SUDDrocess

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Programming (for biologists) BIOL 7800

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code_example.py - /Users/bcf/Dropbox/Classes/BIOL7800/temp/lecture20

#!/usr/bin/env

-*- coding: utf-8 -

code example.pv

.....

(c) 2016 Brant Faircloth || <u>http://faircloth-lab.org/</u> All rights reserved. This code is distributed under a 3-clause BSD license. Please see LICENSE.txt for more information. Created on 17 March 2016 16:01 CDT (-0500) """

import re
import argparse
from collections import Counter

import pdb

def get_args(): """Get arguments from CLI""" parser = argparse.ArgumentParser(description="""Reads a file in; write some stuff out""" parser.add_argument("--infile", required=True, type=str, help="""The path to the input file""" parser.add_argument("--output", required=True, type=str, help="""The path to the output file""" return parser.parse_args() def get_and_clean_file(f): with open(f, 'r') as infile: text = infile.read() return re.findall("\w+['-]*\w*", text.lower()) def pretty_print_counts(cnt, top=20): for word, cnt in cnt.most_common(top): print("{: <20}{}".format(word, cnt))</pre> def pretty_write_counts(o, cnt): with open(o, 'w') as outfile: for word, cnt in cnt.most_common(): outfile.write("{}\t{}\n".format(word, cnt)) def main(): args = get_args() clean_text = get_and_clean_file(args.infile) cnt = Counter(clean_text) pretty_print_counts(cnt) pretty_write_counts(args.output, cnt) if __name__ == '__main__':

Previously...

You've been writing code to accomplish tasks

<u>New</u>

Classes Methods Attributes

Functions

But often...

Programs already exist that do something you want to do

Shell commands	Sequence assembly	<u>Alignment</u>
tail	velvet	bwa
head	trinity	bowtie
WC	abYss	lastz
cat		blast
		mafft
		muscle

Or, <u>any other external program</u> you want to run (from within your Python code)

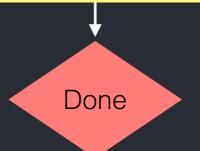
AKA Pipelining

(or building a pipeline)

Python program takes input

Sends to program

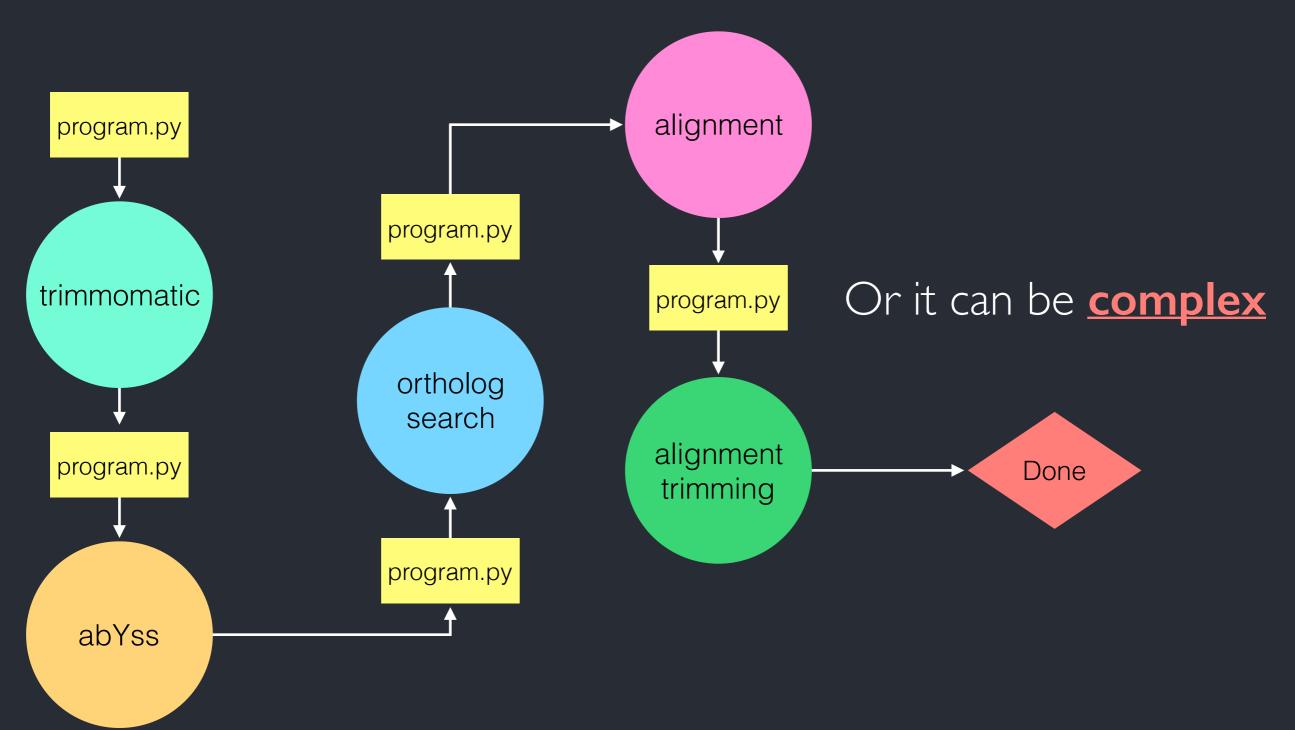
Python program does something with output



This can be simple

AKA Pipelining

(or building a pipeline)



But, how do you do all of this?

subprocess

A python (standard) module that allows you to

"spawn new processes, connect to their input/output/error pipes and obtain their return codes"

- python 3.5 doc

subprocess

What does **subprocess** require to make this magic happen?

Basically, that you have a "<u>scriptable</u>" program you want to run from python

More like command-line

Not so much GUI

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subprocess

What does **subprocess** require to make this magic happen?

Basically, that you have a "<u>scriptable</u>" program you want to run from python

Generally, that means a command-line program but <u>not always</u>

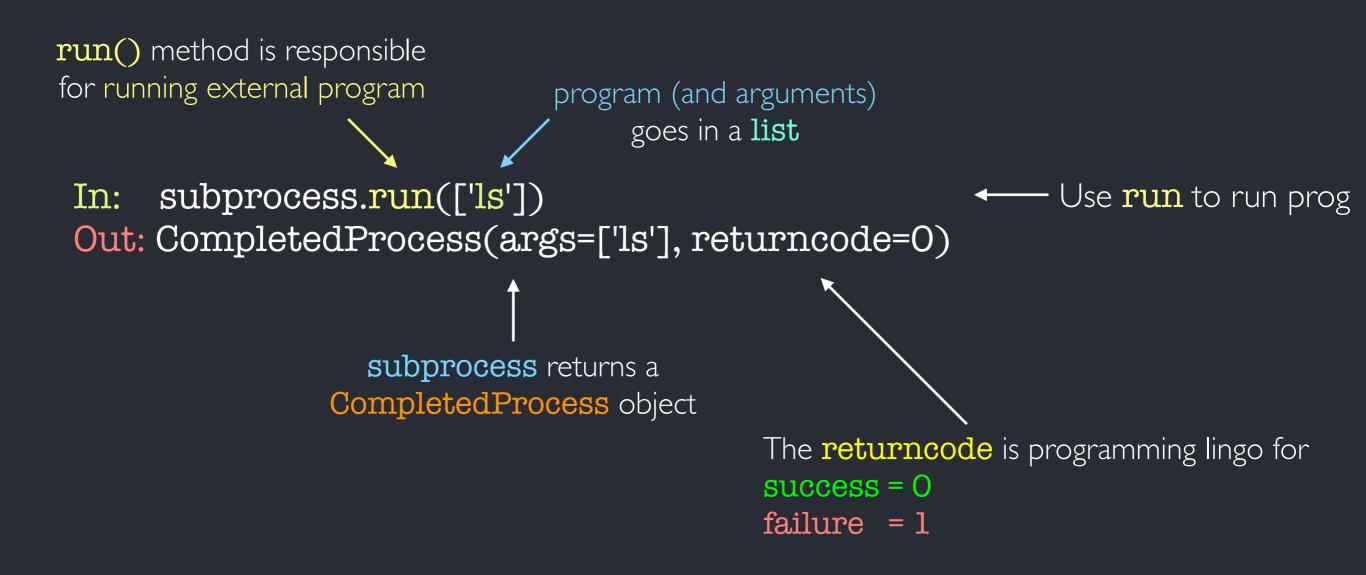
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Reset Load Save ARLEQUIN SETTINGS Calculation settings Genetic structure AMOVA Detecting loci under selection Population comparisons Population differentiation Genotype assignment Haplotype inference ELB algorithm ELInkage disequilibrium Hardy-Weinberg Pariwise linkage Mismatch distribution Molecular diversity indices Neutrality tests 	Project Structure Editor Settings Arlequin Configuration Project wizard Import data			
ARLEQUIN SETTINGS • Calculation settings • Genetic structure • AMOVA • Detecting loci under selection • Population comparisons • Population differentiation • Population differentiation • Population differentiation • Population difference • Palayorithm • EM algorithm • EM algorithm • Painwise linkage • Mismatch distribution • Neutrality tests	Settings	Detecting loci under selection from F-statistics		
	ARLEQUIN SETTINGS	✓ Use hierarchical island model Number of simulations: 50000 Number of demes to simulate (per group): 100 Number of groups to simulate: 10 Min. exp. heterozygosity: 0 Max. exp. heterozygosity: 1 Distance method for AMOVA computations —		

A good example is Arlequin

Has both GUI and command-line interaction

In: import subprocess

-----Import subprocess



In: import subprocess

In: my_process = subprocess.run(['ls'])

In: dir(my_process)

Out:

'args',

'check_returncode',

'returncode',

'stderr',

'stdout'

In: my_process.args

Out: ['ls']

In: my_process.check_returncode() Out:

In: print(my_process.check_returncode()) Out: None

> check_returncode() returns None if program ran successfully

We can store CompletedProcess object of subprocess in a variable

These are the CompletedProcess attributes & methods

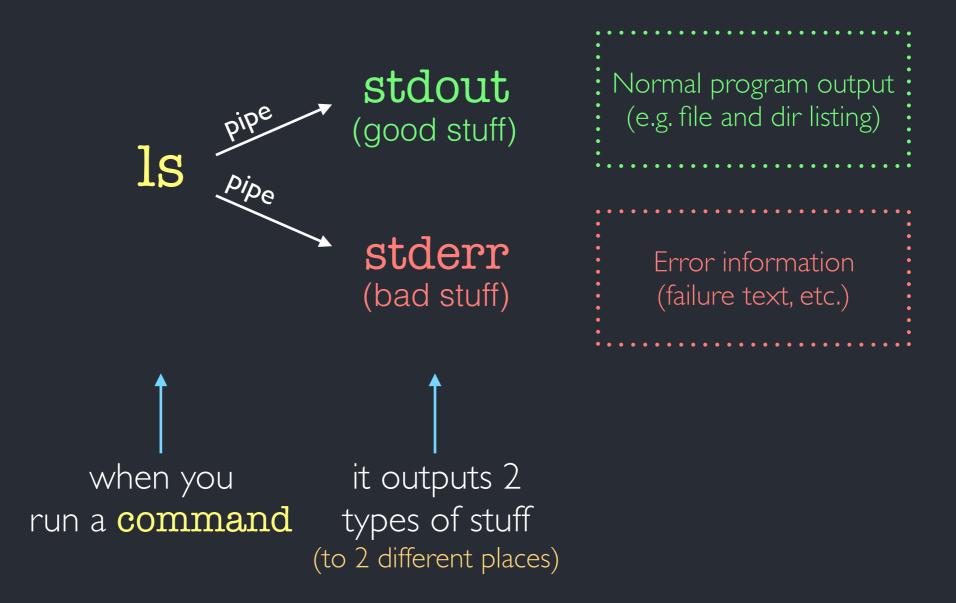
– We can access the **.args** attribute

We can use the check_returncode() method to make sure program ran



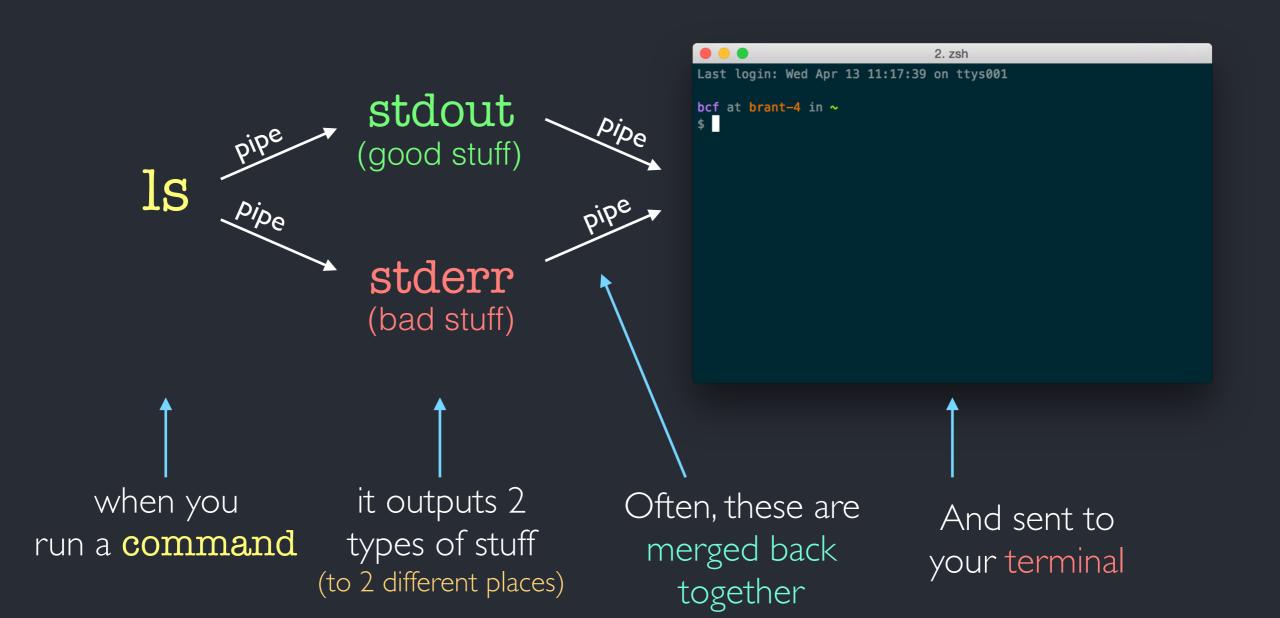
okay, that's great, but where's our output?

(a quick diversion into the land of pipes)



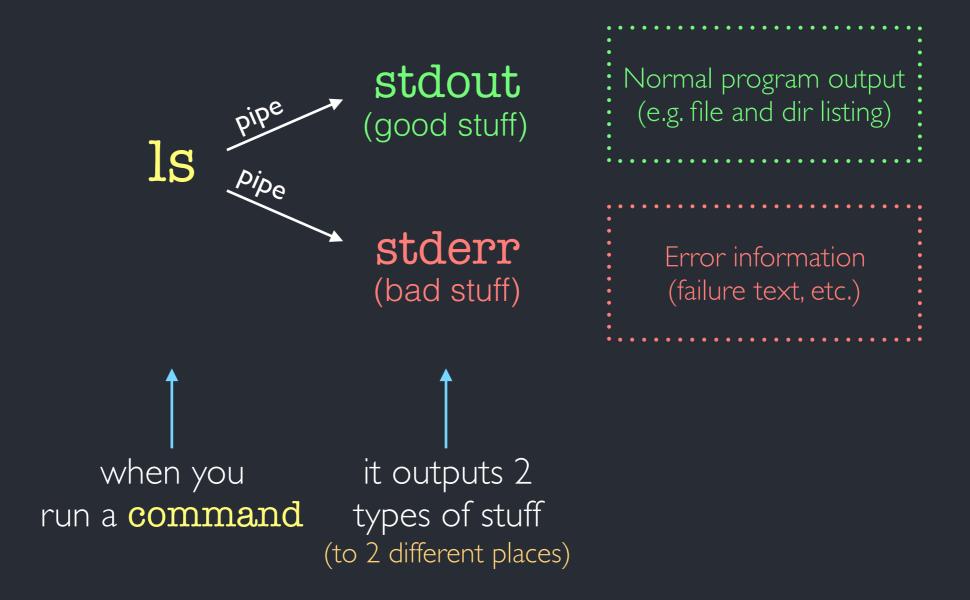
okay, that's great, but where's our output?

When you run a command from your shell



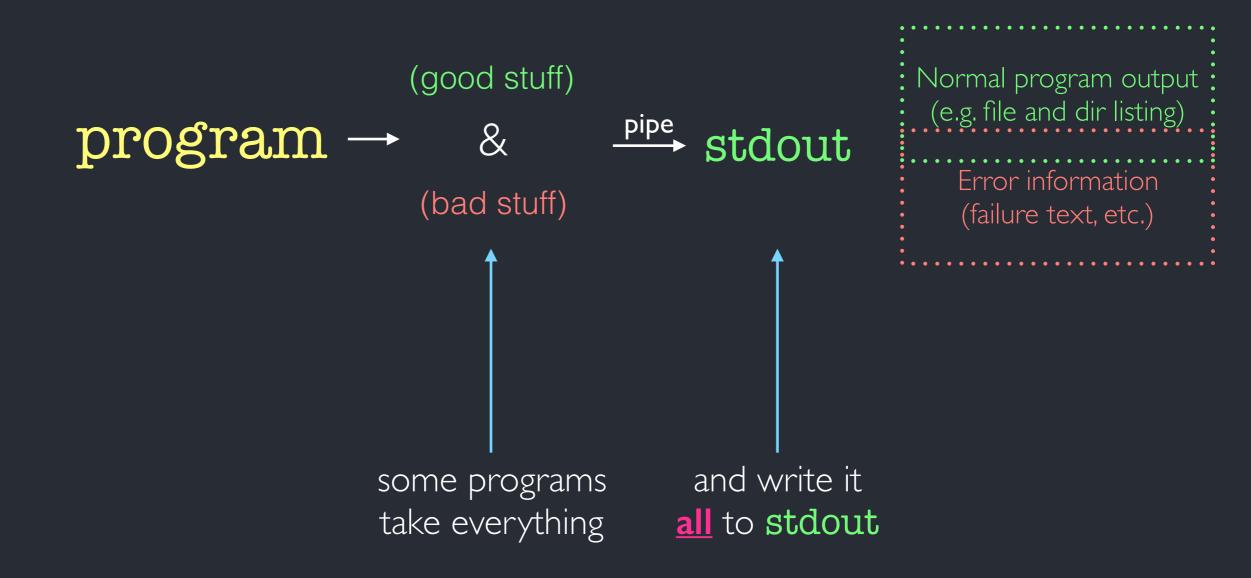
When you run a command from subprocess

The ideal situation



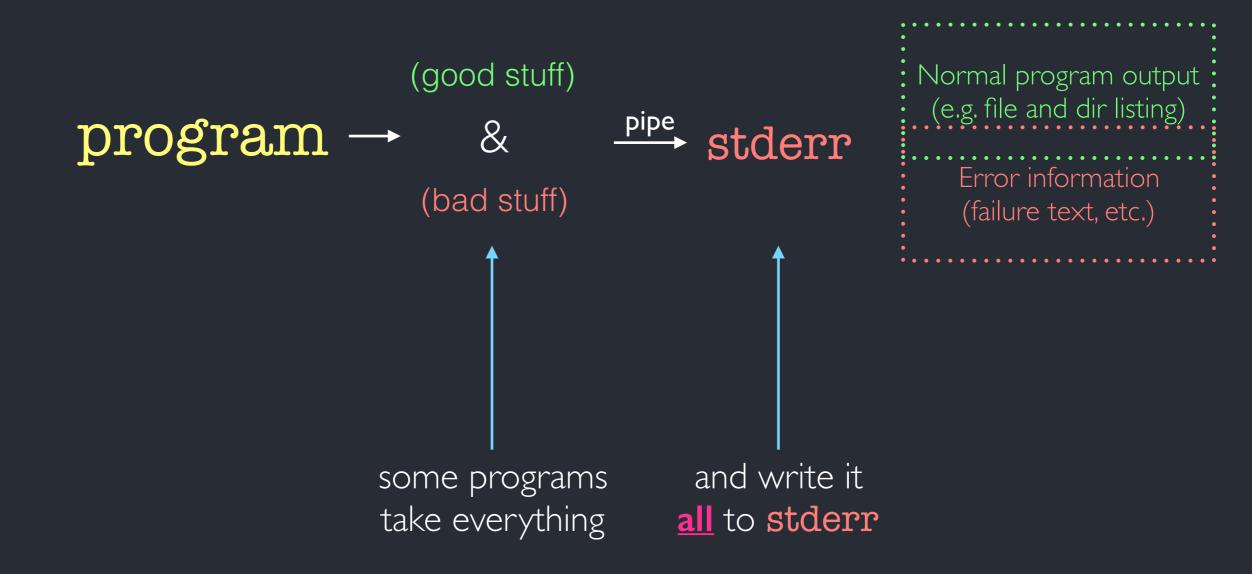
When you run a command from subprocess

But it's not always ideal...

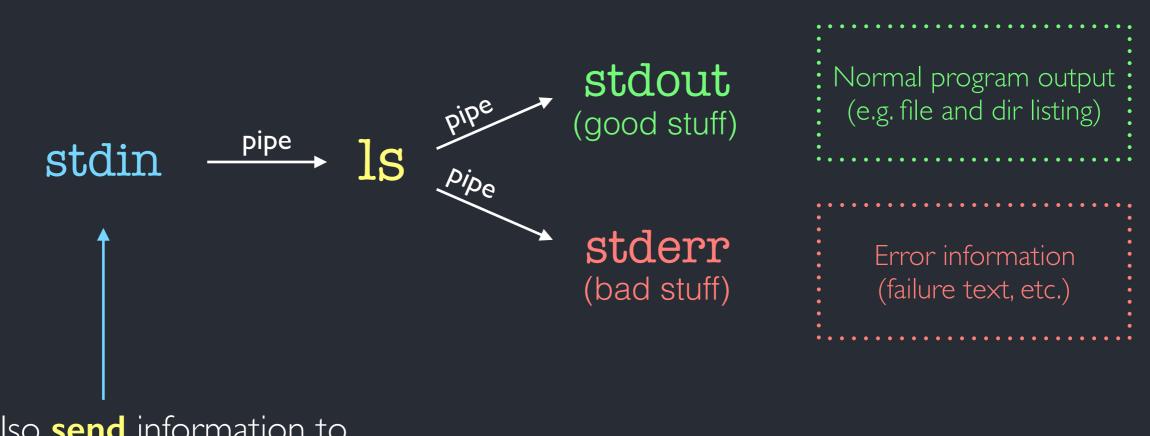


When you run a command from subprocess

But it's not always ideal...



One more little wrinkle...



you can also **send** information to <u>some programs</u> on **stdin**

So, generally, we have 3 types of things to worry about



And, the stdout is <u>sometimes</u> different from what the program can write to a file (although we can also store stdout and stdin in a file)

In: import subprocess

program (and arguments) goes in a **list** set keyword stdout to **subprocess.PIPE** We're only capturing **stdout**

In: my_proc = subprocess.run(['ls'], stdout=subprocess.PIPE)
In: my_proc.args
Out: ['ls']

In: my_proc.returncode Out: 0

In: my_proc.stdout

Out: b'Applications\nCreative Cloud Files
\nDesktop\nDocuments\nDownloads\nDropbox
\nDropbox (faircloth-lab)\nLibrary
\nMesquite_Support_Files\nMovies\nMusic
\nPictures\nPublic\nVirtual Machines
\nanaconda\nbin\ngit\ngithub-app\nnotebooks
\nsrc\ntmp\n'

See if program ran successfully

> stdout is returned as a **bytes** object, which is not the same as a string

> > (more in a minute)



Capture **stdout** and **stderr**

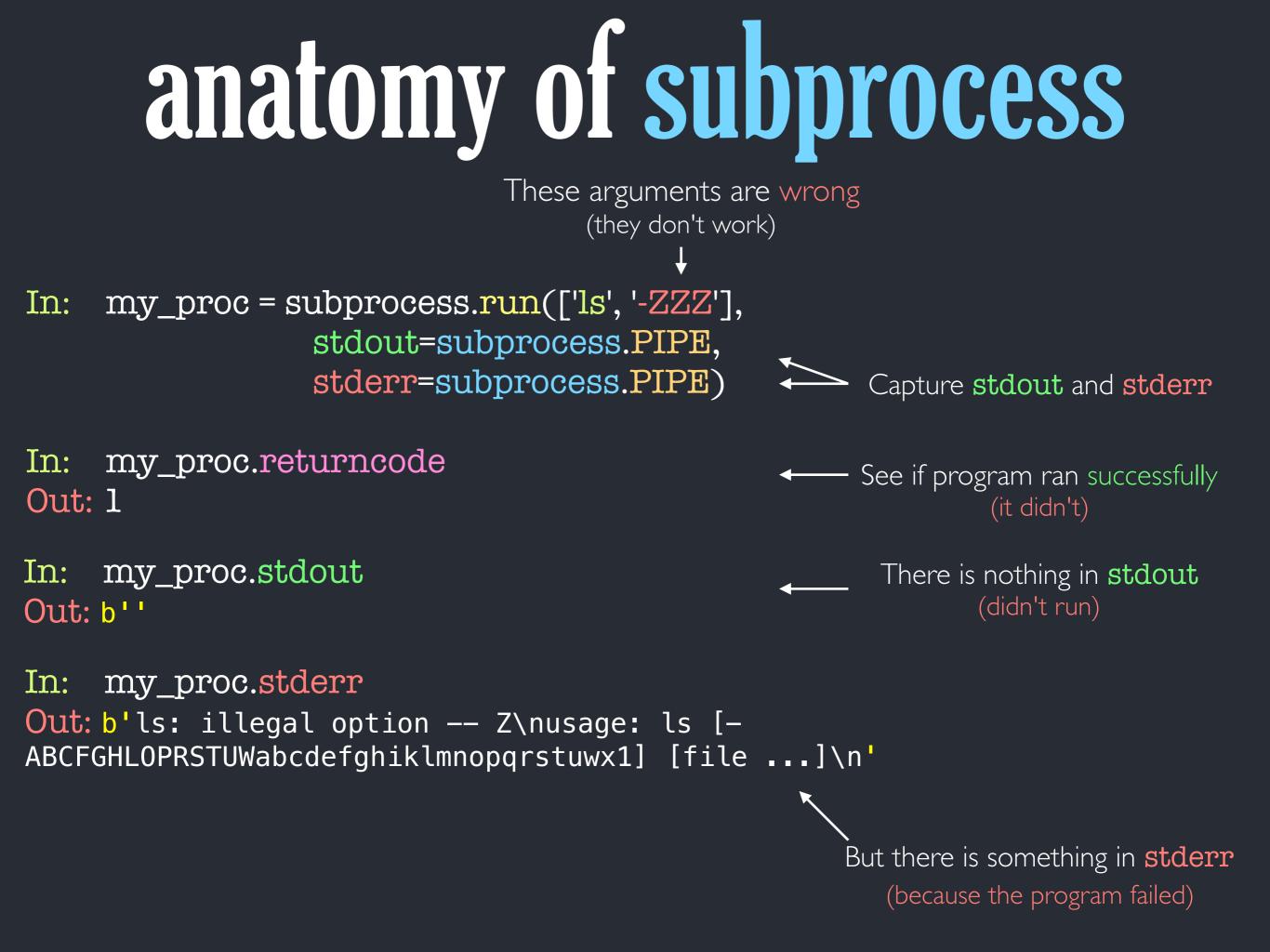
In: my_proc.returncode Out: 0

In: my_proc.stdout
Out: b'Applications\nCreative (...truncated...)'

In: my_proc.stderr Out: b'' See if program ran successfully (it did)

stdout is in the **stdout** attribute

____ There is nothing in **stderr** attribute (program ran successfully)



Can we do something with the **stdout**?



Capture **stdout** and **stderr**

In: my_proc.stdout

Out: b'Applications\nCreative Cloud Files\nDesktop \nDocuments\nDownloads\nDropbox\nDropbox (faircloth-lab) \nLibrary\nMesquite_Support_Files\nMovies\nMusic \nPictures\nPublic\nVirtual Machines\nanaconda\nbin\ngit \ngithub-app\nnotebooks\nsrc\ntmp\n'

In: type(my_proc.stdout) Out: bytes stdout is returned as a **bytes** object, which is not the same as a string

stdout is returned as a **bytes** object, which is not the same as a string

bytes objects are a primitive way to encode a string

Can we do something with the **stdout**?



Capture **stdout** and **stderr**

In: my_proc.stdout

Out: b'Applications\nCreative Cloud Files\nDesktop \nDocuments\nDownloads\nDropbox\nDropbox (faircloth-lab) \nLibrary\nMesquite_Support_Files\nMovies\nMusic \nPictures\nPublic\nVirtual Machines\nanaconda\nbin\ngit \ngithub-app\nnotebooks\nsrc\ntmp\n'

In: my_proc.stdout.split("\n") Out: TypeError: a bytes-like object is required, not 'str' And bytes objects need to be encoded to string objects byte

stdout is returned as a **bytes** object, which is not the same as a **string**

This fails, because my_proc.stdout is a bytes object, not a string

Two ways around the problem

Method I

my_proc.stdout.decode("utf-8").split("\n") \leftarrow Use the bytes object's In: Out: **decode()** method to convert ['Applications', it to "utf-8" (or other) encoding 'Creative Cloud Files', 'Desktop', 'Documents', 'Downloads', 'Dropbox', 'Dropbox (faircloth-lab)', 'Library', 'Mesquite_Support_Files', 'Movies', (...truncated...) **''**]

Two ways around the problem

Method 2

Pass the universal_newlines argument to — subprocess.run()

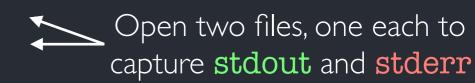
In: type(my_proc.stdout) Out: str

```
In: my_proc.stdout.split("\n")
Out:
['Applications',
 'Creative Cloud Files',
 'Desktop',
 'Documents',
 'Downloads',
 'Dropbox',
(..truncated..)
'''
```

_ And, we can easily split a **string**

Pipes are nice, but we may want to write **stdout/stderr** to a file (particularly when there is a **lot** of it - our pipes can get full)

In: with open('stdout.txt', 'w') as stdout_file: with open('stderr.txt', 'w') as stderr_file: my_proc = subprocess.run(['ls'], stdout=stdout_file, stderr=stderr_file, universal_newlines=True)



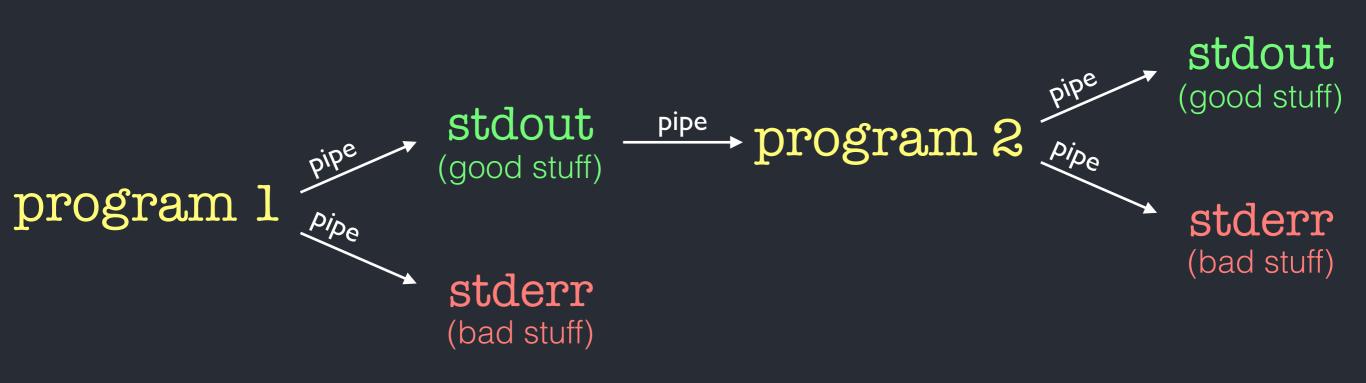
In: print(open('stdout.txt', 'r').read())
Out:
Applications
Creative Cloud Files
Desktop
Documents
Downloads
Dropbox
(...truncated...)

The lines that <u>were</u> going to our **stdout** pipe are now being written to a file

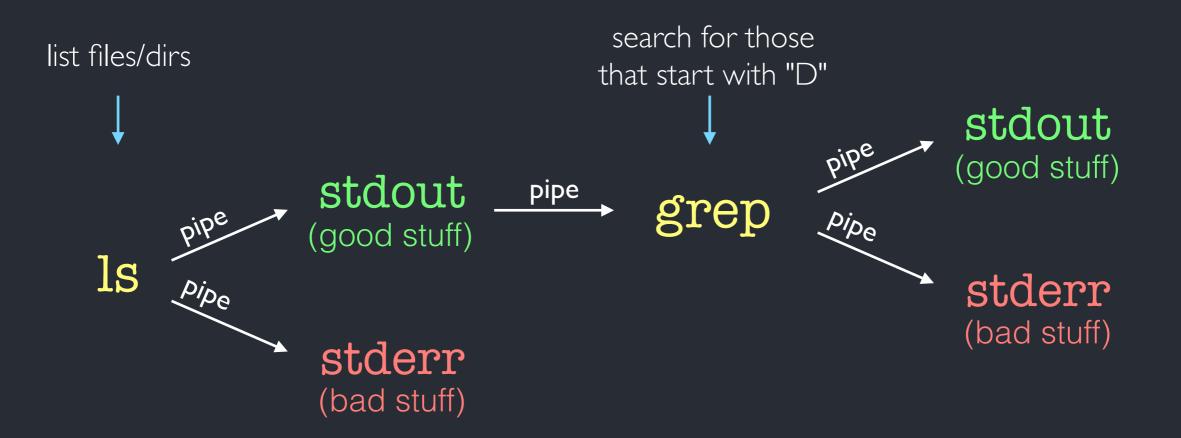
Same for **stderr** (but there's nothing there)

We can now do anything we want with these file (parse them, etc.)

What if we want to chain several programs together ?



What if we want to chain several programs together ?

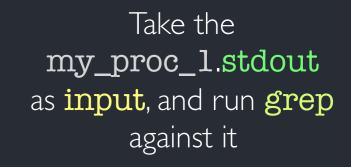


or, as we would type it in the shell

ls | grep "^D"

Chaining programs together by pipes

Run ls, send the output to stdout



print(my_proc_2.stdout)

Out: b'Desktop\nDocuments\nDownloads\nDropbox\nDropbox (faircloth-lab)\n'

stdout is returned as a **bytes** object

Chaining programs together by pipes (with string output)

 We need to specify **universal_newlines** in both processes for **string** output

print(my_proc_2.stdout)

Out: Desktop Documents Downloads Dropbox Dropbox (faircloth-lab)

stdout is returned as a **string**

What about programs with lots of parameters?

e.g.

java -jar /usr/bin/gatk -T UnifiedGenotyper -nt 12 -R genome.fasta -I genome.bam -gt_mode DISCOVERY -glm INDEL

You make a really long list of all the parameters...

Each part of a parameter is a list item

Numbers **must** be converted to strings

anatomy of subprocess What about programs with lots of parameters?

e.g.

java -jar /usr/bin/gatk -T UnifiedGenotyper -nt 12 -R genome.fasta -I genome.bam -gt_mode DISCOVERY -glm INDEL

In: command = ['java', '-jar', '/usr/bin/gatk', '-T', 'UnifiedGenotyper', '-nt', '12', '-R', 'genome.fasta', '-I', 'genome.bam', '-gt_mode', 'DISCOVERY', '-glm', 'INDEL']

Because this is just a **list**, you can make the list and place it in a variable...

Then, pass the variable to subprocess.run

What about programs with lots of parameters?

e.g.

java -jar /usr/bin/gatk -T UnifiedGenotyper -nt 12 -R genome.fasta -I genome.bam -gt_mode DISCOVERY -glm INDEL

```
In: import shlex
```

```
In: shlex.split('java -jar /usr/bin/gatk -T UnifiedGenotyper
-nt 12 -R genome.fasta -I genome.bam -gt_mode DISCOVERY -glm
INDEL')
```

```
You can also use
the shlex module
to help you split
<u>complex</u> command
line statements
```

Then, use the list that
 shlex makes as your
 input

```
Out:
['java',
 '-jar',
 '/usr/bin/gatk',
 '-T',
 'UnifiedGenotyper',
 '-nt',
 '12',
 '-R',
 'genome.fasta',
 '-I',
 'genome.bam',
 '-gt_mode',
 'DISCOVERY',
 '-qlm',
 'INDEL']
```