Principles of Computer Science II

Sequence Similarity

Ioannis Chatzigiannakis

Sapienza University of Rome

Lecture 19

Equivalent Words

Transform one English word v into another word w by going through a series of intermediate English words, where each word in the sequence differs from the next by only one substitution (1 character).

- Given two words v, w and a dictionary, find out whether the words are equivalent.
- Your program should output the series of transformations for v to become w
- Use the following dictionary: `https://goo.gl/hBvqqr`
- Example: To transform head into tail one can use four intermediates:
  head → heal → teal → tell → tall → tail

Generalized Equivalent Words

Find an algorithm to solve a generalization of the Equivalent Words problem when insertions, deletions, and substitutions are allowed (rather than only substitutions).

- Given two words v, w and a dictionary, find out whether the words are equivalent.
- Your program should output the series of transformations for v to become w
- Use the following dictionary: `https://goo.gl/hBvqqr`
- Example: To transform head into tea one can use four intermediates:
  head → heal → teal → tea

Edit Distance

- We looked for repeating patterns within DNA sequences.
- How can we measure the similarity between different sequences?
- We use the notion of Vladimir Levenshtein introduced in 1966
- Edit distance – the minimum number of editing operations needed to transform one string into another (insert/delete symbol or substitute one symbol for another).

Alignment of ATATATAT vs TATATATA

```
A T A T A T A T -
  : : : : : : :
- T A T A T A T A
```

Sequence Similarity

Alignment of ATATATAT vs TATAAT

```
A T A T A T A T
  : : : : : : :
- T A T A - A T
```

Sequence Similarity

Alignment of TGCATAT vs ATCCGAT

TGCATAT
↓ delete last T
TGCATA
↓ delete last A
TGCAT
↓ insert A at the front
ATGCAT
↓ substitute C for G in the third position
ATCCAT
↓ insert a G before the last A
ATCCGAT

Five operations.

Sequence Similarity

Alignment of TGCATAT vs ATCCGAT

TGCATAT
↓ insert A at the front
ATGCATAT
↓ delete T in the sixth position
ATGCAAT
↓ substitute G for A in the fifth position
ATGCGAT
↓ substitute C for G in the third position
ATCCGAT

Four operations.

Edit Distance

- Vladimir Levenshtein defined the notion of Edit distance
- Did not provide an algorithm to compute it.

Edit Distance Algorithm using Dynamic Programming

- Assume two strings:
  - v (of n characters)
  - w (of m characters)
- The alignment of v, w is a two-row matrix such that
  - first row: contains the characters of v (in order)
  - second row: contains the characters of w (in order)
  - spaces are interpersed throughout the table.
- Characters in each string appear in order, though not necessarily adjacently.

A	T	-	G	T	T	A	T	-
A	T	C	G	T	-	A	-	C

- No column contains spaces in both rows.
- At most $n + m$ columns.

Edit Distance Algorithm using Dynamic Programming

A	T	-	G	T	T	A	T	-
A	T	C	G	T	-	A	-	C

- Matches – columns with the same letter,
- Mismatches – columns with different letters.
- Columns containing one space are called indels
  - Space on top row: insertions
  - Space on bottom row: deletions

$$\#\text{matches} + \#\text{mismatches} + \#\text{indels} < n + m$$

Representing the rows

v	A	T	-	G	T	T	A	T	-
w	A	T	C	G	T	-	A	-	C

- One way to represent v
  - AT-CGTAT-
- One way to represent w
  - ATCGT-A-C
- Another way to represent v
  - AT-CGTAT-
  - 122345677
  - number of symbols of v present up to a given position
- Similarly, to represent w
  - ATCGT-A-C
  - 123455667

Representing the rows

v	A	T	-	G	T	T	A	T	-
w	A	T	C	G	T	-	A	-	C

v	1	2	2	3	4	5	6	7	7
w	1	2	3	4	5	5	6	6	7

can be viewed as a coordinate in 2-dimensional $n \times m$ grid:

$$\binom{0}{0} \binom{1}{1} \binom{2}{2} \binom{2}{3} \binom{3}{4} \binom{4}{5} \binom{5}{5} \binom{6}{6} \binom{7}{6} \binom{7}{7}$$

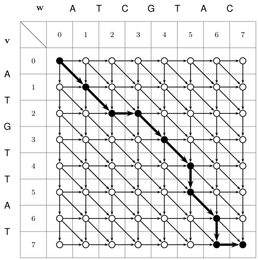
The entire alignment is simply a path:

$(0,0) \to (1,1) \to (2,2) \to (2,3) \to (3,4) \to (4,5) \to (5,5) \to (6,6) \to (7,6) \to (7,7)$

Edit distance graph

- Edit graph: a grid of n, m size.
- The edit graph will help us in calculating the edit distance.
- Alignment: a path from $(0,0)$ to (n,m).
- Every alignment corresponds to a path in the edit graph.
- Diagonal movement at point i,j correspond to column $\begin{pmatrix} v_i \\ w_j \end{pmatrix}$
- Horizontal movement correspond to column $\begin{pmatrix} - \\ w_j \end{pmatrix}$
- Vertical movement correspond to column $\begin{pmatrix} v_i \\ - \end{pmatrix}$

Edit distance graph



↘	↘	→	↘	↘	↓	↘	↓	→
A	T	-	G	T	T	A	T	-
A	T	C	G	T	-	A	-	C

Profile most-frequent k-mer

```
def edit_distance(s1, s2):
    m=len(s1)+1
    n=len(s2)+1

    tbl = {}
    for i in range(m): tbl[i,0]=i
    for j in range(n): tbl[0,j]=j
    for i in range(1, m):
        for j in range(1, n):
            cost = 0 if s1[i-1] == s2[j-1] else 1
            tbl[i,j] = min(tbl[i, j-1]+1,
                           tbl[i-1, j]+1,
                           tbl[i-1, j-1]+cost)

    return tbl[i,j]
```

Profile most-frequent k-mer

```
def levenshteinDistance(s1, s2):
    if len(s1) > len(s2):
        s1, s2 = s2, s1

    distances = range(len(s1) + 1)
    for i2, c2 in enumerate(s2):
        distances_ = [i2+1]
        for i1, c1 in enumerate(s1):
            if c1 == c2:
                distances_.append(distances[i1])
            else:
                distances_.append(1 + min((distances[i1],
                                           distances[i1 + 1],
                                           distances_[-1])))
        distances = distances_
    return distances[-1]
```