Scalable Solutions for DNA Sequence Analysis

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Outline

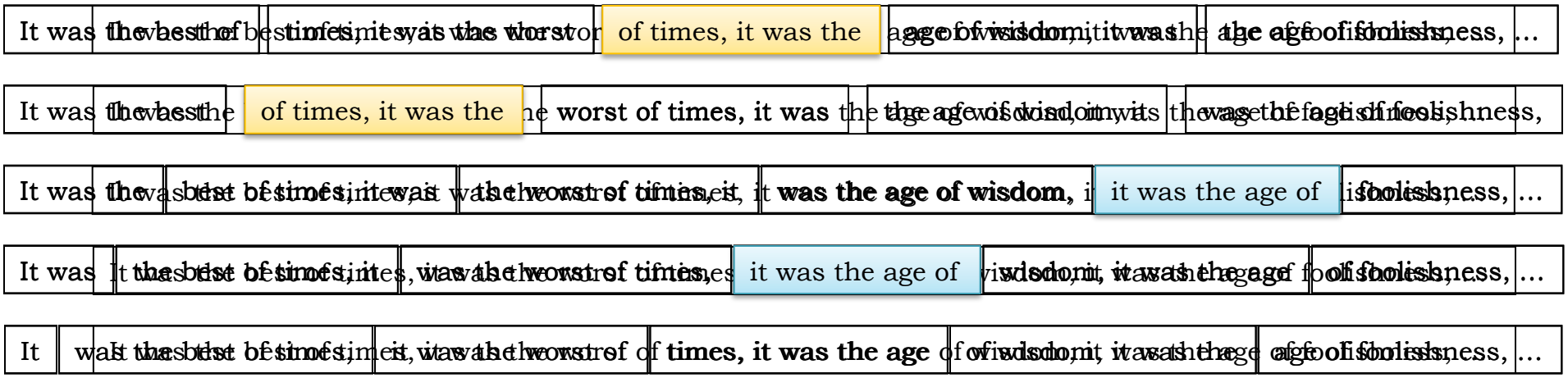
1. Genome Assembly by Analogy

2. DNA Sequencing and Genomics

3. MapReduce for Sequence Analysis
    1. K-mer counting
    2. Read Mapping & Genotyping
    3. Genome Assembly

Shredded Book Reconstruction

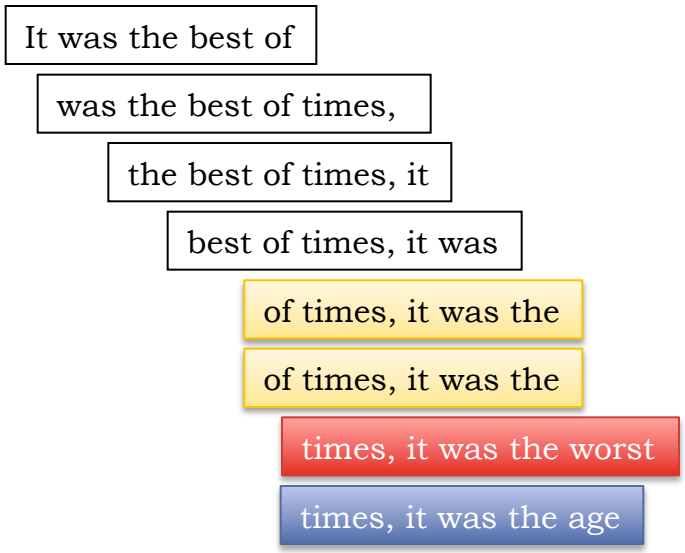
- Dickens accidentally shreds the first printing of A Tale of Two Cities
  - Text printed on 5 long spools



- How can he reconstruct the text?
  - 5 copies x 138, 656 words / 5 words per fragment = 138k fragments
  - The short fragments from every copy are mixed together
  - Some fragments are identical

Greedy Reconstruction

It was the best of
age of wisdom, it was
best of times, it was
it was the age of
it was the age of
it was the worst of
of times, it was the
of times, it was the
of wisdom, it was the
the age of wisdom, it
the best of times, it
the worst of times, it
times, it was the age
times, it was the worst
was the age of wisdom,
was the age of foolishness,
was the best of times,
was the worst of times,
wisdom, it was the age
worst of times, it was



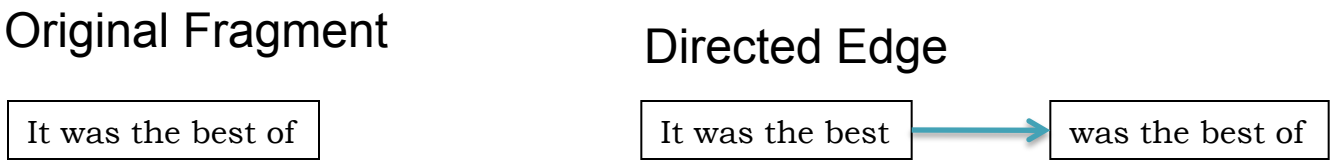
The repeated sequence make the correct reconstruction ambiguous

- It was the best of times, it was the [worst/age]

Model sequence reconstruction as a graph problem.

de Bruijn Graph Construction

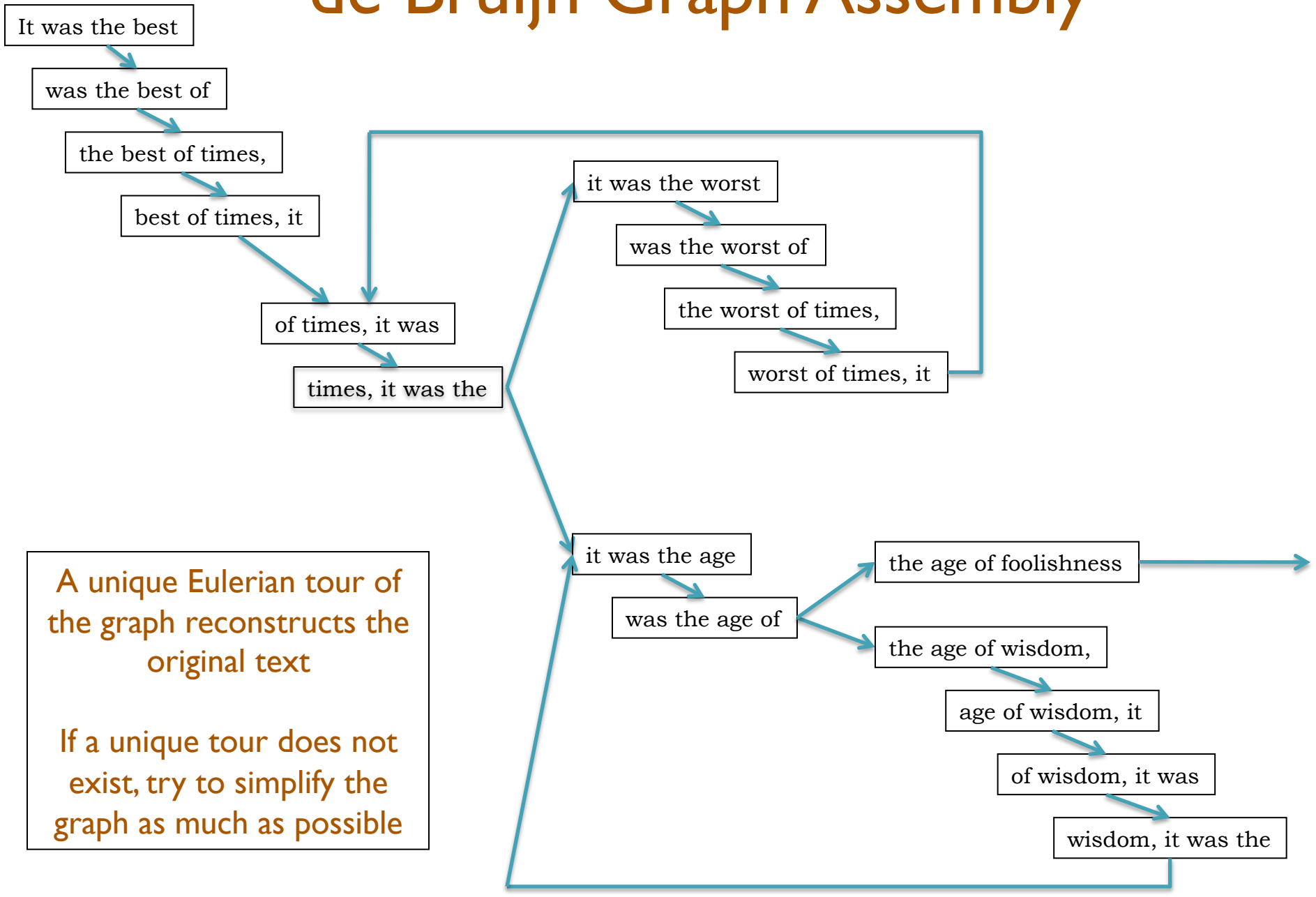
- $D_k = (V,E)$
  - V = All length-k subfragments (k < l)
  - E = Directed edges between consecutive subfragments
    - Nodes overlap by k-1 words



- Locally constructed graph reveals the global sequence structure
  - Overlaps between sequences implicitly computed

de Bruijn, 1946
Idury and Waterman, 1995
Pevzner, Tang, Waterman, 2001

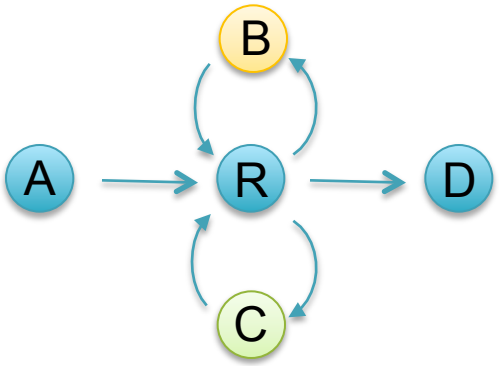
de Bruijn Graph Assembly



A unique Eulerian tour of the graph reconstructs the original text

If a unique tour does not exist, try to simplify the graph as much as possible

Counting Eulerian Tours



ARBRCRD
or
ARCRBRD

Generally an exponential number of compatible sequences

– Value computed by application of the BEST theorem (Hutchinson, 1975)

$$\mathcal{W}(G,t) = (\det L)\left\{\prod_{u\in V}(r_u-1)!\right\}\left\{\prod_{(u,v)\in E} a_{uv}!\right\}^{-1}$$

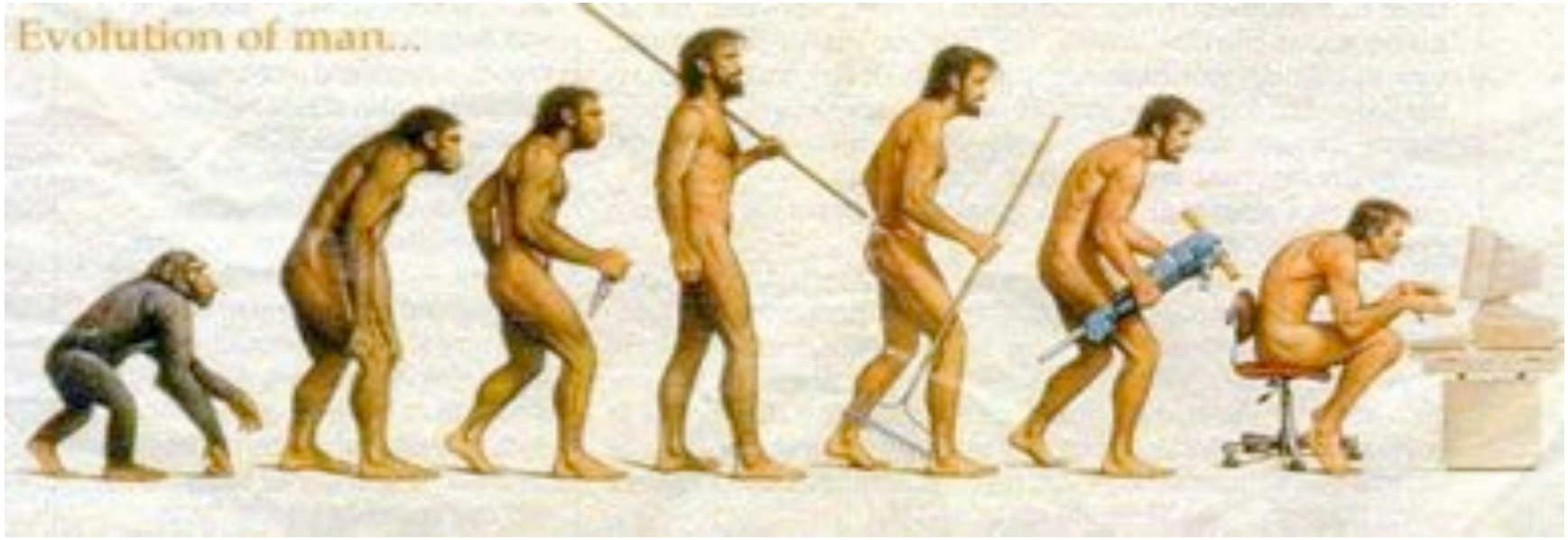
L = *n x n* matrix with r_u-a_{uu} along the diagonal and -a_{uv} in entry uv

$r_u = d^+(u)+1$ if $u=t$, or $d^+(u)$ otherwise

a_{uv} = multiplicity of edge from *u* to *v*

Assembly Complexity of Prokaryotic Genomes using Short Reads.
Kingsford C, Schatz MC, Pop M (2010) *BMC Bioinformatics*.

Genomics



Your genome influences (almost) all aspects of your life

- Anatomy & Physiology: 10 fingers & 10 toes, organs, neurons
- Diseases: Sickle Cell Anemia, Down Syndrome, Cancer
- Psychological: Intelligence, Personality, Bad Driving

Your environment also influences your life

- Genome as a recipe, not a blueprint

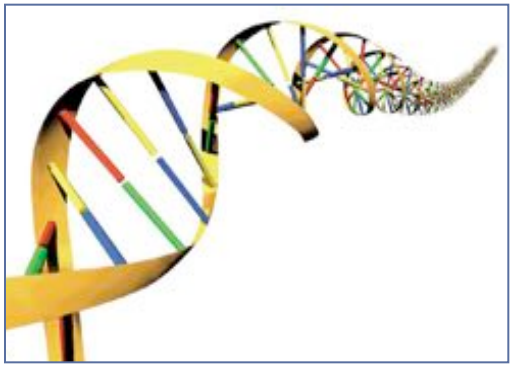
Genomics across the Tree of Life

Selected Genomes

- *M. gallopavo* (Folkerts *et al.*, 2010*)
- *A. dorsata* (Ruepell *et al.*, 2010*)
- *V. destructor* (Cornman *et al.*, 2010*)
- *N. ceranae* (Cornman *et al.*, 2009)
- *B. taurus* (Zimin *et al.*, 2009)
- *C. papaya* (Ming *et al.*, 2008)
- *X. oryzae* (Salzberg *et al.*, 2008)
- *T. vaginalis* (Carlton *et al.*, 2007)
- Drosophila (Drosophila 12 genomes consortium, 2007)
- *B. malayi* (Ghedin *et al.*, 2007)
- *A. aegypti* (Nene *et al.*, 2007)
- Campylobacter (Fouts *et al.*, 2005)

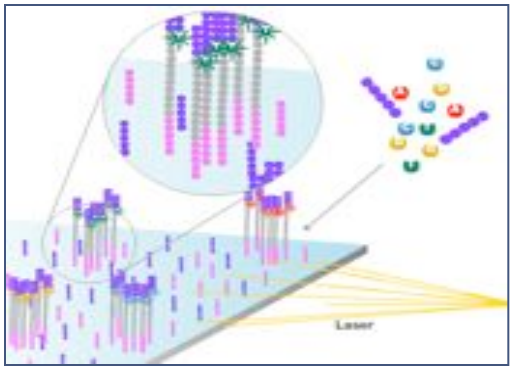
* In preparation or under review

DNA Sequencing



Genome of an organism encodes the genetic information in long sequence of 4 DNA nucleotides: ACGT

- Bacteria: ~3 million bp
- Humans: ~3 billion bp



Current DNA sequencing machines can generate 1-2 Gbp of sequence per day, in millions of short reads

- Per-base error rate estimated at 1-2% (Simpson *et al*, 2009)
- Sequences originate from random positions of the genome

ATCTGATAAGTCCCAGGACTTCAGT

GCAAGGCAAACCCGAGCCCAGTTT

TCCAGTTCTAGAGTTTCACATGATC

GGAGTTAGTAAAAGTCCACATTGAG

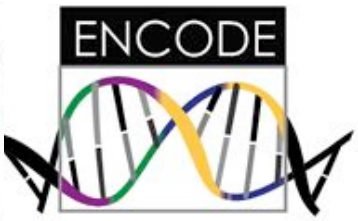
Recent studies of entire human genomes analyzed 3.3B (Wang, et al., 2008) & 4.0B (Bentley, et al., 2008) 36bp reads

- ~100 GB of compressed sequence data

The Evolution of DNA Sequencing

Year	Genome	Technology	Cost
2001	Venter *et al.*	Sanger (ABI)	$300,000,000
2007	Levy *et al.*	Sanger (ABI)	$10,000,000
2008	Wheeler *et al.*	Roche (454)	$2,000,000
2008	Ley *et al.*	Illumina	$1,000,000
2008	Bentley *et al.*	Illumina	$250,000
2009	Pushkarev *et al.*	Helicos	$48,000
2009	Drmanac *et al.*	Complete Genomics	$4,400

(Pushkarev *et al.*, 2009)



Critical Computational Challenges: Alignment and Assembly of Huge Datasets

Hadoop MapReduce

- MapReduce is the parallel distributed framework invented by Google for large data computations.
  - Data and computations are spread over thousands of computers, processing petabytes of data each day (Dean and Ghemawat, 2004)
  - Indexing the Internet, PageRank, Machine Learning, etc…
  - Hadoop is the leading open source implementation

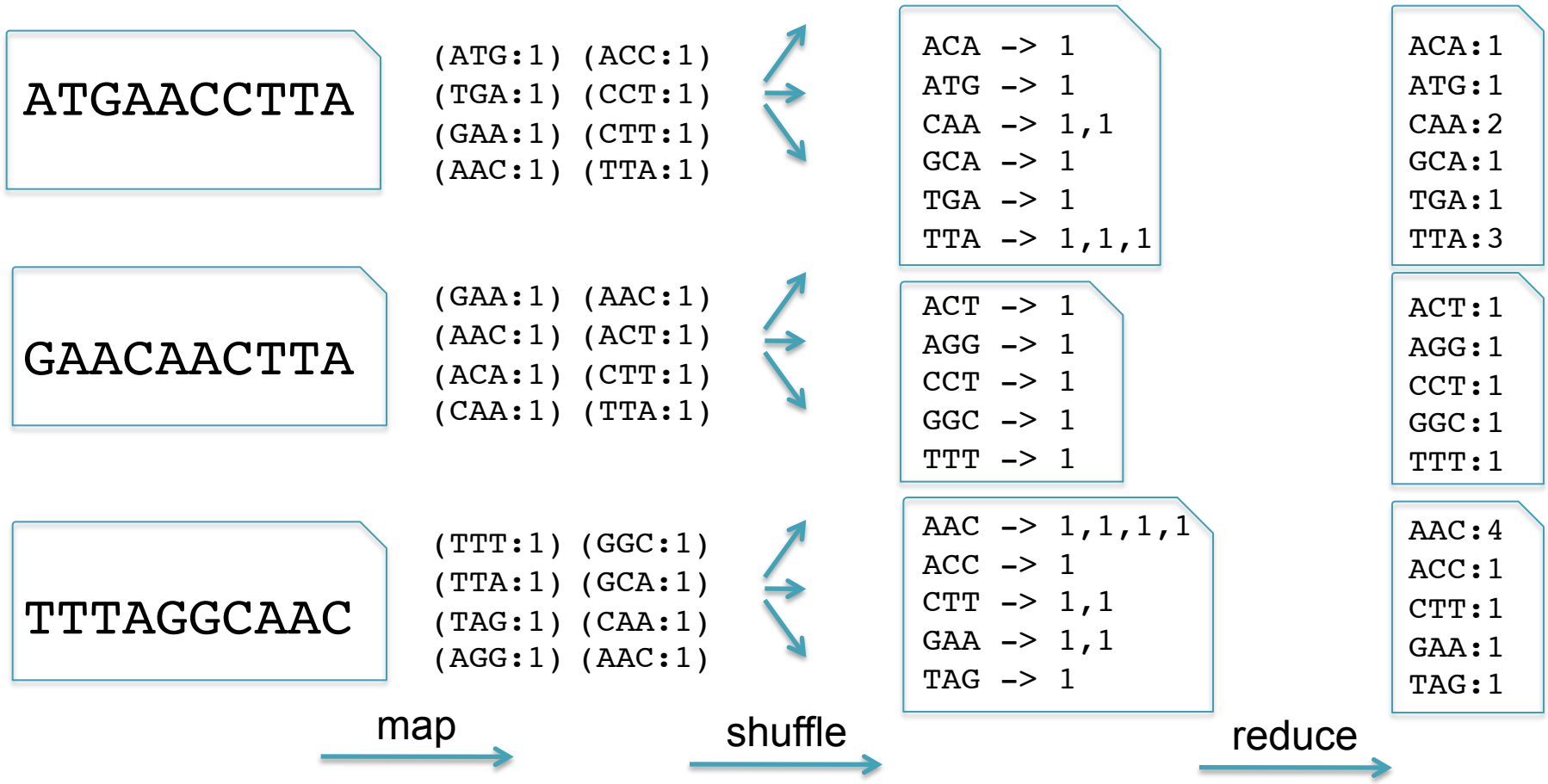
- Benefits
  - Scalable, Efficient, Reliable
  - Easy to Program
  - Runs on commodity computers

- Challenges
  - Redesigning / Retooling applications
    - Not Condor, Not MPI
    - Everything in MapReduce

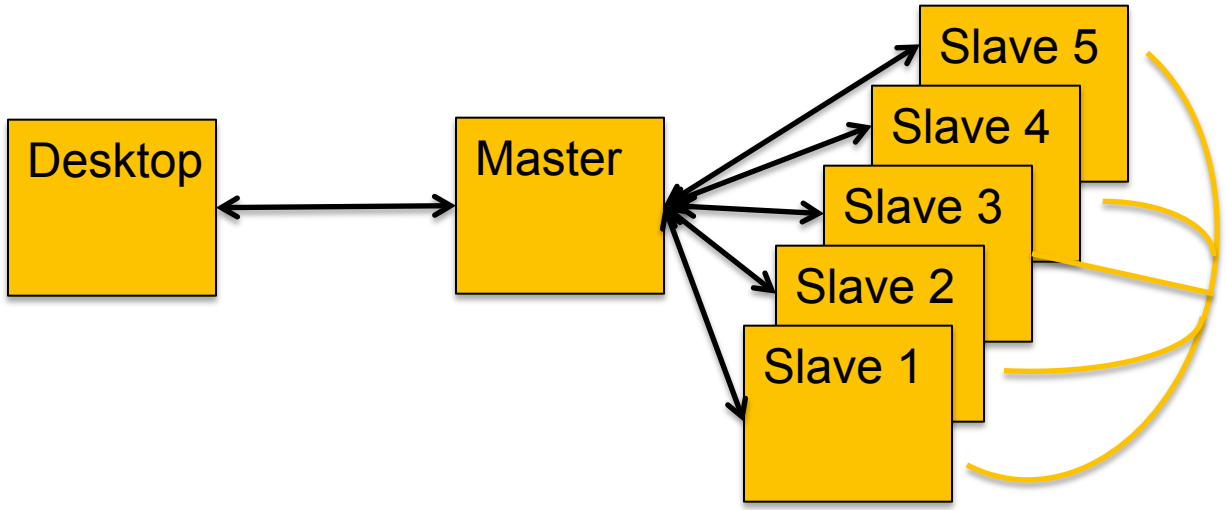
K-mer Counting

- Application developers focus on 2 (+1 internal) functions
  - Map: input ➔ key:value pairs
  - Shuffle: Group together pairs with same key
  - Reduce: key, value-lists ➔ output

Map, Shuffle & Reduce
All Run in Parallel

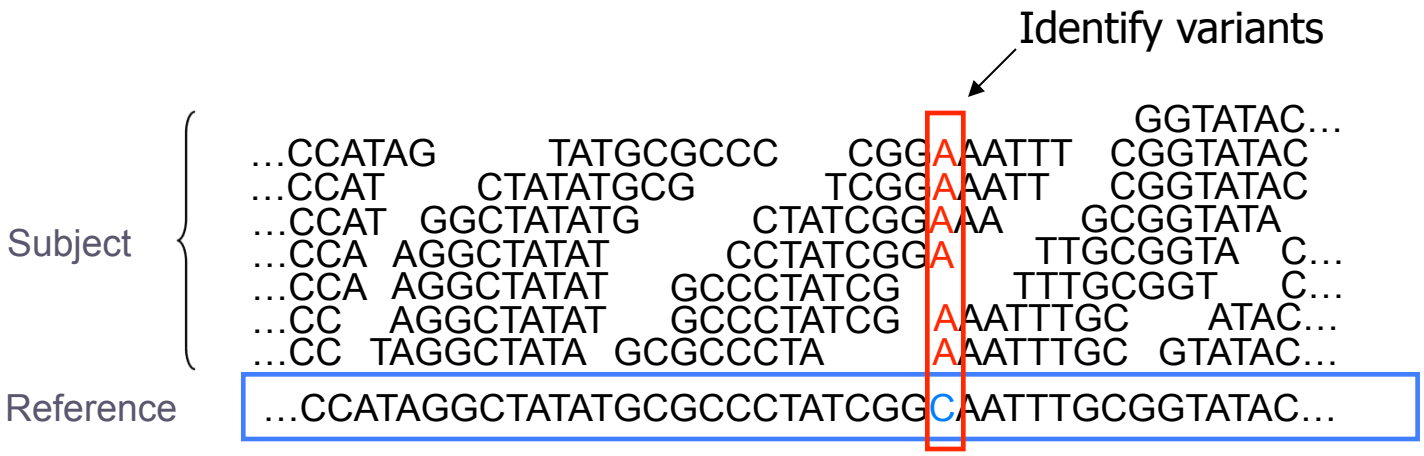


Hadoop Architecture



- Hadoop Distributed File System (HDFS)
  - Data files partitioned into large chunks (64MB), replicated on multiple nodes
  - NameNode stores metadata information (block locations, directory structure)
- Master node (JobTracker) schedules and monitors work on slaves
  - Computation moves to the data, rack-aware scheduling
- Hadoop MapReduce system won the 2009 GreySort Challenge
  - Sorted 100 TB in 173 min (578 GB/min) using 3452 nodes and 4x3452 disks

Short Read Mapping



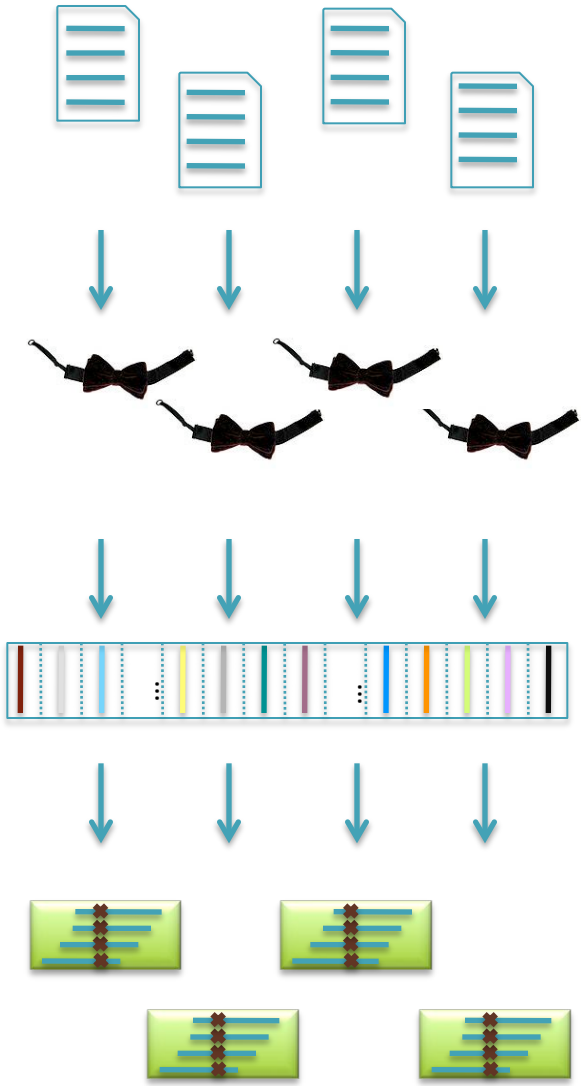
- Given a reference and many subject reads, report one or more "good" end-to-end alignments per alignable read
  - Find where the read most likely originated
  - Fundamental computation for many assays
    - Genotyping
    - Structural Variations
    - RNA-Seq
    - Chip-Seq
    - Methyl-Seq
    - Hi-C-Seq

- Desperate need for scalable solutions
  - Single human requires >1,000 CPU hours / genome

Crossbow

http://bowtie-bio.sourceforge.net/crossbow

- Align billions of reads and find SNPs
  - Reuse software components: Hadoop Streaming
- Map: Bowtie (Langmead *et al.*, 2009)
  - Find best alignment for each read
  - Emit (chromosome region, alignment)
- Shuffle: Hadoop
  - Group and sort alignments by region
- Reduce: SOAPsnp (Li *et al.*, 2009)
  - Scan alignments for divergent columns
  - Accounts for sequencing error, known SNPs



Performance in Amazon EC2

http://bowtie-bio.sourceforge.net/crossbow

	Asian Individual Genome		
Data Loading	3.3 B reads	106.5 GB	$10.65
Data Transfer	1h :15m	40 cores	$3.40
Setup	0h : 15m	320 cores	$13.94
Alignment	1h : 30m	320 cores	$41.82
Variant Calling	1h : 00m	320 cores	$27.88
End-to-end	4h : 00m		$97.69

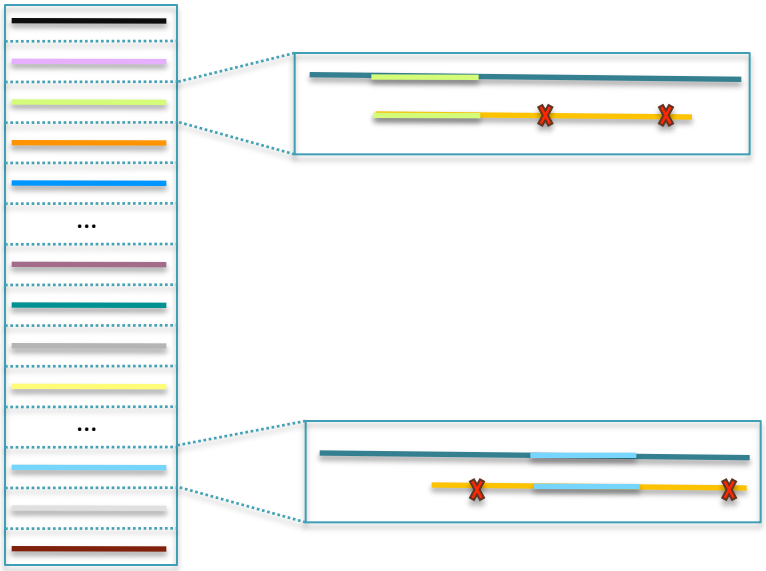
Analyze an entire human genome for ~$100 in an afternoon.
Accuracy validated at >99%

Searching for SNPs with Cloud Computing.
Langmead B, Schatz MC, Lin J, Pop M, Salzberg SL (2009) *Genome Biology.*

Related Approaches

CloudBurst

Highly Sensitive Short Read Mapping with MapReduce

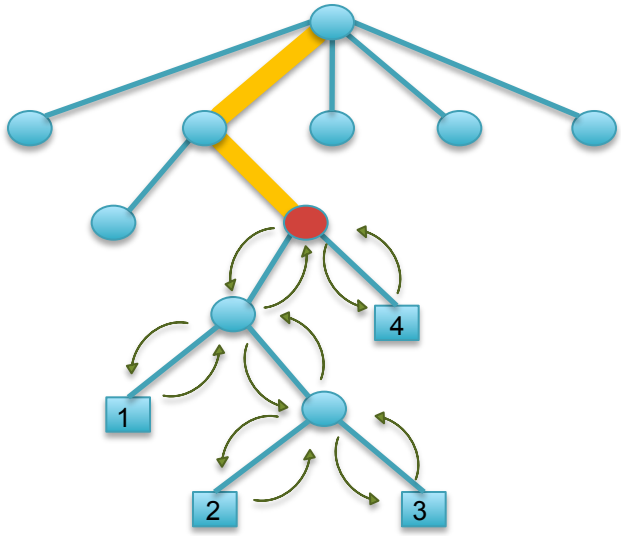


100x speedup on 96 cores @ Amazon

(Schatz, 2009)

MUMmerGPU

High Throughput Sequence Alignment using GPGPUs



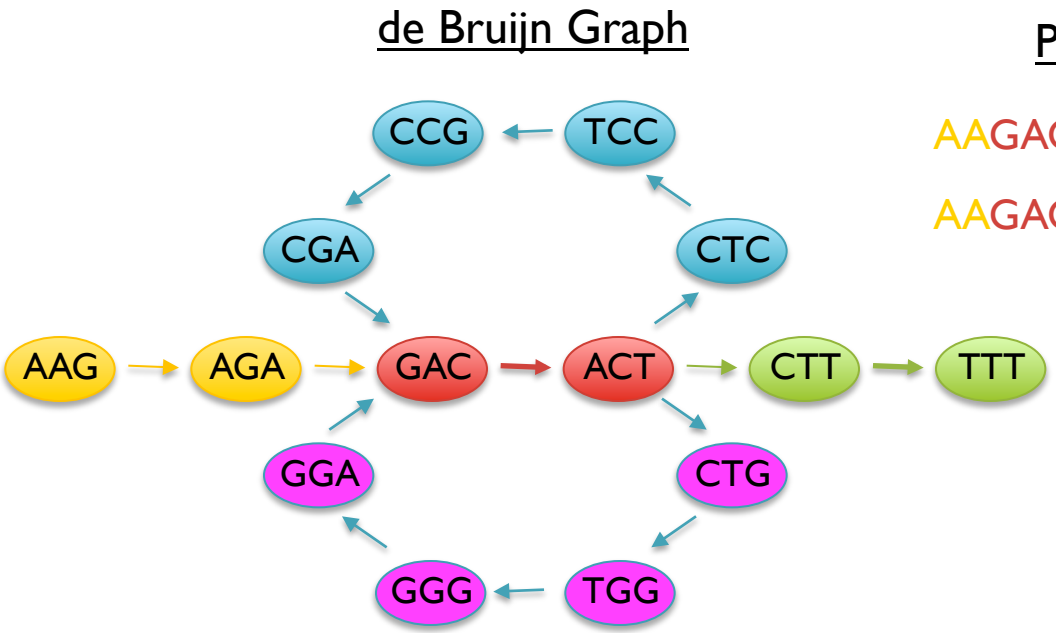
~10x speedup on nVidia GTX 8800

(Schatz, Trapnell, *et al.*, 2007)
(Trapnell & Schatz, 2008)

Short Read Assembly

Reads

AAGA
ACTT
ACTC
ACTG
AGAG
CCGA
CGAC
CTCC
CTGG
CTTT
…



Potential Genomes

AAGACTCCGACTGGGACTTT

AAGACTGGGACTCCGACTTT

- Genome assembly as finding an Eulerian tour of the de Bruijn graph
  - Human genome: >3B nodes, >10B edges
- The new short read assemblers require tremendous computation
  - Velvet (Zerbino & Birney, 2008) serial: > 2TB of RAM
  - ABySS (Simpson *et al.*, 2009) MPI: 168 cores x ~96 hours
  - SOAPdenovo (Li *et al.*, 2010) pthreads: 40 cores x 40 hours, >140 GB RAM

K-mer Counting

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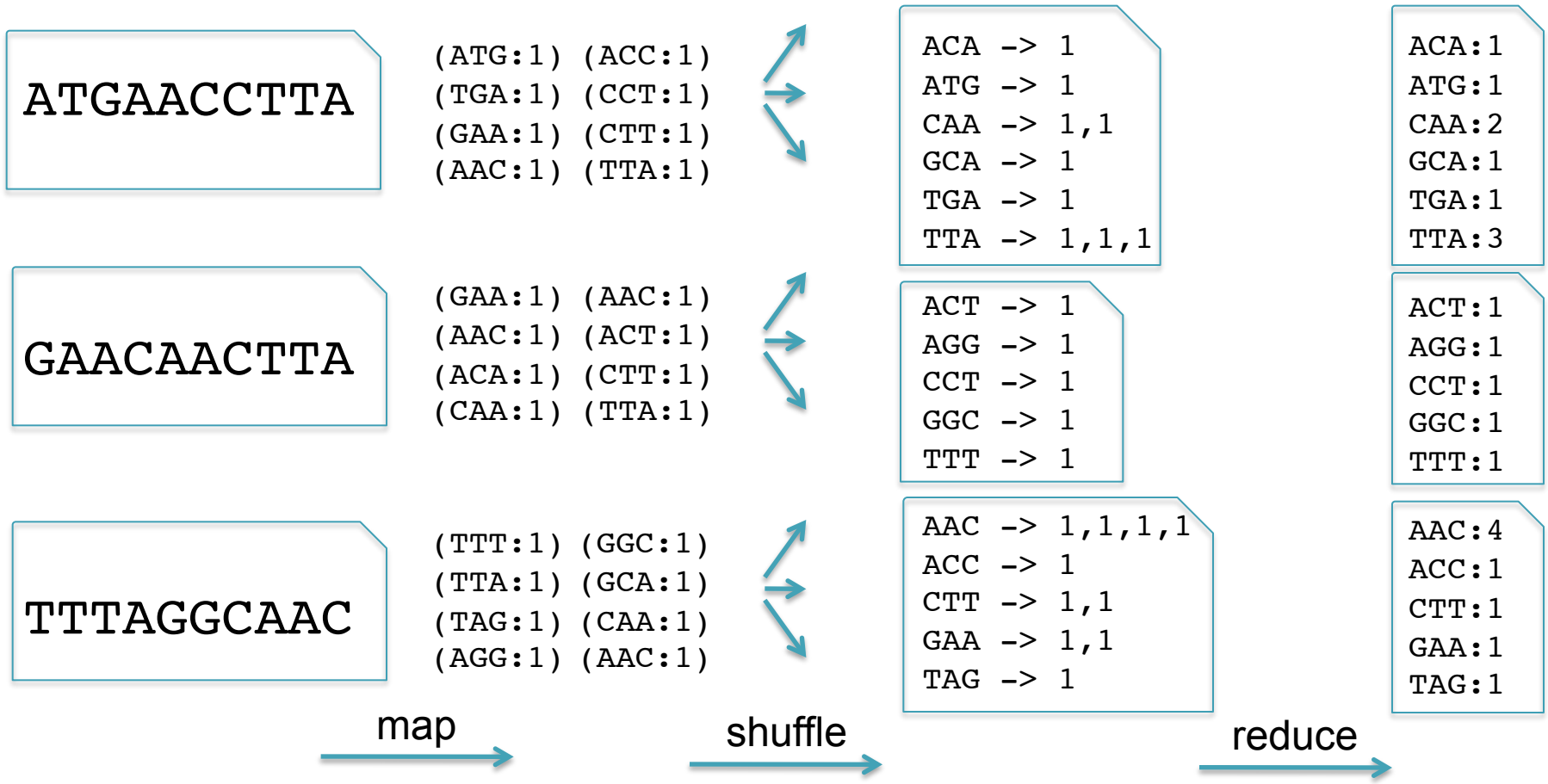
  - Map: input ➔ key:value pairs
  - Shuffle: Group together pairs with same key
  - Reduce: key, value-lists ➔ output

Map, Shuffle & Reduce
All Run in Parallel



Graph Construction

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Map, Shuffle & Reduce
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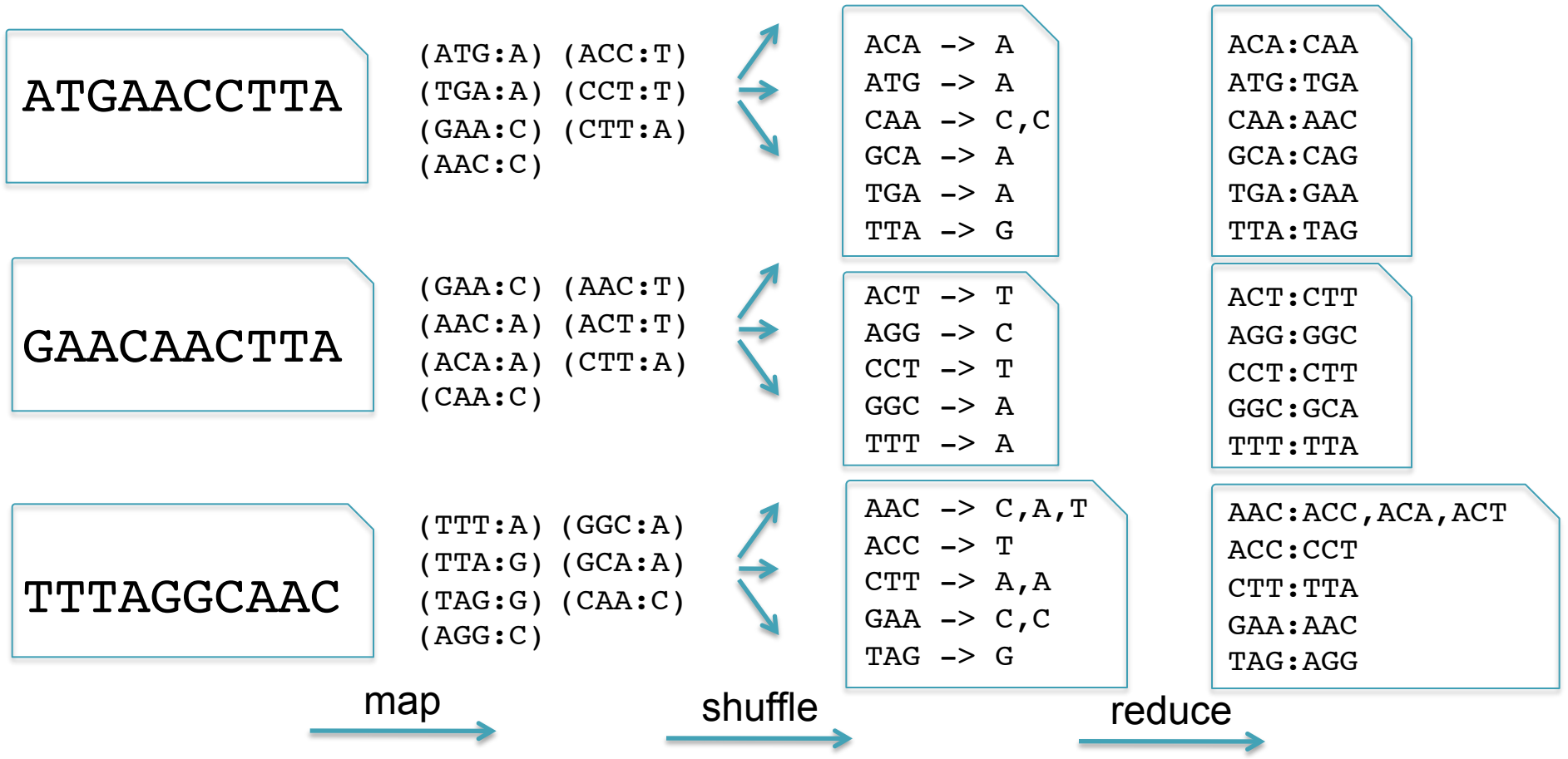
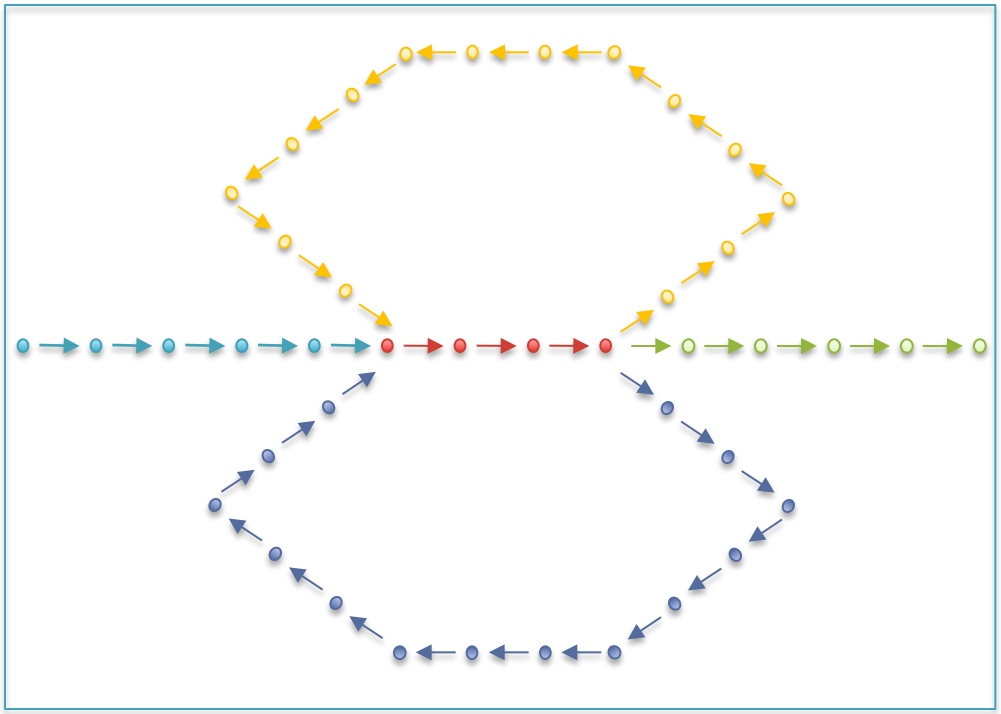
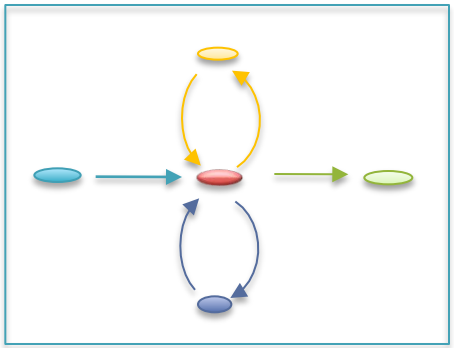


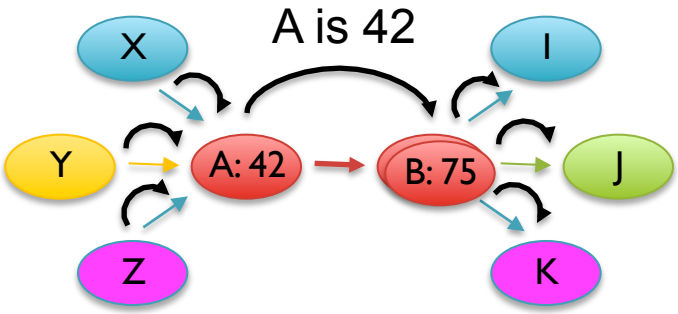
Graph Compression

- After construction, many edges are unambiguous
  - Merge together compressible nodes
  - Graph physically distributed over hundreds of computers





Distributed Graph Processing



MapReduce
Message Passing

Input:

– Graph stored as node tuples

```
A: (N E:B W:42)
B: (N E:I,J,K W:33)
```

Map

– For all nodes, re-emit node tuple

– For all neighbors, emit value tuple

```
A: (N E:B W:42)
B: (V A 42)
B: (N E:I,J,K W:33)
…
```

Shuffle

– Collect tuples with same key

```
B: (N E:I,J,K W:33)
B: (V A 42)
```

Reduce

– Add together values, save updated node tuple

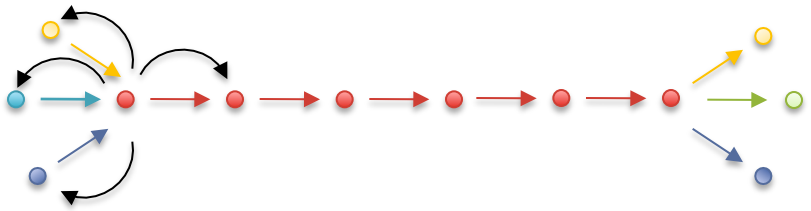
```
B: (N E:I,J,K W:75)
```

Iterative Path Compression

Iteratively identify and collapse the beginning of each chain

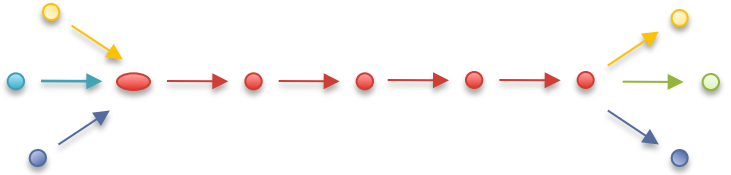
Map:

- Emit messages to the neighbors of the head of each chain



Reduce:

- Update links, node label



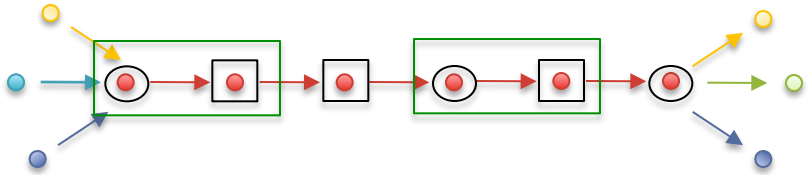
Requires S MapReduce cycles, where S is the length of the longest simple path

- *B. anthracis*: L=5.2Mbp S=268,925
- *H. sapiens* chr 22: L=49.6Mbp S=33,832
- *H. sapiens* chr 1: L=247.2Mbp S=37,172

Fast Path Compression

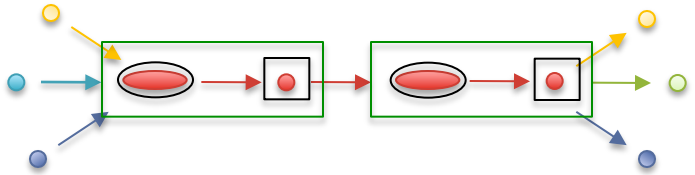
Challenges

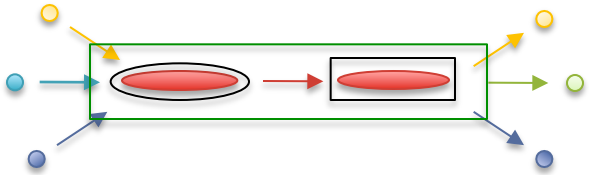
- Nodes stored on different computers
- Nodes can only access direct neighbors



Randomized List Ranking

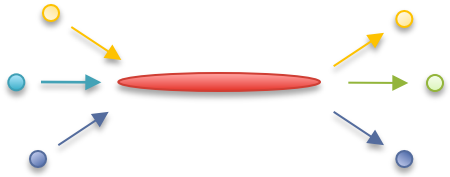
- Randomly assign Ⓗ / T to each compressible node
- Compress Ⓗ → T links





Performance

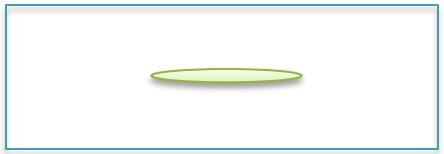
- Compress all chains in log(S) rounds (<20)
- If <1024 nodes to compress (from any number of chains), assign them all to the same reducer (save 10 rounds)



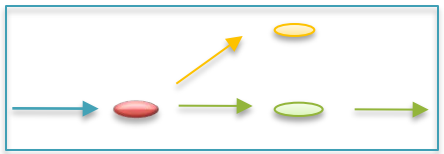
Randomized Speed-ups in Parallel Computation.
Vishkin U. (1984) *ACM Symposium on Theory of Computation. 230-239.*

Node Types

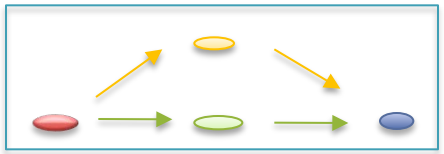
(Chaisson, 2009)



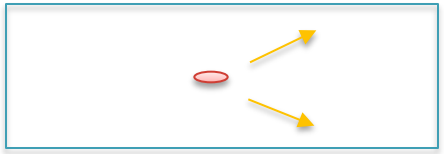
Isolated nodes (10%)
- Contamination



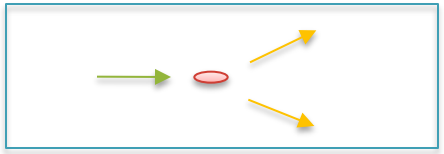
Tips (46%)
- Clip short tips



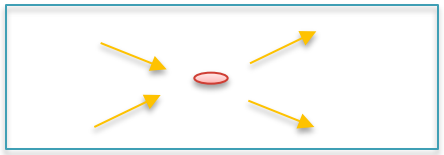
Bubbles/Non-branch (9%)
- Pop bubbles



Dead Ends (.2%)
- Split forks



Half Branch (25%)
- Unzip



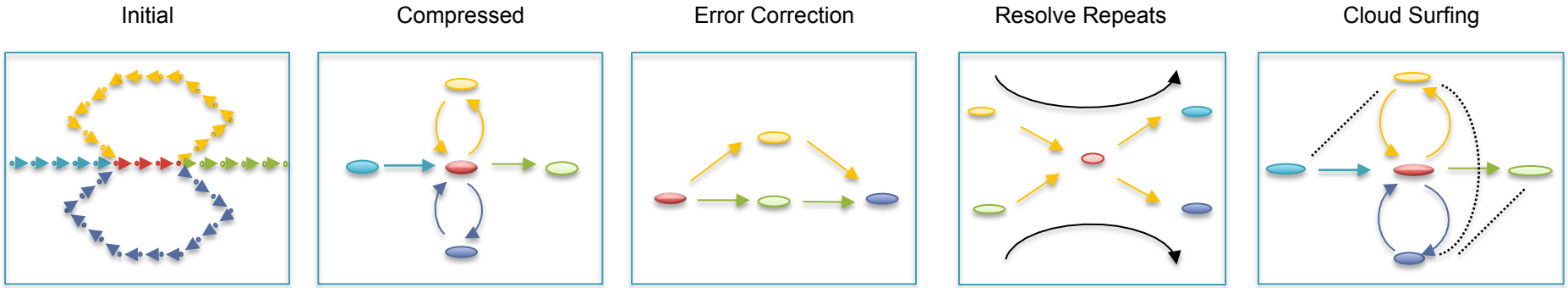
Full Branch (10%)
- Thread reads, cloud surfing

Contrail

http://contrail-bio.sourceforge.net

Scalable Genome Assembly with MapReduce

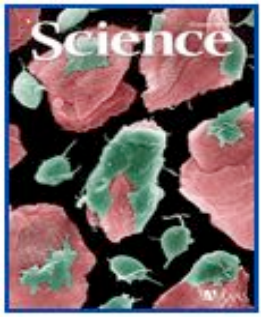
- *Genome: E. coli* 4.6Mbp bacteria
- *Input: 20*M 36bp reads, 200bp insert
- *Preprocessor*: Quality-Aware Error Correction



N	5.1 M	245,131	2,769	1,909	300
Max	27 bp	1,079 bp	70,725 bp	90,088 bp	149,006 bp
N50	27 bp	156 bp	15,023 bp	17,058 bp	54,807 bp

Assembly of Large Genomes with Cloud Computing.
Schatz MC, Sommer D, Kelley D, Pop M, *et al. In Preparation.*

Selected Related Work



AutoEditor & AutoJoiner

Improving Genome Assemblies without Resequencing

(Gajer, Schatz, Salzberg, 2004)
(Carlton *et al.*, 2007)

PhyloTrac

Integrated survey analysis of prokaryotic communities

(Schatz, Phillippy, et al., 2010*)

Hawkeye

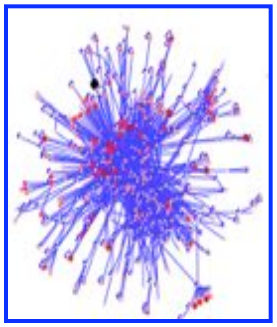
Assembly Visualization & Analytics

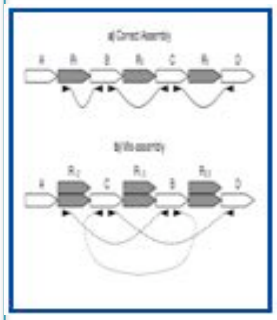
(Schatz, Phillippy, Shneiderman, Salzberg, 2007)

Graph Summarization

Revealing Biological Modules via Graph Summarization.

(Navlakha, Schatz, Kingsford, 2008)





Assembly Forensics

Finding the Elusive Mis-assembly

(Phillippy, Schatz, Pop, 2008)

Transgenic Hunt

Characterization of Insertion Sites in Rainbow Papaya

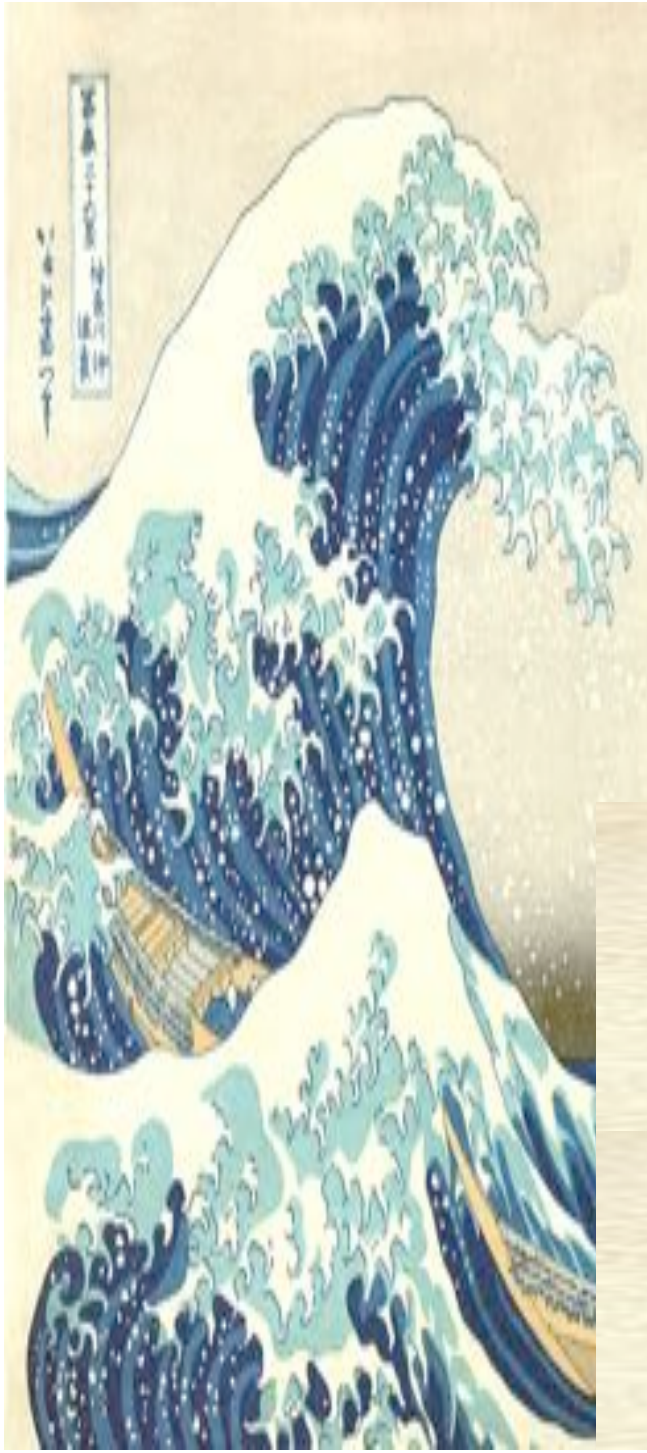
(Suzuki et al., 2008)

Research Directions

- Scalable Sequencing
  - Genomes, Metagenomes, *-Seq, Personalized Medicine
  - How do we survive the tsunami of sequence data?
    - Efficient indexing & algorithms, multi-core & multi-disk systems

- Practically Parallel
  - Managing n-tier memory hierarchies, crossing the PRAM chasm
  - How do we solve problems with 1000s of cores?
    - Locality, Fault Tolerance, Programming Languages & Parallel Systems

- Computational Discovery
  - Abundant data and computation are necessary, but not sufficient
  - How do we gain insight?
    - Modeling, Machine Learning, Databases, Visualization & HCI



Summary

"NextGen sequencing has completely outrun the ability of good bioinformatics people to keep up with the data and use it well… We need a MASSIVE effort in the development of tools for 'normal' biologists to make better use of massive sequence databases."

Jonathan Eisen – JGI Users Meeting – 3/28/09

- Computational Biology
  - Make the problems of genotyping and assembly of large genomes from short reads feasible and accessible to individual researchers
- High Performance Computing
  - Developed Novel Parallel Algorithms for MapReduce and Multicore systems

Acknowledgements

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Steven Salzberg

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CBCB Students

Adam Phillippy, Cole Trapnell,
Saket Navlakha, Ben Langmead,
James White, David Kelley

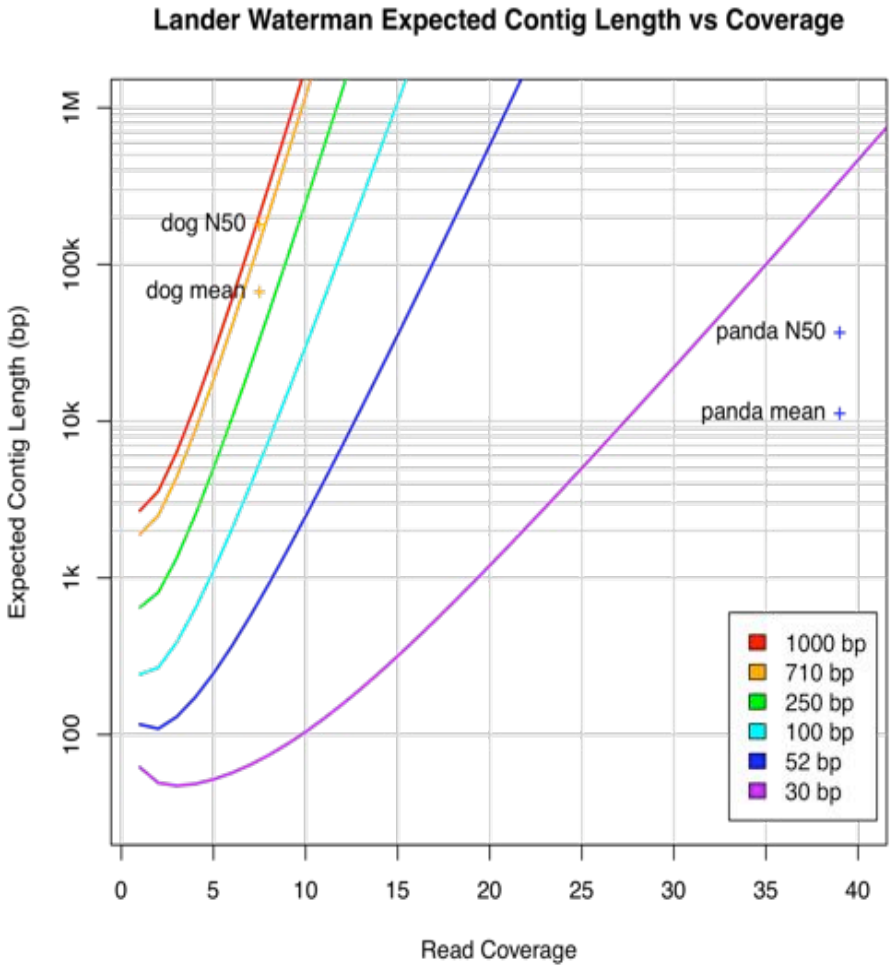
Thank You!

http://www.cbcb.umd.edu/~mschatz

Genome Coverage

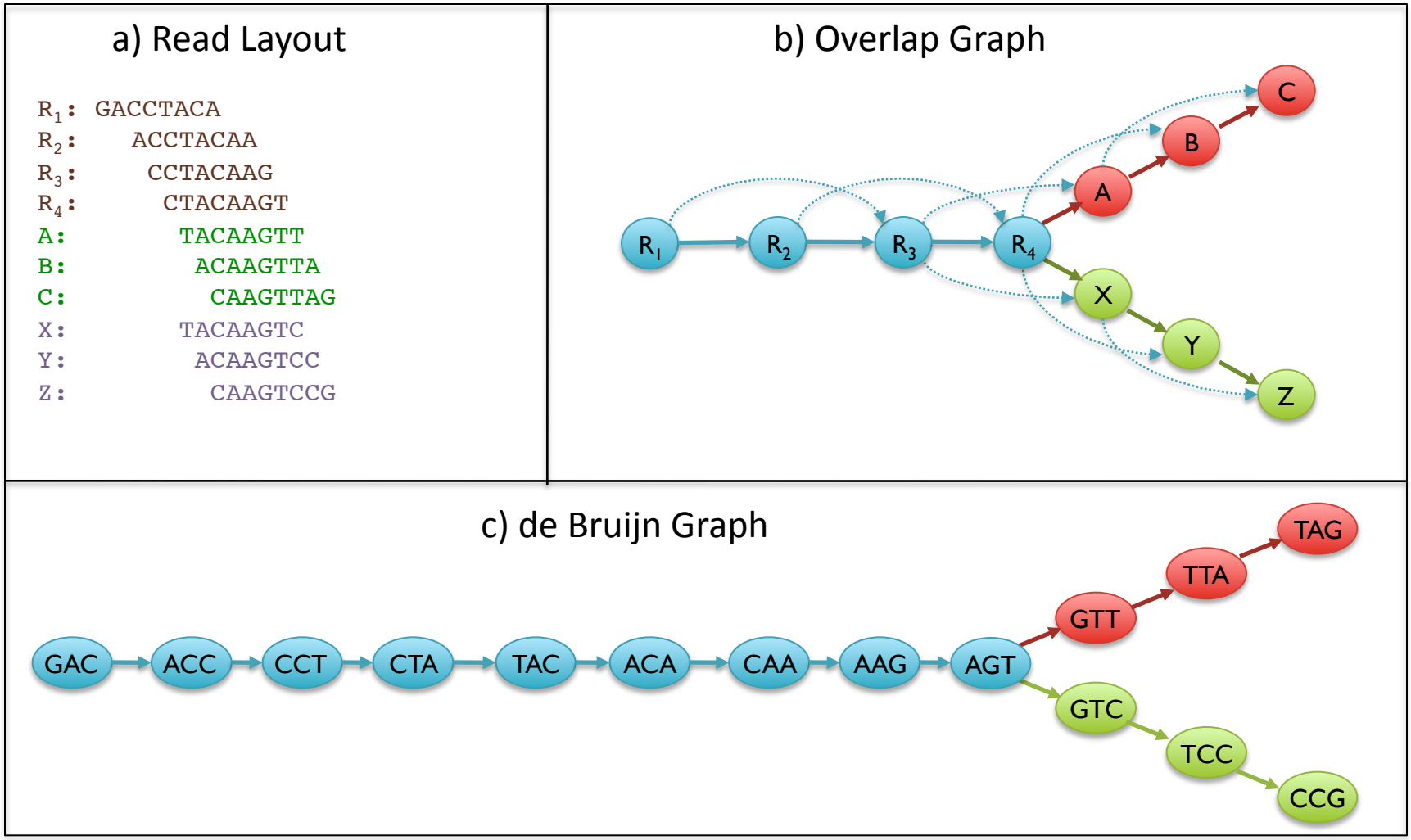
Idealized assembly

- Uniform probability of a read starting at a given position
  - p = G/N
- Poisson distribution in coverage along genome
  - Contigs end when there is no overlapping read
- Contig length is a function of coverage and read length
  - Short reads require much higher coverage



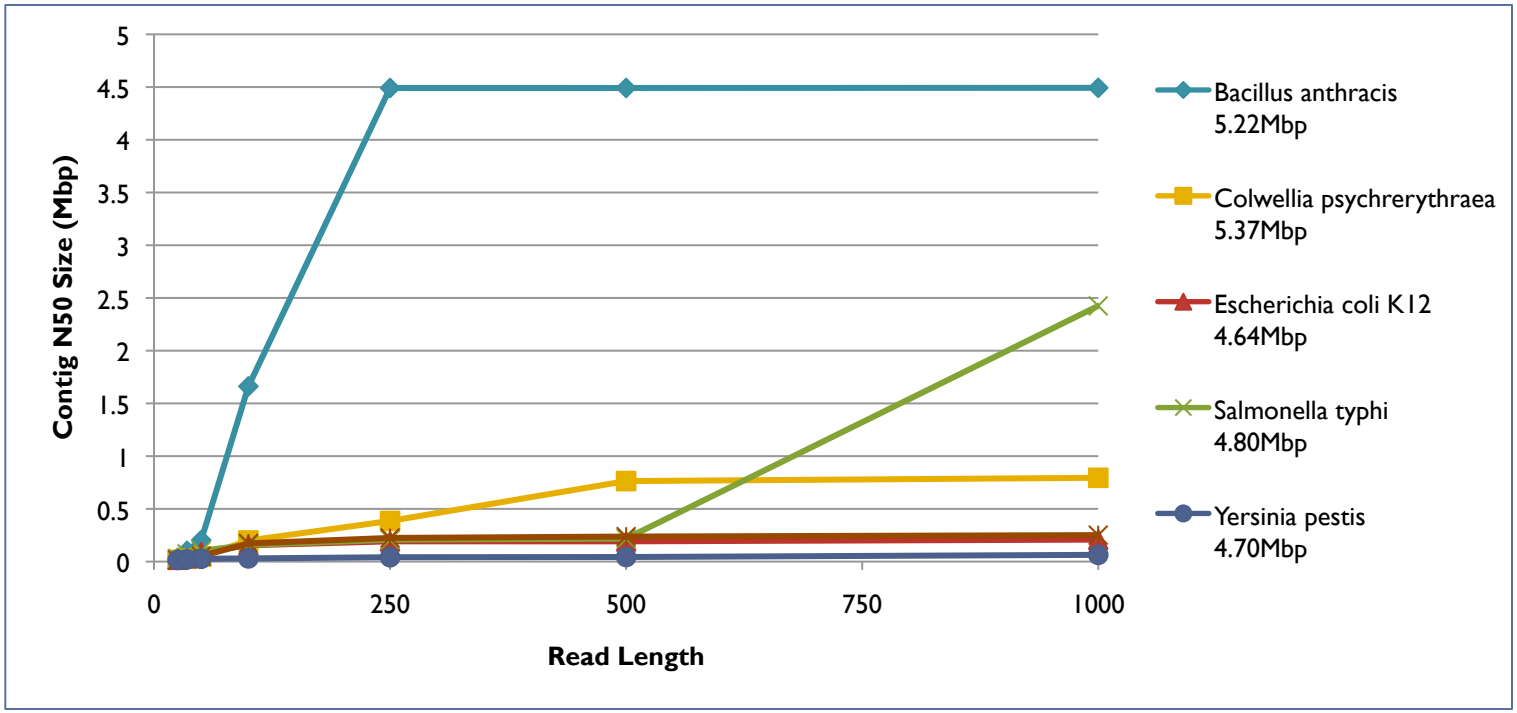
Large-Scale Genome Assembly from Short Reads.
Schatz MC, Delcher AL, Salzberg SL (2010) *Manuscript Under Review.*

Two Paradigms for Assembly



Large-Scale Genome Assembly from Short Reads.
Schatz MC, Delcher AL, Salzberg SL (2010) *Manuscript Under Review.*

Short Reads and Mate-pairs



- Explore the relationship between read length and contig N50 size
  - Perfect reads, lengths: 25, 35, 50, 100, 250, 500, 1000
  - Long reads are limiting case for short mated reads, perfectly compute the insert sequence

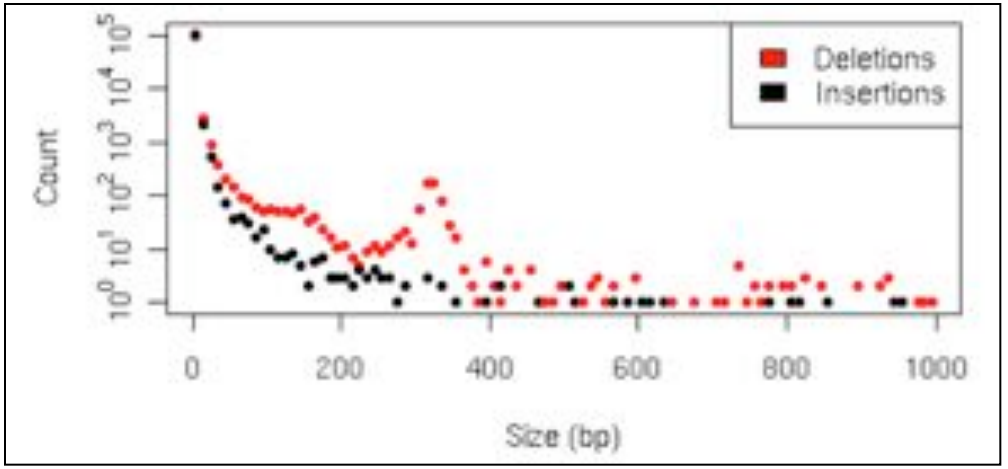
Assembly Complexity of Prokaryotic Genomes using Short Reads.
Kingsford C, Schatz MC, Pop M (2010) *BMC Bioinformatics*.

ABySS Results

- Assemble 42x 36bp reads
- Mate pairs double the size of the contigs
  - Insert size 210bp
- Identify 100k insertions and deletions
  - Pronounced deletion peak corresponds to *Alu* family of retrotransposons

Table 3. Assembly statistics for data from the NA18507 Yoruba individual

Contig Statistics	$k = 27$, Without Paired-End Information		$k = 27$, With Paired-End Information	
	Contigs ≥100bp	Contigs ≥1,000bp	Contigs ≥100bp	Contigs ≥1,000bp
# Contigs	4,348,132	549,522	2,762,173	680,203
Median size (bp)	253	1,463	435	1,696
Mean size (bp)	484	1,703	791	2,093
Max. size (bp)	15,911	15,911	18,800	18,800
N50 size	870	1,731	1,499	2,282
# Contigs > N50	674,953	188,171	408,890	202,166
Sum (Gbp)	2.10	0.94	2.18	1.42



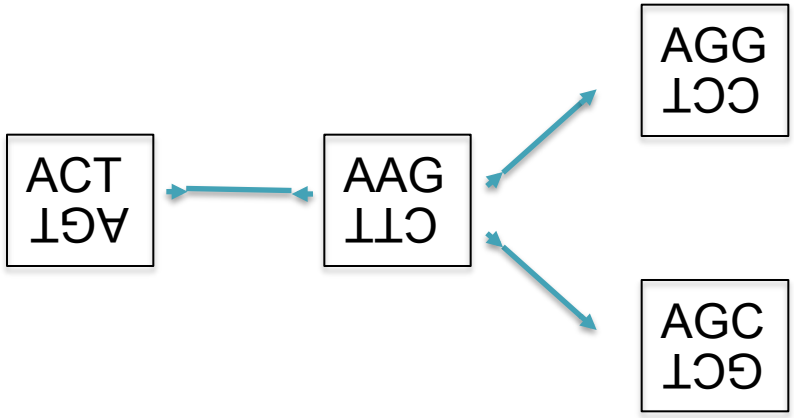
Bidirectional de Bruijn Graph

- Designate a representative mer for each mer/rc(mer) pair
  - Use the lexigraphically smaller mer

- Bidirected edges record if connection is between forward or reverse mer

- In practice, keep separate adjacency lists for the forward and reverse mers

AAGG [CCTT]: AAG^{+} -> AGG^{+}
ACTT [AAGA]: ACT^{+} -> AAG^{-}
GCTT [AAGC]: AGC^{-} -> AAG^{-}
AAG^{+} -> AGC^{+}



(Medvedev et al, 2007)

Find Compressible Nodes

Input: Graph stored as (n : (nodeinfo, ni))

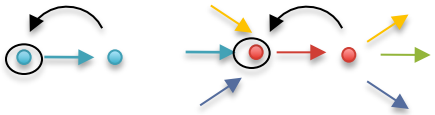
Map:

- For all nodes, emit (n : (nodeinfo, ni))
- If node n has unique predecessor p, emit (p : (unique-pred, n))

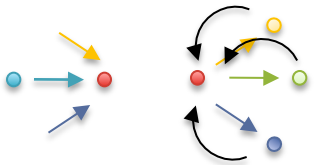
Reduce:

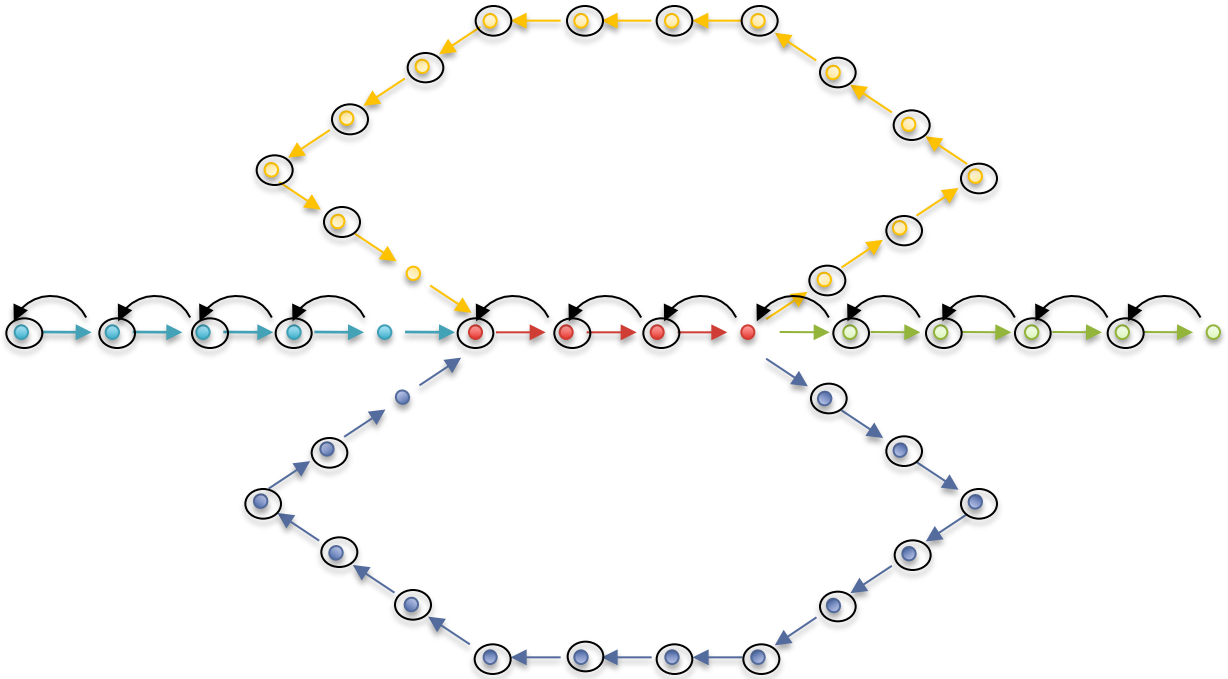
- If node n has unique successor s, and received (unique-pred, s),
  - Mark ni as compressible
- Save (n : (nodeinfo, ni))

Compressible



Not Compressible

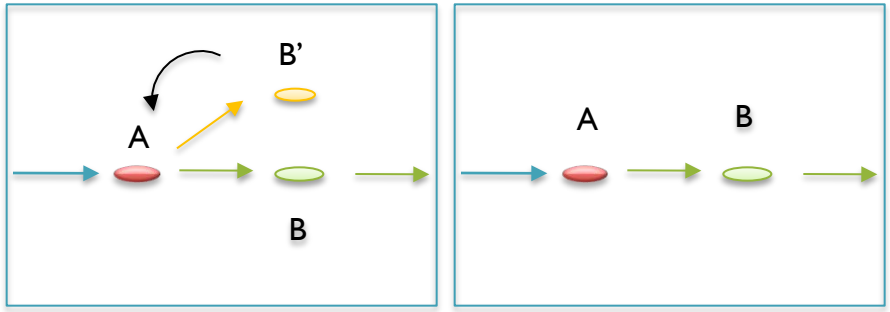




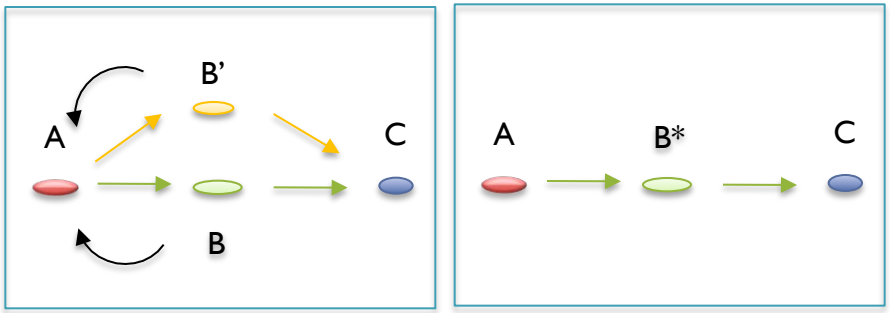
Error Correction

Sequencing error distorts graph structure

- Errors at end of read
  - Trim off 'dead-end' tips
  - B' passes *trim* message to A



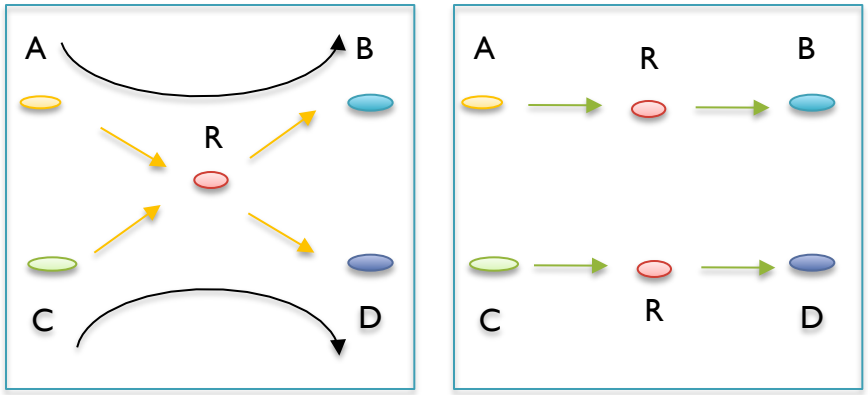
- Errors in middle of read
  - Pop Bubbles
  - B' and B pass *bubble* messages to A
    - A is lexicographically smaller than C



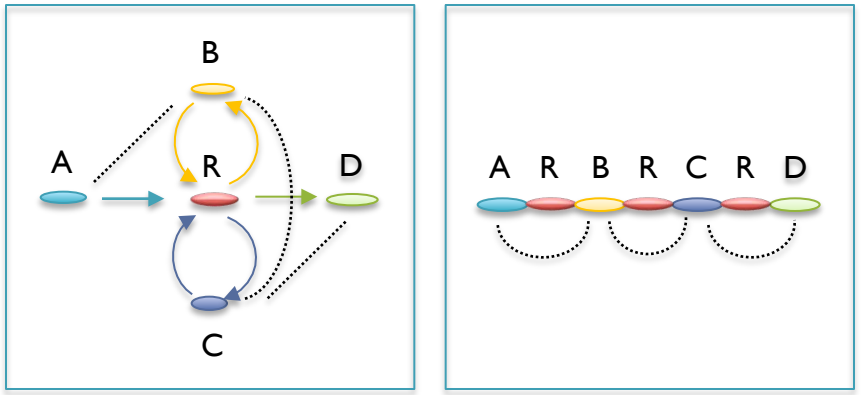
- Recursively apply, rerun path compression between each iteration

Repeat Analysis

- X-cut
  - Annotate edges with spanning reads
  - Separate fully spanned nodes
    - (Pevzner *et al.*, 2001)



- Scaffolding
  - If mate pairs are available search for a path consistent with mate distance
  - Use message passing to iteratively collect linked and neighboring nodes



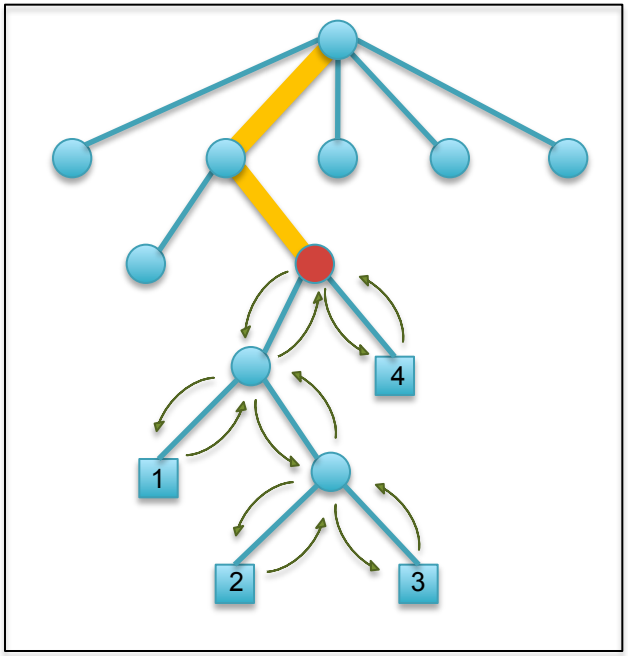
- Other simplifications possible

Parallel Frontier Search

MUMmerGPU

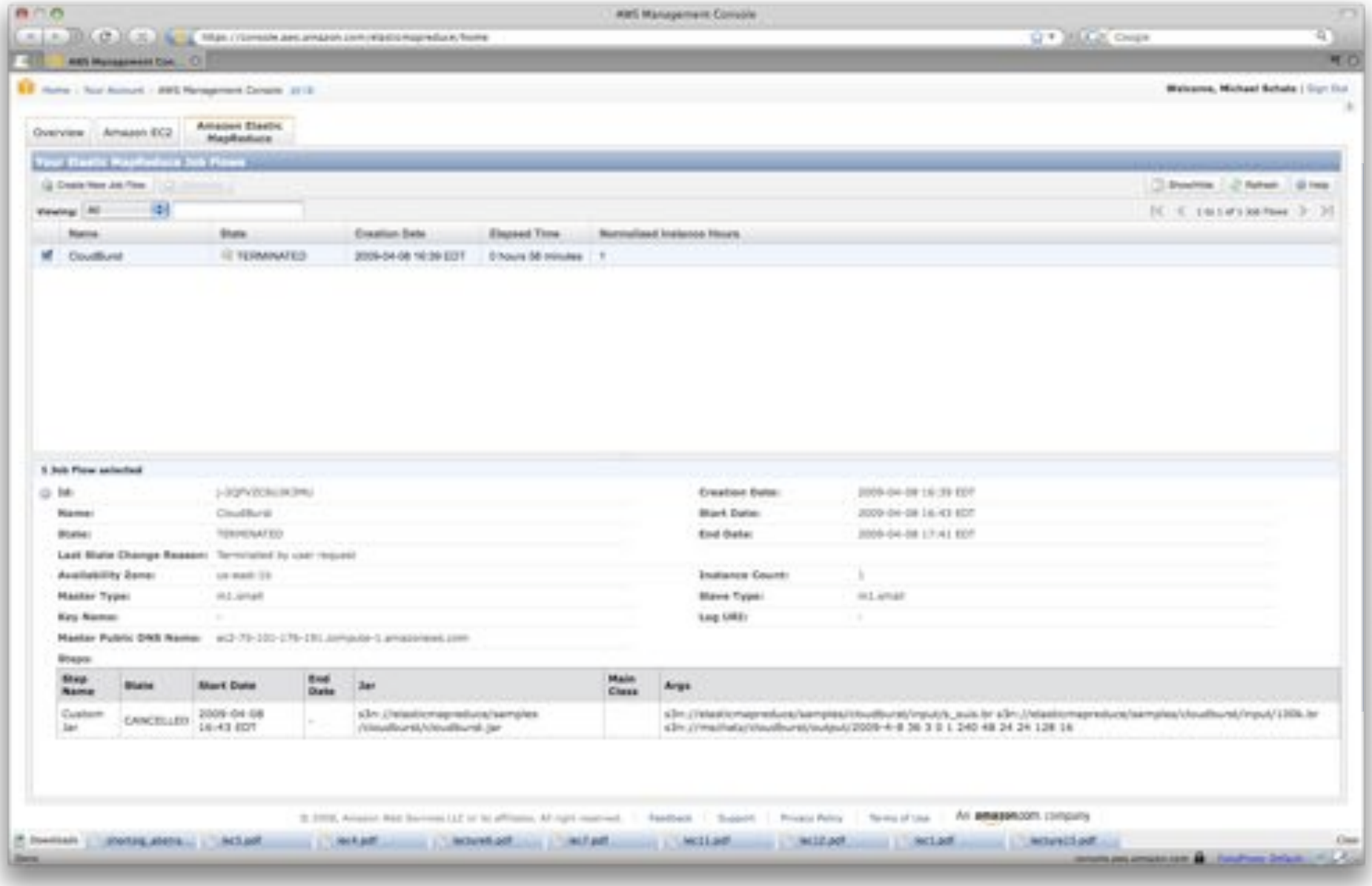
http://mummergpu.sourceforge.net

- Index reference using a suffix tree
  - Each suffix represented by path from root
  - Reorder tree along space filling curve
- Map many reads simultaneously on GPU
  - Find matches by walking the tree
  - Find coordinates with depth first search
- Performance on nVidia GTX 8800
  - Match kernel was ~10x faster than CPU
  - Search kernel was ~4x faster than CPU
  - End-to-end runtime ~4x faster than CPU



Optimizing data intensive GPGPU computations for DNA sequence alignment.
Trapnell C, Schatz MC. (2009) *Parallel Computing.* 35(8-9):429-440.

Amazon Elastic MapReduce



EC2 Pricing

Pricing

Amazon Elastic MapReduce currently is available in the US region only. Pay only for what you use – there is no minimum fee. Amazon Elastic MapReduce pricing is in addition to normal Amazon EC2 and Amazon S3 pricing.

Standard Amazon EC2 Instances	Amazon EC2 Price per hour (On-Demand Instances)	Amazon Elastic MapReduce Price per hour
Small (Default)	$0.10 per hour	$0.015 per hour
Large	$0.40 per hour	$0.06 per hour
Extra Large	$0.80 per hour	$0.12 per hour
High CPU Instances	**Amazon EC2 Price per hour (On-Demand Instances)**	**Amazon Elastic MapReduce Price per hour**
Medium	$0.20 per hour	$0.03 per hour
Extra Large	$0.80 per hour	$0.12 per hour

Amazon EC2 and Amazon S3 charges are billed separately. Pricing for Amazon Elastic MapReduce is per instance-hour consumed for each instance type, from the time job flow began processing until it is terminated. Each partial instance-hour consumed will be billed as a full hour. For additional details on Amazon EC2 Instance Types, Amazon EC2 Reserved Instances Pricing, or Amazon S3 Pricing, follow the links below:

Amazon EC2 Instance Types

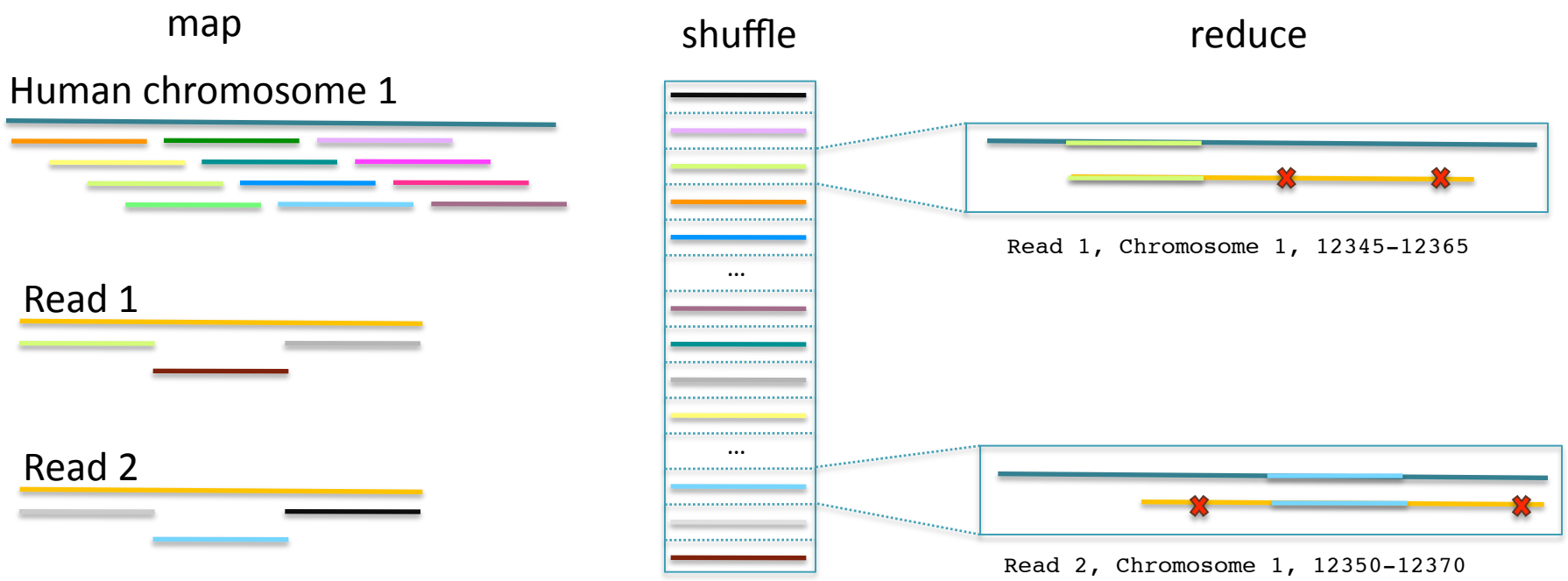
Amazon EC2 Reserved Instances Pricing

Amazon S3 Pricing

CloudBurst

http://cloudburst-bio.sourceforge.net

- Leverage Hadoop to build a distributed inverted index of k-mers and find end-to-end alignments
- 100x speedup over RMAP with 96 cores at Amazon EC2

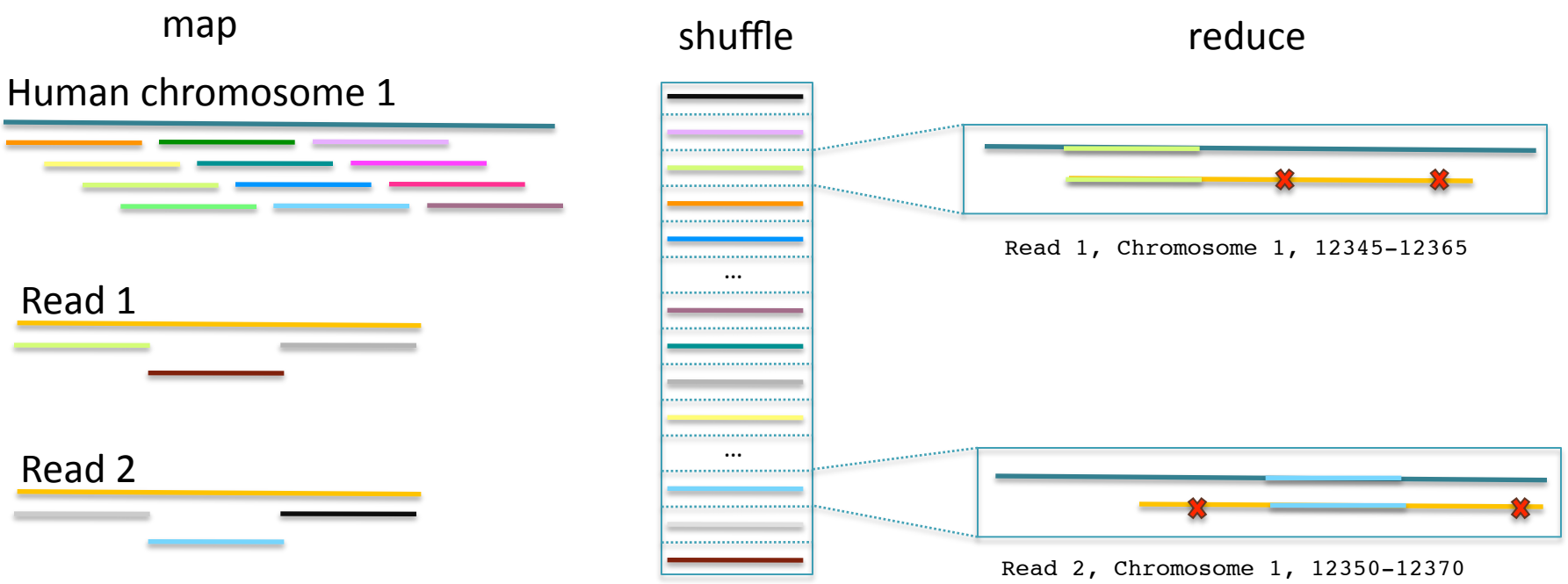


CloudBurst: Highly Sensitive Read Mapping with MapReduce.
Schatz MC (2009) *Bioinformatics*. 25:1363-1369

CloudBurst: Highly Sensitive Read Mapping with MapReduce

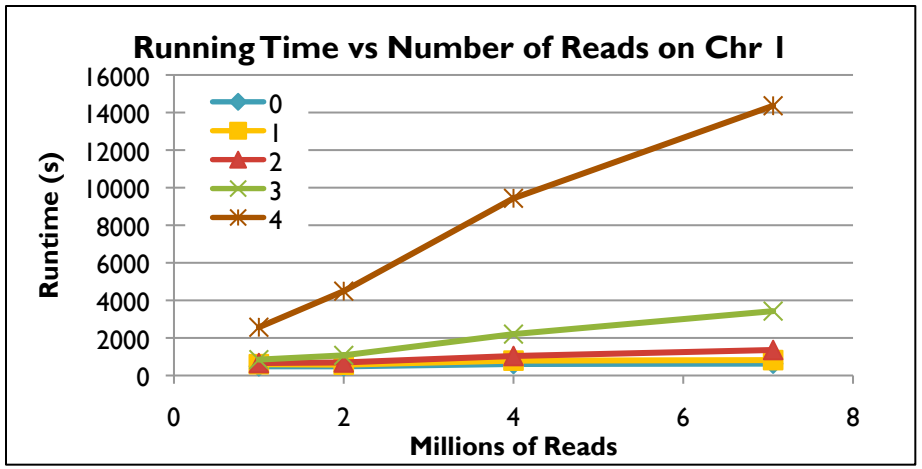
(Schatz, 2009)

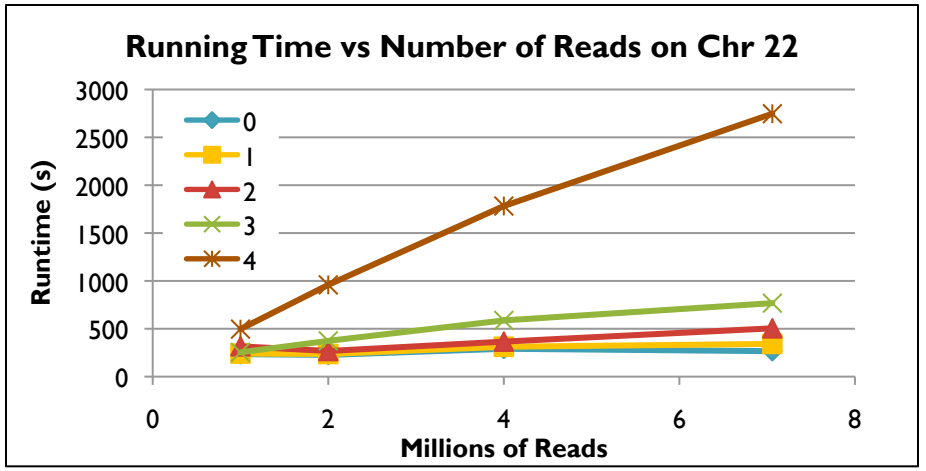
1. Map: Catalog K-mers
   - Emit every k-mer in the genome and non-overlapping k-mers in the reads
   - Non-overlapping k-mers sufficient to guarantee an alignment will be found
2. Shuffle: Coalesce Seeds
   - Hadoop internal shuffle groups together k-mers shared by the reads and the reference
   - Conceptually build a hash table of k-mers and their occurrences
3. Reduce: End-to-end alignment
   - Locally extend alignment beyond seeds by counting mismatches, or with Landau-Vishkin k-difference algorithm to allow for indels.
   - If read aligns end-to-end, record the alignment



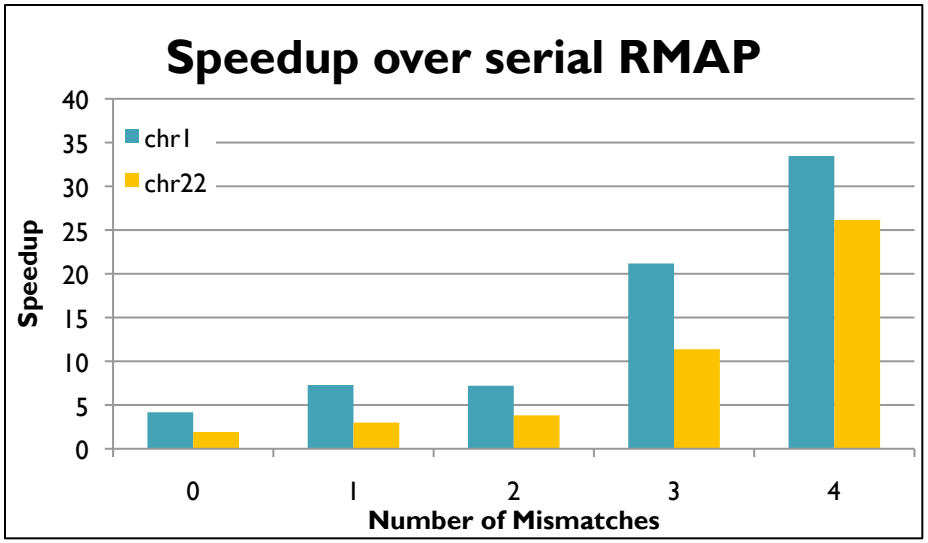
CloudBurst Results on Local CBCB Cluster

- Evaluation of CloudBurst running time while scaling the number of reads and the number of allowed mismatches while mapping to human chromosomes 1 (top) and 22 (bottom) on the local cluster with 24 cores.
- Colored lines indicate timings allowing 0 (fastest) through 4 (slowest) mismatches between a read and the reference.
- As the number of reads increases, the running time increases linearly.
- As the number of allowed mismatches increases, the running time increases super-linearly from the exponential increase in seed instances.





Comparison to RMAP

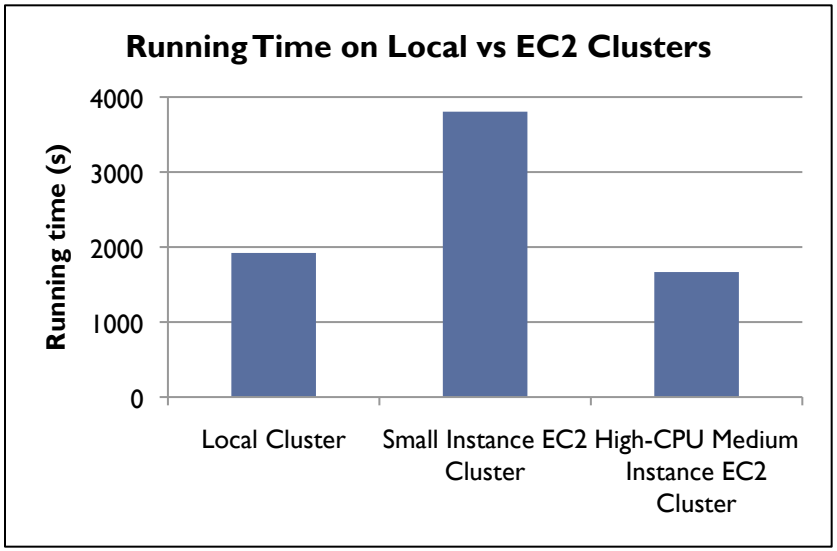


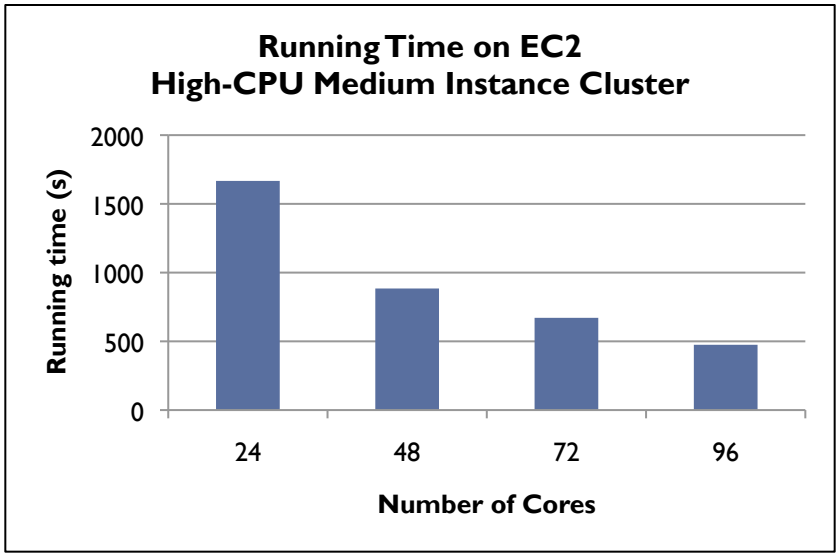
- CloudBurst running time compared to *RMAP* for mapping 7M reads, showing the speedup of CloudBurst running on 24 cores compared to *RMAP* running on 1 core.

- As the number of allowed mismatches increases, the relative overhead decreases allowing CloudBurst to meet and exceed 24x linear speedup.

- Produces identical results in a fraction of the time, especially for highly sensitive alignments.

Amazon EC2 Evaluation

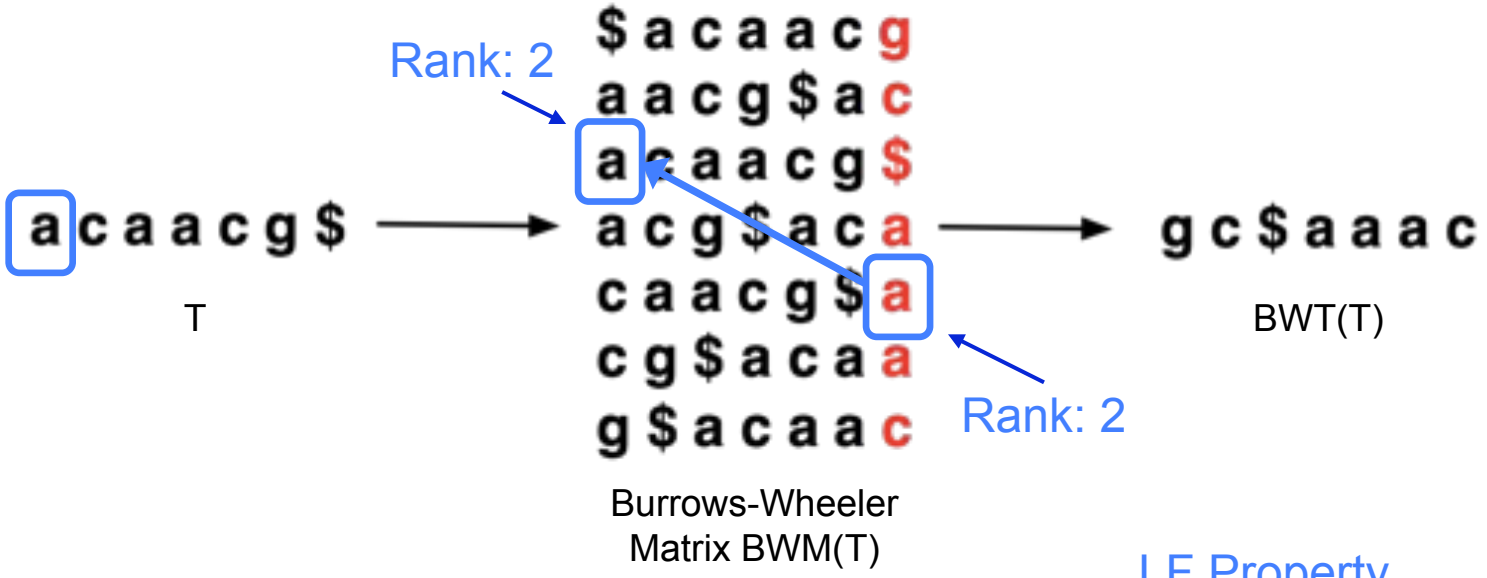




- CloudBurst running times for mapping 7M reads to human chromosome 22 with at most 4 mismatches on the local and EC 2 clusters.
- The 24-core Amazon High-CPU Medium Instance EC2 cluster is faster than the 24-core Small Instance EC2 cluster, and the 24-core local dedicated cluster.
- As the number of cores increase, the running time decreases with near linear speedup. The 96-core cluster is 3.5x faster than the 24-core, and 100x faster than a serial run of RMAP.

Burrows-Wheeler Transform

- Reversible permutation of the characters in a text



LF Property implicitly encodes Suffix Array

- BWT(T) is the index for T

A block sorting lossless data compression algorithm.
Burrows M, Wheeler DJ (1994) *Digital Equipment Corporation.* Technical Report 124

Bowtie algorithm

Reference

BWT(Reference)

Query:
A A T G A T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

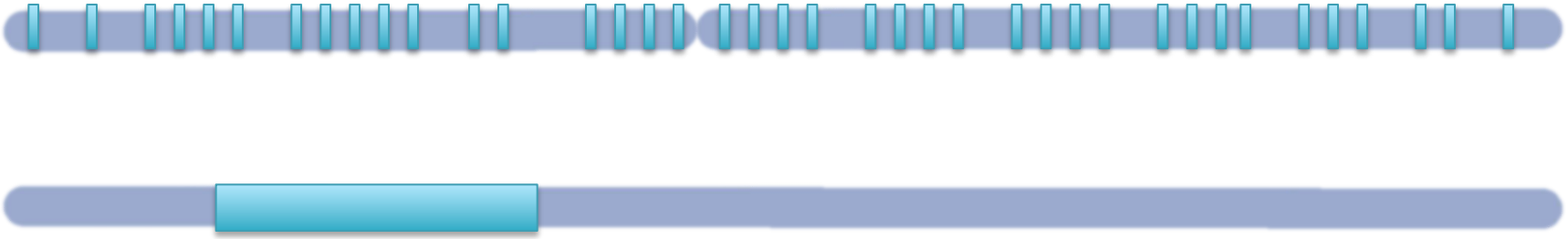
Reference

BWT(Reference)

Query:
A A T G A T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

Reference

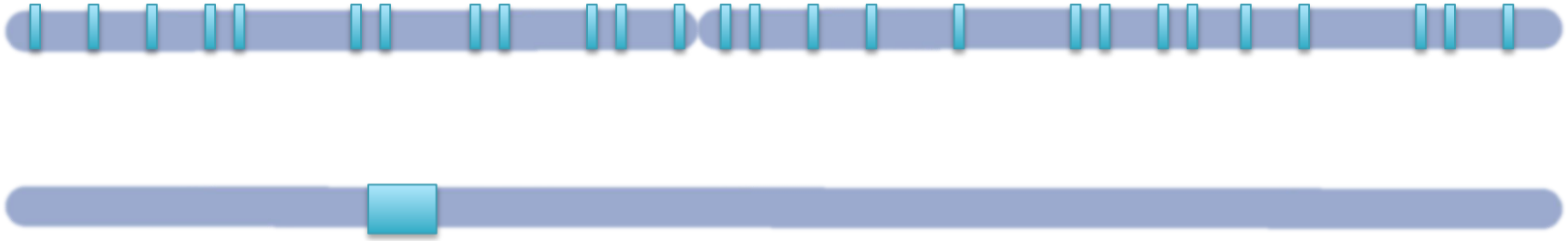


BWT(Reference)

Query:
A A T G A T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

Reference



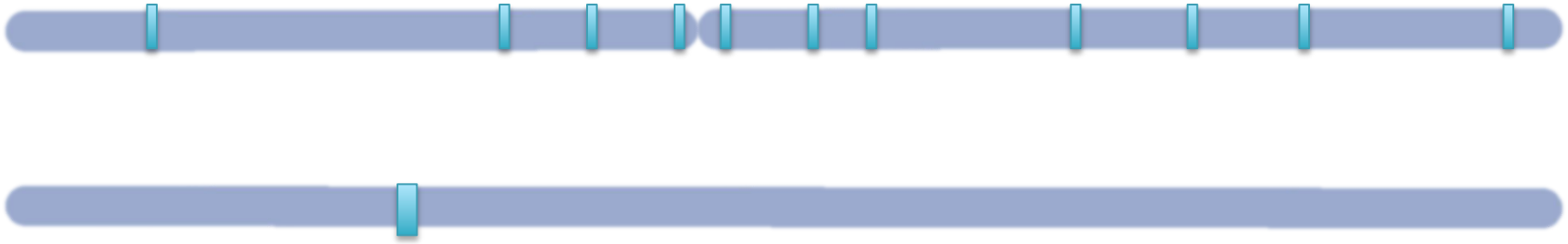
BWT(Reference)

Query:

A A T G A T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

Reference



BWT(Reference)

Query:

A A T G A T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

Reference

BWT(Reference)

Query:
A A T G A T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

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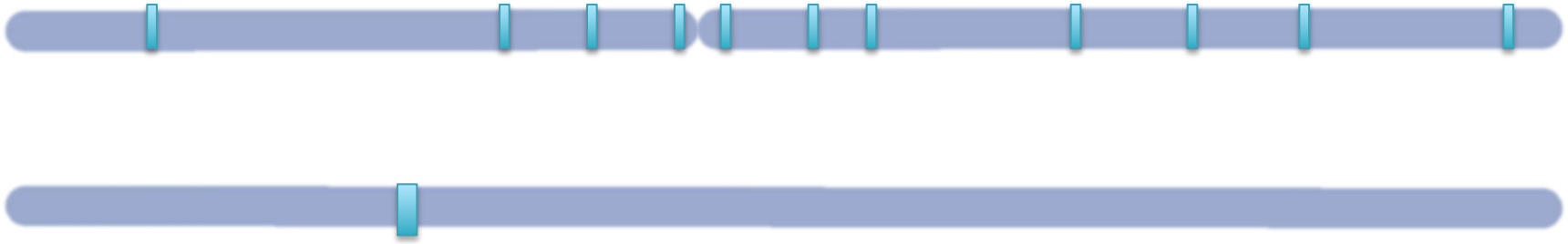

BWT(Reference)

Query:

A A T G T T A C G G C G A C C A C C G A G A T C T A

Bowtie algorithm

Reference

BWT(Reference)

Query:

A A T G T T A C G G C G A C C A C C G A G A T C T A