SI 506: Programming I
Fall 2019
Lecture 09

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Slide deck revisions

errata: corrections and other changes

Slide no(s).	Fix ver.	Description
	v1p1	

Class exercise

open file, read contents, write to file

Canvas Files

`lectures/lecture_09/`

`lecture_08_exercise.py`

`whale_names.txt`

Upload to pythonanywhere.com

Place in same directory

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preliminaries

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Midterm exam

key concepts

files (read, write)

nested lists

functions

splitting and slicing

conditional statements

for loops (*not* while loops)

lists

strings

arithmetic, assignment, logical, identity, membership operators

built in functions()

objects, variables, variable assignment

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Next week

Lectures, lab exercise, problem set

all review

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working with files

old school

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Files: open, read, close

open existing file, return file handle, read content, close

```
path = 'whale_names.txt'

# Create a file handle, read content
file_handle = open(path)
whale_names = file_handle.read()
file_handle.close()

print(f"whale_names = {whale_names}")
```

Files: open, read, close

open existing file, return file handle, read content, close

```
path = 'whale_names.txt'

# Create a file handle,                    tent
file_handle = open(path)
whale_names = file_handle.read()
file_handle.close()

print(f"whale_names = {whale_names}")
```

open

read content

you must close

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Files: gotcha

once closed, you must (re)open file, or trigger a traceback

```
path = 'whale_names.txt'

# Create a file handle, read contents
file_handle = open(path)
whale_names = file_handle.read()
file_handle.close()
names = file_handle.read()

print(f"names = {names}")
```

Files: close() means closed

once closed, you must (re)open file, or trigger a traceback

```
Traceback (most recent call last):
  File "…/whales.py", line 18, in <module>
    names = file_handle.read()
ValueError: I/O operation on closed file.
```

Files: open, read line, close

readline() reads one line at a time; advances to next line

```
path = 'whale_names.txt'

# Create a file handle, read 2 lines
file_handle = open(path)
header = file_handle.readline()
whale = file_handle.readline()
file_handle.close()
```

advances to next line

```
print(f"header = {header}")
print(f"whale = {whale}\n")
```

Files: gotcha

one read operation limit; call different type returns empty value

```
path = 'whale_names.txt'

# Create a file handle
file_handle = open(path)
whale_names = file_handle.read()
line = file_handle.readline()
file_handle.close()

print(f"whale_names = {whale_names}")
print(f"line = {line}\n")
```

blank string

Files: open, read lines, return list, close

readlines() returns a list of lines (note: includes trailing '\n')

```
path = 'whale_names.txt'

# Create a file handle, return list
file_handle = open(path)
lines = file_handle.readlines()
file_handle.close()

print(f"lines = {lines}")
```

returns list

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Files: iterate over each line; create list

loop over file_handle (note: includes trailing '\n')

```
path = 'whale_names.txt'

# Create a file handle, return list
lines = []
file_handle = open(path)
for line in file_handle:
    lines.append(line)
file_handle.close()

print(f"lines = {lines}\n")
```

File: whale list returned

using readlines() or for loop with file_handle

```
lines = ['species,common_name\n',
         'Balaenoptera musculus,Blue Whale\n',
         'Eschrichtius robustus,Grey Whale\n',
         'Eubalaena glacialis,North Atlantic Right Whale\n',
         'Eubalaena japonica,North Pacific Right Whale\n',
         'Physeter macrocephalus,Sperm Whale\n',
         'Megaptera novaeangliae,Humpback Whale\n',
         "Balaenoptera edeni,Bryde's Whale\n",
         'Balaenoptera physalus,Fin Whale\n',
         'Balaena mysticetus,Bowhead Whale\n',
         'Balaenoptera acutorostrata,Minke Whale']
```

newline escape char appended to each line

double quotes surround single quote

Note: Bryde's whale pronounced "Broodus" whale

File: optional parameter modes

open()

```
file_handle = open(path, '<mode>')
```

‘r’: read

‘w’: write

‘x’: create, write (new file)

‘a’: append (existing file)

‘r+’: read, write (same file)

Files: open, write line, close

anatomy

```
# Create a file handle, return list
path = 'whale_lines.txt'
file_handle = open(path, 'w')
#  Get whale names, write to file
for line in lines:
    file_handle.write(f"{line}")
file_handle.close()
```

warning: if file does not exist it will be created; if file exists it will be *overwritten*.

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Files: open, write line, close

anatomy

optional mode parameter 'w' (write)

```
# Create a file handle, return list
path = 'whale_lines.txt'
file_handle = open(path, 'w')
#  Get whale names, write to file
for line in lines:
    file_handle.write(f"{line}")
file_handle.close()
```

always close

warning: if file does not exist it will be created; if file exists it will be *overwritten*.

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File: exercise

write whale common names to file

```
# Create a file handle, return list
path = 'whale_names.txt'
file_handle = open(path)
lines = #FIX ME
file_handle.close()

# Extract headers (first row)
headers = lines[0].rstrip().split(',')

# Get whales only (skip header)
whales = []
for line in lines[#FIX ME]:
    whales.append(#FIX ME)
```

```
# Get common name by index position lookup
def get_common_name(names):
    """Return common name."""
    return names[headers.index(#FIX ME)]


# Open new file in write mode, get file handle
# Iterate over whales list, call function to return common name, write to file
path = 'whale_common_names.txt'
file_handle = open(path, '#FIX ME')
#  Get whale names, write to file
for whale in whales:
    common_name = #FIX ME
    file_handle.write(f"{#FIX ME}\n")
file_handle.close()
```


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File: output file

whale_common_names.txt

```
Blue Whale
Grey Whale
North Atlantic Right Whale
North Pacific Right Whale
Sperm Whale
Humpback Whale
Bryde's Whale
Fin Whale
Bowhead Whale
Minke Whale
```

In class exercise

fix broken file: open file, read lines, write lines new file

1a. Use open() to open `whale_names.txt` and obtain a file handle.
1b. Return a list of lines using `.readlines()`; assign to list named `lines`.
1c. Close file handle.
2. Assign first element of `lines` to a list named `headers`; use `str.split(',')` to return list of species and common names; use `str.rstrip()` to strip out newline ('\n'); syntax:
`headers = lines[?].rstrip().split(',')`
3a. Create an empty list named `whales = []`
3b. Use a `for` loop to iterate over line elements containing *only* whales (use list slicing to skip header line); split the string on the comma returning a list; use `str.rstrip()` to remove '\n'
4. In the function named `get_common_name(names)` reference the header index position associated with `common_name` in the return statement in order to return the common name in the evaluated list.
5a. Use `open()` with optional mode parameter 'w' to create a file named `whale_common_names.txt` and obtain a file handle.
5b. Use a `for` loop to iterate over the `whales` list; use the file handle to write to the file each whale's common name, calling the `get_common_name(names)` function to return the common name of each whale. Add newline '\n' escape char to string you create.
5c. Close the file handle.

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Files: open, write line, close

anatomy

optional mode parameter 'w' (write)

```
# Create a file handle, return list
path = 'whale_common_names.txt'
file_handle = open(path, 'w')
#  Get whale names, write to file
for whale in whales:
    file_handle.write(f"{get_common_name(whale)}\n")
file_handle.close()
```

add newline

call function, write line to file

always close

warning: if file does not exist it will be created; if file exists it will be *overwritten*.

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finis

directors cut

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Functions: quick review

anatomy

‘definition’ keyword

name

arguments

default value

```
def create_email_address(name, domain=umich_domain):
    """Combine local part and domain to form an email address."""
    return ''.join([name, '@', domain])
```

docstring

return statement gives back a value

code block (indented)

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Functions: quick review

have: uniqnames; need: U-M email addresses

```
umich_domain = 'umich.edu' # default domain value
uniqnames = ['arwhyte', 'csev', 'nantin'] # source
umich_email_addresses = [] # target


def create_email_address(name, domain=umich_domain):
    """Combine local part & domain."""
    return ''.join([name, '@', domain])


# Loop over uniqnames list and call create_email_address
for name in uniqnames:
    umich_email_addresses.append(create_email_address(name))

print(f"uniqnames = {uniqnames}\n")
print(f"umich_email_addresses = {umich_email_addresses}\n")
```


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List slicing: problem 1

extract indices using range() and list indexing operation

```
regions = ['Eastern Africa', 'Western Africa', 'Southern Africa']

countries_regions = ['Botswana, Southern Africa', 'Kenya, Eastern Africa',
                     'Ghana, Western Africa', 'Uganda, Eastern Africa',
                     'Nigeria, Western Africa']

# PROBLEM 1
# Extract indices of Eastern African countries from
# countries_regions list (source) and store in list
# named eastern_african_indices (target)

eastern_african_indices = []

for index in range(len(countries_regions)):
    if countries_regions[index].split(', ')[1] == regions[0]:
        eastern_african_indices.append(index)

print(f"eastern_african_indices = {eastern_african_indices}\n")
```

List slicing: problem 1

extract indices using range() and index position

```
regions = ['Eastern Africa', 'Western Africa', 'Southern Africa']

countries_regions = ['Botswana, Southern Africa', 'Kenya, Eastern Africa',
                     'Ghana, Western Africa', 'Uganda, Eastern Africa',
                     'Nigeria, Western Africa']

# PROBLEM 1
# Extract indices of Eastern Af      tries from
# countries_regions list (source) and store in list
# named eastern_africa       (target

eastern_african_indices = []

for index in range(len(countries_regions)):
    if countries_regions[index].split(', ')[1] == regions[0]:
        eastern_african_indices.append(index)

print(f"eastern_african_indices = {eastern_african_indices}\n")
```

split

position

index

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List slicing: problem 2

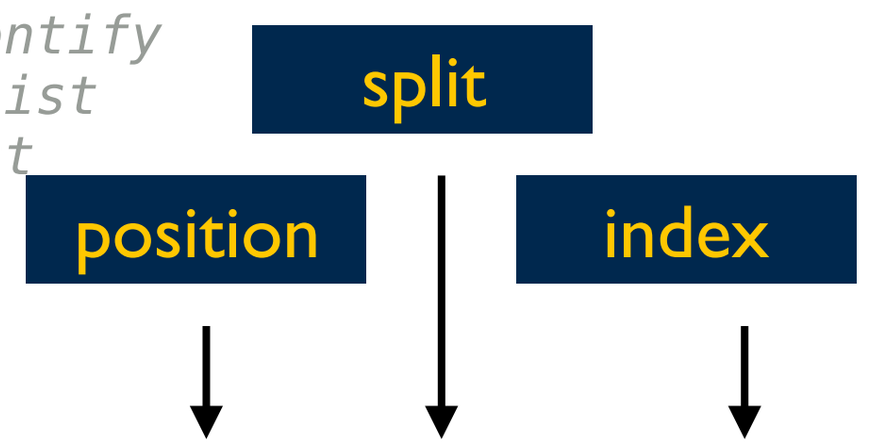
use indices to identify East African countries

```
countries_regions = ['Botswana, Southern Africa', 'Kenya, Eastern Africa',
                     'Ghana, Western Africa', 'Uganda, Eastern Africa',
                     'Nigeria, Western Africa']

eastern_african_indices = [1, 3] # derived from problem 1


# PROBLEM 2
# Use the indices in eastern_african_indices to identify
# East African countries in the countries_regions list
# and then store the country name (only) in the list
# eastern_african_countries.

eastern_african_countries = []

for index in eastern_african_indices:
    eastern_african_countries.append(countries_regions[index].split(', ')[0])

print(f"eastern_african_countries = {eastern_african_countries}\n")
```

List slicing: problem 2

use indices to identify East African countries

```
countries_regions = ['Botswana, Southern Africa', 'Kenya, Eastern Africa',
                     'Ghana, Western Africa', 'Uganda, Eastern Africa',
                     'Nigeria, Western Africa']

eastern_african_indices = [1, 3] # derived from problem 1


# PROBLEM 2
# Use the indices in eastern_african_indices to identify
# East African countries in the countries_regions list
# and then store the country name (only) in the list
# eastern_african_countries.

eastern_african_countries = []

for index in eastern_african_indices:
    eastern_african_countries.append(countries_regions[index].split(', ')[0])

print(f"eastern_african_countries = {eastern_african_countries}\n")
```



Python console

write/execute Python code (only)

Python3.7 console 13351686

Share with others

```
Python 3.7.0 (default, Aug 22 2018, 20:50:05)
[GCC 5.4.0 20160609] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> import json
>>> console = 'command line interpreter'
>>> purpose = 'accept user input in the form of Python code and attempt to execute it.'
>>> use = 'typically used for quick prototyping and exploration of the language (i.e., teaching).'
>>> data = {}
>>> data['console'] = console
>>> data['purpose'] = purpose
>>> data['use'] = use
>>> json_data = json.dumps(data)
>>> print(json_data)
{"console": "command line interpreter", "purpose": "accept user input in the form of Python code and attempt to execute i
t.", "use": "typically used for quick prototyping and exploration of the language (i.e., teaching)."}
>>>
```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Unix shell (Bash)

interact with operating system, issue commands, run scripts

Bash console 13351749

Share with others

```
01:43 ~ $ pwd
/home/arwhyte
01:43 ~ $ ls
README.txt  SI506
01:43 ~ $ cd SI506
01:44 ~/SI506 $ ls -la
total 16
drwxrwxr-x 4 arwhyte registered_users 4096 Sep  5 04:14 .
drwxrwxr-x 5 arwhyte registered_users 4096 Sep  5 22:01 ..
drwxrwxr-x 2 arwhyte registered_users 4096 Sep  5 02:28 lab_exercises
drwxrwxr-x 2 arwhyte registered_users 4096 Sep  2 00:43 problem_sets
01:44 ~/SI506 $ cd lab_exercises
01:44 ~/SI506/lab_exercises $ ls -la
total 12
drwxrwxr-x 2 arwhyte registered_users 4096 Sep  5 02:28 .
drwxrwxr-x 4 arwhyte registered_users 4096 Sep  5 04:14 ..
-rw-rw-r-- 1 arwhyte registered_users 1483 Sep  5 02:28 si506_lab_01.py
01:44 ~/SI506/lab_exercises $ python3 si506_lab_01.py arwhyte
Huzzah! arwhyte writes first Python program at 2019-09-11T21:44:51.572295-04:00
01:44 ~/SI506/lab_exercises $
```


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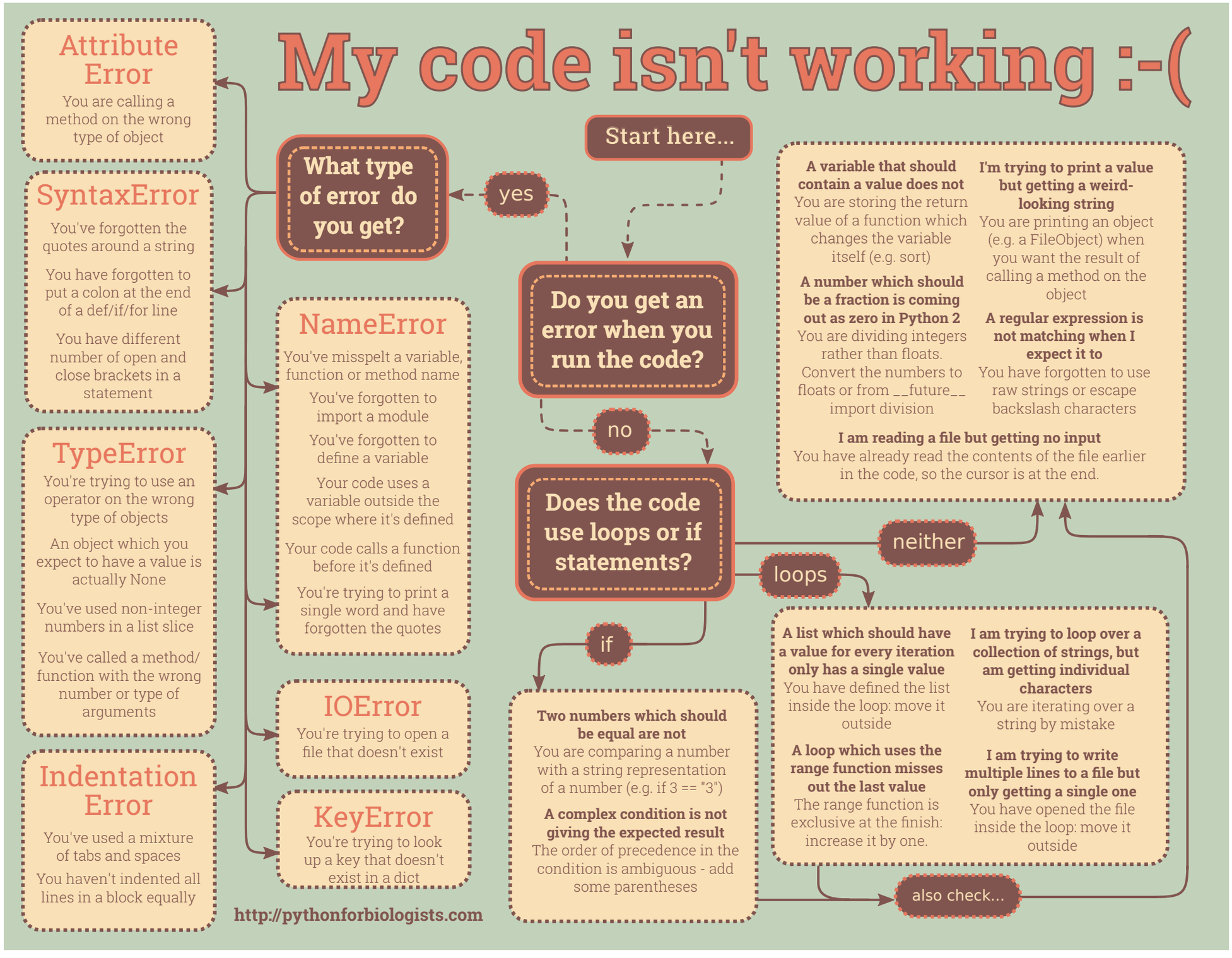
When your code misbehaves

debug flowchart



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Files: open, write, close

write whale common names to file

```
# Create a file handle, return list
path = 'whale_names.txt'
file_handle = open(path)
lines = file_handle.readlines()
file_handle.close()

# Extract headers (first row)
headers = lines[0].rstrip().split(',')

# Get whales only (skip header)
whales = []
for line in lines[1:]:
    whales.append(line.rstrip().split(','))
```

```
# Get common name by index position lookup
def get_common_name(names):
    """Return common name."""
    return names[headers.index('common_name')]


# Open new file in write mode, get file handle
# Iterate over whales list, call function to return common name, write to file
path = 'whale_common_names.txt'
file_handle = open(path, 'w')
#  Get whale names, write to file
for whale in whales:
    common_name = get_common_name(whale)
    file_handle.write(f"{common_name}\n")
file_handle.close()
```


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