Comp 555 - BioAlgorithms - Spring 2021

COMBINATORIAL PILLOW TAIK

How do I love thee? Let me count the ways. Suppose there are n ways of loving someone and I can love you in any k of them. Assuming order doesn't matter, there are simply (k) ways. If order does matter - eq. if buying you flowers on Monday and taking you to de on Tuesday dilluss from taking you to a show on Monday and buying you flowers on Tuesday then we have (n-k1), or (k)k! - but what if then we have (n-k!), or (k)k! - but ways? I can love you in k ways, then me ways? This scenario requires the multichoose operation, This scenario requires the multichoose operation, k!(n-k)! m!(n-k-m)! COULTNEY GIBBONS 2006

• PROBLEM SET #2 IS DUE TONIGHT

Combinatorial Pattern Matching

A Recurring Problem

- Finding patterns within sequences
- Variants on this idea
 - Finding repeated motifs amongst a set of strings
 - What are the most frequent k-mers
 - How many times does a specific k-mer appear



- Fundamental problem: *Pattern Matching*
 - Find all positions of a particular substring in given sequence?

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Pattern Matching



The most fundamental of pattern matching problems-does a pattern, *p*, appear in a text, *t*? And if so, where?

- Goal: Find all occurrences of a pattern in a text
- **Input:** Pattern $p = p_1, p_2, \dots, p_n$ and text $t = t_1, t_2, \dots, t_m$
- <u>Output:</u> All positions 1 < i < (m n + 1) such that the *n*-letter substring of t starting at i matches p

```
In [2]: M def bruteForcePatternMatching(p, t):
    locations = []
    for i in range(0, len(t)-len(p)+1):
        if t[i:i+len(p)] == p:
            locations.append(i)
        return locations
    print(bruteForcePatternMatching("ssi", "imissmissmississippi"))
    [11, 14]
```

Pattern Matching Performance

- Performance:
 - m length of the text t
 - \circ *n* the length of the pattern *p*
 - Search Loop executed *O(m)* times
 - Comparison *O*(*n*) symbols compared
 - Total cost *O(mn)* per pattern
- In practice, most comparisons will terminate early. Why?
- But worst-case data examples exist:

 \circ t = "AAAAAAAAAAAAAAAAAAAAAAAAAA



We can do better!



If we preprocess our pattern we can search more efficiently (O(n)).

Example: FindPattern("ssi", "imissmissmississippi"):

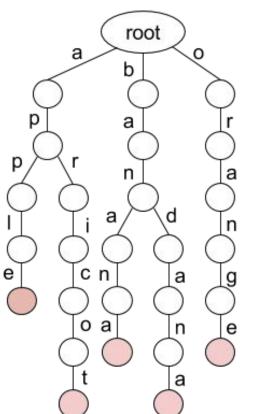
imissmissmississippi

| 1. | S | |
|-----|-----|---------------|
| 2. | S | |
| 3. | S | |
| 4. | SSi | |
| 5. | S | |
| 6. | SSi | |
| 7. | S | |
| 8. | SSI | - match at 11 |
| 9. | SSI | - match at 14 |
| 10. | S | |
| 11. | S | |
| 12. | S | |

- At steps 4 and 6 after finding the mismatch "i" ≠ "m" we can skip over all positions tested because we know that the suffix "sm" is not a prefix of our pattern "ssi".
- Even works for our worst-case example "AAAAT" in "AAAAAAAAAAAAAT" by recognizing the shared prefixes ("AAA" in "AAAA").
- How about finding multiple patterns [p₁,p₂,...,p₃] in t

Keyword Trees

- We can preprocess the set of strings we are seeking to minimize the Inumber of comparisons
- Idea: Combine patterns that share prefixes, to share those comparisons
 - Stores a set of keywords in a rooted labeled tree
 - Each edge labeled with a letter from an alphabet
 - All edges leaving a given vertex have distinct labels
 - Leaf vertices are indicated
 - Every keyword stored can be spelled on a path from the root to some leaf vertex
 - Searches are performed by "threading" the target pattern through the tree
- A *Tree* is a special graph as discussed previously
 - One connected component
 - N nodes, N-1 edges, No loops
 - Exactly one path from any.
- A *Trie* is a tree that is related to a sequence.
 - Generally, there is a 1-to-1 correspondence between either nodes or edges of the *trie* and a symbol of the sequence





Prefix Trie Match



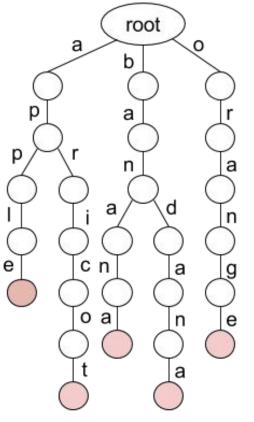
- Input: A text *t* and a trie *P* of patterns
- **Output:** True if *t* leads to a leaf in *P*; False otherwise

What is output for:

- apple
- band
- april

Performance:

- O(m) the length of the text, t
- Independent of how many strings are in the Keyword Trie



Prefix Trie code



```
In [2]: def path(string, parent):
            if (len(string) > 0):
                if (string[0] in parent):
                    child = parent[string[0]]
                else:
                    child = {}
                    parent[string[0]] = child
                path(string[1:], child)
            else:
                parent['$'] = True
        class PrefixTrie:
            def __init (self):
                """ Tree is a dictionary of the children at each node"""
                self.root = {}
            def add(self, string):
                """ Add a path from the Trie's root"""
                path(string, self.root)
            def match(self, string):
                """ Check if there is a path from the root to a '$' """
                parent = self.root
                for c in string:
                    if c not in parent:
                        break
                    parent = parent[c]
                else:
                    return '$' in parent
                return False
```

Prefix Trie code



| In [3]: | <pre>T = PrefixTrie() T.add("apple") T.add("banana") T.add("apricot") T.add("hendene")</pre> |
|---------|---|
| | T.add("bandana") T.add("orange") print(T.root) print(T.match('orange')) print([T.match(v) for v in ['apple', 'banana', 'apricot', 'orange', 'band', 'april', 'bandana', 'bananapple']]) |
| | {'o': {'r': {'a': {'n': {'g': {'e': {'\$': True}}}}, 'b': {'a': {'n': {'a': {'n': {'a': {'\$': True}}}, 'd': {'a': {'n': {'a': {'\$': True}}}}, 'a': {'p': {'r': {'i': {'c': {'c': {'\$': True}}}, 'p': {'l': {'e': {'\$': True}}}} True [True, True, True, True, False, False, True, False] |



Suppose that we have a long string, *t*, like a genome, and we want to find if any of the strings in a previously constructed prefix trie, *P*, appear within it.

- *t* the text to search through
- *P* the trie of patterns to search for

```
def multiplePatternMatching(t, P):
    locations = []
    for i in xrange(0, len(t)):
        if PrefixTrieMatch(t[i:], P):
            locations.append(i)
    return locations
```

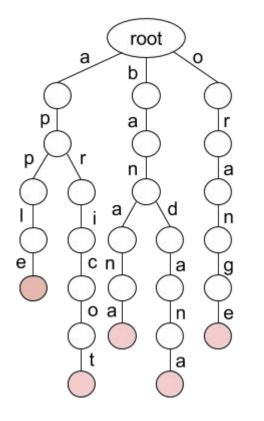


Multiple Pattern Matching Example

multiplePatternMatching("bananapple", P):

- 0: PrefixTrieMatching("bananapple", P) = True
- 1: PrefixTrieMatching("ananapple", P) = False
- 2: PrefixTrieMatching("nanapple", P) = False
- 3: PrefixTrieMatching("anapple", P) = False
- 4: PrefixTrieMatching("napple", P) = False
- 5: PrefixTrieMatching("apple", P) = True
- 6: PrefixTrieMatching("pple", P) = False
- 7: PrefixTrieMatching("ple", P) = False
- 8: PrefixTrieMatching("le", P) = False
- 9: PrefixTrieMatching("e", P) = False

locations = [0, 5]



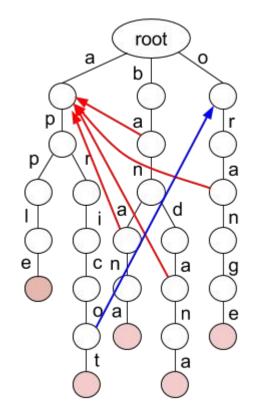
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Trie Improvements

- Based on our previous speed-up
- We can add failure edges to our Trie Add an edge to any *prefix* from the root that matches a *suffix* on our failed path
- Aho-Corasick Algorithm

The concept of "threading" one string through another

bapple bap apple



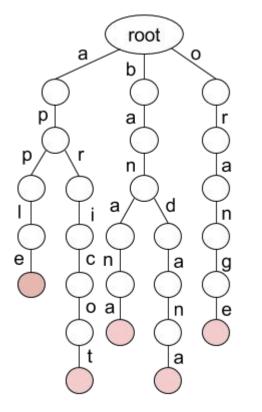




Multiple Pattern Matching Performance

- m len(t)
- d max depth of P (longest pattern in P)
- O(md) to find all patterns
- Can be decreased further to O(m) using Aho-Corasick Algorithm
 - Add links for pattern suffixes that match text prefixes
- Pattern matching data structure is query specific

Idea: Rather than building a search data structure for indexing the prefixes of the pattern, why not build one for indexing the suffixes of the text.



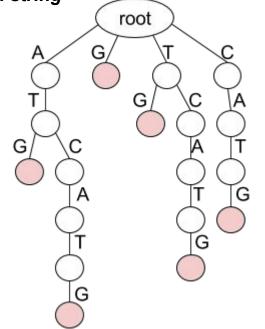
Now for a Twist



• What if our list of keywords were simply all suffixes of a single given string

Example: ATCATG TCATG CATG ATG TG G

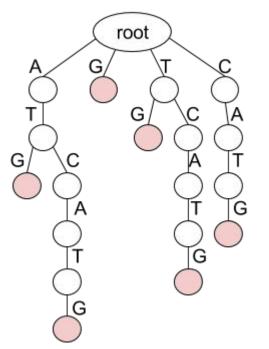
- The resulting keyword tree:
- A Suffix Trie
- How would you find "CAT"
- It is a prefix of one of our suffixes
- If there is a path for our entire pattern, we know which suffix it came from
- Try "AT"



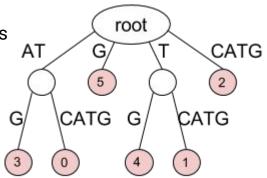
Suffix Tree



A compressed Suffix Trie



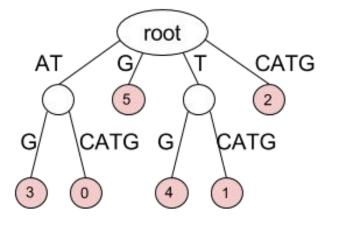
- Combine nodes with in and out degree 1
- Make edges of these substrings
- All internal nodes have at least 3 edges
- All leaf nodes are labeled with an index of the suffix's index



Uses for Suffix Trees

They are

- Suffix trees hold all suffixes of a text, T
 - i.e., ATCATG: ATCATG, TCATG, CATG, ATG, TG, G
- Can be built in O(m) time for text of length m
- To find any pattern P in a text:
 - \circ Build suffix tree for text, O(m), m=|T|
 - Thread the pattern through the suffix tree
 - Can find pattern in O(n) time! (n=|P|)
- O(|T|+|P|) time for "Pattern Matching Problem" (better than Naïve O(|P||T|)
- Build suffix tree and lookup pattern
- Multiple Pattern Matching in O(|T|+k|P|)



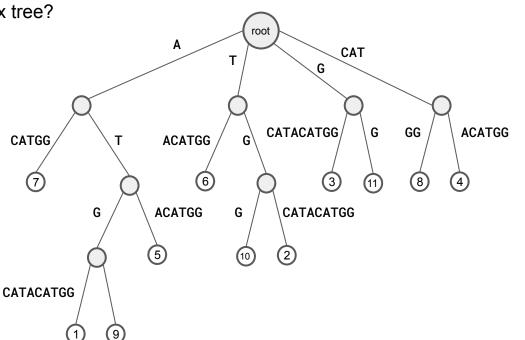
Suffix Tree Overhead

Mar

- Input: text of length m
- Computation
 - O(m) to compute a suffix tree
 - Does not require building the suffix trie first
- Memory
 - O(m) nodes are stored as offsets and lengths
- Huge hidden constant, best implementations
- Requires about 20*m bytes
- 3 GB human genome = 60 GB RAM

Suffix Tree Examples

- What is the string represented in the suffix tree? Find path that leads to "1"
- What letter occurs most frequently? Find edge from the root leads to the most leafs
- How many times does "ATG" appear, and where?
 Match "ATG" to tree and count the number of leafs from that path
- How long is the longest repeated k-mer?
 Find longest path leading to two leafs

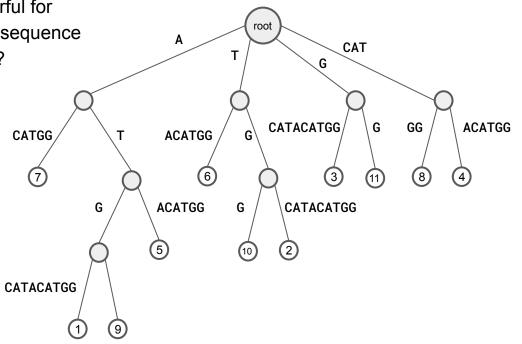




Suffix Trees: Theory vs. Practice



- In theory, suffix trees are extremely powerful for making a variety of queries concerning a sequence
 - What is the shortest unique substring?
 - How many times does a given string appear in a text?
- Despite the existence of linear-time construction algorithms, and O(m) search times, suffix trees are still rarely used for genome-scale searching
- Large storage overhead



Substring Searching



- Is there some other data structure to gain efficient access to all of the suffixes of a given string with less overhead than a suffix tree?
- Some things we know
 - Searching an unordered list of items with length *n* generally requires *O(n)* steps
 - However, if we sort our items first, then we can search using O(log(n)) steps
 - Thus, if we plan to do frequent searches there is some advantage to performing a sort first and amortizing its cost over many searches
- For strings *suffixes* are interesting *items*. Why?

| Suffixes: | panamabananas anamabananas namabananas amabananas amabananas abananas abananas bananas ananas ananas nanas anas | Sorted Suffixes: | abananas amabananas anamabananas ananas anas anas as bananas mabananas namabananas nanas nanas nanas |
|-----------|--|------------------|--|
| | S | | S |

Questions you can ask

Is there any use for a list of sorted suffixes?

Sorted Suffixes: abananas amabananas anamabananas ananas anas anas as bananas mabananas namabananas namabananas nas panamabananas s

- Does the substring "nana" appear in the original string?
- How many times does "ana" appear in the string?
- What is the most/least frequent letter in the original string?
- What is the most frequent two-letter substring in the original string?



Mes



Properties of a sorted "suffix array"

- Size of the sorted list if the given text has a length of m? O(m²)
- Cost of the sort? O(m²log(m))
- Not practical for big *m*
- There are many ways to sort
 - What is an "*in place*" sort?
 - What is a "stable" sort?
 - What is an "arg" sort?





consider the list:

[72,27,45,36,18,54,9,63]

When sorted it is simply:

```
[9,18,27,36,45,54,63,72]
```

Its "arg" sort is:

[6, 4, 1, 3, 2, 5, 7, 0]

- The *ith* element in the arg sort is the *index* of the *ith* element from the original list when sorted.
- Thus, [A[i] for i in argsort(A)] == sorted(A)

Code for Arg Sorting



```
In [7]: M def argsort(input):
    return sorted(range(len(input)), key=input._getitem_)
    A = [72,27,45,36,18,54,9,63]
    print(argsort(A))
    print([A[i] for i in argsort(A)])
    print()
    B = ["TAGACAT", "AGACAT", "GACAT", "ACAT", "CAT", "AT", "T"]
    print(argsort(B))
    print([B[i] for i in argsort(B)])
    [6, 4, 1, 3, 2, 5, 7, 0]
```

[9, 18, 27, 36, 45, 54, 63, 72]

```
[3, 1, 5, 4, 2, 6, 0]
['ACAT', 'AGACAT', 'AT', 'CAT', 'GACAT', 'T', 'TAGACAT']
```

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Next Time

- We'll see how arg sorting can be used to simplify representing our sorted list of suffixes
- Suffix arrays
- Burrows-Wheeler Transforms
- Applications in sequence alignment

