COMP 204: Sequence alignment examples, more dictionaries

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Midterm materials coverage and practice midterms

- ▶ Midterm is held on February 22 at 6:30-8:00 pm in LEA 219.
- Our midterm will cover up to Lecture 17 (Feb 13)
- ▶ Past midterms in COMP 204 Fall 2018 and COMP 364 Fall 2017 are posted on myCourses for practice

A couple more Needleman-Wunsch examples on blackboard

The most important of Assignment 2 is to understand Needleman-Wunsch global sequence alignment algorithm. Let's do a couple of examples together:

Example 1

Sequence 1: G

Sequnece 2: GCG

Example 2

Sequence 1: TCGA

Sequnece 2: TTCG

A matrix in Python is just a list of lists of the same length

In Assignment #2, we will need to represent two-dimensional tables or matrices, with a fixed number of rows and columns.

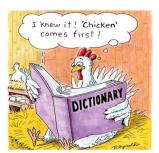
Two-dimensional lists can be used to do this in Python.

A 2D list is a list of lists, where each of the lists is of the same length. Example: A tic-tac-toe grid:

To create a new matrix with zeros we can use list comprehension:

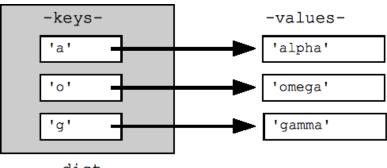
Dictionaries Recap

- A dictionary is said to be a mapping type because it maps key objects to value objects.
- ▶ Dictionaries are immensely useful and are the magic behind a lot of Python functionality
- Syntax: my_dict = {[key]: [value], ...,}
- ► The analogy to a real dictionary works. The word you look up is the **key** and the definition is the **value**



Dictionaries: picture

- Keys map to values.
- ▶ We use dictionaries when we want to access data using something other than an index (i.e. lists).



dict

Dictionaries: keys and values

- ► A dictionary's keys can be many different types of **immutable** objects (i.e. int, str, tuple)
- You can access a key's value like a list. Syntax: my_dict[key]
- ► You can mix and match key types
- ▶ Values can be any object type. You can also mix and match.

```
record_sales = {
    "Kanye": 2.4,
    "Beyonce": 1.5,
    "Chance": 1.2,
    ("a", 12): "bob"
    }

print(record_sales["Beyonce"]) # 1.5

print(record_sales[("a", 12)]) # "bob"
```

Adding keys to a dictionary

- Syntax: my_dict["key"] = value
- ► If the key does not yet exist, a new key/value pair is created.
- ▶ If the key already exists, its previous value is overwritten

```
>>> d = {"bob": 28}
2 >>> print(d)
3 {"bob": 1.2}
4 >>> d["charlie"] = 33
5 >>> print(d)
6 {"bob": 1.2, "charlie": 2.5}
7 >>> d["bob"] = "woooo"
8 {"bob": "woooo", "charlie": 33}
   >>> del d["bob"] # we can delete keys with the del
   → operator
10 {"charlie": 33}
```

Important properties of dictionaries

Dictionaries are mutable We can modify the contents of the dictionary as much as we want.

```
>>> d = {"bob": 24, "tina": 11}

>>> d["tameeka"] = 42

>>> d['bob'] = [1, 2, 3, 4]

>>> del d["bob"]

>>> mystring = 'AAAGGG'

>>> mystring[2] = 'T' # this is an error. strings

are immutable
```

Important properties of dictionaries

- ► Key-value pairs are **NOT** always stored in order. (for the current Python 3.7 they are, but assume it won't be like this forever)
- ▶ If you want to iterate over the keys in a dictionary use the dict.keys() function.

Useful dictionary methods and operators

d.items() produces an iterator which yields tuples of the form (key, value)

- k in d evaluates to True if the key exists in the dictionary and False otherwise.
- ▶ d.update(d2) "merges" two dictionaries into one.

```
1 >>> d = {"a": 3, "b": 4}
2 >>> d.update({"c": 5})
3 {"a": 3, "c": 5, "b": 4}
```

Quick dictionary example: mini BLAST

- BLAST is a very popular bioinformatics tool used to compare DNA sequences. One of the main innovations is to index a genome by 'words'.
- words are short sequences. AT, CG, CC, GG, AA
- ► Goal: Given a genome and a list of words return a dictionary with a list of positions where each given word occurs.
- ► Example: for words AAG, AAT in genome GAAGAAGGGAATGGAAGAAT we should return 'AAG': [1,4,14], 'AAT': [9,17].

Note BLAST is a *heuristic approach* to do fast sequence search but Needleman-Wunsch global alignment algorithm (or Smith-Waterman local alignment) is a more principled way to find optimal match(es) at the cost of speed.

Building genomic dictionary

```
1 #Args: genome_seq: a DNA sequence as a string
2 # words: an iterable of sequences
3 #Returns:
4 # genomeDict: a dict with a key for each word mapping to
      list of indices.
5 def buildGenomeDict(genome_seq, words):
      genomeDict = \{\}
6
      for w in words:
7
          for i in range (len (genome_seq)-len (w)+1):
8
               if genome_seq[i:i+len(w)] == w:
9
                   if w not in genomeDict:
10
                       genomeDict[w] = []
11
                   genomeDict[w].append(i)
12
      return genomeDict
13
14
15 genome_seq = "AGCGACGTATAATCGACTA"
16 words=["CG", "TATA"]
  genomeDict = buildGenomeDict(genome_seq, words)
18 print (genomeDict)
19 # { 'CG': [2, 13], 'TATA': [7]}
```

Searching genomic dictionary

```
1 #Args: genomeDict: build from genome_index
         genome_seq: DNA sequence corresponding to genomeDict
         queries: a list of query sequences
4 #Returns: blasthits: a dict with a key for each query and
      their genomic location(s)
5 def searchGenomeDict(genomeDict, genome_seq, queries):
      blasthits={}
6
      for q in queries:
           blasthits[q]=[] # initialize query hit list
8
           for genomeDictKey in genomeDict.keys():
9
               for i in range(len(q)-len(genomeDictKey)+1):
10
                   wordlen = len(genomeDictKey)
11
                   querySubstr = q[i:i+wordlen]
12
                   if querySubstr == genomeDictKey:
13
                       genomePosList = genomeDict[querySubstr]
14
                       for pos in genomePosList:
15
                            if genome_seq[pos-i:pos+len(q)-i] =
16
       q: # mistake: genome_seq[pos:pos+len(q)] == q:
                                blasthits [q]. append (pos-i)
           if len(blasthits[q]) > 0:
18
               blasthits[q] = set(blasthits[q]) # set returns
19
      unique values (more info on set in the next lecture)
      return blasthits
20
  queries = ["ACGT", "CGACGT", "TATAAT", "CGACT", "XYZ"]
  myhits = searchGenomeDict(genomeDict, genome_seq, queries)
print (myhits) # \{ \Delta CGT : \{A\} \} \{ CGACGT : \{2\} \} \{ TATAAT : \{7\} \}
```

A convenient method: setdefault

Let's look at line 15 in the previous example:

- You will find yourself writing this statement many times.
- mydict.setdefault(key, [default]) If key is in the dictionary, return its value. If not, insert key with a value of default and return default.
- ► We can replace it with one line using setdeafult

```
word_index.setdefault(w, []).append(i)
```

Dictionaries Pop Quiz

- ► True or False: dictionaries are immutable.
- ► Error? myd = {[1,2]: "hello"}
- True or False: dictionary keys must be unique.
- ► Error? d2 = {'bob': 2, 'susan': 3, 'bob':4}
- Error? d = {}; d['bob'].append(3)
- ► True/False: once a key-value is stored we can't update it.

Dictionaries Pop Quiz Answers

- ► True or False: dictionaries are immutable.
- ► Error? myd = {[1,2]}: "hello" Yes. Keys must be immutable.
- ► True or False: dictionary keys must be unique.
- Error? d2 = {'bob': 2, 'susan': 3, 'bob':4} No.
 Duplicate keys are overwritten
- ► Error? d = {}; d['bob'].append(3) Yes. Key 'bob'
 has not been created.
- ► True/False: once a key-value is stored we can't update it. d['bob'] = 3; d['bob']='hi' is valid.