Wide-SIMD Parallelization of Streaming Dataflow, with Applications to Bioinformatics

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For CSE 591

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Take-Home Message

- **Biological sequence analysis** is a source of high-impact computational problems
- Using SIMD parallel computing for these problems requires dealing with **irregularity**
- **MERCATOR** is an ongoing research effort to make irregular application development on SIMD platforms easier.

Who Am I?

- I study how to accelerate high-impact bioinformatics problems.
- One way to do this is via parallelization on modern architectures (FPGAs, GPUs, …)

- Along the way, many interesting CS questions…
  - Streaming computation [FCCM'07, JVSP'07,M&M'09]
  - Systolic array design [FPL'09,FCCM'10,ASAP'10]
  - Deadlock avoidance [SPAA'10,PPoPP'12,DFM'13,JPDC'17]
  - SIMD mapping [ISPDC'14,DFM'15,HPCS'17]

Talk Overview

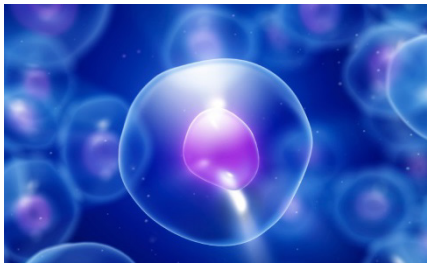
- Problems: DNA comparison and read mapping
- Algorithmic approach – Why SIMD?
- MERCATOR overview and performance
- Research challenges

Molecular Biology is Fundamental

- **Genetic basis** of disease and disease risk
- **Systems biology** – what are your cells doing?
- Studying **natural history** and evolution
- **Engineering** cells' behavior for medicine, industry, agriculture

The First Step: DNA Sequencing

- Sequencing can tell us what is in a genome…
- … but also the basis of experiments to probe gene expression, protein binding, chromosome conformation, epigenetic marks, polymorphism, copy number variants …



…acaggatagtaccgataccat
cacccggataggacctatgag
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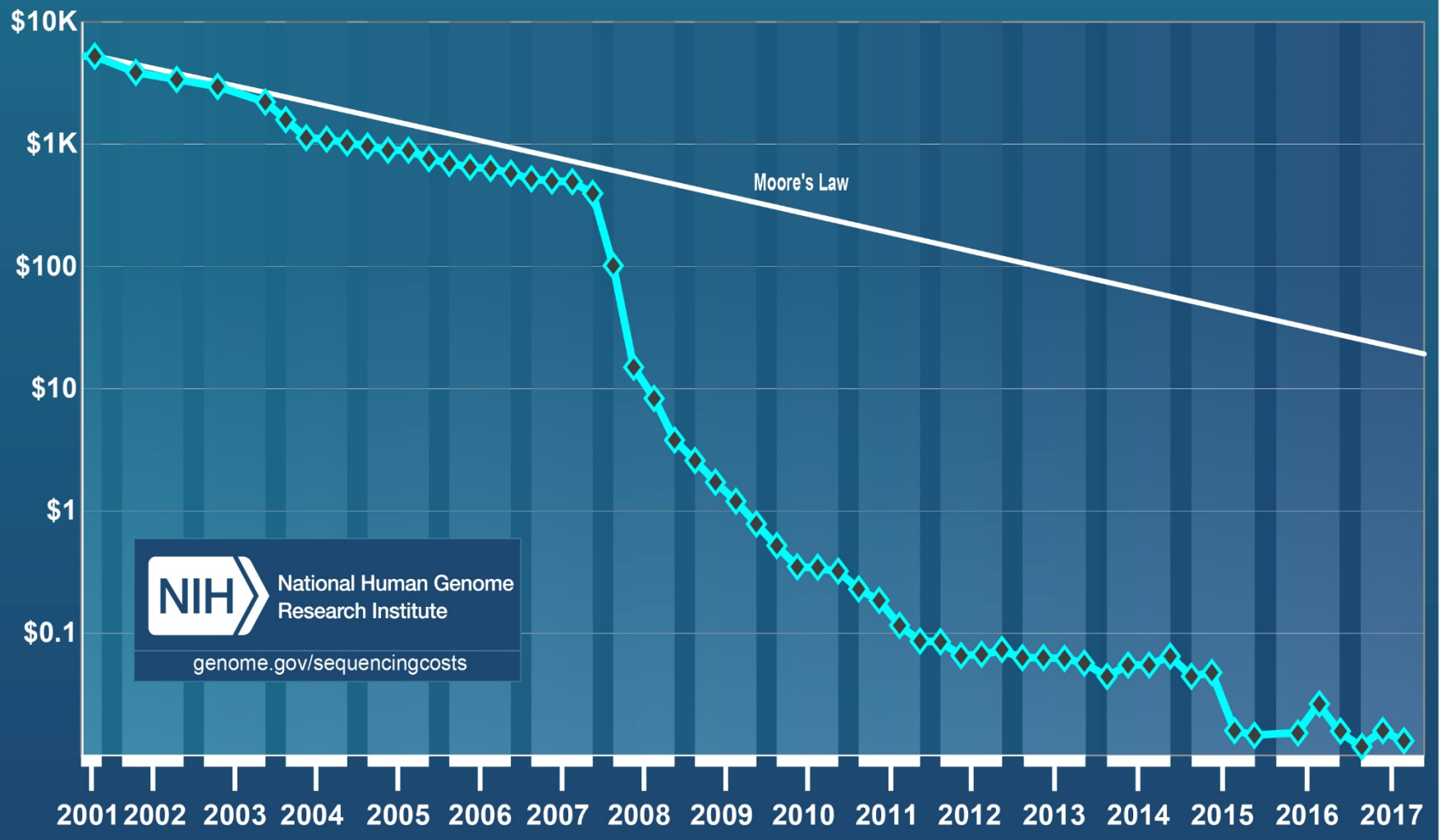
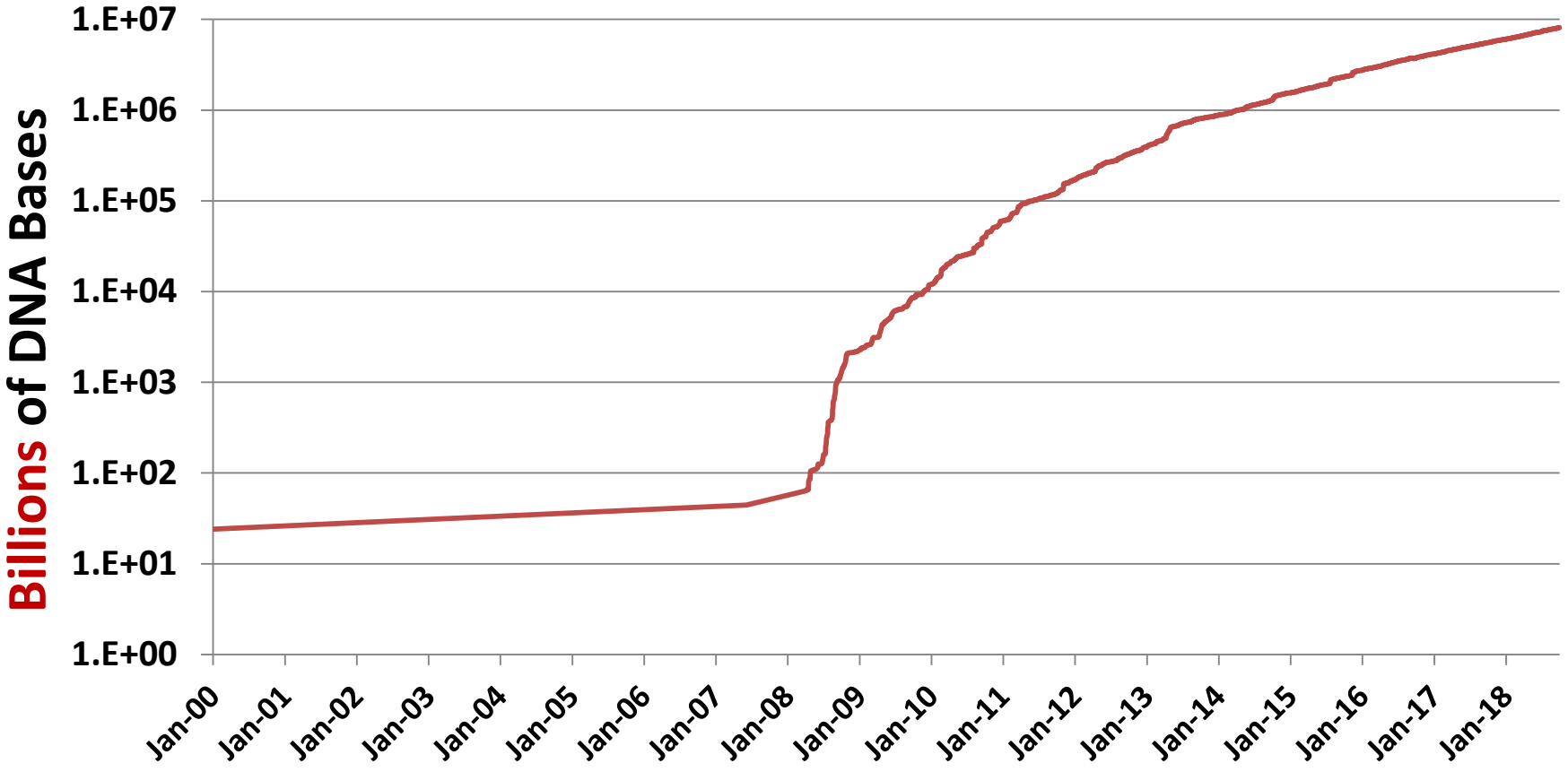
Cost per Raw Megabase of DNA Sequence



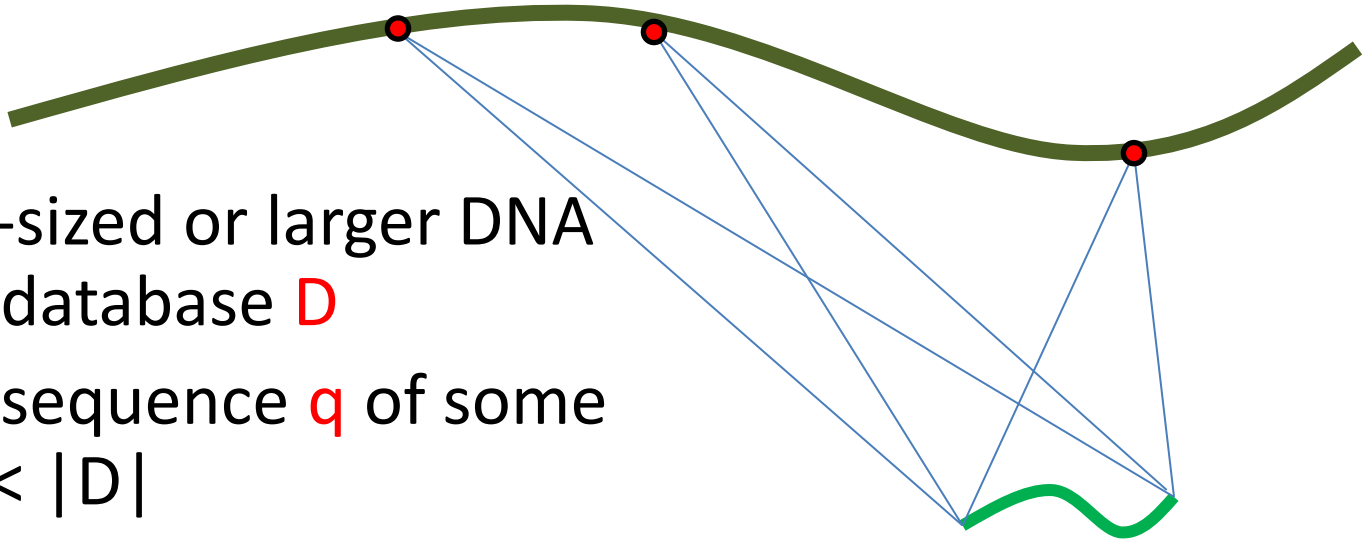
NIH Sequence Read Archive Size

(Open Access Only)



http://www.ncbi.nlm.nih.gov/Traces/sra/

Problem: Classical Similarity Search



- Given
  - a genome-sized or larger DNA sequence database D
  - a "query" sequence q of some length L << |D|

- *Does q appear in D with at most k differences*, and if so, where?

Typical Parameters

- Database D has size $10^9 – 10^{10}$ bases
- Query q has size $10^2 – 10^4$ bases
- # differences k is 5-25% of |q| (bases added, deleted, changed)

Tools for Similarity Search

- **BLAST** [Altschul et al. 1990, 1996]

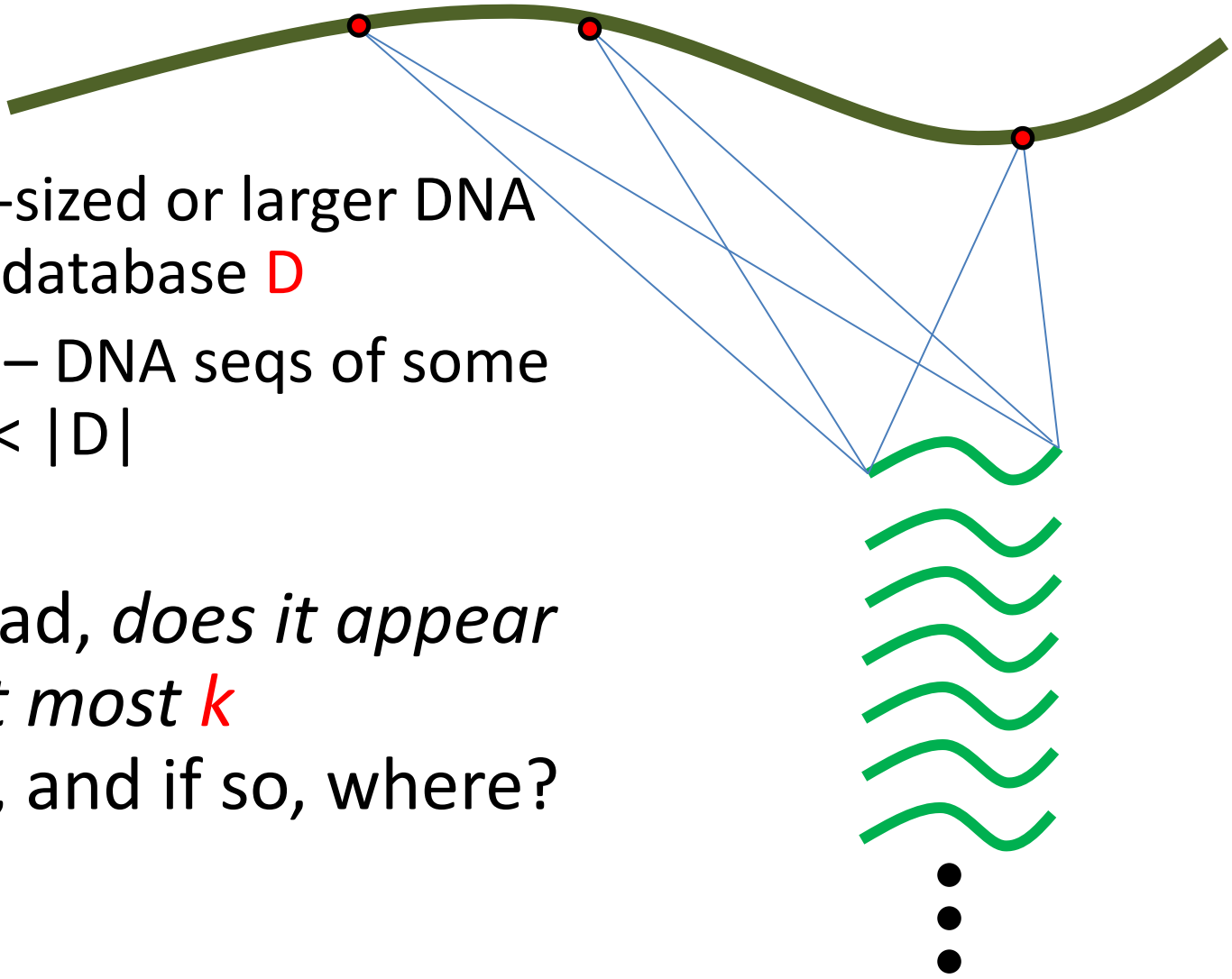
- **BLAT** [Kent 2002]

These tools use variants of same basic search algorithm.

Problem: Short-Read Mapping

- Given
  - a genome-sized or larger DNA sequence database D
  - N "reads" – DNA seqs of some length L << |D|

- For each read, *does it appear in D with at most k differences*, and if so, where?



Typical Parameters

- Database D has size $10^9 – 10^{10}$ bases
- Number of reads N is $10^6 – 10^8$
- Length L is 75-150 (may vary among reads)
- # differences k is 0-3 (added, deleted, changed)

Tools for Mapping

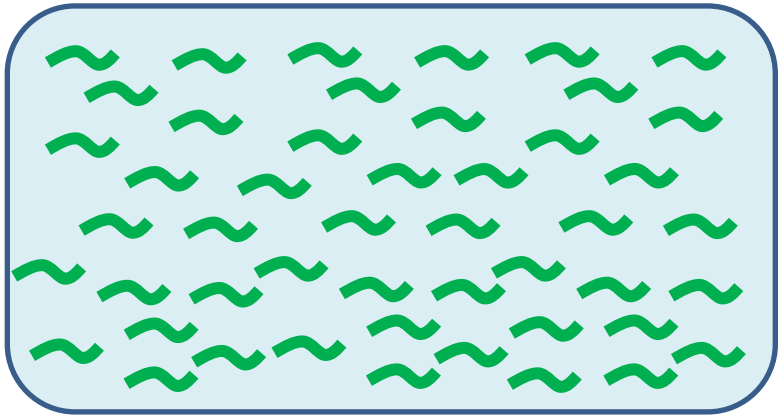
- **Bowtie** [Langmead et al. 2009, 2012]
- **BWA** [Li & Durbin 2009, 2010]
- **SOAP2** [Li et al. 2009]

All these tools use variants of same basic search algorithm.

Why Short-Read Mapping?

- Some experimental procedure selects a subset of everything in the database
- Reads are sampled from this subset by your sequencing machine
- Mapping tells you which parts of database are present in your sample

Problem: Alignment-Free Organism ID



- Given
  - a metagenome-sized DNA sequence database D
  - N microbial genomes – DNA seqs of some length L << |D|

- For each genome, *do (some of) its sequences appear in D?*

Alignment-Free Techniques

- **Min-Hash Sketching** – convert a seq to a small sample (m ~ 1000) of hash values

- **Approximate Containment**: how much of (the sketch for) a genome overlaps (the sketch for) a metagenome?

- MASH (Ondov et al. 2016)
- SourMASH (Brown et al. 2016)

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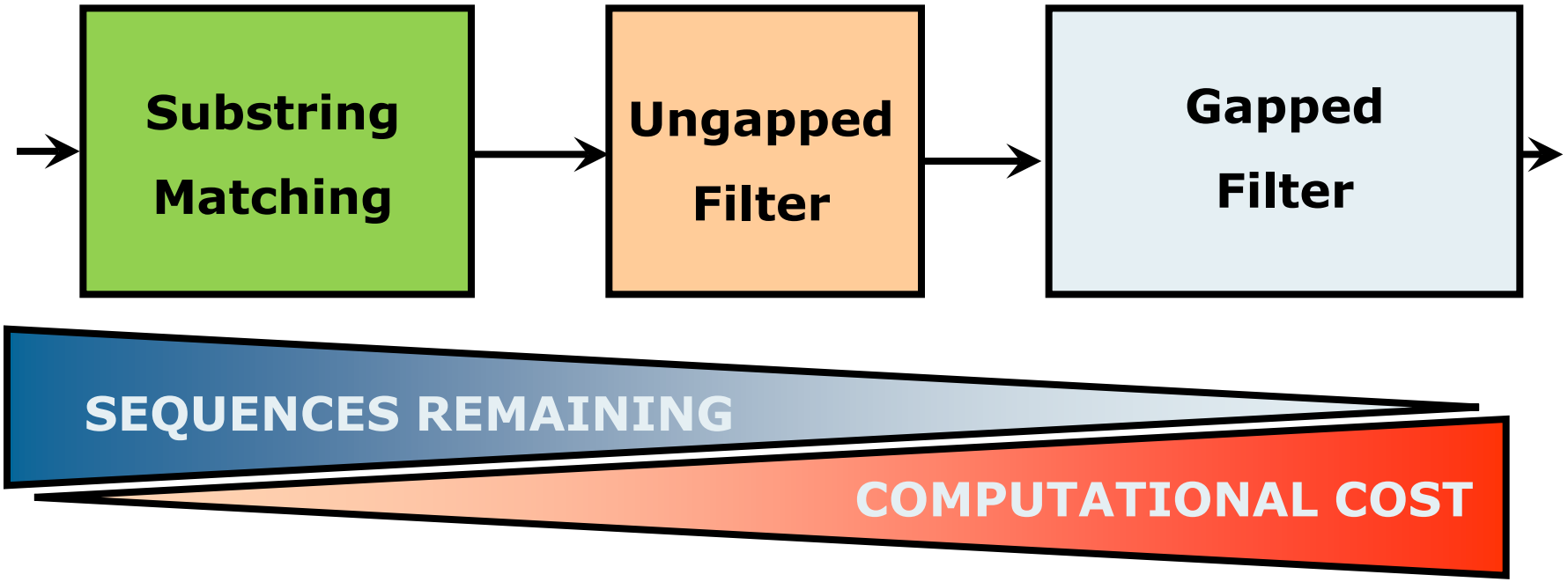
How BLAST Works



BLAST operates as a pipeline of computational stages.

Stages of BLAST

- Stage 1: identify *potential match locations* between q, D
- Stage 2: keep only those locations that look somewhat promising
- Stage 3: keep only those locations that actually yield high-similarity alignments

Generating Possible Matches

- Every place where some 11-mer from q matches an 11-mer from D *exactly* is a candidate.

  accagatacatagcactcgctacgtcagatgggtaca

  gttaagtcagatgggtagactcaggatgacagtggaca

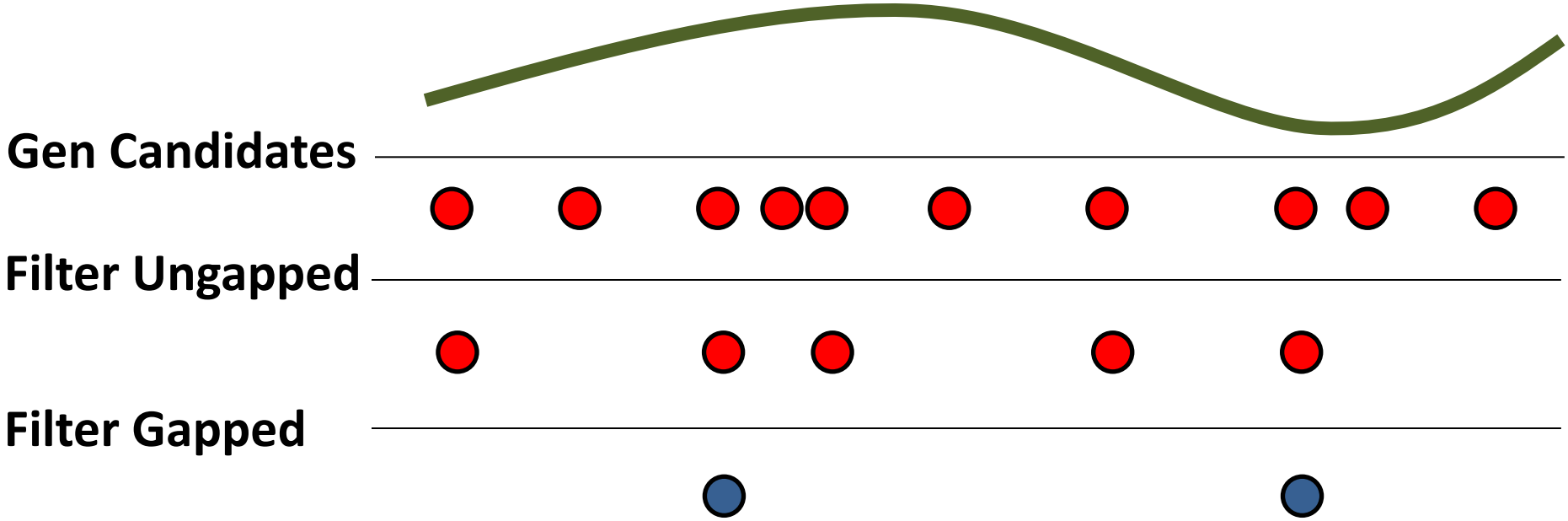
- Can rapidly find all such matching locations using hash table of 11-mers in sequence q

Filtering Candidates

- Uses explicit edit distance computation between q, part of D (Smith-Waterman algo)
- Expensive dynamic programming!
- “Easy” version (substitutions only), followed by hard version (add/delete chars allowed)

BLAST Parallelization

- Can generate candidates in parallel at each DB location, then filter them in parallel.



What About Read Mapping?

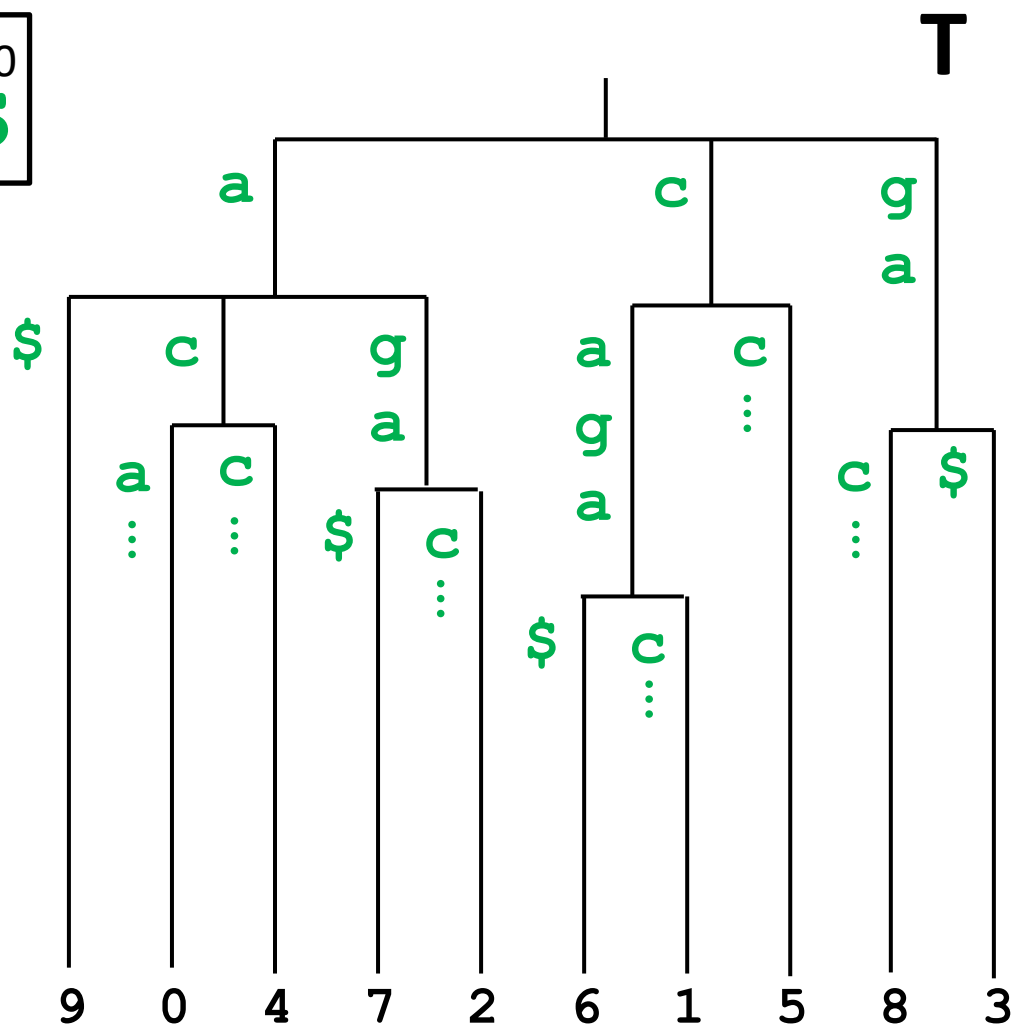
- Uses an index (virtual suffix tree) of database
- Matching involves tracing a path down index tree for each read
- (must try several paths if differences are allowed)
- *Can do in parallel for many reads at once!*

Suffix Tree Example

D = 0 1 2 3 4 5 6 7 8 9 10
acagaccaga$

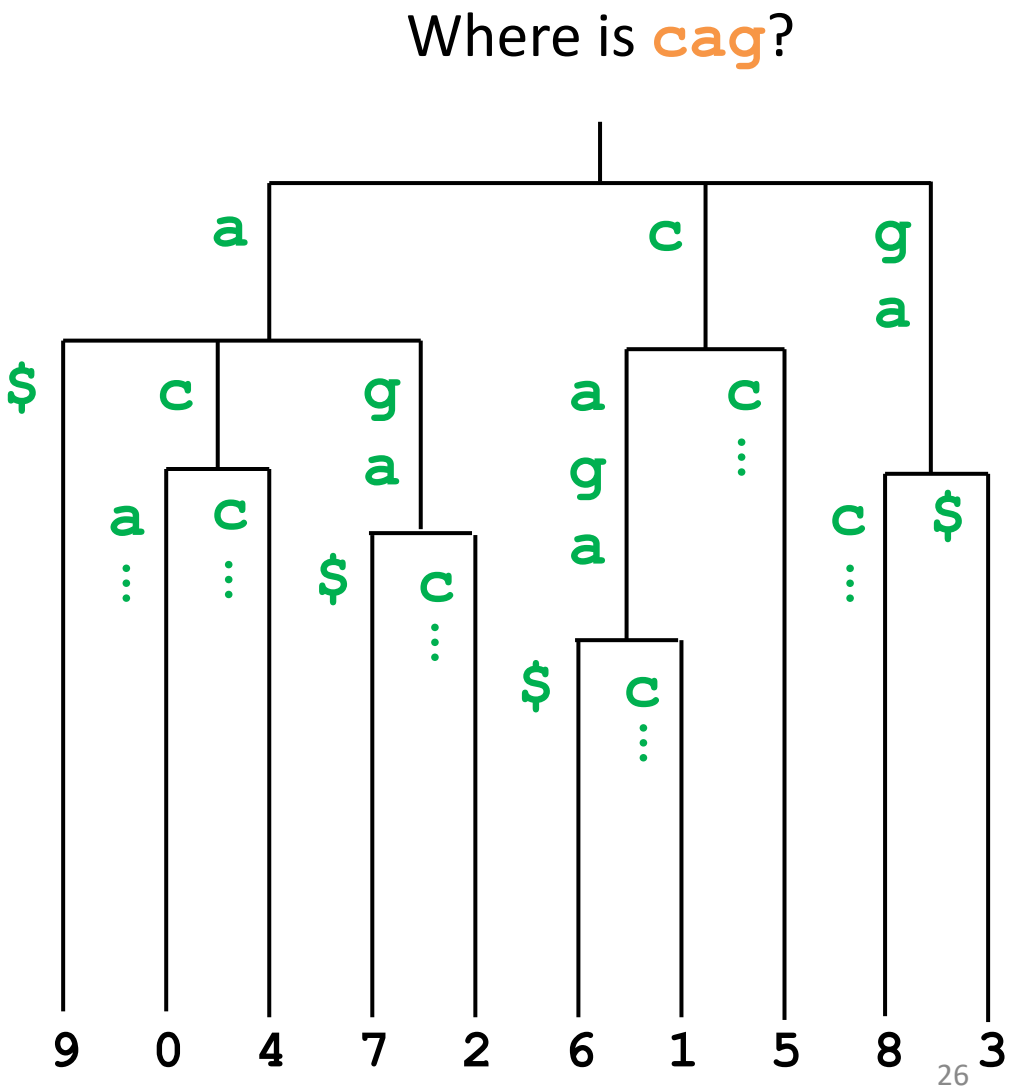
A

10	$
9	a$
0	aca…
4	acc…
7	aga$
2	agac…
6	caga$
1	cagac…
5	cca…
8	ga$
3	gac…



Rapid Matching vs Suffix Tree

- Can find all matches to a read in D in time proportional to read length L.



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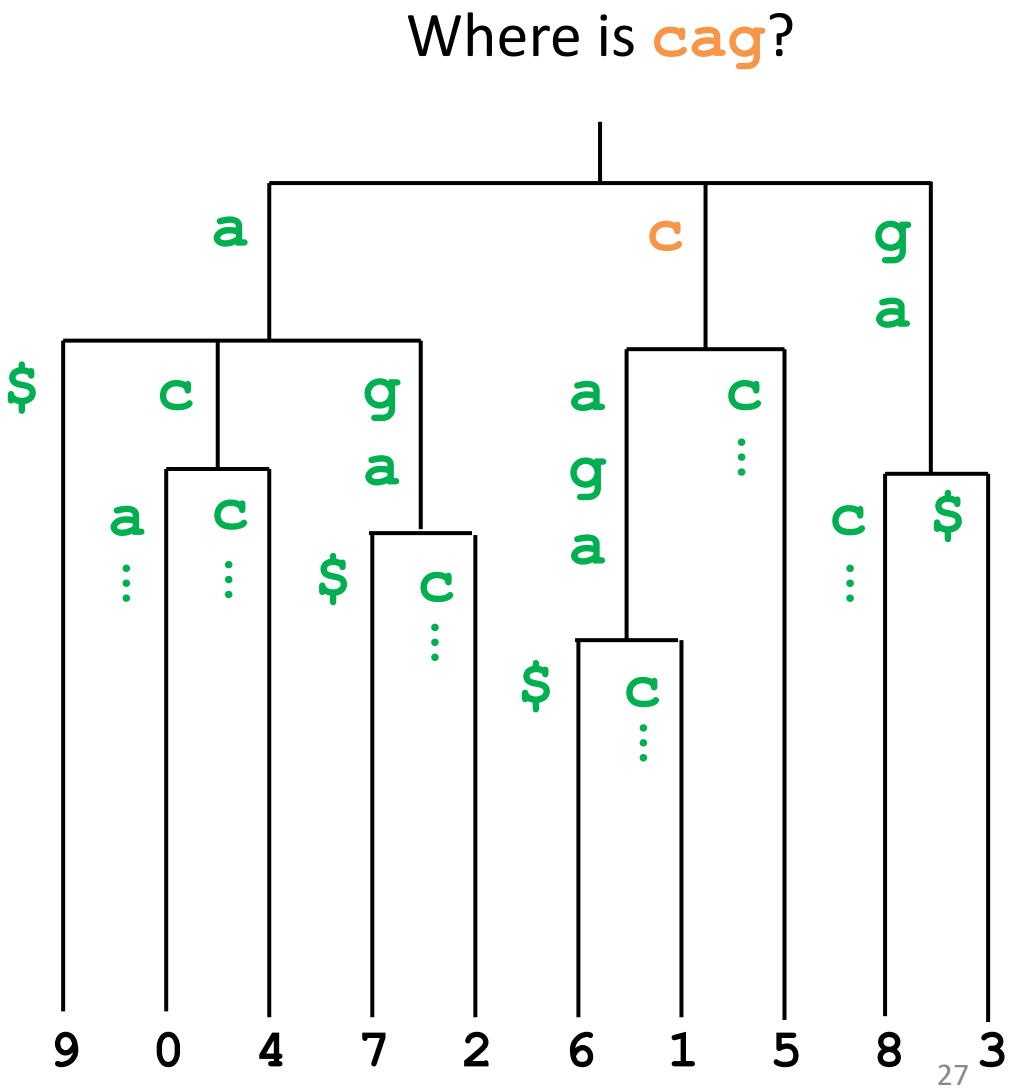

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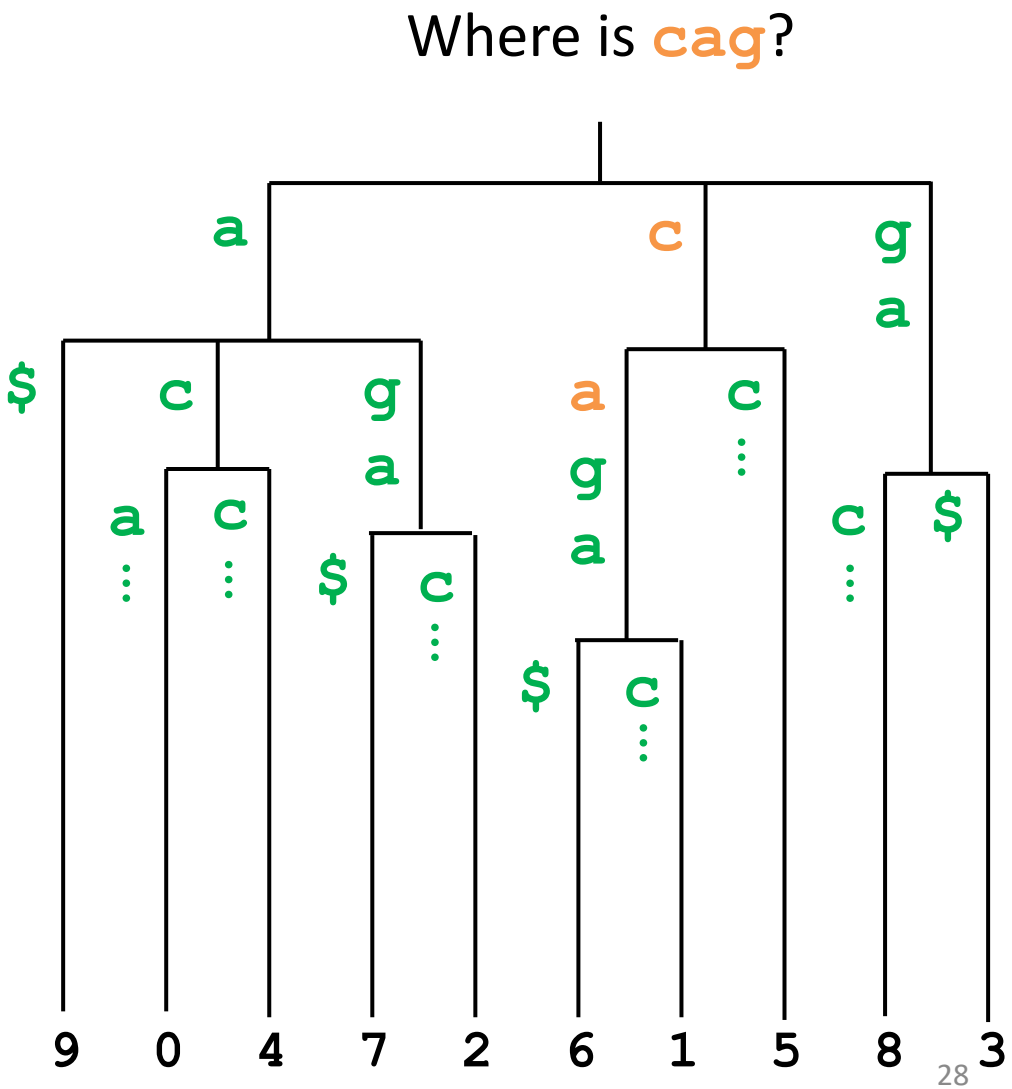

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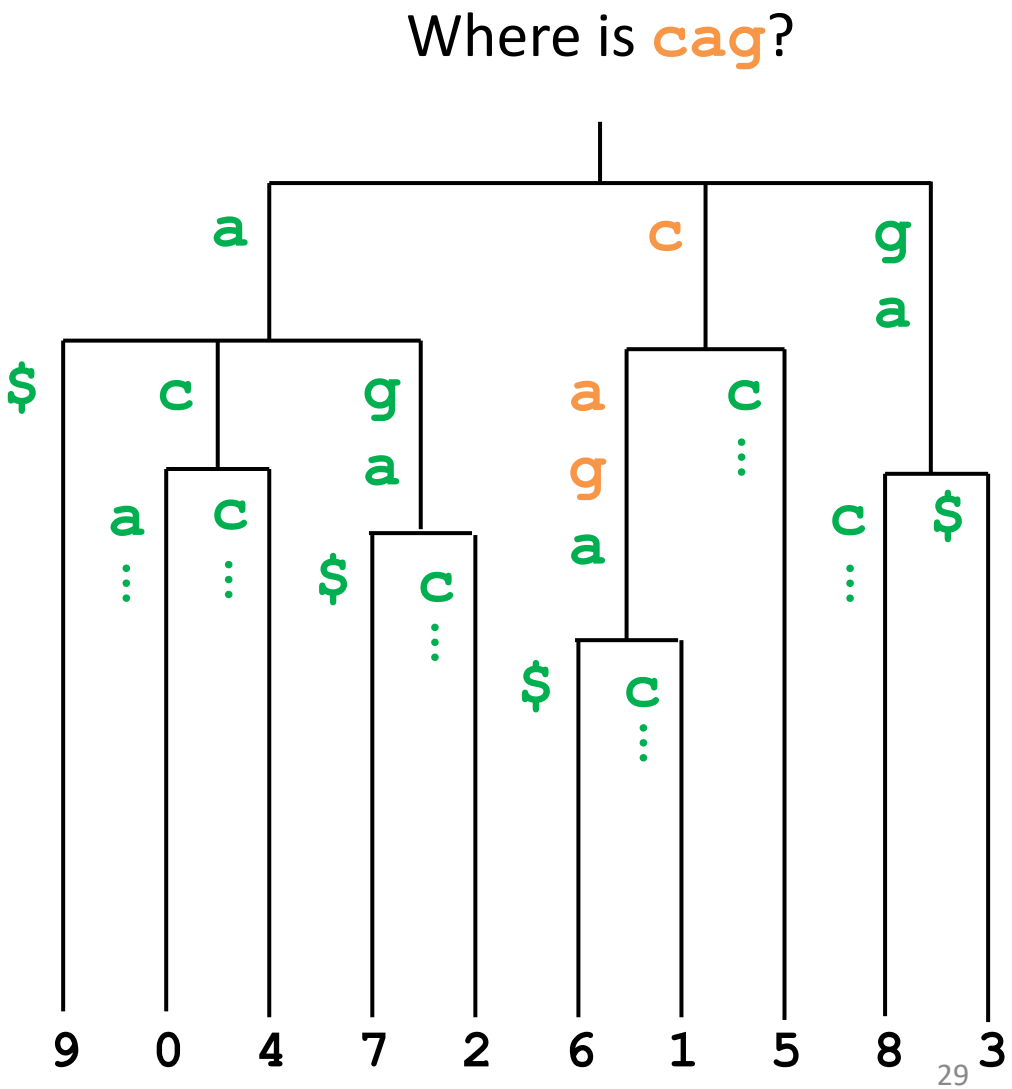

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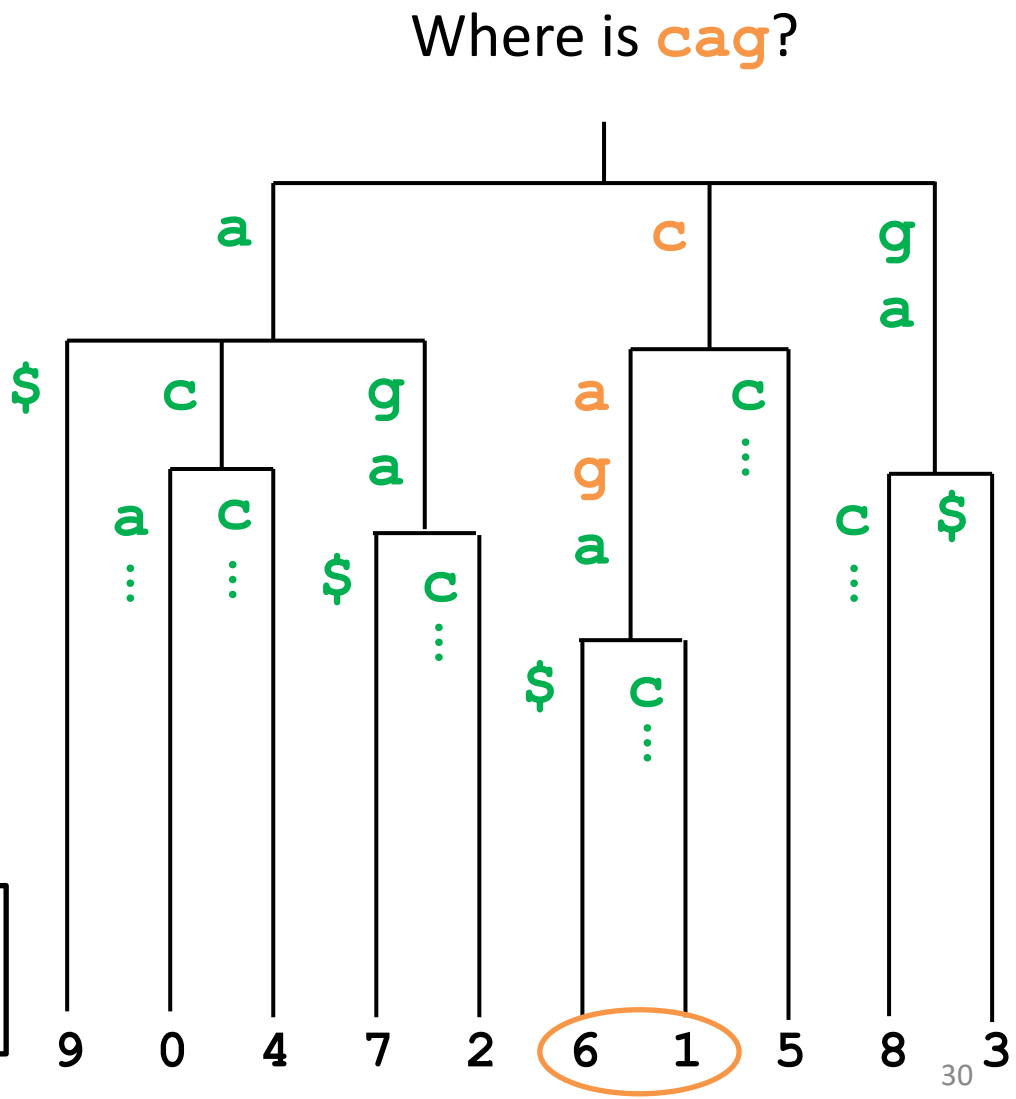


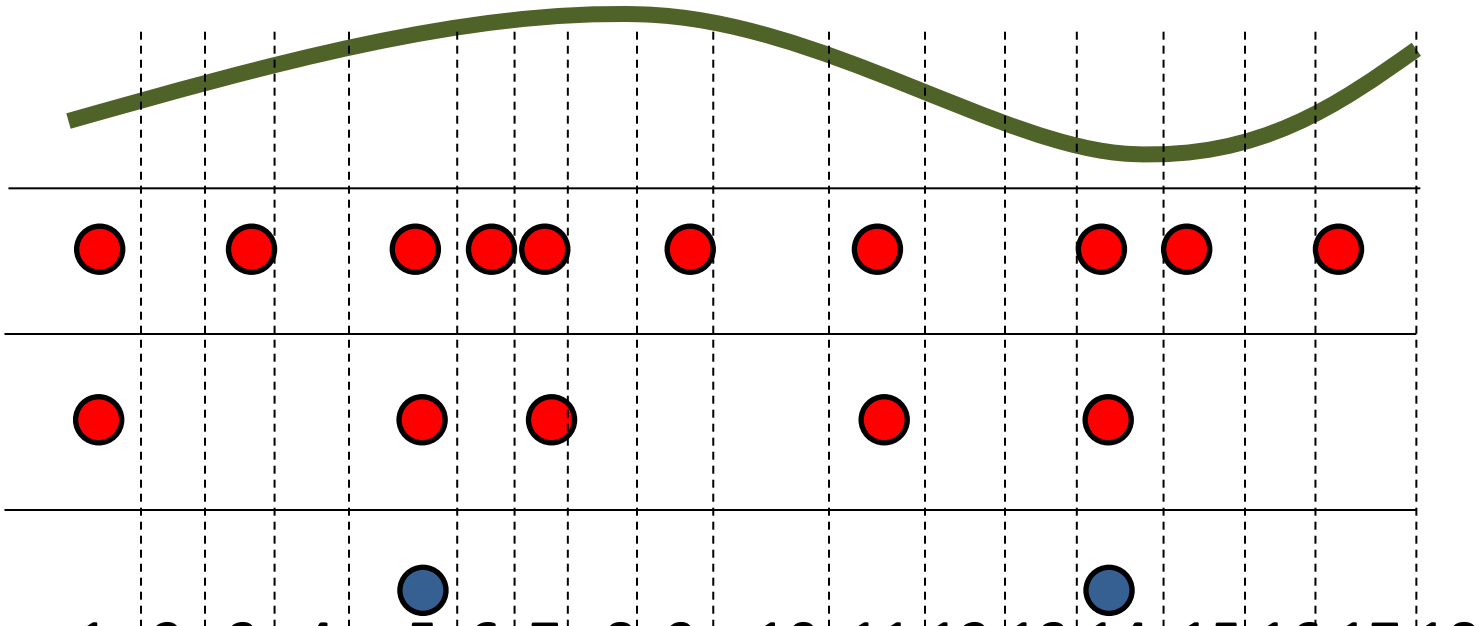
D = acagaccaga$ (0 1 2 3 4 5 6 7 8 9 10)

Extension to Inexact Matching

- To permit matches with k substitutions, try multiple paths, but charge for each mismatch.
- To permit matches with k differences, we do dynamic programming to compute edit distance of read against each path in tree.
- Descent stops for a read when we hit bottom of tree or find that path requires > k differences.

Parallel Alignment is a SIMD Computation

- We process every BLAST starting loc / every read through *same* filtering computation
- ***S**ingle **I**nstruction stream, **M**ultiple **D**ata items*



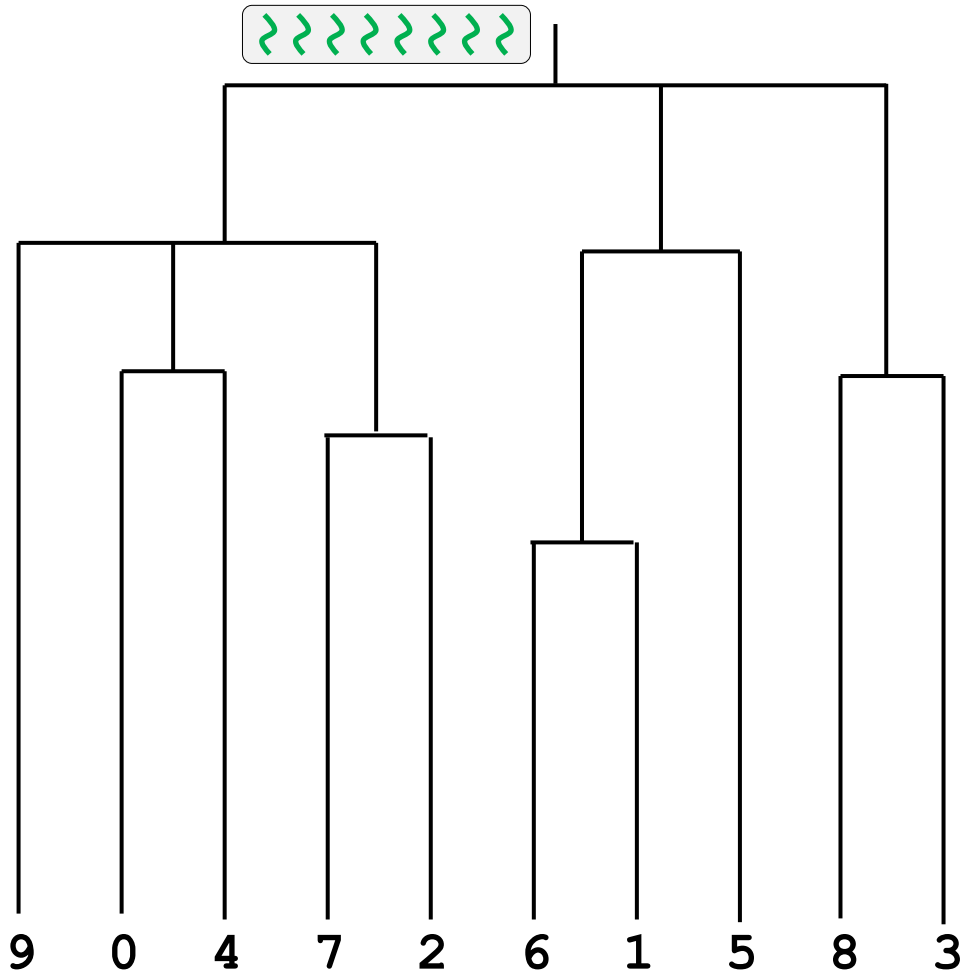
SIMD Targets

- Our work: **NVIDIA GPUs**
  (32 SIMD lanes x 4+ threads x 2-64 cores)

- Other possibilities: any multicore with wide vector instructions (Intel Xeon, AMD, ARM, …)

- ~All modern processors have wide SIMD!

Batched Traversal (Short Reads)



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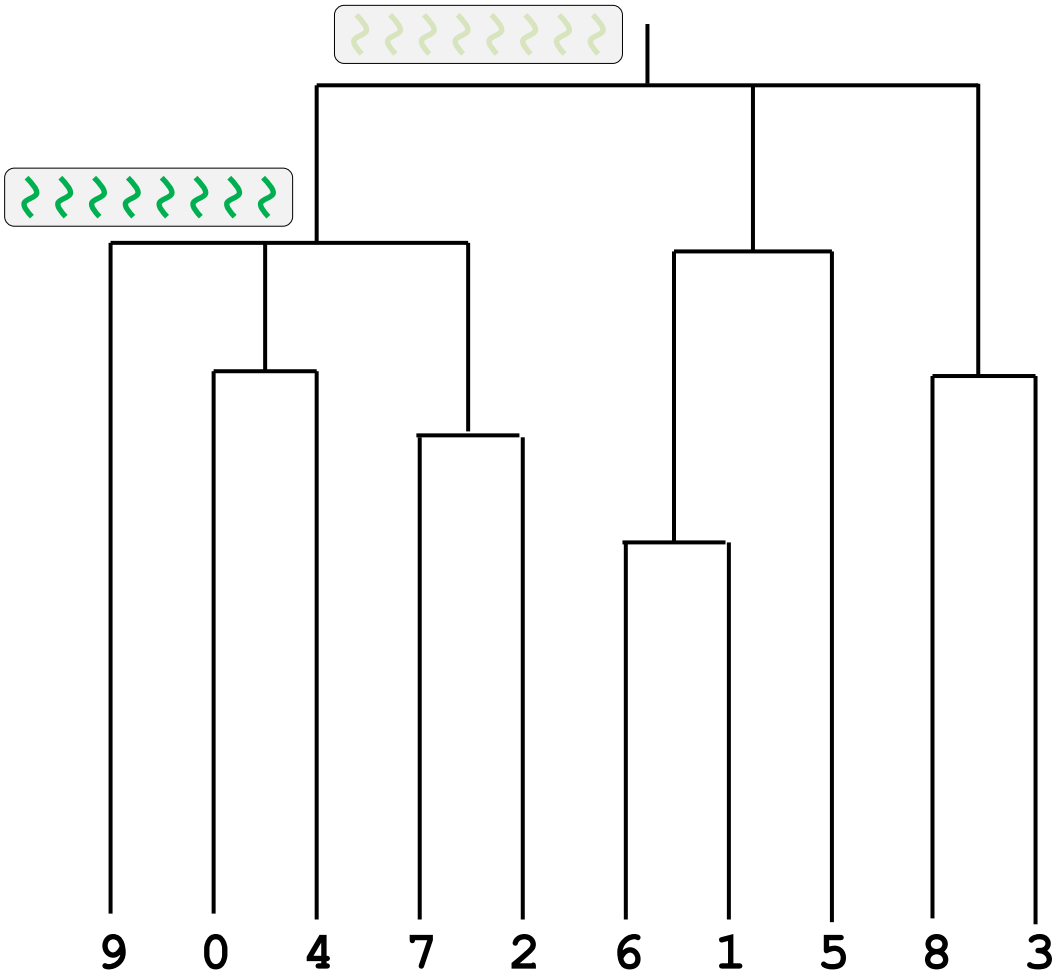
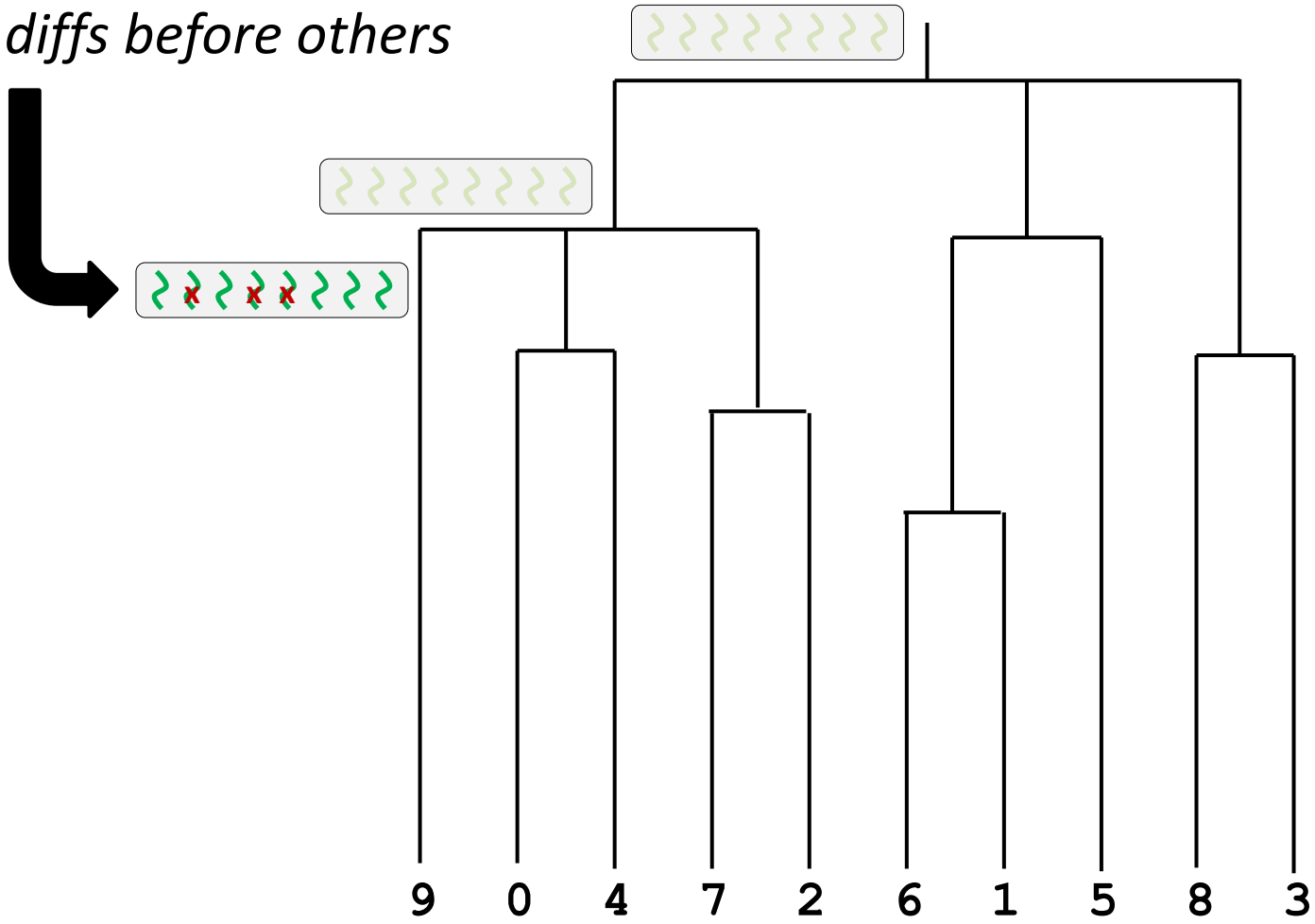


Batched Traversal

Some reads may accumulate > k diffs before others



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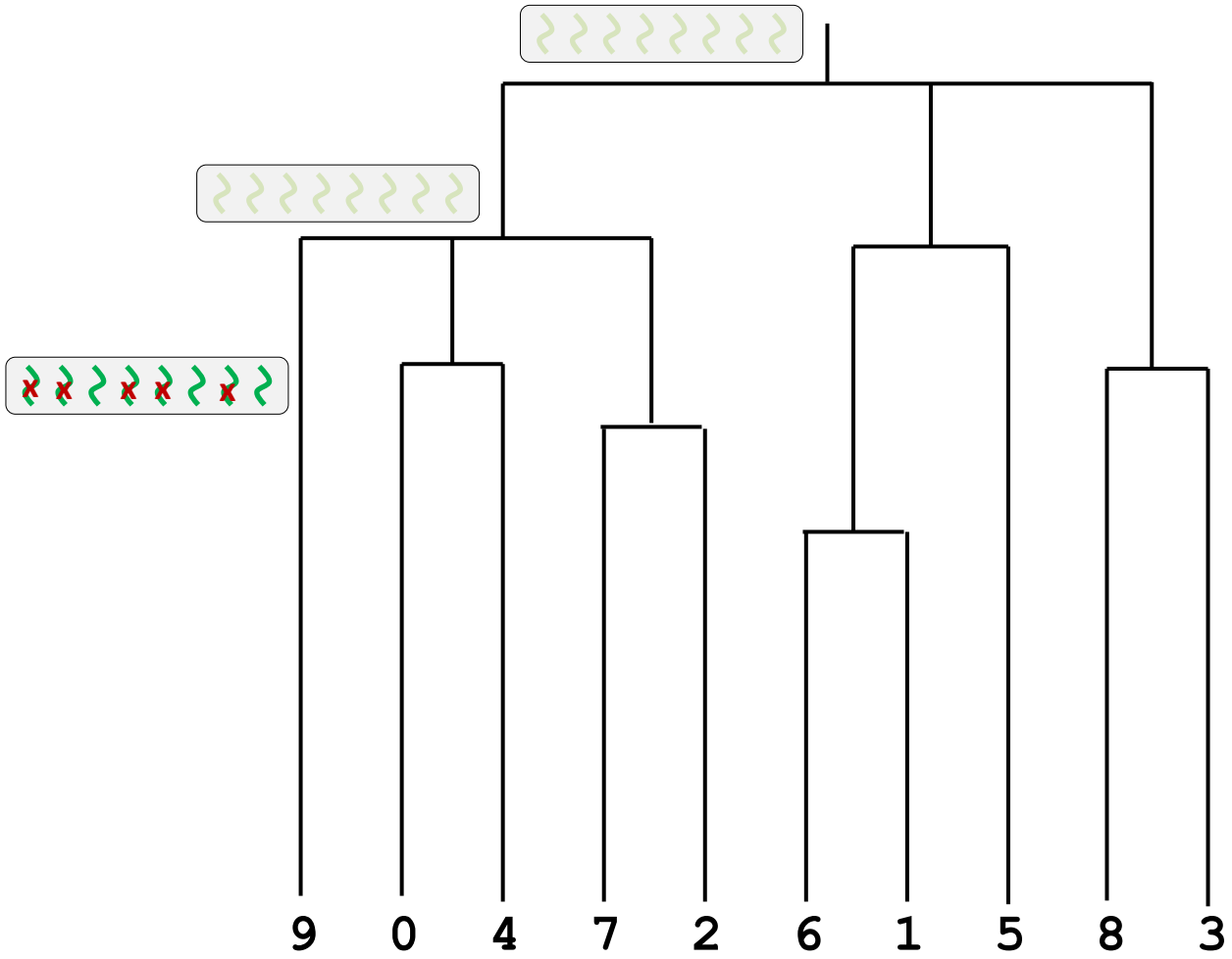

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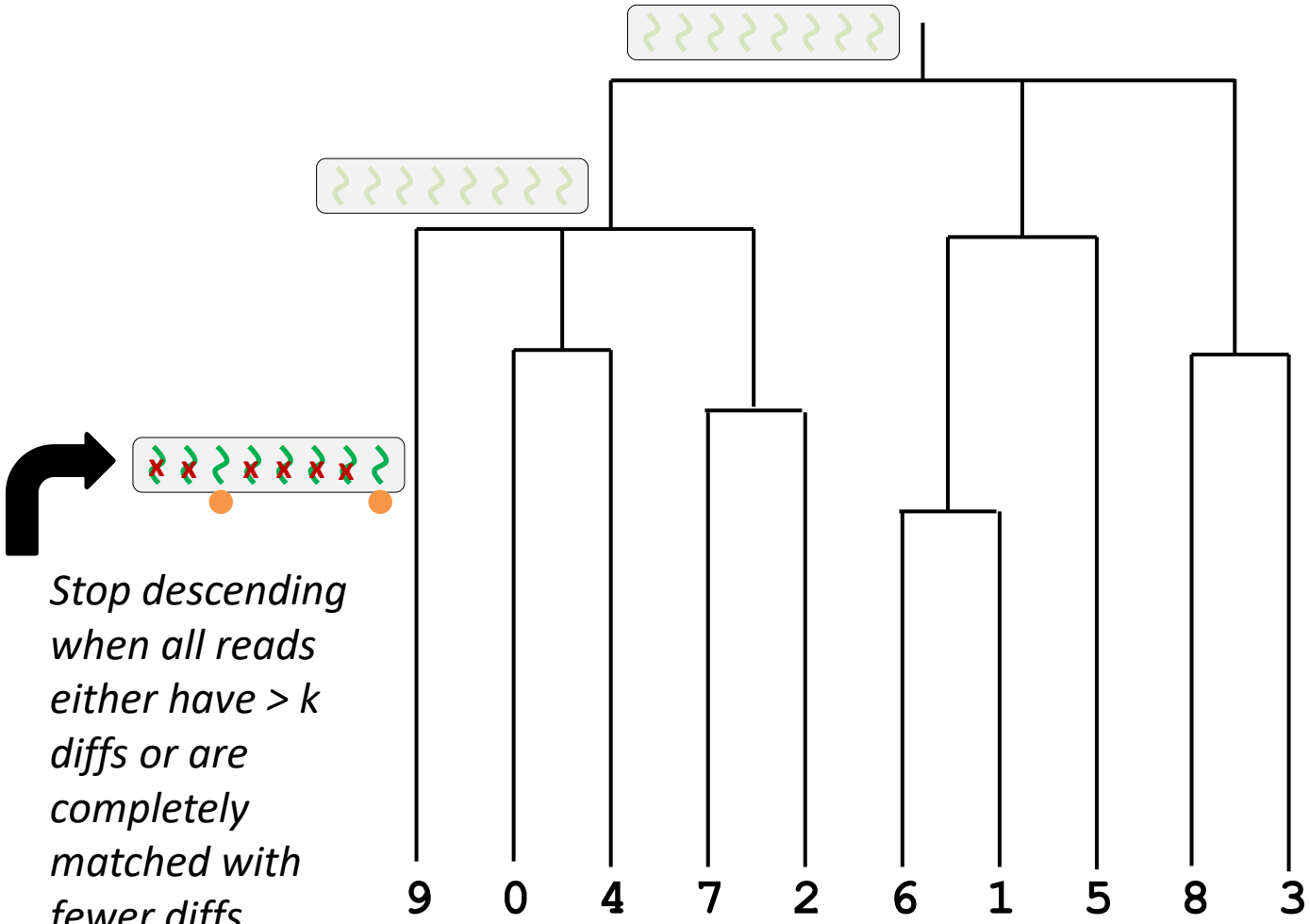
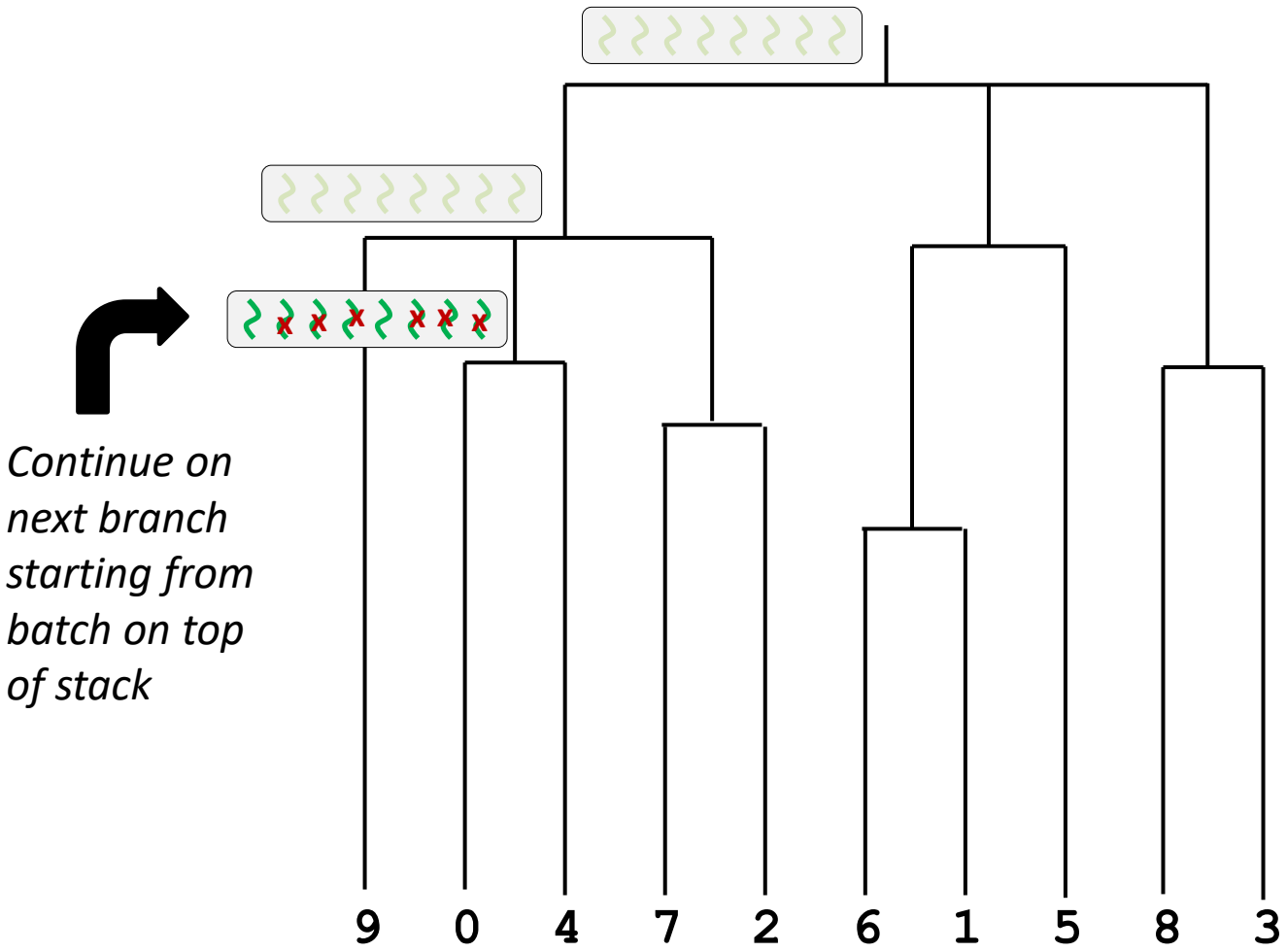


Stop descending when all reads either have > k diffs or are completely matched with fewer diffs

Batched Traversal



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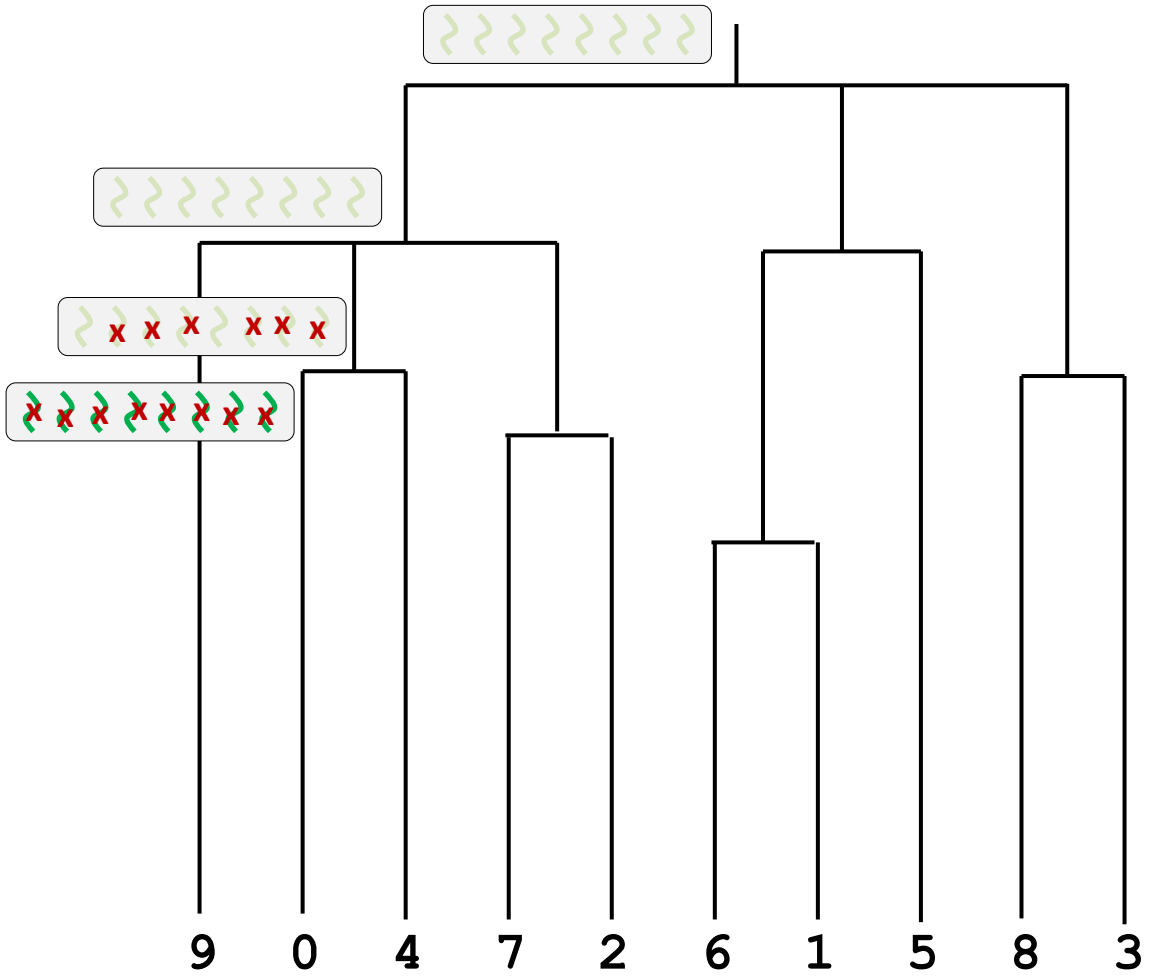

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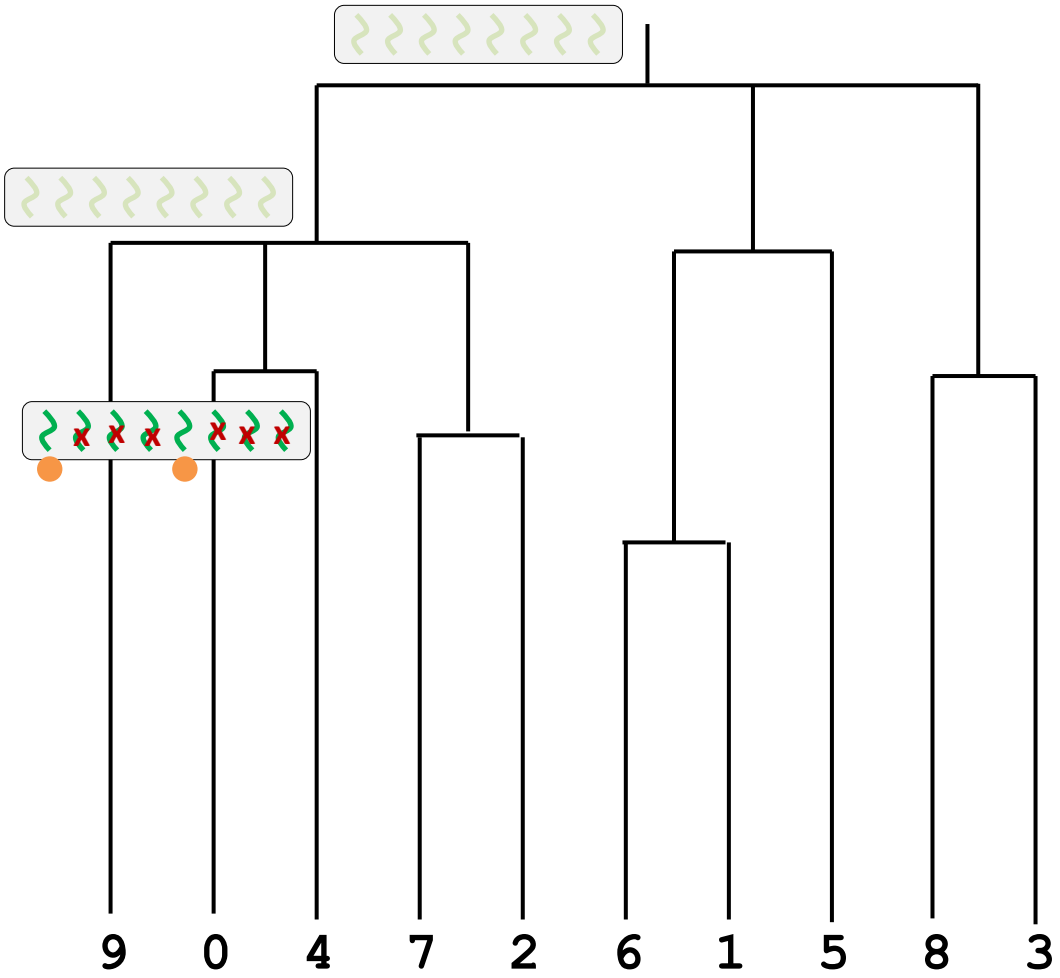

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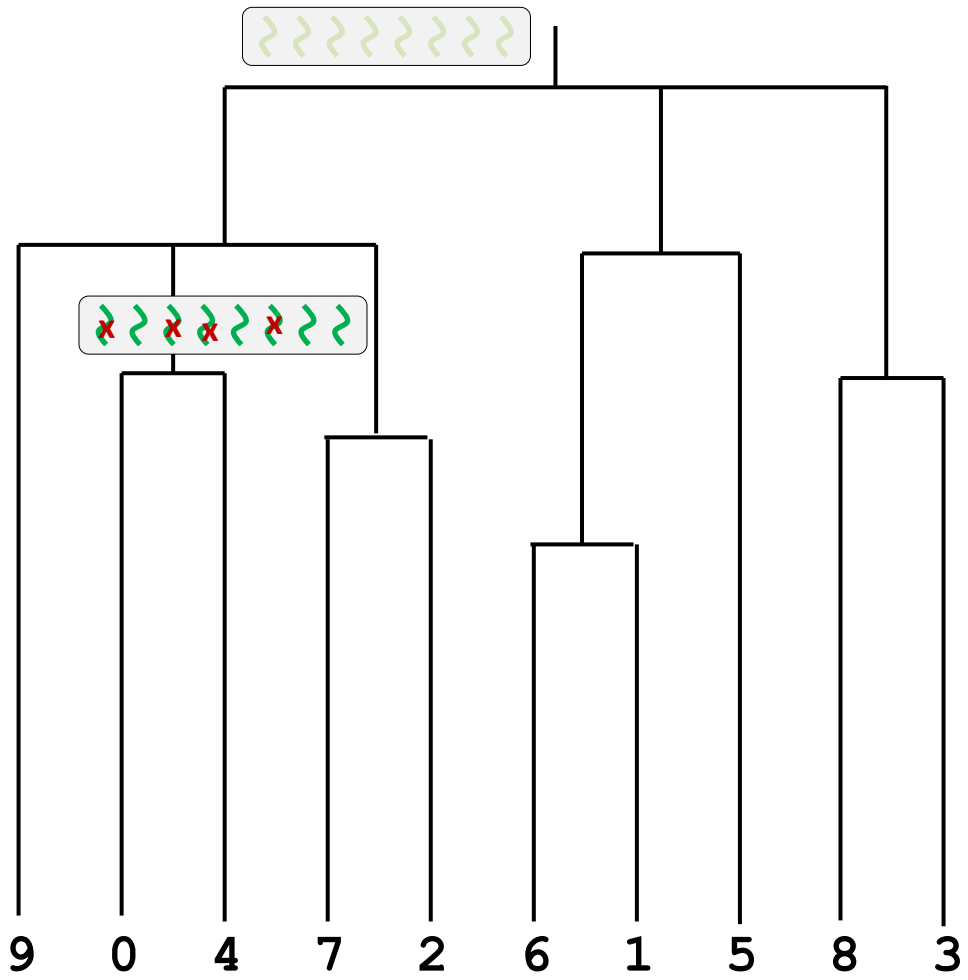
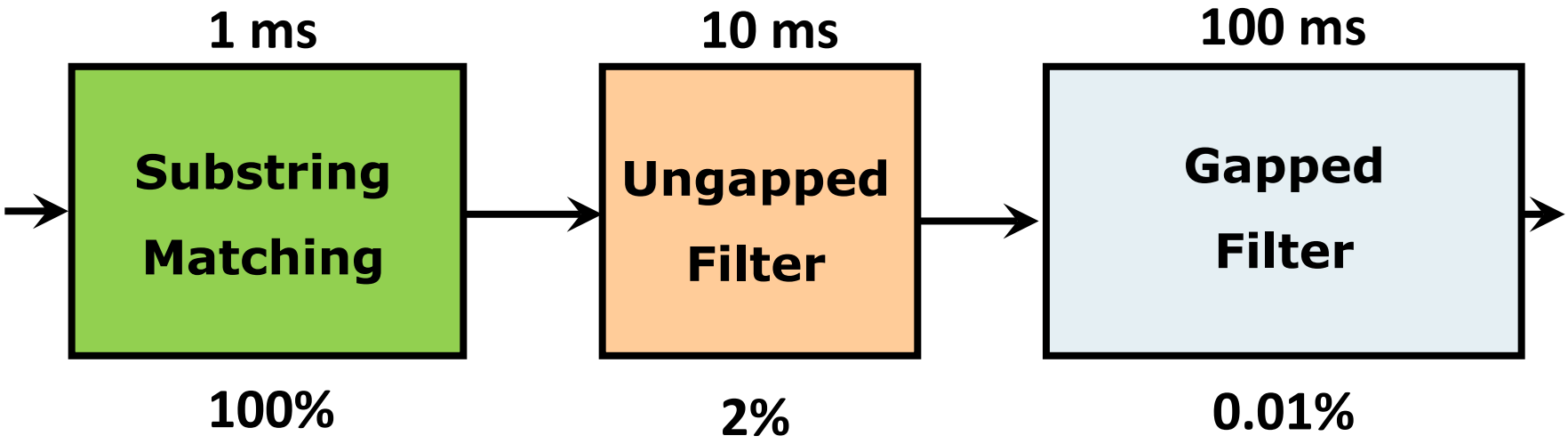


Performance?

- Each stage of BLAST costs more but processes less input.



- 98% of threads idle for 110/111 ms
- 1.99% of threads idle for 100/111 ms
- **SIMD EFFICIENCY**: 1.1%

Irregular Computations

- DNA alignment is an irregular computation: different inputs (*i.e. DB locations, reads*) require different amounts of work to process.

- Antithesis of, e.g., linear algebra calculations that are easily vectorized

- *Irregular computations are highly inefficient if naively implemented on SIMD processors.*

The Key Problem

- **How can we *efficiently* map irregular computations onto a SIMD architecture?**

Talk Overview

- Problems: DNA alignment and read mapping
- Algorithmic approach – Why SIMD?
- MERCATOR overview and performance
- Research challenges

Pause for MERCATOR demo

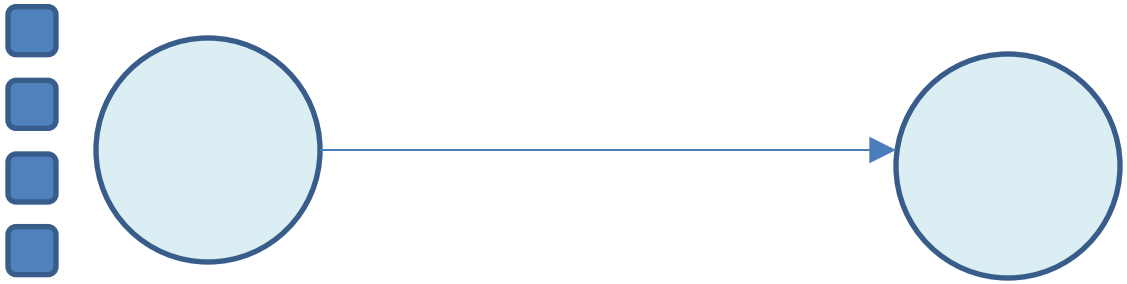
MERCATOR Paradigm

- Application processes a long **stream** of inputs
- **Application graph** consists of nodes (computations), edges (data transfer)
- Data flows through graph of computations
- **Irregularity**: paths differ per input, each input to a node generates 0, 1, or multiple outputs

Handling Irregularity

- Each edge between nodes has a **queue**
- MERCATOR queues inputs to a node until there are enough to fill all its SIMD lanes
- Node is only fired when it has “full ensemble” of inputs in all lanes.

Illustration of Queues



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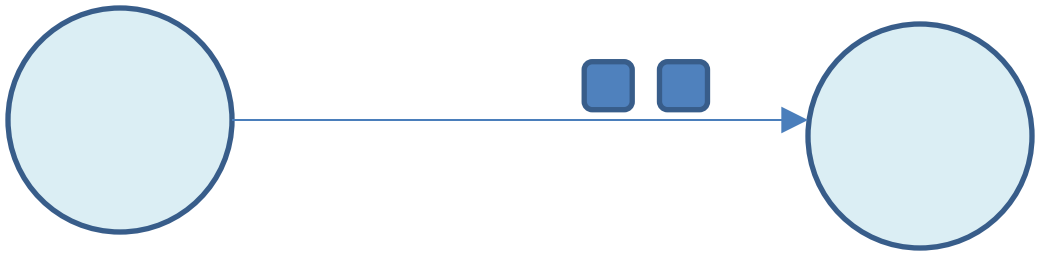

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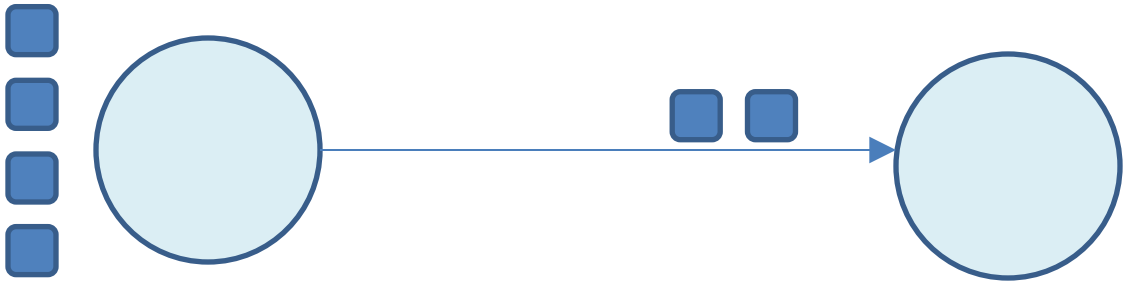

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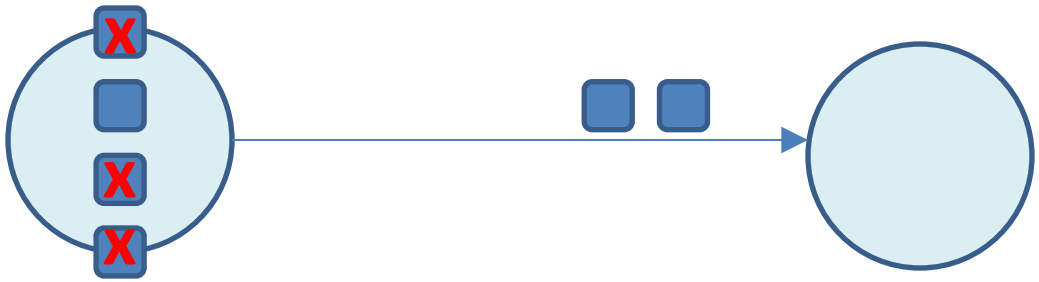

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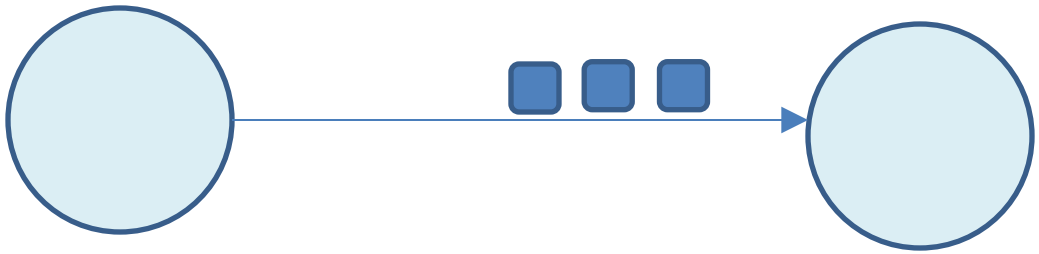

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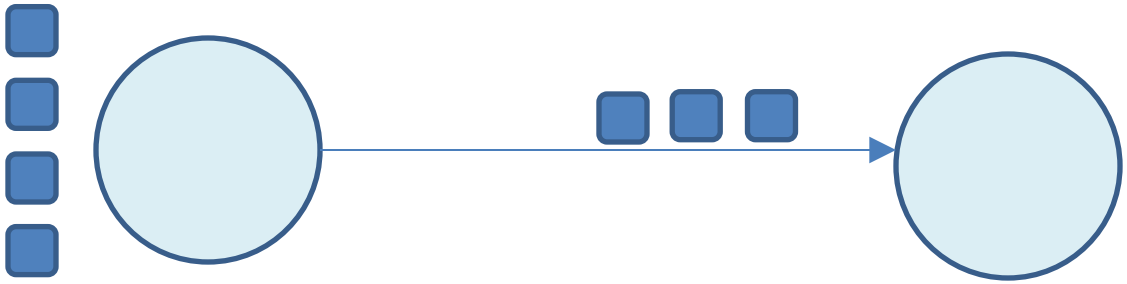

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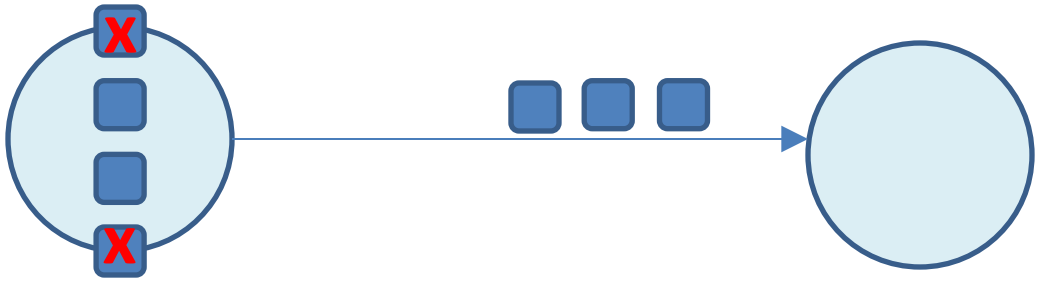

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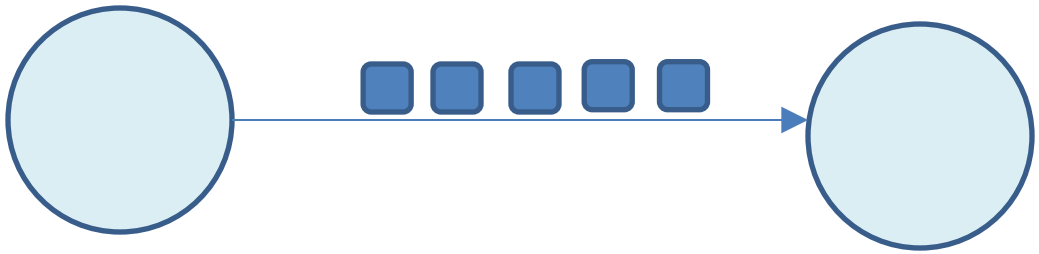


Illustration of Queues

A Few Complications

- **Shared Code** – two or more nodes may do same thing (e.g. Viola-Jones)
- **Overhead** – queueing isn't free
- **Asynchrony** – must use multiple processors, each with multiple SIMD lanes
- **Ordering** – are inputs processed "in order"?

Exploiting Shared Code

- "Module type" ←→ CUDA code
- Multiple nodes with same function have same module type
- *We execute all nodes of a given module type in parallel!*
- [Requires pulling data from each node's queue concurrently]

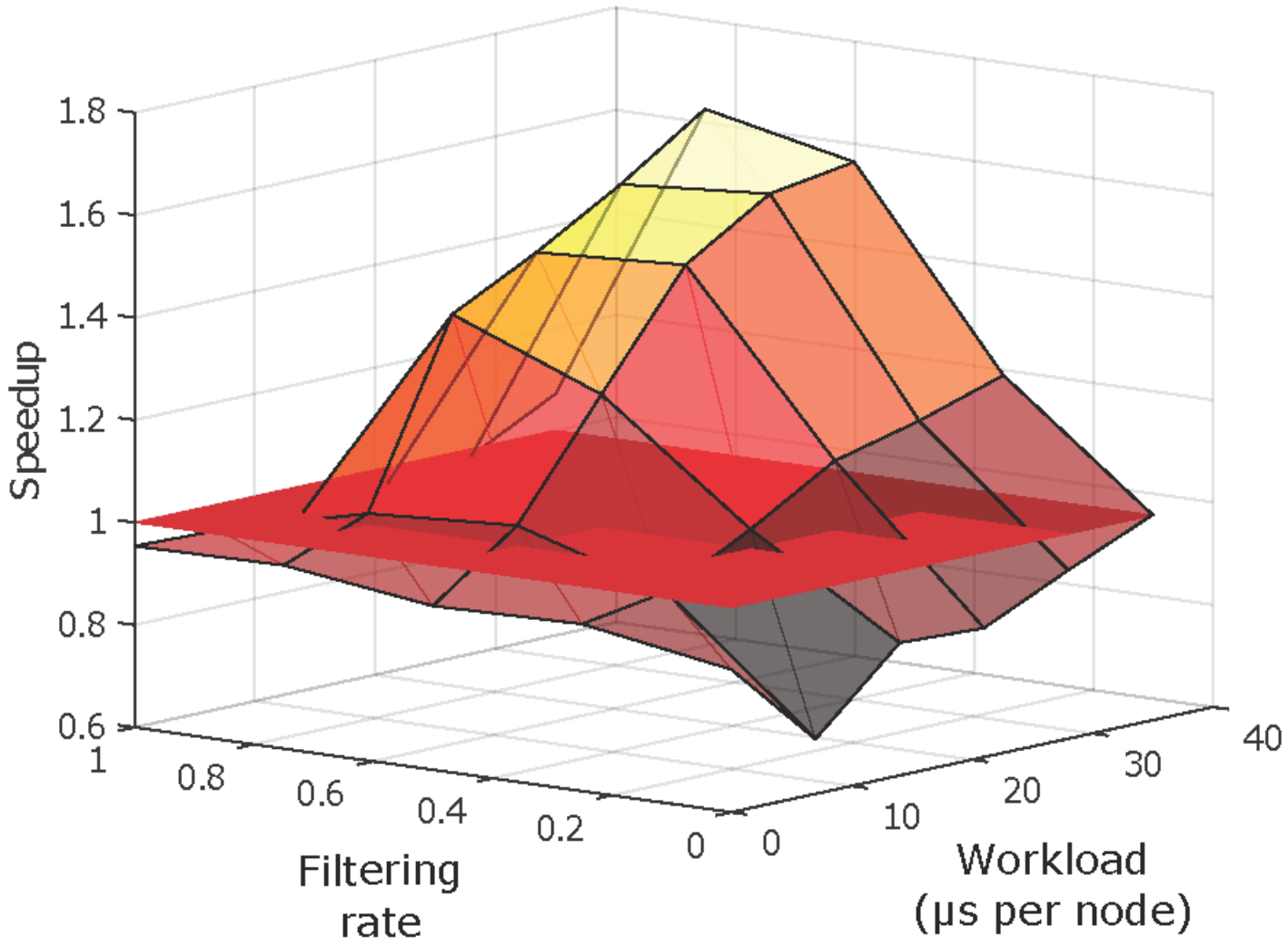
Minimizing Overhead

- Queue manipulation is itself parallelized
- *Easy case*: “read next k inputs from queue into threads 1..k.”
- *More fun*: “read k total inputs from all queues combined into threads 1..k, and remember which queue each input came from.”

Sneaky Tricks

- Parallel scan
- Branch-free binary search
- Parallel output compaction
- *[exploits, maintains input ordering]*

Results of Synthetic Trial



Dealing with Asynchrony

- Shared input / output buffers
- Output order with multiple processors?
- *[Need **stream-synchronized signaling**]*
- Associative (and commutative?) reductions

Applications with Cycles

- App graph can have *back edges*
- **Issue***:* deadlock prevention
- [*topology restrictions, queueing policy*]
- **Order preservation?**

Optimization Opportunities

- Parameter tuning (queue sizes, **scheduler**, …)
- Latency-sensitive applications *vs* occupancy
- Fusing nodes to elide queueing (at what cost to occupancy?)

Want to Play?

- *https://github.com/jdbuhler/mercator*
- MERCATOR will be a testing ground for SIMD-aware irregular streaming computation
- Many interesting problems still to be solved!
- → **thesis topics**