# CMSC423: Bioinformatic Algorithms, Databases and Tools 

Exact string matching: introduction

## Sequence alignment: exact matching

```
ACAGGTACAGTTCCCTCGACACCTACTACCTAAG
```

for i = 0 .. len(Text) {

```
for i = 0 .. len(Text) {
    for j = 0 .. len(Pattern) {
    for j = 0 .. len(Pattern) {
            if (Pattern[j] != Text[i]) go to next i
            if (Pattern[j] != Text[i]) go to next i
        }
        }
    if we got there pattern matches at i in Text
    if we got there pattern matches at i in Text
}
```

}

```

\author{
Pattern
}

Running time \(=O(\) len(Text \() * \operatorname{len}(\) Pattern \())=O(m n)\)
What string achieves worst case?

\section*{Worst case?}

АААААААААААААААААААААААААААААААААААААААААААААА AAAAAAAAAAAAT
\[
(m-n+1)^{*} n \text { comparisons }
\]

\section*{Can we do better?}

\section*{the \(Z\) algorithm (Gusfield)}

For a string \(T, Z[i]\) is the length of the longest prefix of \(T[i . . m]\) that matches a prefix of \(T\). \(Z[i]=0\) if the prefixes don't match.
\(T[0\).. \(Z[i]]=T[i \quad . . i+Z[i]-1]\)


\section*{Example \(Z\) values}

\section*{ACAGGTACAGTTCCCTCGACACCTACTACCTAAG 0010004010000000003020002002000110}

\section*{Can the \(Z\) values help in matching?}

Create string Pattern\$Text where \(\$\) is not in the alphabet


If there exists \(\mathrm{i}, \mathrm{s.t} . \mathrm{Z}[\mathrm{i}]=\) length(Pattern)
Pattern occurs in the Text starting at i

\section*{example matching}

\section*{CCTACT\$ACAGGTACAGTTCCCTCGACACCTACTACCTAAG 01001000100000100002310100106100100410000}
- What is the largest \(Z\) value possible?

\section*{Can \(Z\) values be computed in linear time?}

AAAGGTACAGTTCCCTCGACACCTACTACCTAAG
\(\mathrm{Z}[1]\) ? compare \(\mathrm{T}[1]\) with \(\mathrm{T}[0], \mathrm{T}[2]\) with \(\mathrm{T}[1]\), etc. until mismatch \(Z[1]=2\)

This simple process is still expensive:
\(\mathrm{T}[2]\) is compared when computing both \(\mathrm{Z}[1]\) and \(\mathrm{Z}[2]\).
Trick to computing \(Z\) values in linear time: each comparison must involve a character that was not compared before

Since there are only \(m\) characters in the string, the overall \# of comparisons will be \(O(m)\).

\section*{Basic idea: 1-D dynamic programming}

Can \(Z[i]\) be computed with the help of \(Z[j]\) for j < \(i\) ?


Assume there exists \(\mathrm{j}<\mathrm{i}\), s.t. \(\mathrm{j}+\mathrm{Z}[\mathrm{j}]-1>\mathrm{i}\) then \(Z[i-j+1]\) provides information about \(Z[i]\)

If there is no such j , simply compare characters \(\mathrm{T}[i .\).\(] to \mathrm{T}[0 .\). since they have not been seen before.

\section*{Three cases}

Let j < i be the coordinate that maximizes \(\mathrm{j}+\mathrm{Z}[\mathrm{j}]-1\) (intuitively, the \(Z[j]\) that extends the furthest)
I. \(Z[i-j+1]<Z[j]-i+j-1=>Z[i]=Z[i-j+1]\)

II. \(Z[i-j+1]>Z[j]-i+j-1=>Z[i]=Z[j]-i+j-1\) \(i-j+1 \quad j\)

III. \(Z[i-j+1]=Z[j]-i+j-1=>Z[i]=\) ??, compare from
i-j+1
j
\[
i+Z[i-j+1]
\]

\section*{Time complexity analysis}
- Why do these tricks save us time?
1. Cases I and II take constant time per Z-value computed total time spent in these cases is \(\mathrm{O}(\mathrm{n})\)
2. Case III might involve 1 or more comparisons per Z-value however:
- every successful comparison (match) shifts the rightmost character that has been visited
- every unsuccessful comparison terminates the "round" and algorithm moves on to the next Z-value
total time spent in III cannot be more than \# of characters in the text
Overall running time is \(\mathrm{O}(\mathrm{n})\)

\section*{Space complexity?}
- If using \(Z\) algorithm for matching, how many \(Z\) values do we need to store?

\section*{PPPPPPPPPP\$TTTTTTTTTTTTTTTTTTTTTTTT}
- Only need to remember Z-values for pattern and the "farthest reaching Z-value" (Z[j] in what we discussed before)

\section*{Some questions}
- What are the Z-values for the following string:

TTAGGATAGCCATTAGCCTCATTAGGGATTAGGAT
- In the string above, what is the longest prefix that is repeated somewhere else in the string?
- Trace through the execution of the linear-time algorithm for computing the \(Z\) values for the string listed above. How many times do rules I, II, and III apply?

\section*{Z algorithm, not just for matching}
- Lempel-Ziv compression (e.g. gzip)

if \(Z[i]=0\), just send/store the character T[i], otherwise, instead of sending \(T[i . . i+Z[i]-1]\) ( \(Z[i]-1\) characters/bytes) simply send \(Z[i]\) (one number)
- Note: other exact matching algorithms used for data compression (e.g. Burrows-Wheeler transform relates to suffix arrays)

\section*{Knuth-Morris-Pratt algorithm}

Given a Pattern and a Text, preprocess the Pattern to compute \(s p[i]=\) length of longest prefix of \(P\) that matches a suffix of \(P[0 . . i]\)

P

\(P^{\prime} \square \square\)
- Compare P with T until finding a mis-match (at coordinate \(i+1\) in \(P\) and \(j+1\) in \(T\) ).
- Shift \(P\) such that first \(s p[i]\) characters match \(T[j-s p[i]+1\).. j].
- Continue matching from T[i+1], P[sp[i]+1]

\section*{Knuth-Morris-Pratt (KMP) Algorithm}

Given a pattern ( \(\mathbf{P}\) ) and a text block ( \(\mathbf{T}\) ) you preprocess \(\mathbf{P}\) to compute a zero-indexed array \(\mathbf{s p}[]\) where \(\mathbf{s p}[\mathrm{pos}]\) contains the length of longest prefix of \(\mathbf{P}\) that matches a suffix of \(\mathbf{P}[0 .\). pos]
\[
\begin{aligned}
& \downarrow \text { pos=11 } \\
& \mathrm{sp}[\mathrm{pos}]=4 \uparrow
\end{aligned}
\]

\section*{Tracing KMP}

\section*{\(\downarrow\) pos=11 \\ P ABCD|EFGH|ABCD \\ \[
\mathbf{s p}[\mathrm{pos}]=4 \uparrow
\]}

We compare \(\mathbf{P}\) with \(\mathbf{T}\) until finding a mismatch.
We'll call that position \(i+1\) in \(\mathbf{P}\) and \(j+1\) in \(\mathbf{T}\).


We then logically shift \(\mathbf{P}\) using the \(\mathbf{s p}\) value.
This allows the first \(\mathbf{s p}[1]\) characters to match \(\mathrm{T}[(j-\mathrm{sp}[1]+1)\).. \(j]\). We then continue comparing from \(\mathrm{P}[\mathrm{sp}[1]+1]\) and \(\mathrm{T}[j+1]\)
index: 0123456
pattern: AAAAAAA
sp: 0123456
index: 0123456
pattern: AAAAAAB
sp: 0123450

AAAAABAAAAAABAAAAAAA
\begin{tabular}{ll} 
index: & 0123456 \\
pattern: & ABACABC \\
sp: & 0010120
\end{tabular}

\section*{ABABBABAABABACABC}

\section*{Boyer-Moore algorithm}

Preprocess the pattern, computing, for every \(\mathrm{i}, \mathrm{L}[\mathrm{i}]=\) largest coordinate < n, s.t. P[i..n] matches a suffix of P[1..L[i]] (inverted Z function)


Match the pattern backwards (starting at the right) until mismatch. Shift the pattern such that \(P[L[i]-n+i+1]\) matches at \(T[j]\) Repeat.

Bad character rule: find character \(T[j-1]\) in \(P\) and shift until it matches. Choose the longest shift (btwn. suffix \& char. rules)

\section*{Boyer-Moore ... cont}
- What if \(P[i . . n]\) does not occur elsewhere prior to \(i\) ?
- Find k > i s.t. P[1..(n-k)] matches P[k..n]

- Also bad character rule:
- if \(P[i]\) mismatches with \(T[j]\) - can shift \(P\) until we find a character equal to \(T[j]\) in \(P\) (above, shift until an \(A\) in \(P\) lines up to the \(A\) in \(T\) )
- Putting it all together: compute the shift according to the suffix rules and the bad character rule and pick the largest

\section*{Questions}
- Can you use the Z-values to efficiently compute the \(s p()\) values used in the KMP algorithm?
- How about the values used by the Boyer-Moore algorithm?```

