

# Introduction To Python Programming

## II: How to Use It

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# Today:

- **Use a python module**
  - Example: Generate random values
- **Install a Python package as a user**
  - Often useful when installing software
- **Exercise: Read a file, filter and output another file**
  - Reading and writing files
  - splitting lines and finding bits of information
- **Create a Slurm job and submit from a Python script**
  - Create text file from template ("here" document)
  - run system commands from inside a script

# Use a Python module

We will use the random module

```
import random                # import the random module
random.randint(0,10)         # a random integer in [0, 10]
2

import random as rn          # give module a shorter name
rn.randint(0,10)
9

from random import randint   # import a module function
randint(0,10)                # directly
6

from random import *         # import all functions - dangerous
```

# Make your own Python module

- Modules are just Python files
  - You can organize and import your own code

main.py

```
# use mymodule

import mymodule as mm
print(mm.double(2))
```

mymodule.py

```
# mymodule example

def double(x):
    return x*2
```

Use modules to:

- Organize your program
  - Split up a large program into modules with related code
  - Makes organization and debugging easier
- Reuse useful code
  - Example: data analysis and graphing code
  - Build a library of useful tools for interactive analysis of your data sets

# Python *packages*

- Python Packages: a directory with
  - One or more module files, and
  - An `__init__.py` file
    - It can be empty
    - It's run when you load the package

```
packagename/  
├── __init__.py  
├── module1.py  
└── module2.py  
    ...
```

You don't often write packages yourself

- Useful for large projects
- When you want to share a package in public

# Install a Python package

Problem: You want to install a program in Deigo.

The instructions tell you to run:

```
pip install <some package>
```

or you download it, unpack, then run:

```
python setup.py install
```

But **this fails** with an error about not having permission

**What do you do?**

# Install a Python package

## 1. Load our Python module

Load python 3:

```
$ module load python/3.7.3
```

Use 'pip3' and 'python3'

Use our python modules,  
never the system Python

# Install a Python package

## 1. Load our Python module

Load python 3:

```
$ module load python/3.7.3
```

Use 'pip3' and 'python3'

Use our python modules,  
never the system Python

Packages are at PyPi:

<https://pypi.org/>

Over **300 000** (!) projects

Anything you need may already  
be available there



# Install a Python package in your home

## 2. Install locally using the '--user' option

for pip3:

```
$ pip3 install --user <package>
```

for setup.py:

```
$ python3 setup.py --user
```

This installs the package into your home.

Programs go to:

`~/.local/bin`

packages go to:

`~/.local/lib/python3.7/site-packages`

this depends on your Python version

# Install a Python package in your home

## 2. Install locally using the '--user' option

Example:

```
$ pip3 install --user cli-weather
```

```
$ ~/.local/bin/cli-weather city Naha -f
```

This installs the package into your home.

Programs go to:

`~/.local/bin`

packages go to:

`~/.local/lib/python3.7/site-packages`

this depends on your Python version

# Install a Python package in /apps

You can choose the installation directory with PYTHONUSERBASE:

```
$ export PYTHONUSERBASE="/apps/unit/UnitU"  
$ pip3 install --user <package>
```

Programs go to:

/apps/unit/UnitU/bin

packages go to:

/apps/unit/UnitU/lib/python3.7/site-packages/

Remember this path  
←

# Install a Python package in /apps

## 3. Tell Python where the local library and binary is

Add the path to site-packages to PYTHONPATH:

```
export PYTHONPATH="/apps/unit/UnitU/lib/python3.7/site-packages:$PYTHONPATH"
```

Add the path to bin to PATH

```
export PATH="/apps/UnitU/bin:$PATH"
```

# Install a Python package in /apps

## 3. Tell Python where the local library is

Add the path to site-packages to PYTHONPATH:

```
export PYTHONPATH="/apps/unit/UnitU/lib/python3.7/site-packages:$PYTHONPATH"
```

separate paths  
with ':'

set PYTHONPATH to

our new path

followed by whatever is  
already in PYTHONPATH

export makes PYTHONPATH available to the entire  
shell environment

# Exercise:

## Convert a file from one format to another

We will convert a FASTA file from one format to another

- "Fasta" is a bioinformatics sequence file format
- This kind of problem shows up in any field; the specific file format here is not important.

# Exercise:

## Convert a file from one format to another

We will convert a FASTA file from one format to another

- "Fasta" is a bioinformatics sequence file format
- This kind of problem shows up in any field; the specific file format here is not important.

Copy the session data files:

```
cp -r /apps/share/training/Python/session2 .
```

# Exercise:

## Convert a file from one format to another

### Input file:

```
>NODE_130_length_9368_cov_2.522454  
GCGCCGTTTTTCATA...  
  
>NODE_357_length_6506_cov_2.493338  
GCCTCACCTGTGGAA...
```

### Output file:

```
>sequence_number_1_[cov=2.52]  
GCGCCGTTTTTCATA...  
  
>sequence_number_2_[cov=2.49]  
GCCTCACCTGTGGAA...
```

the gene data is just copied right over

Copy the session data files:

```
cp -r /apps/share/training/Python/session2 .
```



# Exercise:

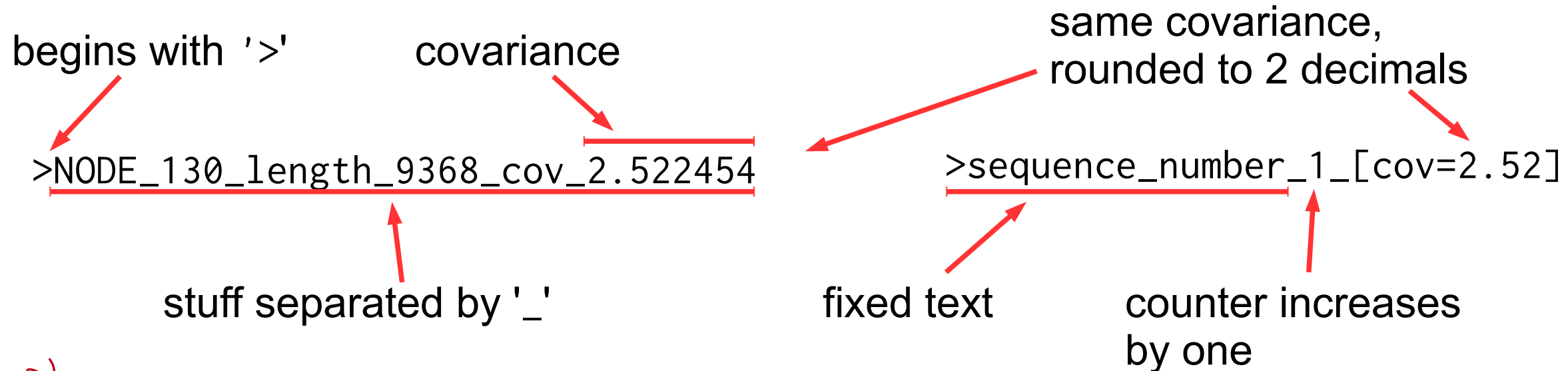
## Convert a file from one format to another

### Input file:

```
>NODE_130_length_9368_cov_2.522454  
GCGCCGTTTTTCATA...  
>NODE_357_length_6506_cov_2.493338  
GCCTCACCTGTGGAA...
```

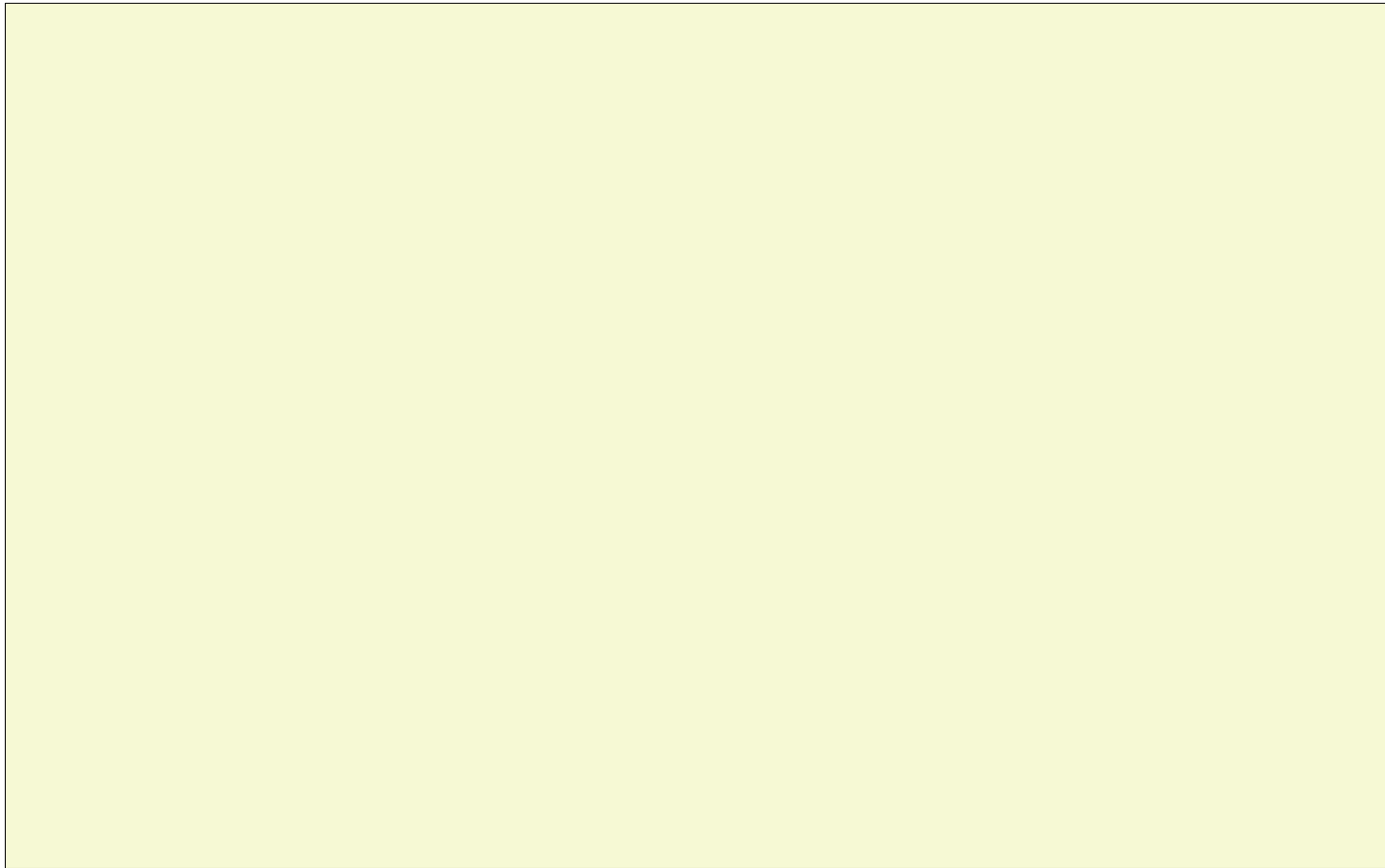
### Output file:

```
>sequence_number_1_[cov=2.52]  
GCGCCGTTTTTCATA...  
>sequence_number_2_[cov=2.49]  
GCCTCACCTGTGGAA...
```



# Exercise:

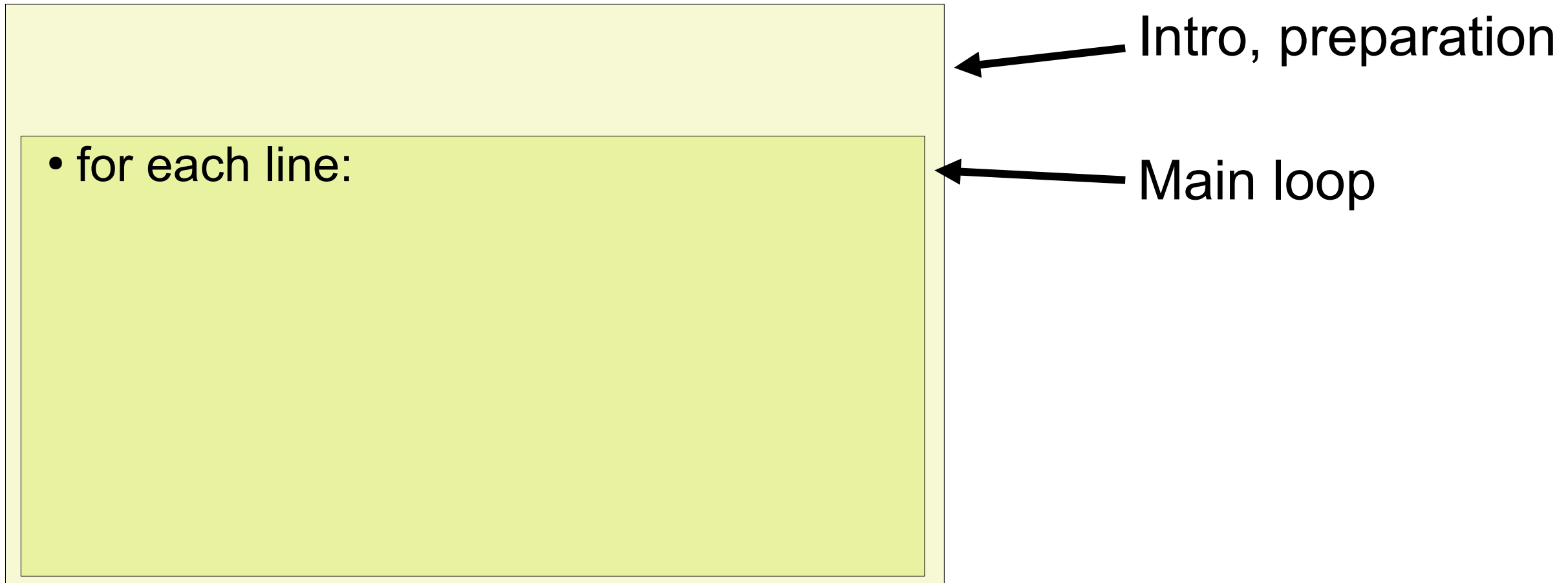
## Convert a file from one format to another



← Our program

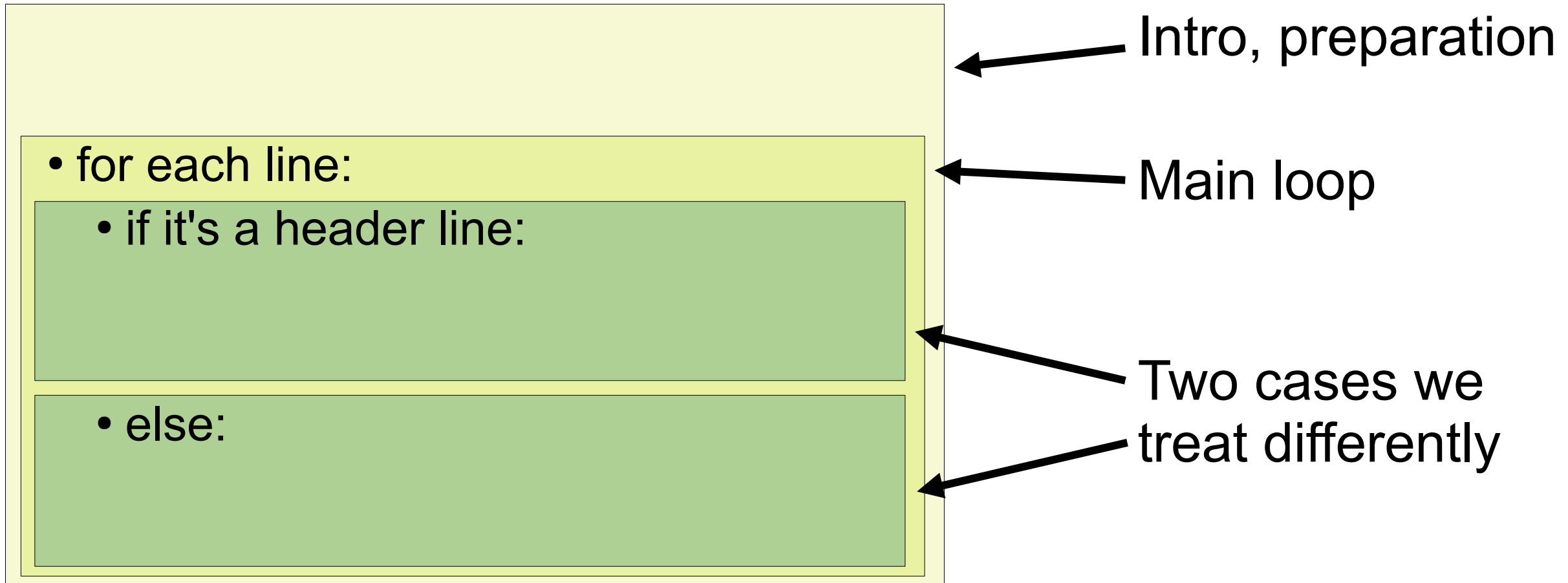
# Exercise:

## Convert a file from one format to another



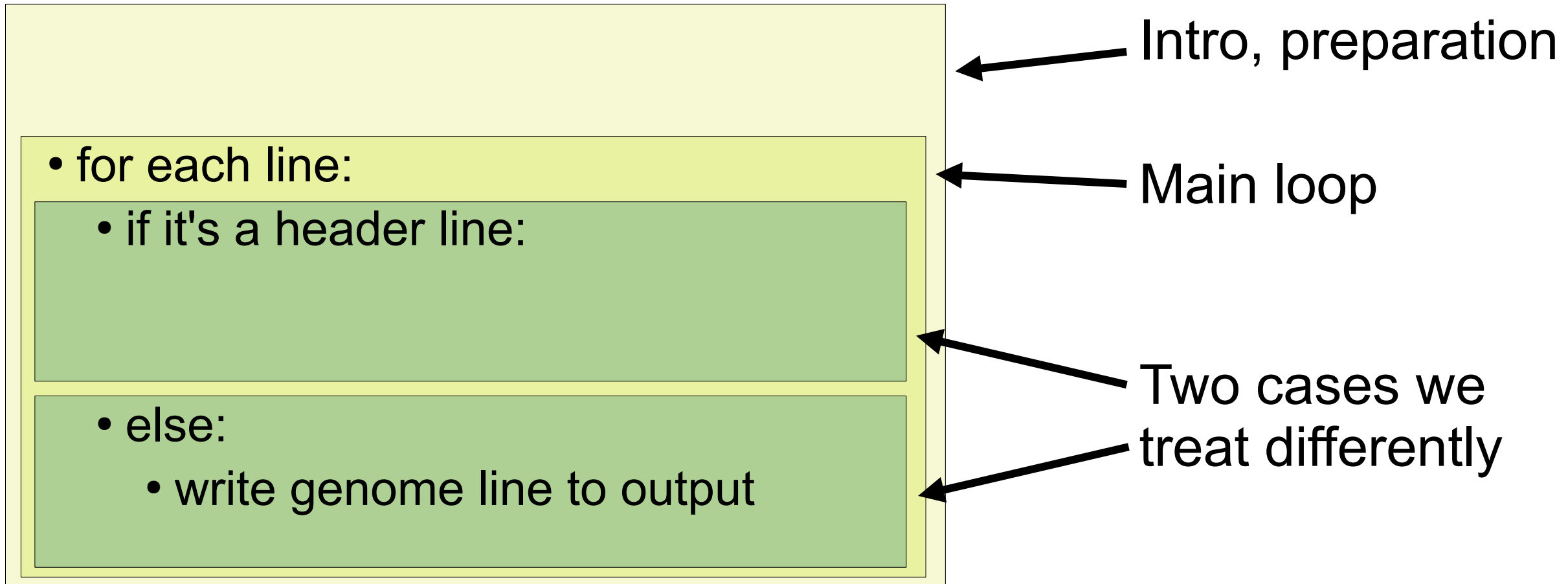
# Exercise:

## Convert a file from one format to another



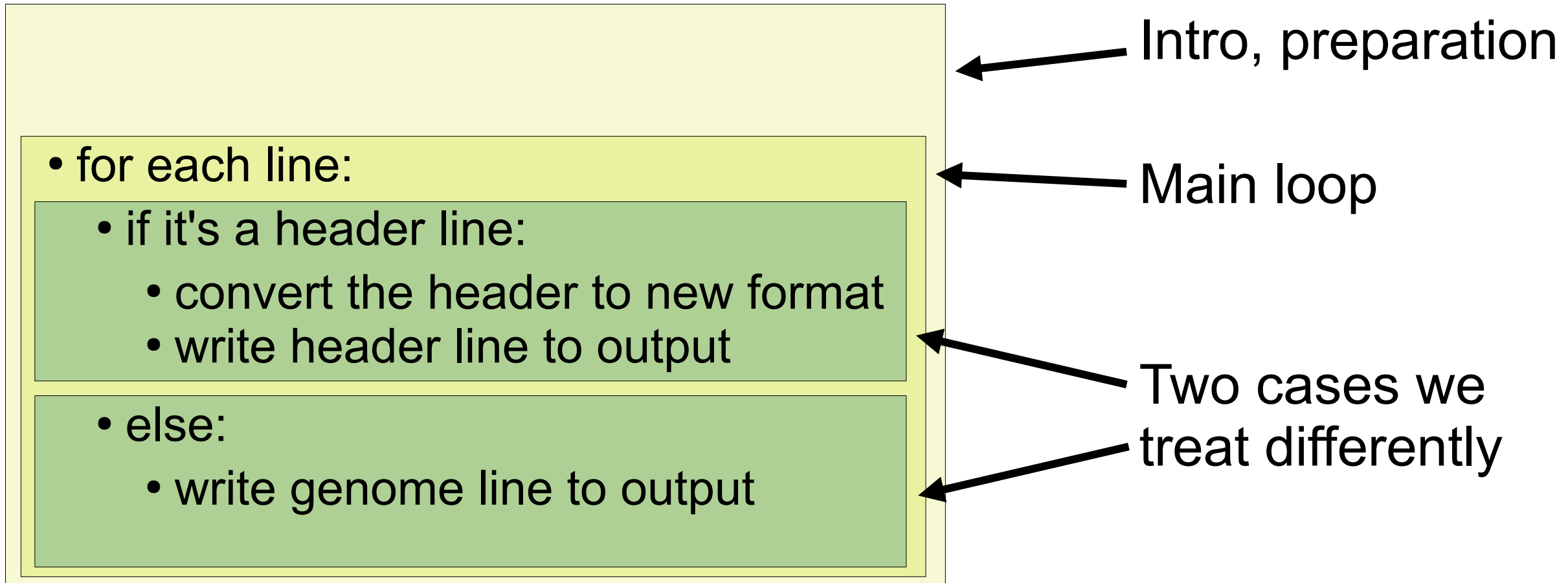
# Exercise:

## Convert a file from one format to another



# Exercise:

## Convert a file from one format to another



# Exercise:

## Convert a file from one format to another

- get input and output file names
- open input and output files

- for each line:

- if it's a header line:

- convert the header to new format
- write header line to output

- else:

- write genome line to output

Intro, preparation

Main loop

Two cases we  
treat differently

# Exercise:

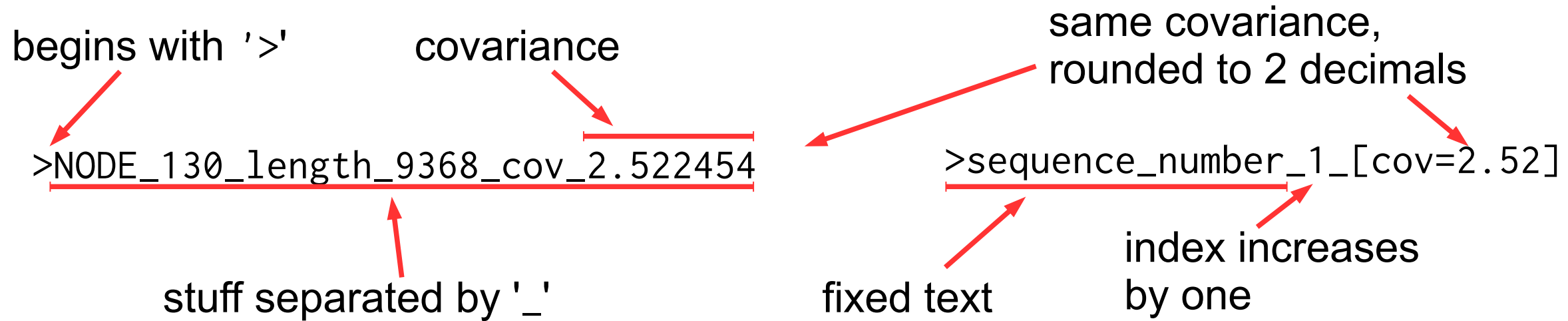
## Convert a file from one format to another

- get input and output file names
- open input and output files
- for each line:
  - if it's a header line:
    - convert the header to new format
    - write header line to output
  - else:
    - write genome line to output

Questions: How do we ...

- convert the header?
- open files?
- read and write from files?
- get our filenames?





## Convert the header: write a function

- take as input an index value "index", and input header text line "line"
- output a new header line (using "return")
- see `string.split()` - split line into a list
  - `split()` splits a line between spaces
  - `split('_')` splits a line between '\_'

```
def myfunction(a,b,c):  
    ...  
    return result  
  
"string: {} bipp".format(value)
```

begins with '>'      covariance

>NODE\_130\_length\_9368\_cov\_2.522454

stuff separated by '\_'

same covariance,  
rounded to 2 decimals

>sequence\_number\_1\_[cov=2.52]

fixed text      index increases  
by one

## Convert the header: write a function

- take as input an index value "index", and input header text line "line"

- output a new header line (using "return")
- see `string.split()` - split line into a list
  - `split()` splits a line between spaces
  - `split('_')` splits a line between '\_'

```
def convert_header(index, line):  
  
    split_line = line.split('_')  
    cov = float(split_line[-1])  
    return '>sequence_number_{0}_[cov={1:.2f}]\n'.format(index, cov)
```

# Exercise:

## Convert a file from one format to another

- Opening files: use the "with" syntax

```
with open('filename', 'r') as f:                # open filename for reading
    <do stuff with filehandle f>

# open two files at once:

with open('file1', 'r') as fin, open('file2', 'w') as fout:
    <read from fin, write to fout>
```

# Exercise:

## Convert a file from one format to another

- read and write from files:

```
with open('filename', 'r') as fin:           # open filename for reading
    all_lines = fin.readlines()              # read all lines in file

with open('filename', 'r') as fin:           # open filename for reading
    for line in fin:
        <do something with each line>

with open('filename', 'w') as fout:
    fout.writelines(lines)                  # write a line or a list
                                           # of lines
```

# Exercise:

## Convert a file from one format to another

Our main loop:

```
infile = 'inputfile.fa'
outfile = 'output.txt'

with open(infile, 'r') as fin, open(outfile, 'w') as fout:
    for line in fin:
```

# Exercise:

## Convert a file from one format to another

Our main loop:

```
infile = 'inputfile.fa'
outfile = 'output.txt'

with open(infile, 'r') as fin, open(outfile, 'w') as fout:

    for line in fin:
        if line[0] == '>':

            else:
```

# Exercise:

## Convert a file from one format to another

Our main loop:

```
infile = 'inputfile.fa'
outfile = 'output.txt'

with open(infile, 'r') as fin, open(outfile, 'w') as fout:

    for line in fin:
        if line[0] == '>':

            else:
                fout.writelines(line)
```

# Exercise:

## Convert a file from one format to another

Our main loop:

```
infile = 'inputfile.fa'
outfile = 'output.txt'

with open(infile, 'r') as fin, open(outfile, 'w') as fout:

    for line in fin:
        if line[0] == '>':
            outline = convert_header(index, line)
            fout.writelines(outline)
        else:
            fout.writelines(line)
```



# Exercise:

## Convert a file from one format to another

Our main loop:

```
infile = 'inputfile.fa'
outfile = 'output.txt'
index = 1

with open(infile, 'r') as fin, open(outfile, 'w') as fout:

    for line in fin:
        if line[0] == '>':
            outline = convert_header(index, line)
            fout.writelines(outline)
            index += 1
        else:
            fout.writelines(line)
```

# Exercise:

## Convert a file from one format to another

Get the input and output files: use the 'sys' module:

```
import sys

infile = sys.argv[1]
outfile = sys.argv[2]
```

Run like:

```
$ python3 convfasta.py inputfile.fa output.txt
```

# Exercise:

## Convert a file from one format to another

Make our program a "real" program

1. Tell linux that python3 knows what to do with it:

```
#!/bin/env python3
import sys
...
```

Run like:

```
$ ./convfasta.py input.fa out.txt
```

2. Make it executable:

```
$ chmod +x convfasta.py
```

# Generate and run a Slurm script from Python

Take a look at this Slurm script:

```
#!/bin/bash

#SBATCH -t 1:00
#SBATCH --mem=2G

tail mylittlefile.txt
```

What if we wanted to choose the input file when we submit?

Let's write a Python script that:

- 1) gets the filename
- 2) creates a multi-line string with this Slurm script and the filename filled in
- 3) saves it to a file
- 4) Runs it with sbatch

we already know how to do these!

# Generate and run a Slurm script from Python

Remember **multi-line strings**  
and format substitutions:

```
s='''#!/bin/bash

#SBATCH -t 1:00
#SBATCH --mem=2G

tail {}
'''

s.format(...)
```

**Run a command:**

```
import subprocess as sb

# just run a command
sb.run(['sbatch', 'myscript.slurm'])

# run command, get the output
ret=sb.run(..., stdout=sb.PIPE,
            universal_newlines=True)

# output as a list
ret.stdout.split()
```

# The final script

```
import sys
import subprocess as sb
sfile = sys.argv[1]           # Get first argument

script='''#!/bin/bash
#SBATCH -t 10:00
#SBATCH --mem=2G
tail {}
'''

with open('myscript.slurm', 'w') as f:
    f.writelines(script.format(sfile))    # substitute and write

sb.run(['sbatch', 'myscript.slurm'])     # start job
```

# The final script - get the job ID

```
import sys
import subprocess as sb
sfile = sys.argv[1]           # Get first argument

script='''#!/bin/bash
#SBATCH -t 10:00
#SBATCH --mem=2G
tail {}
'''

with open('myscript.slurm', 'w') as f:
    f.writelines(script.format(sfile))    # substitute and write

ret = sb.run(['sbatch', 'myscript.slurm'],
             stdout=sb.PIPE, universal_newlines=True)
jobid = ret.stdout.split()[3]
print(jobid)
```

# Generate and run a Slurm script from Python

**WARNING!!!!!!**

**Don't** use this to submit lots and lots of jobs!!!!

you can break Slurm for everyone  
and we may need to kill your jobs if you do

*Always* use Slurm Array jobs for this



# Next Session

Let's get Scientific!

- Numpy and Scipy
  - The workhorses for all scientific Python programming
- Matplotlib
  - Plot your data