# Tries and Suffix Trees

# String Data Structures

- Our last topic for the quarter is the wonderful world of string data structures.
- Why are they worth studying?
  - *They're practical*. These data structures were developed to meet practical needs in data processing. Lots of important data can be encoded as strings.
  - *They're different*. The questions typically asked about strings involve properties of sequences, not individual elements, in a way that you don't normally otherwise see.
  - *They're algorithmically interesting*. The techniques that power these data structures involve some truly beautiful connections and observations.

# Where We're Going

- Today, we'll cover tries and suffix trees, two powerful data structures for exposing shared structures in strings.
- On Thursday, we'll see the *suffix array* and *LCP array*, which are a more space-efficient way of encoding suffix trees.
- Next Tuesday, we'll see the *SA-IS algorithm*, which quickly builds suffix trees and suffix arrays, and is probably the most beautiful divide and conquer algorithm ever invented.

Part I: Tries and Patricia Tries

## A Motivating Problem



what is the cutest ani



what is the cutest animal in the world

what is the cutest animal

what is the cutest animal on earth

what is the cutest animal ever

what is the cutest animal in the whole entire world

what is the cutest animal in the whole world

what is the cutest animal alive

what is the cutest animal on the planet

what is the cutest animal in australia

what is the cutest animal in the sea

Google Search

I'm Feeling Lucky

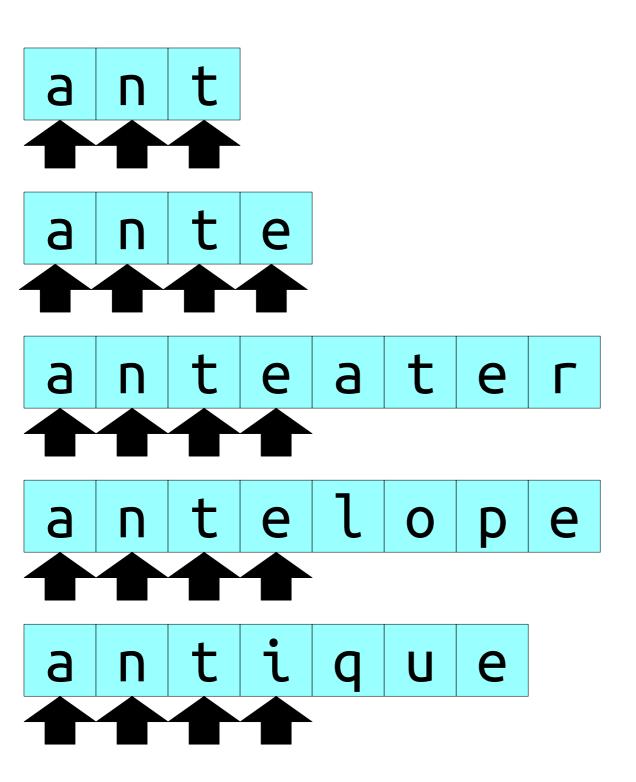
Report inappropriate predictions

How is this done so quickly?

# The Autocomplete Problem

- We have a series of text strings  $T_1, T_2, ..., T_k$  of total length m.  $(|T_1| + ... + |T_k| = m)$
- We have a pattern string P of length n. (|P| = n).
- *Goal:* Find all text strings that start with *P*.
- If we just do a single query, then we can solve this pretty easily.
  - Just scan over all the strings and see which ones start with **P**.
- *Question:* If we have a set of fixed text strings and varying patterns, can we speed this up?

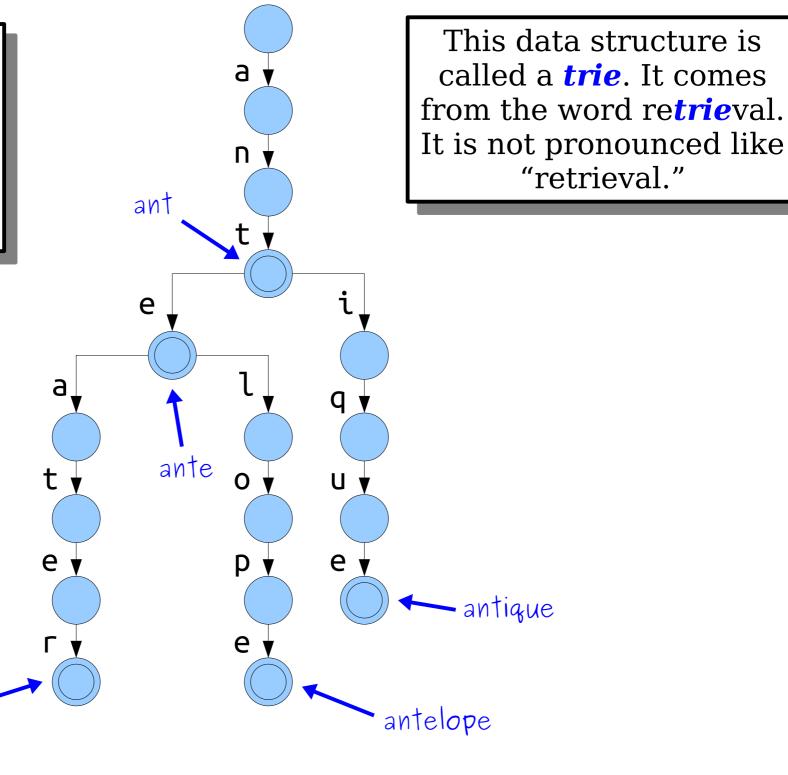
### A Naive Solution



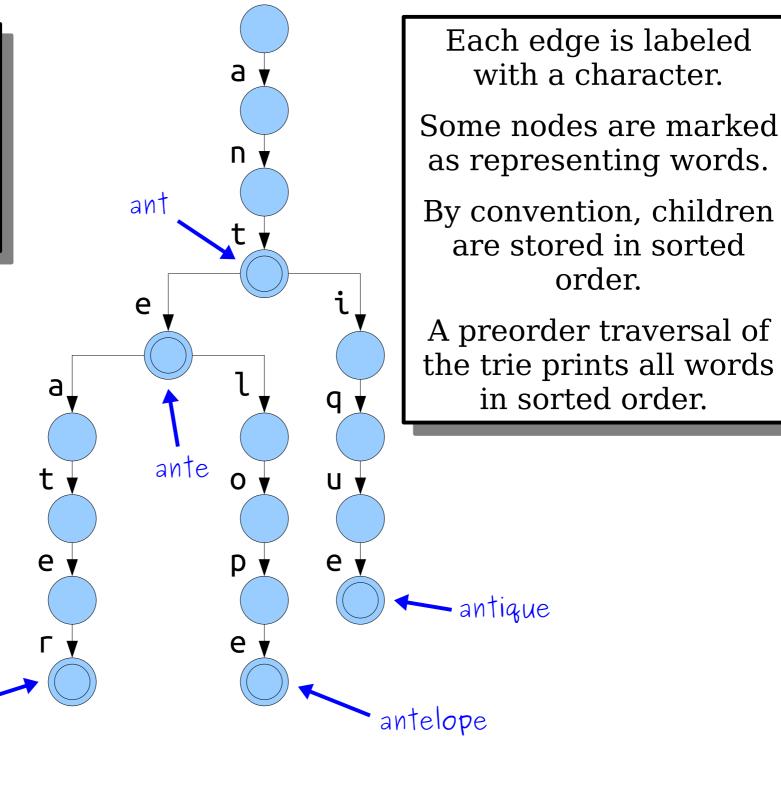
a n t e

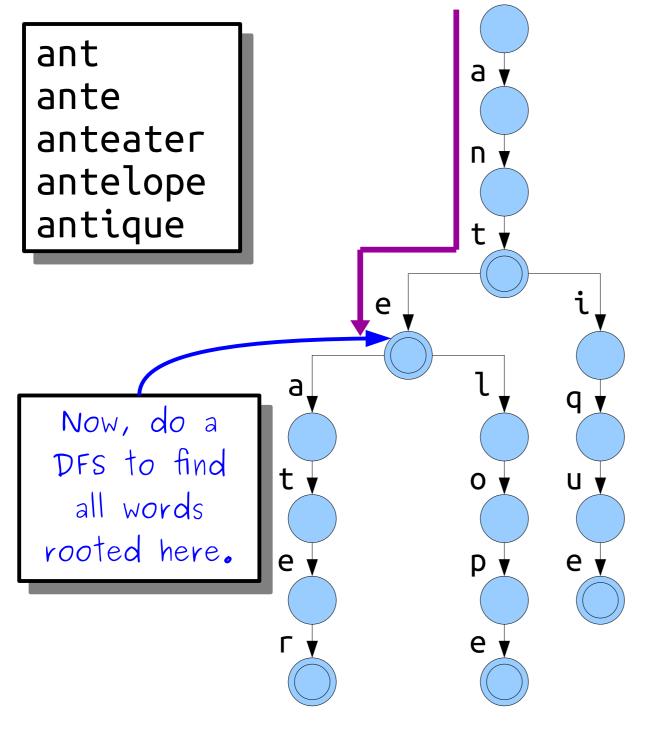
We're spending a lot of time scanning shared prefixes. Is there a way to avoid this?

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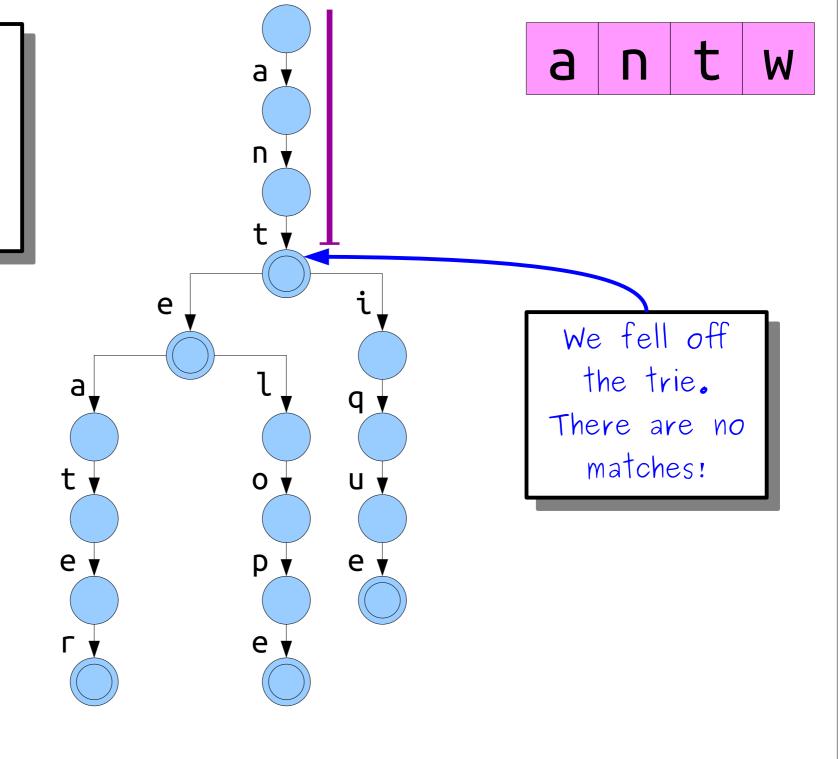


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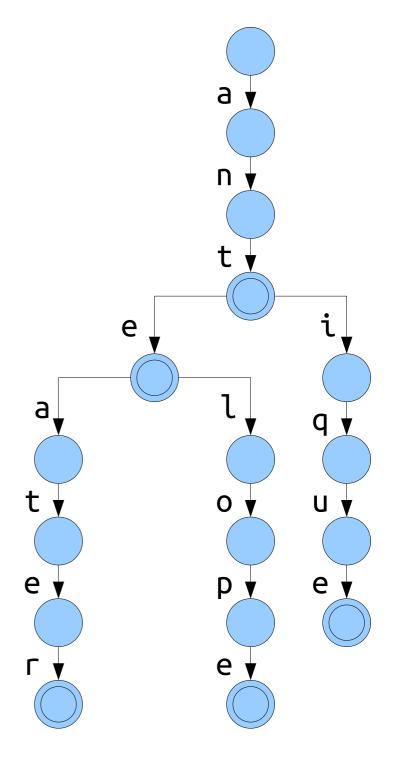




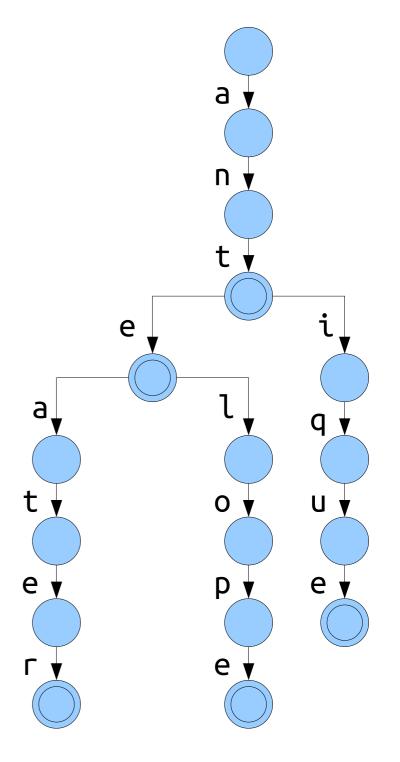
a n t e



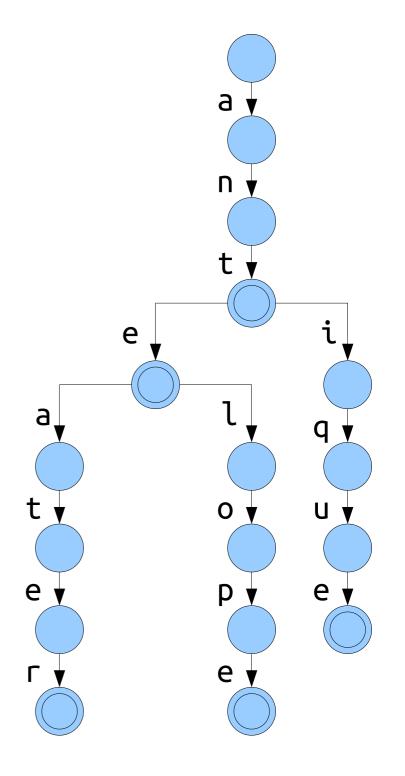
- *Recall:* The total length of our text strings is *m*, and the length of our pattern string is *n*.
- How long does it take to build our trie?
- Claim: Ignoring the size of the alphabet, the runtime is O(m).



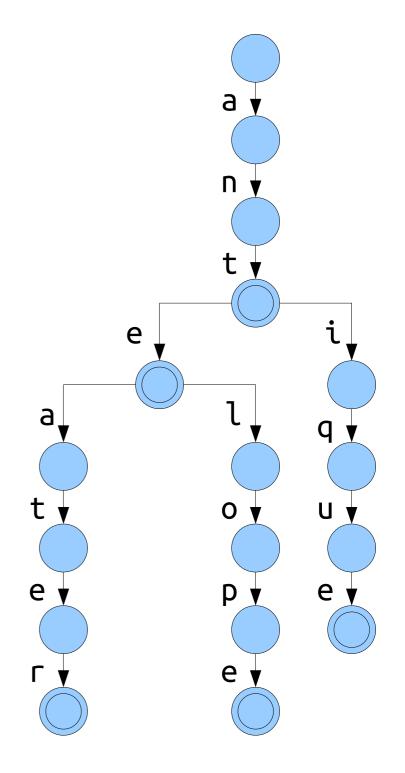
- *Recall:* The total length of our text strings is *m*, and the length of our pattern string is *n*.
- How long does it take to check if the pattern is a prefix of any string?
- Claim: Ignoring the size of the alphabet, the runtime is O(n).



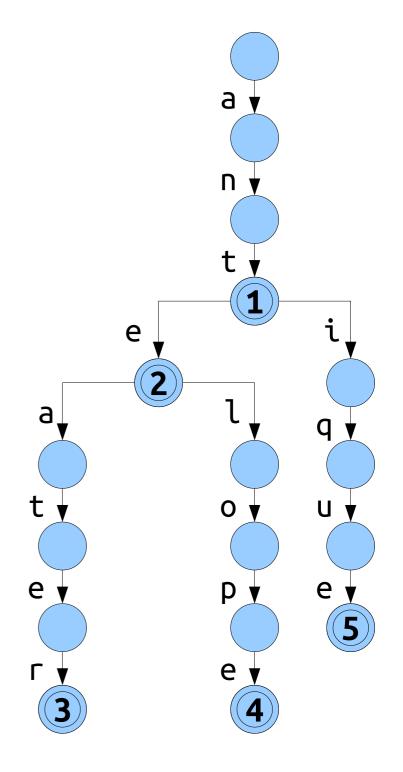
- *Recall:* The total length of our text strings is *m*, and the length of our pattern string is *n*.
- How long does it take to find all text strings that start with the pattern?
- That's a trickier question.

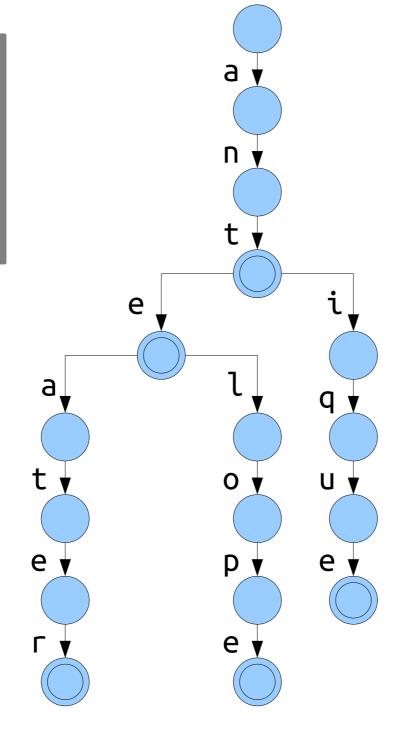


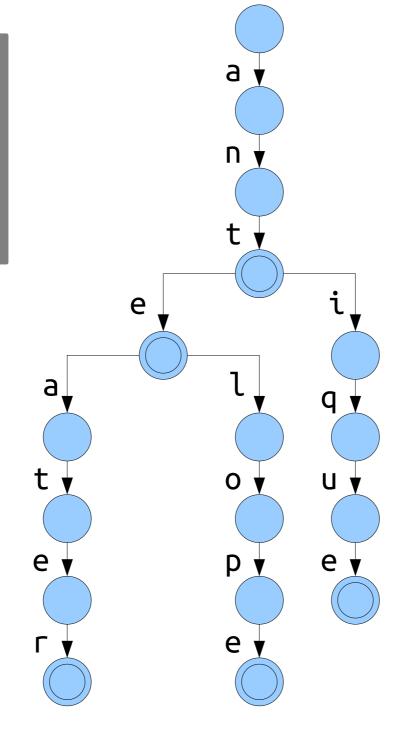
- *Question:* In what format do we want our matches?
- *Option 1:* Just print out all the matches.
  - Search for the prefix as usual.
  - Do a DFS, recording the letters seen on each branch, to rebuild all the words.
- We can upper-bound runtime at O(m + n), but it's hard to say much more than that.
  - (We could upper-bound this expression at O(m) if we'd like, but I like showing both costs here.)

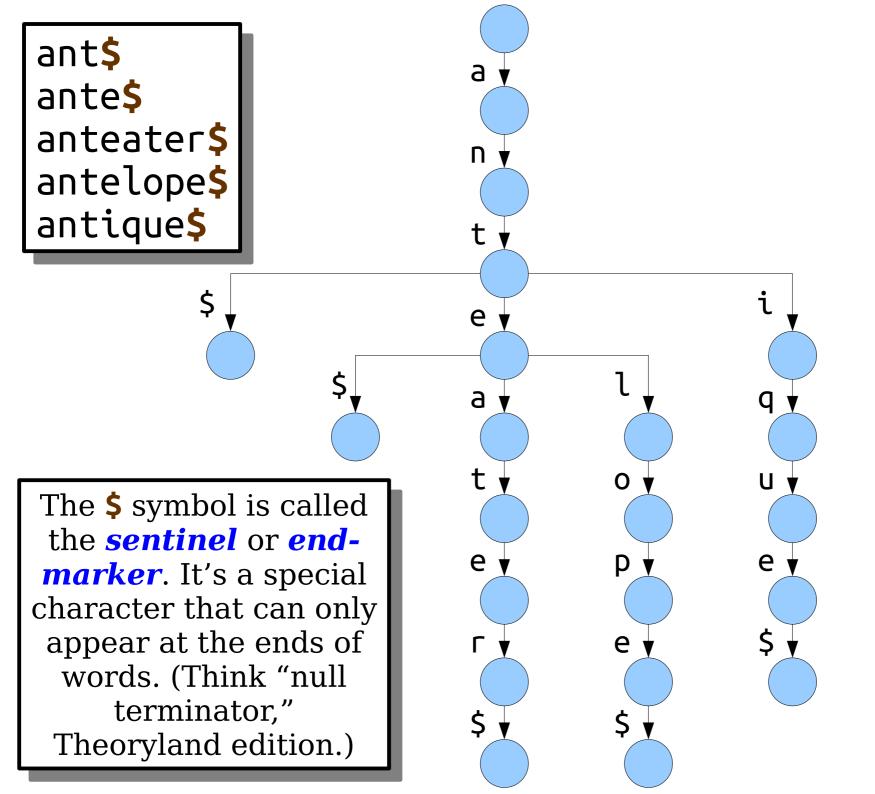


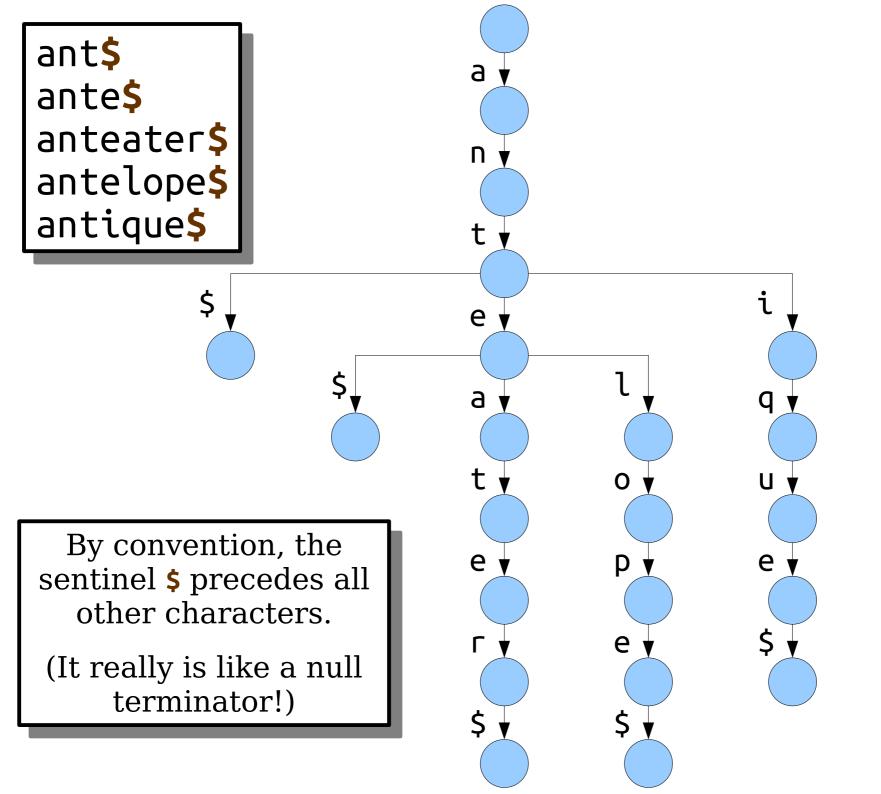
- *Question:* In what format do we want our matches?
- *Option 2:* Assume each text string has some numeric ID, and we want all matching IDs.
- Ideally, we'd like a time complexity of something like
   O(n + z), where z is the number of matches.
- Our current DFS can't achieve this; the lengths of the strings matter.
- Can we do better?

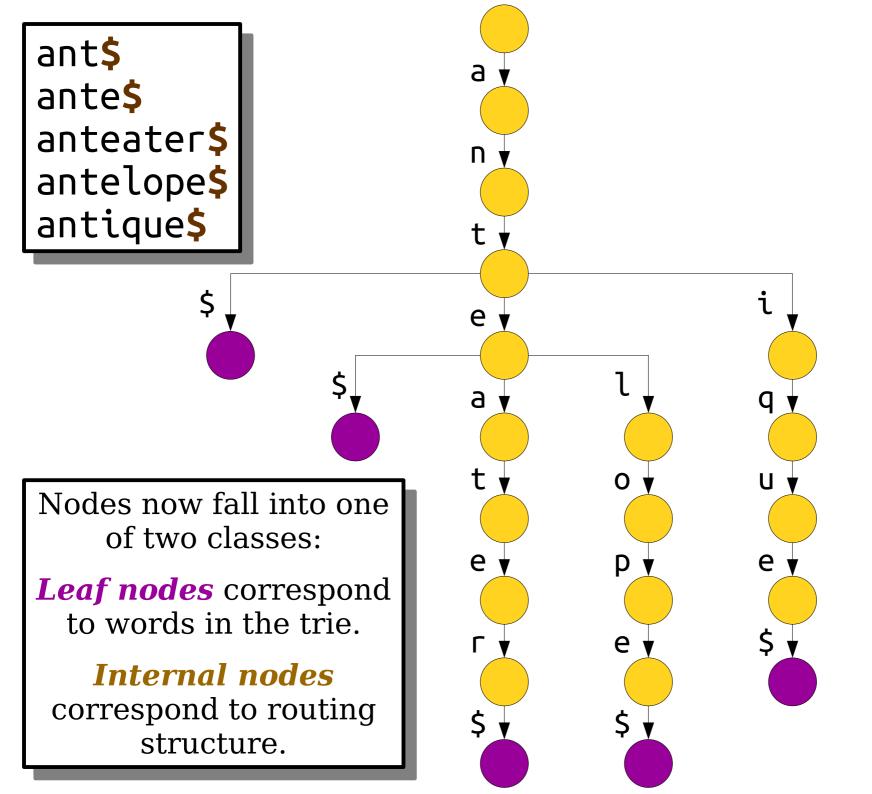


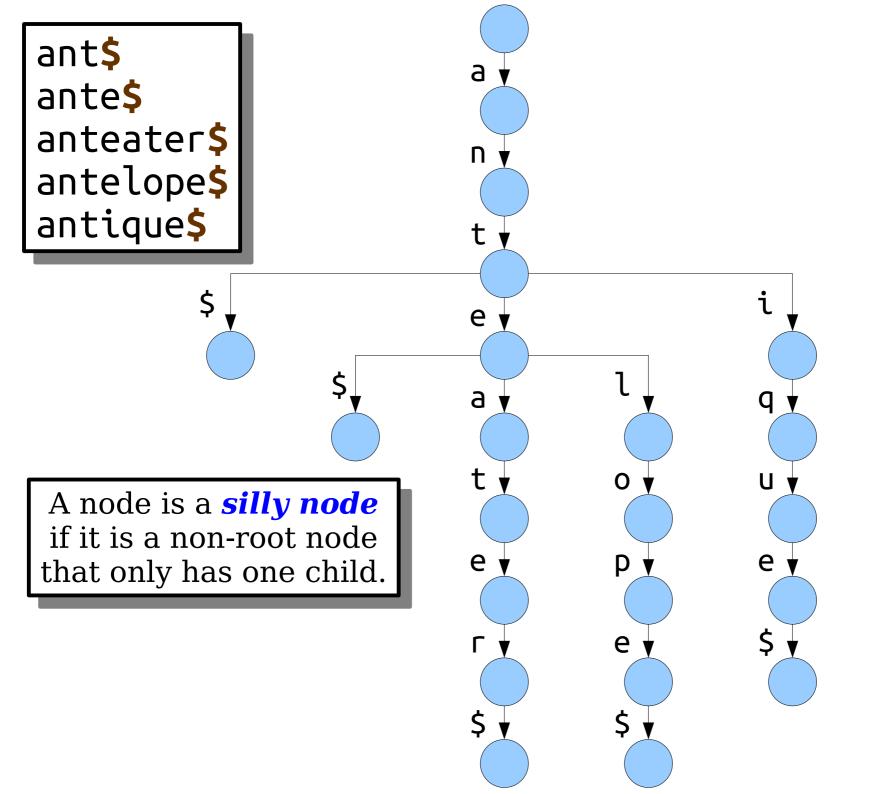


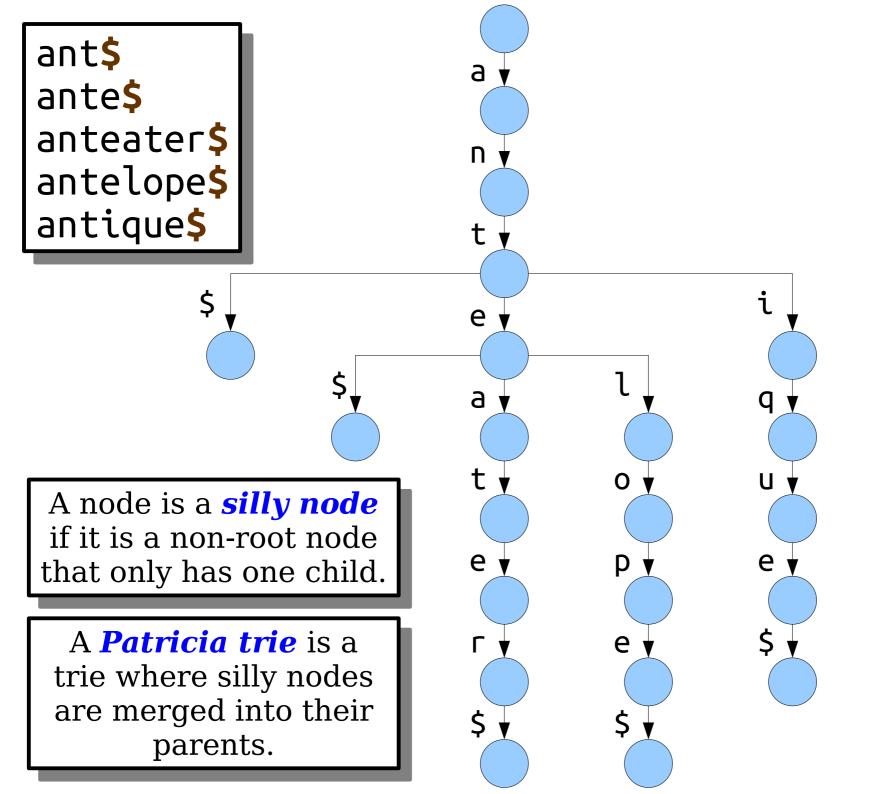


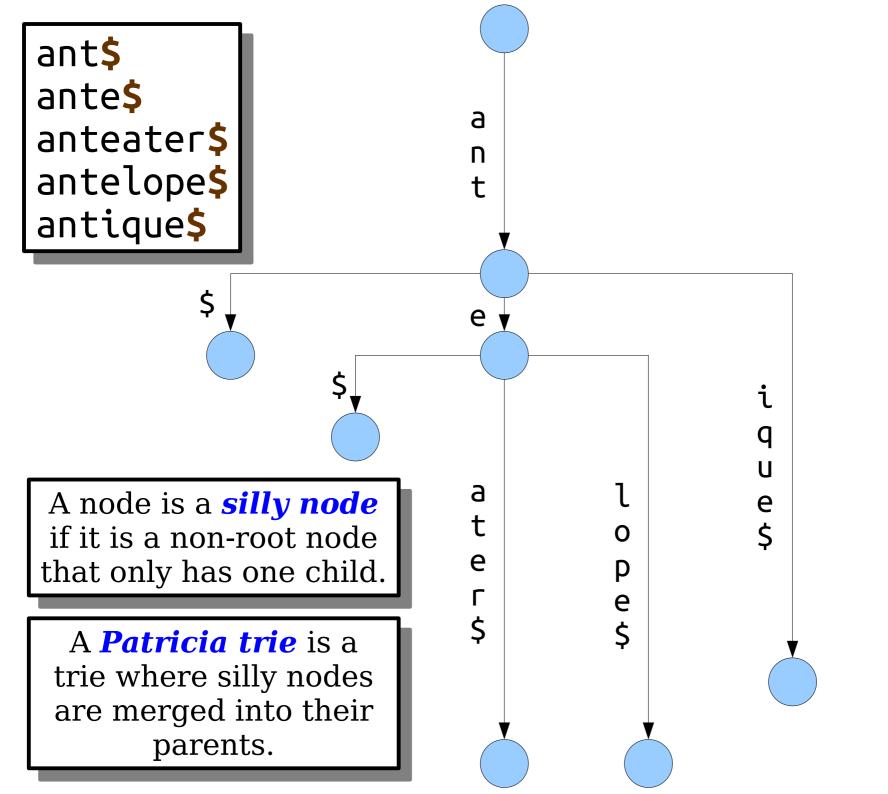


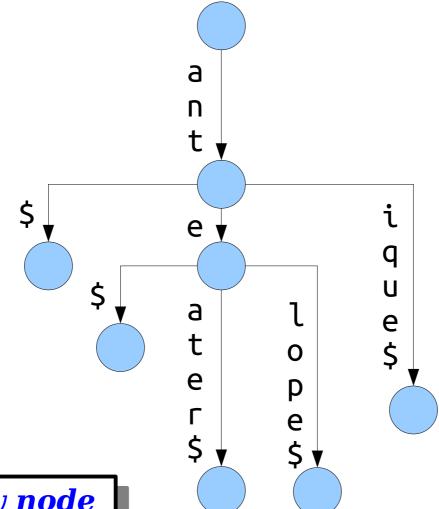






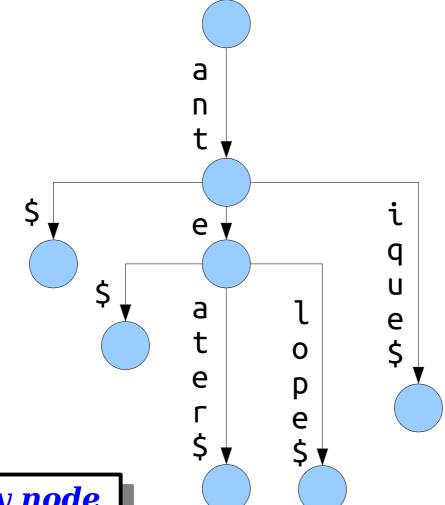






A node is a *silly node* if it is a non-root node that only has one child.

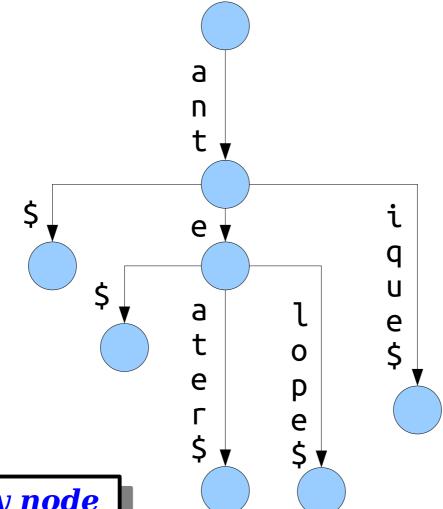
A *Patricia trie* is a trie where silly nodes are merged into their parents.



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A *Patricia trie* is a trie where silly nodes are merged into their parents.

Observation 1: Every internal node in a Patricia trie (except possibly the root) has two or more children.



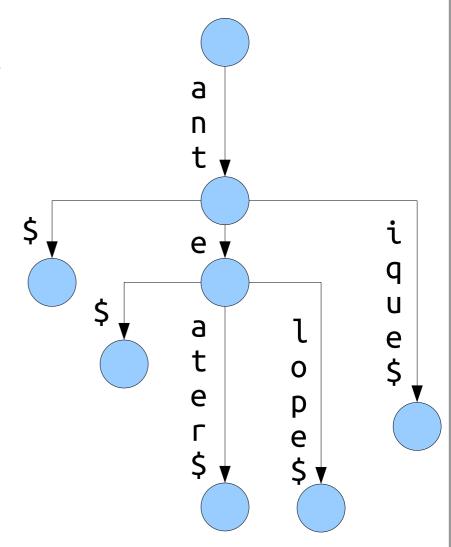
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#### **Observation 2:**

Leaves correspond to words; internal nodes are there for routing purposes.

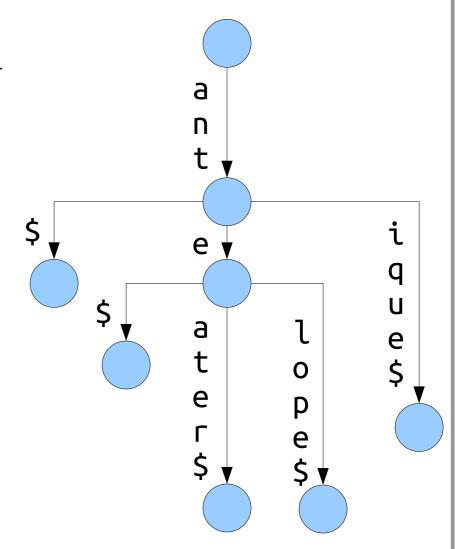
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### Why?

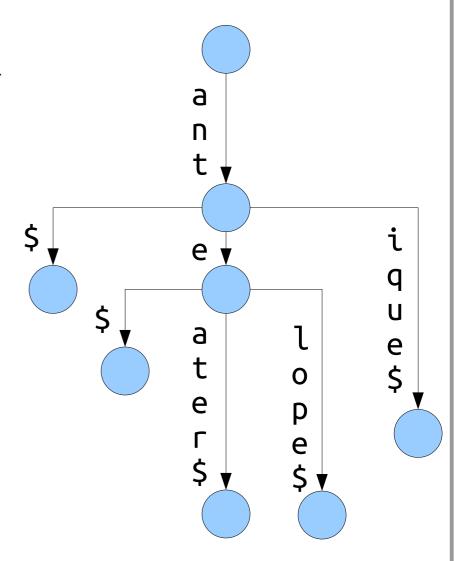
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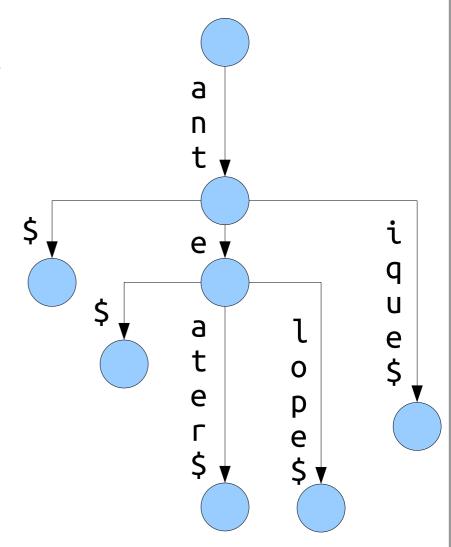
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### Why?

Now, private chat me your best guess. Not sure? Just answer "??."



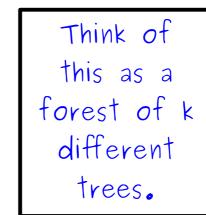
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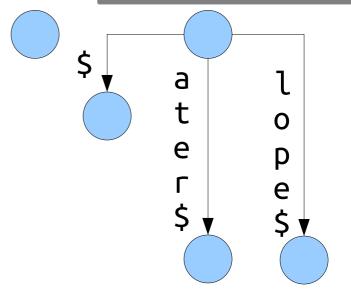
There are k leaves, one per word in the trie.

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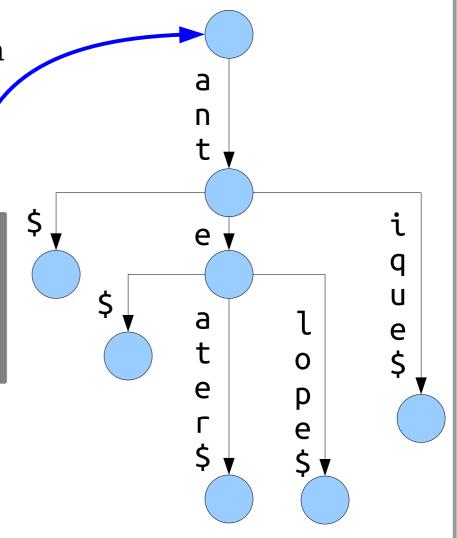
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Adding an internal node merges two or more trees together, decreasing the number of trees by at least one.



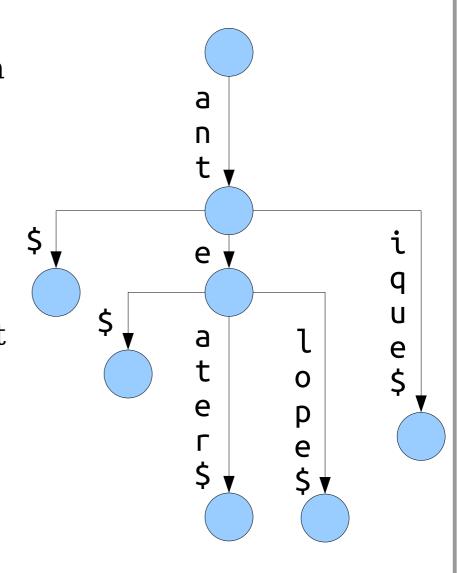
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Adding the root might not decrease the number of trees, but there's only one root.



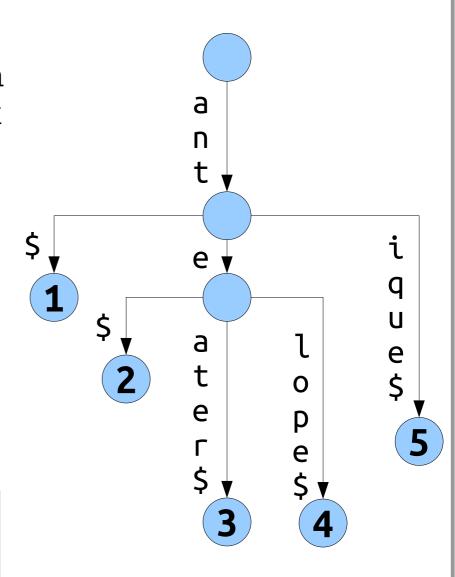
- **Theorem:** The number of nodes in a Patricia trie with k words is always O(k), regardless of what those words are.
- **Proof Sketch:** There are *k* leaves, one per word. Remove all internal nodes, leaving a forest of *k* trees.

Add the internal nodes back one at a time. Each addition (except possibly root) decreases the number of trees in the forest by at least one, since each (non-root) internal node has at least two children. This means there are at most k internal nodes, for a total of O(k) nodes.  $\blacksquare$ 



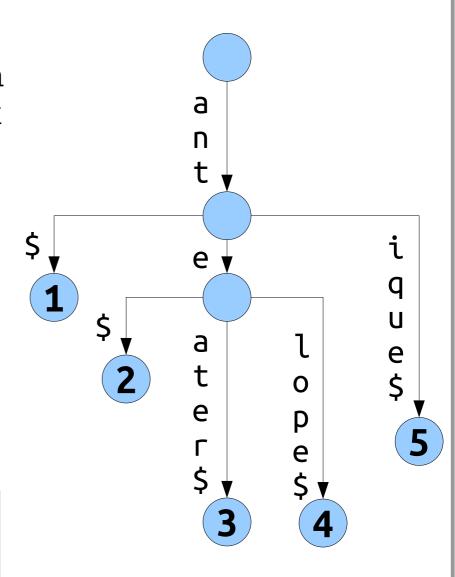
- **Claim:** If each leaf in a Patricia trie is annotated with the index of the word it comes from, the indices of strings starting with a given prefix can be found in time O(n + z), where n is the length of that prefix and z is the number of matches.
- *Question:* How is this possible?

Formulate a hypothesis, but don't post anything in chat just yet.

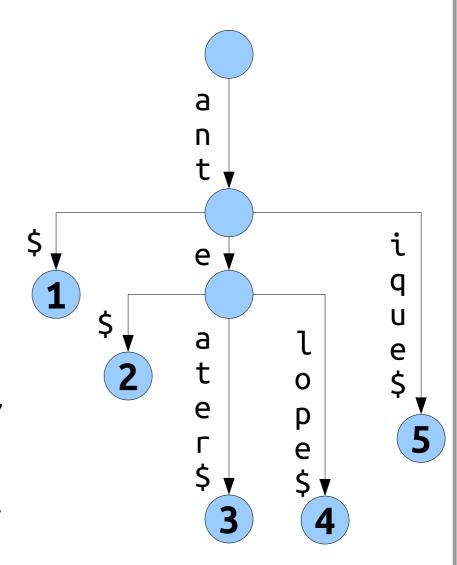


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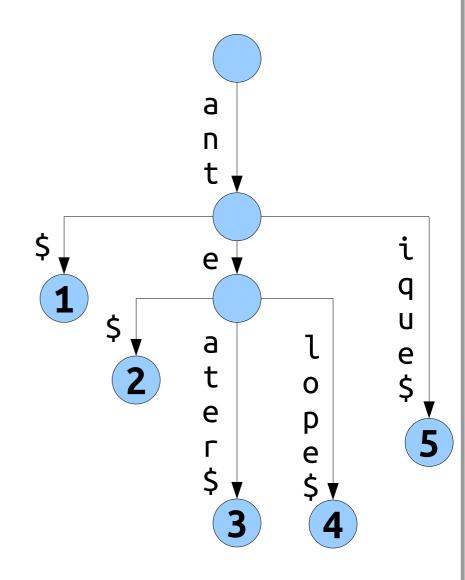


- Use a two-phase search algorithm!
- *(Character-aware)* Read the prefix to search for, matching characters as you walk down the Patricia trie.
  - Time required: O(n), since we have to read all the characters of the prefix.
- (Character-blind) If you didn't walk off the trie, do a DFS below your current point to find all leaves, ignoring the strings on the edges.
  - Time required: O(z). If there are z matches, there are z leaves to explore. As we saw earlier, in a Patricia trie, a subtree with z leaves has O(z) total nodes.



### The Story So Far

- Adopting our notation from RMQ, a Patricia trie gives an  $\langle O(m), O(n+z) \rangle$  solution to prefix matching.
- Those runtimes hide the effect of the alphabet size; take some time to evaluate those tradeoffs!



Part II: Suffix Trees

Two Motivating Problems



The *United States Statutes at Large* contains all legislation ever passed in the United States.

Make it searchable.



Cancers often have repeated copies the same gene.

Given a cancer genome (length ~3,000,000,000), find the longest repeated DNA sequence.

Patricia tries are great tools for finding *prefixes*.

These problems involve looking for *substrings*.

Can we use what we've developed so far?

• The *fundamental theorem of stringology* says that, given two strings *w* and *x*, that

w is a substring of x
if and only if
w is a prefix of a suffix of x

b e

f | l | i | b | b | e | r | t | i | g | i | b | b | e | t

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f l i b b a c + i a i b b a +

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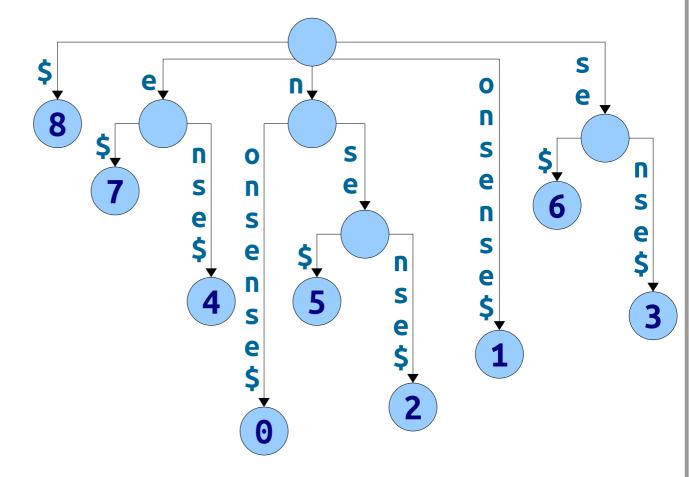
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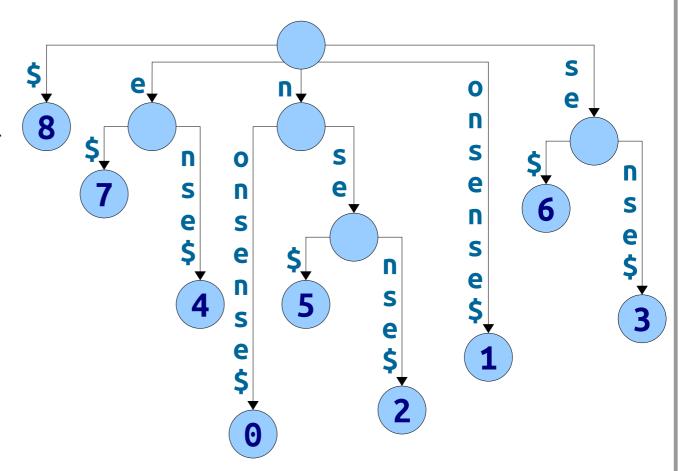
• To find all matches of *w* in *x*, we just need to find all suffixes of *x* that start with *w*.

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onsense\$
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nse\$
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se\$



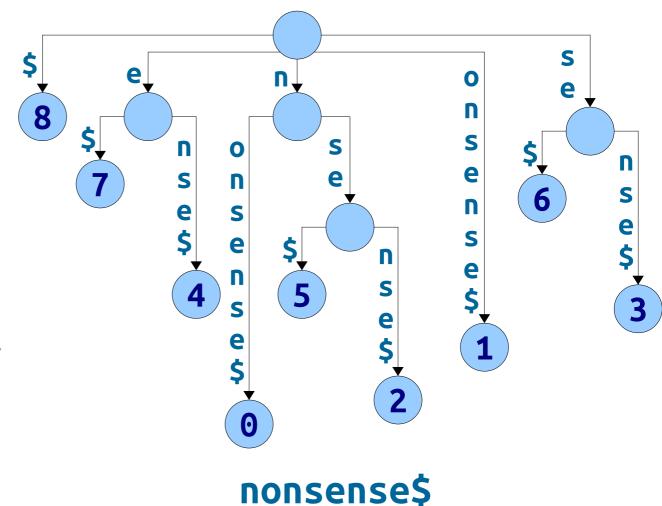
#### Suffix Trees

- A *suffix tree* for a string *T* is a Patricia trie of all suffixes of *T*.
- Each leaf is labeled with the starting index of that suffix.



## Substring Search

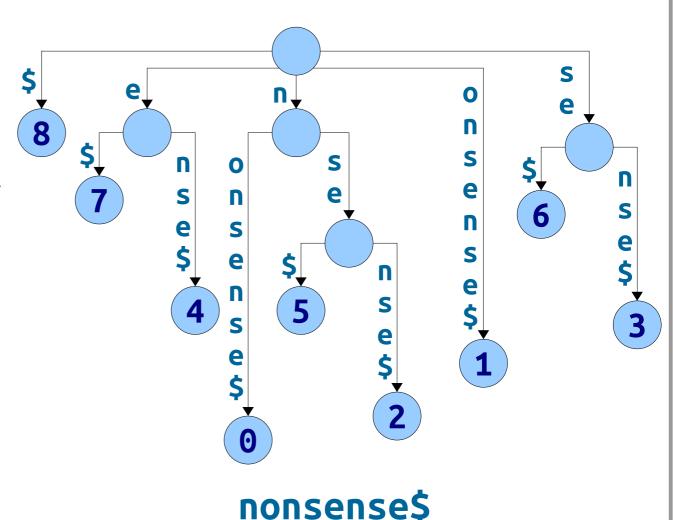
- Claim: Once we have a suffix tree for a string T, we can find all matches of a pattern P of length n in time O(n + z), where z is the number of matches.
- *Idea:* Use the standard Patricia trie search from before!



012345678

## Substring Search

- *Algorithm:* Use the standard Patricia trie search!
- Look up the pattern in the suffix tree, then use a DFS to find all matches.
- Looking up the pattern takes time O(n).
- Finding all matches takes time O(z).



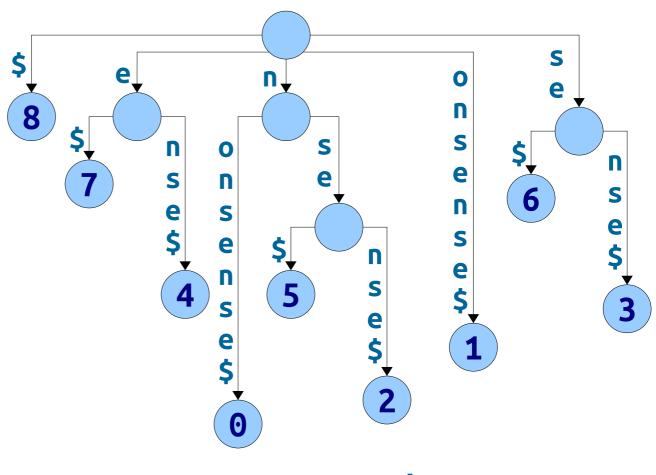
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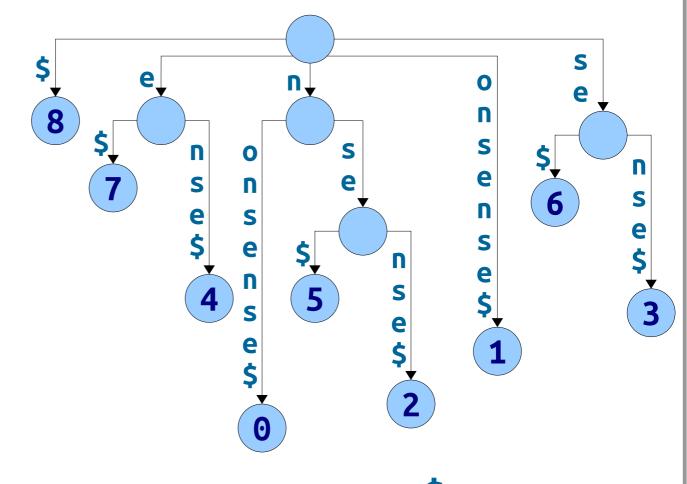
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Given a cancer genome (length ~3,000,000,000), find the longest repeated DNA sequence.

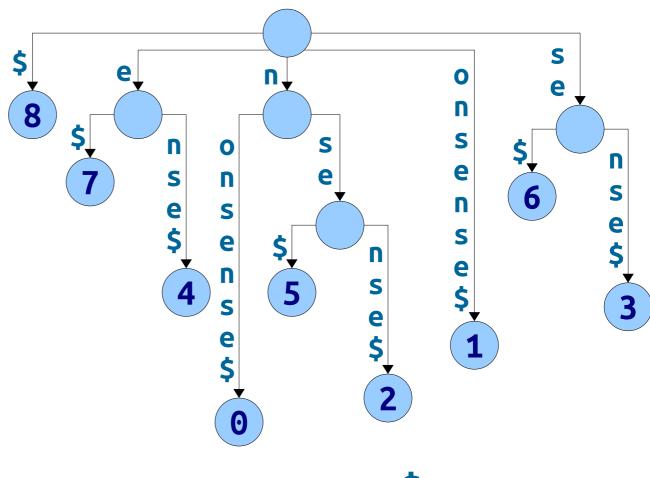
- Think back to Cartesian trees. We can describe them in two ways.
  - *Mechnically:* Hoist the minimum element up to the root, then recursively process the two subarrays.
  - *Operationally:* It's a min-heap whose inorder traversal gives the original array.
- We now have a
   mechanical definition of
   a suffix tree. Can we get
   can operational one?



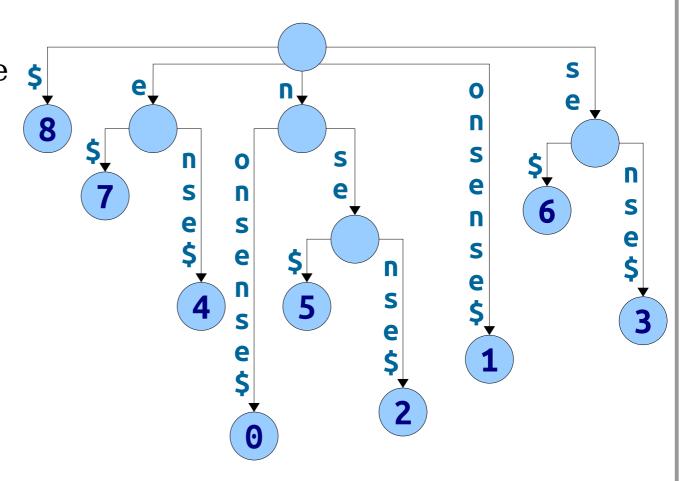
- The leaves of a suffix tree correspond to the suffixes of the text string *T*.
- Question: What do the internal nodes of the suffix tree correspond to?



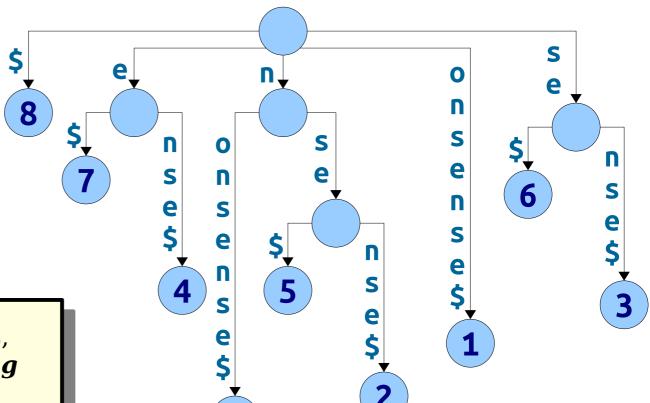
- In this suffix tree, there are internal nodes for the substrings e, n, nse, and se.
- All these substrings appear at least twice in the original string!
- More generally: if there is an internal node for a substring  $\alpha$ , then  $\alpha$  appears at least twice in the original text.



Question: why is
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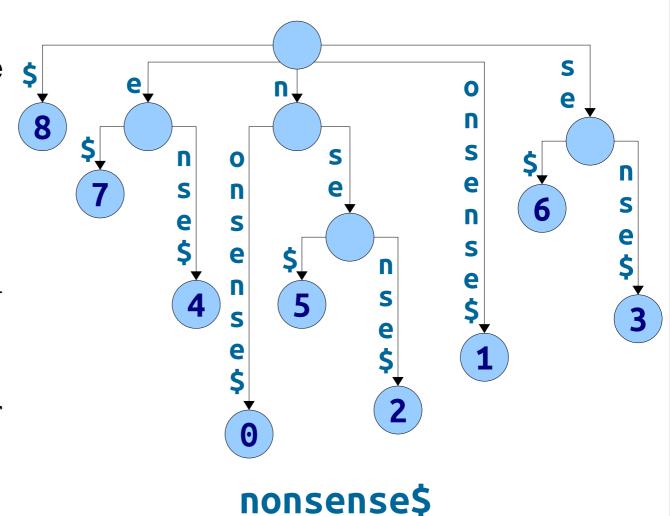
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N N e 5

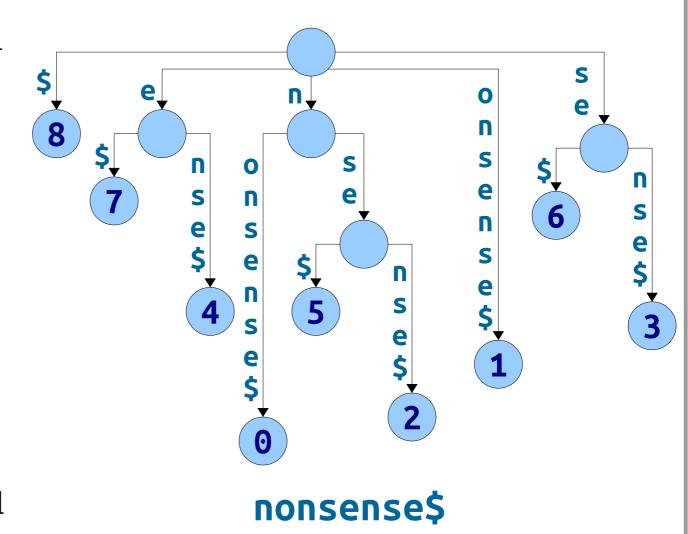
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- Question: why is
   there an internal node
   for the substring n,
   but isn't there an
   internal node for the
   substring ns?
- *Every* occurrence of **ns** can be extended by appending the same character (**e**).
- Not all occurrences of n can be extended by appending the same character.



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- A **branching word** in T\$ is a string  $\omega$  such that there are characters  $a \neq b$  where  $\omega a$  and  $\omega b$  are substrings of T\$.
  - Edge case: the empty string is always considered branching.
- *Theorem:* The suffix tree for a string T has an internal node for a string  $\omega$  if and only if  $\omega$  is a branching word in T\$.

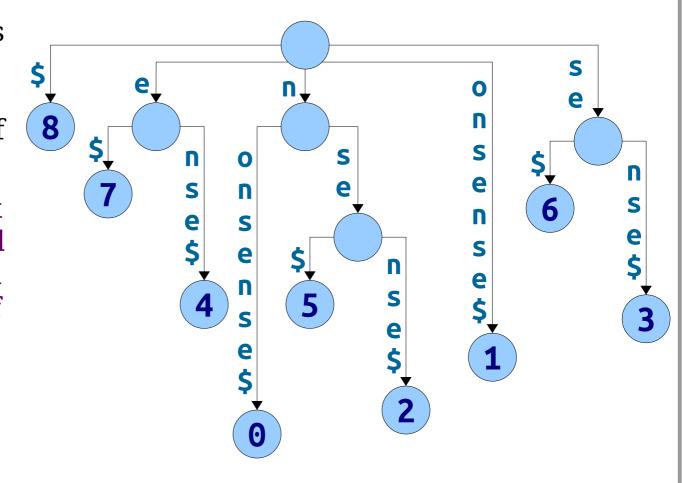


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 Combining our previous points together, we can give a (partial) operational definition of a suffix tree:

The leaves of a suffix tree for T correspond to suffixes of T\$, and the internal nodes of a suffix tree for T correspond to branching words of T\$.

 We'll make extensive use of this fact going forward.



- *Theorem:* The longest repeated substring of a string T must be a branching word in T\$.
- **Proof idea:** If  $\omega$  isn't branching, it can't be the longest repeated substring.

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The substring berti isn't repeated.

It therefore can't be the longest repeated substring.

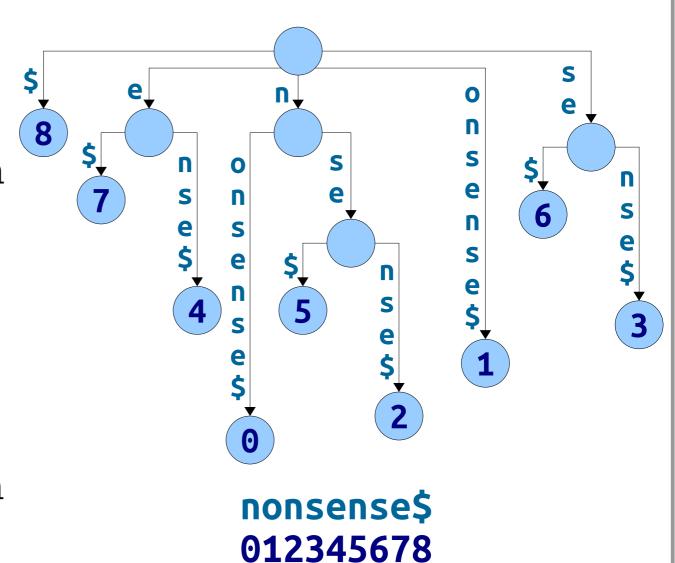
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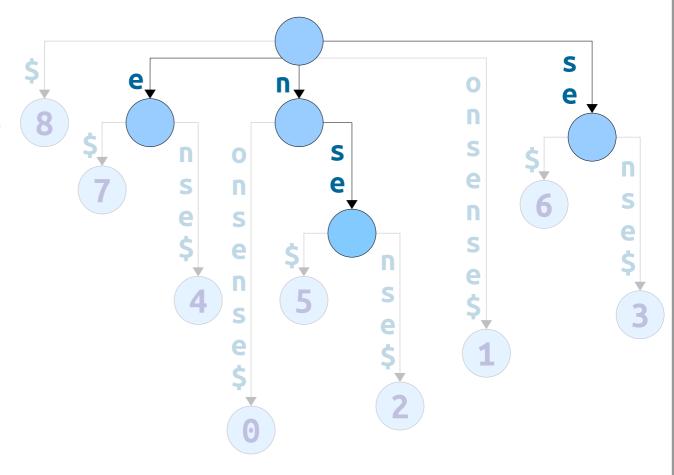
Every instance of bb can be extended to bbe.

It therefore can't be the longest repeated substring.

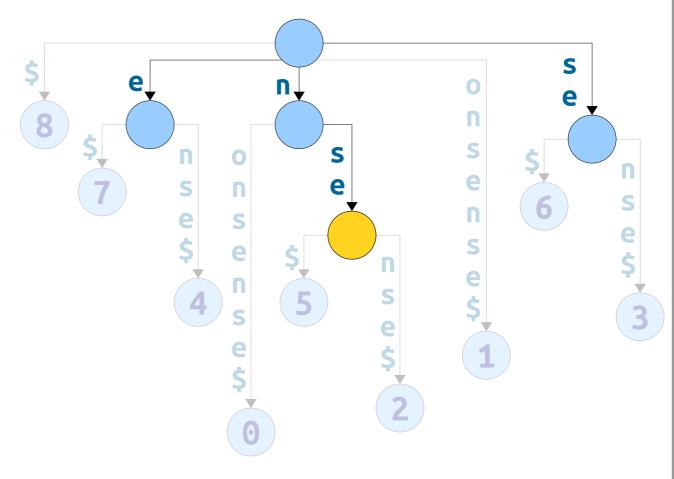
- *Theorem:* The longest repeated substring of *T* is a branching word in *T*\$.
- To find the longest repeated substring of a string *T*, we just need to find the internal node with the longest label!



- Given a suffix tree for a string T of length m, there is an O(m)-time algorithm for finding the longest repeated substring of m.
- **Basic idea:** Run a DFS over the tree and find the internal node with the longest string on its path from the root.
- There are some subtle details required to get this to run in time O(m). Think this over! See what you find.



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### More to Explore

- We've barely scratched the surface of suffix trees. They can be used for tons of other problems.
- A sampling:
  - *Generalized suffix trees*: Solves fast substring searching over multiple text strings, not just a single text string.
  - *Approximate string matching*: Given a text string T and a pattern P, see the closest match to P in T.
  - *Fast matrix multiplication*: The matrix multiplications needed in computing word embeddings can, amazingly, be optimized using suffix trees.
- This is a rich space to explore and I encourage you to do so!

#### Next Time

- Suffix Arrays
  - A space-efficient alternative to suffix trees.
- LCP Arrays
  - Implicitly capturing suffix tree structure.