BINF2111 – Introduction to Bioinformatics Computing

Dictionaries: The Merriam-Webster of python



Richard Allen White III, PhD RAW Lab Lecture 22 - Thursday Nov 18th, 2021

Learning Objectives

- Dictionaries
- Dictionaries vs. lists vs. tuples
- Uses
- Translation
- Coding a translator
- Quiz 22

Python Dictionary

In Python, a dictionary is mapping between a set of indices (keys) and a set of values.

The items in a dictionary are key-value pairs

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Some Examples of Dictionaries:

Key Value

trinucleotide count

Name protein sequence

name restriction enzyme motif

codon amino acid residue

name email address

sample coordinates

word definition

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Python Dictionary vs. others

Data Structure	Ordered	Mutable	Constructor	Example
List	Yes	Yes	[] or list()	[5.7, 4, 'yes', 5.7]
Tuple	Yes	No	() or tuple()	(5.7, 4, 'yes', 5.7)
Set	No	Yes	{}* or set()	{5.7, 4, 'yes'}
Dictionary	No	Yes**	{ } or dict()	{'Jun': 75, 'Jul': 89}

Python Dictionary vs. others detailed

Lists	Sets	Dictionaries	Tuples
List = [10, 12, 15]	Set = {1, 23, 34} Print(set) -> {1, 23,24} Set = {1, 1} print(set) -> {1}	Dict = {"Ram": 26, "mary": 24}	Words = ("spam", "egss") Or Words = "spam", "eggs"
Access: print(list(0))	Print(set). Set elements can't be indexed.	print(dict["ram"])	Print(words[0])
Can contains duplicate	Can't contain duplicate	Can't contain duplicate keys,	Can contains duplicate
elements	elements. Faster compared to Lists	but can contain duplicate values	elements. Faster compared to Lists
List[0] = 100	set.add(7)	Dict["Ram"] = 27	Words[0] = "care" ->TypeError
Mutable	Mutable	Mutable	Immutable - Values can't be changed once assigned
List = []	Set = set()	Dict = {}	Words = ()
Slicing can be done print(list[1:2]) -> [12]	Slicing: Not done.	Slicing: Not done	Slicing can also be done on tuples
Usage: Use lists if you have a collection of data that doesn't need random access. Use lists when you need a simple, iterable collection that is modified frequently.	Usage: - Membership testing and the elimination of duplicate entries when you need uniqueness for the elements.	Usage: - When you need a logical association b/w key:value pair when you need fast lookup for your data, based on a custom key.	Usage: Use tuples when your data cannot change. A tuple is used in comibnation with a dictionary, for example, a tuple might represent a key,

The syntax for creating a dictionary is similar to that for creating a list, but we use curly brackets rather than square ones.

- Each pair of data, consisting of a key and a value, is called an item.
- When storing items in a dictionary, we separate them with commas.
- Within an individual item, we separate the key and the value with a colon.

eng2sp = {'one': 'uno', 'two': 'dos', 'three': 'tres'}

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```
eng2sp = {'one': 'uno', 'two': 'dos', 'three': 'tres'}
```

The dictionary is called eng2sp (English to Spanish)
The keys are one, two, and three.
The values are uno, dos, and tres.

To lookup the values for a particular key in a dictionary, we use the following syntax.

```
eng2sp = {'one': 'uno', 'two': 'dos', 'three': 'tres'}
```

Print(eng2sp['one'])

This looks very similar to a list, but instead of giving the index of the element that we want, we're using the key for the value that we want to retrieve.

Note that the dictionary is created using {}, but [] is used to lookup the value.

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Restrictions on Python Dictionary

Restrictions on dictionaries:

The only types of data we are allowed to use as keys are strings and numbers. These must be **unique**!

Values can be whatever type of data we like.

Most commonly, we create a dictionary, then add keys and values to it.

```
eng2sp = {}
eng2sp['one'] = 'uno'
eng2sp['two'] = 'dos'
eng2sp['three'] = 'tres'
```

Making Python Dictionary from a list

You can zip two lists together using a zip (think of a zipper)

```
1 #!/usr/bin/python3
3 import re
 5 english = ["one","two","three","four","five"]
 6 spanish = ["uno","dos","tres","cuatro","cinco"]
7 zippedList = {}
 8 for i in range(0,len(english)):
      zippedList[english[i]] = spanish[i];
10 print(zippedList)
```

Python Dictionary Methods

dict.get(key) – get a value dict.clear() - removes everything in a dictionary dict.items() - returns the key-value pairs from a dictionary dict.keys() - returns a list of keys dict.values()

Find Trinucleotides

```
1 #!/usr/bin/python3
 3 dna = 'AATTGGCC'
4 counts = {} # was a list, not dictionary
5 # For loops did not end in colon:
 6 for base1 in ['A', 'T', 'G', 'C']:
      for base2 in ['A', 'T', 'G', 'C']:
          for base3 in ['A', 'T', 'G', 'C']:
               trin = base1 + base2 + base3
               count = dna.count(trin)
10
               counts[trin] = count
12 print(counts)
```

Find Trinucleotides (Loops)

```
1 #!/usr/bin/python3
 3 dna = 'AATTGGCC'
 4 bases = ['A', 'T', 'G', 'C']
 5 counts = {} # variable name was different in the loops, changing this one fixed it
6 for base1 in bases:
      for base2 in bases:
          dinucleotide = base1 + base2
          count = dna.count(dinucleotide)
          counts[dinucleotide] = count
10
11
12 for dinucleotide in counts.keys():
      if counts.get(dinucleotide) == 2:
13
          print(dinucleotide)
14
```

Find Trinucleotides - single

```
1 #!/usr/bin/python3
 3 dna = 'AATTGGCC'
4 counts = {}
5 # For loops did not end in colon :
6 for base1 in ['A', 'T', 'G', 'C']:
      for base2 in ['A', 'T', 'G', 'C']:
          for base3 in ['A', 'T', 'G', 'C']:
               trin = base1 + base2 + base3
               count = dna.count(trin)
               counts[trin] = count
12 print(counts['TGG'])
```

10

Find dinucleotides

Why Use a Dict over a List?

A list keeps order, dict doesn't. When you care about order, you must use list.

List contains just values
Dict associates with each key a value

AAAAAACCCCACAGATACAT >seq2 ACATTAGATATATTACATAT

>seq1

When we parsed this using a list, we had to create a sequence list and a header list. With a dictionary, we can assign the sequence to the header.

Dictionary

In Python, a dictionary is mapping between a set of indices (keys) and a set of values.

```
>>> dict([(1,'a'), (2,'e'), (3,'i'), (4,'o'), (5,'u')]) {1: 'a', 2: 'e', 3: 'i', 4: 'o', 5: 'u'}
```

Remember, the great thing about dictionaries is we can find a value instantly, without needing to search through the whole dictionary manually.

```
You can use the form

value = my_dict['key']

value = my_dict.get('key').
```

Translation

GTC V Val

GTA V Val

GCC A Ala

GCA A Ala

Write a program that will translate a DNA sequence into protein.

Your program should use the standard genetic code (64 types):

GAC D Asp

GAA E Glu

TTT F Phe	TCT S Ser	TAT Y Tyr	TGT C Cys
TTC F Phe	TCC S Ser	TAC Y Tyr	TGC C Cys
TTA L Leu	TCA S Ser	TAA * Ter	TGA * Ter
TTG L Leu	TCG S Ser	TAG * Ter	TGG W Trp
CTT L Leu	CCT P Pro	CAT H His	CGT R Arg
CTC L Leu	CCC P Pro	CAC H His	CGC R Arg
CTA L Leu	CCA P Pro	CAA Q GIn	CGA R Arg
CTG L Leu	CCG P Pro	CAG Q GIn	CGG R Arg
ATT I lle	ACT T Thr	AAT N Asn	AGT S Ser
ATC I Ile	ACC T Thr	AAC N Asn	AGC S Ser
ATA I Ile	ACA T Thr	AAA K Lys	AGA R Arg
ATG M Met	ACG T Thr	AAG K Lys	AGG R Arg
GTT V Val	GCT A Ala	GAT D Asp	GGT G GIV

GGC G Gly

GGA G Gly

Here is an example gene: starts with the amino acid M and ends in *

ATGTCGAGATTACCATGGGACAATATACAGTGA

Each triplet in the DNA when translated becomes one of these amino acids

ATGTCGAGATTACCATGGGACAATATACAGTGA

MSRLPWDNIQ*

IIIFPne	ici S Ser	IAI Y IYr	IGI C Cys
TTC F Phe	TCC S Ser	TAC Y Tyr	TGC C Cys
TTA L Leu	TCA S Ser	TAA * Ter	TGA * Ter
TTG L Leu	TCG S Ser	TAG * Ter	TGG W Trp
			_

CTT L Leu	CCT P Pro	CAT H His	CGT R Arg
CTC L Leu	CCC P Pro	CAC H His	CGC R Arg
CTA L Leu	CCA P Pro	CAA Q GIn	CGA R Arg
CTG L Leu	CCG P Pro	CAG Q GIn	CGG R Arg

ATT I IIe	ACT T Thr	AAT N Asn	AGT S Ser
ATC I Ile	ACC T Thr	AAC N Asn	AGC S Ser
ATA I IIe	ACA T Thr	AAA K Lys	AGA R Arg
ATG M Met	ACG T Thr	AAG K Lys	AGG R Arg

GTT V Val	GCT A Ala	GAT D Asp	GGT G Gly
GTC V Val	GCC A Ala	GAC D Asp	GGC G Gly
GTA V Val	GCA A Ala	GAA E Glu	GGA G Gly
GIA V Vai	GCA A Ala	GAA E GIU	GGA G GIY

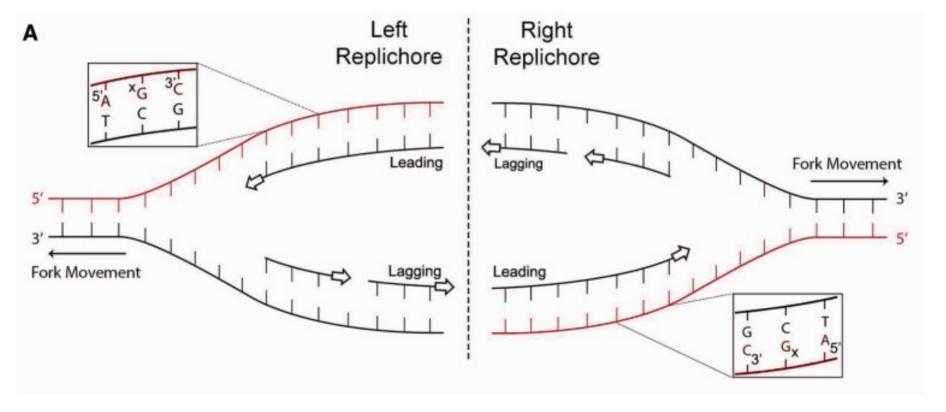
Most DNA is double stranded, so for every strand of DNA there is a **reverse complement**.

The reverse complement is a reverse string with complementary DNA G>C, A>T, T>A, C>G.

5' ATGTCGAGATTACCATGGG 3'

3' TACAGCTCAAATGGTACCC 5'

Most DNA is double stranded, so for every strand of DNA there is a **reverse complement.** During DNA replication the leading and lagging strand are synthesized using leading and lagging strand synthesis from 5'>3'.



Asymmetric Context-Dependent Mutation Patterns Revealed through Mutation-Accumulation Experiments. Sung et al., 2015. MBE

In a single piece of double stranded DNA, there are six frames, forward and reverse. On each strand, there are three frames.

5' ATCGAACAA 3' #Frame 1, starts at index position 0 = encodes

IEQ

3' TAGCTTGTT 5'

#Frame 2, starts at index position 1 = encodes5' ATCGAACAA 3'

SN

5' ATCGAACAA 3'

3' TAGCTTGTT 5'

RT

3' TAGCTTGTT 5'

#Frame 3, starts at index position 2 = encodes

In a single piece of double stranded DNA, there are six frames, forward and reverse. On each strand, there are three frames. Forward strand frames:

```
5' ATCGAACAA 3'
                       #Frame 1, starts at index position 0
3' TAGCTTGTT 5'
                       #Frame 1 is ATC (I), GAA (E), CAA (Q)
5' ATCGAACAA 3'
                       #Frame 2, starts at index position 1 = \text{encodes SN}
3' TAGCTTGTT 5'
                       #Frame 2 is TCG (S), AAC (N)
5' ATCGAACAA 3'
                       #Frame 3, starts at index position 2 = \text{encodes RT}
3' TAGCTTGTT 5'
                       #Frame 3 is CGA (R), ACA (T)
5' ATCGAACAA 3'
                       #The fourth index is in the same frame as frame one
```

3' TAGCTTGTT 5'

In a single piece of double stranded DNA, there are six frames, forward and reverse. On each strand, there are three frames. Reverse strand frames.

Note these frames are reverse complement of the string. (reverse order, and A>T, T>A, G>C, C>G)

5' ATCGAACAA 3' #Frame 4, starts at index position last index 3' TAGCTTGTT 5' #Frame 4 is TTG (L), TTC (F), GAT (D)

5' ATCGAACAA 3' #Frame 5, starts at index position -1

3' TAGCTTGTT 5' #Frame 5 is TGT (C), TCG (S)

5' ATCGAACAA 3' #Frame 6, starts at index position -2 3' TAGCTTGTT 5' #Frame is GTT (V), CGA (R)

In a single piece of double stranded DNA, there are six frames, forward and reverse. In each strand, there are three frames.

```
5' ATCGAACAA 3' #Frame 1, starts at index position 0 = encodes IEQ
```

3' TAGCTTGTT 5'

5' ATCGAACAA 3' #Frame 2, starts at index position 1 = encodes SN 3' TAGCTTGTT 5'

5' ATCGAACAA 3'

3' TAGCTTGTT 5'
When working with DNA sequencing, we often don't know where genes (or other elements) begin. However, we do know that most genes start with a start codon M

#Frame 6, starts in reverse at index position 7 = encodes CS

elements) begin. However, we do know that most genes start with a start codon M (ATG), and end with a stop codon * (TAA, TGA, TAG).

In a single piece of double stranded DNA, there are six frames, forward and reverse. In each strand, there are three frames.

- 5' ATCGAACAA 3' #Frame 1, starts at index position 0 = encodes IEQ
- 3' TAGCTTGTT 5'
- 5' ATCGAACAA 3' #Frame 2, starts at index position 1 = encodes SN
- 3' TAGCTTGTT 5'
- 5' ATCGAACAA 3' #Frame 6, starts in reverse at index position 7 = encodes CS3' TAGCTTGTT 5'
- Today, you will work on translating DNA into amino acids. We will perform 6-frame
- DNA translation. You will use all the tools that you learned to identify all possible genes within a single piece of DNA.

Quiz 22

- On canvas now