

File writing and dictionaries

Programming Bootcamp 2015

Day 5 – 6/16/15

Today's schedule

1. File writing
2. Dictionaries

1. File writing

File writing

Opening an output file is almost identical to input, with a small difference:

```
var = open(fileName, 'w')
```

Example:

```
outFile = open("seqs.txt", 'w')
```

File writing

Opening an output file is almost identical to input, with a small difference:

```
var = open(fileName, 'w')
```

Important: opening a file in 'w' mode will overwrite the file if it already exists.



Example:

```
outFile = open("seqs.txt", 'w')
```

Writing to an output file

Once the output file is opened, we use:

```
var.write(someStr)
```

Example:

```
outFile.write("This is output!\n")
```

Writing to an output file


Once the output file is opened, we use:

```
var.write(someStr)
```

Example:

```
outFile.write("This is output!\n")
```

Don't forget the newline!
Unlike `print`, `.write()` does
not insert this for you.



Simple example

Code

```
fileName = "output.txt"
outFile = open(fileName, 'w')
outFile.write("This is me,")
outFile.write("printing to \n a file.")
outFile.close()
```

output.txt

```
This is me,printing to
a file.
```



Note the spacing
and newline

Weird spacing for educational purposes.

Only strings can be printed

Code

```
fileName = "output.txt"
outFile = open(fileName, 'w')
outFile.write(25)
outFile.close()
```


Error:

```
Traceback (most recent call last):
  File "test.py", line 3, in <module>
    outFile.write(25)
TypeError: expected a character buffer object
```

Only strings can be printed

Code

```
fileName = "output.txt"
outFile = open(fileName, 'w')
outFile.write(str(25))
outFile.close()
```



A simple fix.

output.txt

25

Reading and writing can be done at the same time (as long as it's to different files)

Code

```
infile = "genes.txt"
outfile = "output.txt"
infile = open(infileName, 'r')
outfile = open(outfileName, 'w')
for line in infile:
    line = line.rstrip('\n')
    outfile.write("Found " + line + "\n")
outfile.close()
infile.close()
```

genes.txt

```
uc007zss.1
uc009akk.1
uc009eyb.1
uc008wzq.1
uc007hnl.1
```

output.txt

```
Found uc007zss.1
Found uc009akk.1
Found uc009eyb.1
Found uc008wzq.1
Found uc007hnl.1
```

This can pretty much be used as a template for most situations.

2. Dictionaries

Lists vs Dictionaries

Two main differences:

1. You retrieve elements from a dictionary using a "key", rather than an index
2. Dictionaries are unordered

1. Indexing by keys

A dictionary is similar to a list, except instead of accessing elements by their index, you access them by a name ("key") that you pick.

	'age'	'animal'	'num'	203	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

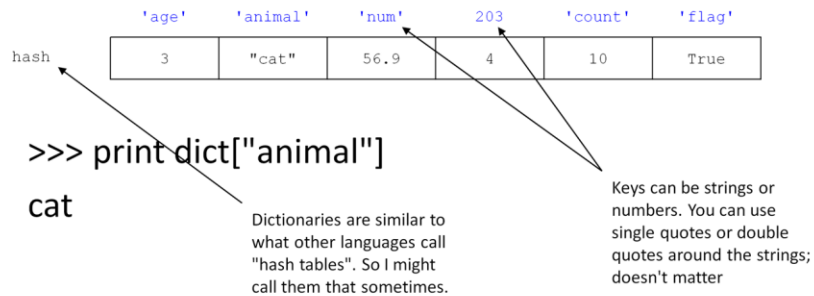
```
>>> print dict["animal"]
```

```
cat
```

Single or double quotes are fine.

1. Indexing by keys

A dictionary is similar to a list, except instead of accessing elements by their index, you access them by a name ("key") that you pick.



Dictionaries are similar to what other languages call "hash tables". So I might call them that sometimes.

2. Unordered

Lists are all about keeping elements in some order. Though you may change the ordering from time to time, it's still in *some* order.

You should think of **dictionaries** more like magic grab bags. You mark each piece of data with a key, then throw it in the bag. When you want that data back, you just tell the bag the key and it spits out the data assigned to that key.

2. Unordered

Lists are all about keeping elements in some order. ~~Though you may change the ordering from time to time.~~

Technicality:

Ok, so in reality, there *is* an order to your dictionary. But it is an order that Python picks that obeys complex rules and is essentially unpredictable by us. So for all intents and purposes, it may as well be unordered. Don't worry about it too much... just treat it like a magic grab bag and all will be well.

You should think of a dictionary like magic grab bags. You throw data with a key, then throw it in the bag. When you want that data back, you just tell the bag the key and it spits out the data assigned to that key.

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
print hash['count']
```

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
print hash['count']
```

Result:

10

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
print hash['num']
```

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
print hash['num']
```

Result:

56.9

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
print hash[age]
```

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
print hash[age]
```

Result:

```
Traceback (most recent call last):  
  File "<stdin>", line 1, in <module>  
NameError: name 'age' is not defined
```

(we didn't put quotes
around "age")

Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
var = 'animal'  
print hash[var]
```


Practice with dictionary keys

	'age'	'animal'	'num'	205	'count'	'flag'
hash	3	"cat"	56.9	4	10	True

What will this code print?

```
var = 'animal'  
print hash[var]
```

Result:

cat

So if you store the key in a variable, you can use that variable to index into the hash at that key.

Creating a dictionary

Create an empty dictionary:

```
hash = {}
```

Create a dictionary with elements:

```
hash = {"Joe": 25, "Sally": 35}
```



```
{'Joe': 25, 'Sally': 35}
```

Commas separate entries. Keys precede their values and are separated by a colon

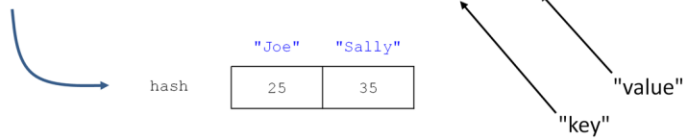
Creating a dictionary

Create an empty dictionary:

```
hash = {}
```

Create a dictionary with elements:

```
hash = {"Joe": 25, "Sally": 35}
```



```
{'Joe': 25, 'Sally': 35}
```

Commas separate entries. Keys precede their values and are separated by a colon

Adding to a dictionary

Add entry:

```
hash[newKey] = newVal
```

Example:

```
>>> hash = {}  
>>> hash["Joe"] = 25  
>>> hash["Bob"] = 39  
>>> print hash  
{'Bob': 39, 'Joe': 25}
```

Adding to a dictionary


Add entry:

```
hash[newKey] = newVal
```

Example:

```
>>> hash = {}  
>>> hash["Joe"] = 25  
>>> hash["Bob"] = 39  
>>> print hash  
{'Bob': 39, 'Joe': 25}
```

Note that Python printed
them in a different order
than we entered them.



Removing from a dictionary

Delete entry:

```
del hash[existingKey]
```

Example:

```
>>> hash = {"name": "Joe", "age": 35, "job": "plumber"}
>>> print hash
{'job': 'plumber', 'age': 35, 'name': 'Joe'}

>>> del hash["age"]
>>> print hash
{'job': 'plumber', 'name': 'Joe'}
```

Phonebook example

Code:

```
phonebook = {}  
phonebook["Joe Shmo"] = "958-273-7324"  
phonebook["Sally Shmo"] = "958-273-9594"  
phonebook["George Smith"] = "253-586-9933"  
  
name = raw_input("Lookup number for: ")  
print phonebook[name]
```

Output example:

```
Lookup number for: <we enter>Sally Shmo  
958-273-9594
```

Phonebook example

Code:

```
phonebook = {}  
phonebook["Joe Shmo"] = "958-273-7324"  
phonebook["Sally Shmo"] = "958-273-9594"  
phonebook["George Smith"] = "253-586-9933"
```

```
name = raw_input("Lookup number for: ")  
print phonebook[name]
```

Notice that we can store the name of a key in a variable, and then use that variable to access the desired element. In this case, name holds the name that we input in the terminal, Sally Shmo.

What would happen if we entered a name that was not in the phonebook?

Output example:

```
Lookup number for: <we enter>Sally Shmo  
958-273-9594
```


Checking if something is in the dict

This is the same as with a list. Use `in`:

```
ages = {}
ages["Joe"] = 35
ages["Sally"] = 36
ages["George"] = 39

if "Joe" in ages:
    print "Yes, Joe is in the dictionary"
else:
    print "No, Joe is not in the dictionary"
```

Result:

```
Yes, Joe is in the dictionary
```

Dictionary methods

Here are some useful dictionary methods:

- `dict.keys()` - returns a **list** of the keys only
- `dict.values()` - returns a **list** of the values only
- `dict.items()` - returns a **list** of key-value pairs

Example:

```
>>> colors = {"apple": "red", "banana": "yellow", "grape": "purple"}
>>> colors.keys()
['grape', 'apple', 'banana']
>>> print colors.values()
['purple', 'red', 'yellow']
>>> print colors.items()
[('grape', 'purple'), ('apple', 'red'), ('banana', 'yellow')]
```

Using .keys()

Code:

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39  
  
for name in ages.keys():  
    print name, "is in the dictionary."
```

Output:

```
Sally is in the dictionary.  
Joe is in the dictionary.  
George is in the dictionary.
```

← Once again, notice that things are printed in a seemingly random order.


Using .keys ()

Code:

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39  
  
for name in ages.keys():  
    print name, "is", ages[name]
```

Output:

```
Sally is 36  
Joe is 35  
George is 39
```



This gets the value associated
with the name


Using .keys ()

Code:

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39
```

```
for name in ages:  
    print name, "is", ages[name]
```

Note that in a `for` loop, you can actually leave off the `.keys()`, because this is what python loops over by default when a dict is the iterable.



Output:

```
Sally is 36  
Joe is 35  
George is 39
```

Using `.values()`

Code:

```
ages = {}
ages["Joe"] = 35
ages["Sally"] = 36
ages["George"] = 39

for age in ages.values():
    print "There is a person who is", age
```

Output:

```
There is a person who is 36
There is a person who is 35
There is a person who is 39
```

← The order is still random-seeming, but note that it's the same order as when we printed the keys.


Using `.items()`

Code:

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39
```

```
for (name, age) in ages.items():  
    print name, "is", age
```

`.items()` returns two variables each time it is called: a key and its value. This is why we can simultaneously assign the result to two variables



Output:

```
Sally is 36  
Joe is 35  
George is 39
```


Sorting a dictionary

You can **not** sort a dictionary. However, you can emulate sorting in the following way:

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39  
  
for name in sorted(ages.keys()):  
    print name, "is", ages[name]
```

Output:

```
George is 39  
Joe is 35  
Sally is 36
```



Sorted based on person's name

This prints in a sorted order, but the hash itself is unaffected!

Basically, what we are sorting is the list returned by `ages.keys()`, then we are indexing into the dict in that order

Sorting by values

Occasionally, you'll also want to sort the keys of your dictionary based on their *value*, rather than the key itself. Here's one way to do it:

```
ages = {}
ages["Joe"] = 35
ages["Sally"] = 36
ages["George"] = 39

for name in sorted(ages, key=ages.get):
    print name, "is", ages[name]
```

Output:

```
Joe is 35
Sally is 36
George is 39
```

← Sorted based on age rather than name

Terminology quiz

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39
```

"Joe" is most accurately referred to as...

- a. an element
- b. an index
- c. a key
- d. a value

Terminology quiz

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39
```

"Joe" is most accurately referred to as...

- a. an element
- b. an index
- c. a key**
- d. a value

Terminology quiz

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39
```

35 is most accurately referred to as...

- a. an element
- b. an index
- c. a key
- d. a value

Terminology quiz

```
ages = {}  
ages["Joe"] = 35  
ages["Sally"] = 36  
ages["George"] = 39
```

35 is most accurately referred to as...

- a. an element
- b. an index
- c. a key
- d. a value**

"an element" is OK too, but value is the more common terminology

Terminology quiz

```
ages = []          #this is a list  
ages[0] = 35  
ages[1] = 36  
ages[2] = 39
```

0 is most accurately referred to as...

- a. an element
- b. an index
- c. a key
- d. a value

Terminology quiz

```
ages = []          #this is a list  
ages[0] = 35  
ages[1] = 36  
ages[2] = 39
```

0 is most accurately referred to as...

- a. an element
- b. an index**
- c. a key
- d. a value

Terminology quiz

```
ages = []          #this is a list  
ages[0] = 35  
ages[1] = 36  
ages[2] = 39
```

39 is most accurately referred to as...

- a. an element
- b. an index
- c. a key
- d. a value

Terminology quiz

```
ages = []          #this is a list  
ages[0] = 35  
ages[1] = 36  
ages[2] = 39
```

39 is most accurately referred to as...

- a. an element**
- b. an index
- c. a key
- d. a value

Appendix

A longer example, complete with R code for
graphing

Why use a dictionary?

Technically, anything you can do with a dictionary you could also just do with a list instead. But dictionaries make coding certain tasks much easier.

Example: matching across files

One problem I encounter a lot is where I have two files with different information about a transcript, and I need to integrate the info.

REAL LIFE SITUATION (!!!)

I have a file with transcript ids and translation start sites. I need to normalize these start positions by transcript length so that I can graph the distribution of start sites across all transcripts in my dataset. To do this, I need to divide the start site position by the full length of the transcript. Unfortunately, I have transcript lengths stored in a separate file, so I need to **match up start sites with their full transcript lengths**.



Ex. cont.: data files

Here are the formats of my data files:

Start site file:

knownGene	Gene	InitCodon	DistCDS	Frame	InitContext	CDSLen	PeakSt	PeakWidth	#Reads	PeakScore	Codon	Product
uc007afd.1	Mpl15	248	79	1	AATATGG	15	247	2	368	2.61	aug	internal-out-of-frame
uc007afh.1	Lyplal	36	5	0	AACATGT	225	34	4	783	3.27	aug	n-term-trunc
uc007afi.1	Tceal	28	-24	0	GGCTTGT	325	27	3	446	1.43	nearcog	n-term-ext
uc007afi.1	Tceal	100	0	0	GCCATGG	301	99	3	3852	3.79	aug	canonical
uc007afn.1	Atp6v1h	100	-13	-1	GCTATCC	10	99	3	728	0.77	nearcog	uorf
uc007afn.1	Atp6v1h	149	3	0	AAGATGG	480	147	3	1407	1.36	aug	n-term-trunc
uc007agb.1	Pcmt1	120	-97	-1	GCGCTGG	45	119	3	65	0.75	nearcog	uorf
uc007agb.1	Pcmt1	265	-49	0	GCGCTGC	42	264	3	133	0.86	nearcog	uorf
...												

Transc. length file:

SeqID	Len
uc009gmc.1	4900
uc008mue.1	459
uc007hzr.1	4578
uc007gtm.1	1257
uc007axo.1	2311
uc007wps.1	2694
uc007gqc.1	30
uc009smc.1	1530
...	

The common piece of information between these files is the **transcript ID**, so this is what we will use to match up start sites to transcript lengths.

Ex. cont.: Plan

When working with more than one file, it sometimes helps to write down a step-by-step plan before you start coding.

Here's my plan:

1. Open length file
2. For each line in length file:
 - a. Extract the id (1st column) and length (2nd column)
 - b. Store lengths in hash based on id
`hash[id] --> length`
3. Open output file
4. Open tss file
5. For each line in tss file:
 - a. Extract the id (1st column) and start site (3rd column)
 - b. Using the id, lookup the length of the transcript from the hash
 - c. Divide the start position by the length of the transc.
 - d. Print the result to the output file

Ex. cont.: Code pt. 1

```
# input files
tssFile = "all_start_sites.txt"
lenFile = "transc_lengths.txt"

# output files
normOut = "normalized_tss.txt"

# data
lengths = {}

# read in lengths, store in hash
input = open(lenFile, 'r')
input.readline() #don't forget to skip the header!
for line in input:
    line = line.rstrip('\n')
    (id, len) = line.split() #split on whitespace
    lengths[id] = len #store len in hash labeled by the id
input.close()
```

... continued on next slide

Ex. cont.: Code pt. 2

```
# read in TSS, use stored lengths to normalize,
# then print. No need to store TSS.
output = open(normOut, 'w')
output.write("RelativePos\n")           #header line for output file
input = open(tssFile, 'r')
input.readline()                       #skip header in input file
for line in input:
    line = line.rstrip('\n')
    data = line.split()                #data is now a LIST
    id = data[0]                       #id is the first data value in the list
    tss = float(data[2])               #start site is third data value in the list
    if id in lengths:                 #make sure there is an entry in hash for this id**
        fullLen = int(lengths[id])    #using hash, lookup the length of this transc
        norm = tss / fullLen          #divide start position by full length
        output.write(str(norm) + "\n") #output the result to a file
input.close()
output.close()
```

** If there are transcript ids in the TSS file that were not in the length file, then we will get an error when we try to look up that id in the hash (because it's just not there). If you think there is a chance this might happen (and there almost always is) just add this quick `if` statement to skip over any ids that would cause an error.

Ex. cont.: Output

Here's what the output looks like:

```
RelativePos  
0.0147118921128  
0.0506072874494  
0.0754048582996  
0.0229226361032  
0.0506208213945  
0.0787010506208  
0.140783190067  
0.170009551098  
0.0329929300864  
0.0675569520817  
0.0523469608479  
0.0627298291153  
0.0752757949384  
0.100800346096  
...
```

This file can now be easily imported
into R for graphing.

Bonus: Graphing the data

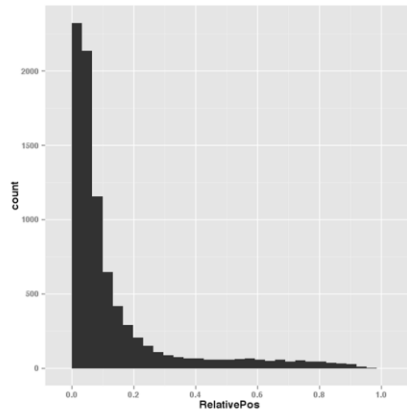
This type of data is best represented using a histogram. Here's how you can easily create a histogram using the ggplot2 package for R (run this code in R, not python):

```
library("ggplot2")
startSites <- read.table("normalized_tss.txt", header=T)
ggplot(startSites, aes(x=RelativePos)) + geom_histogram()
```

Note: You must first install both R and the ggplot2 package to do this. If you already have R installed, you can install ggplot2 by typing `install.packages("ggplot2")` into your R terminal. The ggplot2 docs (found at <http://had.co.nz/ggplot2/>) are very useful and give lots of examples of what you can do.

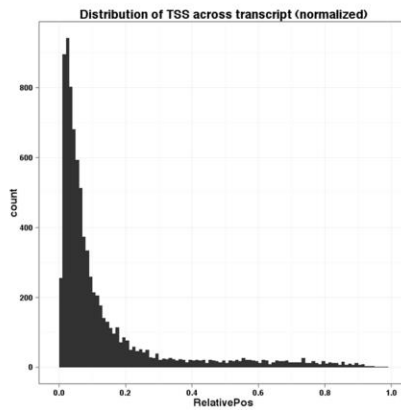
Using ggplot2

The previous commands produce this graph:



Using ggplot2

```
ggplot(startSites, aes(x=RelativePos)) +  
  geom_histogram(binwidth=0.01) +  
  opts(title="Distribution of TSS across transcript (normalized)") +  
  theme_bw()
```



Using ggplot2

We could also use a density plot instead of a histogram:

```
ggplot(startSites, aes(x=RelativePos)) +  
  geom_density() +  
  opts(title="Distribution of TSS across transcript (normalized)") +  
  theme_bw()
```

