Memory Efficient Minimum Substring Partitioning

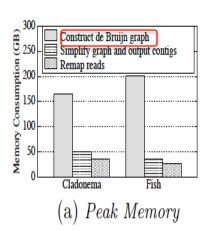
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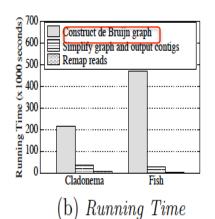
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Motivation - Challenges

- De Bruijn graph based sequence assembly
- Building de Bruijn graph is both time intensive and memory consuming

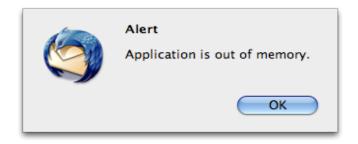




DNA extraction Library construction NGS sequencing Read1: TTCAGACTAATTGCGCTACTAGACG Read2: CGGTTCAGACTAATTGCGCTACTAG Read3: AGACTAATTGCGCTACTAGACGTTC Read4: ACTACCGGTTCAGACTAATTGCGCT Read5: TTCAGACTAATTGCGCTACTAGACG Billions of **Nodes** de Bruijn graph ACTACCGGTTCAGACTAATTGCGCTACTAGACGTTC Contig

Motivation - Existing solutions

- In-memory solution
 - Small running time
 - Huge memory footprint



- Classic disk-based approach
 - Small memory footprint
 - Huge disk space consumption
 - Very large running time



Objectives

- De Bruijn graph construction
 - with small running time
 - with small memory footprint
 - with small disk space consumption
- Minimum Substring Partitioning

A disk-based method with a SMART partitioning strategy ©

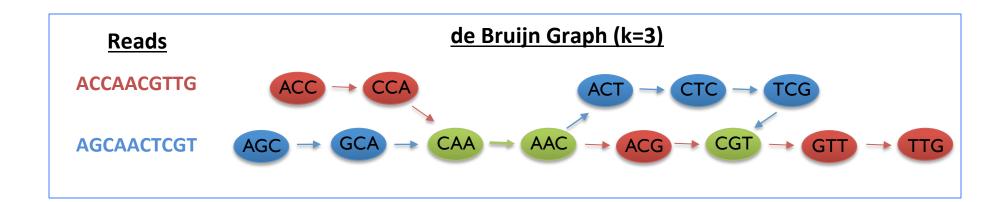


Outline

- Backgrounds
- Minimum Substring Partitioning (MSP)
- MSP-based de Bruijn graph construction
- Experiments
- Conclusions

Backgrounds - de Bruijn graph

- De Bruijn graph
 - $G_k = (V,E)$
 - V = All unique k-mers (length-k substrings)
 - E = Directed edges between consecutive k-mers
 - consecutive k-mers overlap by k-1 symbols
 - Human genome: >3B nodes, >10B edges



Backgrounds - Classic partitioning methods (1)

- Goal: deduplicate k-mers
- Horizontal Partition (*H-Partition*)
 - partition reads S horizontally into disjoint subsets S_i
 - 2. for each S_i, build a hash table H_i of k-mers in memory
 - 3. output a sorted copy H_i to disk
 - 4. merge all such sorted hash tables
- Pro: partitioning is simple and straightforward
- Con: merging is very expensive (time consuming)
 - same k-mer may appear in different partitions

Backgrounds - Classic partitioning methods (2)

- Goal: deduplicate k-mers
- Bucket Partition (*B-Partition*)
 - partition(hash) all k-mers from S into disjoint subsets K_i
 - 2. for each K_i, build a hash table H_i of k-mers in memory
 - 3. output H_i (no need to sort) to disk
 - 4. merge all such hash tables
- Pro: merging is simple and straightforward
- Con: partitioning is very expensive (time consuming)
 - k-mer set size is much larger than sequence set size
 - huge I/O costs and disk space occupations

Minimum Substring Partitioning

Intuition

• if several adjacent k-mers are distributed to the same partition, we can compress them to reduce I/O costs



Observation

• since two adjacent k-mers overlap with length k-1 substring, the chance for them to have the same minimum p-substring (p < k) could be very high.

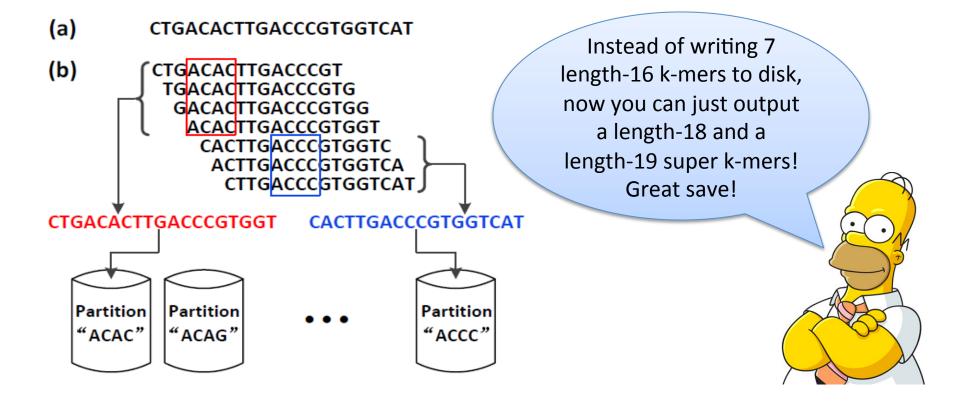


Idea

• partition k-mers w.r.t minimum substring

Minimum Substring Partitioning

Given a string $s = s_1 s_2 ... s_m$, $p \le k \le m$, minimum substring partitioning breaks s to substrings with maximum length $\{s[i,j]|i+k-1 \le j, 1 \le i, j \le m\}$, s.t., all k-mers in s[i,j] share the same minimum p-substring. s[i,j] is also called super k-mer.



Minimum Substring Partitioning - Theorems

- We employ a random string model to derive theorems
- Total Partition Size

critical for running time & disk space usage

Theorem 1

In a random string model, the total partition size is O(pn) or $\Theta(n)$

Largest Partition Capacity

critical for peak memory

Theorem 2

In a random string model, the maximum percentage of distinct kmers covered by one p-substring is bounded by $3k/(4^p+1)$, when $p \ge 2$.

MSP-based de Bruijn graph construction

Partitioning

A simple yet efficient scan algorithm for MSP



Mapping

Assign ID to each k-mer and generate ID replacement tables



Merging

Merge ID replacement tables to produce a disk-based de Bruijn graph

Experiments - Setup

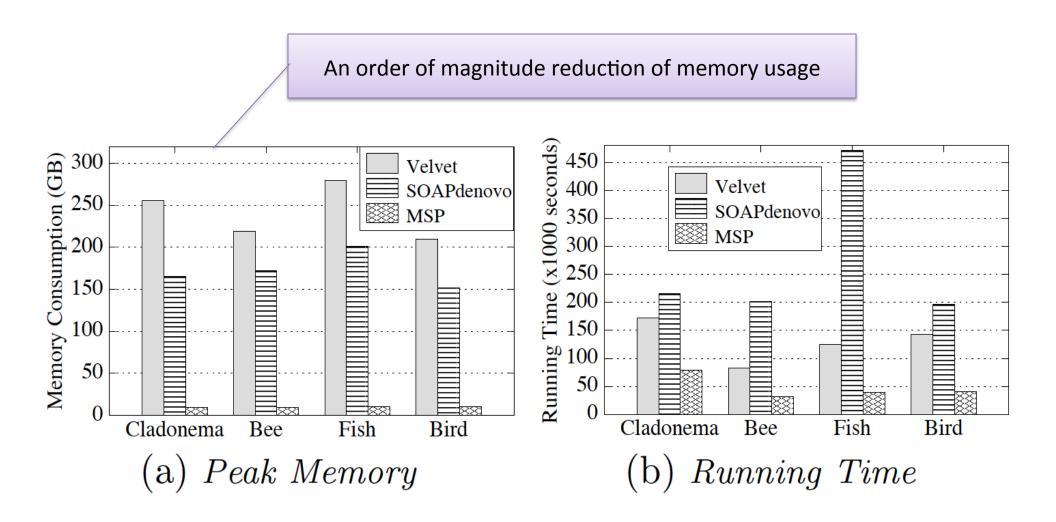
Datasets

	Cladonema	Bee	Fish	Bird
Size (GB)	258.7	93.8	137.5	106.8
Avg Read Length (bp)	101	124	101	150
# of Reads (million)	894	303	598	323

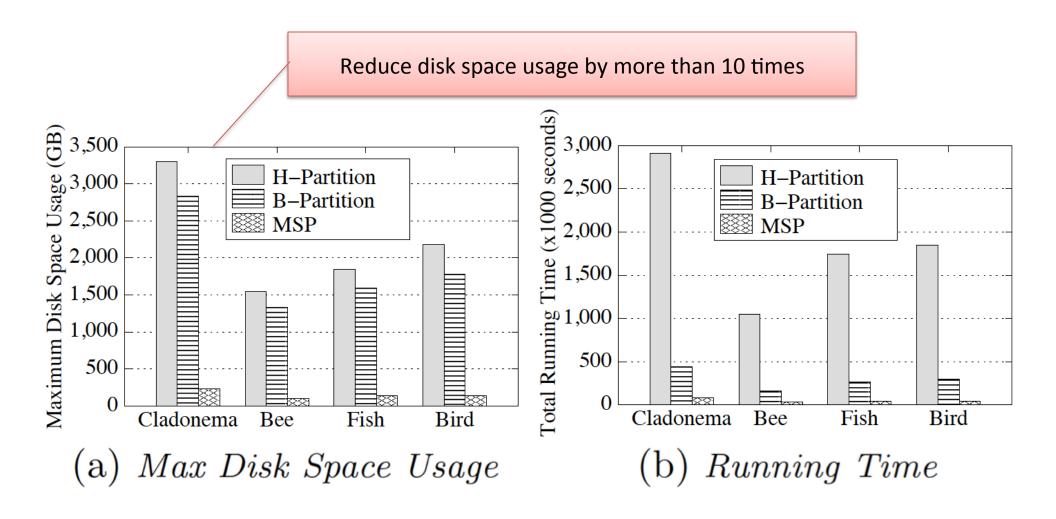
- Environment
 - a server with 2.40GHz Intel Xeon CPU and 512GB RAM
- Evaluation criteria
 - Peak memory
 - Running time
 - Disk space usage

The smaller, the better!

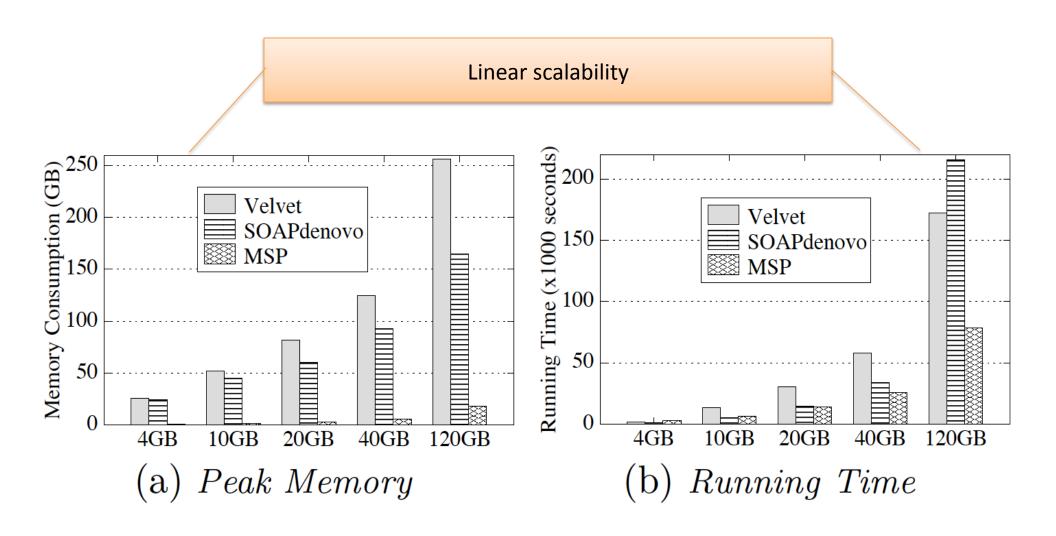
Experiments - Efficiency



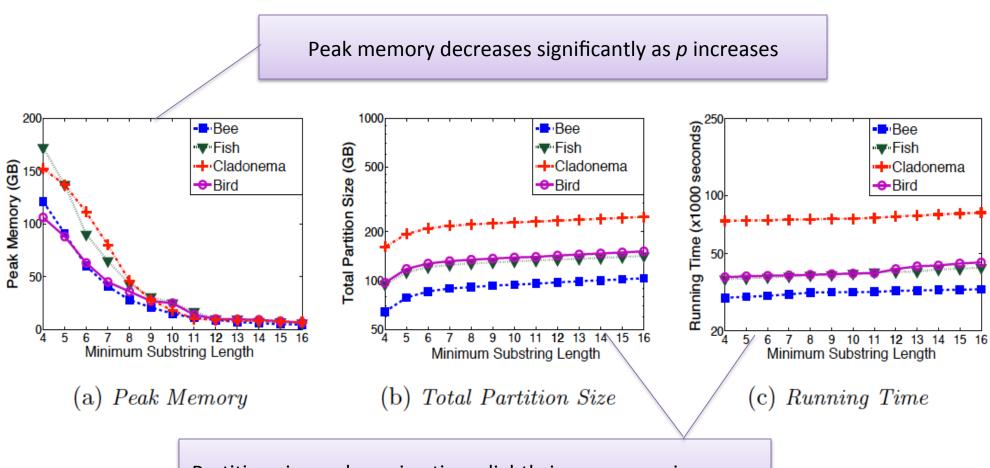
Experiments - Effectiveness



Experiments - Scalability

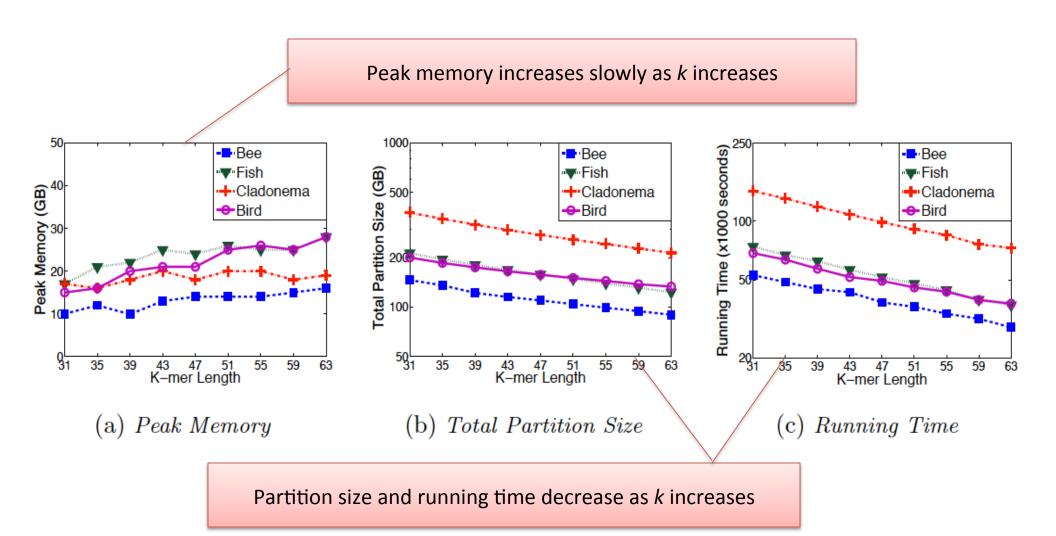


Experiments - Properties (1)



Partition size and running time slightly increase as p increases

Experiments - Properties (2)



Conclusions

- Minimum Substring Partitioning
 - with small running time
 - with small memory footprint
 - with small disk space consumption
- Project Homepage
 - http://grafia.cs.ucsb.edu/msp

Remaining Challenges

Sequence Assembly

Construct de Bruijn graph



Load graph & generate sequence



