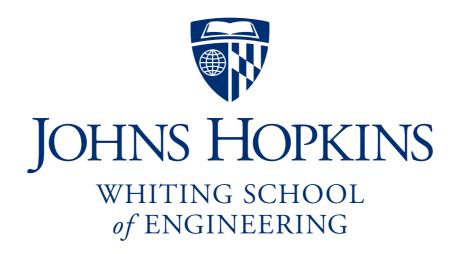
# Suffix arrays

Ben Langmead

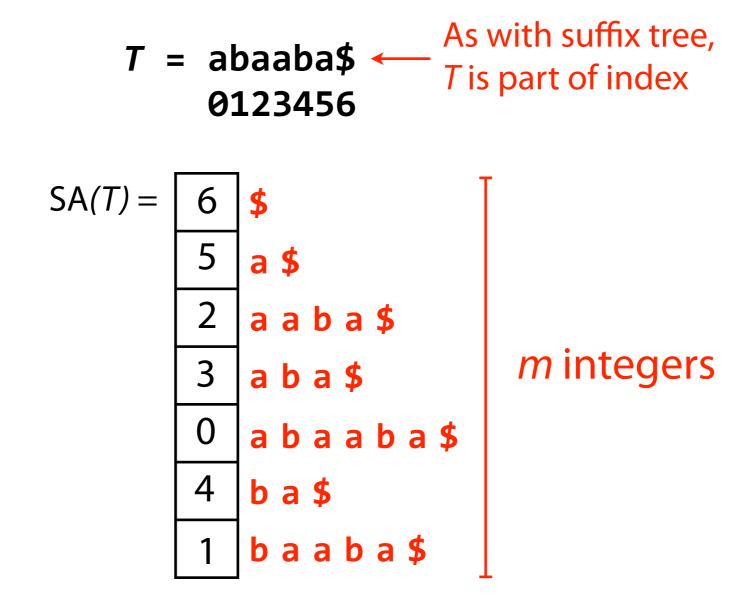


Department of Computer Science



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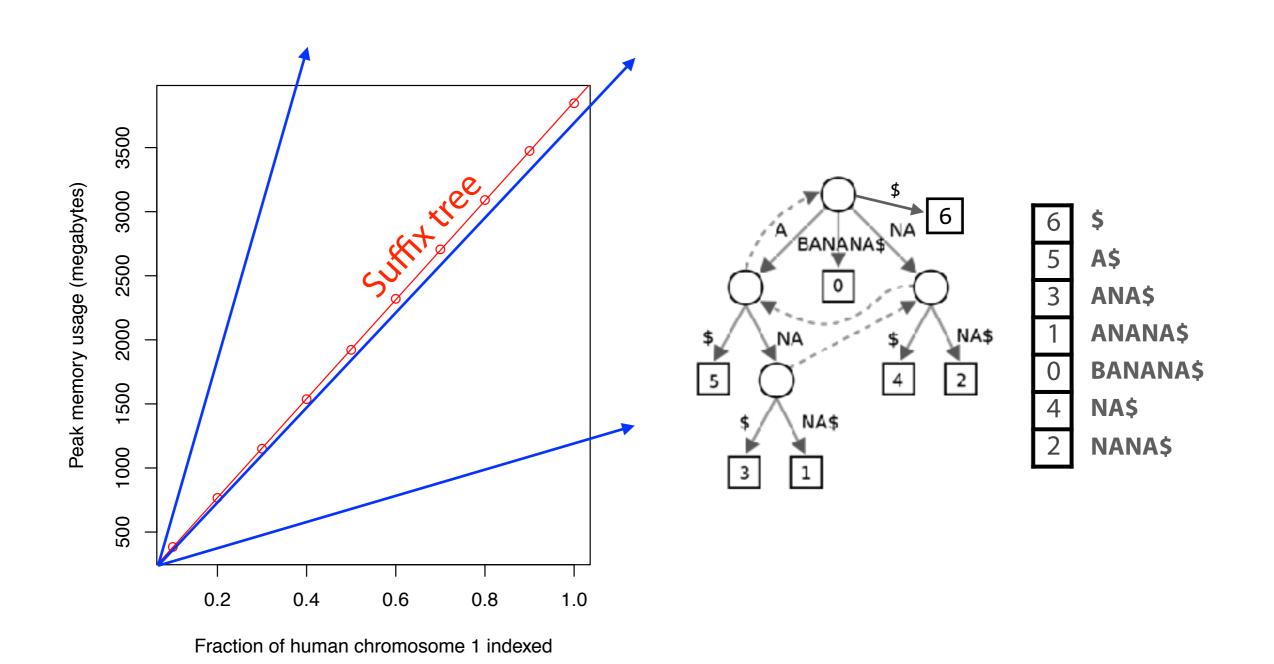
# Suffix array



Suffix array of T is an array of integers in [0, m) specifying lexicographic (alphabetical) order of T's suffixes

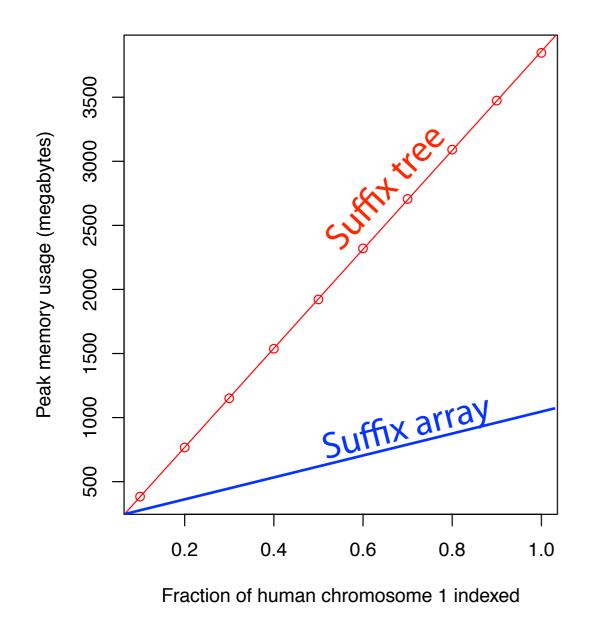
# Suffix array

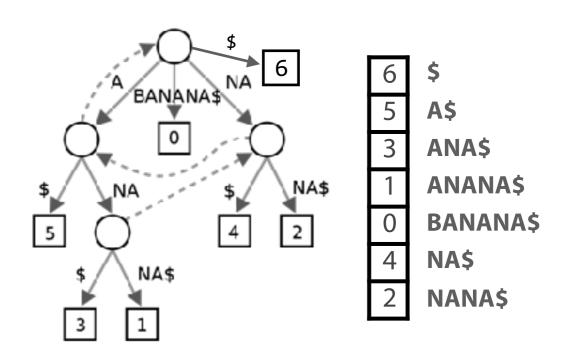
O(m) space, like suffix tree Is "constant factor" worse, better, same?



### Suffix array

32-bit integers sufficient for human genome, so fits in ~4 bytes/base  $\times$  3 billion bases  $\approx$  12 GB. Suffix tree is >45 GB.





# Suffix array: querying

Is P a substring of T?

- 1. For P to be a substring, it must be a prefix of  $\geq 1$  of T's suffixes
- 2. Suffixes sharing a prefix are consecutive in the suffix array

Use binary search

T = abaaba\$

```
5
a $
2
a a b a $
a b a $
0
a b a a b a $
b a $
b a a b a $
```

# Suffix array: querying

Is P a substring of T?

Do binary search, check whether *P* is a prefix of the suffix there

Query time is O(?)...

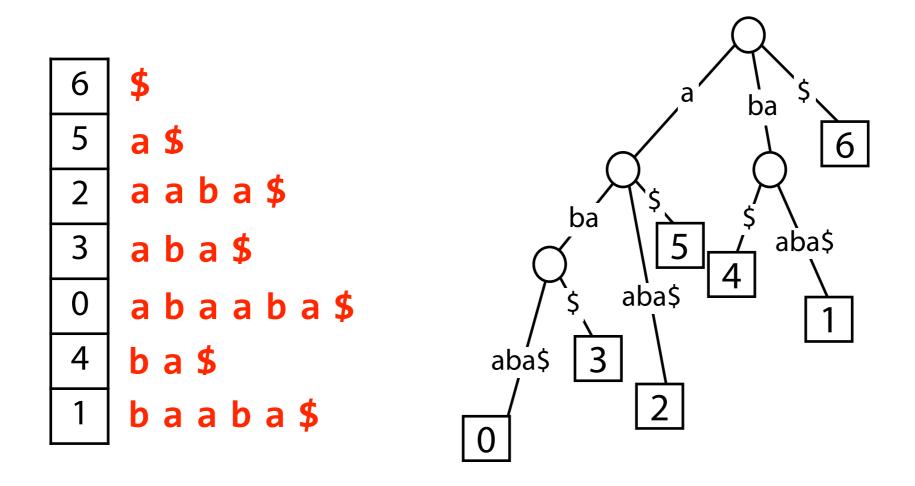
... $O(\log_2 m)$  bisections, O(n) comparisons per bisection, so  $O(n \log m)$ 

T = abaaba\$

5 a \$ aaba\$ aba\$ 3 abaaba\$ b a \$ baaba\$

### Suffix array: querying

Contrast suffix array query time:  $O(n \log m)$  with suffix tree: O(n)



Time can be improved to  $O(n + \log m)$ , but we won't discuss here (See Gusfield 7.17.4). For this class, we'll consider it  $O(n \log m)$ .

### Suffix array: sorting suffixes

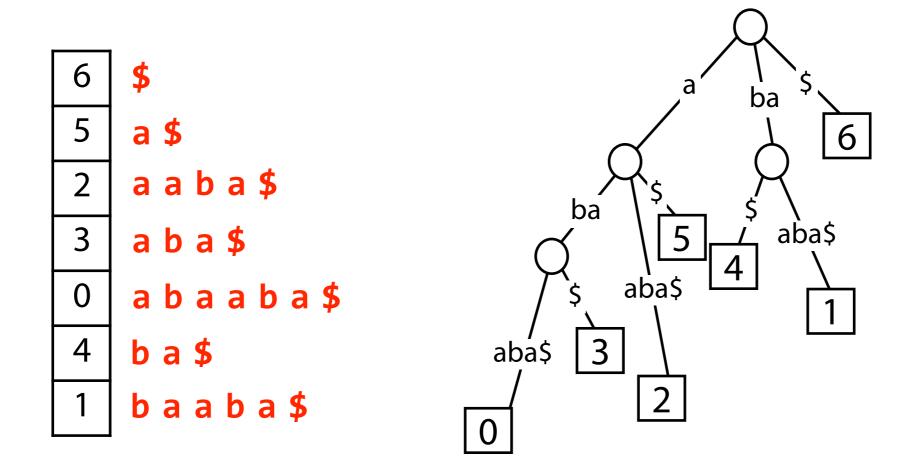
Use your favorite sort, e.g., quicksort

```
abaaba$
                        def quicksort(q):
                            lt, gt = [], []
     baaba$
                            if len(q) <= 1:
     aaba$
                                return q
                            for x in q[1:]:
     aba$
                                if x < q[0]: ←
     b a $
                                    lt.append(x)
                                else:
                                    gt.append(x)
                            return quicksort(lt) + q[0:1] + quicksort(gt)
Expected time: O(m^2 \log m)
```

Not  $O(m \log m)$  because a suffix comparison is O(m) time

# Suffix array: building

How to build a suffix array?



- (a) Build suffix tree, (b) traverse in alphabetical order,
- (c) upon reaching leaf, append suffix to array

# Suffix array: sorting suffixes

Another idea: Use a sort algorithm that's aware that the items being sorted are all suffixes of the same string

Original suffix array paper suggested an  $O(m \log m)$  algorithm

Manber U, Myers G. "Suffix arrays: a new method for on-line string searches." SIAM Journal on Computing 22.5 (1993): 935-948.

Other popular  $O(m \log m)$  algorithms have been suggested

Larsson NJ, Sadakane K. Faster suffix sorting. Technical Report LU-CS-TR: 99-214, LUNDFD6/(NFCS-3140)/1-43/(1999), Department of Computer Science, Lund University, Sweden, 1999.

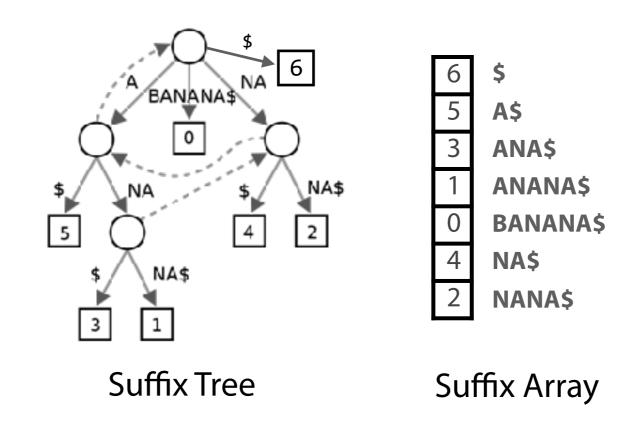
#### More recently O(m) algorithms have been demonstrated!

Kärkkäinen J, Sanders P. "Simple linear work suffix array construction." Automata, Languages and Programming (2003): 187-187.

Ko P, Aluru S. "Space efficient linear time construction of suffix arrays." *Combinatorial Pattern Matching*. Springer Berlin Heidelberg, 2003.

### Suffix array: summary

Just *m* integers, with O(*n* log *m*) query time



Constant factor greatly reduced compared to suffix tree: human genome index fits in ~12 GB instead of > 45 GB