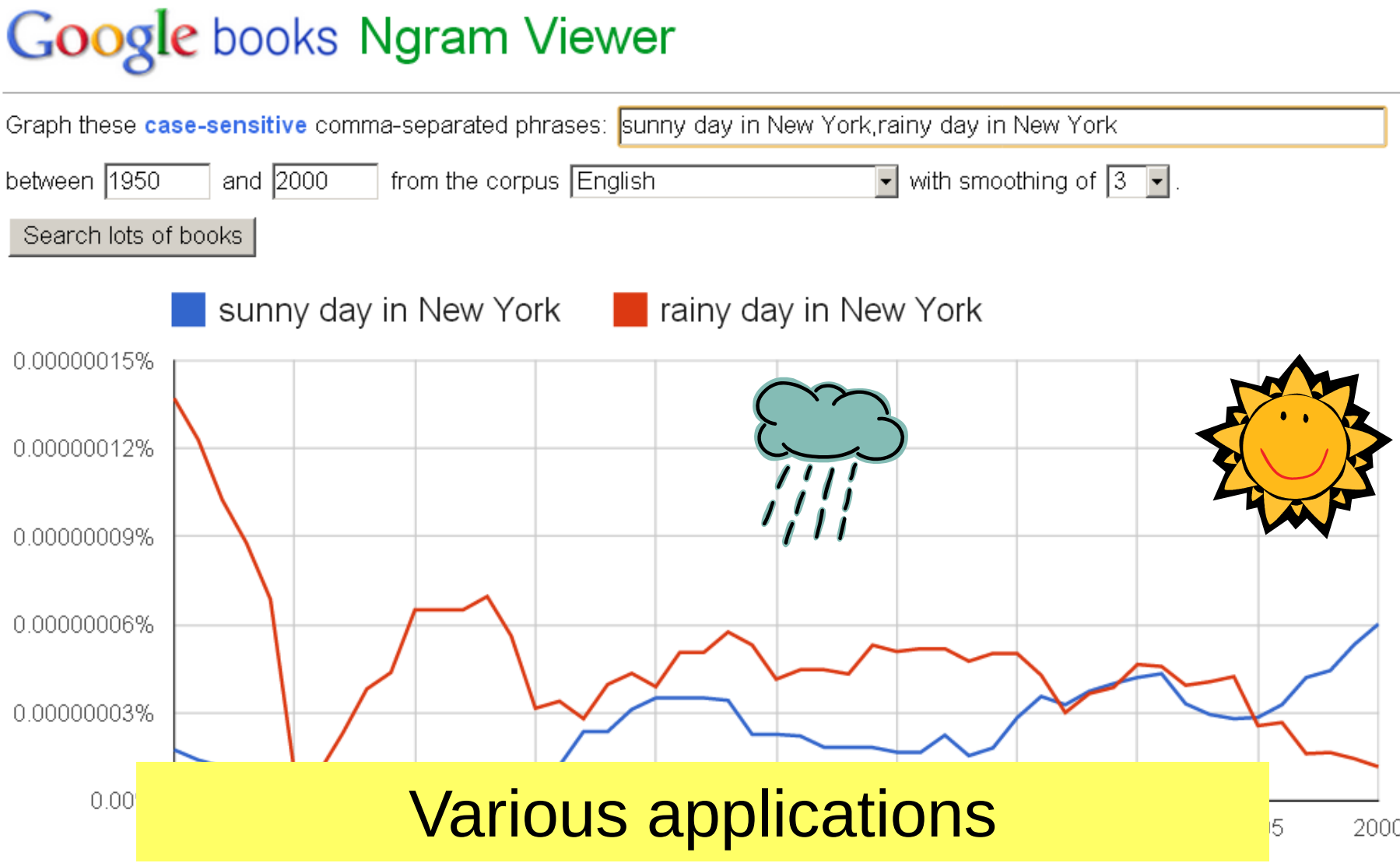
Mind the Gap: Large-Scale Frequent Sequence Mining

Iris Miliaraki Klaus Berberich Rainer Gemulla Spyros Zoupanos

Max Planck Institute for Informatics

Saarbrücken, Germany

Why are sequences interesting?



Various applications

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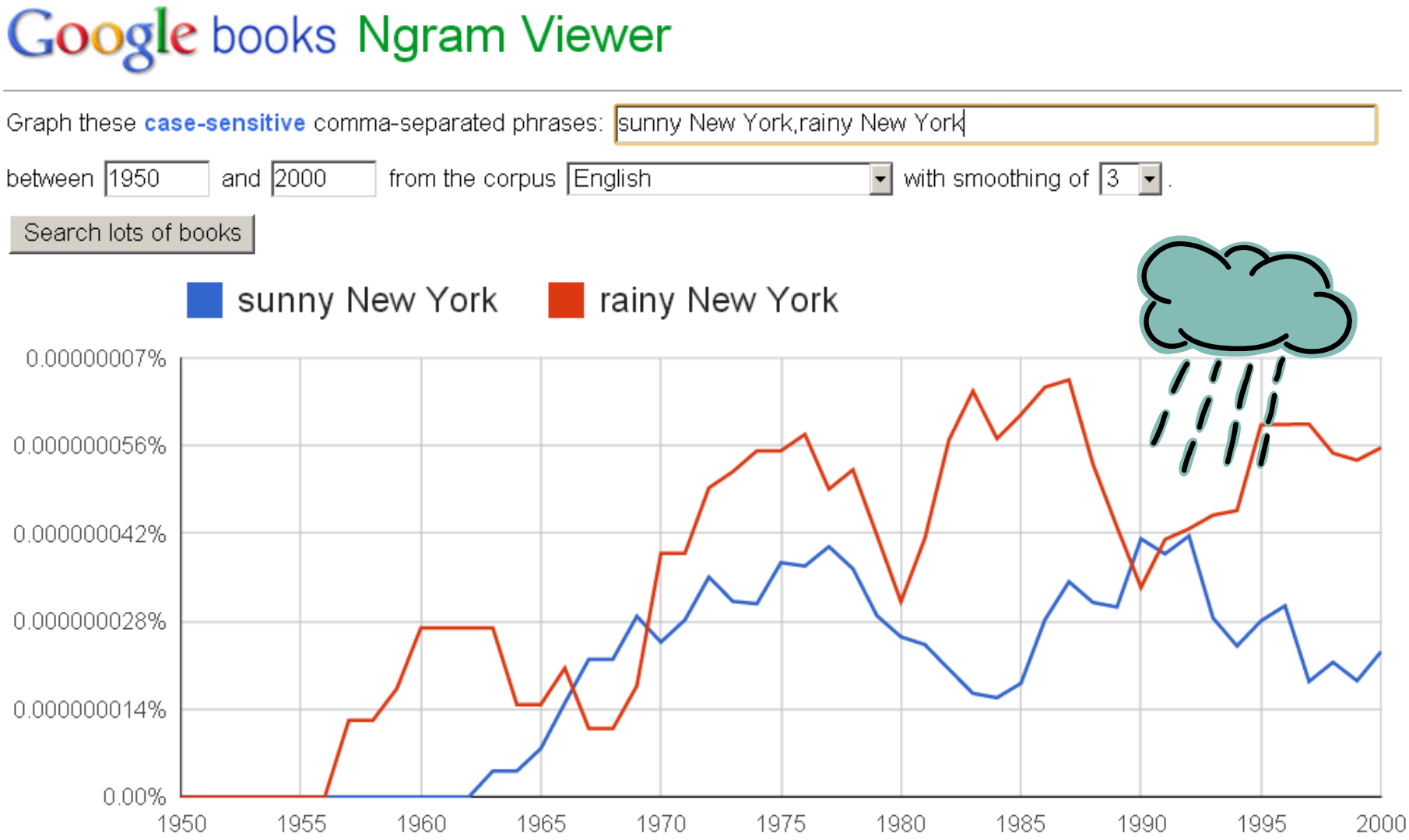


Sequences with gaps

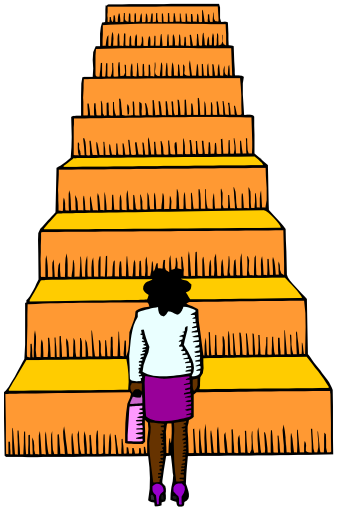
- Generalization of n-grams to sequences with gaps
  - sunny [...] New York
  - rainy [...] New York

- Exposes more structure
  - ✓ Central Park is the best place to be on a **sunny** day in **New York**.
  - ✓ It was a **sunny**, beautiful **New York** City afternoon.

More applications....

- **Text analysis** (e.g., linguistics or sociology)
- **Language modeling** (e.g, query completion)
- **Information extraction** (e.g,relation extraction)
- Also: web usage mining, spam detection, ...

Challenges



Huge collections of sequences

Computationally intensive problem

- $O(n^2)$ n-grams for sequence S where |S| = n
- $O(2^n)$ subsequences for sequence S where |S| = n and gap > n

Sequences with small support can be interesting

Potentially many output patterns

How can we perform frequent sequence mining at such large scales?

Outline

- Motivation & challenges
- **Problem statement**
- The MG-FSM algorithm
- Experimental Evaluation
- Conclusion

Gap-constrained frequent sequence mining

Input: Sequence database

Output: Frequent subsequences that

- Occur in at least σ sequences (support threshold)
- Have length at most λ (length threshold)
- Have gap at most γ between consecutive items (gap threshold)

Central Park is the best place to be on a sunny day in New York.

Monday was a sunny day in New York.

It was a sunny, beautiful New York City afternoon.

Frequent n-gram sunny day in New York for $\sigma = 2$, $\gamma = 0$, $\lambda = 5$

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Frequent n-gram sunny day in New York for $\sigma = 2, \gamma = 0, \lambda = 5$

Frequent n-gram New York for $\sigma = 3, \gamma = 0, \lambda = 2$

Gap-constrained frequent sequence mining

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Output: Frequent subsequences that

- Occur in at least σ sequences (support threshold)
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Frequent n-gram sunny day in New York for $\sigma = 2, \gamma = 0, \lambda = 5$

Frequent n-gram New York for $\sigma = 3, \gamma = 0, \lambda = 2$

Frequent subsequence sunny New York for $\sigma = 3, \gamma \geq 2, \lambda = 3$

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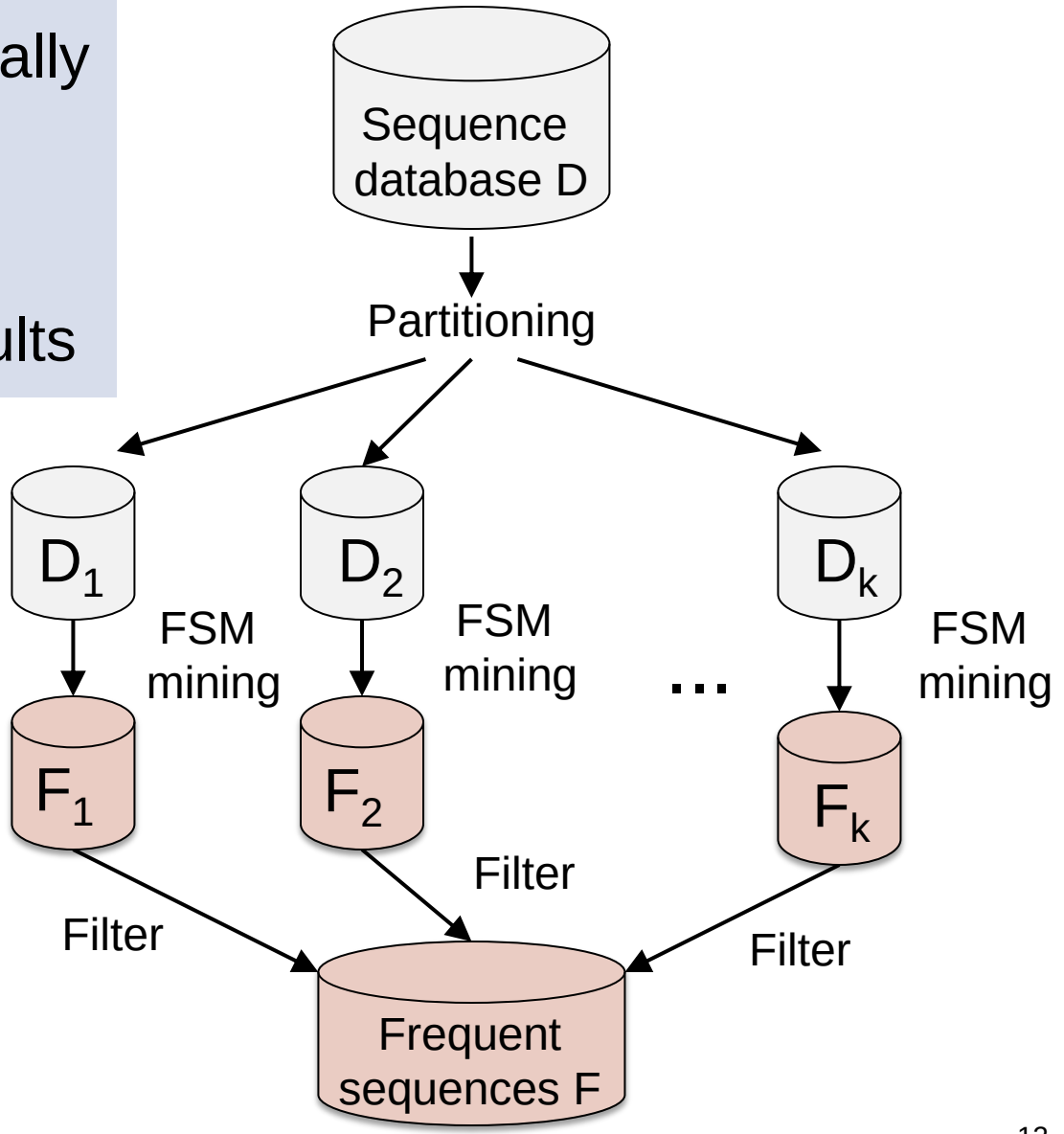
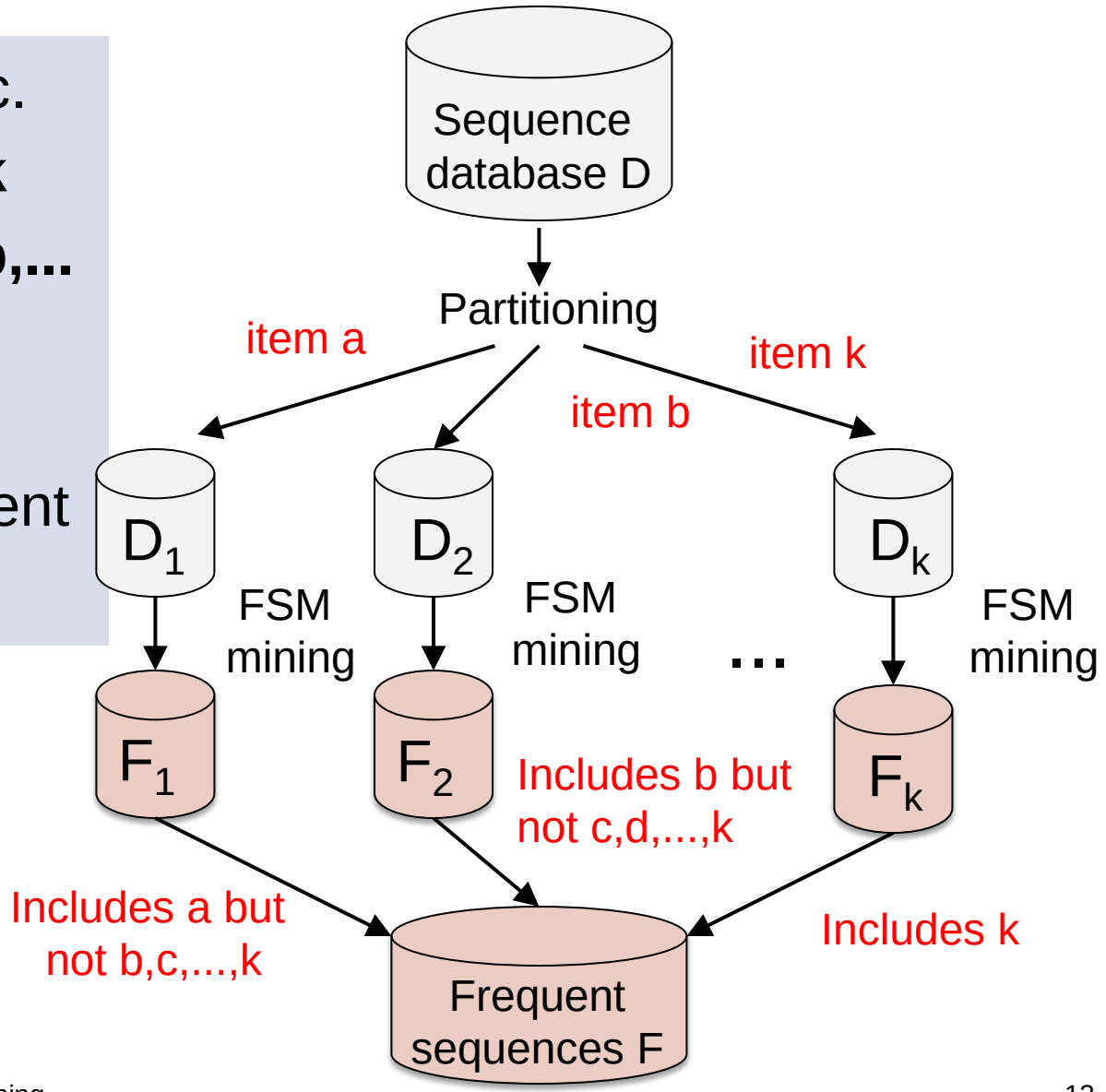
Parallel frequent sequence mining

1. Divide data into potentially overlapping partitions
2. Mine each partition
3. Filter and combine results



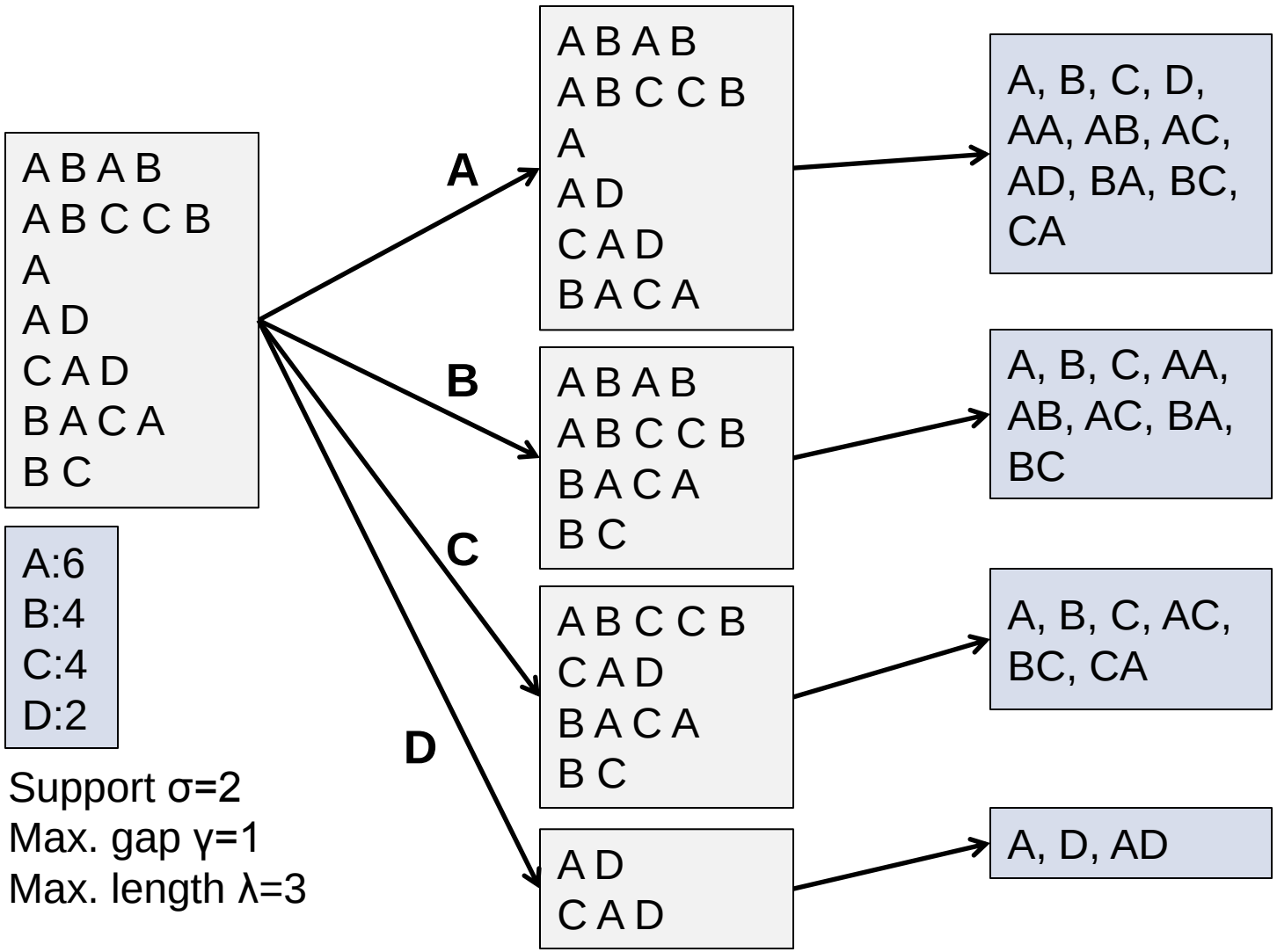
Using item-based partitioning

1. Order items by desc. frequency **a > ... > k**
2. Partition by item **a,b,...** (called **pivot** item)
3. Mine each partition
4. Filter: no less-frequent item

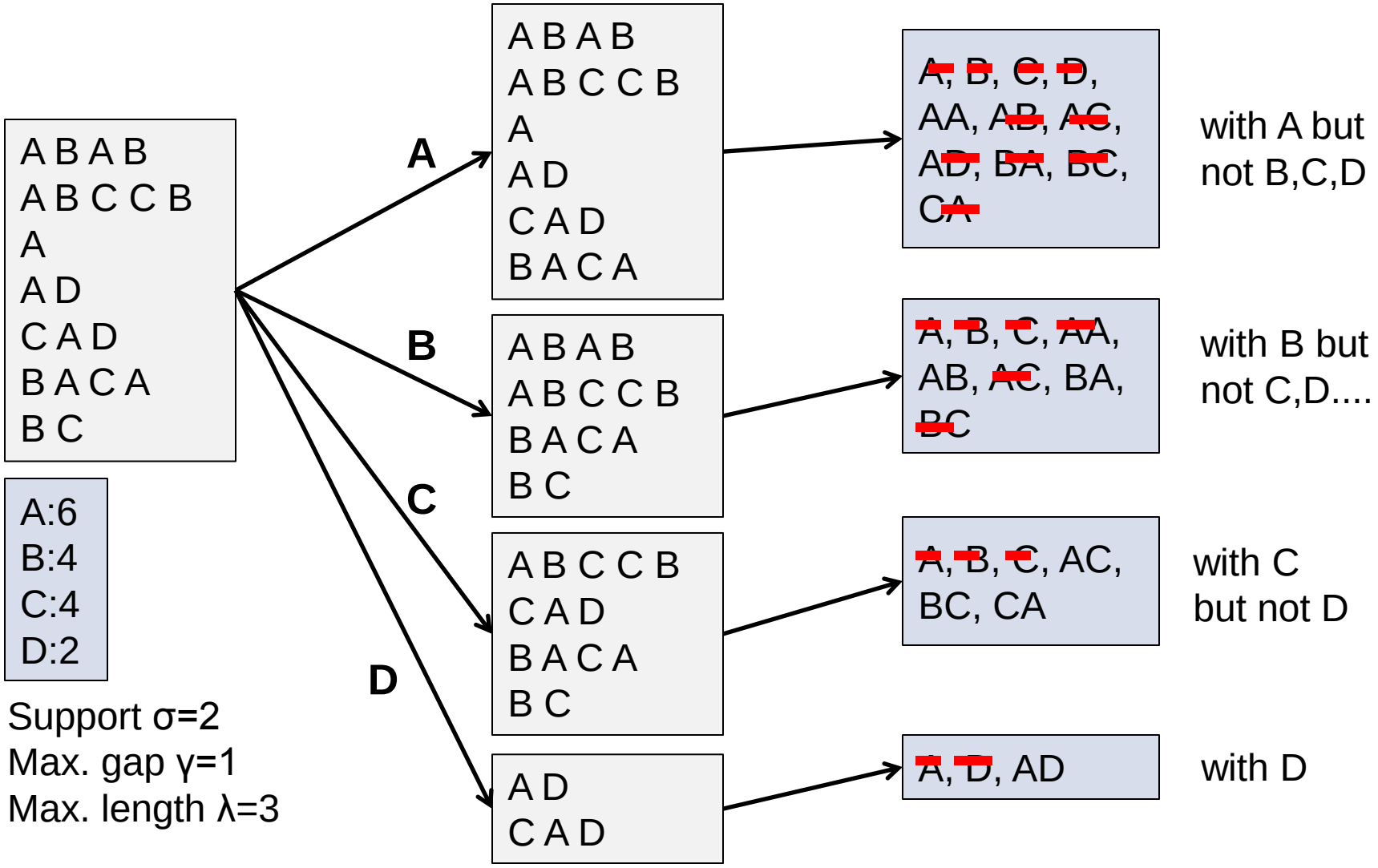


Disjoint subsequence sets computed in-parallel and independently

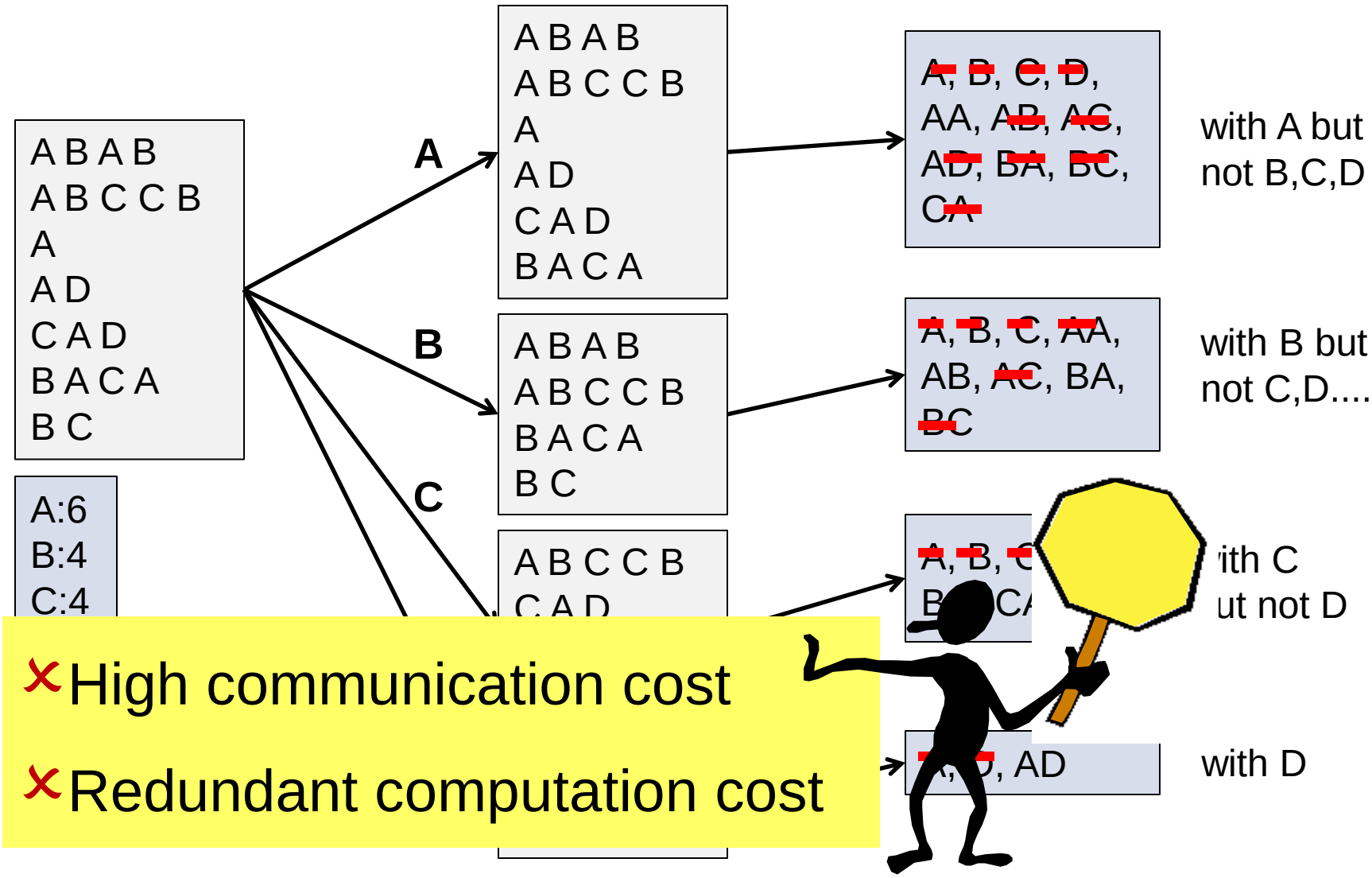
Example: Naive partitioning



Example: Naive partitioning

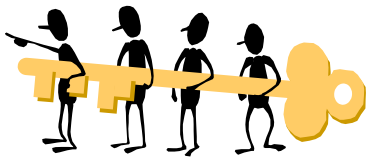


Example: Naive partitioning



Improving the partitioning

Traditional approach



- Derive a partitioning rule (“projection”)
- Prove correctness of the partition rule

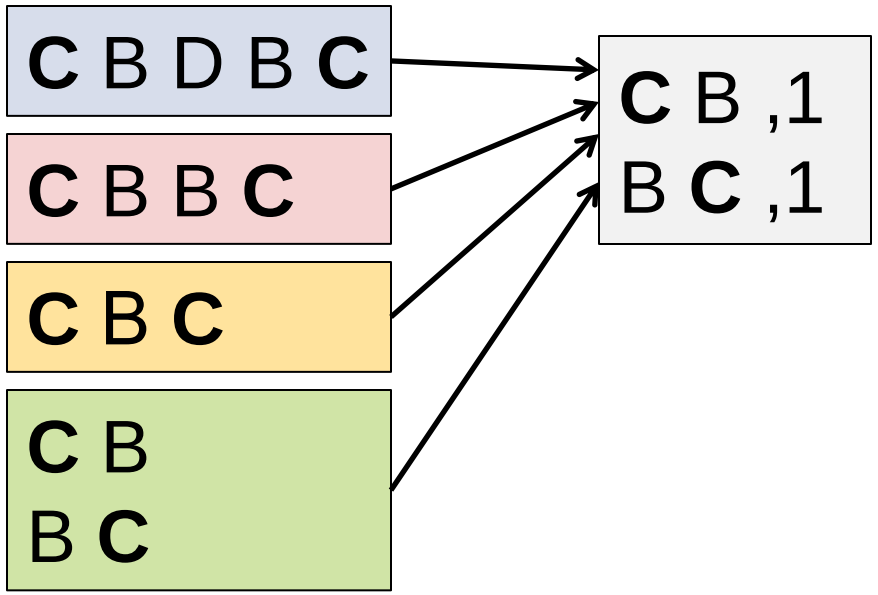
MG-FSM approach

- Use *any* partitioning satisfying correctness
- Rewrite the input sequences →

  ensuring each w-partition generates the set of **pivot sequences** for w

Which is the optimal partition?

Max. gap γ=0
Max. length λ=2
pivot **C**



Many short sequences? Few long sequences?
Optimal partition not clear!

Aim for a “good” partition
using inexpensive rewrites

Trade-off cost & gain

Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B
D A **C** B D
D A **C** B D D B **C** A
B **C** A D D B D
A D D **C** D

γ = 1
λ = 3

1. Replace irrelevant items (i.e., less frequent) by special blank symbol (_)

Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B
D A **C** B **D**
D A **C** B **D** **D** B **C** A
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A **D** **D** **C** **D**

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Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B
_ A **C** B _
_ A **C** B _ _ B **C** A
B **C** A _ _ B _
A _ _ **C** _

γ = 1
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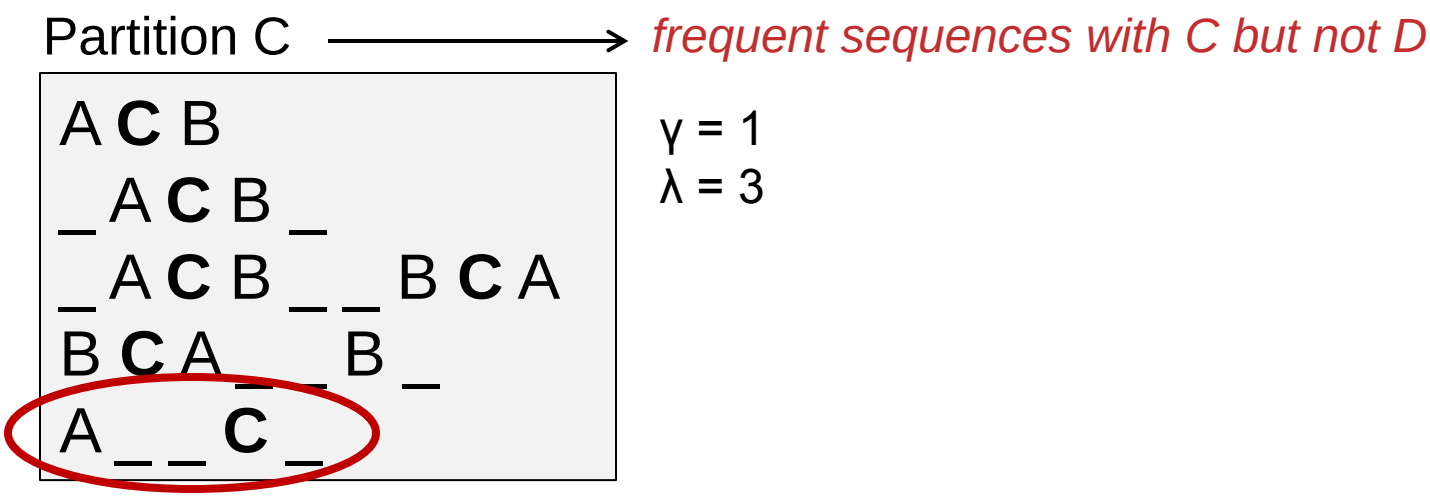
Rewriting partitions



1. Replace irrelevant items (i.e., less frequent) by special blank symbol (_)

2. Drop irrelevant sequences (i.e., cannot generate any pivot sequence)

Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B
_ A **C** B _
_ A **C** B _ _ B **C** A
B **C** A _ _ B _
~~A _ _ **C** _~~

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Partition C → *frequent sequences with C but not D*

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_ A **C** B _
_ A **C** B _ _ B **C** A
B **C** A _ _ **B** _

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1. Replace irrelevant items (i.e., less frequent) by special blank symbol (_)
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3. Remove all unreachable items (provably correct)

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5. Break up sequence at split points (i.e., sequences of γ+1 blanks)

Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B
A **C** B
A **C** B
B **C** A
B **C** A

γ = 1
λ = 3

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Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B **: 3**
~~A **C** B~~
~~A **C** B~~
~~B **C** A~~ **: 2**
B **C** A

γ = 1
λ = 3

A **C** B
D A **C** B D
D A **C** B D D B **C** A
B **C** A D D B D
A D D **C** D

1. Replace irrelevant items (i.e., less frequent) by special blank symbol (_)
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5. Break up sequence at split points (i.e., sequences of γ+1 blanks)
6. Aggregate repeated subsequences

Rewriting partitions

Partition C → *frequent sequences with C but not D*

A **C** B : 3 B **C** A : 2	γ = 1 λ = 3

A **C** B
D A **C** B D
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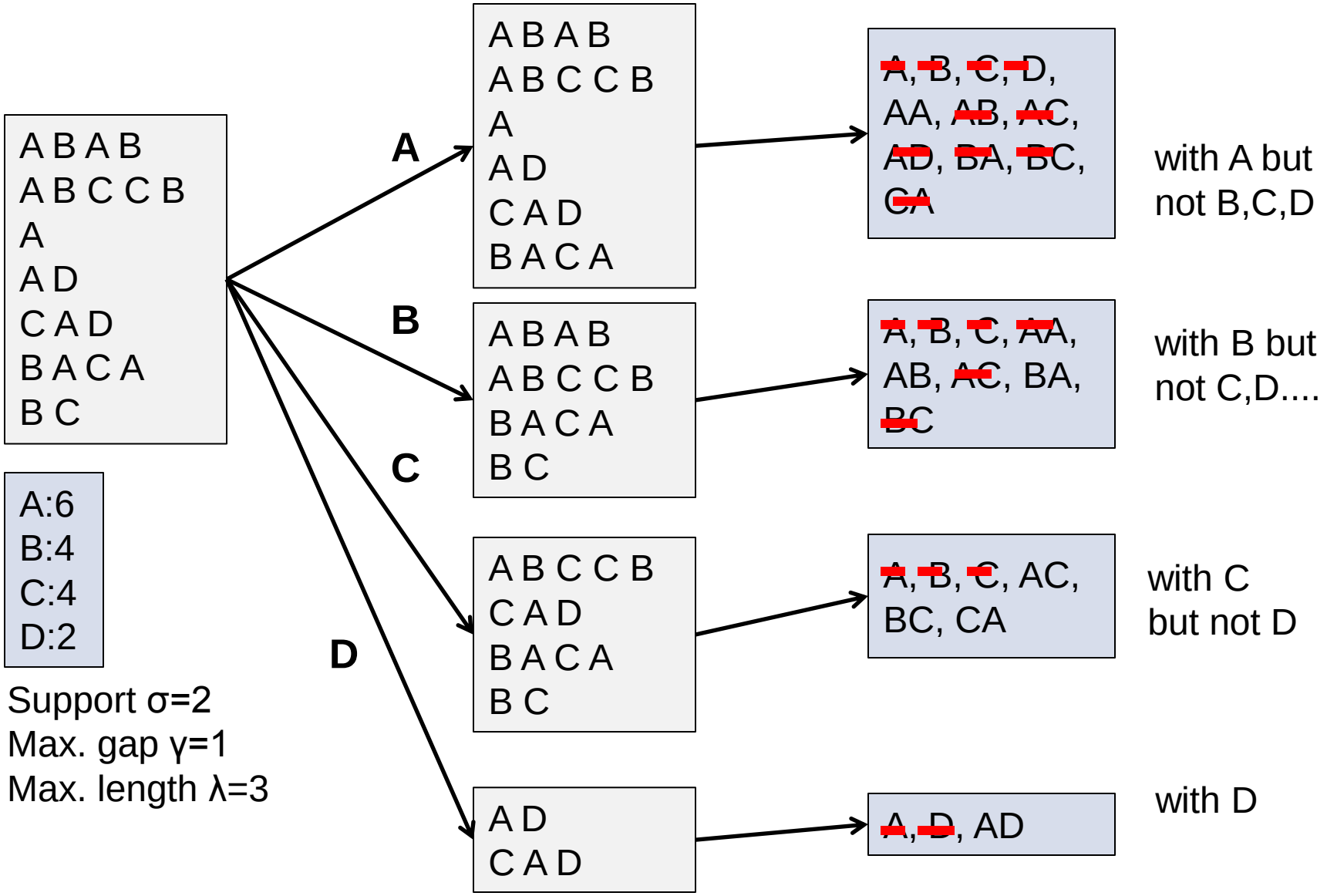
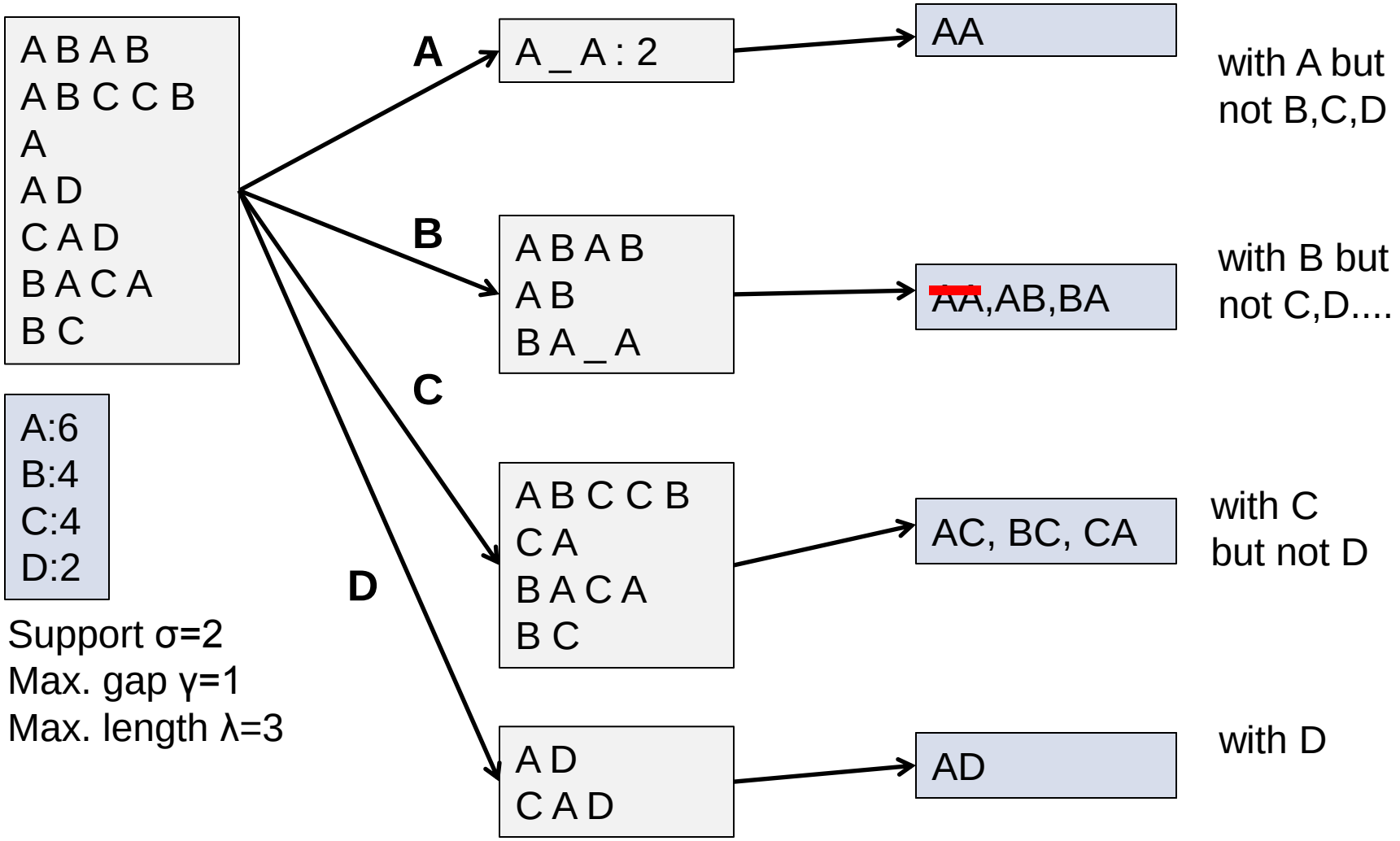
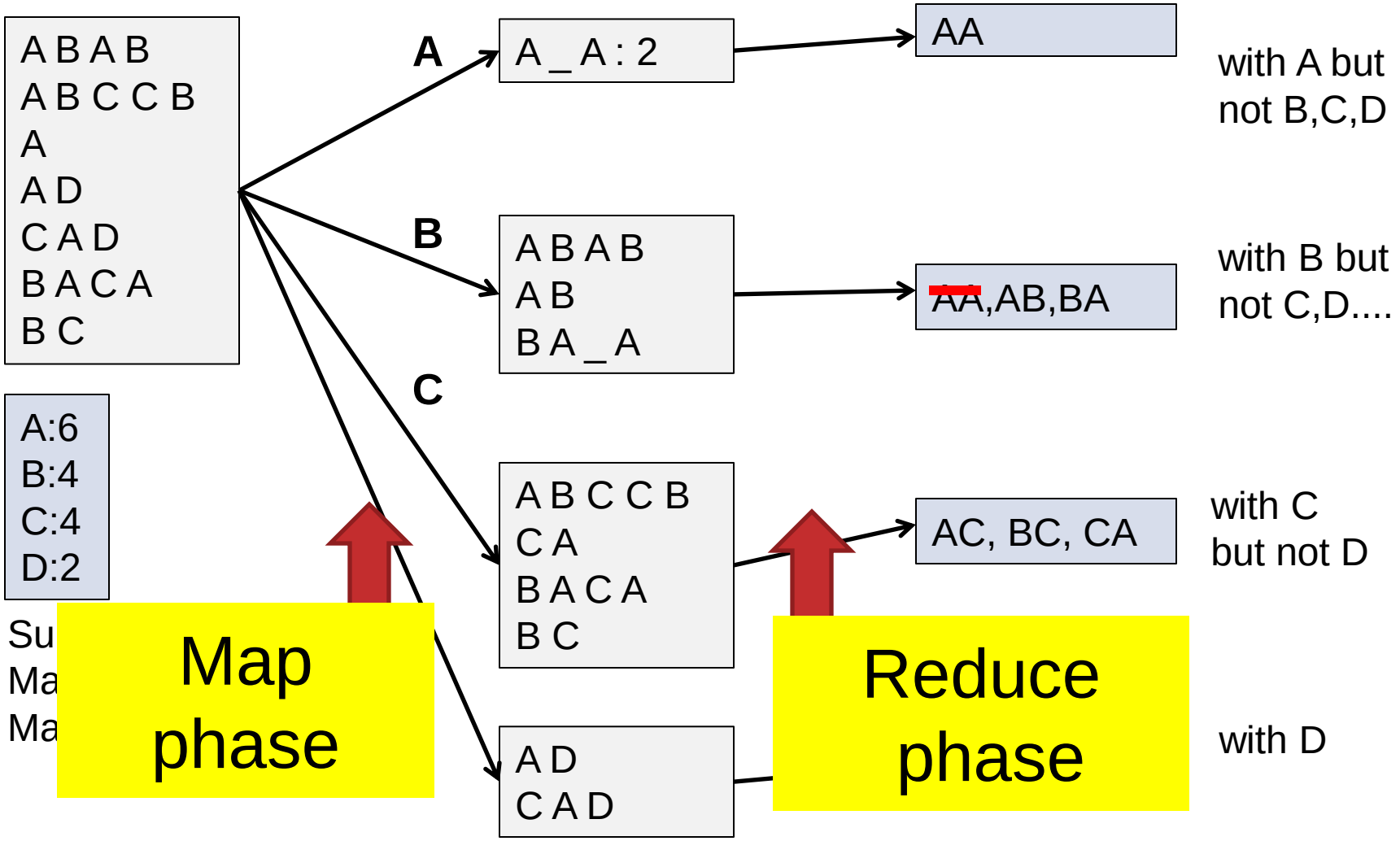
Revisiting example: Naive partitioning



Revisiting example: MG-FSM partitioning



Revisiting example: MG-FSM partitioning



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- The MG-FSM algorithm
- **Experimental Evaluation**
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Experimental evaluation: Setup

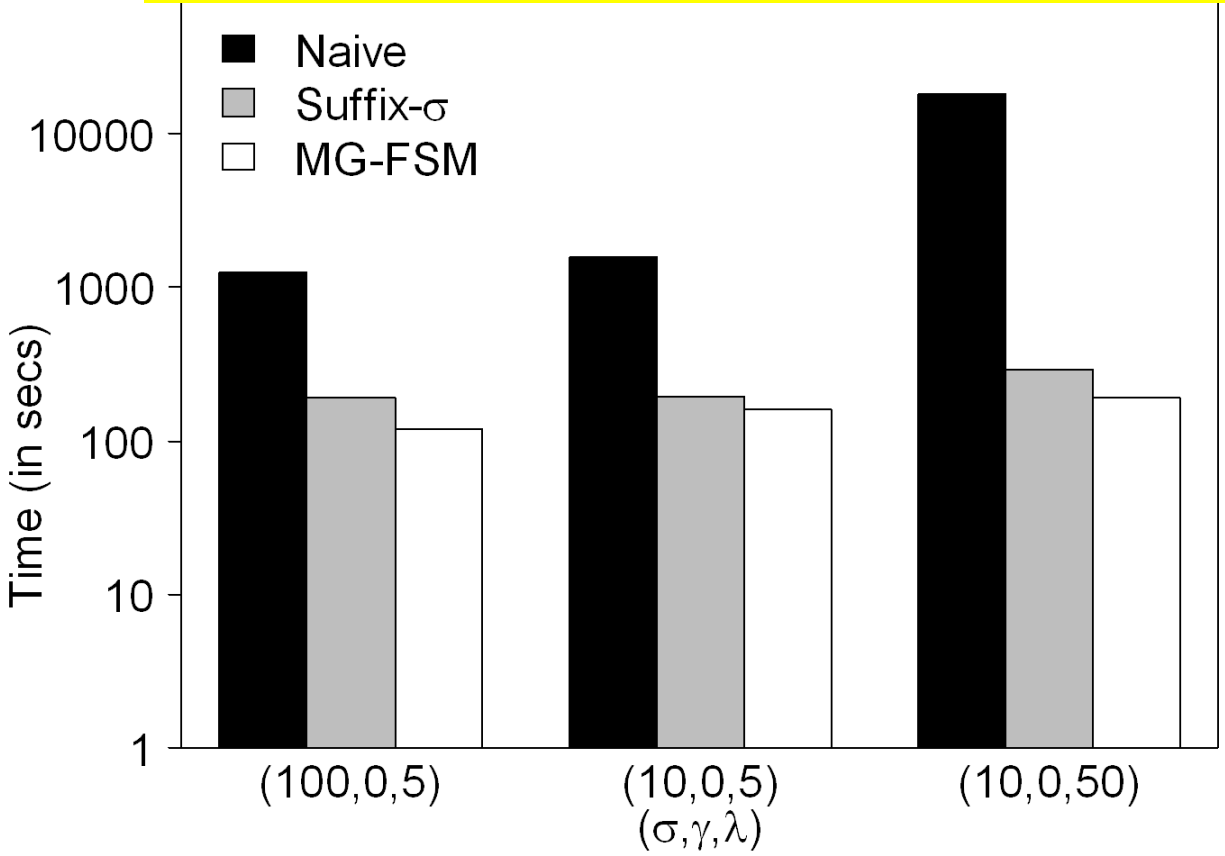
- Algorithms
  - MG-FSM
  - Naive algorithm for MapReduce
  - Suffix-σ (state-of-the-art n-gram miner)
- Setting
  - 10-machine local cluster
  - 10 GBit/64GB of main memory/eight 2TB SAS 7200 RPM hard disks/2 Intel Xeon E5-2640 6-core CPUs
  - Cloudera cdh3u0 distribution of Hadoop 0.20.2.

Experimental evaluation: Datasets

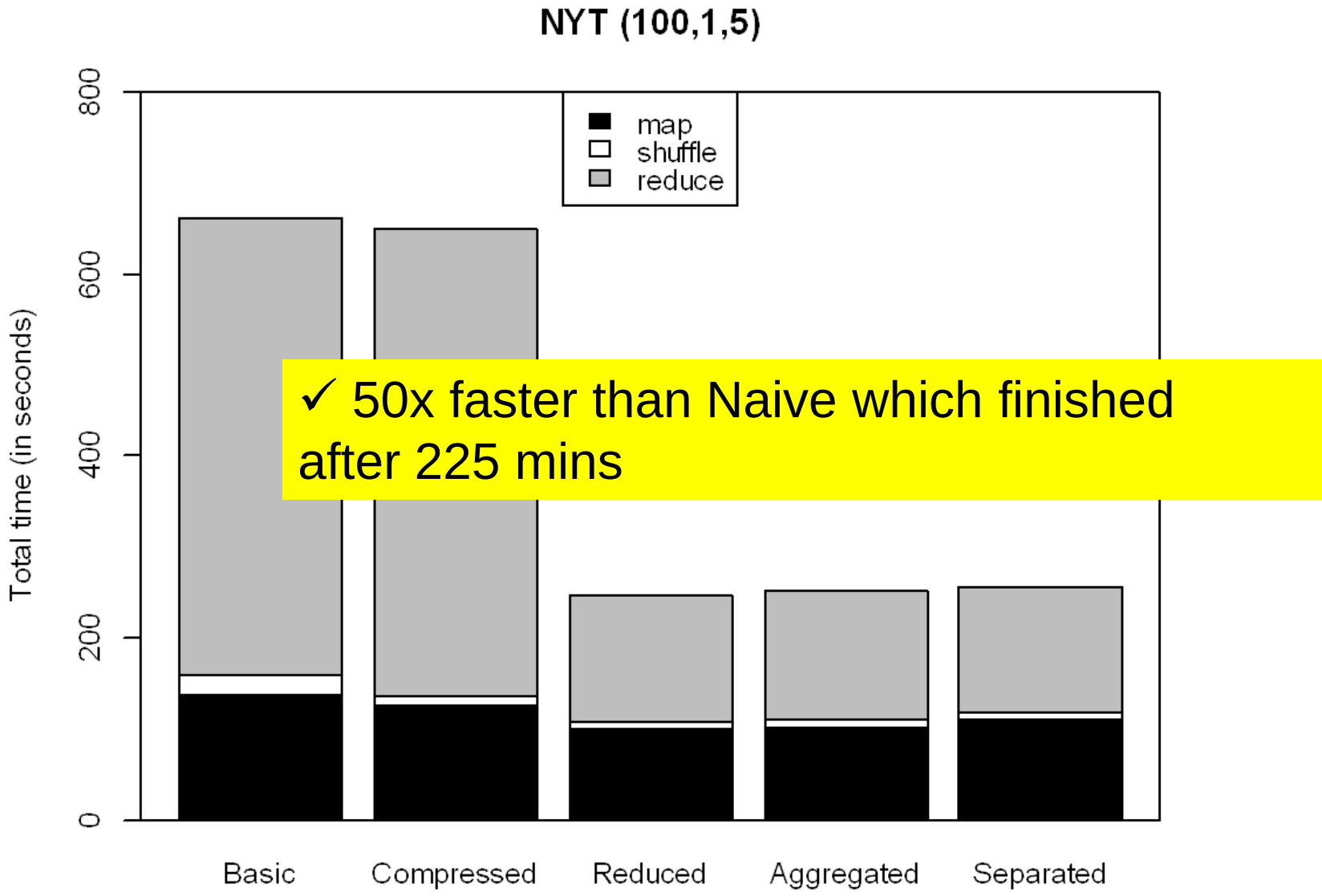
	ClueWeb	New York Times
Average length	19	19
Maximum length	20 993	21 174
Total sequences	1 135 036 279	53 137 507
Total items	21 565 723 440	1 051 435 745
Distinct items	7 361 754	1 577 233
Total bytes	66 181 963 922	3 087 605 146

n-gram mining (γ=0)

✓ Orders of magnitude faster than Naive
✓ Competitive to state-of-the-art n-gram miners



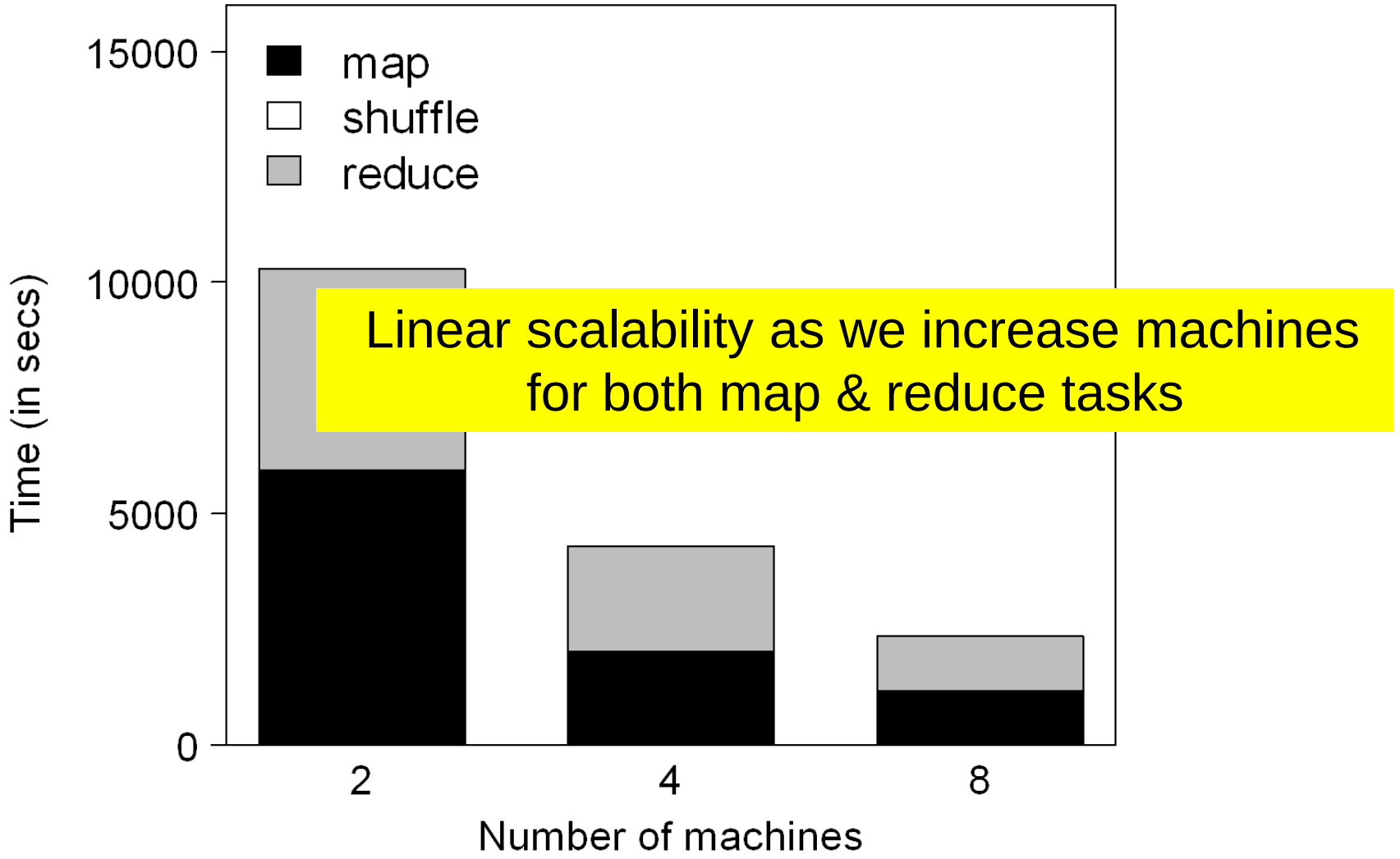
MG-FSM partition optimizations (time)



✓ 50x faster than Naive which finished after 225 mins

Strong scalability

σ=1000,γ=1,λ=5
50% ClueWeb



Linear scalability as we increase machines for both map & reduce tasks

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Summary & Contributions

- MG-FSM mines frequent sequences with gap constraints
- Uses item-based partitioning → partitions can be mined independently and in parallel using *any FSM algorithm*
- Instead of “optimal” partitioning, MG-FSM uses efficient, inexpensive rewrites that ensure correctness
- Fast, low communication cost, scalable

Questions?