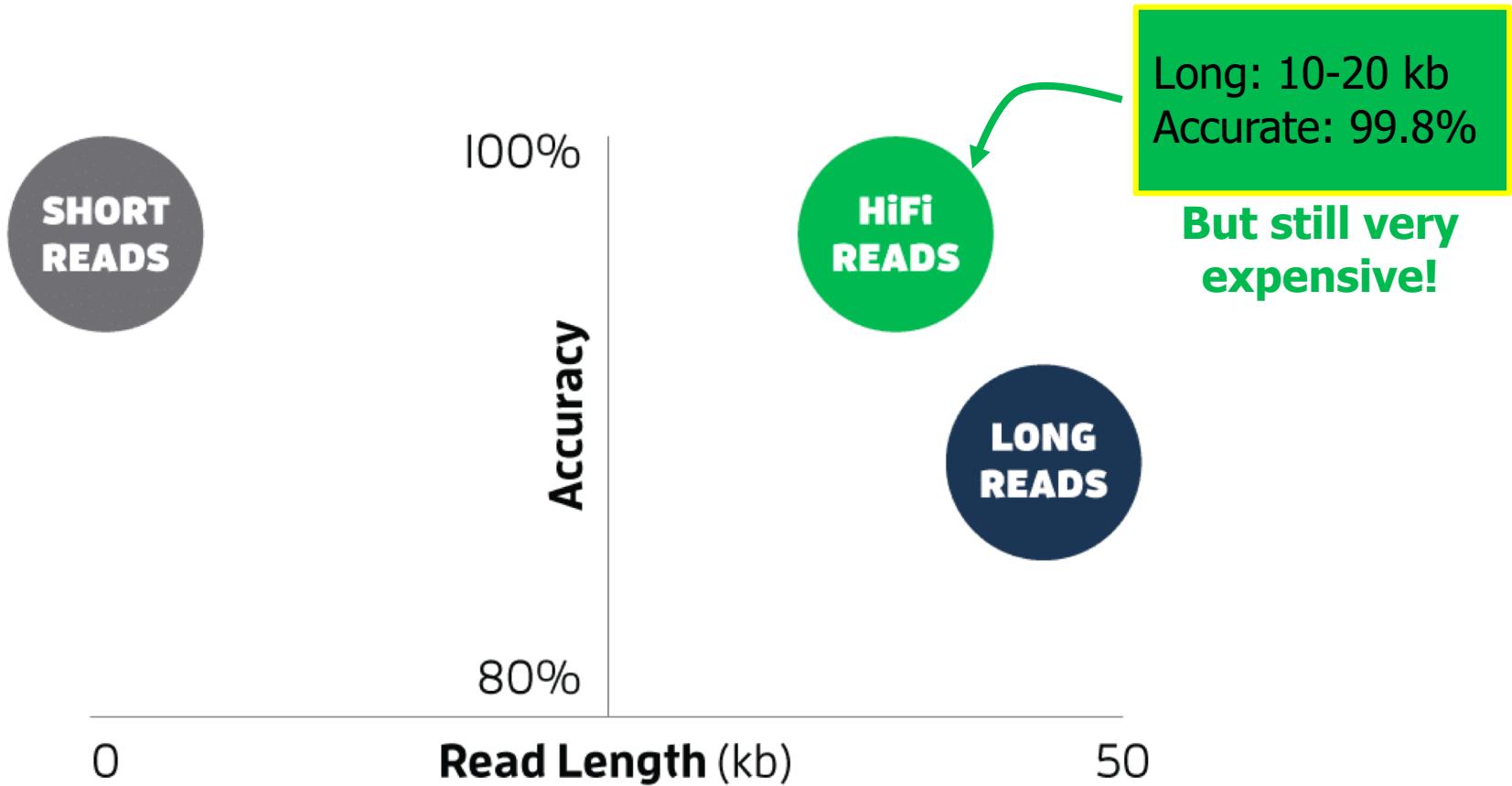
... and more! All produce data with different properties.

Genome Sequencer is a Chopper

Regardless the sequencing machine,
reads still lack information about their order and location
(which part of genome they are originated from)



Types of Genomic Reads



Wenger+, "[Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome](#)", *Nature Biotechnology*, 2019

Solving the Puzzle

.FASTA file



Reference genome

.FASTQ file



Reads

<https://www.pacb.com/smrt-science/smrt-sequencing/hifi-reads-for-highly-accurate-long-read-sequencing/>

Read Mapping in 111 pages!

In-depth analysis of 107 read mappers (1988-2020)

Mohammed Alser, Jeremy Rotman, Dhrithi Deshpande, Kodi Taraszka, Huwenbo Shi, Pelin Icer Baykal, Harry Taegyun Yang, Victor Xue, Sergey Knyazev, Benjamin D. Singer, Brunilda Balliu, David Koslicki, Pavel Skums, Alex Zelikovsky, Can Alkan, Onur Mutlu, Serghei Mangul

["Technology dictates algorithms: Recent developments in read alignment"](#)

Genome Biology, 2021

[\[Source code\]](#)

Alser *et al.* *Genome Biology* (2021) 22:249
<https://doi.org/10.1186/s13059-021-02443-7>

Genome Biology

REVIEW

Open Access



Technology dictates algorithms: recent developments in read alignment

Mohammed Alser^{1,2,3†}, Jeremy Rotman^{4†}, Dhrithi Deshpande⁵, Kodi Taraszka⁴, Huwenbo Shi^{6,7}, Pelin Icer Baykal⁸, Harry Taegyun Yang^{4,9}, Victor Xue⁴, Sergey Knyazev⁸, Benjamin D. Singer^{10,11,12}, Brunilda Balliu¹³, David Koslicki^{14,15,16}, Pavel Skums⁸, Alex Zelikovsky^{8,17}, Can Alkan^{2,18}, Onur Mutlu^{1,2,3†} and Serghei Mangul^{5*†}

Matching Each Read with Reference Genome

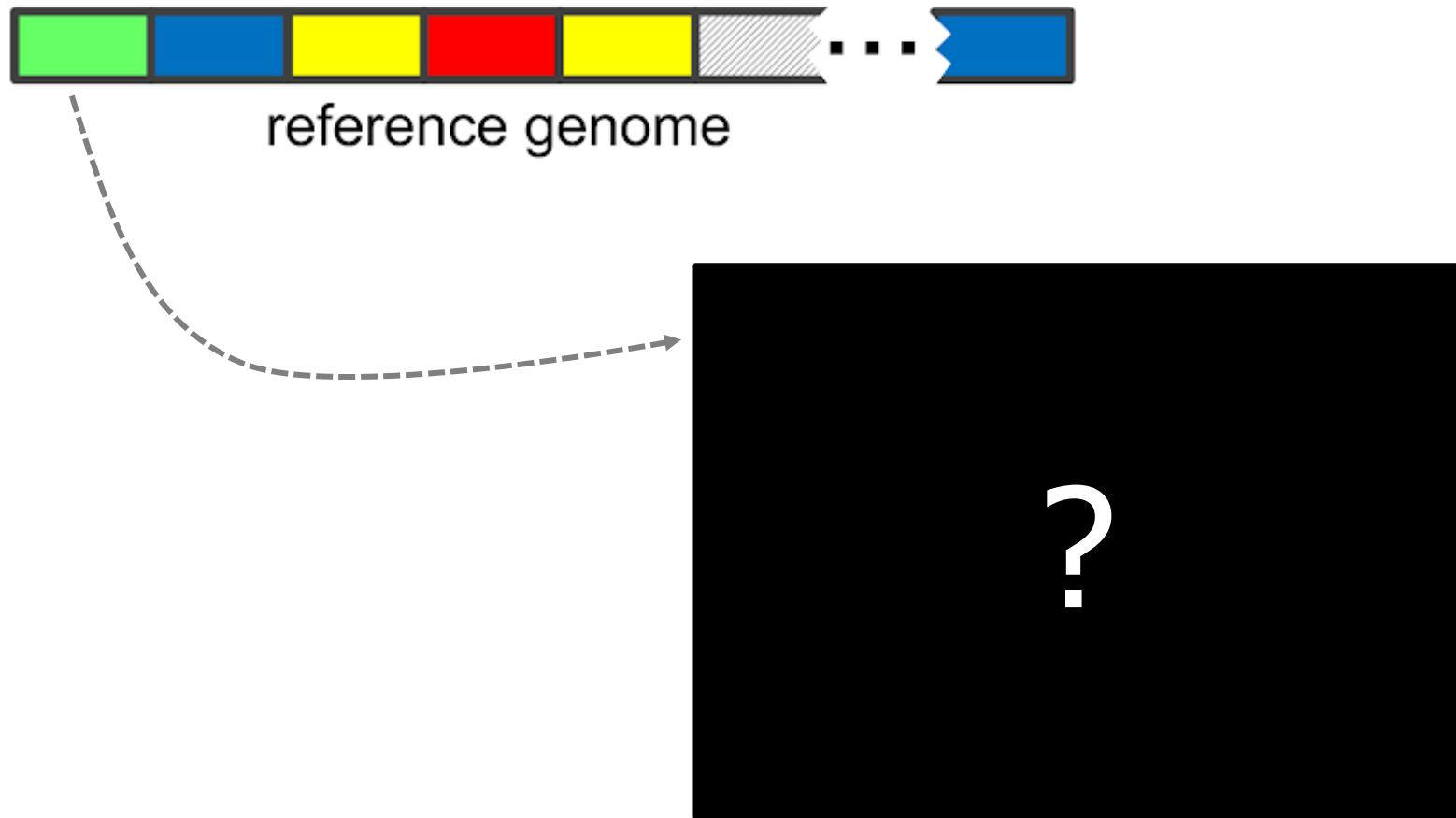
.FASTA file:

```
>NG_008679.1:5001-38170 Homo sapiens paired box 6 (PAX6)
ACCC[T]TCATTGACATTAAACTCTGGGGCAGG[G]GAACGCGGCTGTCAGATCT
GCCACTTCCCCTGCCGAGCGGCGGTGAGAAGTGTGGGAACC GGCGCTGCCAGGCTCACCTGCCTCCCCGC
CCTCCGCTCCCAGGTAACCGCC[CCCCGGCCGGCTCGGGGCCCGCGGGCCTCTCCGCTG
CCAGCGACTGCTGTCCCCAAATCAAAGCCGCCCAAGTGGCCCCGGGGCTTGATTTGCTTTAAAAG
GAGGCATACAAAGATGGAAGCGAGTTACTGAGGGAGGGATAGGAAGGGGGTGGAGGAGGGACTTGTCTT
TGCCGAGGTG[CTCCTAA]TCCAGTCCGGCCCT
GAGCTGGGAGTAGGGGGCGGGAGTCTGCTGCTGTCTGCTAAAGCCACTCGCGACCGCGAAAAATGCA
GGAGGTGGGGACGCACTTGCATCCAGACCTCCTCTGCATCGCAGTTC[CGCTTGGGAAAG
TCCGTACCCGCGCCT[AAGACACCC]TGCAGGTCAGCAGAAGTTCCC
GCGGTTGCAAAGTGCAGATGGCTGGACCGCAACAAAGTCTAGAGATGGGTTCGTTCTCAGAAAGACGC
```

.FASTQ file:

```
@HWI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1
T[AATAAAATCT]TTAGATN[NNNNNNNNNTAG
+
efcfffffcfeffffcfffffffdf`feed]`]_Ba_`__[YBBBBBBBBBRTT
```

Step 1: Indexing the Reference Genome

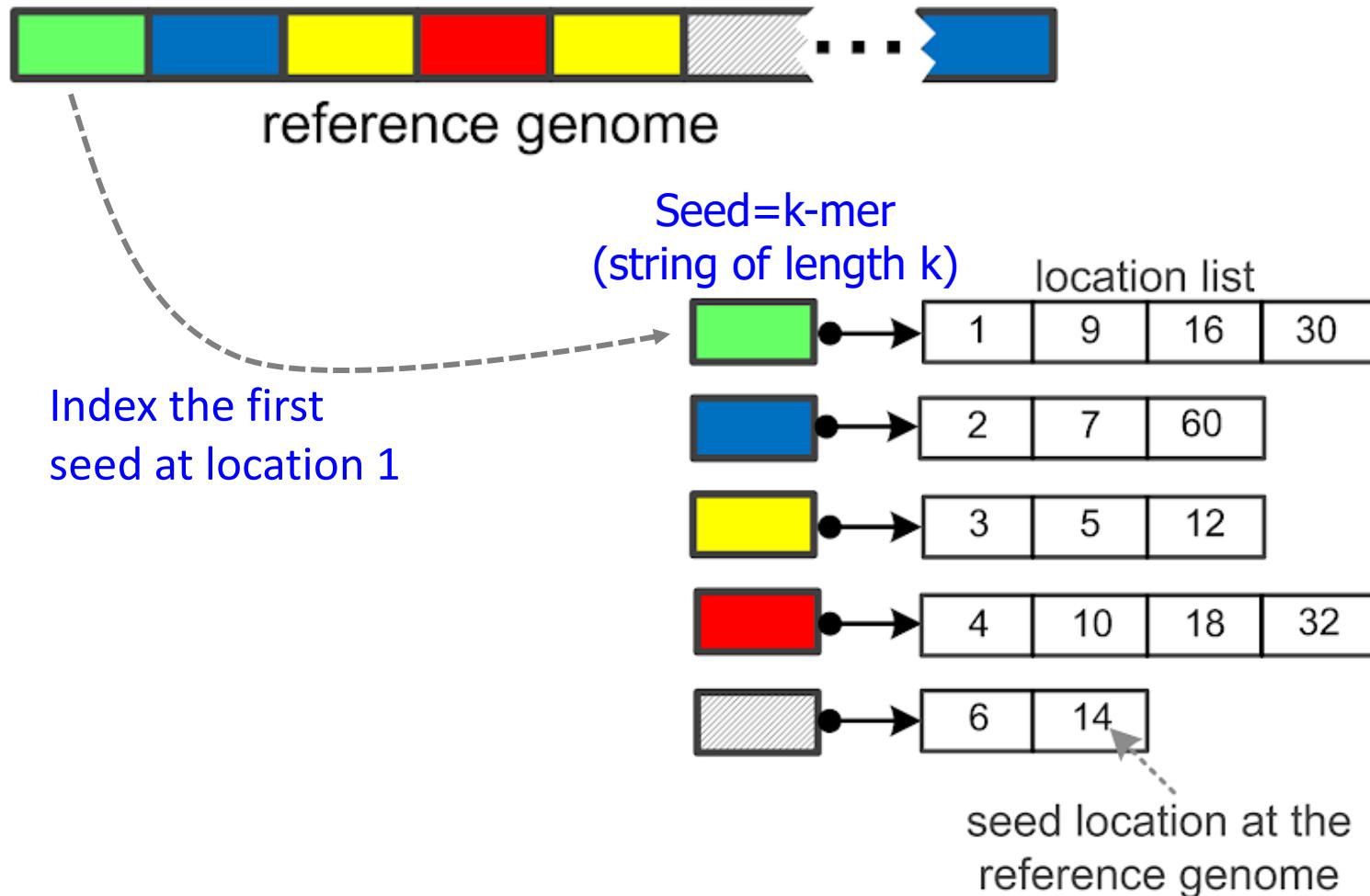


Popular Indexing Technique

Hashing is the most popular indexing technique for read mapping since 1988

Alser+, "[Technology dictates algorithms: Recent developments in read alignment](#)",
Genome Biology, 2021

Step 1: Indexing the Reference Genome



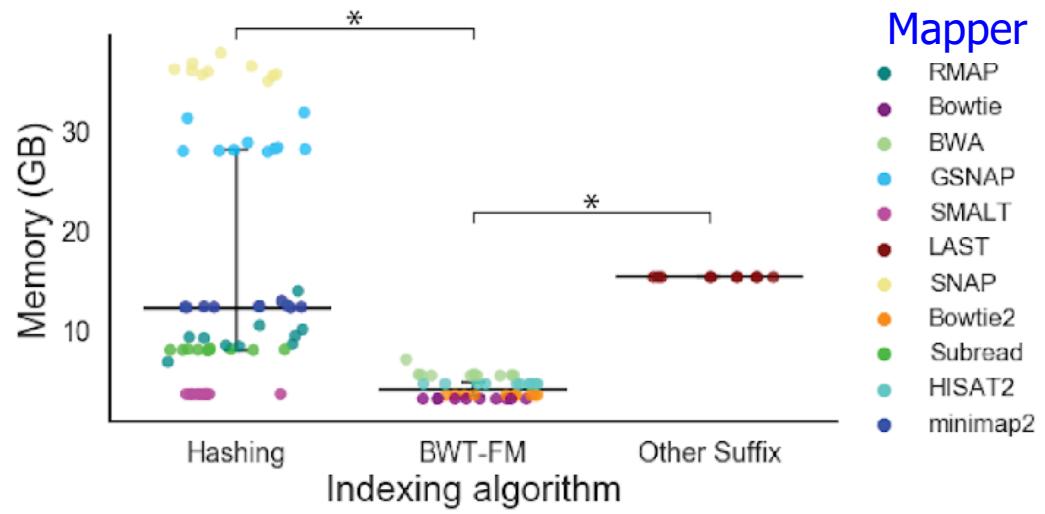
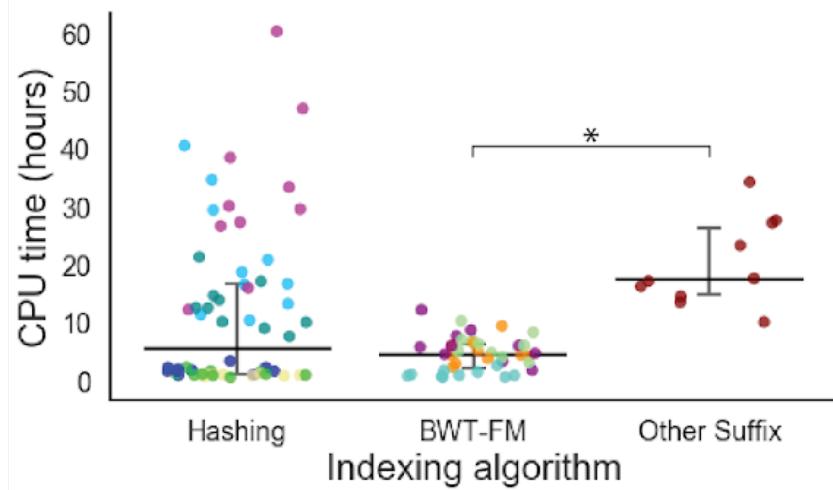
Genome Index Properties

- The index is built **only once** for each reference.
- **Seeds** can be overlapping, non-overlapping, spaced, adjacent, non-adjacent, minimizers, compressed, ...

Tool	Version	Index Size*	Indexing Time
mrFAST	2.2.5	16.5 GB	20.00 min
minimap2	0.12.7	7.2 GB	3.33 min
BWA-MEM	0.7.17	4.7 GB	49.96 min

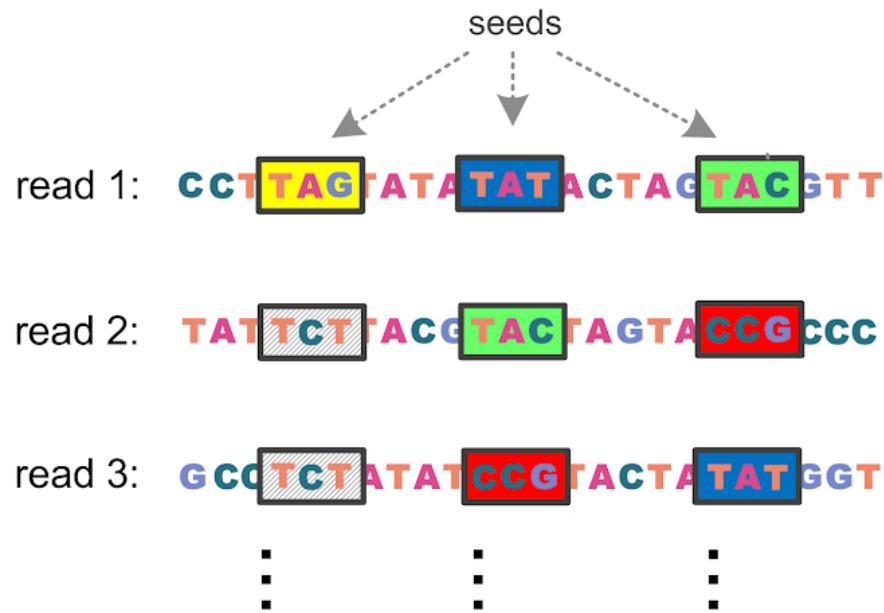
*Human genome = 3.2 GB

Performance of Human Genome Indexing

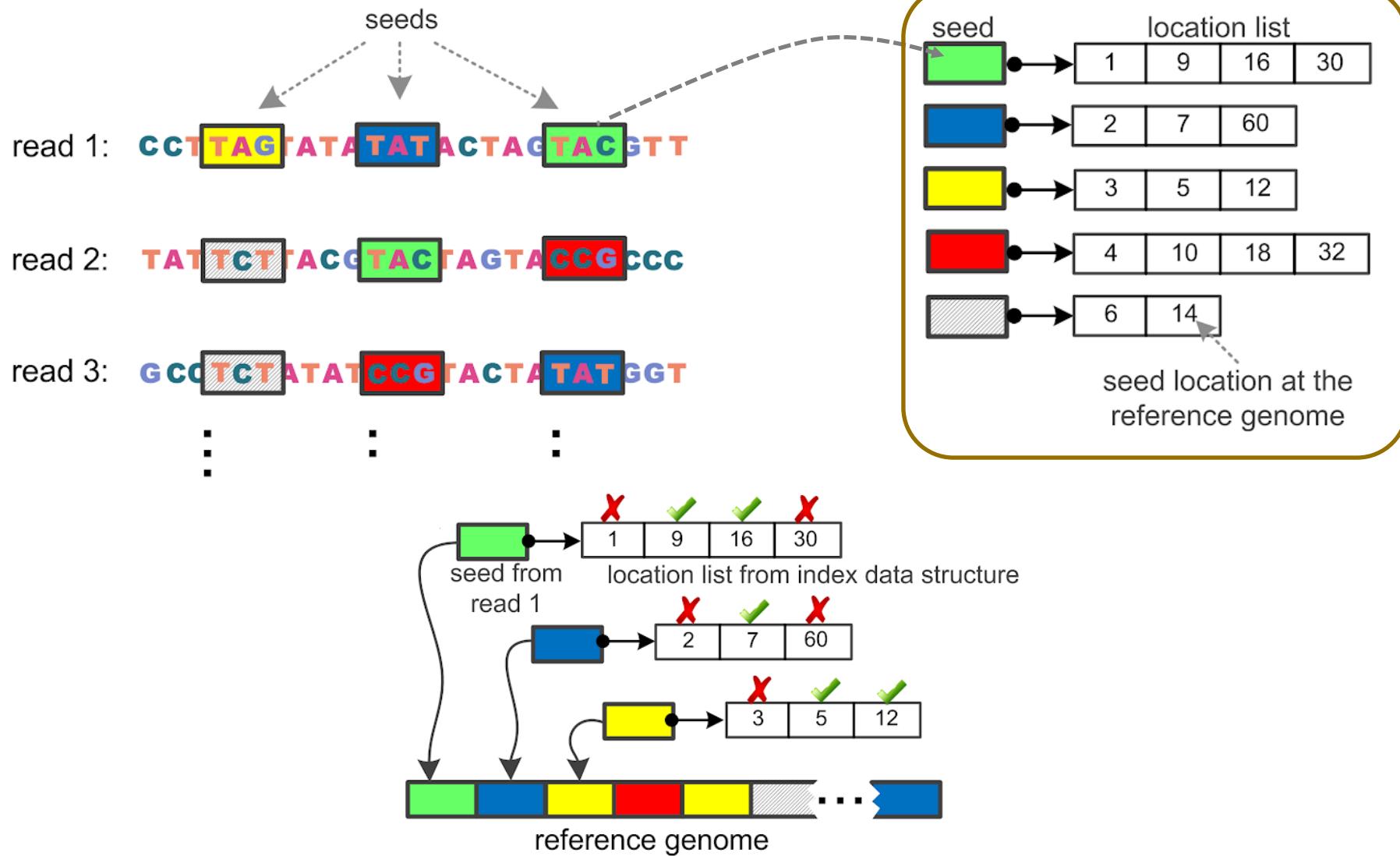


Alser+, "[Technology dictates algorithms: Recent developments in read alignment](#)",
Genome Biology, 2021

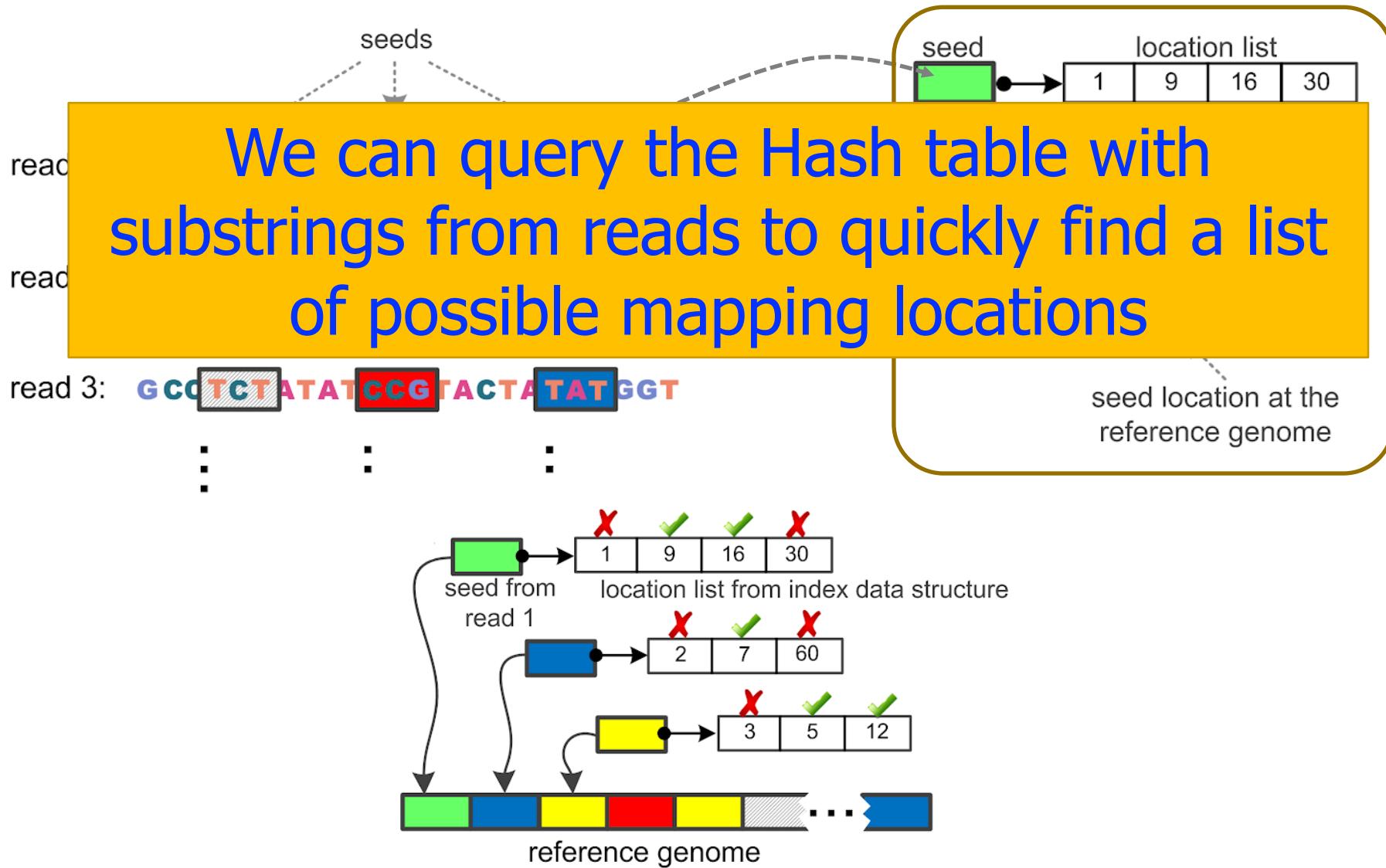
Step 2: Query the Index Using Read Seeds



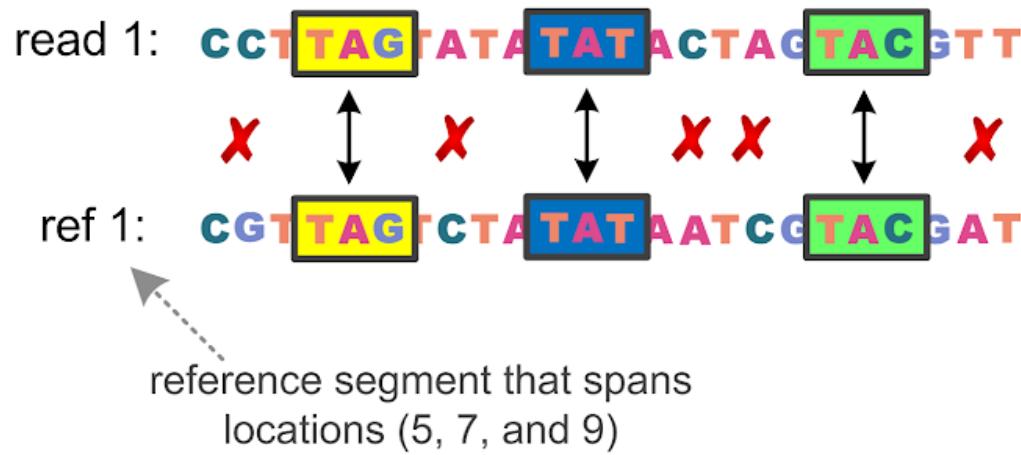
Step 2: Query the Index Using Read Seeds



Step 2: Query the Index Using Read Seeds

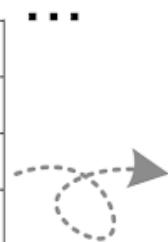


Pre-alignment Filtering



Step 3: Sequence Alignment (Verification)

	C	G	T	T	A	G	T	C	T	A	
C	0	0	0	0	0	0	0	0	0	0	0
C	0	2	2	2	2	2	2	2	2	2	2
T	0	2	3	3	3	3	3	3	4	4	4
T	0	2	3	5	5	5	5	5	5	6	6
T	0	2	3	5	7	7	7	7	7	7	7
A	0	3	3	5	7	9	9	9	9	9	9
G	0	2	4	5	7	9	11	11	11	11	11
T	0	2	4	6	7	9	11	13	13	13	13
A	0	2	4	6	7	9	11	13	14	14	15
T	0	2	4	6	8	9	11	13	14	16	16
:											



.bam/.sam file contains necessary alignment information (e.g., type, location, and number of each edit)

Step 3: Sequence Alignment (Verification)

- **Edit distance** is defined as the minimum number of edits (i.e. insertions, deletions, or substitutions) needed to make the read exactly match the reference segment.

organization x operation

Ref	o	-	-	r	g	a	n	i	z	a	t	o	n
Read	o	p	e	r	-	-	-	-	-	a	t	o	n

Ref	o	-	-	r	g	a	n	o	z	i	z	a	t	o	n
Read	o	p	e	r	-	a	-	-	-	-	-	t	i	o	n

Edit distance = 7



organization x translation

Ref	o	r	g	a	n	i	z	-	a	t	i	o
Read	t	r	-	a	n	-	s	l	a	t	i	o

Ref	o	r	g	a	n	-	i	z	a	t	i	o	n
Read	t	r	-	a	n	s	l	-	a	t	i	o	n

Ref Read

o	r	g	a	n	i	z	a	t	o	n
t	r	-	a	n	s	l	a	t	o	n

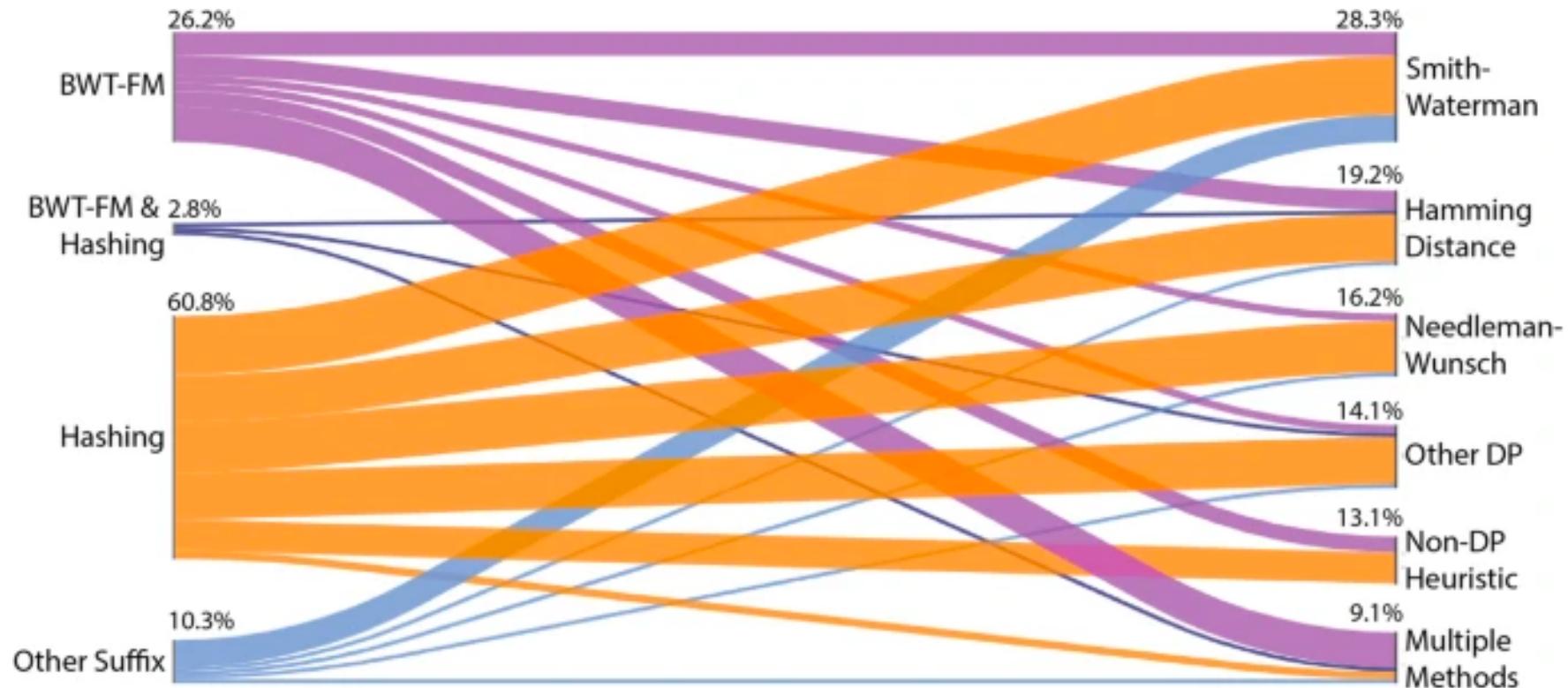
Edit distance = 4

Popular Algorithms for Sequence Alignment

Smith-Waterman remains
the most popular algorithm
since 1988

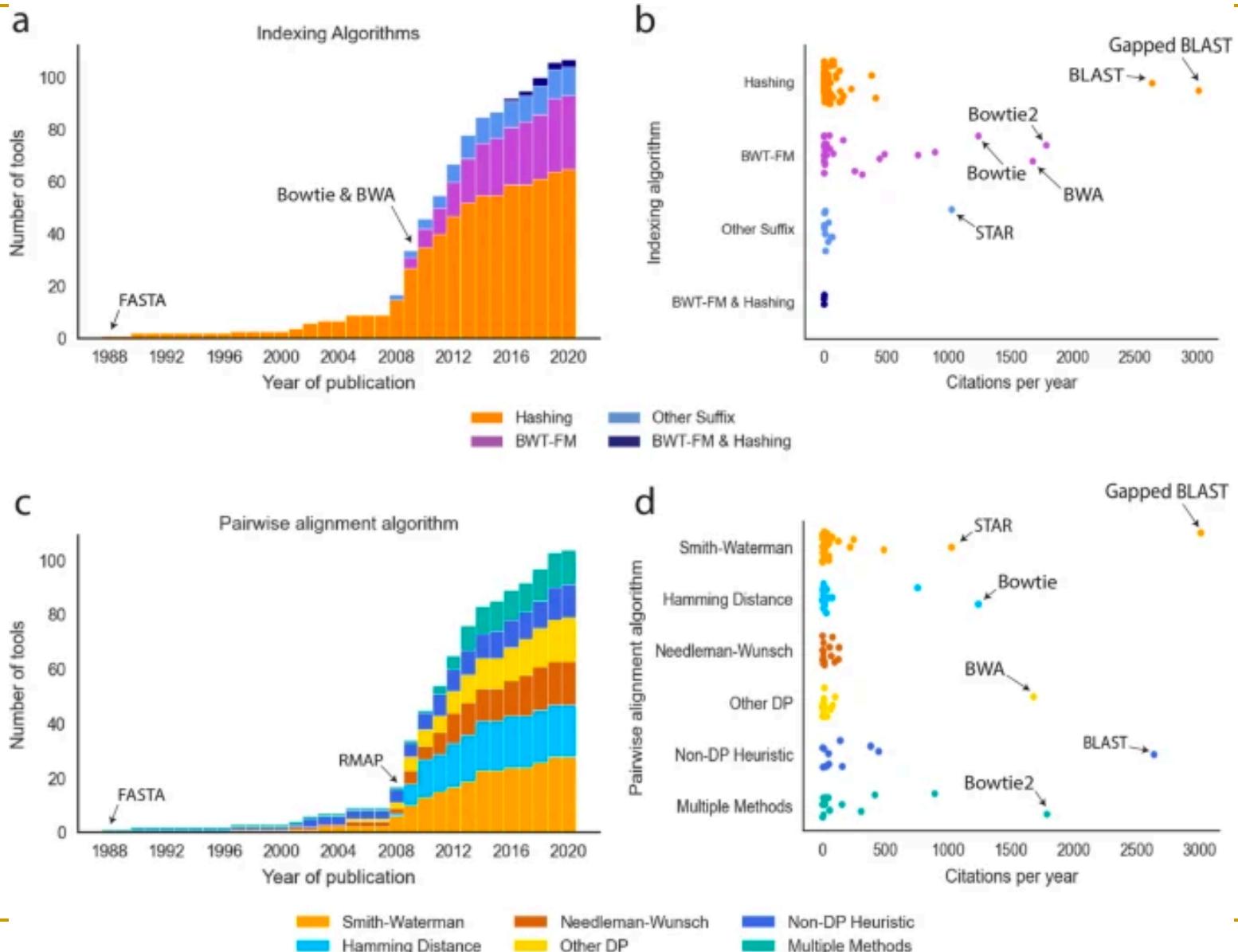
Hamming distance is
the second most popular technique
since 2008

Indexing & Sequence Alignment Algorithms

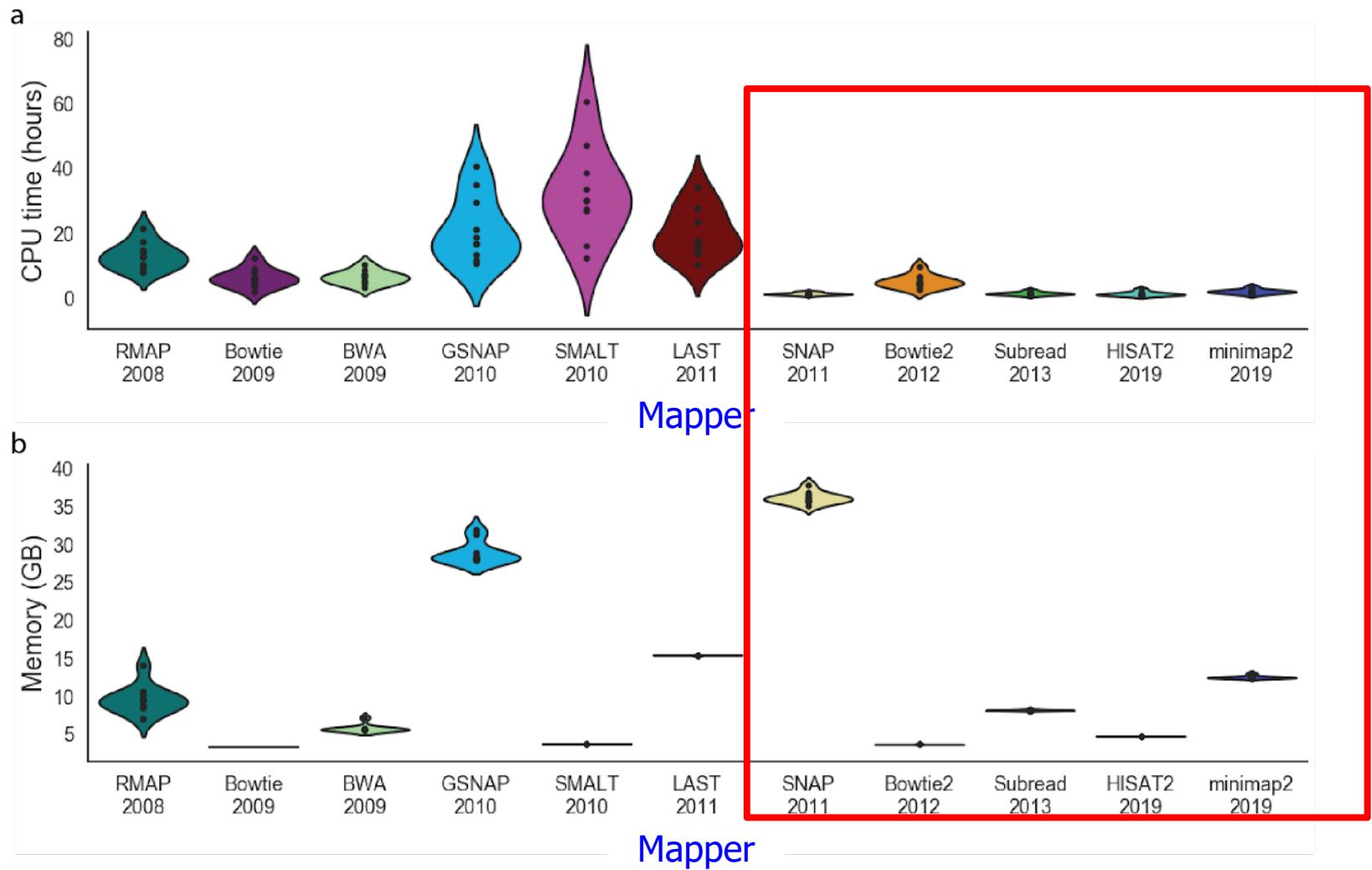


Combination of algorithms utilized by read alignment tools. Sankey plot displaying the flow of surveyed tools using each indexing technique and pairwise alignment.

The landscape of read alignment 1988-2020

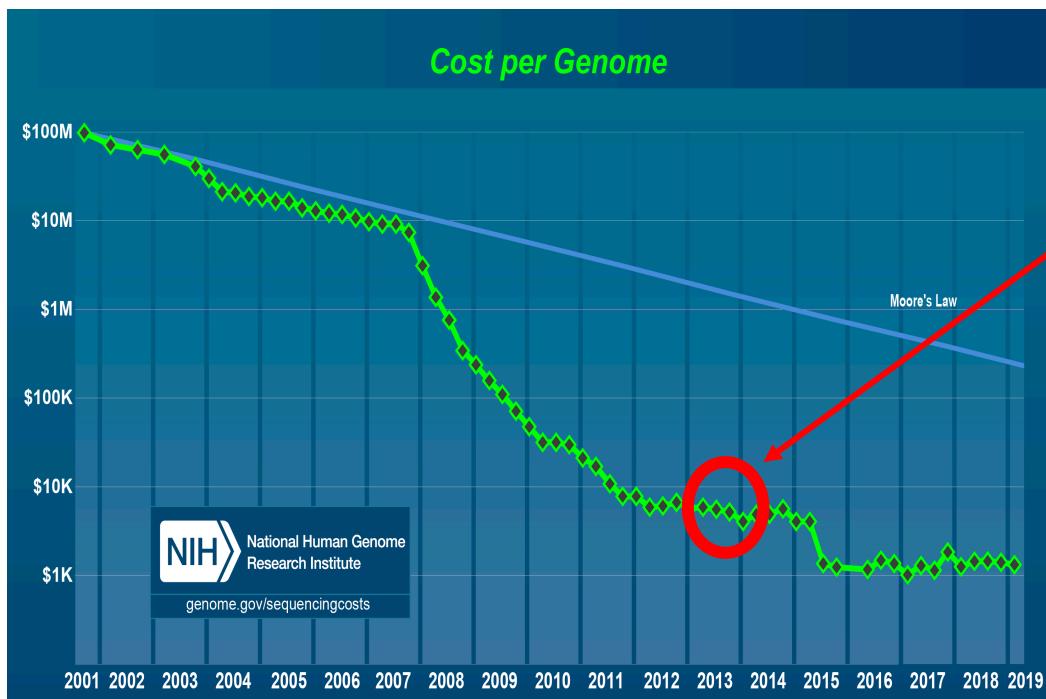


Performance of Read Mapping

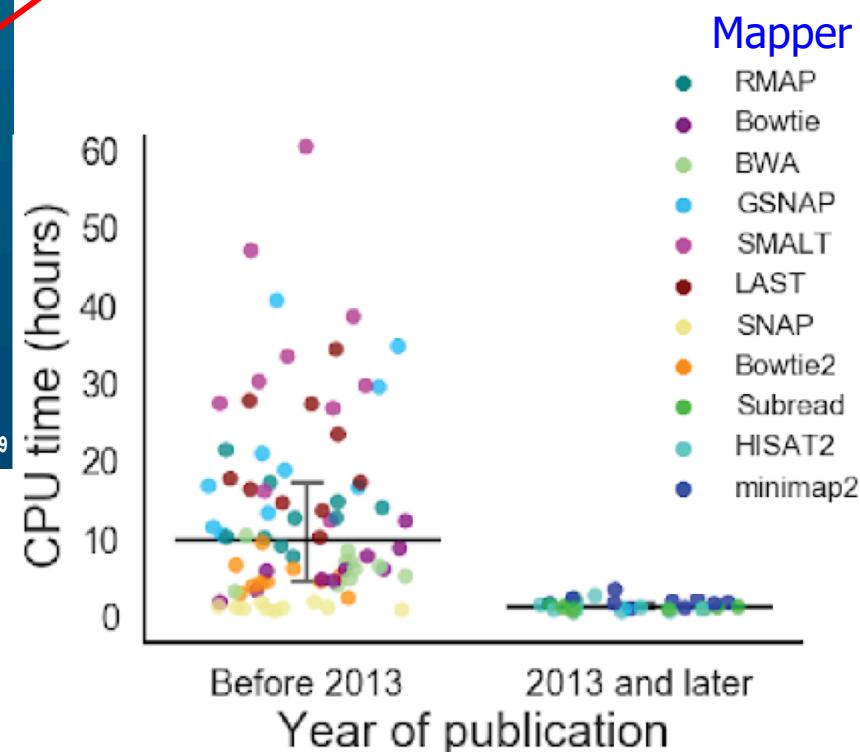


Alser+, "Technology dictates algorithms: Recent developments in read alignment",
Genome Biology, 2021

The Need for Speed



Did we realize the **need** for **faster** genome analysis?

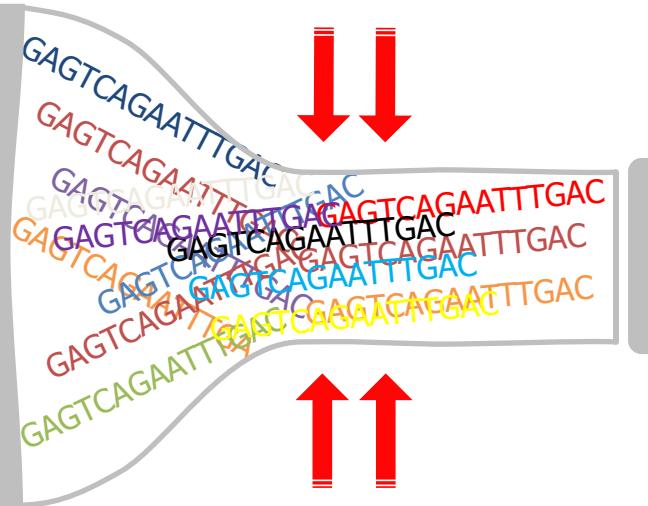


Alser+, "Technology dictates algorithms: Recent developments in read alignment",
Genome Biology, 2021

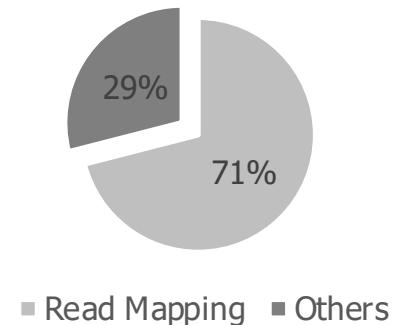
Analysis is Bottlenecked in Read Mapping!!

48 Human whole genomes
at 30× coverage
in about 2 days

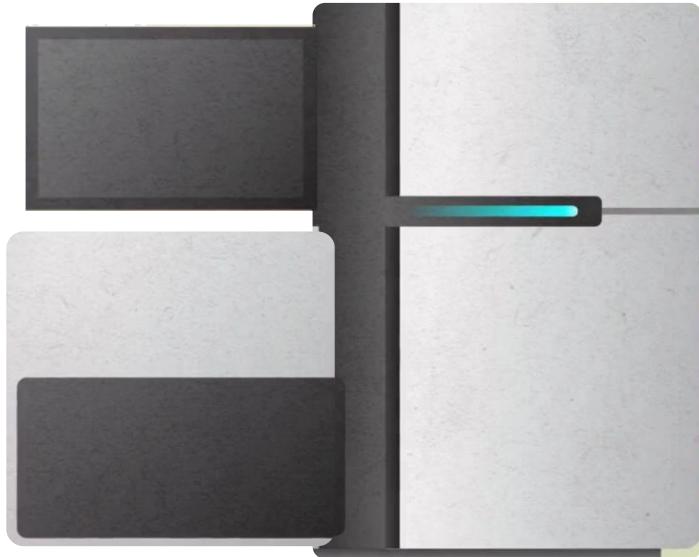
Illumina NovaSeq 6000



1 Human genome
32 CPU hours
on a 48-core processor

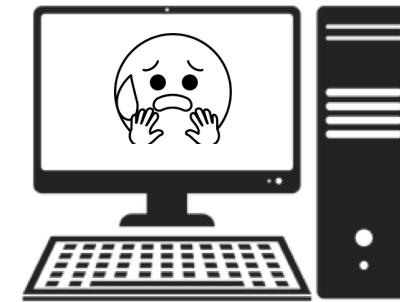
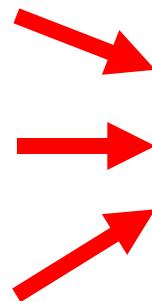


Lack of Specialized Compute Capability



Specialized Machine
for Sequencing

FAST

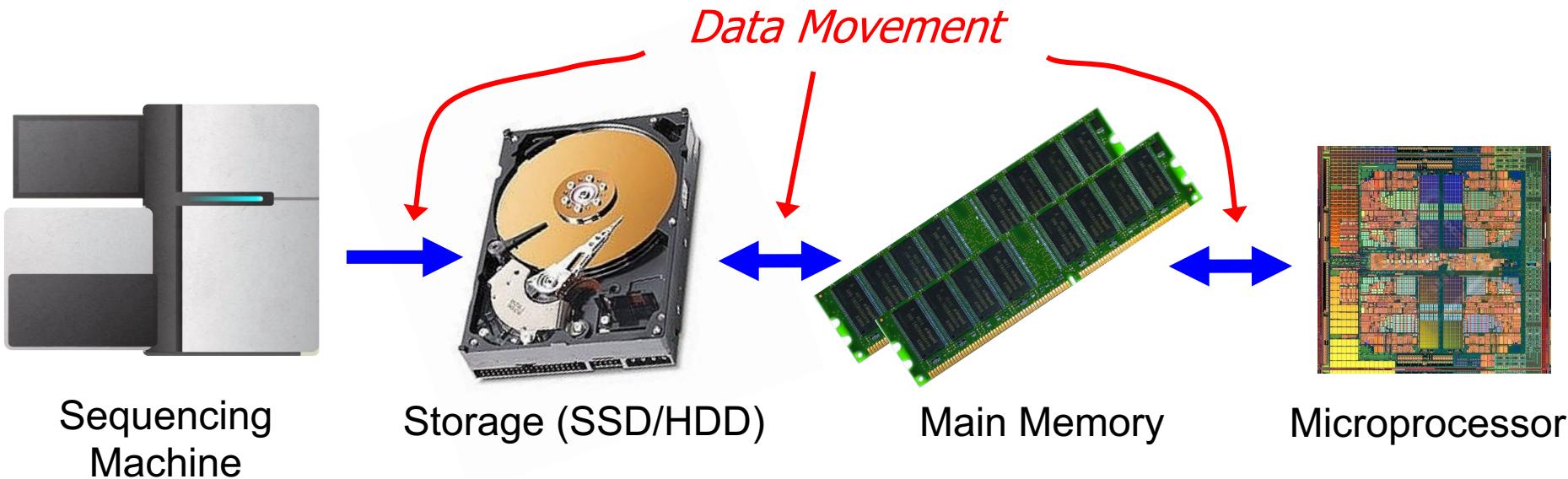


General-Purpose Machine
for Analysis

SLOW

Data Movement Dominates Performance

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



* 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

We need intelligent algorithms
and intelligent architectures
that handle data well

Our Contributions

Near-memory/In-memory
Pre-alignment Filtering

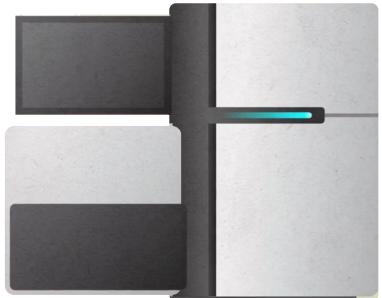
GRIM-Filter [BMC Genomics'18]

SneakySnake [IEEE Micro'21]

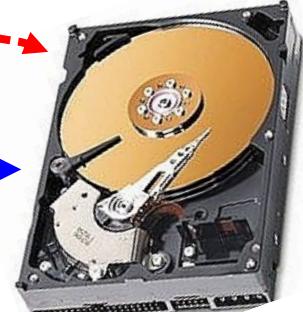
GenASM [MICRO 2020]

In-storage Sequence Alignment

GenStore [ASPLOS 2022]



1



Storage (SSD/HDD)

Near-memory Sequence Alignment

GenASM [MICRO 2020]

SeGraM [ISCA 2022]

Specialized Pre-alignment Filtering
Accelerators (GPU, FPGA)

GateKeeper [Bioinformatics'17]

MAGNET [AACBB'18]

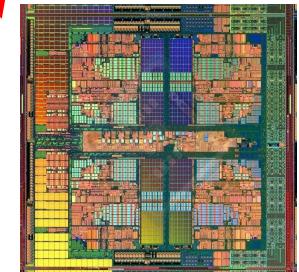
Shouji [Bioinformatics'19]

GateKeeper-GPU [arXiv'21]

SneakySnake [Bioinformatics'20]

Main Memory

32
Microprocessor



2

Our Contributions

Near-memory/In-memory
Pre-alignment Filtering

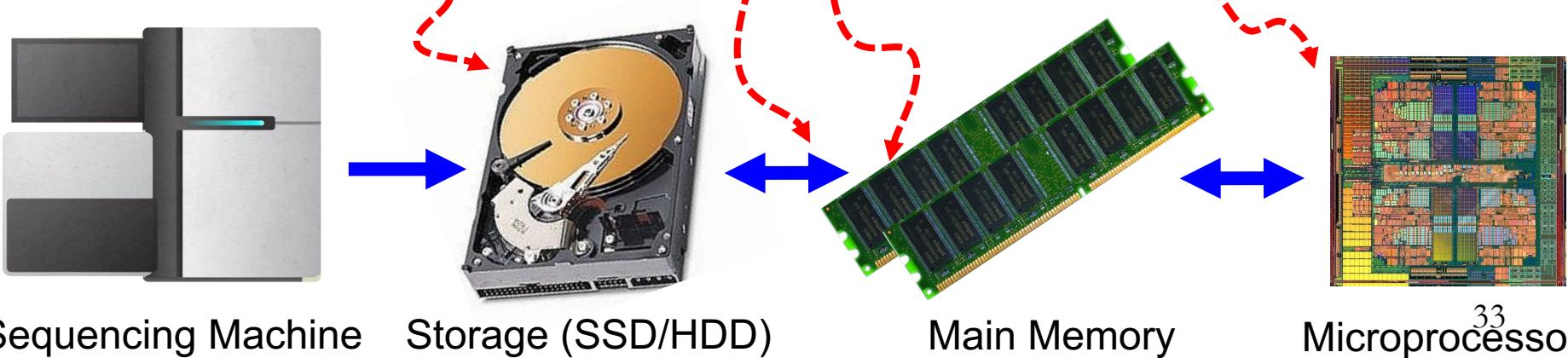
Near-memory Sequence Alignment

GenASM [MICRO 2020]

SeGram [ISCA 2022]

Specialized Pre-alignment Filtering
Accelerators (GPU, FPGA)

Improving **performance** and **energy efficiency**
by 1-3 orders of magnitude



Feedback From Our Community!



James Ferguson

@Psy_Fer_

This is awesome! I've got my evening reading sorted.



Stéphane Le Crom

@sleclrom

Very complete article on the evolution of read alignment algorithms. #NGS #genomics



Svetlana Gorokhova

@SGorokhova

An impressive overview of read alignment methods over the last three decades



BContrerasMoreira @BrunoContrerasM · Sep 10

Replies to [@mealser](#) [@GenomeBiology](#) and 3 others

Buen hilo de repaso sobre la evolución de los algoritmos de alineamiento de secuencias a medida que ha mejorado la tecnología de secuenciación

...

Key Takeaway

Most speedup comes from

parallelism enabled by

novel architectures and algorithms

Intelligent Genome Analysis

<https://arxiv.org/abs/2205.07957>



arXiv > q-bio > arXiv:2205.07957

Quantitative Biology > Genomics

[Submitted on 16 May 2022]

Going From Molecules to Genomic Variations to Scientific Discovery: Intelligent Algorithms and Architectures for Intelligent Genome Analysis

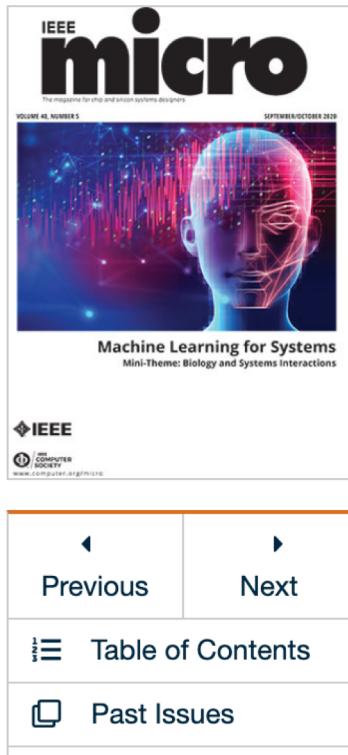
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Accelerating Genome Analysis

Mohammed Alser, Zülal Bingöl, Damla Senol Cali, Jeremie Kim, Saugata Ghose, Can Alkan, Onur Mutlu

["Accelerating Genome Analysis: A Primer on an Ongoing Journey"](#)

IEEE Micro, August 2020.



[Home](#) / [Magazines](#) / [IEEE Micro](#) / [2020.05](#)

IEEE Micro

Accelerating Genome Analysis: A Primer on an Ongoing Journey

Sept.-Oct. 2020, pp. 65-75, vol. 40

DOI Bookmark: [10.1109/MM.2020.3013728](https://doi.org/10.1109/MM.2020.3013728)

Authors

[Mohammed Alser](#), ETH Zürich

[Zulal Bingol](#), Bilkent University

[Damla Senol Cali](#), Carnegie Mellon University

[Jeremie Kim](#), ETH Zurich and Carnegie Mellon University

[Saugata Ghose](#), University of Illinois at Urbana–Champaign and Carnegie Mellon University

[Can Alkan](#), Bilkent University

[Onur Mutlu](#), ETH Zurich, Carnegie Mellon University, and Bilkent University

Read Mapping in 111 pages!

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["Technology dictates algorithms: Recent developments in read alignment"](#)

Genome Biology, 2021

[\[Source code\]](#)

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Genome Biology

REVIEW

Open Access



Technology dictates algorithms: recent developments in read alignment

Mohammed Alser^{1,2,3†}, Jeremy Rotman^{4†}, Dhrithi Deshpande⁵, Kodi Taraszka⁴, Huwenbo Shi^{6,7}, Pelin Icer Baykal⁸, Harry Taegyun Yang^{4,9}, Victor Xue⁴, Sergey Knyazev⁸, Benjamin D. Singer^{10,11,12}, Brunilda Balliu¹³, David Koslicki^{14,15,16}, Pavel Skums⁸, Alex Zelikovsky^{8,17}, Can Alkan^{2,18}, Onur Mutlu^{1,2,3†} and Serghei Mangul^{5*†}

Learning Materials



<https://www.youtube.com/c/OnurMutluLectures/search?query=Mohammed%20alser>

More on Accelerating Genome Analysis ...

- Mohammed Alser,
[**"Accelerating Genome Analysis: A Primer on an Ongoing Journey"**](#)
Talk at [RECOMB 2021](#), Virtual, August 30, 2021.
[\[Slides \(pptx\) \(pdf\)\]](#)
[\[Talk Video \(27 minutes\)\]](#)
[\[Related Invited Paper \(at IEEE Micro, 2020\)\]](#)

Our Contributions

Near-memory/In-memory Pre-alignment Filtering

- GRIM-Filter [BMC Genomics'18]
- SneakySnake [IEEE Micro'21]
- GenASM [MICRO 2020]

Near-memory Sequence Alignment

- GenASM [MICRO 2020]

Specialized Pre-alignment Filtering Accelerators (GPU, FPGA)

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- MAGNET [AACBB'18]
- Shouji [Bioinformatics'19]
- GateKeeper-GPU [arXiv'21]
- SneakySnake [Bioinformatics'20]

(⌚) Premieres in 23 hours
October 5, 4:30 PM

Storage Set reminder

SAFARI

20

More on Intelligent Genome Analysis ...

- Mohammed Alser,

"Computer Architecture - Lecture 10: Intelligent Genome Analysis"

ETH Zurich, Computer Architecture Course, Fall2021, Lecture 10, Virtual, 29 October 2021.

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

[[Talk Video](#) (3 hour 2 minutes, including Q&A)]

[[Related Invited Paper \(at IEEE Micro, 2020\)](#)]



Computer Architecture - Lecture 10: Intelligent Genome Analysis (Fall 2021)

412 views • Streamed live on Oct 29, 2021

19

0

SHARE

SAVE

...

More on Intelligent Genome Analysis ...

■ Mohammed Alser,

[**"Computer Architecture - Lecture 8: Intelligent Genome Analysis"**](#)

ETH Zurich, Computer Architecture Course, Lecture 8, Virtual, 15 October 2021.

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

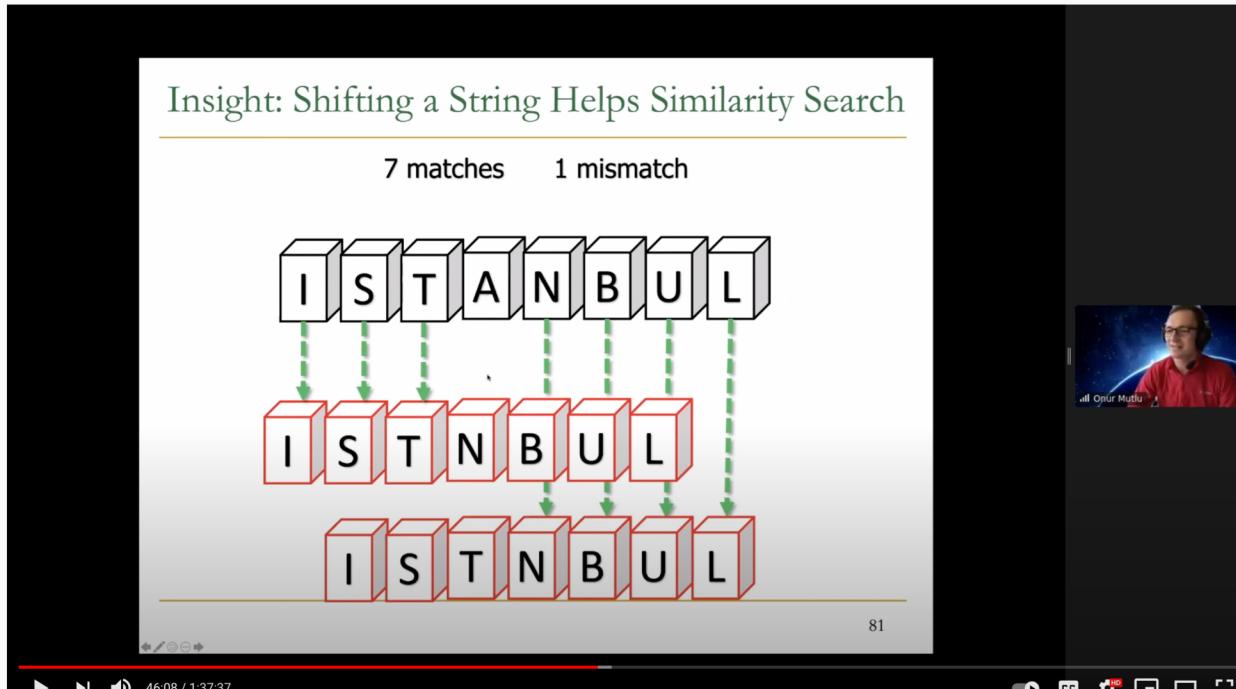
[[Talk Video](#) (2 hour 54 minutes, including Q&A)]

[[Related Invited Paper \(at IEEE Micro, 2020\)](#)]

The screenshot shows a video player interface with a presentation slide. The slide title is "Our Solution: GateKeeper". It features a diagram of an "Alignment Filter" (represented by a yellow cube) combined with an "FPGA-based Alignment Filter" (represented by a photograph of an FPGA board). This combination is labeled as the "1st FPGA-based Alignment Filter". Below the diagram, a flowchart illustrates the process: "High throughput DNA sequencing (HTS) technologies" (labeled 1) produce "Billions of Short Reads" (labeled $\times 10^{12}$ mappings). These reads undergo "Read Pre-Alignment Filtering" (labeled 2), which is described as "Fast & Low False Positive Rate" and achieves "Low Speed & High Accuracy". Finally, the reads are aligned ("Read Alignment", labeled 3), which is described as "Slow & Zero False Positives" and achieves "Medium Speed, Medium Accuracy". A small video window in the top right corner shows a man wearing headphones, likely the speaker. The video player controls at the bottom include a play button, volume, and a progress bar from 2:08:58 to 2:54:18. The slide number 108 is visible in the bottom right corner.

More on Fast Genome Analysis ...

- Onur Mutlu,
[**"Accelerating Genome Analysis: A Primer on an Ongoing Journey"**](#)
Invited Lecture at [Technion](#), Virtual, 26 January 2021.
[\[Slides \(pptx\) \(pdf\)\]](#)
[\[Talk Video\] \(1 hour 37 minutes, including Q&A\)](#)
[\[Related Invited Paper \(at IEEE Micro, 2020\)\]](#)

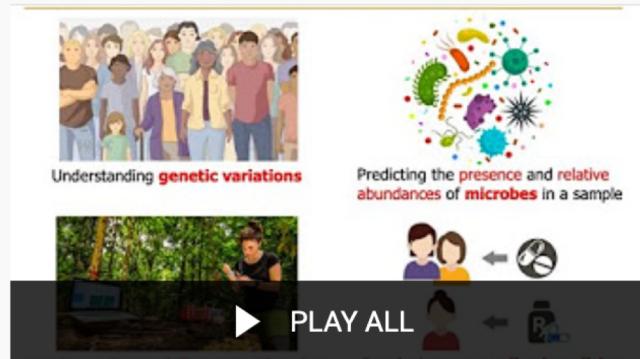


Onur Mutlu - Invited Lecture @Technion: Accelerating Genome Analysis: A Primer on an Ongoing Journey

566 views • Premiered Feb 6, 2021

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Two P&S Genomics Courses



Livestream - P&S Genome Sequencing on Mobile Devices (Fall 2021)

9 videos • 75 views • Updated 5 days ago



Onur Mutlu
Lectures

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https://www.youtube.com/playlist?list=PL5Q2soXY2Zi_U2F8yrrNPD9CjcM6CFQXv

Course Materials

2021 Meetings/Schedule

Week	Date	Livestream	Meeting	Learning Materials	Assignments
W1	5.10 Tue.	YouTube Live	M1: P&S Accelerating Genomics Course Introduction & Project Proposals PDF (PDF) PPT (PPT) YouTube Video	Required Materials Recommended Materials	
W2	20.10 Wed.	YouTube Live	M2: Introduction to Sequencing PDF (PDF) PPT (PPT)		
W3	27.10 Wed.	YouTube Live	M3: Read Mapping PDF (PDF) PPT (PPT)		
W4	3.11 Wed.	YouTube Live	M4: GateKeeper PDF (PDF) PPT (PPT)		
W5	10.11 Wed.	YouTube Live	M5: MAGNET & Shouji PDF (PDF) PPT (PPT)		
W6	17.11 Wed.		M6.1: SneakySnake PDF (PDF) PPT (PPT) Video		
			M6.2: GRIM-Filter PDF (PDF) PPT (PPT) YouTube Video		
W7	24.11 Wed.		M7: GenASM PDF (PDF) PPT (PPT) YouTube Video		

https://safari.ethz.ch/projects_and_seminars/fall2021/doku.php?id=bioinformatics

Detailed Lectures on Genome Analysis

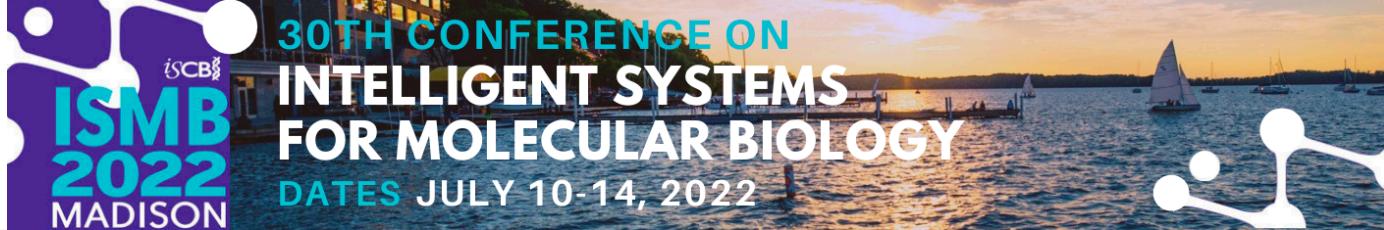
- Computer Architecture, Fall 2020, Lecture 3a
 - **Introduction to Genome Sequence Analysis** (ETH Zürich, Fall 2020)
 - <https://www.youtube.com/watch?v=CrRb32v7SJc&list=PL5Q2soXY2Zi9xidyIgBxUz7xRPS-wisBN&index=5>
- Computer Architecture, Fall 2020, Lecture 8
 - **Intelligent Genome Analysis** (ETH Zürich, Fall 2020)
 - <https://www.youtube.com/watch?v=ygmQpdDTL7o&list=PL5Q2soXY2Zi9xidyIgBxUz7xRPS-wisBN&index=14>
- Computer Architecture, Fall 2020, Lecture 9a
 - **GenASM: Approx. String Matching Accelerator** (ETH Zürich, Fall 2020)
 - <https://www.youtube.com/watch?v=XoLpzmN-Pas&list=PL5Q2soXY2Zi9xidyIgBxUz7xRPS-wisBN&index=15>
- Accelerating Genomics Project Course, Fall 2020, Lecture 1
 - **Accelerating Genomics** (ETH Zürich, Fall 2020)
 - <https://www.youtube.com/watch?v=rgjl8ZyLsAg&list=PL5Q2soXY2Zi9E2bBVAgCqLgwiDRQDTyId>

Prior Research on Genome Analysis (1 / 2)

- Alser + "["SneakySnake: A Fast and Accurate Universal Genome Pre-Alignment Filter for CPUs, GPUs, and FPGAs."](#)" to appear in *Bioinformatics*, 2020.
- Senol Cali+, "["GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis"](#)", *MICRO* 2020.
- Alser+, "["Technology dictates algorithms: Recent developments in read alignment"](#)", to appear in *Genome Biology*, 2021.
- Kim+, "["AirLift: A Fast and Comprehensive Technique for Translating Alignments between Reference Genomes"](#)", *arXiv*, 2020
- Alser+, "["Accelerating Genome Analysis: A Primer on an Ongoing Journey"](#)", *IEEE Micro*, 2020.

Prior Research on Genome Analysis (2/2)

- Firtina+, "[Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm](#)", *Bioinformatics*, 2019.
- Alser+, "[Shouji: a fast and efficient pre-alignment filter for sequence alignment](#)", *Bioinformatics* 2019.
- Kim+, "[GRIM-Filter: Fast Seed Location Filtering in DNA Read Mapping Using Processing-in-Memory Technologies](#)", *BMC Genomics*, 2018.
- Alser+, "[GateKeeper: A New Hardware Architecture for Accelerating Pre-Alignment in DNA Short Read Mapping](#)", *Bioinformatics*, 2017.
- Alser+, "[MAGNET: understanding and improving the accuracy of genome pre-alignment filtering](#)", *IPSI Transaction*, 2017.



Technology Dictates Algorithms: Developments in Read Mapping

Mohammed Alser

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