Persona: A High-Performance Bioinformatics Framework

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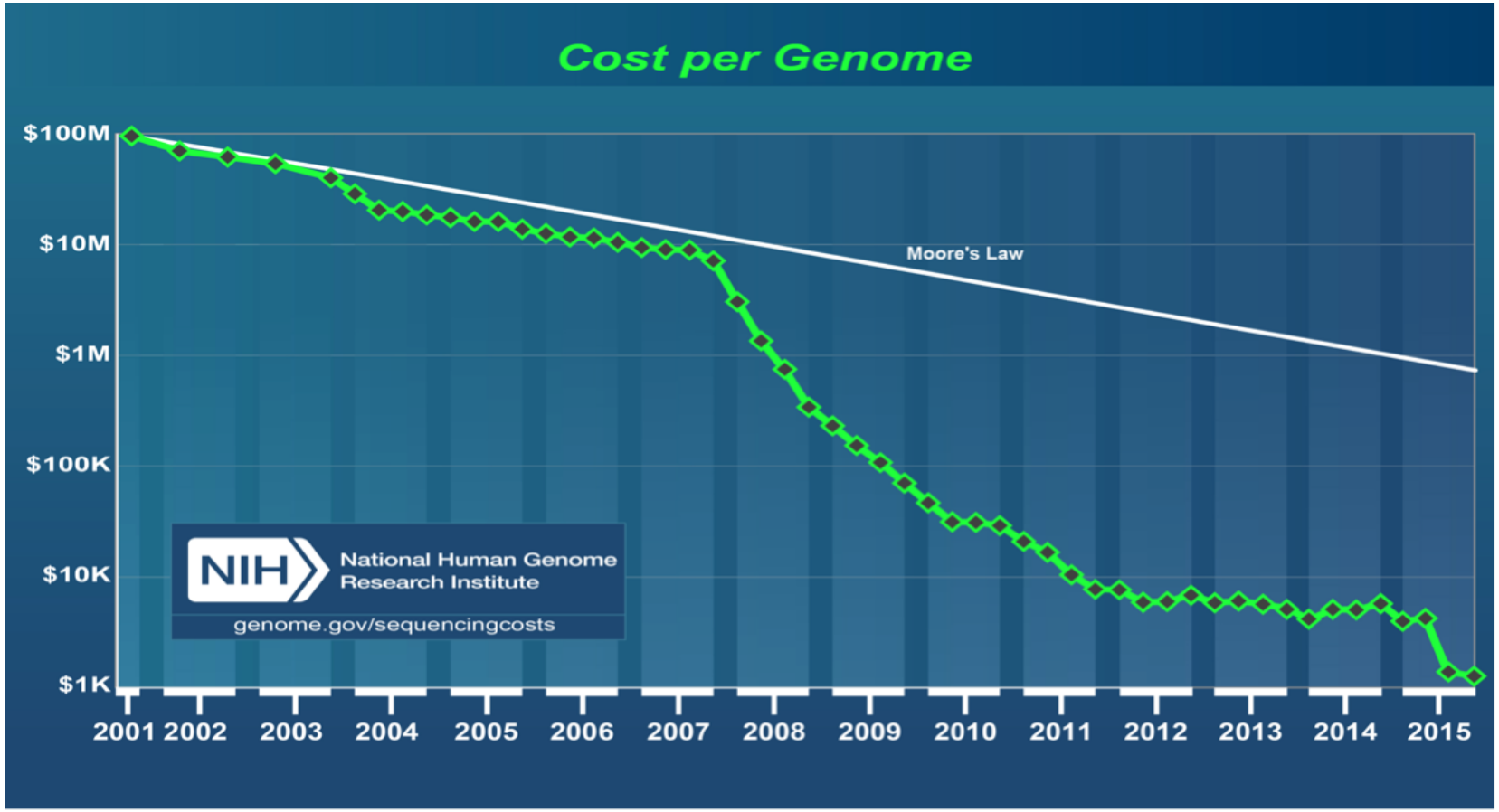
ÉCOLE POLYTECHNIQUE
FÉDÉRALE DE LAUSANNE

12/07/2017

Agenda

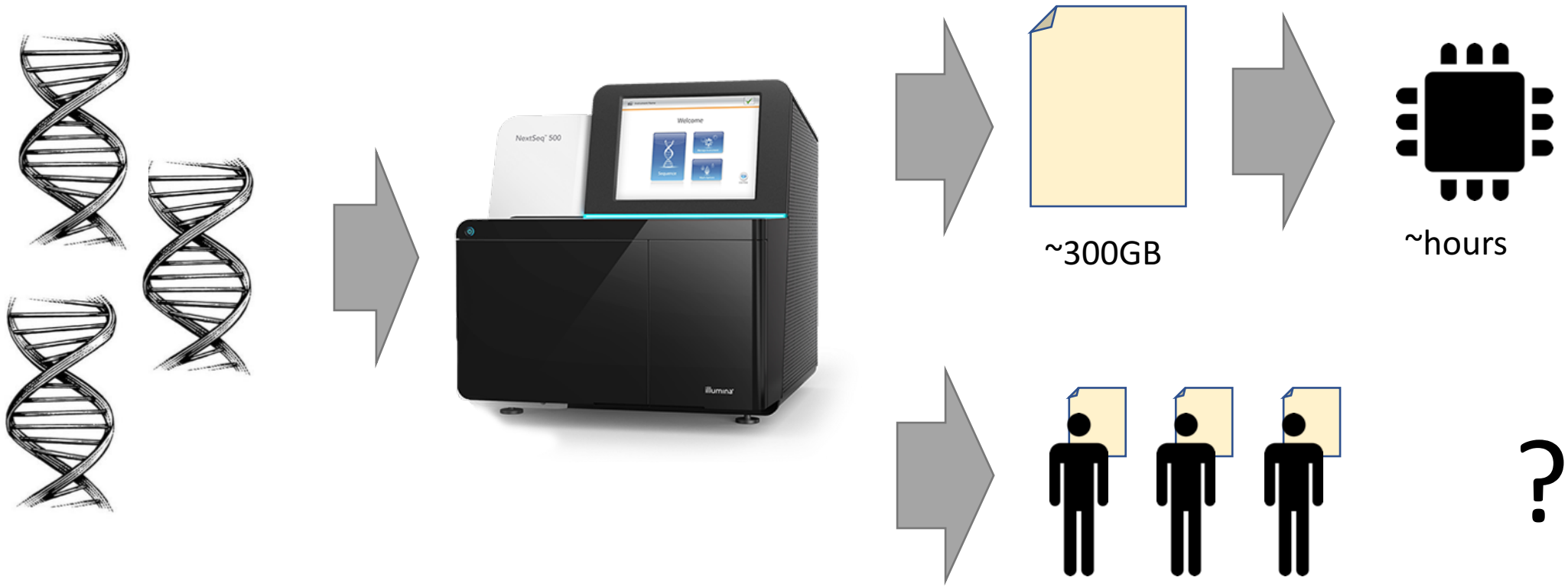
- **Motivation**
- Bioinformatics Data and Tools
- Persona
  - AGD
  - Dataflow Engine
- Performance Results

Sequencing cost



Not a wet lab problem anymore → IT / Systems problem

Implications



Need efficient systems that scale well

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What kind of data?

- Common sequencers produce *Reads*
  - Snippets of DNA → AACCGCTAGCGCGCTAGCTCGAGCTAGAA
  - 100-200 bases

```
@sequence name, metadata
ACGTTTCGATCGCGCCAGGAGGCTAG
+
-+*''))**55CCF@>>>>>CCCCCC
```

times a few hundred million …

Alignment

Reference Genome

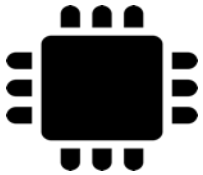
Mismatch

```
...TGACCTATAGCGATATAGCTTATTATTGGG-CAAAAATGGAATCGATTGATCG...
                                 |||||||||||  |||||  |||
Read:                            TATTATTGGGATAAAA-TGG
```

Insertion

Deletion

times a few hundred million …



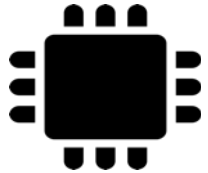
~hours

Aligned Reads

- Stored in SAM/BAM

```
read_name 16      chr12   85500011        70
18M   *       0       0
TTTTACACACATTATCTC    CDDFAEEC>EDDFFBCDEED?FCC@
PL:Z:Illumina   PU:Z:pu LB:Z:lb SM:Z:sm
```

- Followed by
  - Duplicate marking
  - Sorting
  - Recalibrations, analysis (variant calling)



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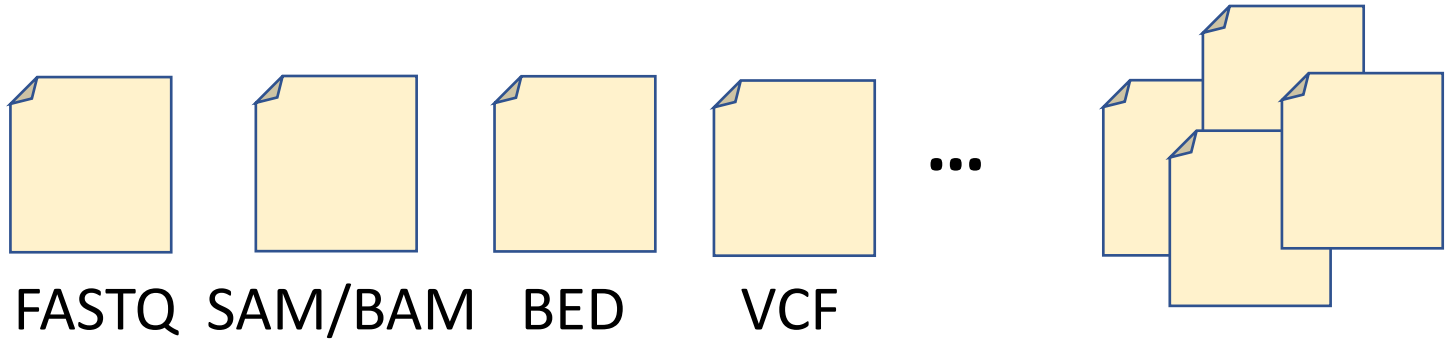
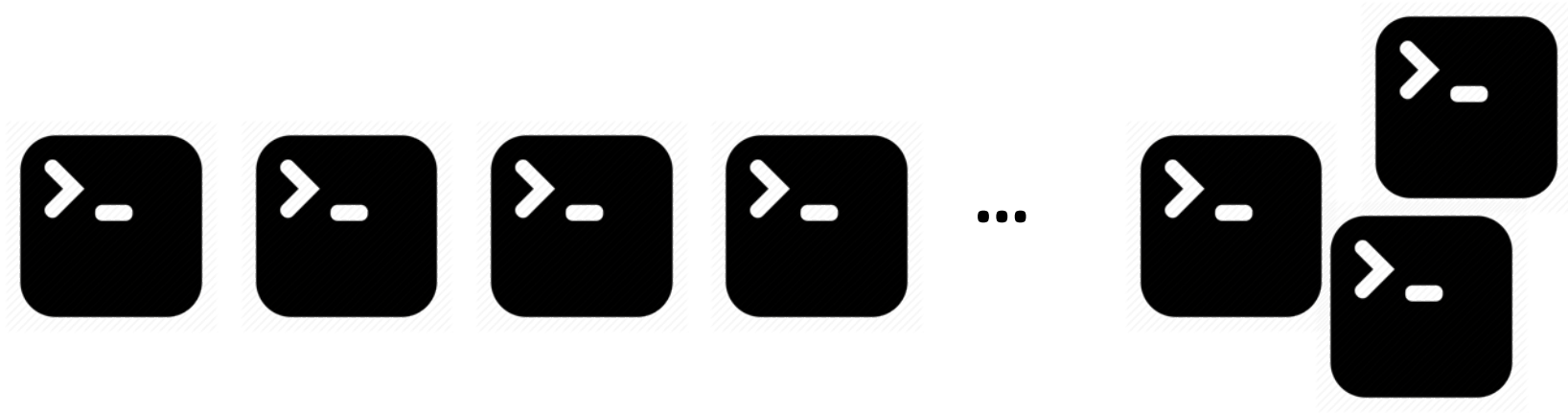
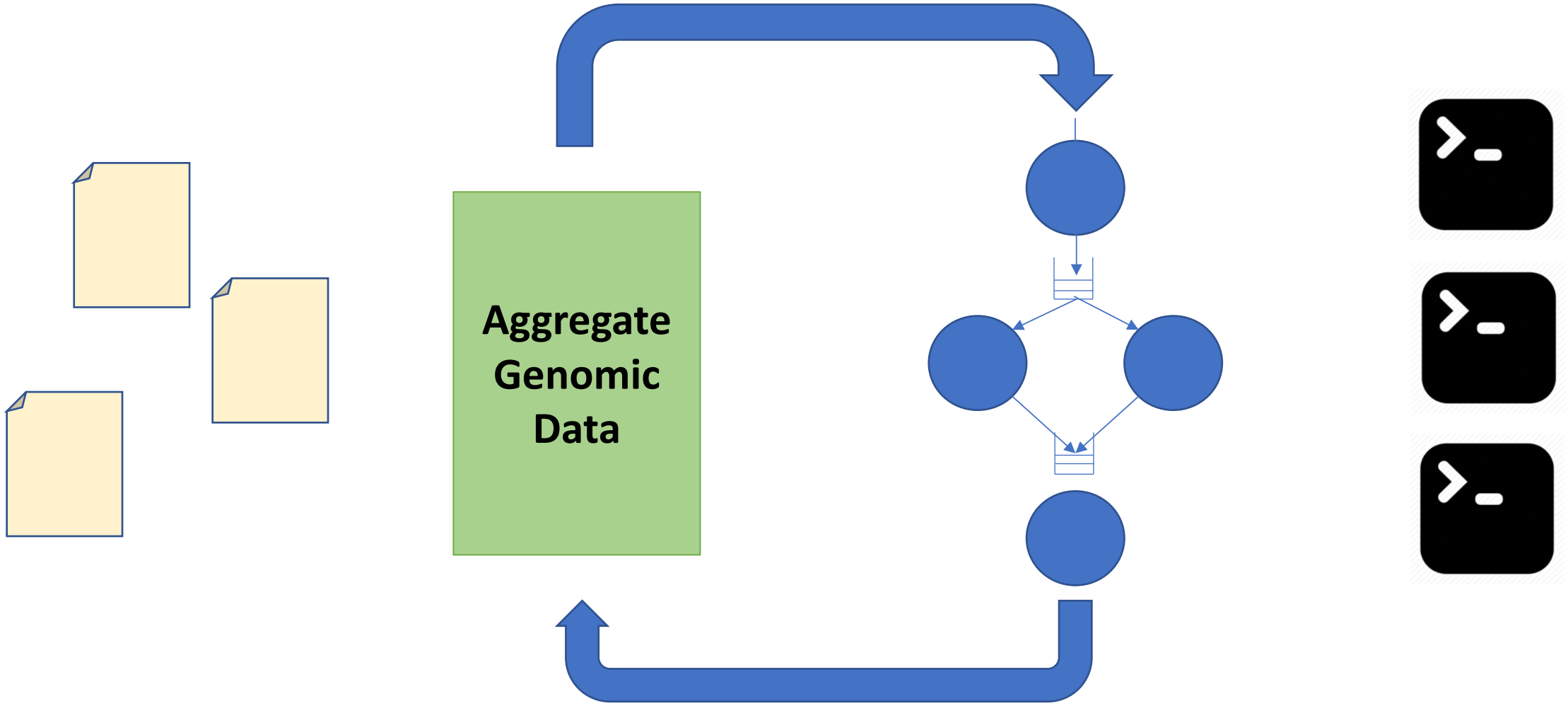
Data and Tool Issues





Persona – Bioinformatics, Unified



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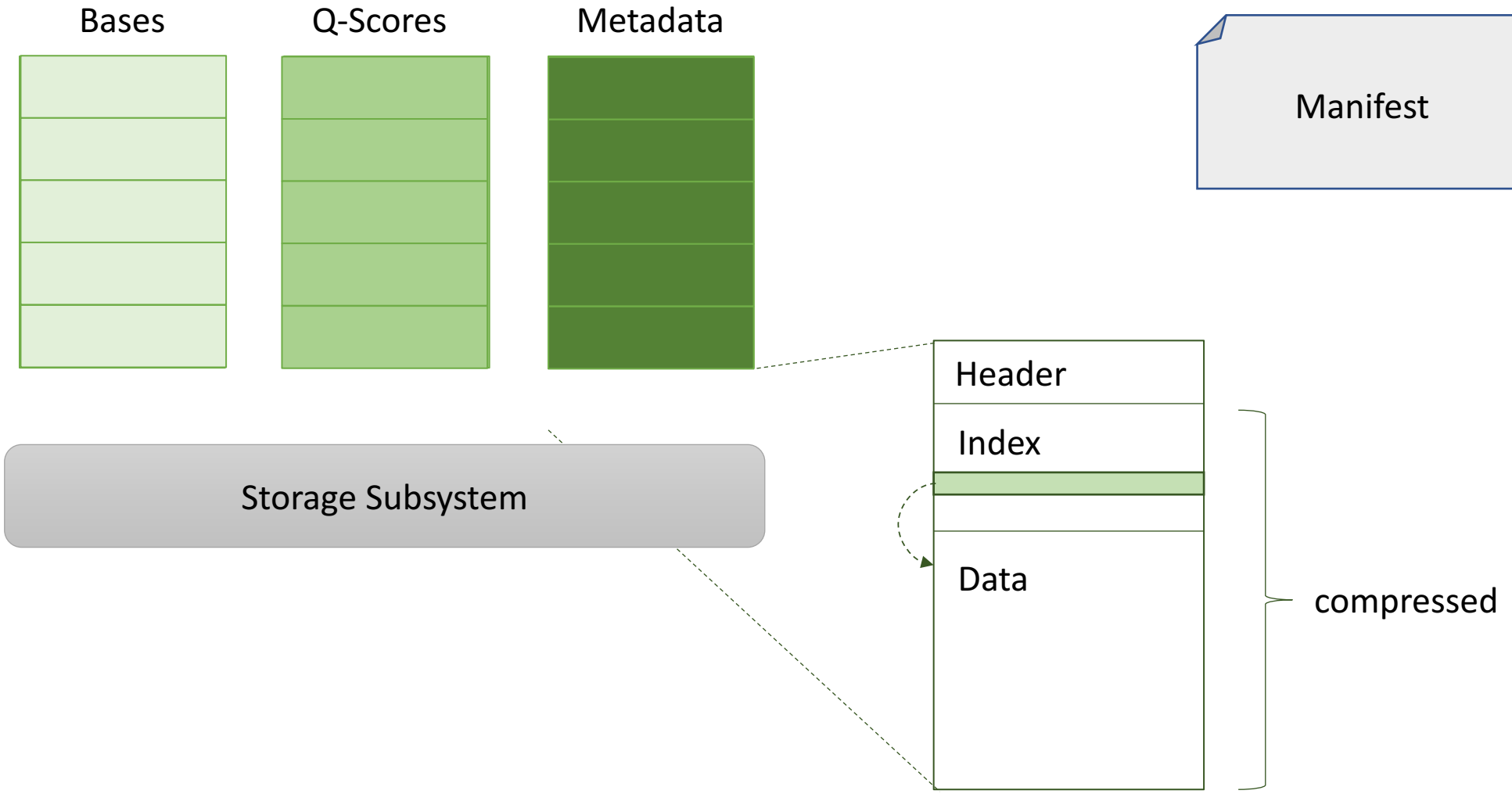
Aggregate Genomic Data



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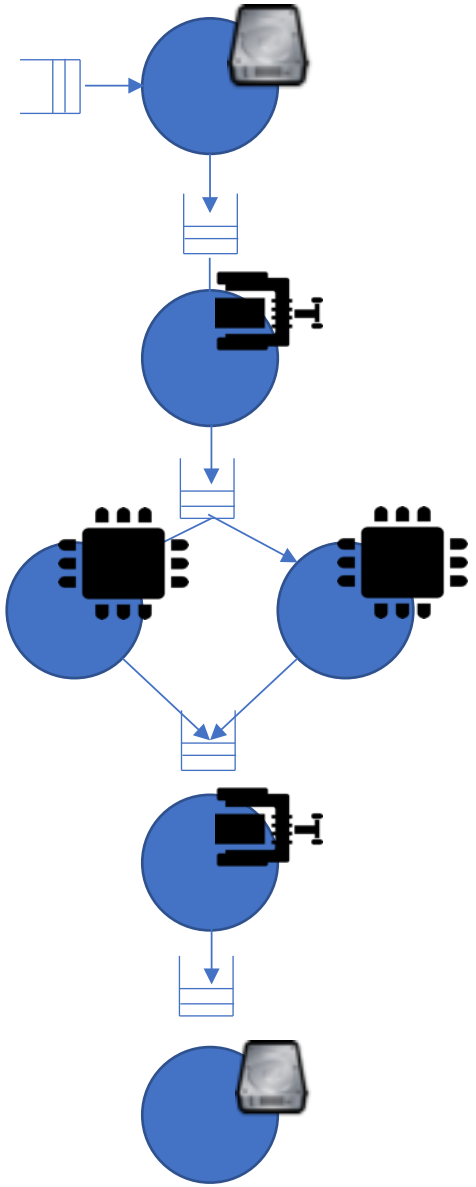
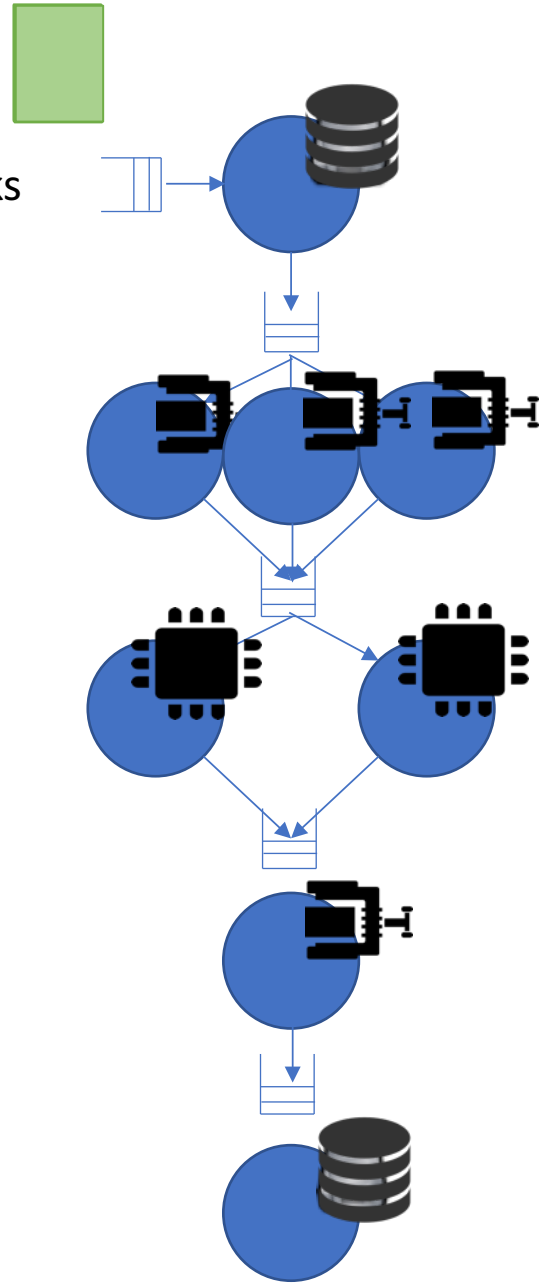
Dataflow

- Dataflow execution framework
  - Base on TensorFlow engine
  - But no machine learning
- Operators perform computation on AGD chunks



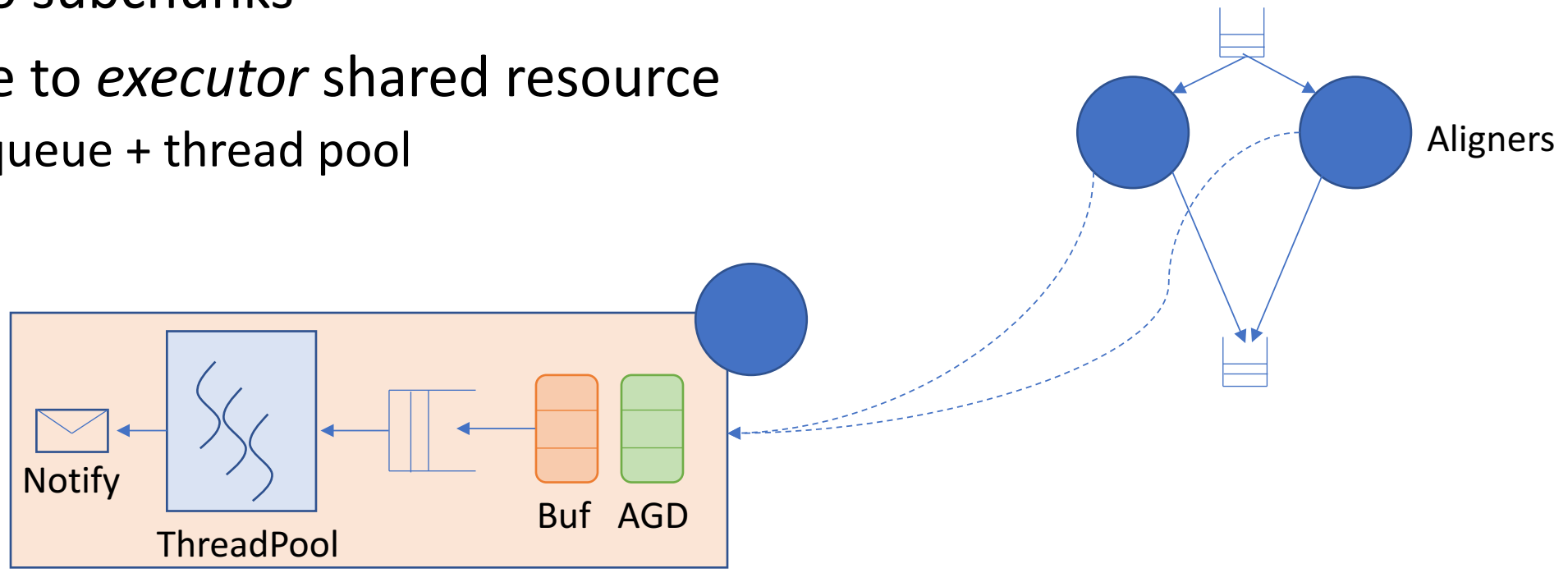
Dataflow

- Modularity
- Balance/tuning
- (bounded) Queueing

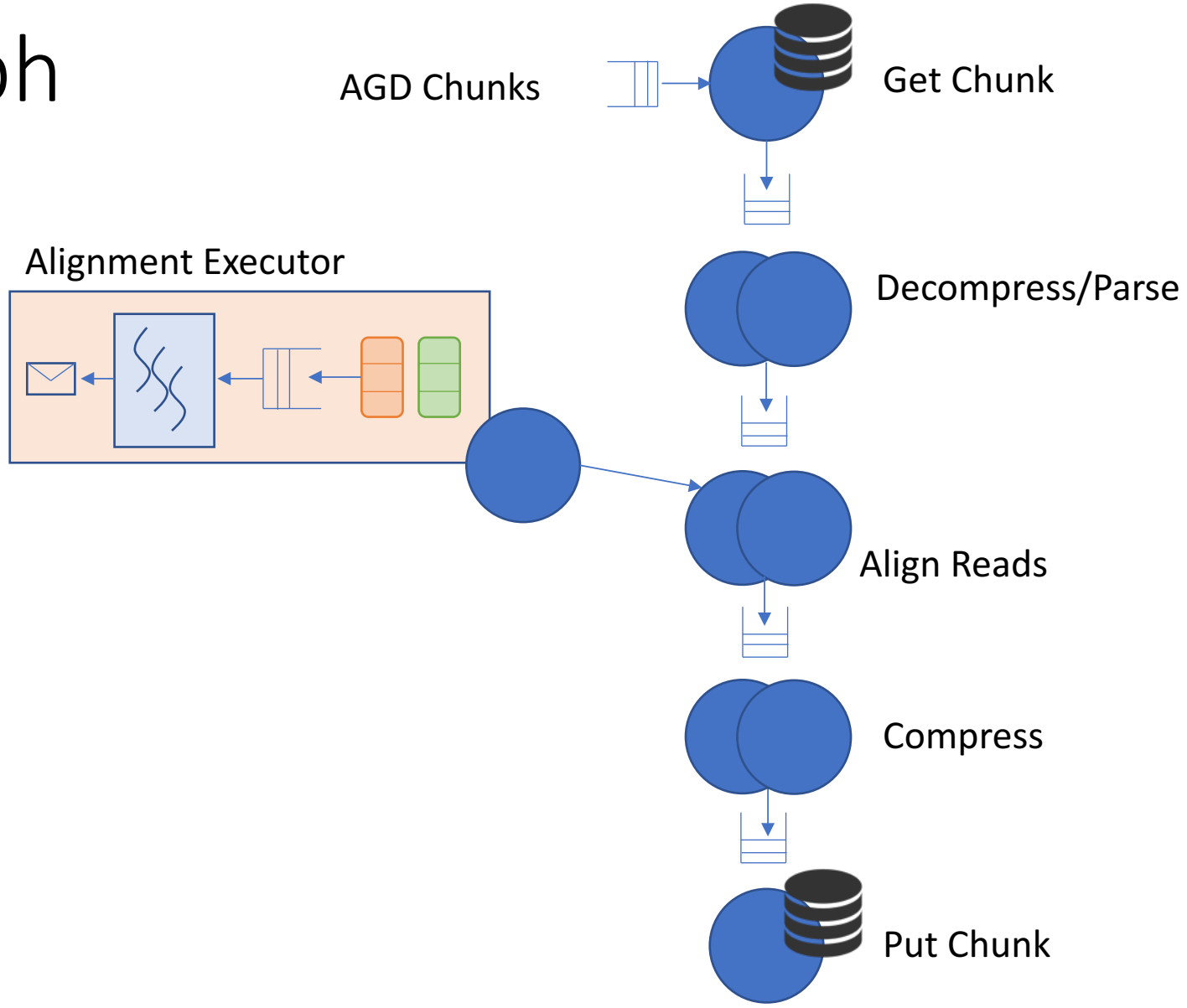


Fine-grained Threading

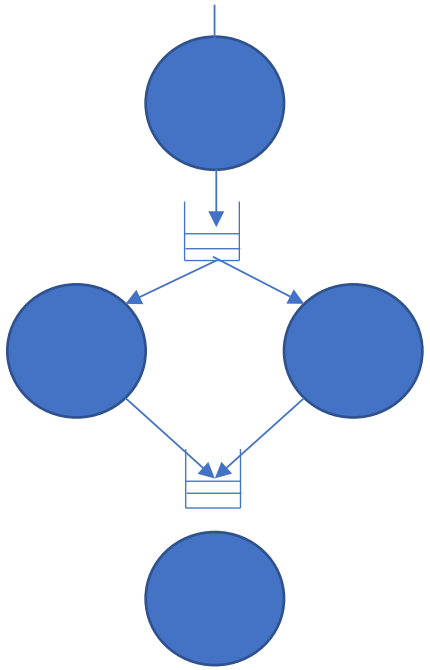
- AGD chunks optimized for storage
  - Too coarse for some tasks
- Split into subchunks
- Delegate to *executor* shared resource
  - Task queue + thread pool



Aligner Graph

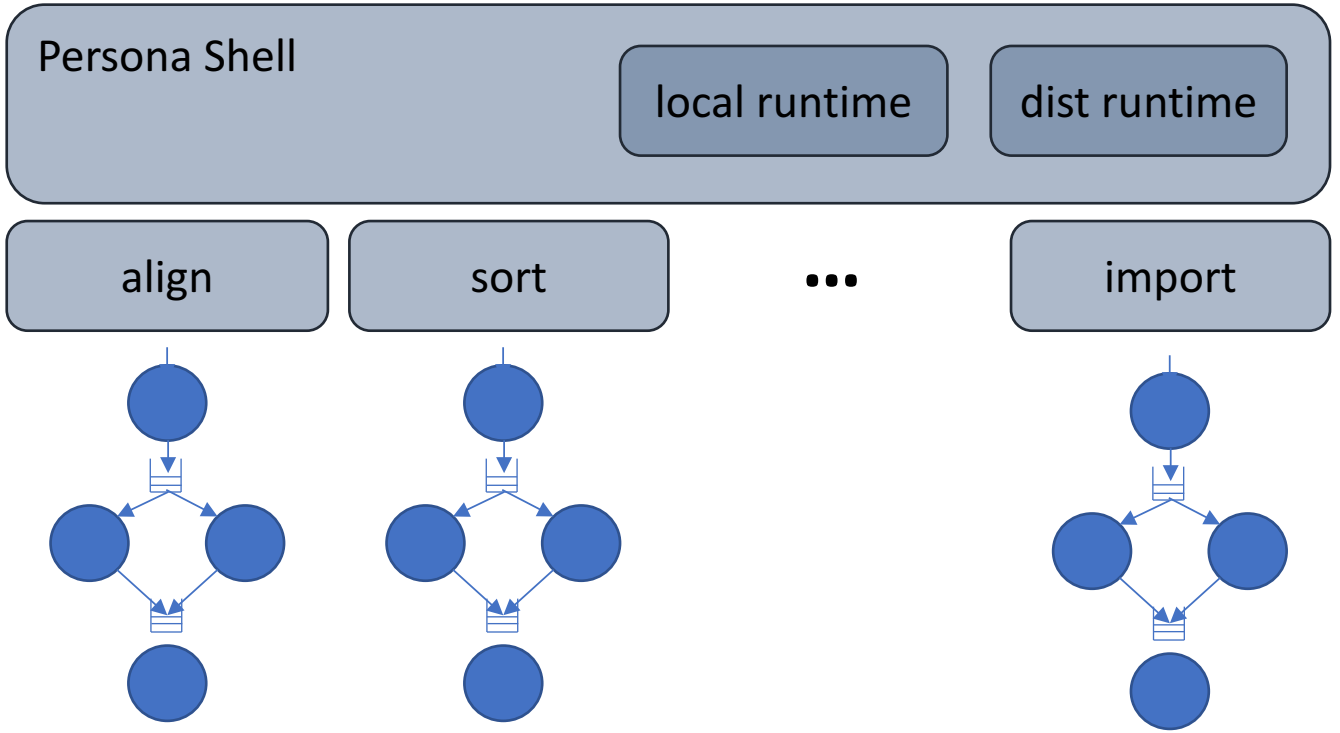


Graph Construction



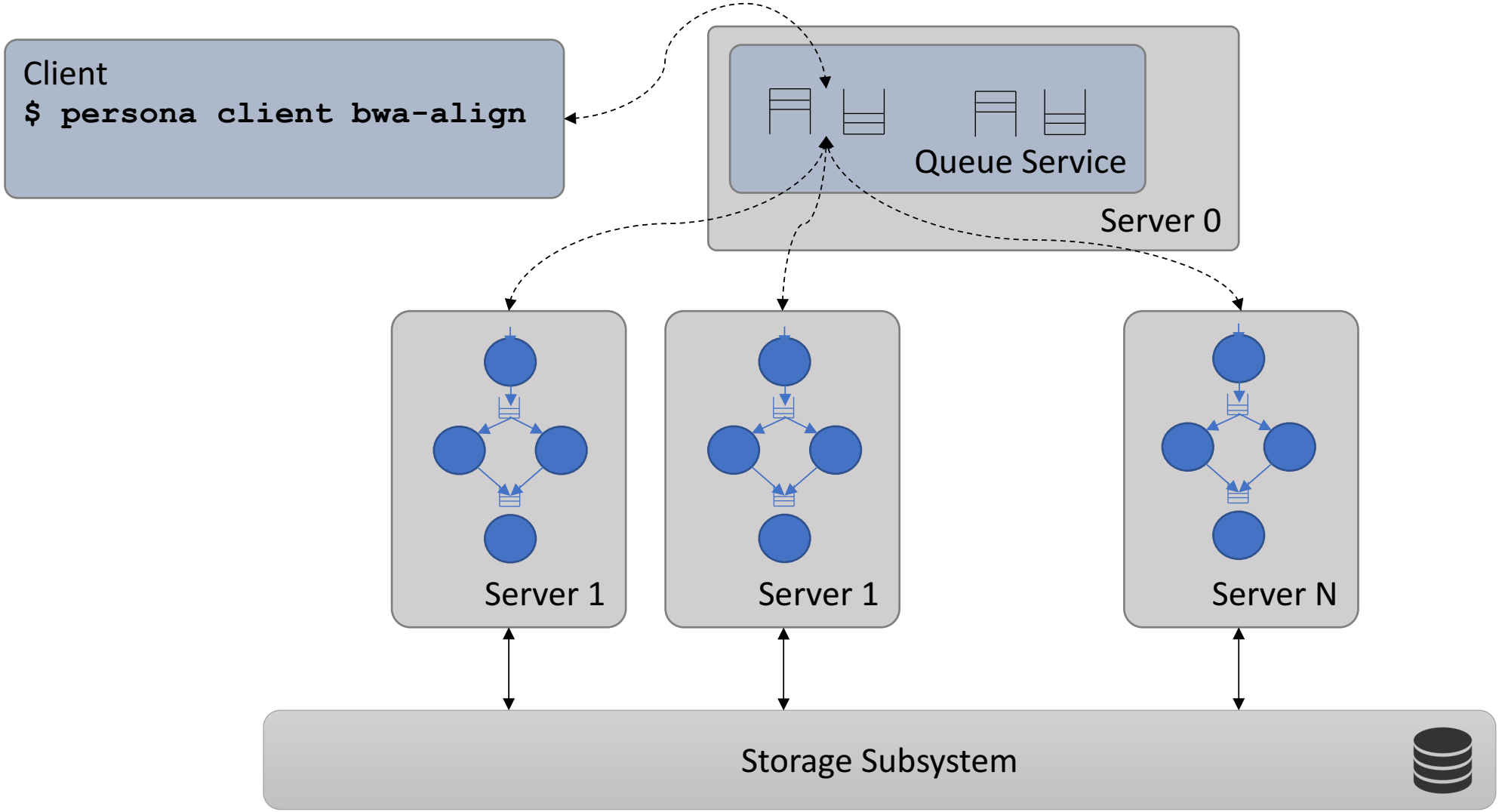
```
c = persona.read_chunk(path)

d = persona.decompress(c)

o = persona.align(d)

sess = tf.Session()
result = sess.run([o])
```

Persona Shell




```
$ persona align local -i hg19 data/my_agd.json
$ persona sort local data/my_agd.json
```

Distributed Computation



Current Features

- Import data from FASTQ/BAM/SRA, export to BAM
- Sequence alignment with BWA-MEM, SNAP
- Dataset sorting
- Duplicate marking
- Dataset statistics (samtools flagstat)
- Read coverage (depth)

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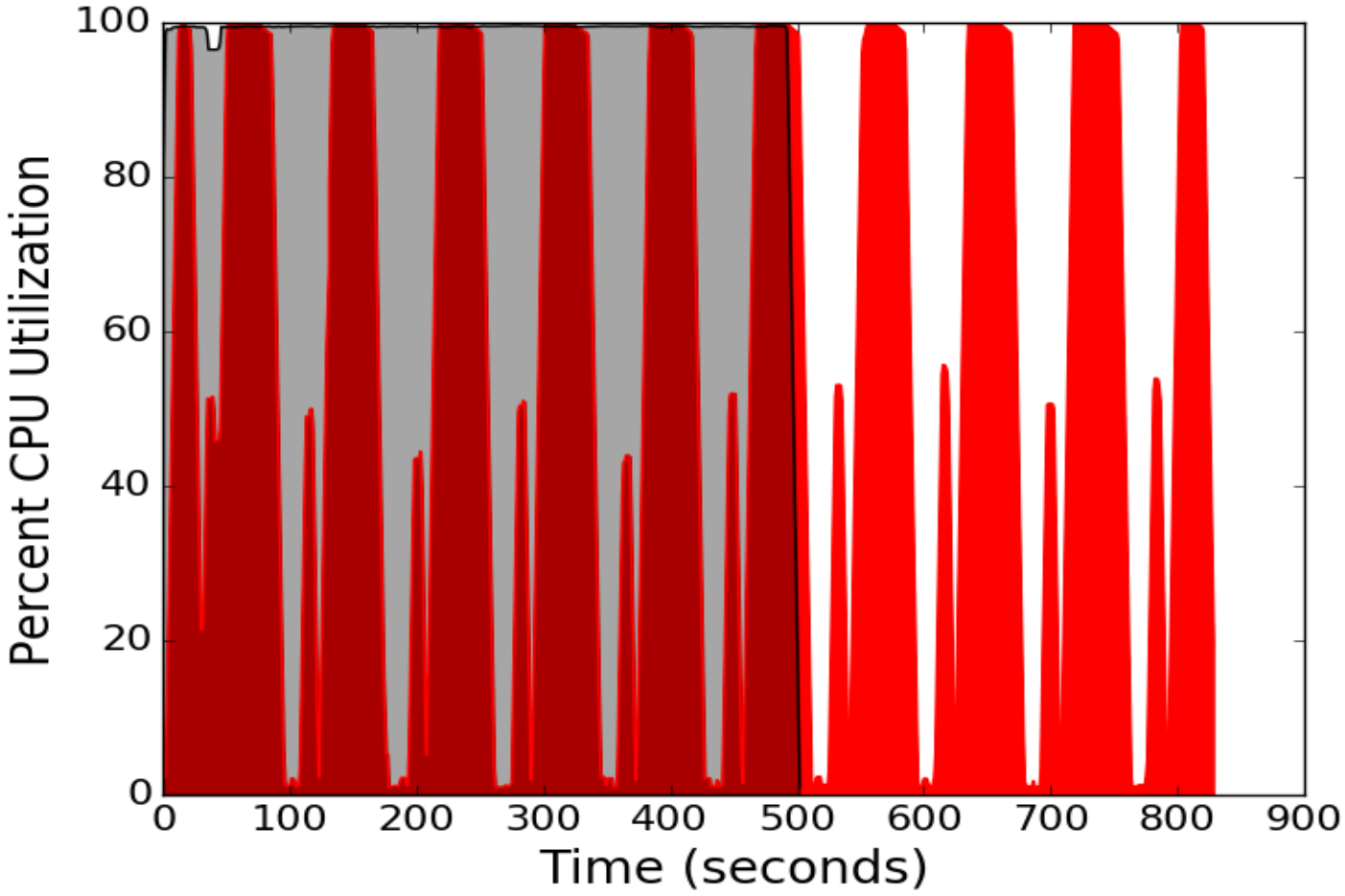
Evaluation -- Setup

- Focused on sequence alignment using SNAP
- Throughput in bases aligned per second
- Data
  - 223 million 101 base reads (~16GB)
  - AGD chunks of 100K records
- Hardware
  - 32X Ubuntu 16.04, 2x12 Xeon E5-2680v3 @ 2.5GHz
  - Data on 6-disk RAID0 and single spindle drive
  - 7 server Ceph object store for distributed execution

Evaluation -- Questions

- What are the bandwidth-saving effects of AGD?
- What is the overhead of the Persona framework?
- How well do Persona and AGD scale?

Performance – AGD



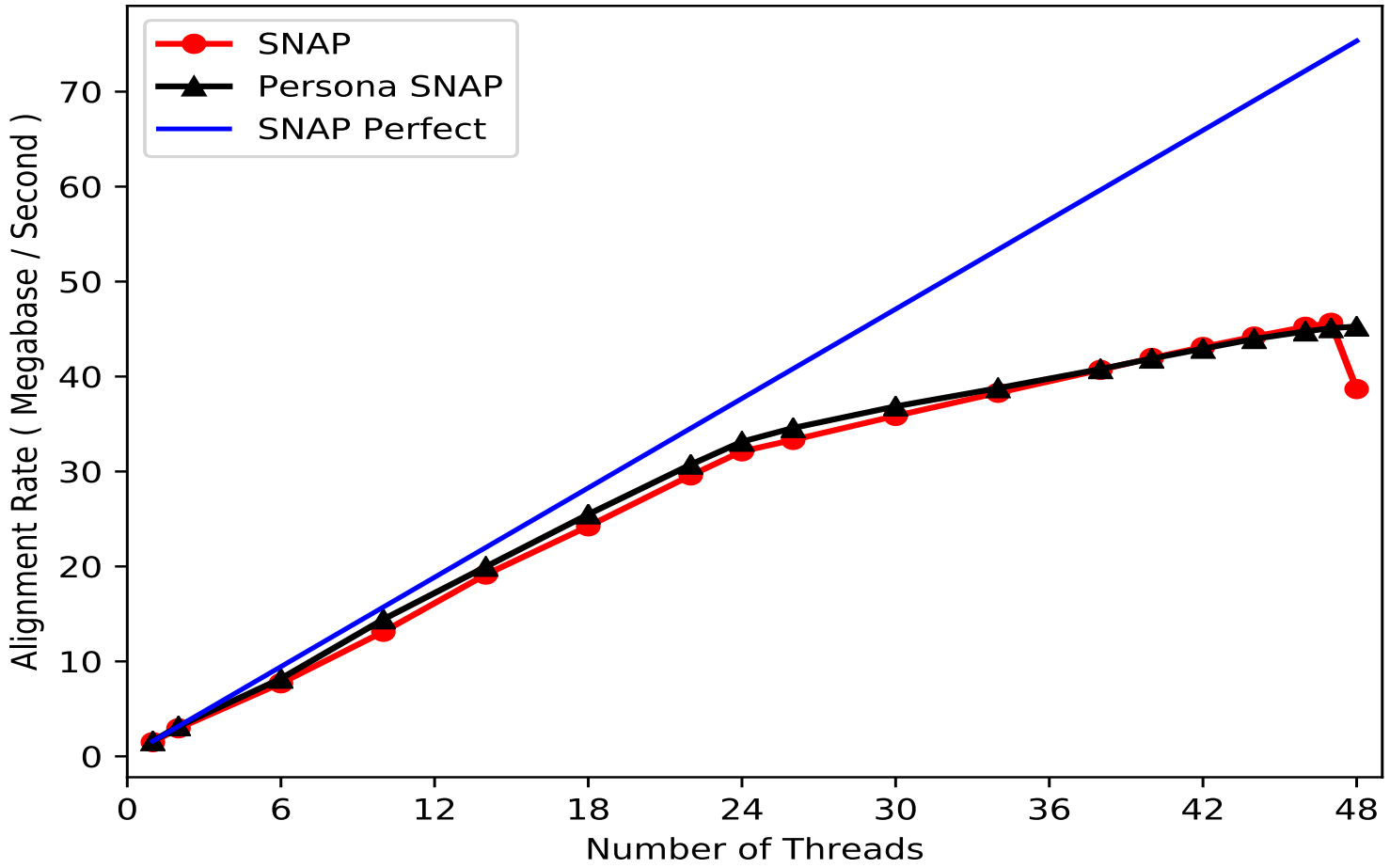
SNAP

Persona SNAP

* single disk

Significantly less I/O → more efficient use of HW, BW

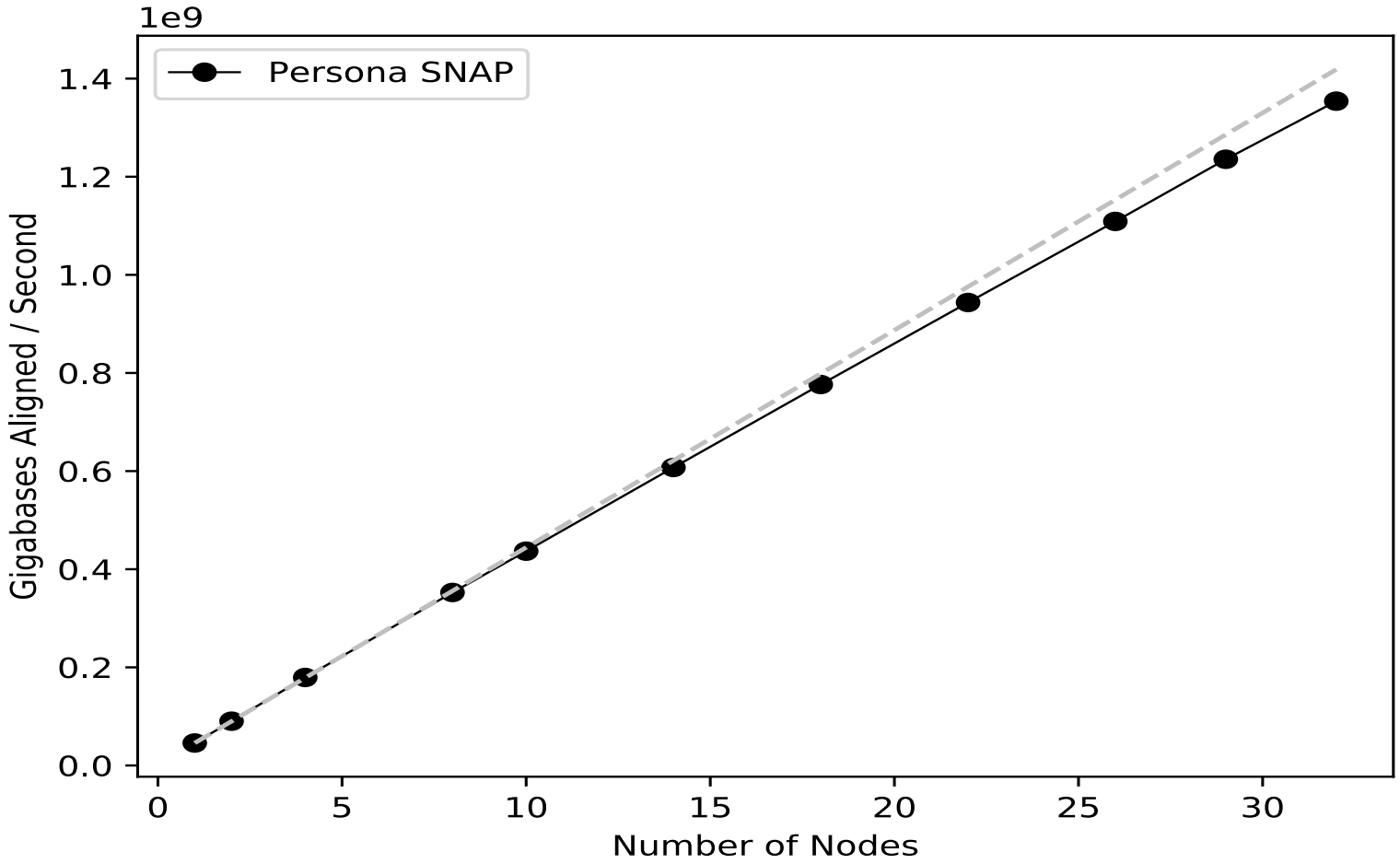
Persona Overhead



* RAID-0

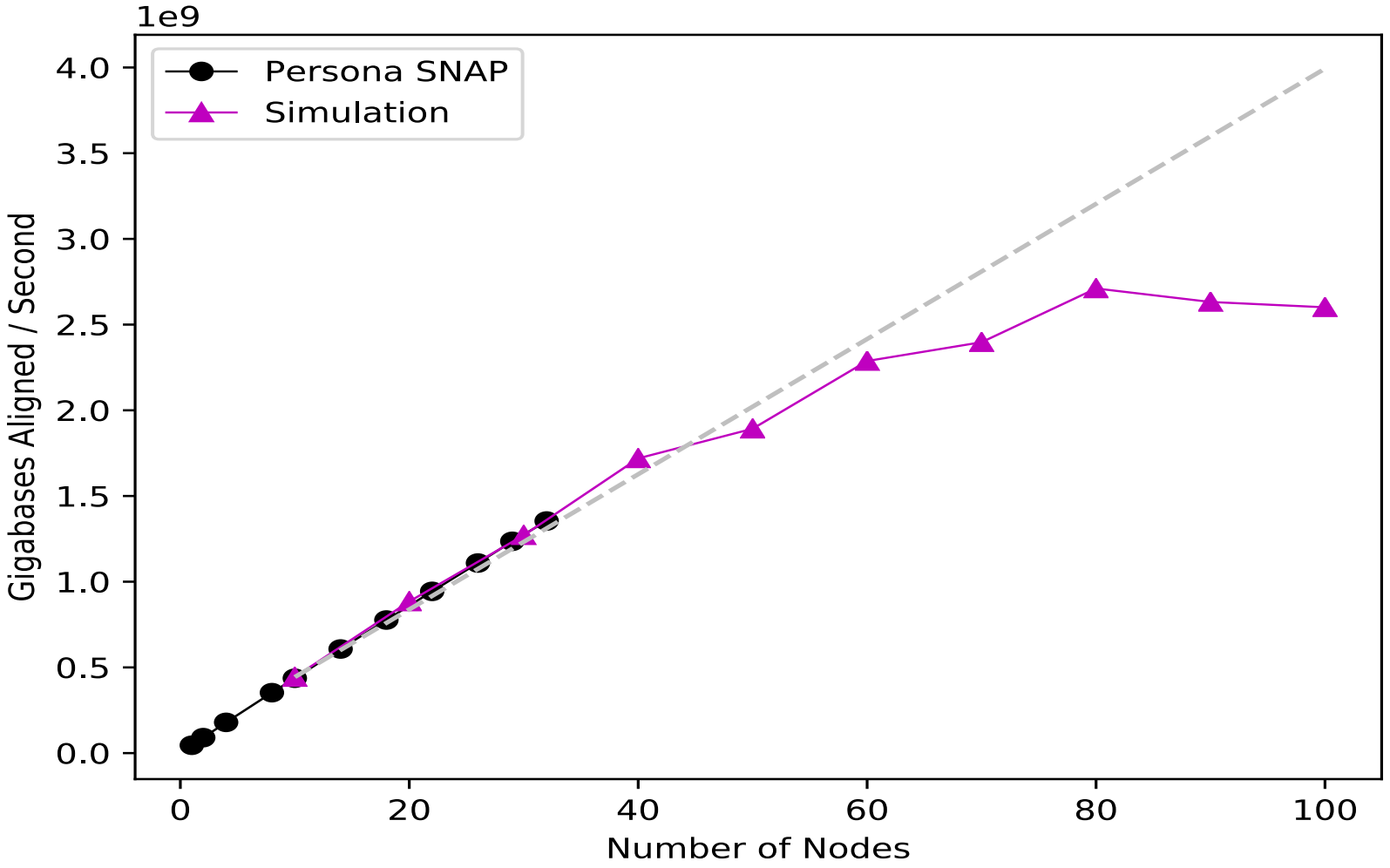
Negligible overhead!

Scaling

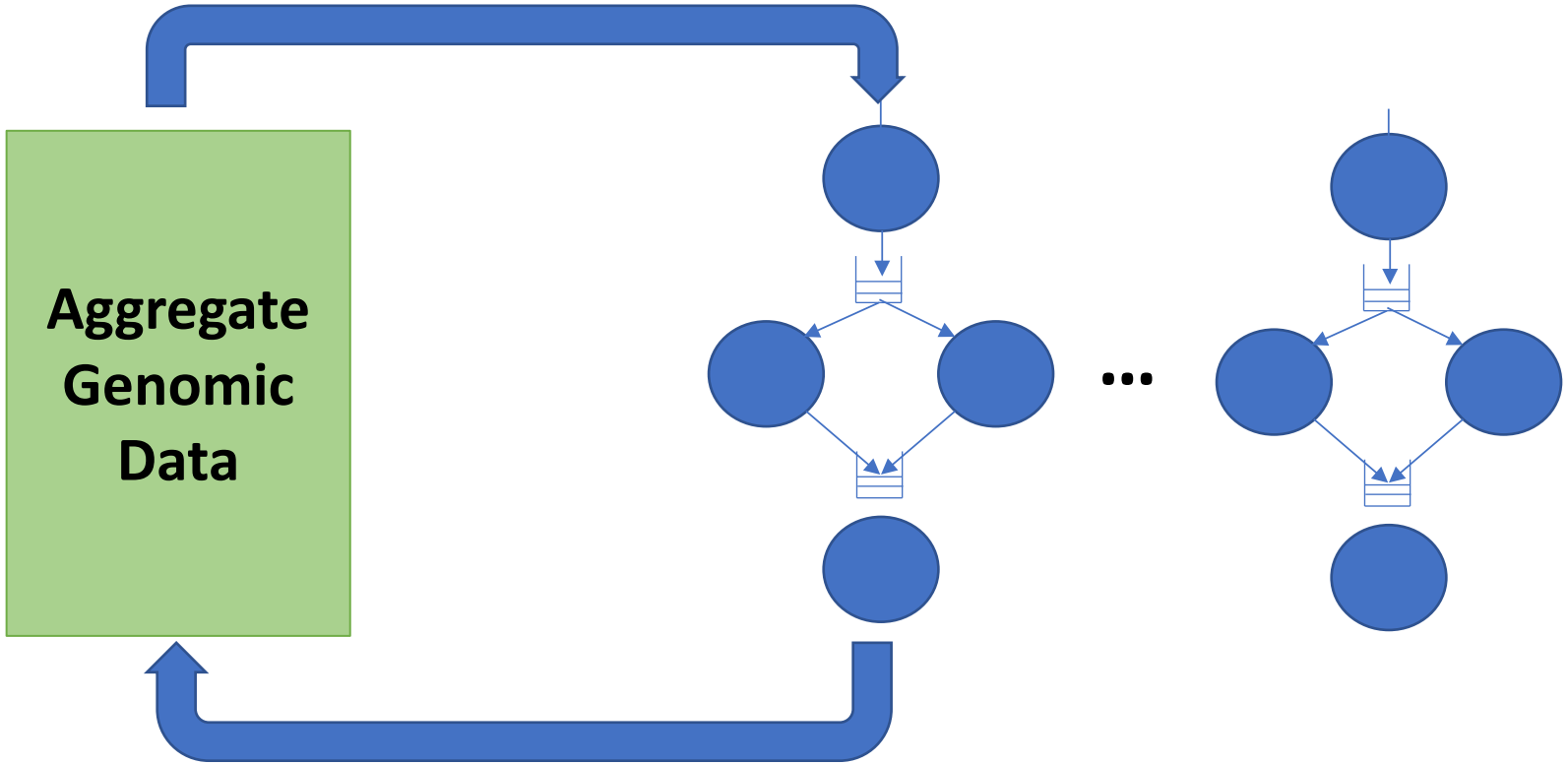


Full dataset aligned in ~17 seconds

Scaling Limits



Persona – Scalable Bioinformatics



https://github.com/epfl-vlsc/persona

backup

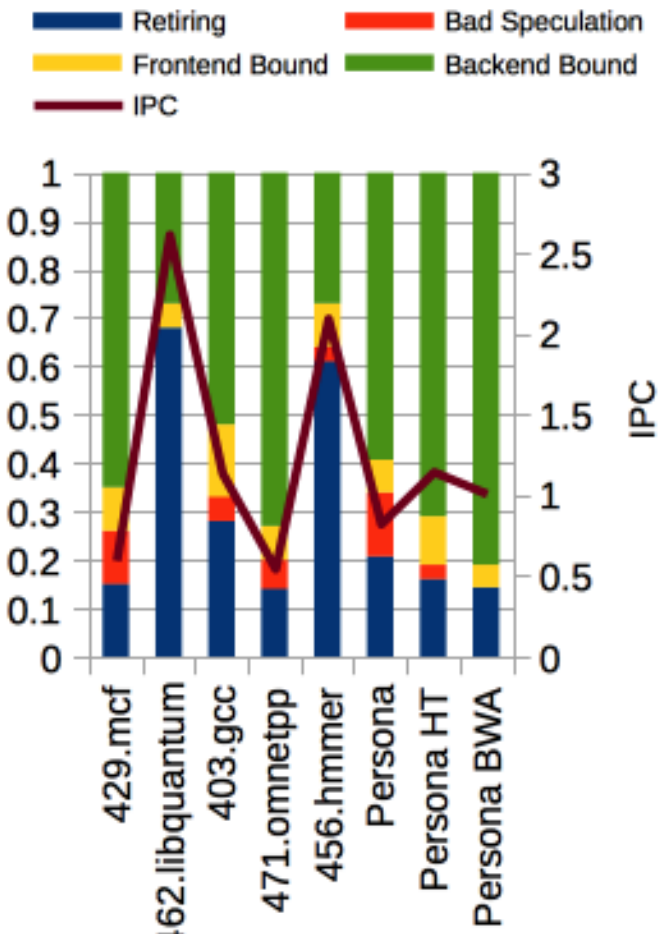
Performance – Sort and Dup. Mark

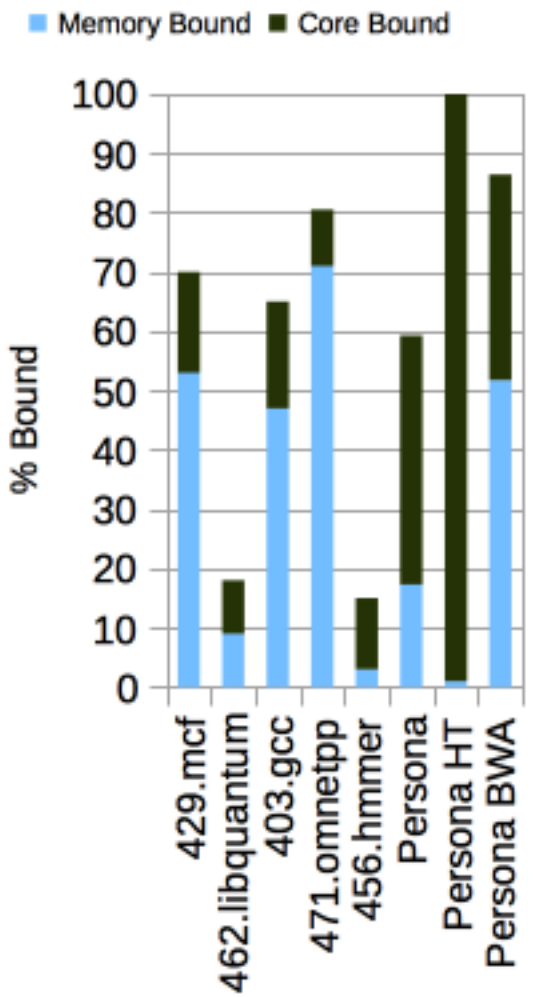
- Sort
  - By metadata or aligned location
  - 1.54x speedup over samtools
  - 5.15x speedup over Picard
- Dataset stats 

  - 2x speedup
- Duplicate marking
  - Same algorithm as samblaster
  - 3.73x faster than samblaster
- Coverage (depth) 

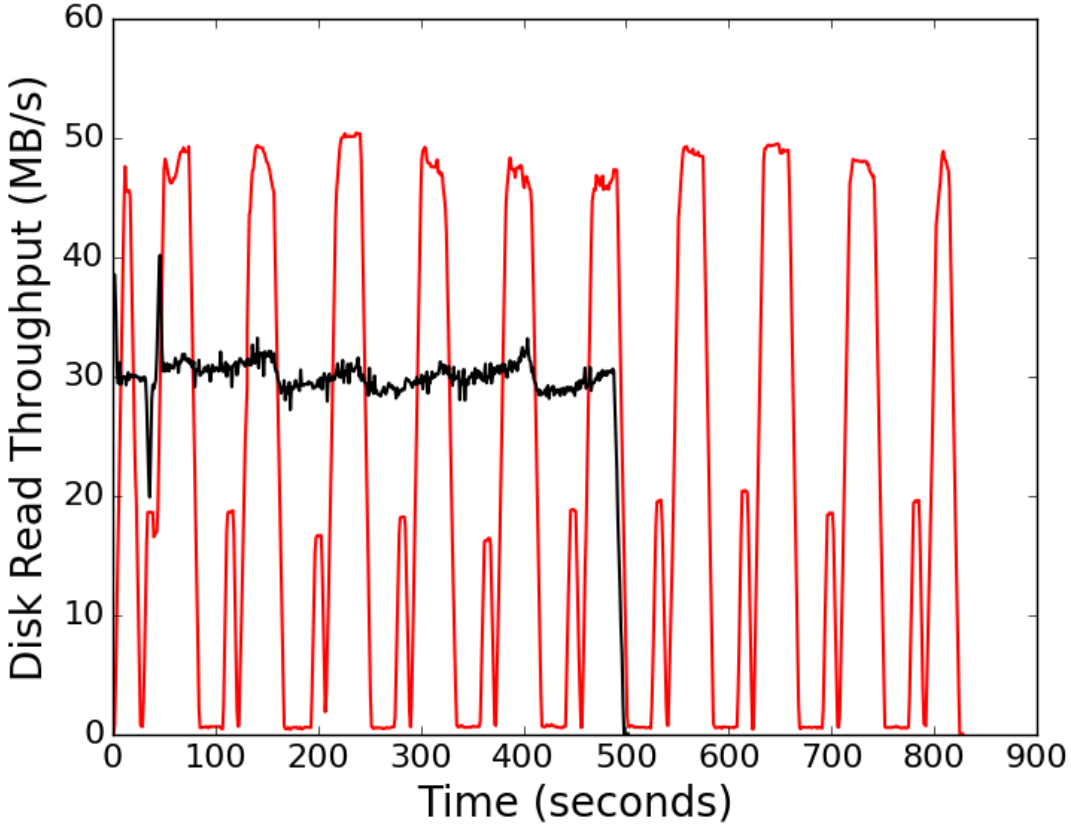
  - 2x speedup

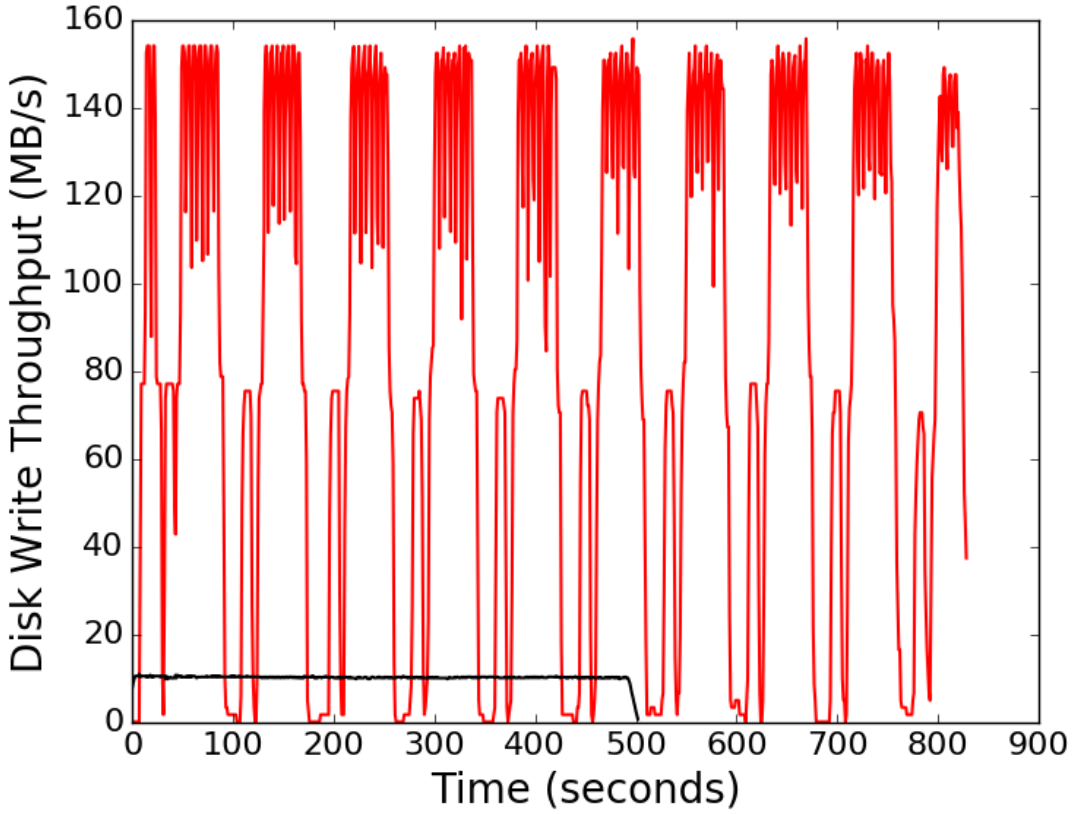
Profiling


Retiring
Bad Speculation
Frontend Bound
Backend Bound
IPC
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
3
2.5
2
1.5
1
0.5
0
IPC
429.mcf
462.libquantum
403.gcc
471.omnetpp
456.hmmer
Persona
Persona HT
Persona BWA


Memory Bound
Core Bound
100
90
80
70
60
50
40
30
20
10
0
% Bound
429.mcf
462.libquantum
403.gcc
471.omnetpp
456.hmmer
Persona
Persona HT
Persona BWA

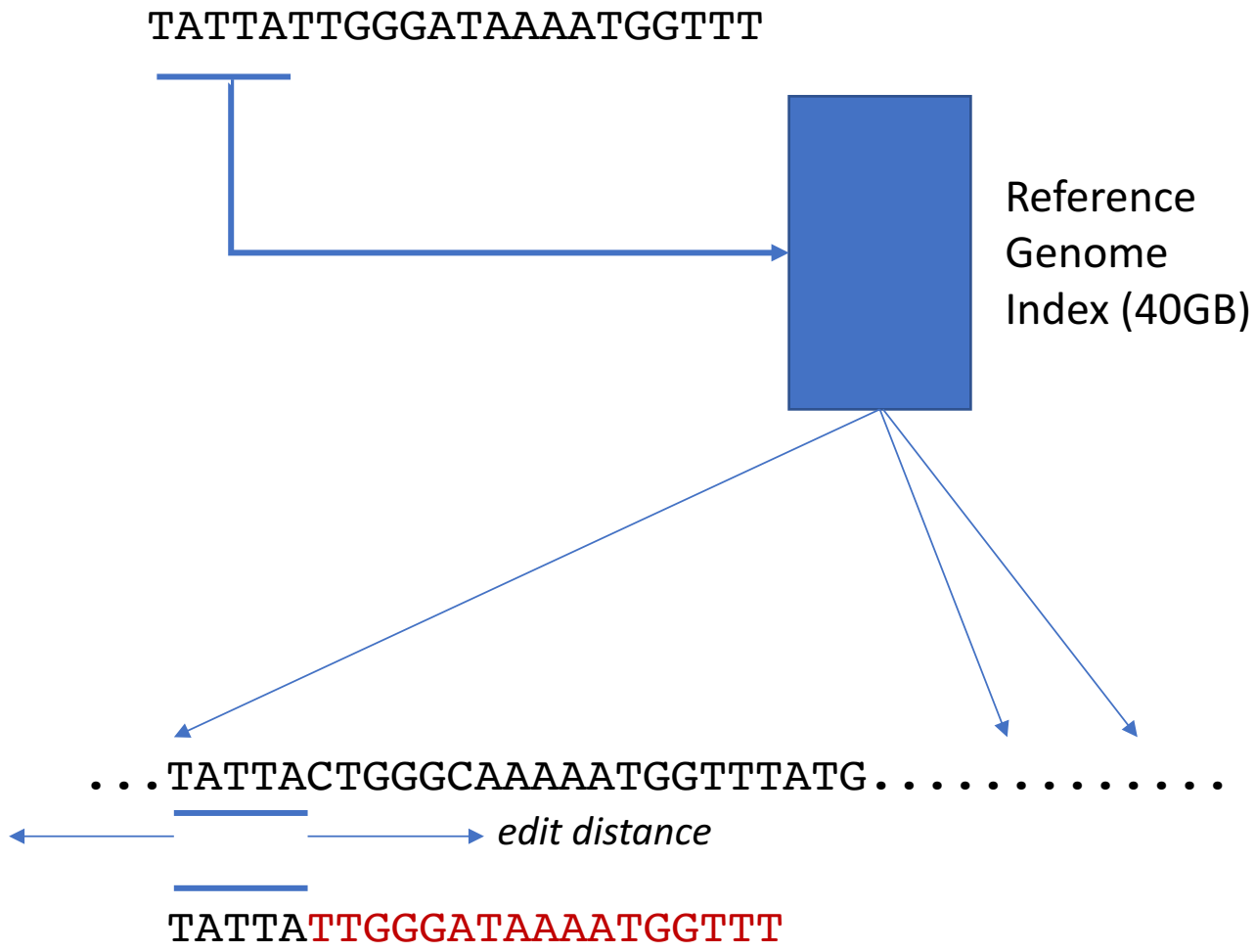
Read/Write Single Disk





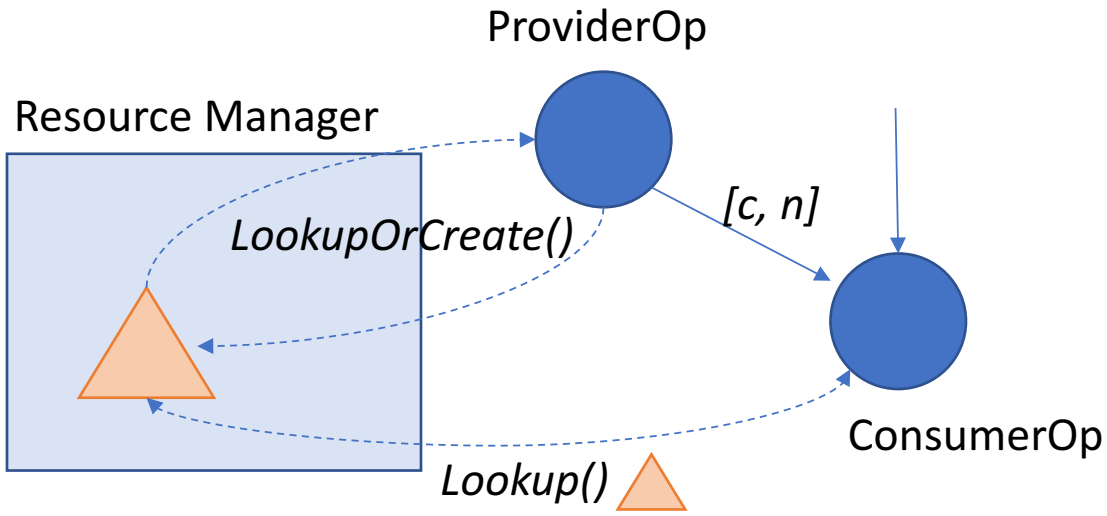
Alignment

- Example: SNAP
- Build hash index of reference
- To align a read:
  - Hash a portion (seed)
  - Lookup
    - Evaluate each hit
    - Edit distance computation
- Cores align reads in parallel



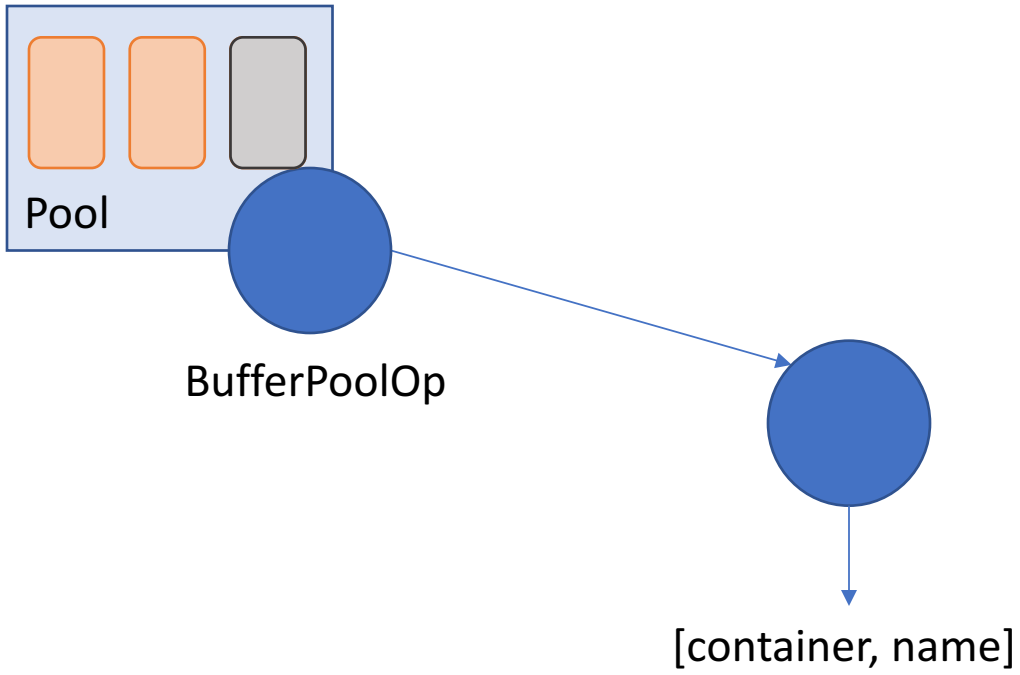
Shared Data

- Sometimes need to share data between ops
  - E.g. multi-GB index of reference genome
- Use TF session resource manager
  - [string, string] → refcount object
- Op can create objects, provide handle to other ops



Data Movement

- Tensors not amenable to bioinfo data
- Leverage TF shared resources
- Implement reusable buffers
  - Stable memory use
  - Avoid syscalls



Bioinformatics?

- Biology, computer science, math, statistics
- Started mid 90's with Human Genome Project
- Broad field
  - Genomics, proteomics, systems biology

- This talk: Whole Genome Sequence (WGS) analysis
  - Reading the letters of your DNA (ATCG …)