## Comp 555 - BioAlgorithms - Spring 2020

## COMBINATORIAL PILLOW TANK

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 $\binom{n}{k}=\frac{n!}{n-l e)!} k$ ! ways. If order does matter - eg, is burying you flowers on Monday and taking you to a show on Tuesday differs from taking you to a show on Monday and baying you flowers on Tuesday, then we have $\left(\frac{n!}{n-k!}\right)$, or $\binom{n}{k} k!$ - but what if I can love you in $k$ ways, then me ways? This scenario requires the multichoose operation, $\binom{n}{k, m)} \frac{n!}{k!(n-k)!} \cdot n!(n-k)!$

2006

- Problem set \#z is due NEXT TUESDAY


## 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?


## Pattern Matching

The most fundemental for pattern matching problems, does a pattern, $p$, appear in a text, $t$ ? If so, where?

- Goal: Find all occurrences of a pattern in a text
- Input: Pattern $p=p_{1}, p_{2}, \ldots p_{n}$ and text $t=t_{1}, t_{2}, \ldots t_{m}$
- Output: All positions $1<\mathrm{i}<(\mathrm{m}-\mathrm{n}+1)$ 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 $(\theta$, len $(t)-\operatorname{len}(p)+1)$ :
if $t[i: i+\operatorname{len}(p)]==p$ :
locations.append(i)
return locations
print(bruteForcePatternMatching("ssi", "imissmissmississippi"))
$[11,14]$

## Pattern Matching Performance

- Performance:
- $m$ - length of the text $t$
- $n$ - 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 sets exist:
- $p=$ "AAAT"
- $t=$ "AAAAAAAAAAAAAAAAAAAAAAAT"


## We can do better!

If we preprocess our pattern we can search more effciently $(O(n))$.
Example: FindPattern("ssi", "imissmissmississippi"):

## imissmissmississippi

1. $s$
2. s
3. s
4. SSi
$5 . \quad$ s
5. SSi
6. 
7. 
8. 
9. 
10. 
11. 
```
                SSI - match at 11
```

                    SSI - match at 14
                s
                    s
    s

- At steps 4 and 6 after finding the mismatch " $i$ " $\neq$ " $m$ " 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 "AAAAAAAAAAAAAAT" by recognizing the shared prefixes ("AAA" in "AAAA").
- How about finding multiple patterns $\left[p_{1}, p_{2}, \ldots, p_{3}\right]$ in $t$


## Keyword Trees

- We can preprocess the set of strings we are seeking to minimize the |number 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
- $\quad N$ 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:

- $\mathrm{O}(\mathrm{m})$ - the length of the text, $t$
- Independent of how many strings are in the Keyword Trie



## Prefix Trie code

```
In [5]: M 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]
        return '$' in parent
T = PrefixTrie()
T.add("apple")
T.add("banana")
T.add("apricot")
T. add("bandana")
.add("bandana")
T.add("orange")
print(T.root)
print([v for v in map(T.match, ['apple', 'banana', 'apricot', 'orange', 'band', 'april', 'bananapple'])])
```


[True, True, True, True, False, False, True]

## Multiple Pattern Matching

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
- $\quad P$ - 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]
```



## 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 matchs a suffix on our failed path
- Aho-Corasick Algorithm

The concept of "threading" one string through another

$$
\begin{aligned}
& \text { bapple } \\
& \text { bap } \\
& \text { apple }
\end{aligned}
$$



## Multiple Pattern Matching Performance

- $\quad m-\operatorname{len}(t)$
- d - max depth of P (longest pattern in P)
- $\quad \mathrm{O}(\mathrm{md})$ to find all patterns
- Can be decreased further to $\mathrm{O}(\mathrm{m})$ 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

- $\quad$ 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:
- Build suffix tree for text, $O(m), m=|T|$
- Thread the pattern through the suffix tree
- Can find pattern in $O(n)$ time! ( $n=|P|$ )
- $\quad \mathrm{O}(|\mathrm{T}|+|\mathrm{P}|)$ time for "Pattern Matching Problem" (better than Naïve $\mathrm{O}(|\mathrm{P}||\mathrm{T}|$ )
- Build suffix tree and lookup pattern
- Multiple Pattern Matching in $\mathrm{O}(|\mathrm{T}|+\mathrm{k}|\mathrm{P}|)$



## Suffix Tree Overhead

- 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 $\mathrm{O}(\mathrm{m})$ 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 efficent 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 searchs there is some advantage to performing a sort first and amortizing its cost over many searchs
- For strings suffixes are interesting items. Why?

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

## Questions you can ask

Is there any use for a list of sorted suffixes?

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

- Does the substring "nana" appear in the orginal string?

Sometimes the questions are complicated
and the answers are
 simple.

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


## Properties of a sorted "suffix array"

- Size of the sorted list if the given text has a length of $m$ ? $\mathrm{O}\left(\mathrm{m}^{2}\right)$
- Cost of the sort? $O\left(m^{2} \log (m)\right)$
- 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?


## Arg Sorting

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 orginal list when sorted.
- Thus, $[\mathrm{A}[\mathrm{i}]$ for i in $\operatorname{argsort}(\mathrm{A})]==$ sorted[ A$]$


## Code for Arg Sorting

In [7]: $\quad$ def argsort(input)
return $\operatorname{sorted}($ 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()
$\mathrm{B}=$ ["TAGACAT", "AGACAT", "GACAT", "ACAT", "CAT", "AT", "T"]
print(argsort(B))
print([B[i] for $i$ in $\operatorname{argsort(B)])}$
$[6,4,1,3,2,5,7,0]$
$[9,18,27,36,45,54,63,72]$
$[3,1,5,4,2,6,0]$
['ACAT', 'AGACAT', 'AT', 'CAT', 'GACAT', 'T', 'TAGACAT']

## 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


