managing text data

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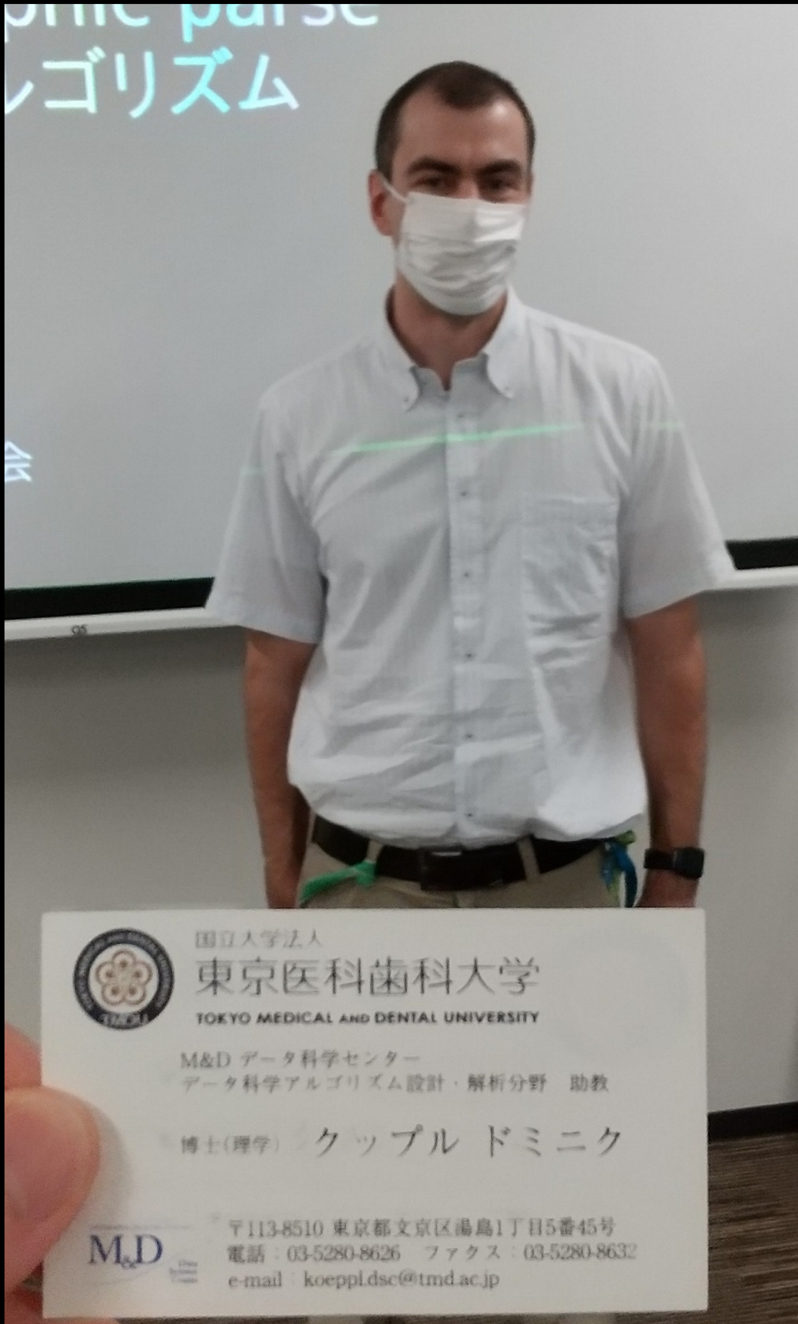


why text data?

text data (strings) are ubiquitous:

- natural texts
- source code

```
namespace C = packed::character;
void print_packed(uint64_t packed) {
   for(size_t i = 0; i < C::FIT_CHARS; ++i) {
      std::cout << C::character(packed, i);
   }
}
```

- DNA

GCTACGT...

- binary code

0110011110101100

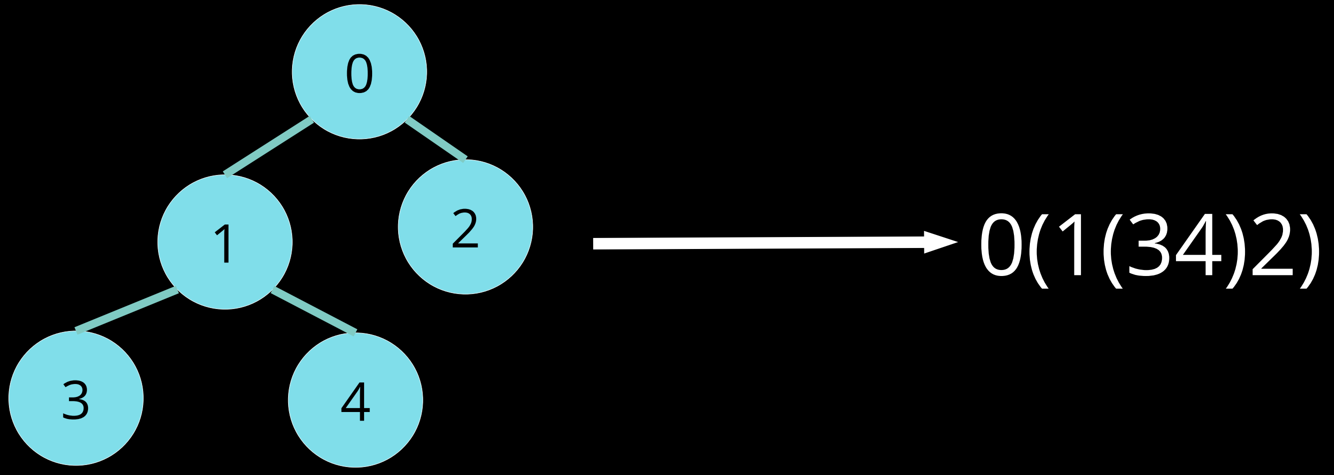
- etc.

why text data?

text data (strings) are ubiquitous:

we can interpret all data one-dimensionally by serialization

- graphs: adjacency lists
- trees: depths first search (mentioned later)



why strings?

string is a simple data type

⇒ already exhaustively treated?

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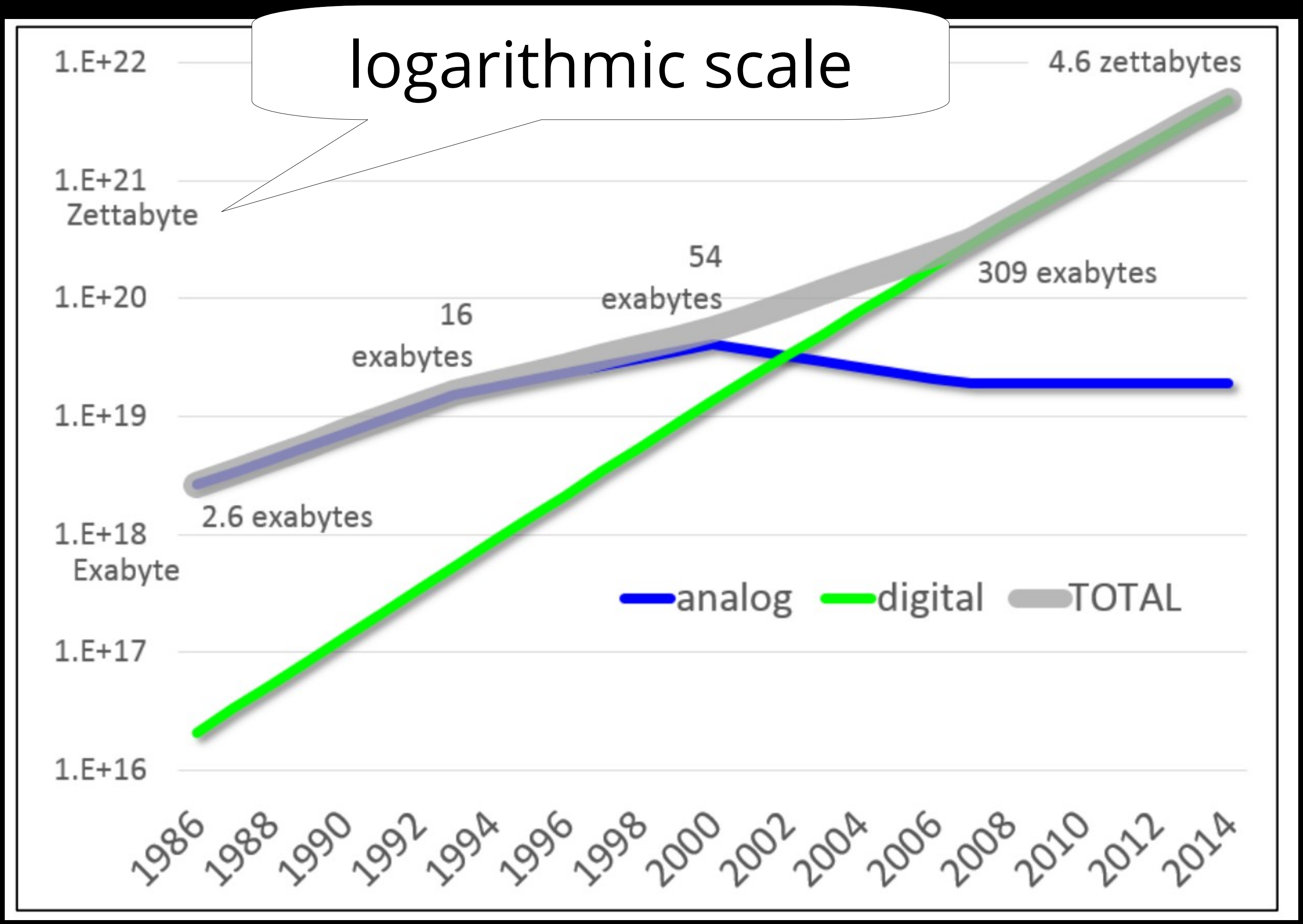
⇒ already exhaustively treated?

many problems occur with big data sizes!

estimated information capacity of the world



[Hilbert, Lopez '11]

big data

- data collections in the web

  Wikipedia, Google Books, etc.

- version control systems

  git, SVN, etc.

- biological data

  1000 Genome Project:

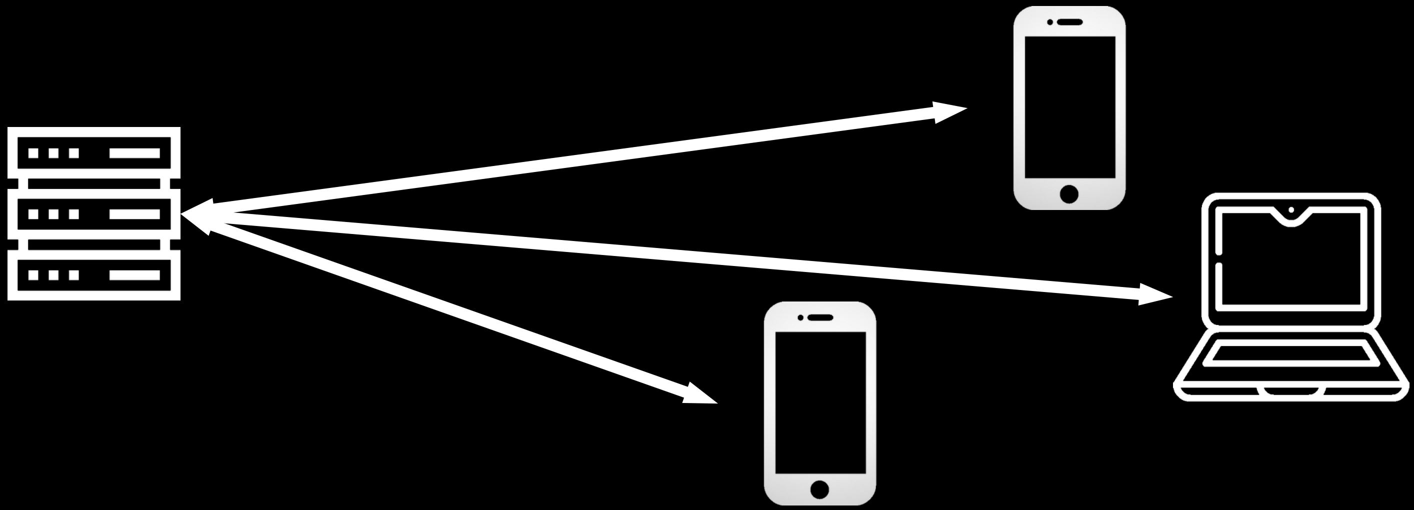
  human genomes, each ~ $3.2 \cdot 10^9$ characters

big data

to manage big data we need

- memory- and
- time-efficient

solutions, in particular for data transfer!



big data

- the problems to solve are often easily describable

    like pattern matching

big data

- the problems to solve are often easily describable

    like pattern matching

but:

- naive solutions are often
    - too slow
    - use too much space

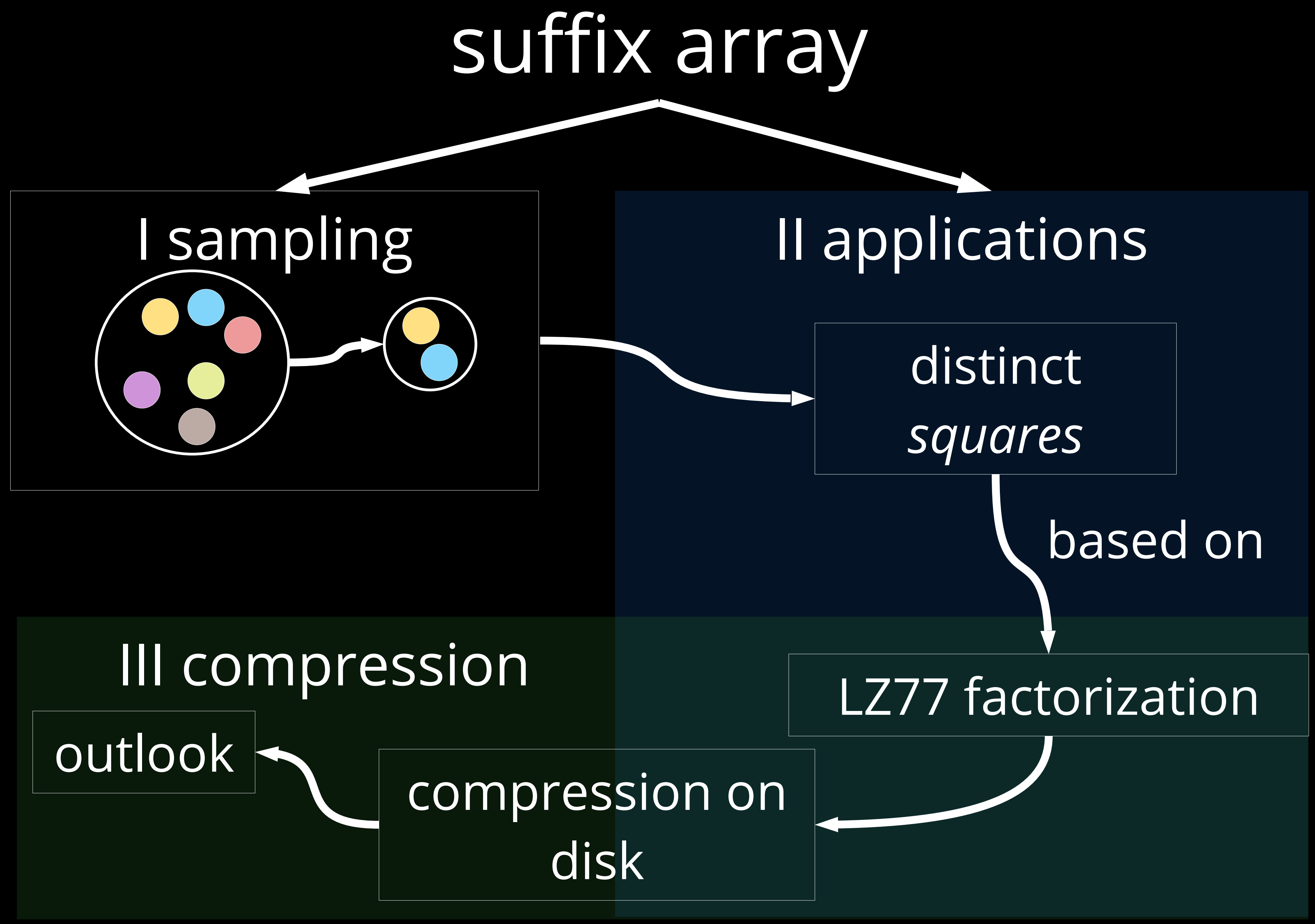
scalability

- how good performs a data structure or an algorithm when scaling the data size?
- goal: given a text with n characters
  - number of steps of an algorithm should be at most linear to n (linear-time algorithm).
    We say: $O(n)$ time
  - same for space (linear-space consumption)
    We say: $O(n)$ space

example text

	1	2	3	4	5	6	7	8	9
T =	a	b	a	b	b	a	b	b	a

- text length: n = |T| = 9
- alphabet Σ = { a , b }
- alphabet size σ = |Σ| = 2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suffix array

1	2	3	4	5	6	7	8	9
a	b	a	b	b	a	b	b	a

T =

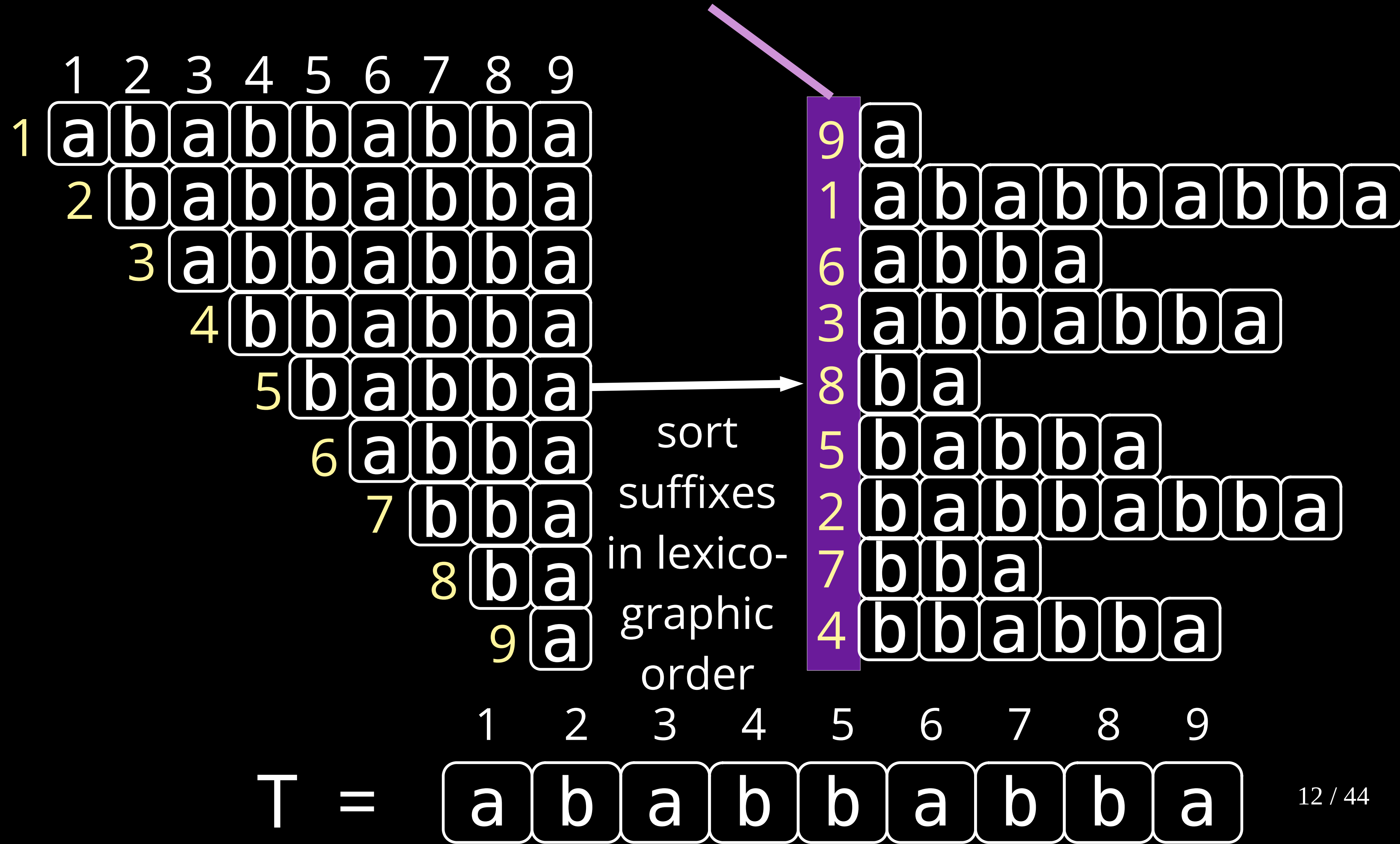
1	2	3	4	5	6	7	8	9
a	b	a	b	b	a	b	b	a

suffix array

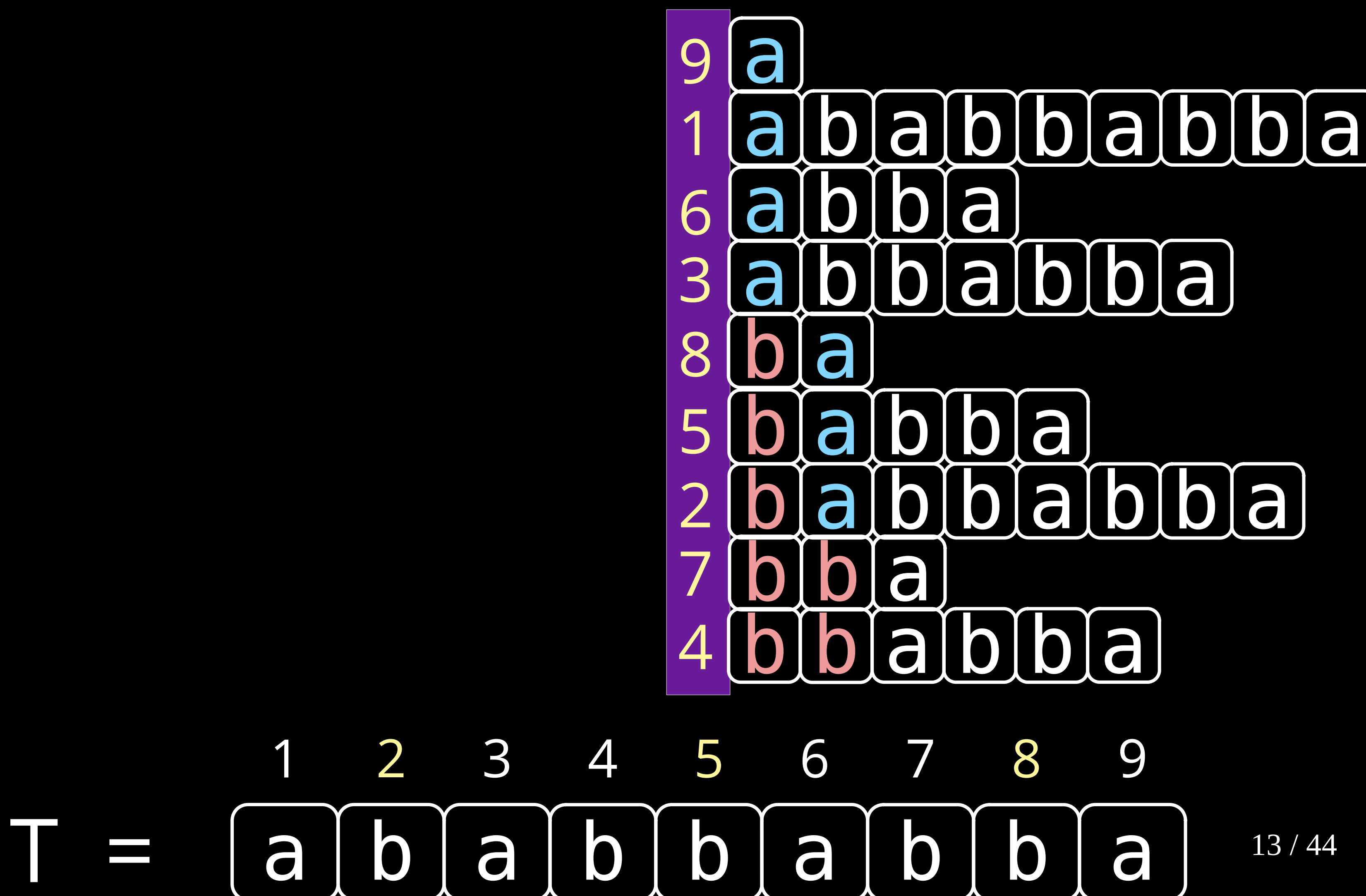
	1	2	3	4	5	6	7	8	9
1	a	b	a	b	b	a	b	b	a
2		b	a	b	b	a	b	b	a
3			a	b	b	a	b	b	a
4				b	b	a	b	b	a
5					b	a	b	b	a
6						a	b	b	a
7							b	b	a
8								b	a
9									a

	1	2	3	4	5	6	7	8	9
T =	a	b	a	b	b	a	b	b	a

suffix array



pattern matching : # ba = ?



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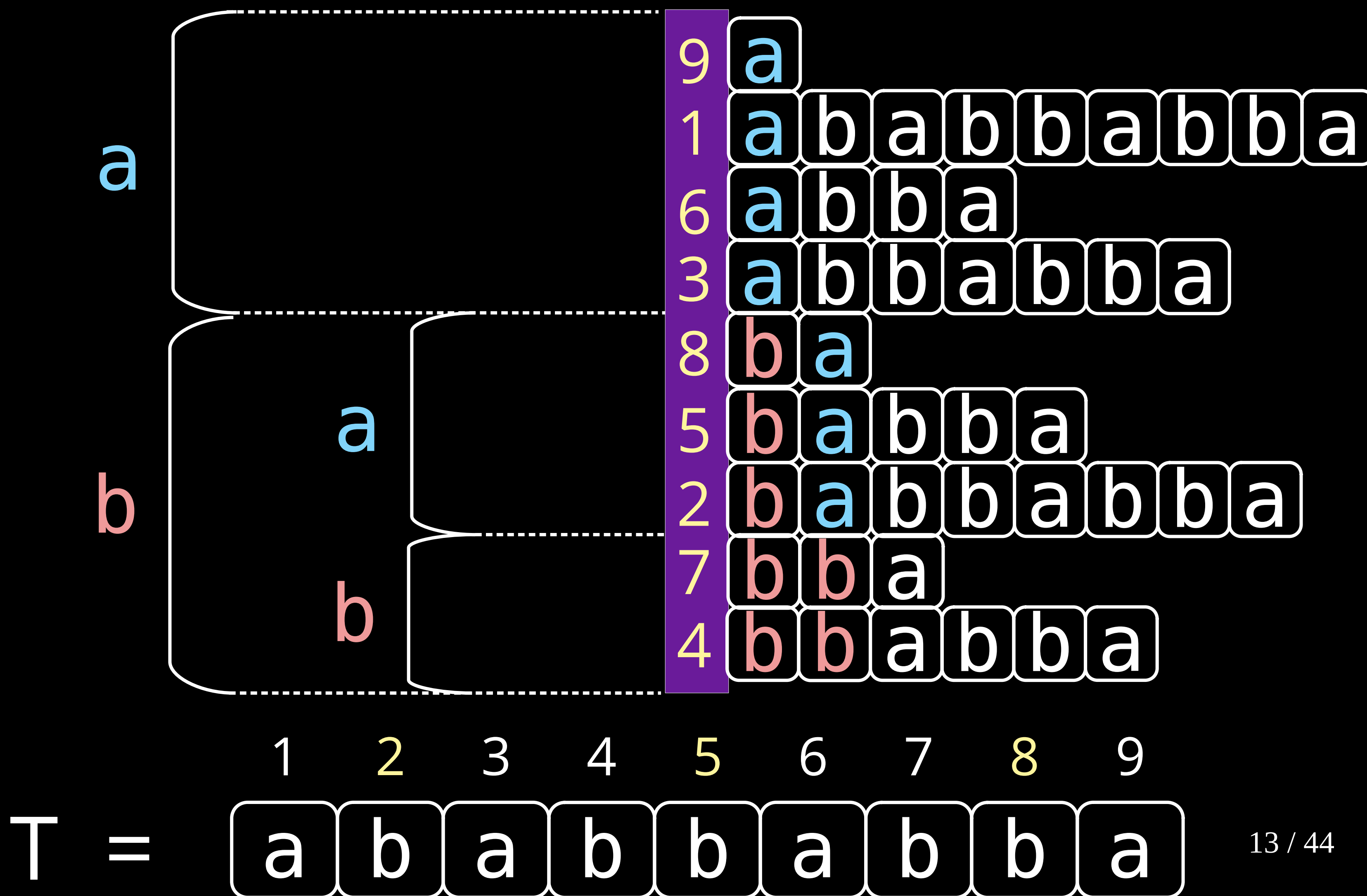
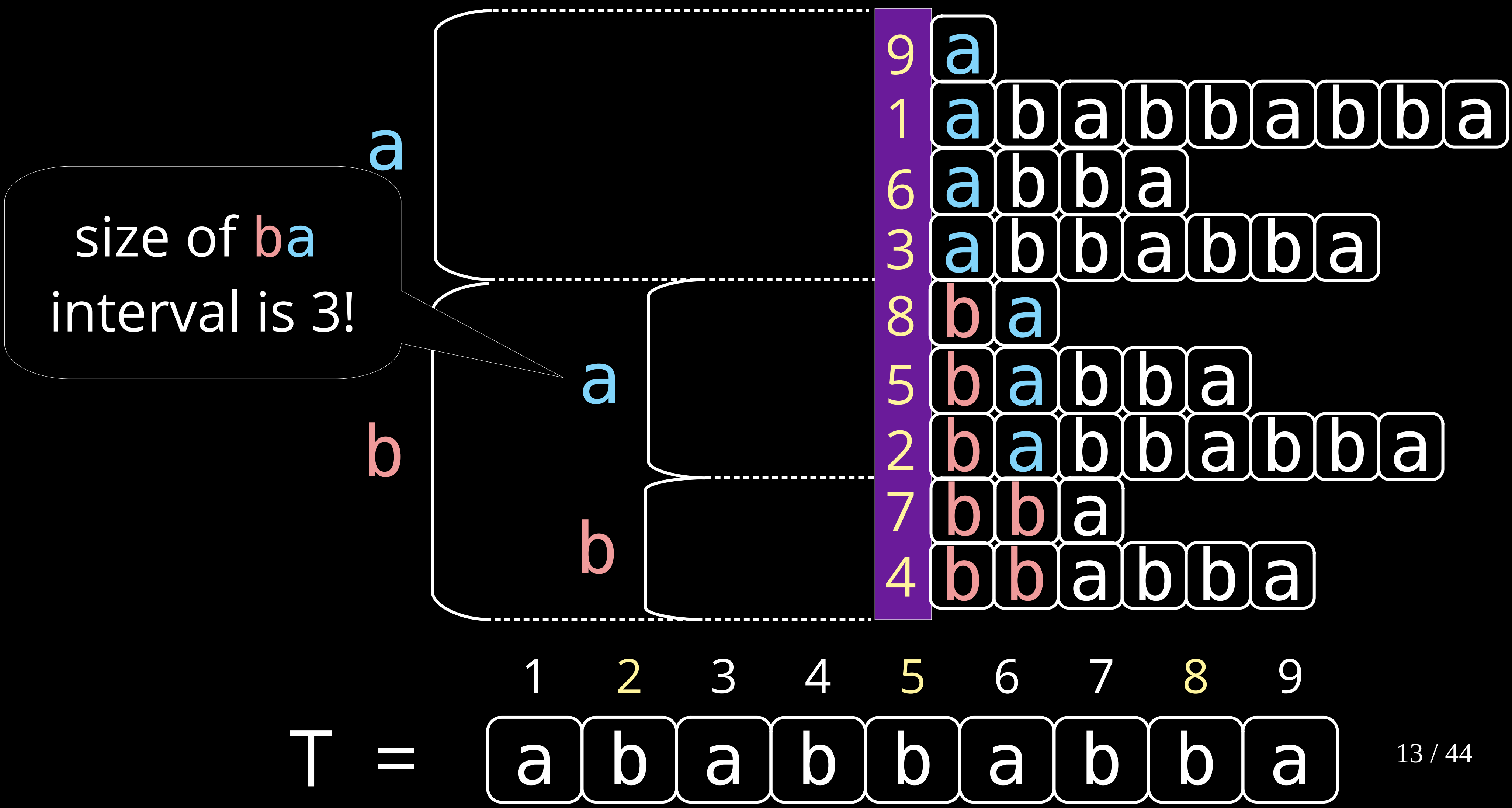
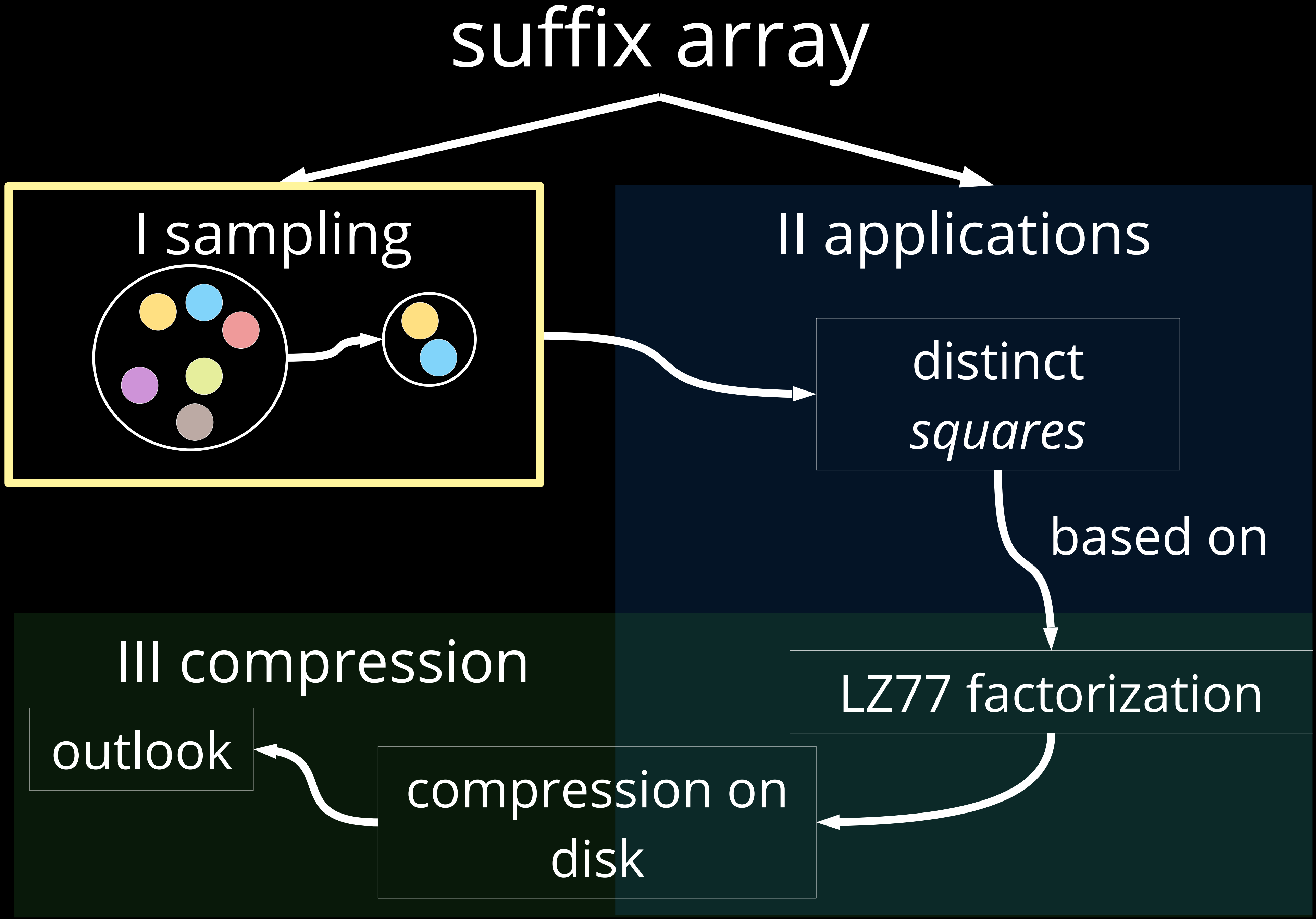


pattern matching : # ba = ?

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I. sampling

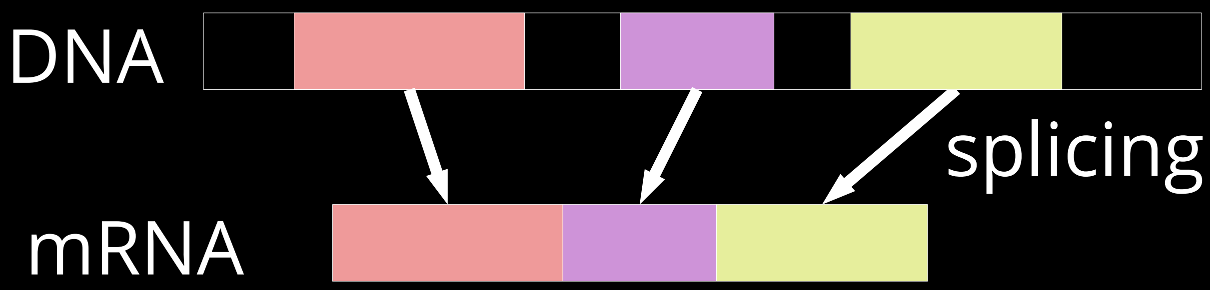
- assume we are only interested in indexing m text positions
- such a suffix array should
  - take $O(n)$ time and
  - $O(m)$ space, also during the construction
    ⇒ *sparse* suffix array

	1	2	3	4	5	6	7	8	9
T =	a	b	a	b	b	a	b	b	a

sparse suffix array

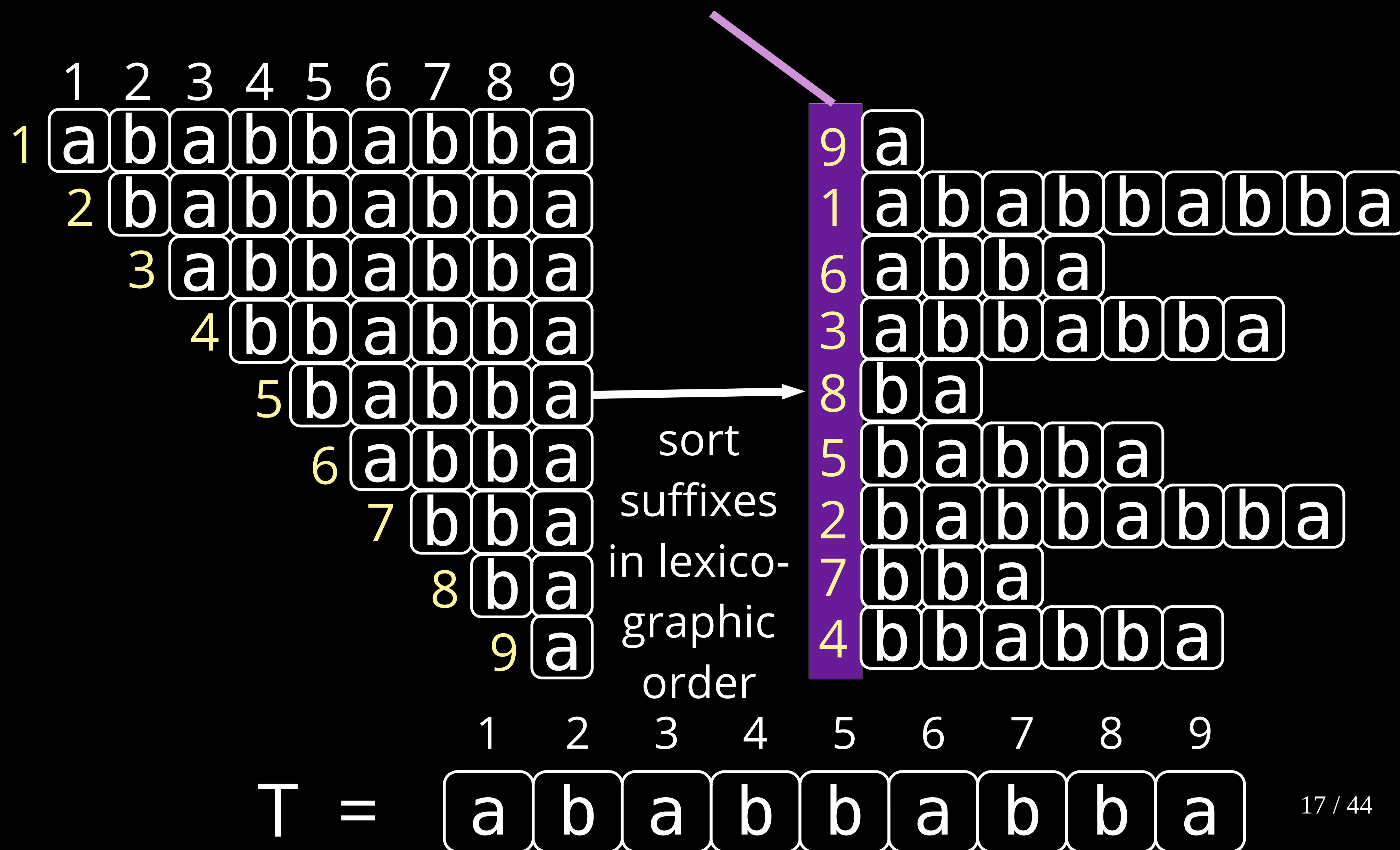
- sort only *m* suffixes
- but why?
  - only interested in word beginnings
  - coding sections of DNA sequences

Once upon a time ....

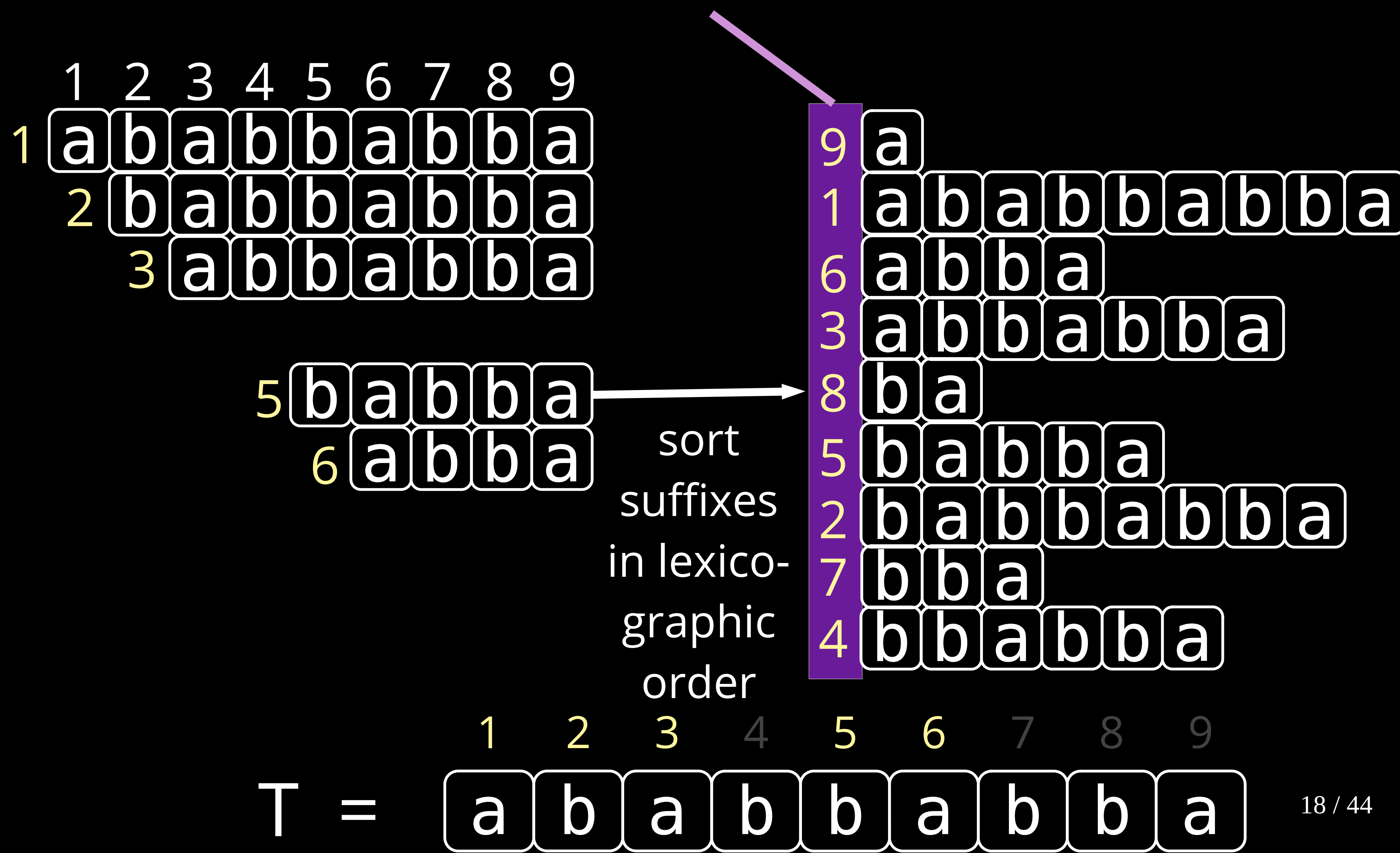


	1	2	3	4	5	6	7	8	9
T =	a	b	a	b	b	a	b	b	a

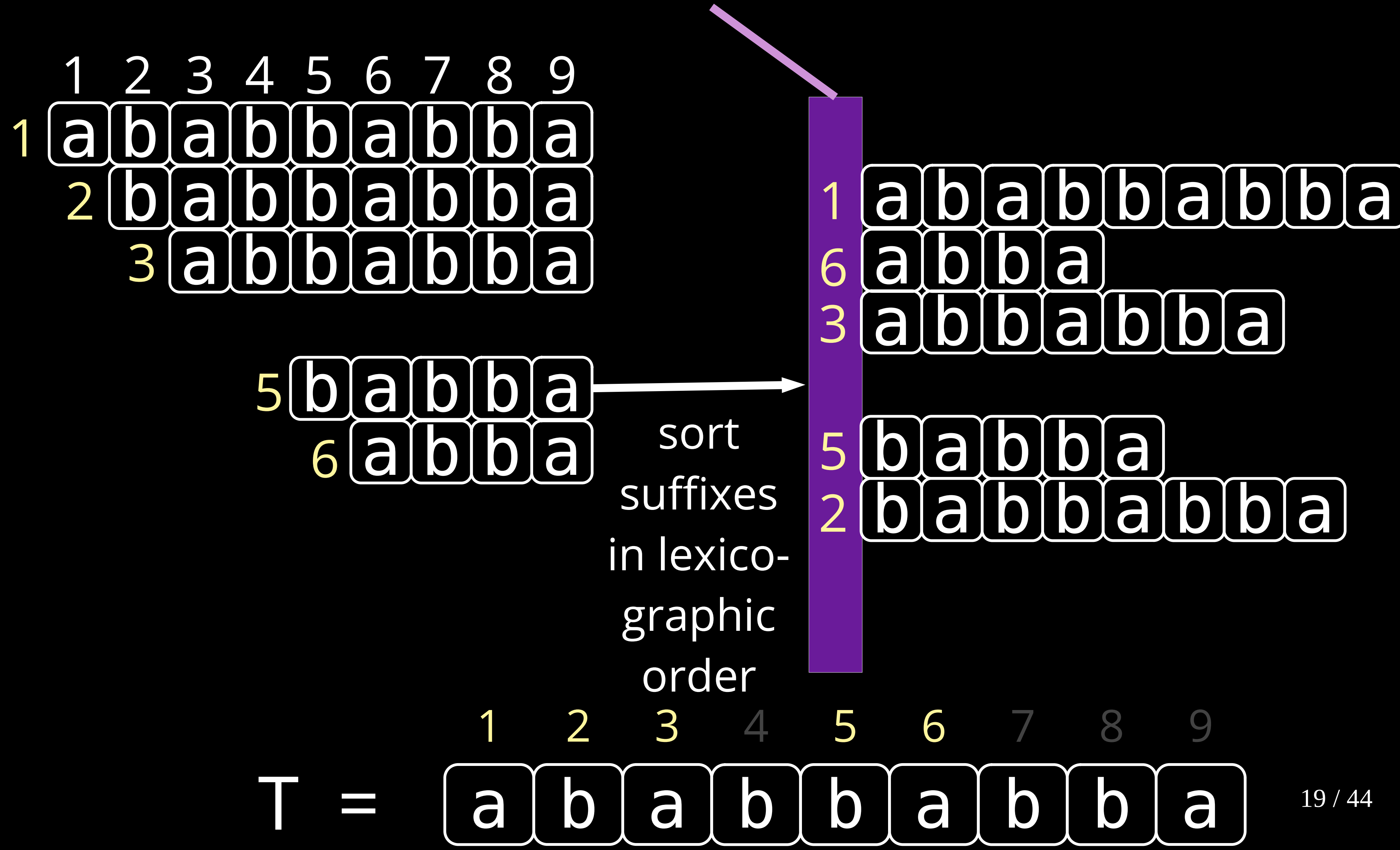
suffix array



suffix array



sparse suffix array



sparse suffix array

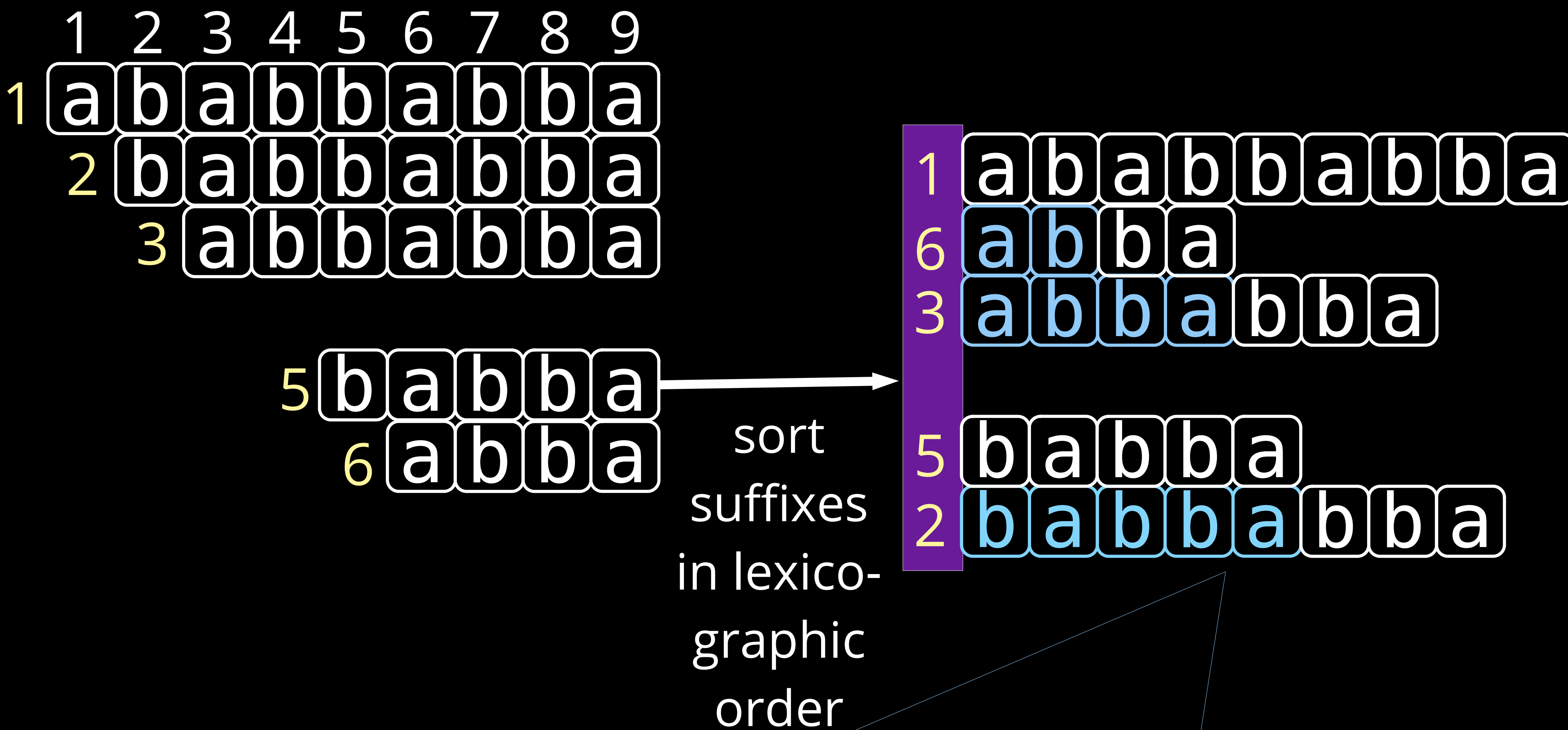
- can construct suffix array in $O(n)$ time and $O(n)$ space [Nong+ '11]
- how much time do we need to construct the sparse suffix array in $O(m)$ space?

naive: $O(mn)$ time (+ sorting integers)

- each suffix has a length of at most n
- sort all m suffixes ⇒ $O(mn)$ character comparisons

2 suffixes

sparse suffix array



LCP: length of the longest common prefix
with its lexicographic predecessor

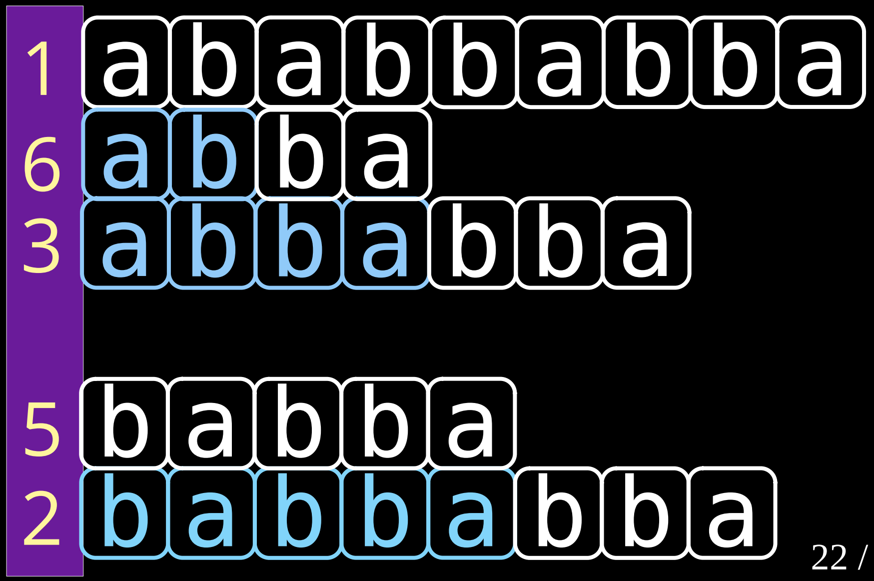
construction of the sparse suffix array

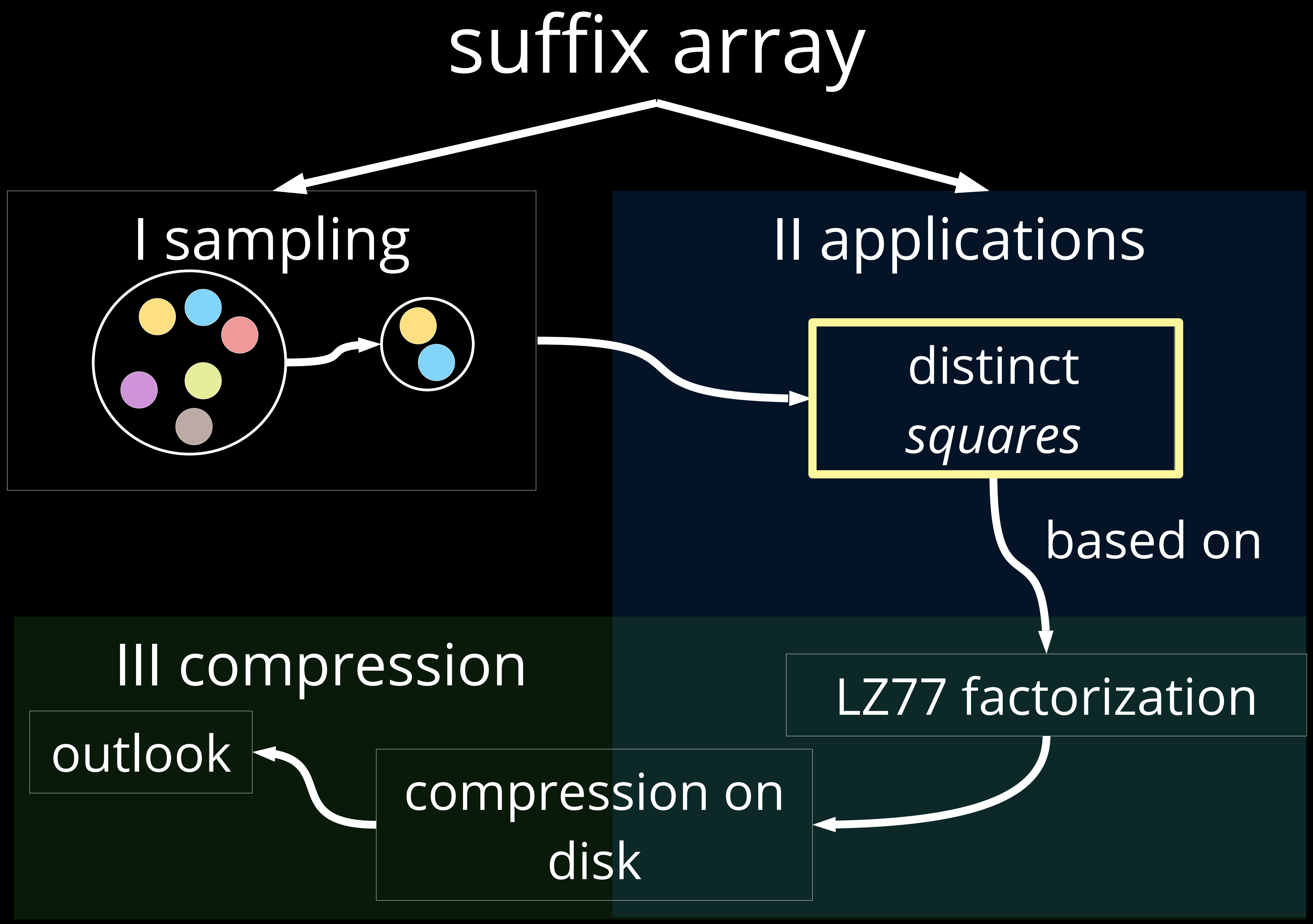
- c : sum of all LCPs
- need to compare c characters to determine the order of the suffixes

⇒ at least c time necessary

[TALG' 20]:

- O(m) space
- O($c \lg n + m \lg^2 n$) time
- fastest (deterministic) solution for small c

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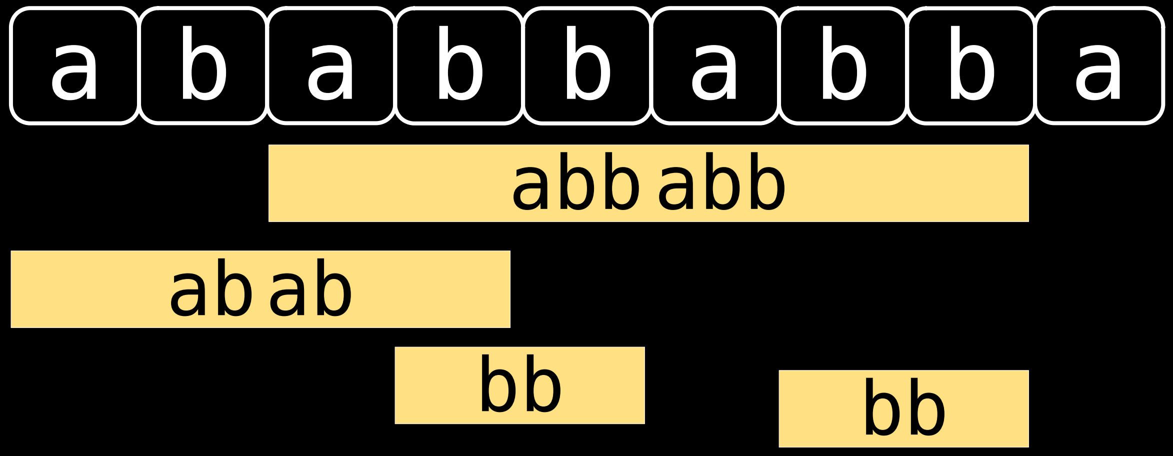
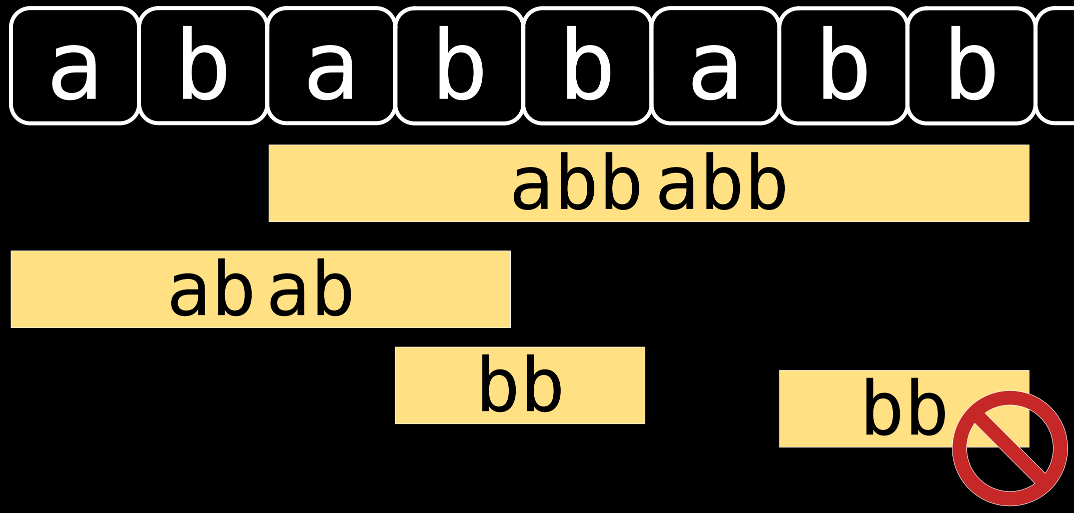
all distinct squares

- square: substring of the form A A



all distinct squares

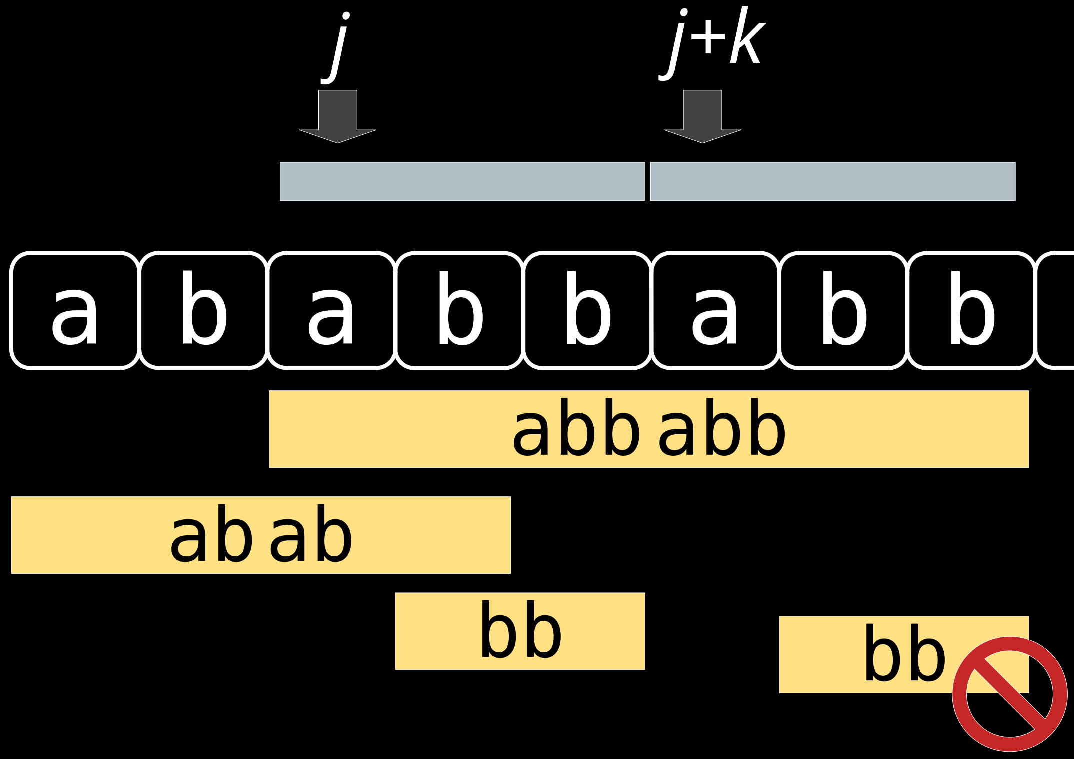
- square: substring of the form A A
- aim: list only all different squares (useful for DNA fingerprinting, etc.)
- at most $2n$ many different squares



naive approach

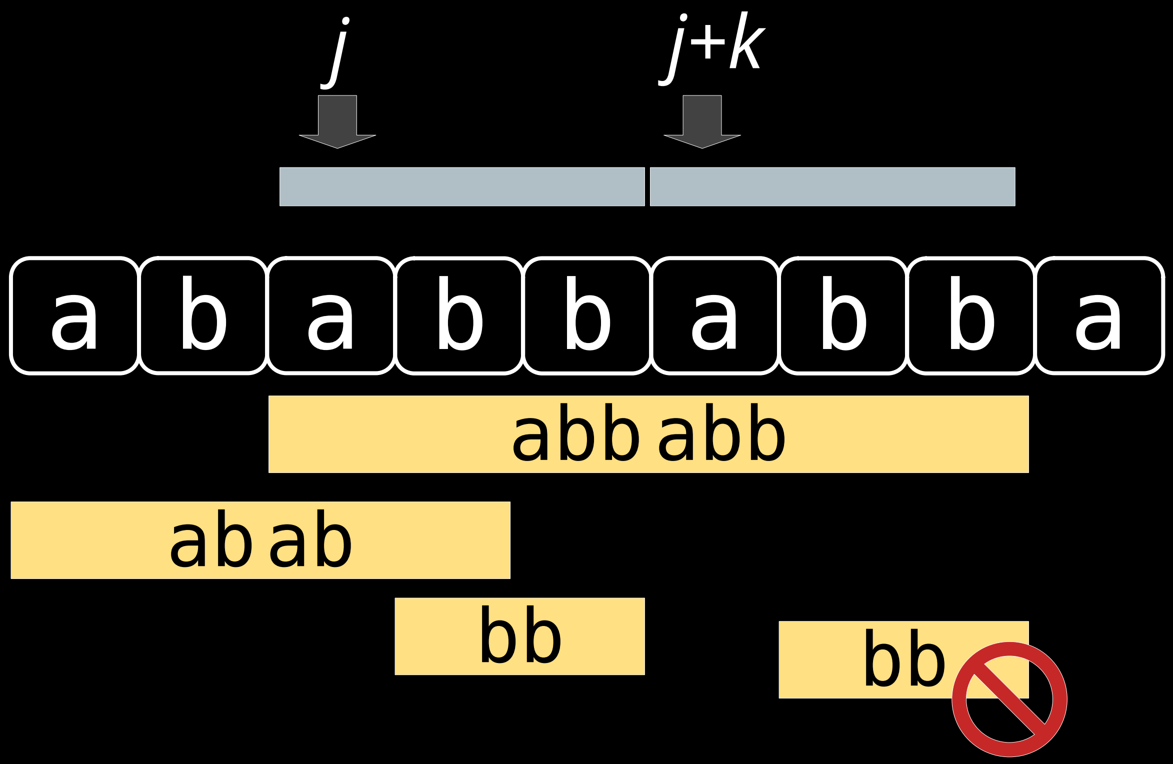
- test for all text positions j and lengths k if $T[j..j+k-1]$ and $T[j+k..j+2k-1]$ make a square

⇒ at least n^2 time



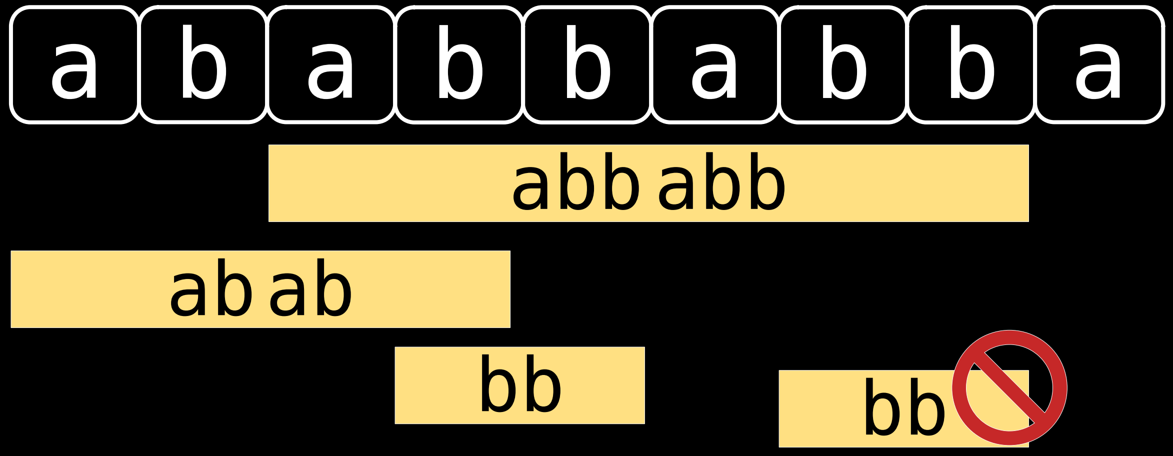
linear time algorithm

- [CPM '17] : O(n) time algorithm
- only choose specific j und k



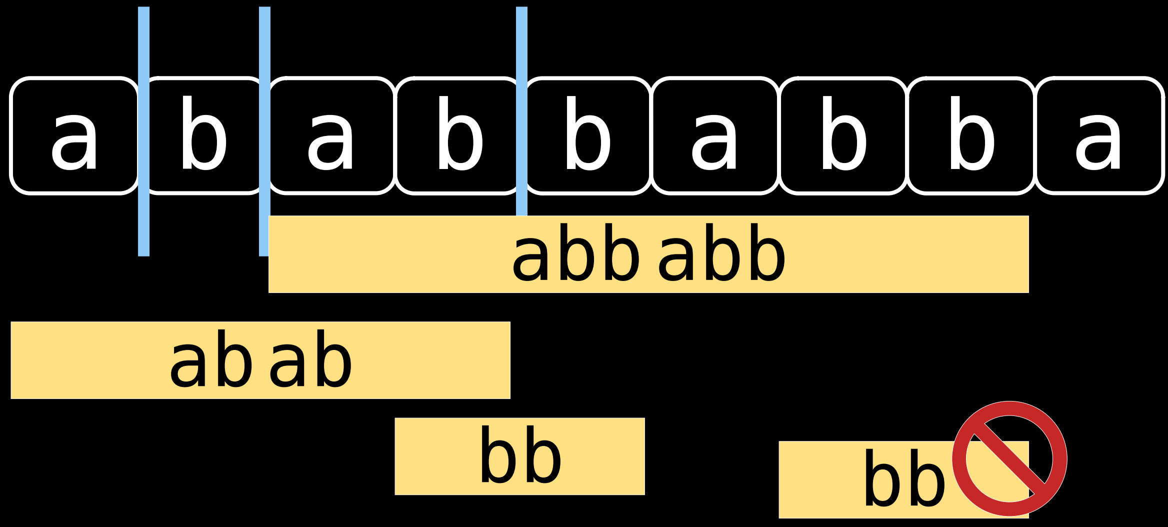
linear time algorithm

- idea: only report the leftmost ones



linear time algorithm

- idea: only report the leftmost ones
- find them with the
  Lempel-Ziv 77 (LZ77) factorization



linear time algorithm

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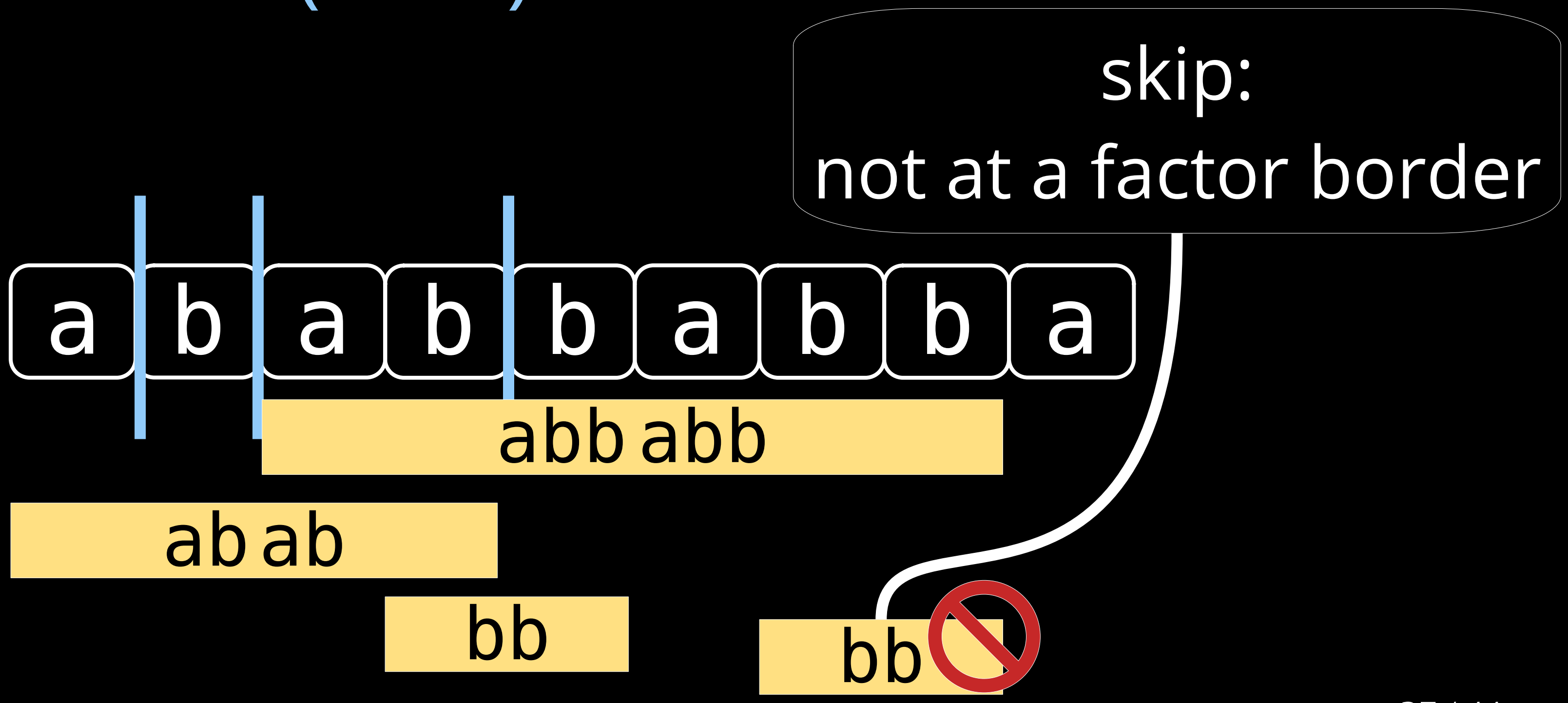

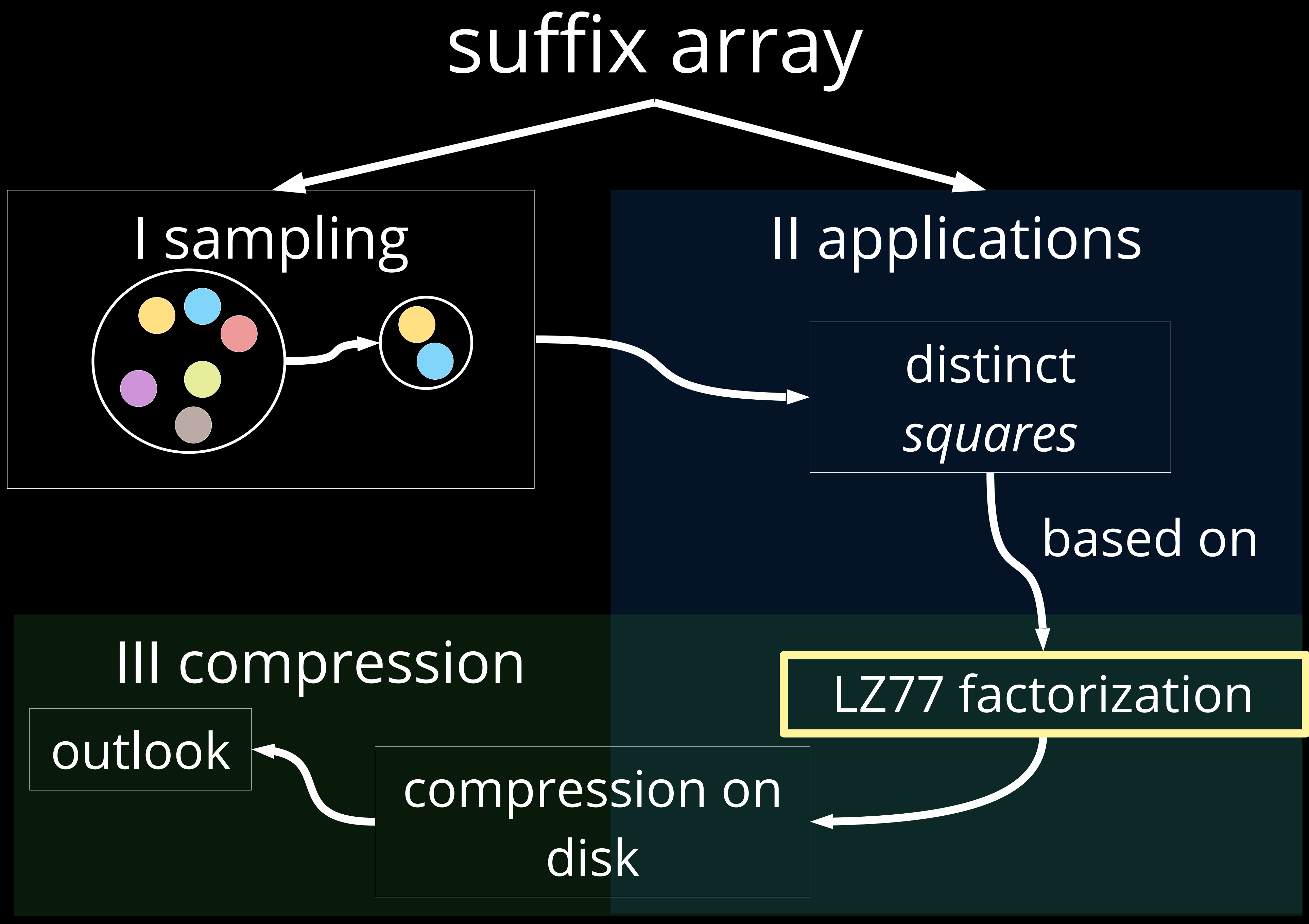
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LZ77

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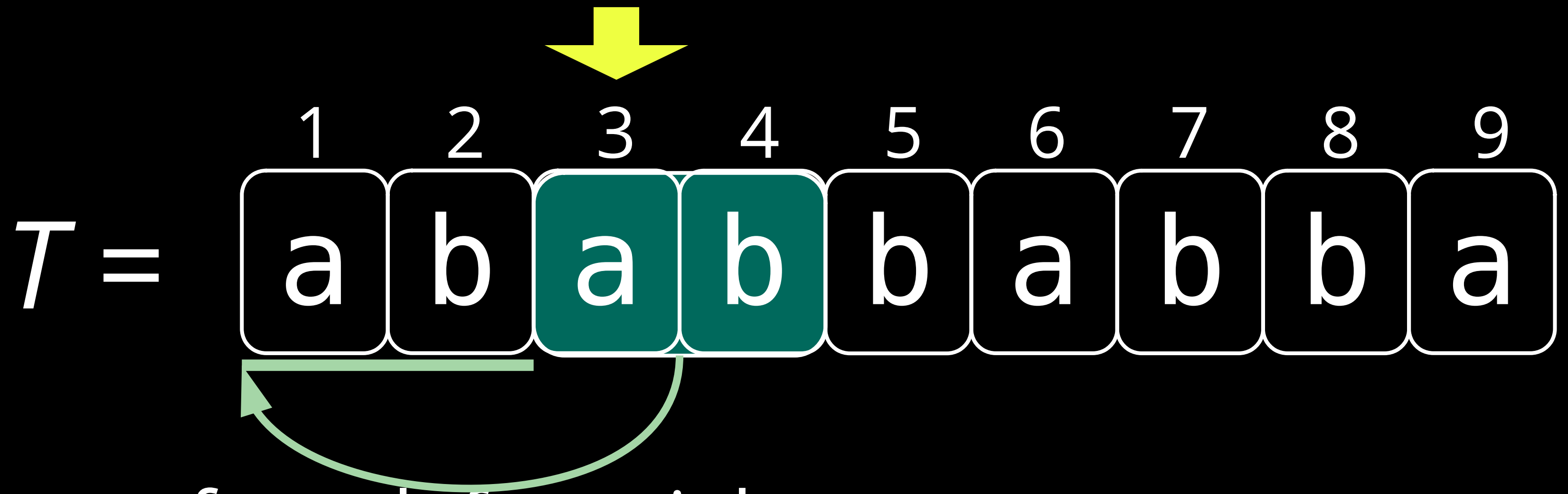
T =	a	b	a	b	b	a	b	b	a

LZ77

	1	2	3	4	5	6	7	8	9
T =	a	b	a	b	b	a	b	b	a

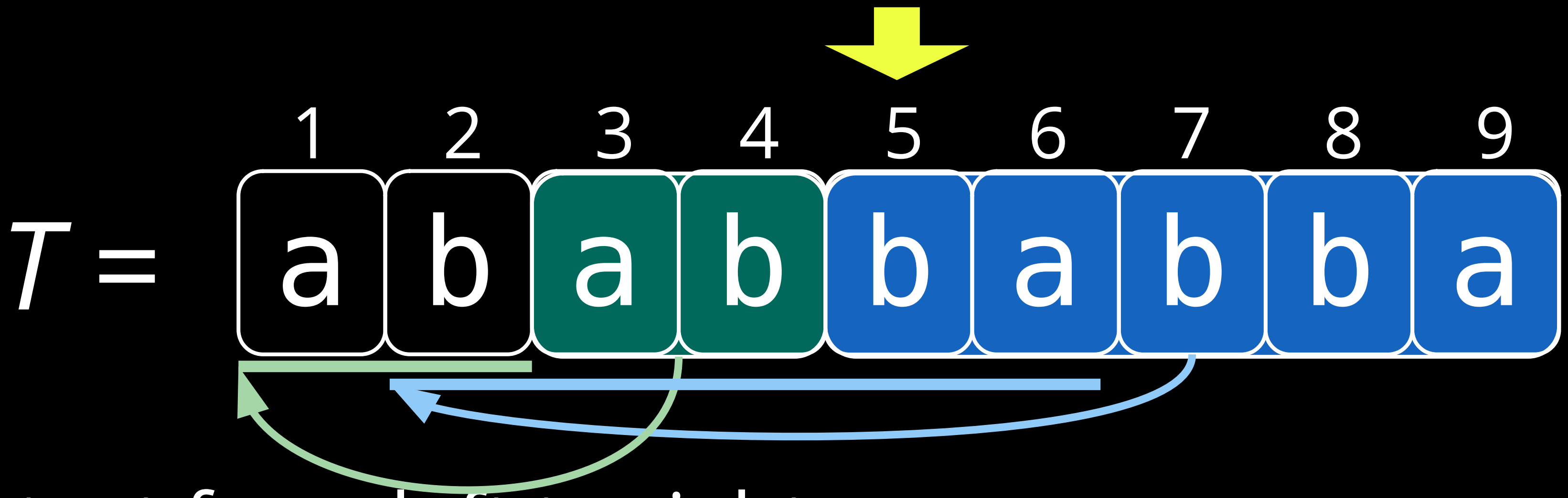
- read text from left to right

LZ77



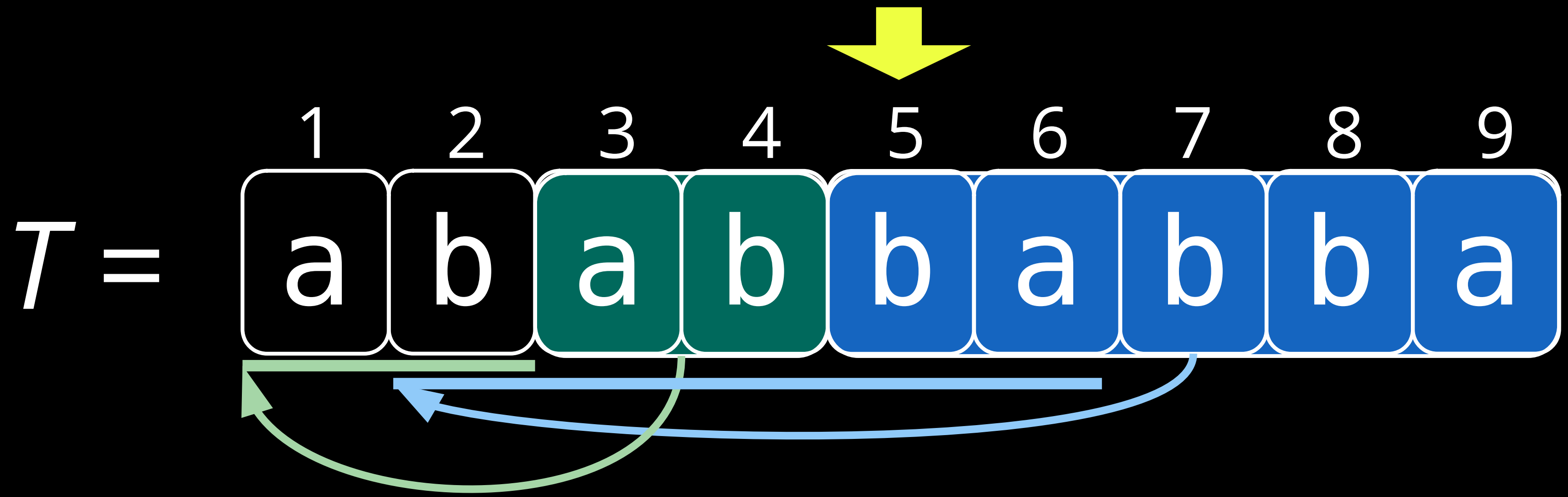
- read text from left to right
- replace longest repetition occurring in read part

LZ77



- read text from left to right
- replace longest repetition occurring in read part
- support overlapping

LZ77



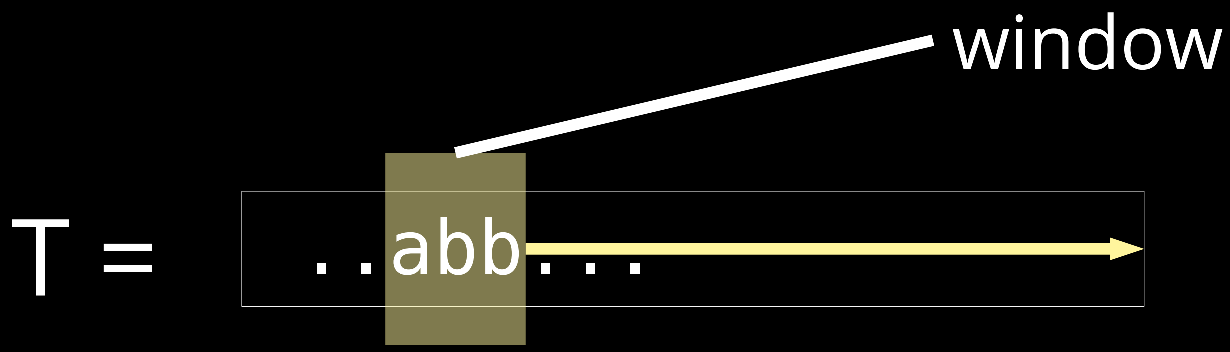
- read text from left to right
- replace longest repetition occurring in read part
- support overlapping

⇒ finds repetitions (and leftmost squares)

LZ77 compression

[Lempel, Ziv '77]

- high compression ratios
- popular: zip, gzip, 7zip, png, ...
- technique: window search



fixed window

search for repetitions only within a fixed window width

- memory-efficient
- but: far redundancies cannot be found

  e.g. compress 100 *identical* human genomes

```
repetitive data with a gap are overlooked repetitively
```

fixed window

search for repetitions only within a fixed window width

- memory-efficient
- but: far redundancies cannot be found

e.g. compress 100 *identical* human genomes

already forgotten

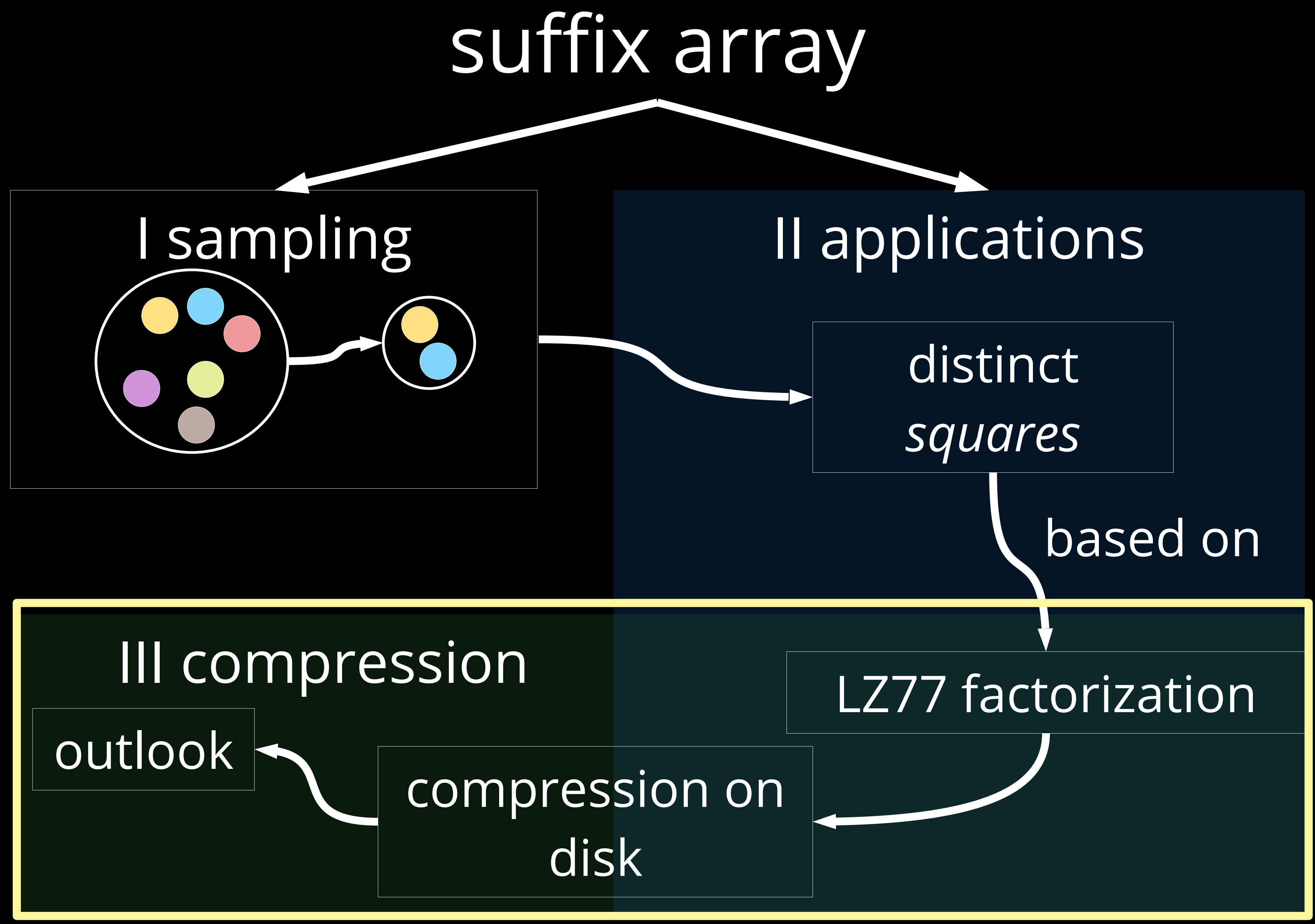
`repetitive data with a gap are overlooked repetitively`

without window

solution: work on the entire input!

- improves compression rate
- for 200 MiB repetitive DNA:

compressor	ratio (less better)	memory
`gzip -1`	30,73%	7 MiB
`gzip -9`	26,22%	7 MiB
LZ77 without window	4,05%	2900 MiB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III. compress big data

if the data does not fit into memory, work

1) with compact data structures for LZ77 [Algorithmica '18]

2) on hard disk [ESA '19]

III. compress big data

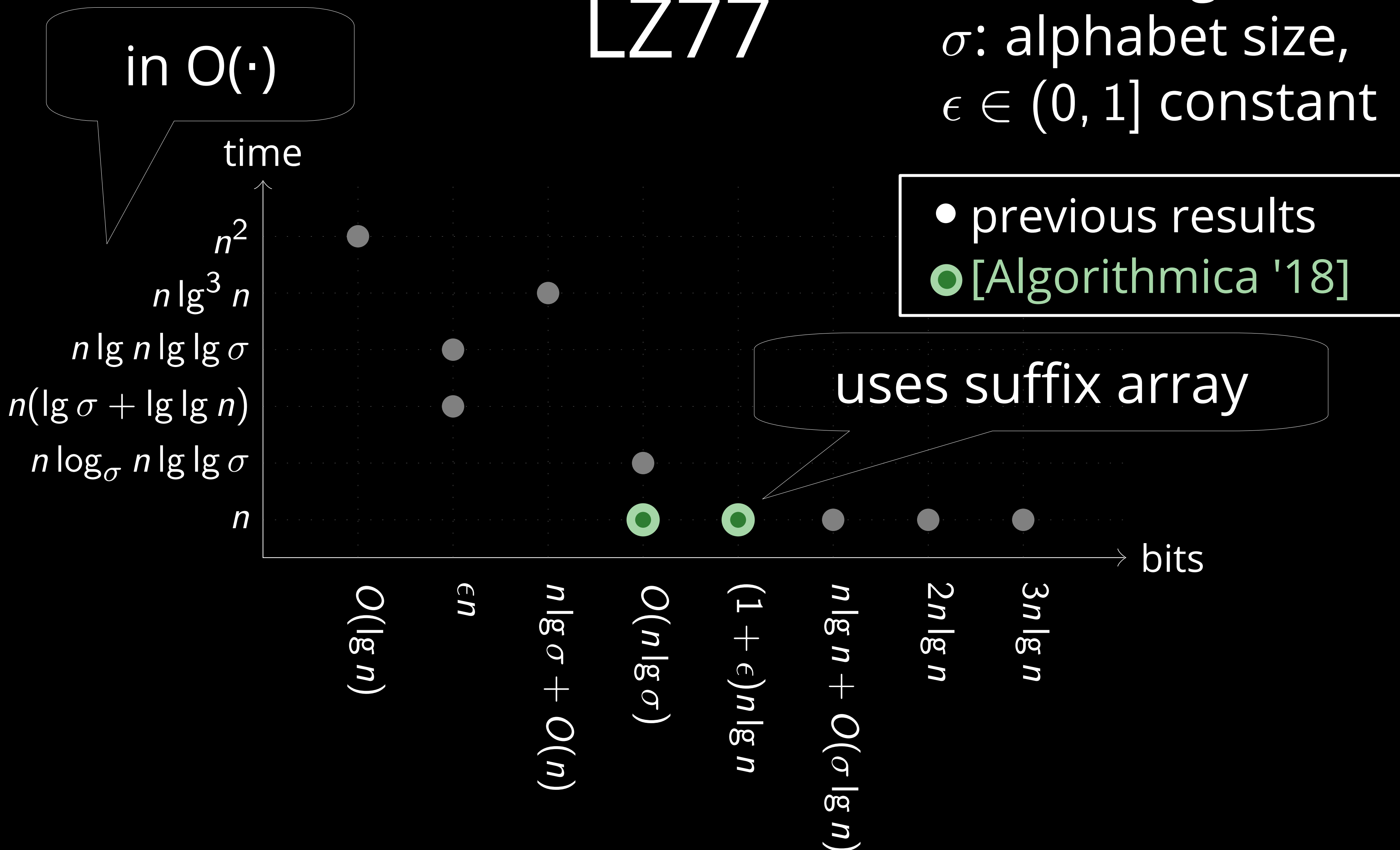
if the data does not fit into memory, work

1) with compact data structures for LZ77
[Algorithmica '18]

2) on hard disk [ESA '19]

LZ77

n: text length,
σ: alphabet size,
$\epsilon \in (0,1]$ constant



smallest space among linear-time algorithms!

III. compress big data

if the data does not fit into memory, work

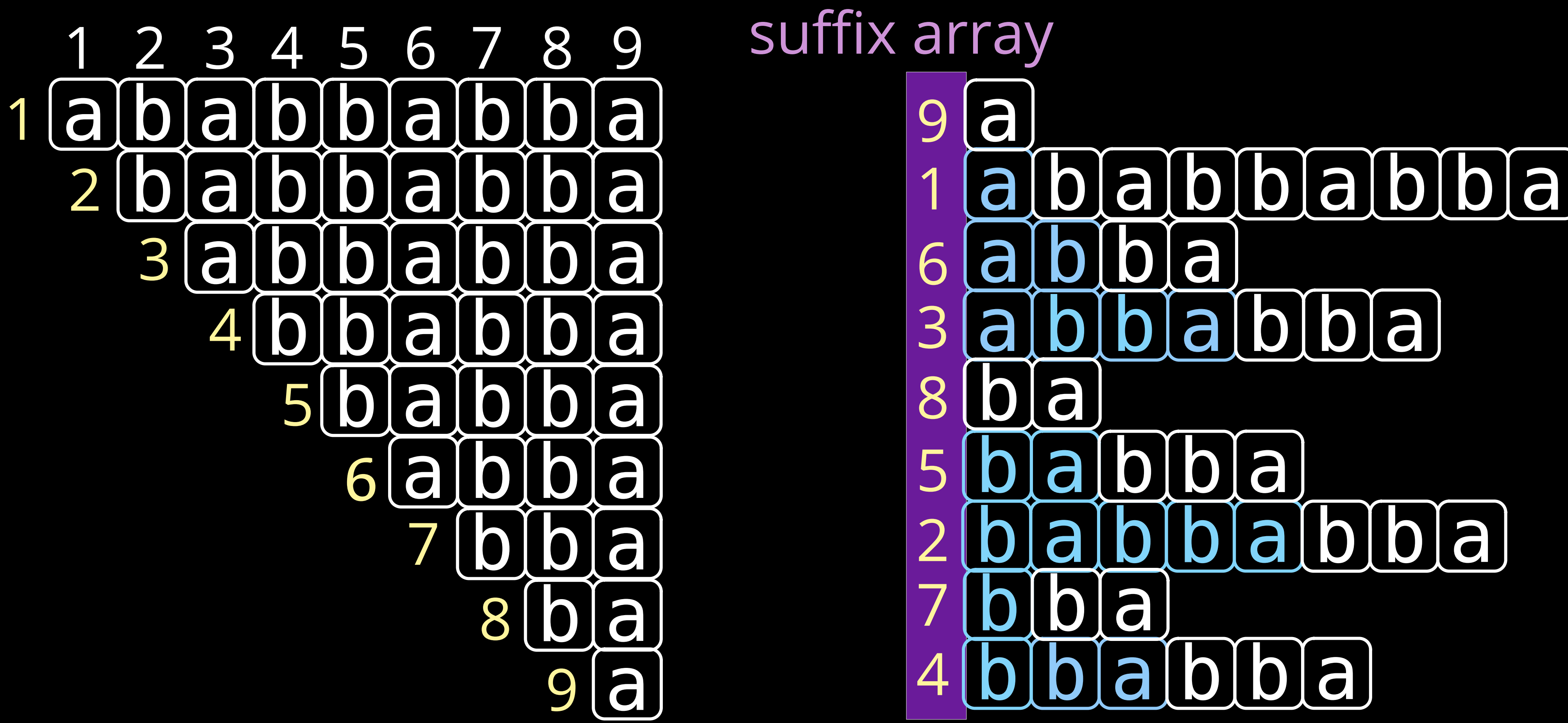
1) with compact data structures for LZ77 [Algorithmica '18]

2) on hard disk [ESA '19]

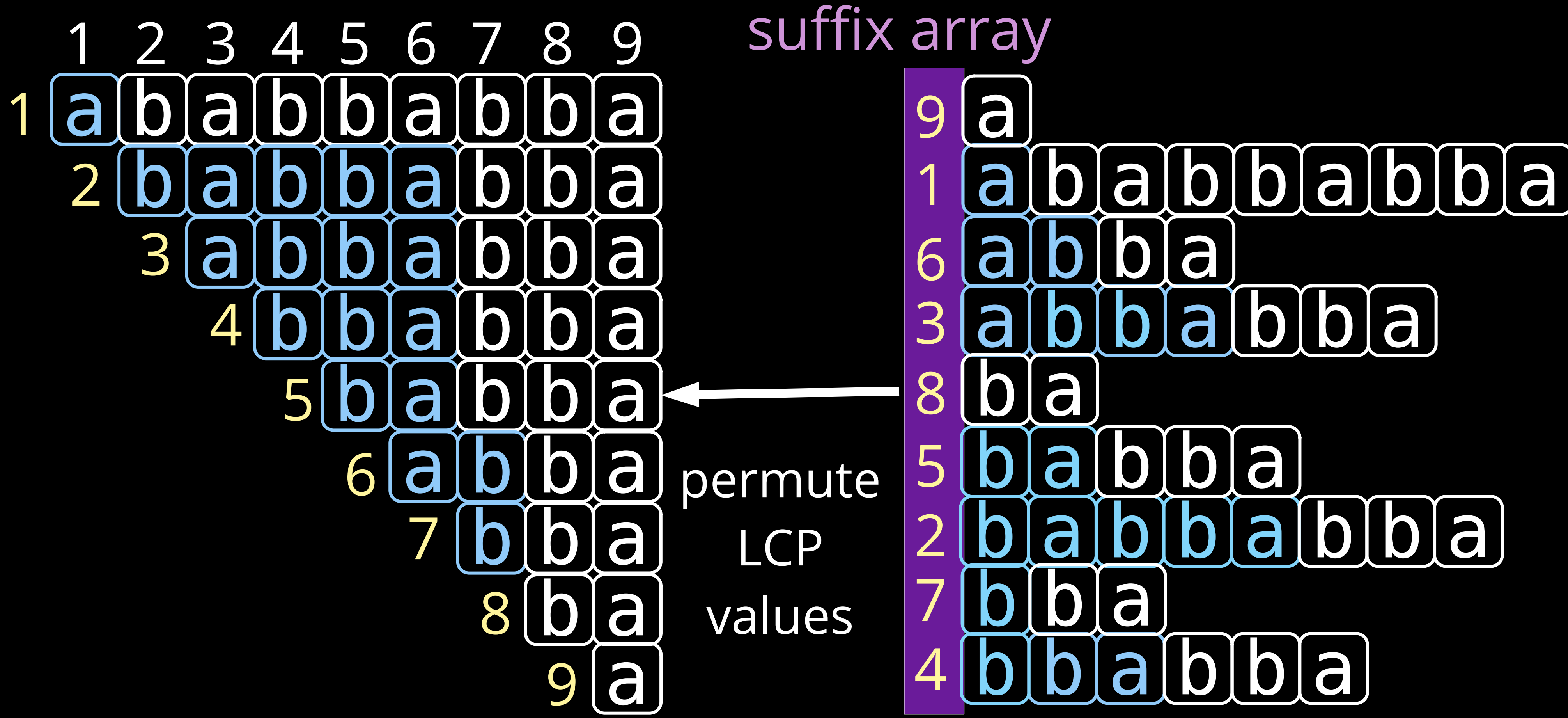
plcpcomp

- variation of LZ77
- works on hard drive for really large data
- idea:
  - search for longest factors first
  - permute LCPs of suffix array

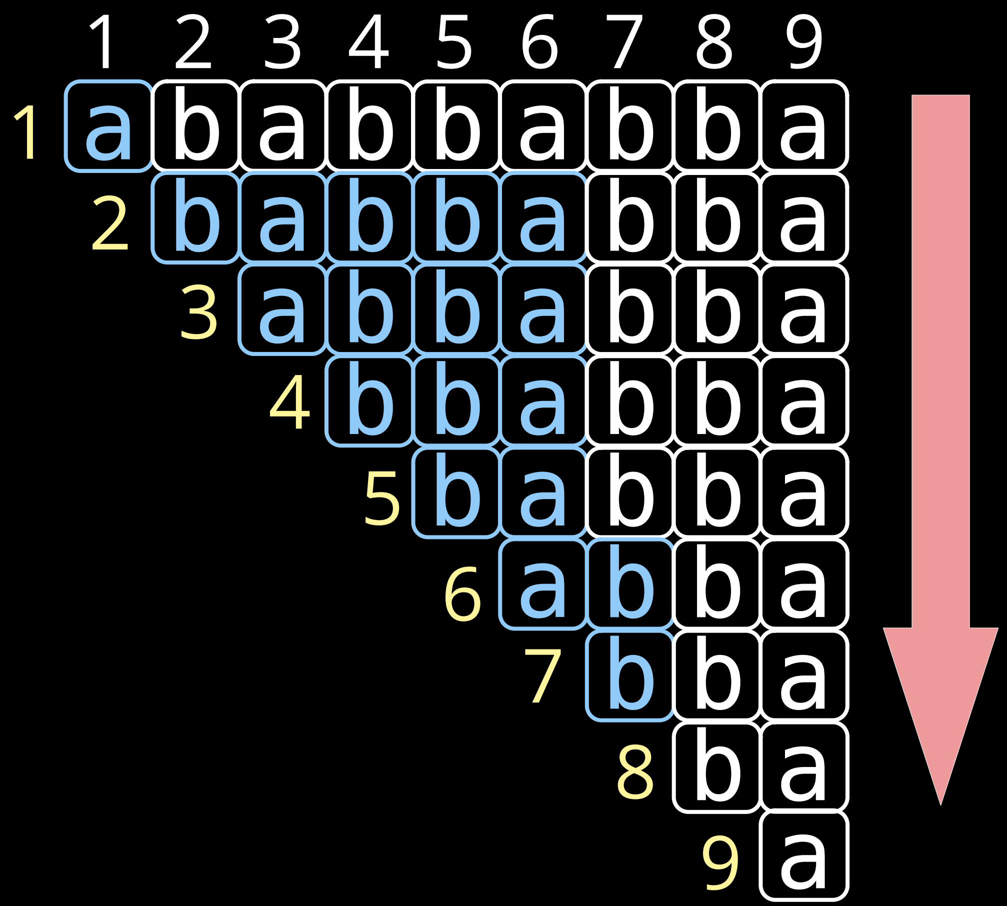
plcpcomp


1 2 3 4 5 6 7 8 9
1 a b a b b a b b a
2 b a b b a b b a
3 a b b a b b a
4 b b a b b a
5 b a b b a
6 a b b a
7 b b a
8 b a
9 a
suffix array
9 a
1 a b a b b a b b a
6 a b b a
3 a b b a b b a
8 b a
5 b a b b a
2 b a b b a b b a
7 b b a
4 b b a b b a

plcpcomp


1 2 3 4 5 6 7 8 9
1 a b a b b a b b a
2 b a b b a b b a
3 a b b a b b a
4 b b a b b a
5 b a b b a
6 a b b a
7 b b a
8 b a
9 a
permute
LCP
values
suffix array
9 a
1 a b a b b a b b a
6 a b b a
3 a b b a b b a
8 b a
5 b a b b a
2 b a b b a b b a
7 b b a
4 b b a b b a

plcpcomp



scan the permuted LCP values in text order

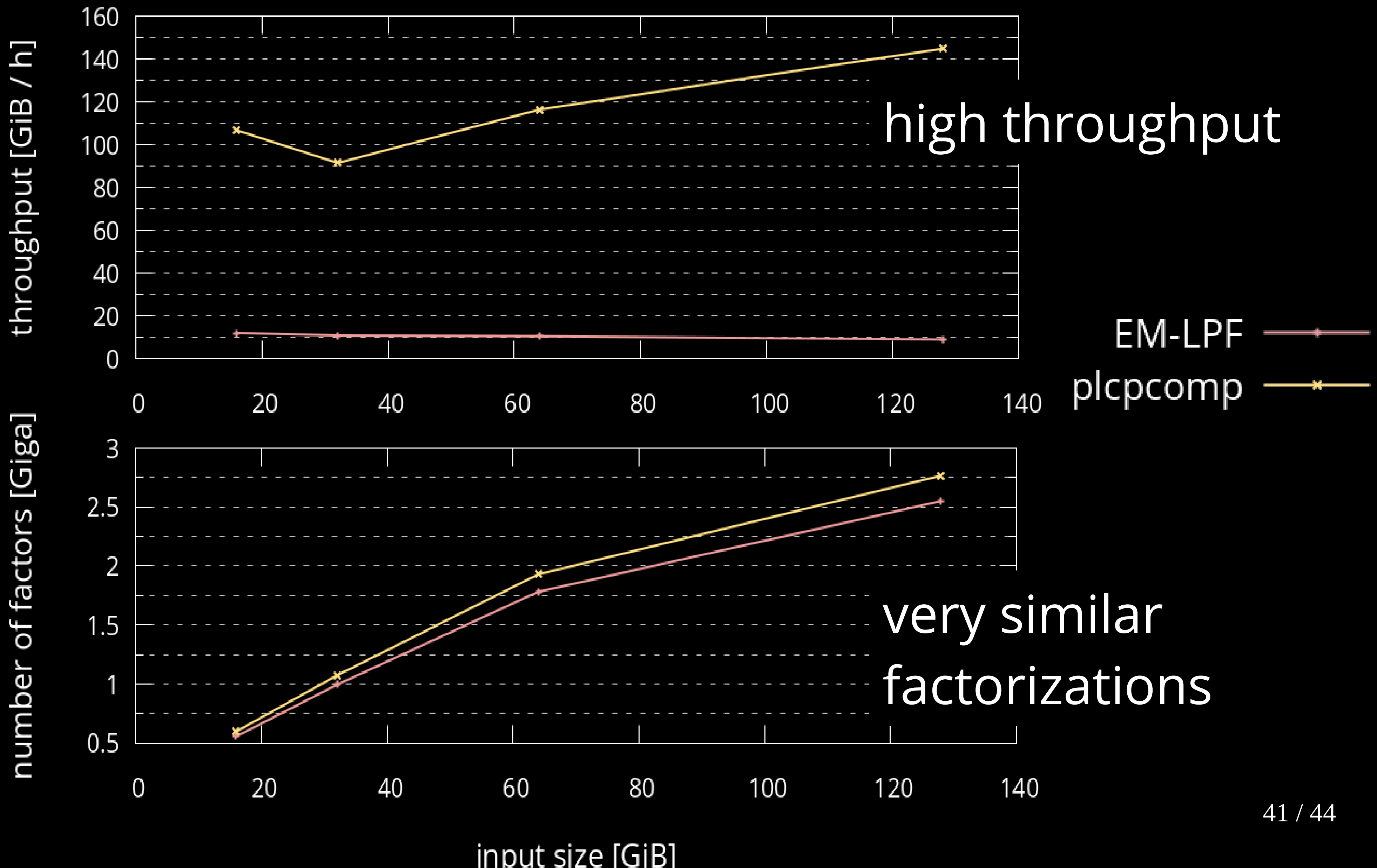
benchmark

1) plcpcomp [ESA '19]

2) EM-LPF [Kärkkäinen+ '14]

currently fastest LZ77 factorization algorithm
on disk space

web pages compression



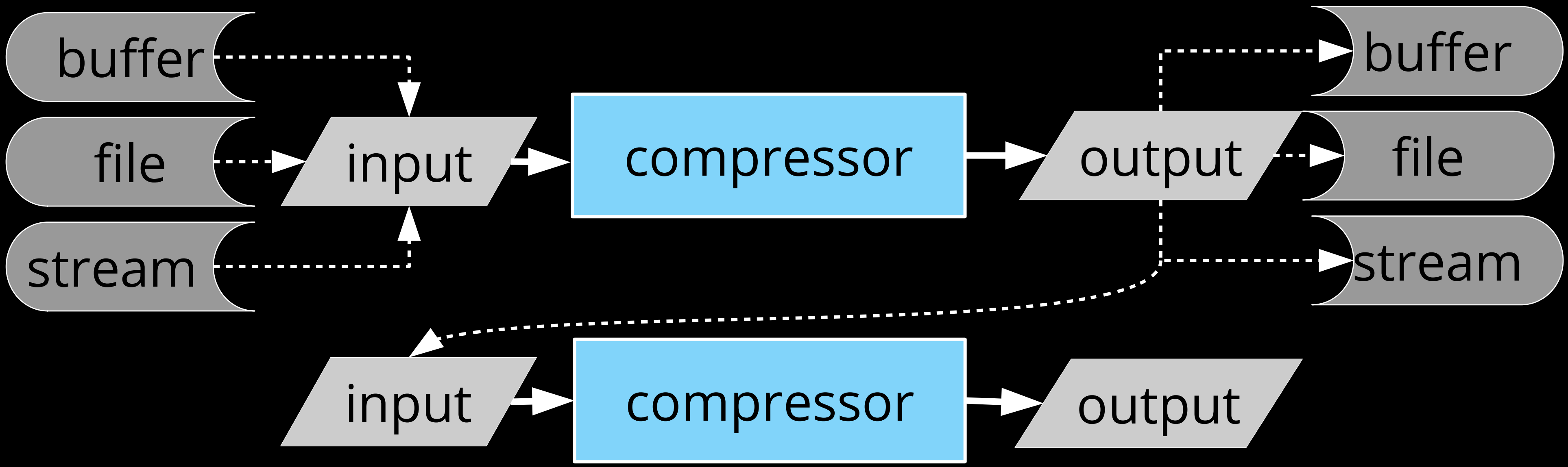
high throughput

very similar factorizations

http://tudocomp.org

C++ compression framework for

- benchmarks
- combinations of compressors



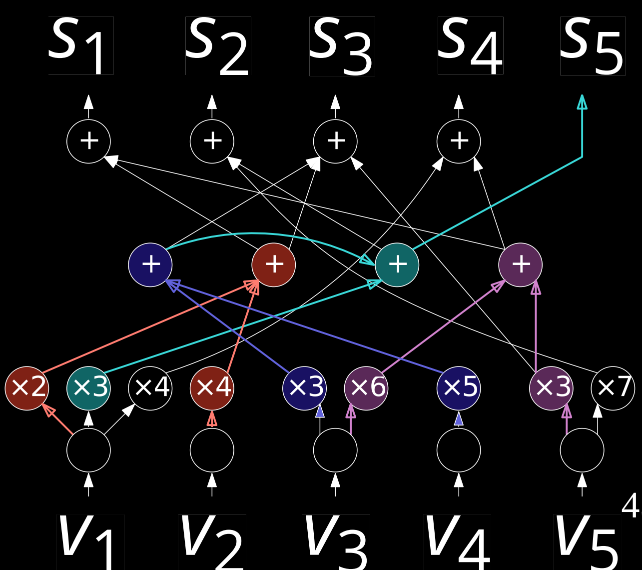
[SEA '17]

current research

compression not only for strings, but also for 2D structures like matrices

faster matrix multiplication
(multi-purpose: e.g., deep learning)

$$\begin{bmatrix} 2 & 4 & 6 & 0 & 3 \\ 3 & 0 & 3 & 5 & 7 \\ 2 & 4 & 3 & 5 & 3 \\ 4 & 0 & 6 & 0 & 3 \\ 3 & 0 & 3 & 5 & 0 \end{bmatrix} \cdot \begin{pmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \\ v_5 \end{pmatrix} = \begin{pmatrix} s_1 \\ s_2 \\ s_3 \\ s_4 \\ s_5 \end{pmatrix}$$



why Japan?

- high number of collaborators
- good research network
- many domestic conferences