Introduction

COMP90049
COMP30018
Knowledge Technologies

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Summary

Week 3:

- Approximate String Search and Matching
- Common Applications
- Methods:
  - Neighbourhood Search
  - Edit Distance
  - N-Gram Distance
  - [Phonetic methods]
- Evaluation
- [Genomics]

Exact String Search

Consider:

- Given a string, is some substring contained within it?
- Given a string (document), find all occurrences of some substring

For example, find `Exxon` in:

```
In exes for foxes rex dux mixes a pox of waxed luxes.
An axe, and an axon, to exo Exxon max oxen.
Grexit or Brexit as quixotic haxxers with buxom rex taxation.
```

Not (really) a Knowledge Technology!

Find `exon` in:

```
In exes for foxes rex dux mixes a pox of waxed luxes.
An axe, and an axon, to exo Exxon max oxen.
Grexit or Brexit as quixotic haxxers with buxom rex taxation.
```

Not present!

...But what is the “closest” or “best” match?

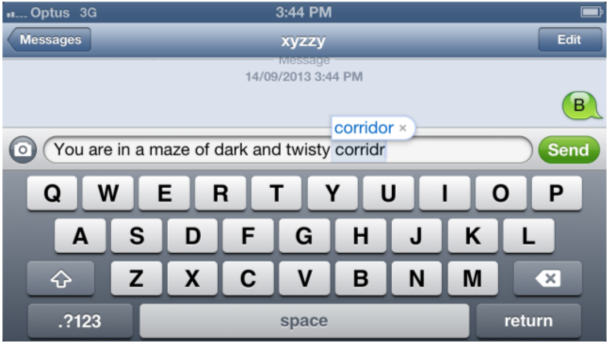
This is a Knowledge Technology!

Important problems

Two main applications for Approximate String Search:

- Spelling correction
- Computational Genomics

Spelling Correction



Need the notion of a **dictionary**:

- Here, a list of entries that are "correct"
- We can break our input into substrings that we wish to match, and compare each of them against the entries in the dictionary
- An item in the input which *doesn't* appear in the dictionary is *misspelled*
- An item in the input which *does* appear in the dictionary might be correctly spelled *or* misspelled (probably slightly beyond the scope of this subject)

Spelling Correction

Therefore, the problem here:

Given some item of interest — which does not appear in our dictionary — which entry from the dictionary was truly intended?

Depends on the person who wrote the original string!

Other Problems of Interest

- Computational Genomics (later, if we have time)
- Name matching
- Query repair
- Phonetic matching (later, if we have time)
- Data cleaning
- ...

What's a "best" match?

Find approximate match(es) for `exon` in:

```
In exes for foxes rex dux mixes a pox of waxed luxes.
An axe, and an axon, to exo Exxon max oxen.
Grexit or Brexit as quixotic haxxers with buxom rex taxation.
```

Neighbourhood Search

For a given string *w* of interest:

- Generate all variants of *w* that utilise at most *k* changes (Insertions/Deletions/Replacements) — **neighbours**
- Check whether generated variants exist in dictionary
- **All** results found in dictionary are returned

Unix command-line utility `agrep` is an efficient mechanism for finding these.

Neighbourhood Search

For example:

`... proceed if you can see no` **ther** `option ...`

Intended word: `other`

Requires 1 insertion (`o`) so intended word will be found using neighbourhood search (and some unintended words...)

Neighbourhood Search Efficiency

Neighbourhood search is suprisingly fast!

Consider: alphabet size is Σ, length of string is $|w|$:

For k edits, roughly $\mathcal{O}(\Sigma^k \cdot |w|^k)$ neighbours

...But Σ is a small constant, string of interest is usually short, and k is usually small

For each neighbour, need a dictionary read (dict has D entries):
Binary search yields $\mathcal{O}(|w|^k \log D)$ string comparisons

Neighbourhood Search Effectiveness

So, efficiency isn't our problem.

(`agrep` example)

Global Edit Distance

Alternative methods:

Scan through each dictionary entry looking for the “best” match

Global Edit Distance

Global Edit Distance:

Transform the string of interest into each dictionary entry, using the operations Insert, Delete, Replace, and Match (character)

Each operation is associated with a score;
Best match is the dictionary entry with best aggregate **score**

Global Edit Distance

For example:

Item of interest: `crat`

Dictionary: `cart`, `arts`

Score: Match +1, Insert -1, Delete -1, Replace -1

`crat` → `cart`:
Match `c` (+1), Delete `r` (-1), Match `a` (+1), Insert `r` (-1), Match `t` (+1) = +1

`crat` → `arts`:
Replace `c` with `a` (-1), Match `r` (+1), Delete `a` (-1), Match `t` (+1), Insert s (-1) = -1

`cart` is the better match

Global Edit Distance Parameter

Confusingly, Global Edit Distance isn't a "distance"

...But depends on parameter

Match (0), Insert (+1), Delete (+1), Replace (+1)
This is the Levenshtein Distance (which is a "distance"): it counts the number of edits required to transform one string into the other

Global Edit Distance Parameter

Hypothetically, any parameter is possible!

But some choices make no sense, e.g.:

Match (+4), Insert (-2), Delete (+8), Replace (0)

`aba`: Which corresponds to best match?

- `foo`: Insert, Delete, Insert, Delete, Insert, Delete = +18
- `aba`: Match, Match, Match = +12
- `cbc`: Replace, Match, Replace = +4

Global Edit Distance Parameter

Often, “direction” doesn’t matter: Insert = Delete (“Indel”)

Sometimes, score of Replace depends on which character is being replaced:

Consider:
Is `faxing` more likely to be `facing` or `faking`?

Global Edit Distance Algorithm

From string f to string t, given array A of $|f| + 1$ columns and $|t| + 1$ rows, we can solve using the Needleman–Wunsch algorithm:

```
lf = strlen(f); lt = strlen(t);
A[0][0]=0;
for (j=1; j<=lt; j++) A[j][0] = j * i;
for (k=1; k<=lf; k++) A[0][k] = k * d;

for (j=1; j<=lt; j++)
   for (k=1; k<=lf; k++)
      A[j][k] = max3( //Or min3 if m<i,d,r
         A[j][k-1] + d, //Deletion
         A[j-1][k] + i, //Insertion
         A[j-1][k-1] + equal(f[k-1],t[j-1])); //Replace or match
```

`equal()` returns m if characters match, r otherwise

Final score is at $A[lt][lf]$

Global Edit Distance in Action

In action: from `crat` to `arts`, Match (+1), Insert/Delete/Replace (-1)

	ε	c	r	a	t
ε	0	-1	-2	-3	-4
a	-1	-1	-2	-1	-2
r	-2	-2	0	-1	-2
t	-3	-3	-1	-1	0
s	-4	-4	-2	-2	-1

Global Edit Distance: -1 (Replace, Match, Delete, Match, Insert)

More parameter concerns

Algorithm actually depends on parameter!

```
A[j][k] = max3(
  A[j][k-1] + d, //Deletion
  A[j-1][k] + i, //Insertion
  A[j-1][k-1] + equal(f[k-1],t[j-1])); //Replace or match
```

$\rightarrow$ Match score greater than Insert/Delete/Replace

e.g. Match (+1), Insert/Delete/Replace (-1)

More parameter concerns

Algorithm actually depends on parameter!

```
A[j][k] = min3(
  A[j][k-1] + d, //Deletion
  A[j-1][k] + i, //Insertion
  A[j-1][k-1] + equal(f[k-1],t[j-1])); //Replace or match
```

→ Match score <u>less</u> than Insert/Delete/Replace

e.g. Match (0), Insert/Delete/Replace (+1)

(Levenshtein Distance)

Local Edit Distance

Local Edit Distance is like Global Edit Distance, but we are searching for the best substring match

Particularly suitable when comparing two strings of very different lengths, e.g. a word and a sentence

Local Edit Distance Algorithm

From string f to string t, given array A of $|f| + 1$ columns and $|t| + 1$ rows, we can solve using the Smith–Waterman algorithm:

```
lf = strlen(f); lt = strlen(t);
A[0][0]=0;
for (j=1; j<=lt; j++) A[j][0] = 0;
for (k=1; k<=lf; k++) A[0][k] = 0;

for (j=1; j<=lt; j++)
   for (k=1; k<=lf; k++)
      A[j][k] = max4( //Or min4 if m<i,d,r
         0,
         A[j][k-1] + d, //Deletion
         A[j-1][k] + i, //Insertion
         A[j-1][k-1] + equal(f[k-1],t[j-1])); //Replace or match
```

`equal()` returns m if characters match, r otherwise

Final score is greatest value in the entire table (or least value, if $m < i, d, r$)

Local Edit Distance in Action

In action: from `cart` to `arts`, Match (+1), Insert/Delete/Replace (-1)

	ε	c	a	r	t
ε	0	0	0	0	0
a	0	0	1	0	0
r	0	0	0	2	1
t	0	0	0	1	3
s	0	0	0	0	2

Best match: `art` with `art` (+3); ties are possible.

Edit Distance Efficiency

For strings f and t, Both algorithms above are $\mathcal{O}(|f||t|)$ in both space and time. (Space can be improved, but time (probably) cannot.)

When approximate matching, we have a constant string f which we want to compare to each string t in the dictionary D:

$\mathcal{O}(|f| \sum_{t \in D} |t|)$

Hence, integer comparisons are roughly the number of characters in the dictionary. Whether this is feasible depends on the size of the dictionary.

N-Gram Distance

N-Gram Distance has same goal as Edit Distance: compare two strings to determine "best" match

(character) *n*-gram: substring of length *n*

2-grams of `crat`: `#c`, `cr`, `ra`, `at`, `t#`
2-grams of `cart`: `#c`, `ca`, `ar`, `rt`, `t#`
2-grams of `arts`: `#a`, `ar`, `rt`, `ts`, `s#`

N-Gram Distance between *n*-grams of string s ($G_n(s)$) and t ($G_n(t)$):
$|G_n(s)| + |G_n(t)| - 2 \times |G_n(s) \cap G_n(t)|$

N-Gram Distance

n-gram: substring of length *n*

2-grams of `crat`: `#c`, `cr`, `ra`, `at`, `t#`
2-grams of `cart`: `#c`, `ca`, `ar`, `rt`, `t#`
2-grams of `arts`: `#a`, `ar`, `rt`, `ts`, `s#`

2-Gram Distance between `crat` and `cart`:
$|G_2(\texttt{crat})| + |G_2(\texttt{cart})| - 2 \times |G_2(\texttt{crat}) \cap G_2(\texttt{cart})|$
$= 5 + 5 - 2 \times 2 = 6$ (better)
2-Gram Distance between `crat` and `arts`:
$|G_2(\texttt{crat})| + |G_2(\texttt{arts})| - 2 \times |G_2(\texttt{crat}) \cap G_2(\texttt{arts})|$
$= 5 + 5 - 2 \times 0 = 10$

N-Gram Distance Efficiency

Occasionally useful as a simpler variant of Edit Distance

More sensitive to long substring matches, less sensitive to relative ordering of strings (matches can be anywhere!)

Despite its simplicity, takes roughly the same time to compare entire dictionary

Quite useless for very long strings and/or very small alphabets (Why?)

Orthography

In English (and some other languages), **orthography** (spelling) isn't a good predictor of **phonetics** (sounds)

Salient concern in speech–to–text systems, e.g.:

```
Georgia Conal
George O'Connell
```

Also relevant in spelling correction (English can be very difficult to spell correctly!)

Soundex

One mechanism: Soundex

Translation table:

aehiouwy	$\rightarrow$	0 (vowels)
bpfv	$\rightarrow$	1 (labials)
cgjkqsxz	$\rightarrow$	2 (misc: fricatives, velars, etc.)
dt	$\rightarrow$	3 (dentals)
l	$\rightarrow$	4 (lateral)
mn	$\rightarrow$	5 (nasals)
r	$\rightarrow$	6 (rhotic)

Four step process:

1. Except for initial character, translate string characters according to table
2. Remove duplicates (e.g. 4444 $\rightarrow$ 4)
3. Remove 0s
4. Truncate to four symbols

Soundex

One mechanism: Soundex

Translation table:

`aehiouwy`	$\rightarrow$	0 (vowels)
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`dt`	$\rightarrow$	3 (dentals)
`l`	$\rightarrow$	4 (lateral)
`mn`	$\rightarrow$	5 (nasals)
`r`	$\rightarrow$	6 (rhotic)

Four step process:

`king`	`kyngge`
`k052`	`k05220`
`k052`	`k0520`
`k52`	`k52`
`k52`	`k52`

Other Phonetic Methods

Better phonetic methods make use of the fact that some letters sounds alike in certain contexts, and different in other contexts

Editex uses the Edit Distance to compare strings based on a similar translation table to Soundex

Ipadist uses a text–to–sound algorithm to represent tokens according to the International Phonetic Alphabet (but context matters a lot)

There are also worse variants, like Phonix.

Evaluating an Approximate Matching System

Evaluation: consider whether the system is effective at solving the user's problem

In this case: for a misspelled word, does the system identify the correct word?

To evaluate, we need:

- A number of cases of misspelled words
- The intended (correct) word for each case
- An **evaluation metric**

Evaluation Metrics for Spelling Correction

We have some cases:

Misspelled Word	Correct Word	Predicted Word	Right/Wrong?
`ther`	`other`	`there`	×
`corridr`	`corridor`	`corridor`	✓
`cracheyt`	`crotchety`	`cachet`	×
...	...	...	...

Accuracy: fraction of correct responses ($\frac{1}{3}$)

Evaluation Metrics for Spelling Correction

More realistic situation:

Misspelled Word	Correct Word	Predicted Word	Right/Wrong?
ther	other	there	$\times$
		other	$\checkmark$
		their	$\times$
corridr	corridor	corridor	$\checkmark$
		carrier	$\times$
cracheyt	crotchety	???	—
...	...	...	

Precision: fraction of correct responses among attempted responses ($\frac{2}{5}$)
Recall: proportion of words with a correct response (somewhere) ($\frac{2}{3}$)

Comparing Systems

Typically, the value of the evaluation metric has little intrinsic meaning

“This system gets 81% accuracy” — useful for users, or not?

“The system based on the Global Edit Distance gets 81% accuracy, whereas the system based on the N-Gram Distance gets 84% accuracy”

“The basic system gets 81% accuracy, but after making some changes, the accuracy becomes 74%”

“System A gets 45% precision and 80% recall;
System B gets 95% precision and 10% recall”
— Which one should we use? (Also: why?)

The answer depends on the problem (and the user)!

Summary

- What is approximate string search?
- What are some common applications of approximate string search; why are they hard?
- What are some methods for finding an approximate match to a string? What do we need to generate them?
- How can we evaluate a typical approximate matching system?

Background Readings

Needleman, Saul B. and Wunsch, Christian D. (1970). “A general method applicable to the search for similarities in the amino acid sequence of two proteins”. Journal of Molecular Biology 48 (3): 44353. doi:10.1016/0022-2836(70)90057-4

(Originally in Russian, published in English as:) Levenshtein, Vladimir I. (1966). “Binary codes capable of correcting deletions, insertions, and reversals”. Soviet Physics Doklady 10 (8): 707710.

Smith, Temple F. and Waterman, Michael S. (1981). “Identification of Common Molecular Subsequences”. Journal of Molecular Biology 147: 195197. doi:10.1016/0022-2836(81)90087-5

Kondrak, Grzegorz (2005). “N-Gram Similarity and Distance”. In Proceedings of the 12th international conference on String Processing and Information Retrieval (SPIRE’05), pp. 115-126, Buenos Aires, Argentina.

Zobel, Justin and Dart, Philip (1996). “Phonetic String Matching: Lessons from Information Retrieval”. In Proceedings of the 19th annual international ACM SIGIR conference on Research and development in information retrieval (SIGIR’96), pp. 166-172, New York, USA.

Extension Readings

Whitelaw, Casey and Hutchison, Ben and Chung, Grace Y and Ellis, Gerard (2009). “Using the Web for Language Independent Spellchecking and Autocorrection”. In Proceedings of the 2009 Conference on Empirical Methods in Natural Language Processing (EMNLP 2009), pp. 890-899, Singapore, Singapore.

Ahmad, Farooq and Kondrak, Grzegorz (2005). “Learning a Spelling Error Model from Search Query Logs”. In Proceedings of the Human Technology Conference and Conference on Empirical Methods in Natural Language Processing (HLT/EMNLP 2005), pp. 955-962, Vancouver, Canada.

Computational Genomics

Typical Genomics problem:

- Given a nucleotide/amino acid sequence (substring)
- Find whether the sequence occurs within a larger sequence (string)
- Possibly with “errors” (nucleotide/amino acid changes)

Computational Genomics

Typical Genomics problem:

- Given a substring, find whether the sequence occurs within a larger string, possibly with "errors"
- Almost the same as spelling correction
- But **much** larger strings: a small genomics problem might involve comparing perhaps 1K character sequence against several 100K character sequences; alphabet is smaller

Suitability for Computational Genomics

Recall: we have a “short” ($\sim$1K character) nucleotide/amino acid sequence to compare against many long ($\sim$100K character) chromosomes/genes/proteins/etc.

For example, if some member of the population has 99% of the sequence of interest, they might be susceptible to some medical condition

We're allowed $\sim$10 errors; alphabet is $\sim$4 or $\sim$20 characters

Suitability for Computational Genomics

Neighbourhood search:

Roughly $4^{10} \times 1000^{10}$ possible neighbours.

... Forget it.

Suitability for Computational Genomics

Global Edit Distance:

One string is $\sim$1K characters, other is $\sim$100K characters.

... Every string comparison involves $\sim$99K insertions.

$\rightarrow$ Prefers shorter chromosomes (not intended behaviour)

Suitability for Computational Genomics

Local Edit Distance:

One string is $\sim$1K characters, other is $\sim$100K characters.

... Seems like the right idea.

Suitability for Computational Genomics

Local Edit Distance:

One string is ~10K characters, other is ~1G characters.

... Can't fit table into memory.
... Requires approximate solutions with heuristics, e.g. BLAST, FASTA

Suitability for Computational Genomics

N-Gram Distance:

With huge *n* (e.g. 80% of length of shorter string) can (almost) work!

Tends to prefer shorter chromosomes like Global Edit Distance

But better methods for using *n*-gram information, e.g. de Bruijn graphs