Suffix arrays

Space-efficient alternative to suffix trees

Lecture 5

Full-text indexes – continued

- In order to be able to find any substring in a large ***static*** string database we need to index all the possible substrings
- How many possible substrings in text of length N?

N^2

- We would like all the substrings to be sorted – this will allow to perform find any substring in time O(N logN) using binary search

Brute-force – not feasible

- We need to ***index*** substrings **only if the text is large** – so large that the linear-time scanning of the text is out-of-question – takes too long
- But if we sort all possible substrings for a very large text of length N – there will be N^2 substrings to store, and what is the size of each substring?

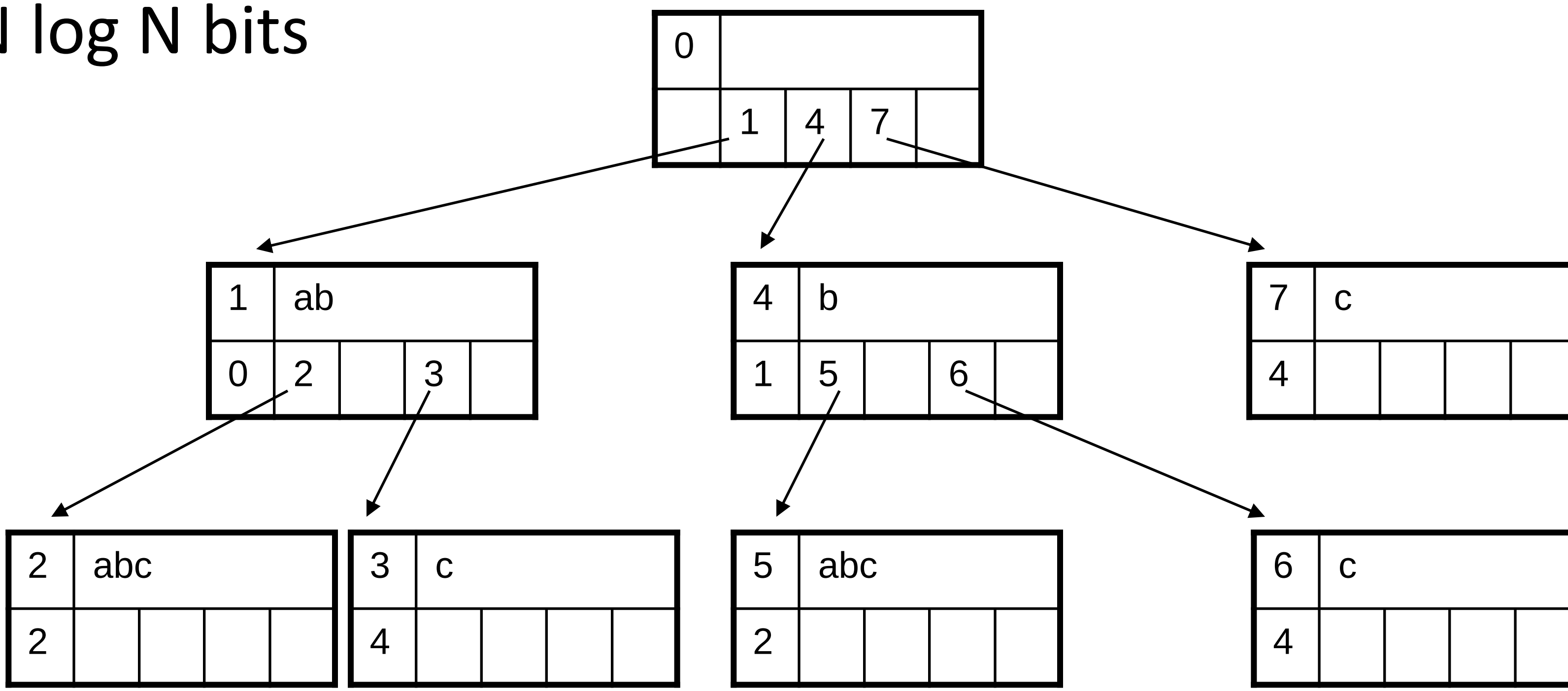
  O(N)
- Thus the brute-force approach will produce an index of **size $O(N^3)$**
- Where are we going to store $\mathbf{N^3}$ values for large N?

$(3*10^9)3 = 27 * 10^{27}$ (bytes) – 27 brontobytes or 1,125,899,906,842,624 terabytes

All different substrings can be exposed through the suffix tree of T

For each byte– 2 x 2 numbers. Each number logN bits

4N log N bits



a	*b*	*a*	*b*	*c*
00	01	00	01	10

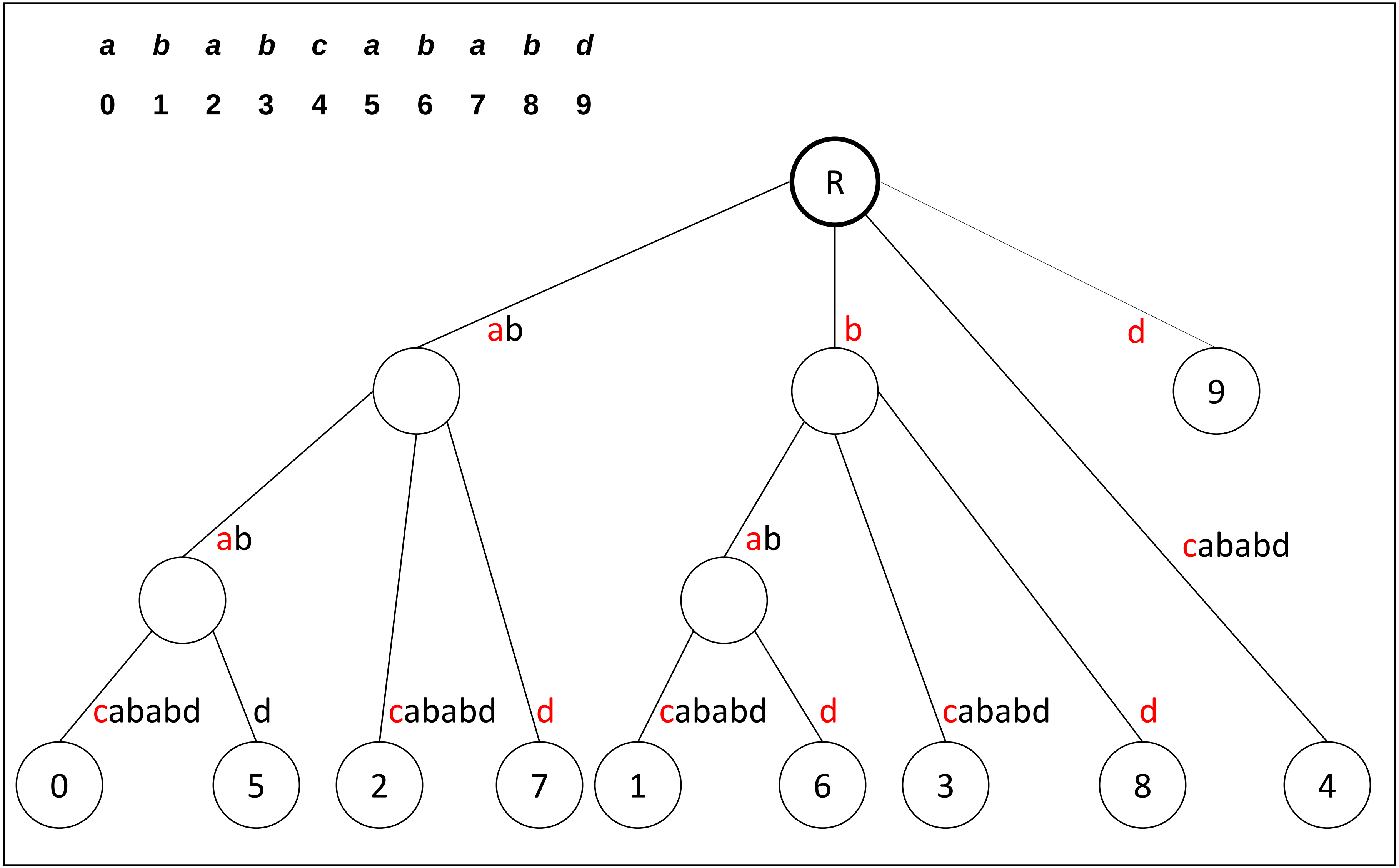
Linear space but heavy constants

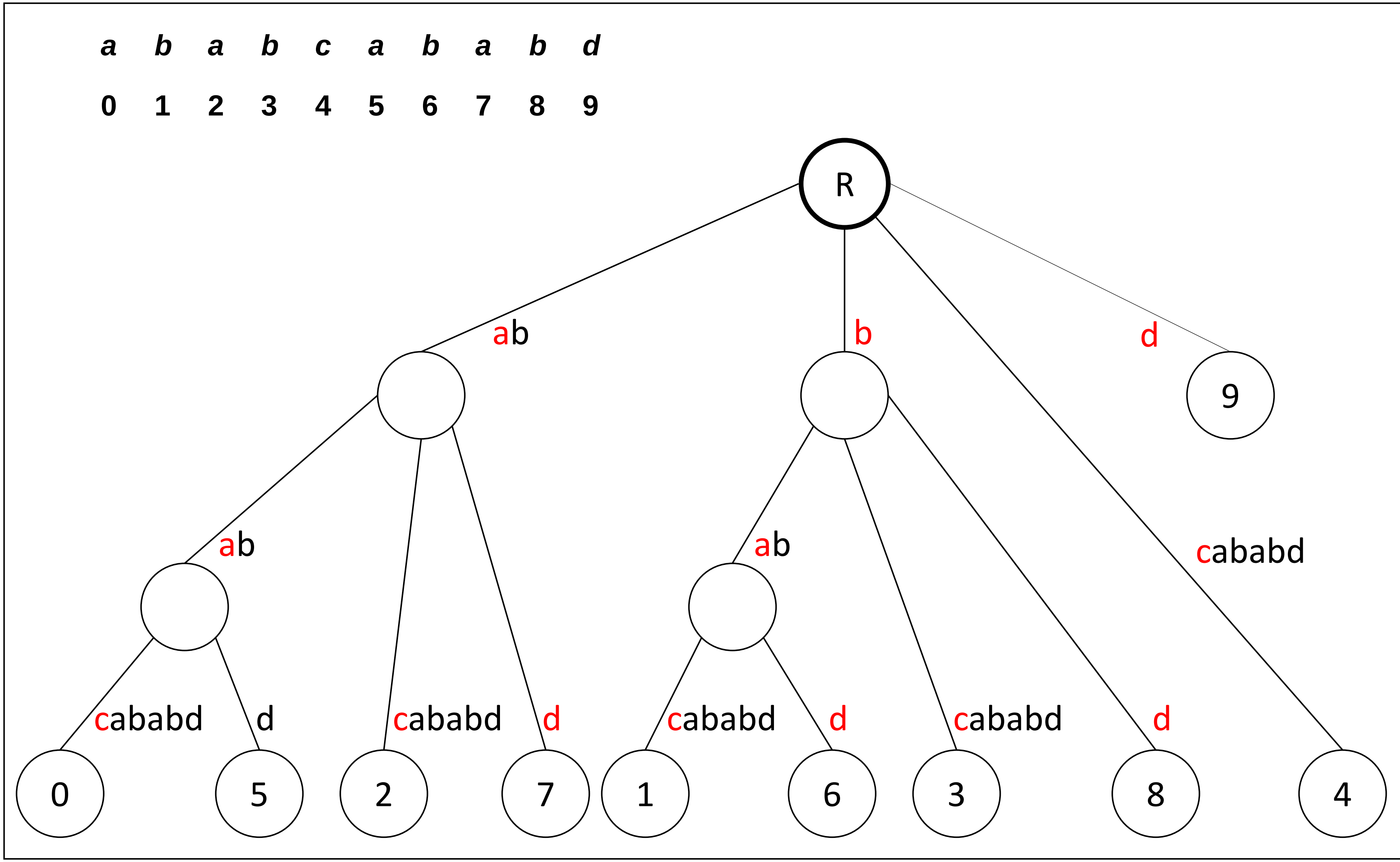
Estimated size of Suffix Trees

	input	suffix tree
• Human genome	3 GB	48 GB
• Corn genome	5 GB	58 GB
• All of GenBank	108 GB*)	1.5 TB
• Amoeba genome	670 GB	~30 TB
• 1000 genomes	20 TB ?	???

*) As of Jan 2010 http://www.cbs.dtu.dk/databases/DOGS/GBgrowth.php

From suffix tree to suffix array





If we traverse the suffix tree by processing children in lexicographical order of their edges, then we can collect all the suffixes in lexicographical order:

0,5,2,7,1,6,3,8,4,9

This sequence of suffix start positions is called a ***Suffix Array***

Suffix array example

S	a	b	a	b	a	a	a	b	b	c
	0	1	2	3	4	5	6	7	8	9

suffix start	4	5	2	0	6	3	1	7	8	9
	a	a	a	a	a	b	b	b	b	c
	a	a	b	b	b	a	a	a	b	
	a	b	a	a	b	a	b	b	c	
	b	b	a	b	c	a	a	b		
	…	…	…	…		…	…	…		
LCP	0	2	1	3	2	0	2	3	1	0

SA

Suffixes in lexicographical order

The *suffix array SA* of string *S* is defined to be an array of integers providing the starting positions of suffixes of *S* in lexicographical order.

Build SA for *cocoa*

c	*o*	*c*	*o*	*a*
0	1	2	3	4

N

Alphabetically sort suffixes: **Suffix array**

4	**2**	**0**	**3**	**1**
a	c	c	o	o
	o	o	a	c
	a	c		o
		o		a
		a		

O(N)

$O(N^2)$

Suffix array space

- For a string of length N bytes
  - Total space is *N numbers*. Each number can be represented with log N bits
  - So the space is just N log N bits
- Also because it is sorted, it can be partitioned, distributed, and searched in parallel

Simple **binary search** using SA for S

S	a	b	a	b	a	a	a	b	b	c
	0	1	2	3	4	5	6	7	8	9

SA	4	5	2	0	6	3	1	7	8	9

Search for pattern: *bab*

N = 10

- String at pos SA [N/2] = SA[5] = 3: baa < *bab*

=> search to the right of N/2

- String at pos SA [N/2+N/4] = SA [5+2]=7: bbc > *bab*

=> Search between N/2 and N/2+N/4

- String at pos SA [N/2 + N/8] = SA [6] = 1: bab = *bab*