File Reading and Writing

MBV-INFx410

Fall 2016

Working with files

- Reading – get info into your program
- Parsing – processing file contents
- Writing – get info out of your program

Reading and writing

- Three-step process
  - Open file
    - create file handle – reference to file
  - Read or write to file
  - Close file
- File will be automatically closed on program end, but bad form to not close

Opening a file

- How to open a file:

  fh = open("filename", "mode")
    - fh = filehandle, reference to a file, NOT the file itself
- Opening modes:

  -"r" - read file

  -"w" - write file

  -"a" - append to end of file

Reading a file

- Three ways to read
  - read([n]), n = bytes to read, default is all
  - readline(), read one line, incl. newline
  - **readlines(), read file into a list, one element per line, including newline**

Reading example

```
>>> fh = open("reading_file.txt", "r")
>>> fh
<open file 'reading_file.txt', mode 'r' at 0x1027e4540>


>>> lines = fh.readlines()
>>> lines
['This is a test file.\n', 'This file contains \n', 'three lines of text.\n']
>>>
```

NOTE: results is a list with strings, each string ending in a newline – a \n

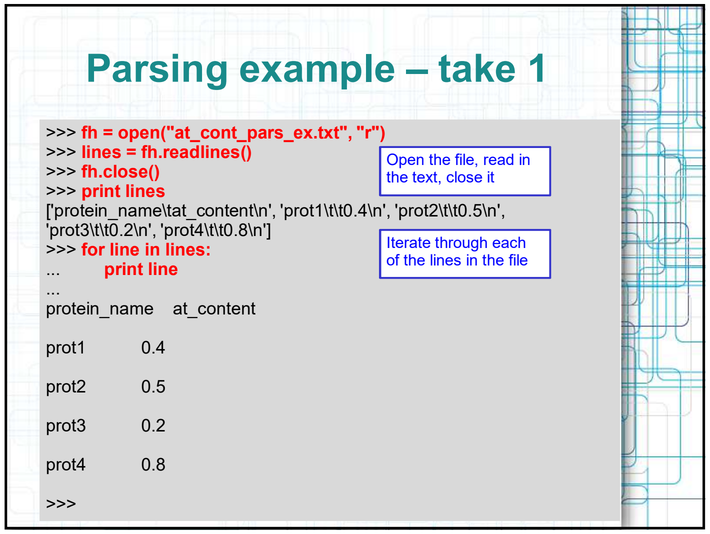
Parsing

- Getting information out of a file
- Commonly used string methods
  - *oneline: variable that contains text*
  - oneline.split("character") – splits line into list on character, default is whitespace
  - oneline.replace("in string", "put into instead")
  - slicing

Parsing example

```
protein_name    at_content
prot1           0.4
prot2           0.5
prot3           0.2
prot4           0.8
```

Goal: calculate the average AT content of the proteins

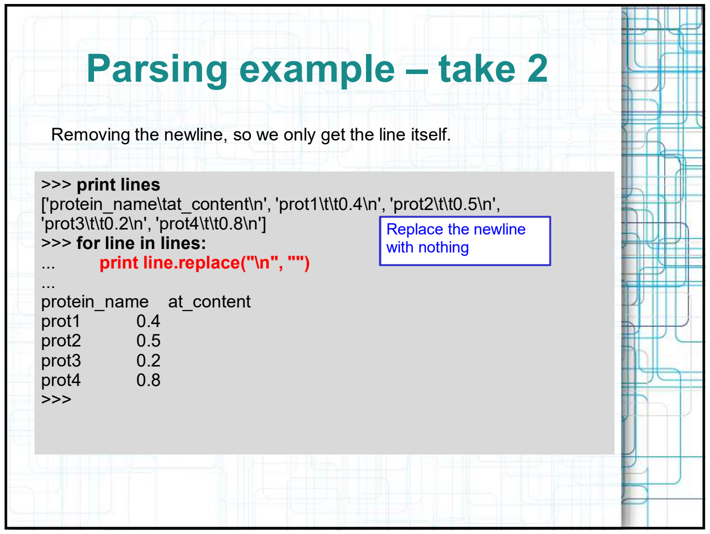


Parsing example – take 1

```
>>> fh = open("at_cont_pars_ex.txt", "r")
>>> lines = fh.readlines()
>>> fh.close()
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> for line in lines:
...       print line
...
protein_name    at_content

prot1           0.4

prot2           0.5

prot3           0.2

prot4           0.8

>>>
```

Open the file, read in the text, close it

Iterate through each of the lines in the file

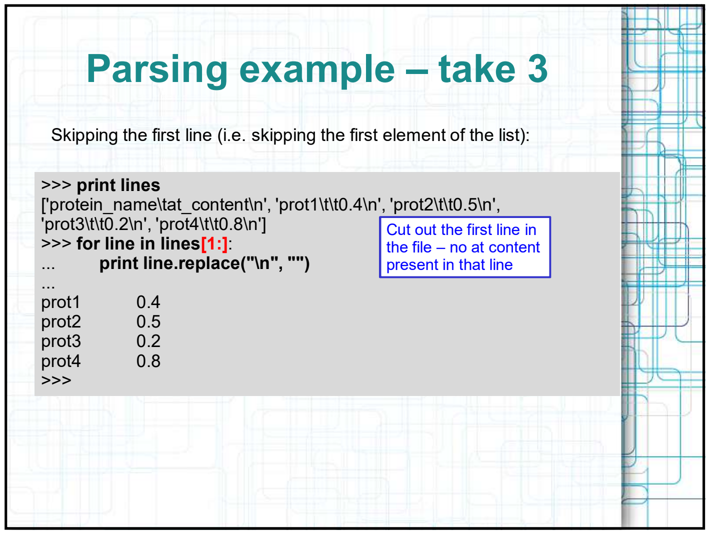


Parsing example – take 2

Removing the newline, so we only get the line itself.

```
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> for line in lines:
...       print line.replace("\n", "")
...
protein_name    at_content
prot1           0.4
prot2           0.5
prot3           0.2
prot4           0.8
>>>
```

Replace the newline with nothing

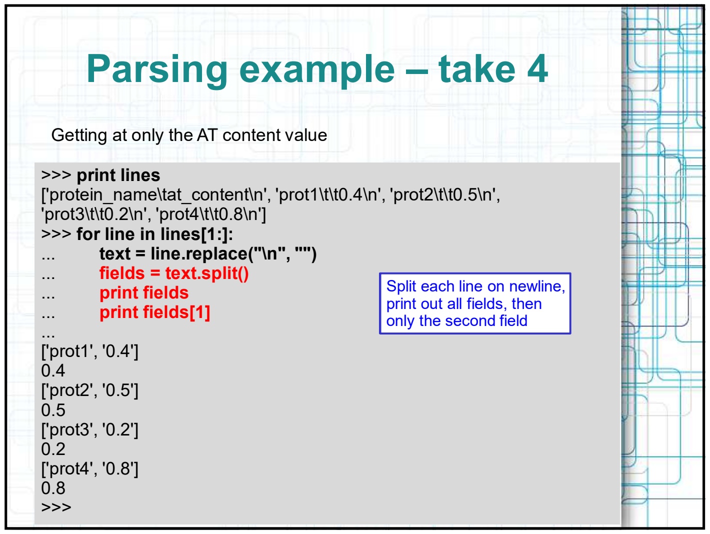


Parsing example – take 3

Skipping the first line (i.e. skipping the first element of the list):

```
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> for line in lines[1:]:
...       print line.replace("\n", "")
...
prot1           0.4
prot2           0.5
prot3           0.2
prot4           0.8
>>>
```

Cut out the first line in the file – no at content present in that line



Parsing example – take 4

Getting at only the AT content value

```
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> for line in lines[1:]:
...       text = line.replace("\n", "")
...       fields = text.split()
...       print fields
...       print fields[1]
...
['prot1', '0.4']
0.4
['prot2', '0.5']
0.5
['prot3', '0.2']
0.2
['prot4', '0.8']
0.8
>>>
```

Split each line on newline, print out all fields, then only the second field

Parsing example – take 5

Putting the AT content value into a list

```
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> at_content_list = []
>>> for line in lines[1:]:
...       text = line.replace("\n", "")
...       fields = text.split()
...       this_at_content = fields[1]
...       at_content_list.append(this_at_content)
...
>>> print at_content_list
['0.4', '0.5', '0.2', '0.8']
>>>
```

Create list to hold the at contents. Created outside of loop, otherwise out of scope

Get only at content value, append it to the list

Print out the resulting list

Parsing example – take 6

Putting the AT content value into a list as NUMBERS

```
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> at_content_list = []
>>> for line in lines[1:]:
...       text = line.replace("\n", "")
...       fields = text.split()
...       this_at_content = float(fields[1])
...       at_content_list.append(this_at_content)
...
>>> print at_content_list
[0.4, 0.5, 0.2, 0.8]
>>>
```

Converting the string with the at content in to float

Parsing example – take 6

Calculating the average

```
>>> print lines
['protein_name\tat_content\n', 'prot1\t\t0.4\n', 'prot2\t\t0.5\n',
'prot3\t\t0.2\n', 'prot4\t\t0.8\n']
>>> at_content_list = []
>>> for line in lines[1:]:
...       text = line.replace("\n", "")
...       fields = text.split()
...       this_at_content = float(fields[1])
...       at_content_list.append(this_at_content)
...
>>> print at_content_list
[0.4, 0.5, 0.2, 0.8]
>>> sum(at_content_list)/len(at_content_list)
0.47500000000000003
>>>
```

Calculating the average

Parsing blast output

```
Isotig13419   contig698252   99.79    472  1   0   1538 2009 1187 716  0.0          928
Isotig13419   contig698252   100.00   114  0   0   1369 1482 1356 1243 1e-56        226
Isotig13419   contig698252   100.00   100  0   0   1247 1346 2243 2144 2e-48        198
Isotig13419   contig698252   98.95    95   1   0   2088 2182 637  543  5e-43        180
isotig13419   contig889828   99.72    361  1   0   570  930  1631 1271 0.0      708
isotig13419   contig889828   99.60    251  0   1   321  570  2064 1814 2e-119    434
Isotig13419   contig889828   100.00   193  0   0   981  1173 266  74   2e-82        311
isotig13419   contig889828   100.00   63   0   0   1185 1247 63   1    3e-26        125
Isotig13419   contig362216   99.72    361  1   0   570  930  364  4    0.0      708
Isotig13419   contig362216   99.60    251  0   1   321  570  797  547  2e-119    434
Isotig13419   contig362215   100.00   193  0   0   981  1173 266  74   2e-82        311
```

- Columns tab separated
- Headings:
  - Query, Subject, % id, aln length, # mismatches, # gap openings, q.start, q.end, s.start, s.end, e-value, bit score

Length of blast matches

- Goal: figure out how long each of the matches in the subject is
- Output: subject name, length of match
- First: read in file into a list
- Second: Per element in list:
  - access columns 2 (subject name), columns 9 and 10 (s.start,
  - convert 9 and 10 to int, substract and print results
- Remember - python is zero based!
- Fill out script in parse_blast.py

Parsing blast file

```
import sys
fh = open(sys.argv[1], "r")
lines = fh.readlines()
fh.close()

for line in lines:
    text = line.replace("\n","")
    fields = text.split()
    name = fields[1]
    start = int(fields[8])
    stop = int(fields[9])
    print name, stop - start
```

python script

run with file named blastout2.txt as input

```
contig698252 -471
contig698252 -113
contig698252 -99
[skipping some lines of output here]
contig539930 90
contig127790 78
contig710791 33
```

Results from running the script – some output in the middle is skipped

How to get absolute length?

- Results from previous slide – some lengths were negative
- Examine input file and figure out why

Absolute lengths

- Some matches are on the reverse strand, i.e. stop < start
- Solution: reverse that
- But: only in cases where the match is actually on the reverse strand
- How to detect: see **if** stop < start

Print absolute lengths, also for reverse strand matches

- Modify code from earlier so that in cases where stop < start, we print start – stop instead

```
import sys
fh = open(sys.argv[1], "r")
lines = fh.readlines()
fh.close()

for line in lines:
    text = line.replace("\n","")
    fields = text.split()
    name = fields[1]
    start = int(fields[8])
    stop = int(fields[9])
    if stop < start:
        print name, start - stop
    else:
        print name, stop - start
```

If statement that lets us print out start – stop if stop < starts, and stop – start otherwise

Writing to files

- Similar procedure as for read
  - Open file, mode is "w" or "a"
  - fo.write(string)
    - Note: one single string
    - Newlines have to be added specifically
  - fo.close()

```
>>> outstring = "Write this to file\n"
>>> fo = open("outputfile.txt", "w")
>>> fo.write(outstring)
>>> fo.close()
>>>
[karinlag@freebee] % cat outputfile.txt
Write this to file
[karinlag@freebee] %
```

Modify script to print to file

- Changes to do:
  - Open output file
  - Write to output file
  - Close output file

Print to file

```
import sys
fh = open(sys.argv[1], "r")
lines = fh.readlines()
fh.close()

fo = open(sys.argv[2], "w")

for line in lines:
    text = line.replace("\n","")
    fields = text.split()
    name = fields[1]
    start = int(fields[8])
    stop = int(fields[9])
    difference = 0
    if stop < start:
        difference = start - stop
    else:
        difference = stop – start

    outstring = name + "\t" + str(difference) + "\n"
    fo.write(outstring)

fo.close()
```

Open output file for writing.

Putting the difference in a separate variable makes it easier to print

Creating output string, and writing it. Notice we added a newline!

Closing the output file

Results

```
contig698252   471
contig698252   113
contig698252   99
contig698252   94
contig889828   360
contig889828   250
contig889828   192
contig889828   62
contig362216   360
contig362216   250
contig362215   192
contig362215   62
contig855826   139
contig701635   138
contig747126   141
contig280145   115
contig560635   99
contig279861   85
contig539930   90
contig127790   78
contig710791   33
```

readFasta.py

- Goal: get fasta sequence into one string
- Create script that
  - opens fasta file - name on command line
  - reads in lines into variable lines
  - closes fasta file
  - create variable to contain fasta sequence
  - keep/cut out first line - out in variable header
  - per remaining line:
    - remove newline
    - add to variable that contains sequence
  - print out header and result

```
# import to get command line variables available
import sys

# Read in fasta file contents
fh = ____(sys.argv[_], "r")
lines = fh._________()
fh.close()

# Store the first line, the description line
firstline = _____[0]
# Replace the newline at the end with nothing
header = _________.replace(__, __)

# Create an empty text variable to store the sequence in
sequence = __

# Iterate over all the read in lines, from the second and onwards
___ line in _____[_:]:
    # Remove the newline
    wo_newline = line._______("\n", "")
    # append this line of text to the sequence we have already
    ________ = sequence _ wo_newline

print header
print sequence
```

```
# import to get command line variables available
import sys

# Read in fasta file contents
fh = open(sys.argv[1], "r")
lines = fh.readlines()
fh.close()

# Store the first line, the description line
firstline = lines[0]
# Replace the newline at the end with nothing
header = firstline.replace("\n", "")

# Create an empty text variable to store the sequence in
sequence = ""

# Iterate over all the read in lines, from the second and onwards
for line in lines[1:]:
    # Remove the newline
    wo_newline = line.replace("\n", "")
    # append this line of text to the sequence we have already
    sequence = sequence + wo_newline

print header
print sequence
```

readWriteFasta.py

- Copy readFasta.py into readWriteFasta.py
- Change script so that you:
  - open/create output file
  - write header to file
  - write dna, in chunks of 60 to file

readWriteFasta.py

```
# rest of script is above
# Iterate over all the read in lines, from the second and onwards
for line in lines[1:]:
    # Remove the newline
    wo_newline = line.replace("\n", "")
    # append this line of text to the sequence we have already
    sequence = sequence + wo_newline

# Open out file
fo = open(sys.argv[2], "w")
# Write header
fo.write(header + "\n")

# Get slices 60 long, and write out with newline on end
i = 0
while i < len(sequence):
    chunk = sequence[i:i+60]
    fo.write(chunk + "\n")
    i = i + 60

fo.close()
```