

All for exact matching

Read ctcaaactcctgacctttggtgatccacccgcctaggccttc

Reference

GATCACAGGTCTATCACCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTT CGTCTGGGGGGTATGCACGCGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTC **ACAATTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCA** AACCCCCCCCCCCCCCCCTTCTGGCCACAGC AAAAC **CTCTGCCAAACCCCAAAA** ACAAAGAACCCTAACACCAGCCTAACC/ TTGGCGGTATGCAC TTTTAACAGTCACCCCCAACTAACA ATTATT CATACTACTAAT CTCATCAATACAACCCCCGCCCATCATACCCAGCAC CTAACCCCATA CCCCGAACCAACCAAACCCCAAAC CCTCCTCAAA GCAATACACTGACCCGCTCAAAC CCTGGATTTTGGATC TTGGCCTAAA CTAGCCTTTCTATTAGCTCTTAG AAGATTACACATGCAAGCA **CCAGTGAGT** TCACCCTCTAAATCACCACGATC AAAGGAACAAGCATCAAGCACG **AATGCAGCTC** AAAACGCTTAGCCTAGCCACACC TCACGGGAAACAGCAGTGATTAA TTAGCAATAA ACGAAAGTTTAACTAAGCTATACT ACCCCAGGGTTGGTCAATTTCG1 CCAGCCACCGC **AGATCACCCC** GGTCACACGATTAACCCAAGTCAAT, GAAGCCGGCGTAAAGAGTGT **FACAAAATAGAC** TCCCCAATAAAGCTAAAACTCACCTGA TTGTAAAAAACTCCAG TACGAAAGTGGCTTTAACATATCTGAACA **GGGATTAGA** TACCCCACTATGCTTAGCCCTAAACCTCAACAC CACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTCA AGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCTT CCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTAC ACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTACATT **AAAACTACGATAGCCCTTATGAAACTTAAGGGTCGAAGGTGGATTTAGCAGTAA** AGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGCGTACACACCGCCCGTCAC AAGTATACTTCAAAGGACATTTAACTAAAACCCCTACGCATTTATATAGAGGAGACA CGTAACCTCAAACTCCTGCCTTTGGTGATCCACCCGCCTTGGCCTACCTGCATAATGAAG GCCCCAAACCCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAA AGTATAGGCGATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATG **AAAAATTATAACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAA** TTAACTAGAAATAACTTTGCAAGGAGAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCT ACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATA GGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAG TTCAACTTTAAATTTGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTC

Differences between read and reference occur because of...

- 1. Sequencing error
- 2. Natural variation

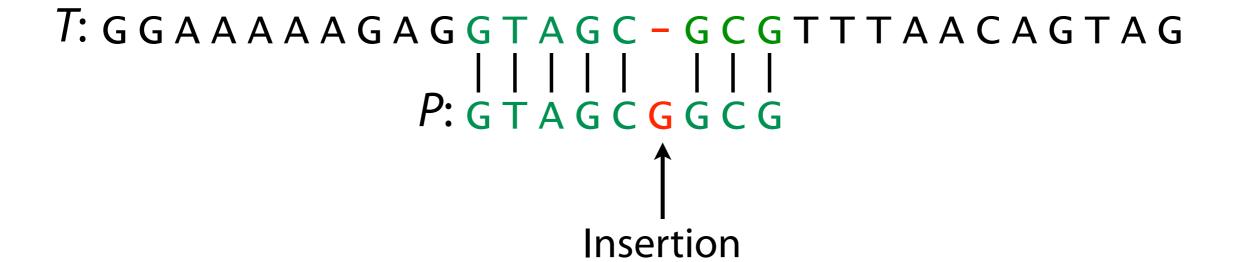
```
T: G G A A A A A G A G G T A G C G G C G T T T A A C A G T A G

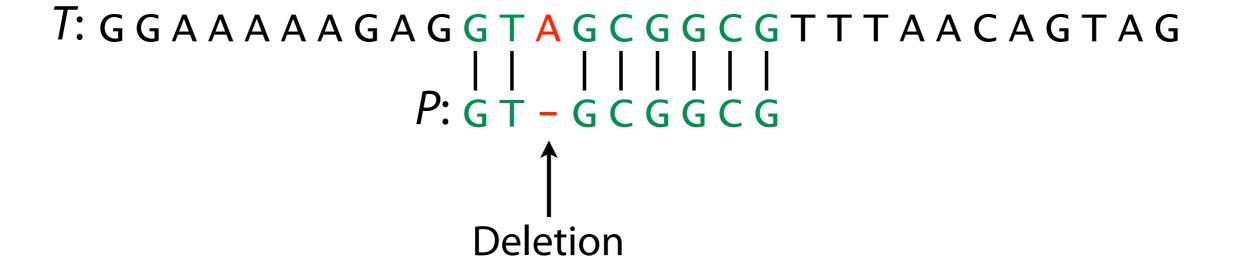
| | | | | | | | |

P: G T A A C G G C G

Mismatch

(Substitution)
```





Hamming distance

For X & Y where |X| = |Y|, hamming distance = minimum # substitutions needed to turn one into the other

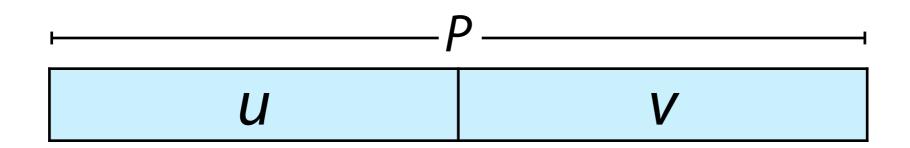
Edit distance

(AKA Levenshtein distance)

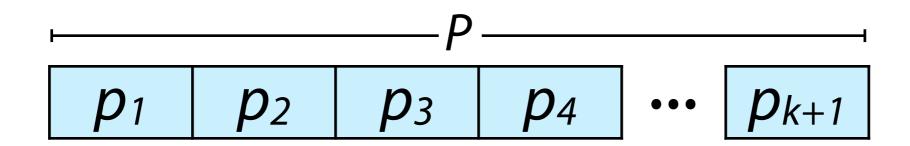
For X & Y, edit distance = minimum # edits (substitutions, insertions, deletions) needed to turn one into the other

```
def naiveHamming(p, t, maxDistance):
    occurrences = []
    for i in xrange(len(t) - len(p) + 1): # loop over alignments
        nmm = 0
        match = True
        for j in xrange(len(p)):
                                  # loop over characters
                                          # compare characters
            if t[i+j] != p[j]:
                nmm += 1
                                          # mismatch
                if nmm > maxDistance:
                    break
                                           # exceeded max hamming dist
        if nmm <= maxDistance:</pre>
          occurrences.append(i)
                                          # approximate match
    return occurrences
```

Wanted: way to apply exact matching algorithms to approximate matching problems



If P occurs in T with 1 edit, then u or v appears with no edits



If *P* occurs in *T* with up to *k* edits, then at least one of $p_1, p_2, ..., p_{k+1}$ must appear with 0 edits



Approximate Boyer-Moore performance

	Boyer-Moore, exact			Boyer-Moore, ≤1 mismatch with pigeonhole			Boyer-Moore, ≤2 mismatches with pigeonhole		
	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches
P: "tomorrow" T: Shakespeare's complete works	786 K	1.91s	17	3.05 M	7.73 s	24	6.98 M	16.83 s	382
P: 50 nt string from Alu repeat* T: Human reference (hg19) chromosome 1	32.5 M	67.21 s	336	107 M	209 s	1,045	171 M	328 s	2,798

^{*} GCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG