Programming Homework 2
Graded Quiz • 30 min

Due Jun 28, 1:59 AM CDT

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TOTAL POINTS 6

1. How many alignments does the naive exact matching algorithm try when matching the string GGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG (derived from human Alu sequences) to the excerpt of human chromosome 1? (Don't consider reverse complements.)

1 point

799954

2. How many character comparisons does the naive exact matching algorithm try when matching the string GGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG (derived from human Alu sequences) to the excerpt of human chromosome 1? (Don't consider reverse complements.)

1 point

984143

3. How many alignments does Boyer-Moore try when matching the string GGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG (derived from human Alu sequences) to the excerpt of human chromosome 1? (Don't consider reverse complements.)

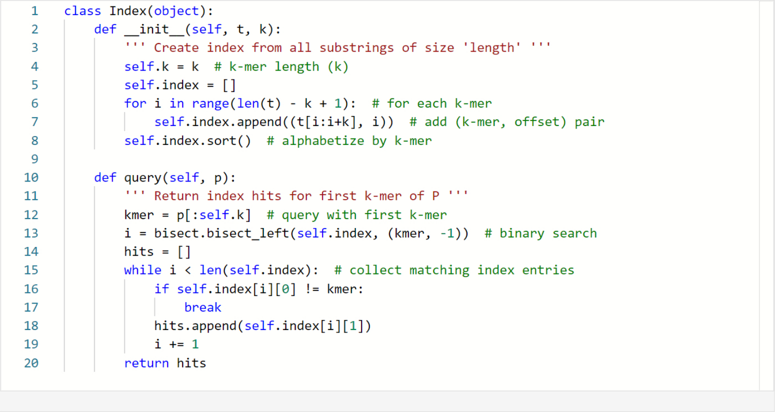
1 point

127974

4. **Index-assisted approximate matching.** In practicals, we built a Python class called Index

1 point

implementing an ordered-list version of the k-mer index. The Index class is copied below.



```python
class Index(object):
    def __init__(self, t, k):
        ''' Create index from all substrings of size 'length' '''
        self.k = k  # k-mer length (k)
        self.index = []
        for i in range(len(t) - k + 1):  # for each k-mer
            self.index.append((t[i:i+k], i))  # add (k-mer, offset) pair
        self.index.sort()  # alphabetize by k-mer

    def query(self, p):
        ''' Return index hits for first k-mer of P '''
        kmer = p[:self.k]  # query with first k-mer
        i = bisect.bisect_left(self.index, (kmer, -1))  # binary search
        hits = []
        while i < len(self.index):  # collect matching index entries
            if self.index[i][0] != kmer:
                break
            hits.append(self.index[i][1])
            i += 1
        return hits
```

We also implemented the pigeonhole principle using Boyer-Moore as our exact matching algorithm.

Implement the pigeonhole principle using Index to find exact matches for the partitions. Assume P always has length 24, and that we are looking for approximate matches with up to 2 mismatches (substitutions). We will use an 8-mer index.

Download the Python module for building a k-mer index.

https://d28rh4a8wq0iu5.cloudfront.net/ads1/code/kmer_index.py

Write a function that, given a length-24 pattern P and given an Index object built on 8-mers, finds all approximate occurrences of P within T with up to 2 mismatches. Insertions and deletions are not allowed. Don't consider any reverse complements.

How many times does the string GGCGCGGTGGCTCACGCCTGTAAT, which is derived from a human Alu sequence, occur with up to 2 substitutions in the excerpt of human chromosome 1? (Don't consider reverse complements here.)

Hint 1: Multiple index hits might direct you to the same match multiple times, but be careful not to count a match more than once.

Hint 2: You can check your work by comparing the output of your new function to that of the naive_2mm function implemented in the previous module.

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5. Using the instructions given in Question 4, how many total index hits are there when searching for occurrences of GGCGCGGTGGCTCACGCCTGTAAT with up to 2 substitutions in the excerpt of human chromosome 1?

1 point

(Don't consider reverse complements.)

Hint: You should be able to use the boyer_moore function (or the slower naive function) to double-check your answer.

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6. Let's examine whether there is a benefit to using an index built using *subsequences* of T rather than substrings, as we discussed in the "Variations on k-mer indexes" video. We'll consider subsequences involving every N characters. For example, if we split `ATATAT` into two *substring* partitions, we would get partitions `ATA` (the first half) and `TAT` (second half). But if we split `ATATAT` into two *subsequences* by taking every other character, we would get `AAA` (first, third and fifth characters) and `TTT` (second, fourth and sixth).

1 point

Another way to visualize this is using numbers to show how each character of P is allocated to a partition. Splitting a length-6 pattern into two substrings could be represented as `111222`, and splitting into two subsequences of every other character could be represented as `121212`

The following class `SubseqIndex` is a more general implementation of `Index` that additionally handles subsequences. It only considers subsequences that take every Nth character:

```python
import bisect

class SubseqIndex(object):
    """ Holds a subsequence index for a text T """

    def __init__(self, t, k, ival):
        """ Create index from all subsequences consisting of k characters
            spaced ival positions apart.  E.g., SubseqIndex("ATAT", 2, 2)
            extracts ("AA", 0) and ("TT", 1). """
        self.k = k  # num characters per subsequence extracted
        self.ival = ival  # space between them; 1=adjacent, 2=every other, etc
        self.index = []
        self.span = 1 + ival * (k - 1)
        for i in range(len(t) - self.span + 1):  # for each subseq
            self.index.append((t[i:i+self.span:ival], i))  # add (subseq, offset)
        self.index.sort()  # alphabetize by subseq

    def query(self, p):
        """ Return index hits for first subseq of p """
        subseq = p[:self.span:self.ival]  # query with first subseq
        i = bisect.bisect_left(self.index, (subseq, -1))  # binary search
        hits = []
        while i < len(self.index):  # collect matching index entries
            if self.index[i][0] != subseq:
                break
            hits.append(self.index[i][1])
            i += 1
        return hits

```

For example, if we do:

```python
ind = SubseqIndex('ATATAT', 3, 2)
print(ind.index)

```

we see:

```
[('AAA', 0), ('TTT', 1)]

```

And if we query this index:

```python
p = 'TTATAT'
print(ind.query(p[0:]))

```

we see:

```
[]

```

because the subsequence `TAA` is not in the index. But if we query with the second subsequence:

```python
print(ind.query(p[1:]))

```

we see:

```
[1]
```

because the second subsequence `TTT` is in the index.

Write a function that, given a length-24 pattern P and given a `SubseqIndex` object built with k = 8 and ival = 3, finds all approximate occurrences of P within T with up to 2 mismatches.

When using this function, how many total index hits are there when searching for `GGCGCGGTGGCTCACGCCTGTAAT` with up to 2 substitutions in the excerpt of human chromosome 1? (Again, don't consider reverse complements.)

Hint: See this notebook for a few examples you can use to test your function.

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