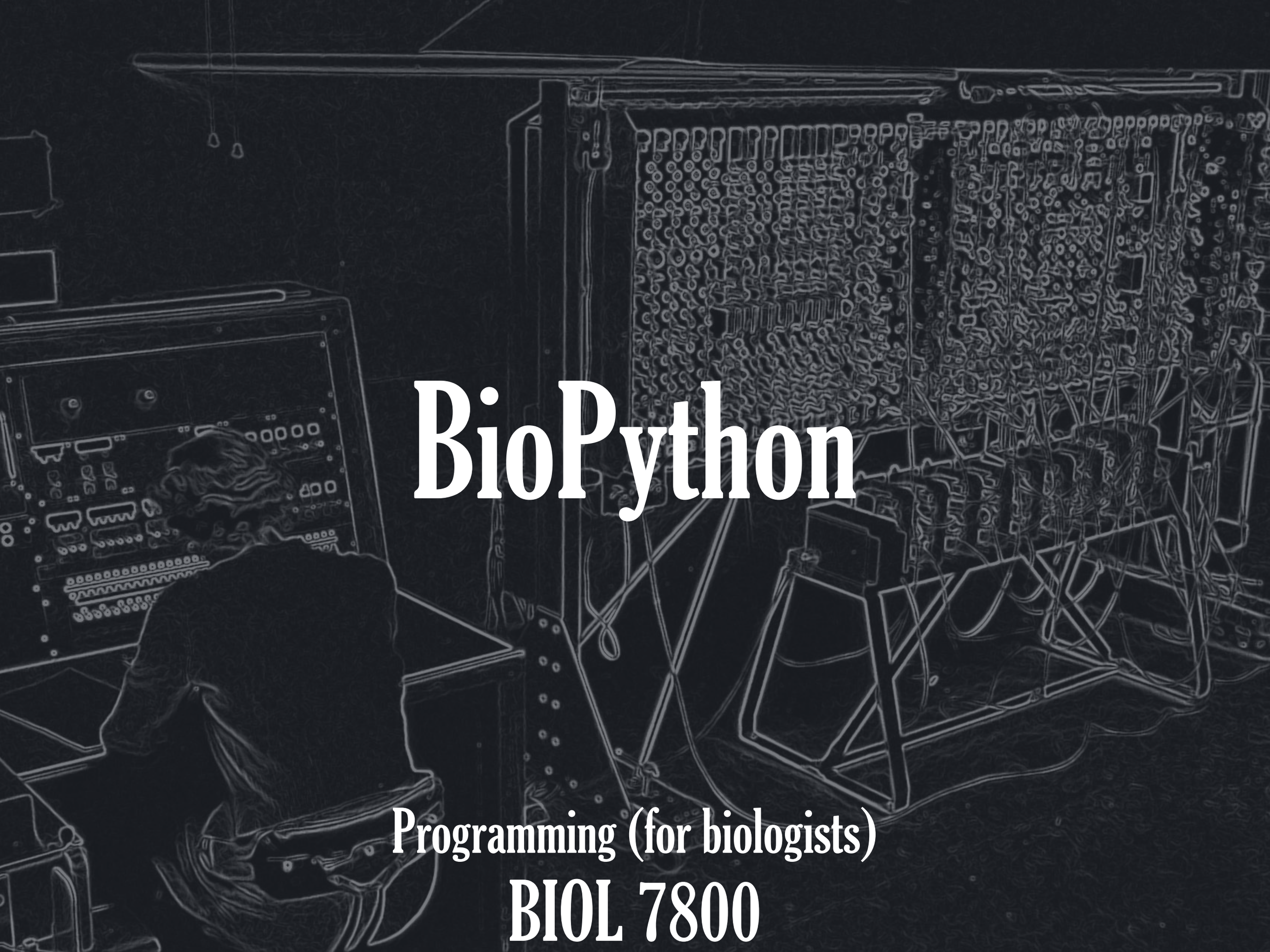


BioPython

Programming (for biologists)

BIOL 7800

3rd Party Libraries

But, Python can be extended with many
external ("third-party") libraries

BioPython

Sequence data
Alignment data
NCBI Interaction

NumPy

Data matrices
Data arrays
array-based computation

Pandas

Data arrays
Data "frames"
frame-based computation

SciPy

Numerical routines
Numerical optimization
Integration

MatPlotLib

Plotting

Requests

Interaction with web-APIs
HTTP requests

3rd Party Libraries

But, Python can be extended with many
external ("third-party") libraries

In many cases, you can easily
manage these libraries using conda

To search for libraries

```
conda search <libraryname>
```

To get info on library

```
conda info <libraryname>
```

To install libraries

```
conda install <libraryname>
```

To remove library

```
conda remove <libraryname>
```

3rd Party Libraries

1. zsh

```
bcf at brant-4 in ~
$ conda search biopython
Fetching package metadata: ......
biopython                 1.60             np17py27_0  defaults
                          1.60             np17py26_0  defaults
                          1.60             np16py27_0  defaults
                          1.60             np16py26_0  defaults
                          1.60             np15py27_0  defaults
                          1.60             np15py26_0  defaults
                          1.61             np17py27_0  defaults
                          1.61             np17py26_0  defaults
                          1.61             np16py27_0  defaults
                          1.61             np16py26_0  defaults
                          1.61             np15py27_0  defaults
                          1.61             np15py26_0  defaults
                          1.62             np17py27_0  defaults
                          1.62             np17py26_0  defaults
                          1.62             np16py27_0  defaults
                          1.62             np16py26_0  defaults
                          1.63             np18py34_0  defaults
                          1.63             np18py33_0  defaults
                          1.63             np18py27_0  defaults
                          1.63             np18py26_0  defaults
                        . 1.63             np17py27_0  defaults
                          1.63             np17py26_0  defaults
                          1.64             np19py34_0  defaults
                          1.64             np19py33_0  defaults
                          1.64             np19py27_0  defaults
                          1.64             np19py26_0  defaults
                          1.64             np18py34_0  defaults
                          1.64             np18py33_0  defaults
                          1.64             np18py27_0  defaults
                          1.64             np18py26_0  defaults
                          1.65             np19py35_0  defaults
                          1.65             np19py34_0  defaults
                          1.65             np19py33_0  defaults
                          1.65             np19py27_0  defaults
                          1.65             np19py26_0  defaults
                          1.65            np110py35_0  defaults
                          1.65            np110py34_0  defaults
                          1.65            np110py27_0  defaults
                        * 1.66            np110py35_0  defaults
                          1.66            np110py34_0  defaults
                          1.66            np110py27_0  defaults
```

Installed version

`conda search <libraryname>`

Searches for particular package

3rd Party Libraries

```
1. zsh
bcf at brant-4 in ~
$ conda info biopython
Fetching package metadata: ......

biopython 1.60 np17py27_0
--------------------------
file name   : biopython-1.60-np17py27_0.tar.bz2
name        : biopython
version     : 1.60
build number: 0
build string: np17py27_0
channel     : defaults
size        : 1.6 MB
date        : 2014-08-22
license     : BSD-like
license_family: BSD
md5         : 3de47cd4189029e828a7d7337032d99a
installed environments:
dependencies:
    numpy 1.7*
    python 2.7*

biopython 1.60 np17py26_0
--------------------------
file name   : biopython-1.60-np17py26_0.tar.bz2
name        : biopython
version     : 1.60
build number: 0
build string: np17py26_0
channel     : defaults
size        : 1.6 MB
date        : 2014-08-22
license     : BSD-like
license_family: BSD
md5         : 08004e151a726994e06e768ae7445c53
installed environments:
dependencies:
    numpy 1.7*
    python 2.6*
```

conda info <libraryname>

Shows info for packages

3rd Party Libraries

1. python2.7

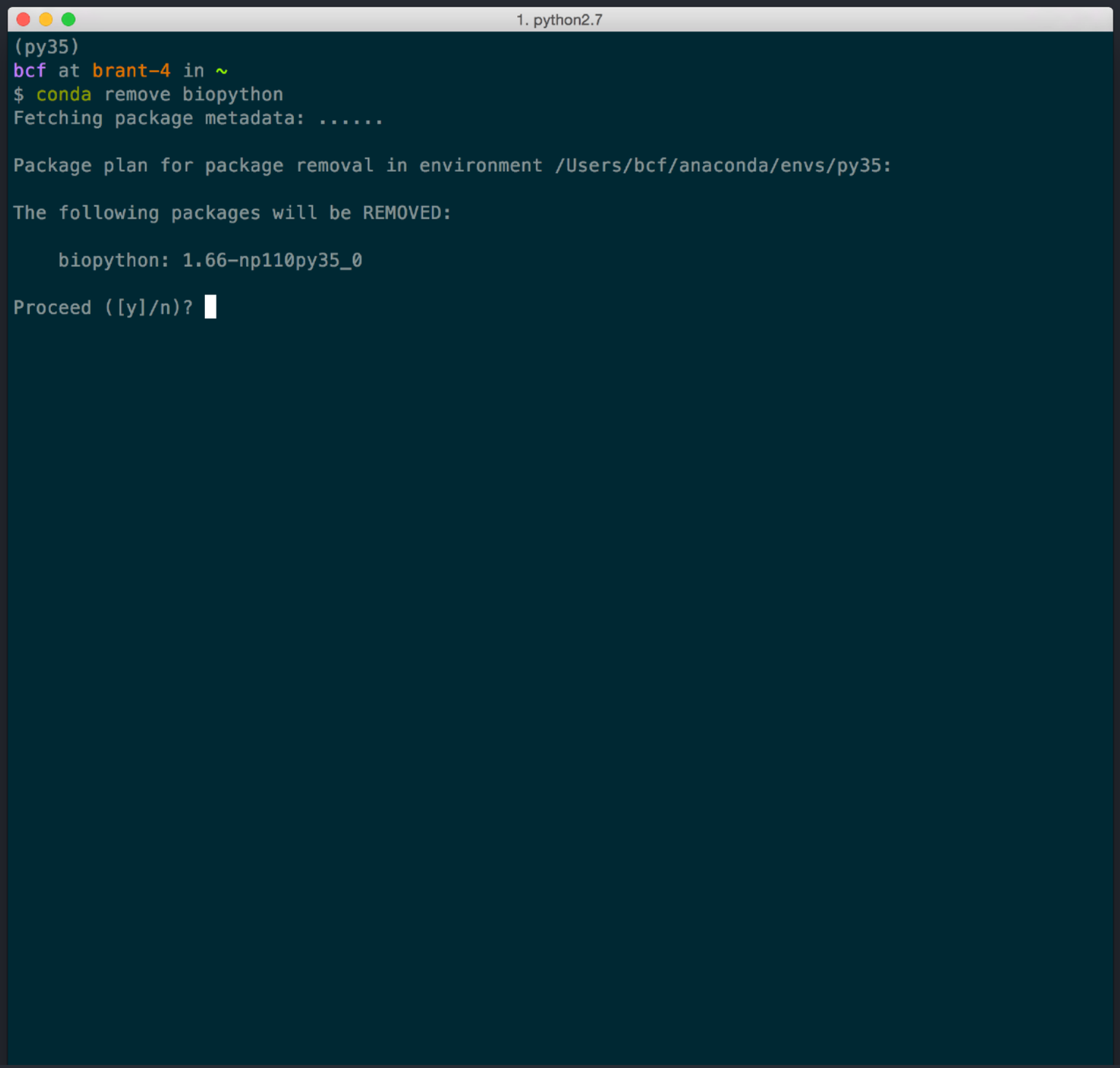
```
(py35)
bcf at brant-4 in ~
$ conda install biopython
Fetching package metadata: ......
Solving package specifications: .............
Package plan for installation in environment /Users/bcf/anaconda/envs/py35:

The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    mkl-11.3.1                 |                0        99.1 MB
    openssl-1.0.2g             |                0         3.0 MB
    xz-5.0.5                   |                1         173 KB
    numpy-1.10.4               |          py35_0         2.6 MB
    setuptools-20.3            |          py35_0         457 KB
    wheel-0.29.0               |          py35_0          82 KB
    pip-8.1.1                  |          py35_0         1.6 MB
    ------------------------------------------------------------
                                          Total:       107.0 MB

The following NEW packages will be INSTALLED:

    mkl:        11.3.1-0

The following packages will be UPDATED:

    numpy:      1.10.2-py35_0 --> 1.10.4-py35_0
    openssl:    1.0.2f-0      --> 1.0.2g-0
    pip:        8.0.2-py35_0  --> 8.1.1-py35_0
    setuptools: 19.6.2-py35_0 --> 20.3-py35_0
    wheel:      0.26.0-py35_1 --> 0.29.0-py35_0
    xz:         5.0.5-0       --> 5.0.5-1

Proceed ([y]/n)?
```

BioPython dependencies

conda info <libraryname>

Installs packages
(and dependencies)

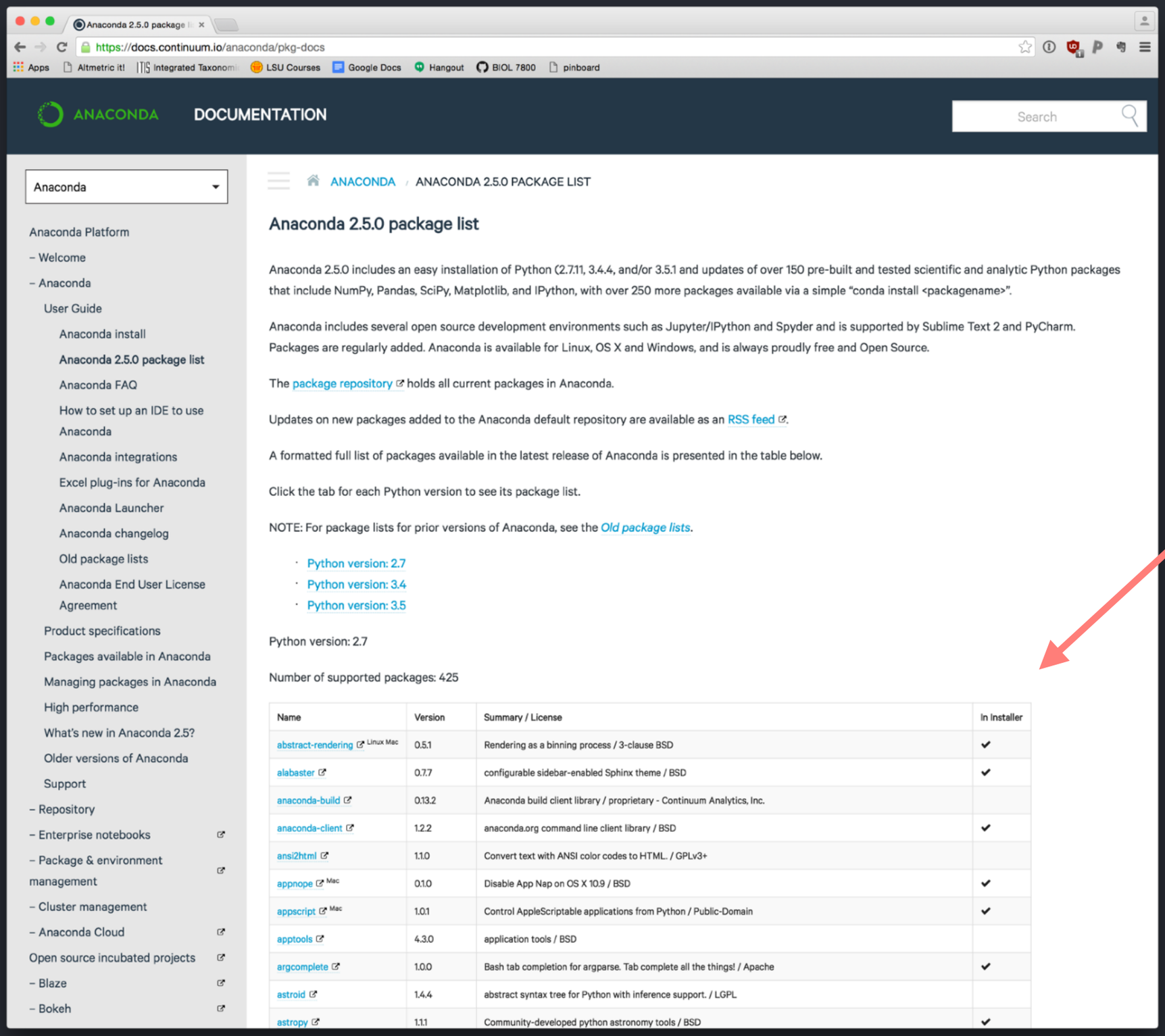
3rd Party Libraries



conda info <libraryname>

Removes packages
(but not dependencies)

3rd Party Libraries



Anaconda
distribution

Includes over 150 packages, pre-installed

3rd Party Libraries

But, Python can be extended with many
external ("third-party") libraries

BioPython

Sequence data
Alignment data
NCBI Interaction

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Data matrices
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Numerical routines
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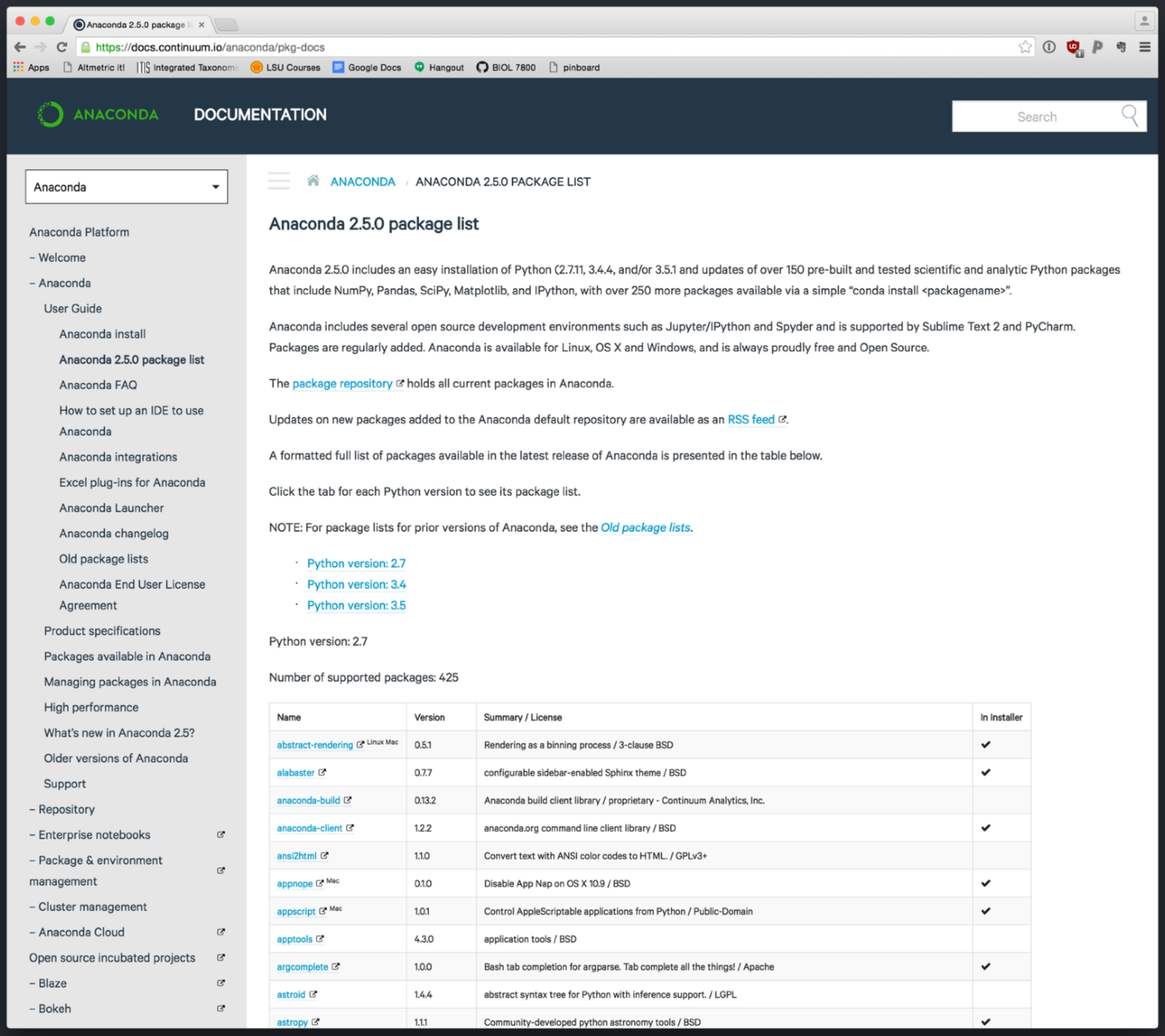
Interaction with web-APIs
HTTP requests

3rd Party Libraries



Anaconda
distribution

Includes over 150 libraries, pre-installed

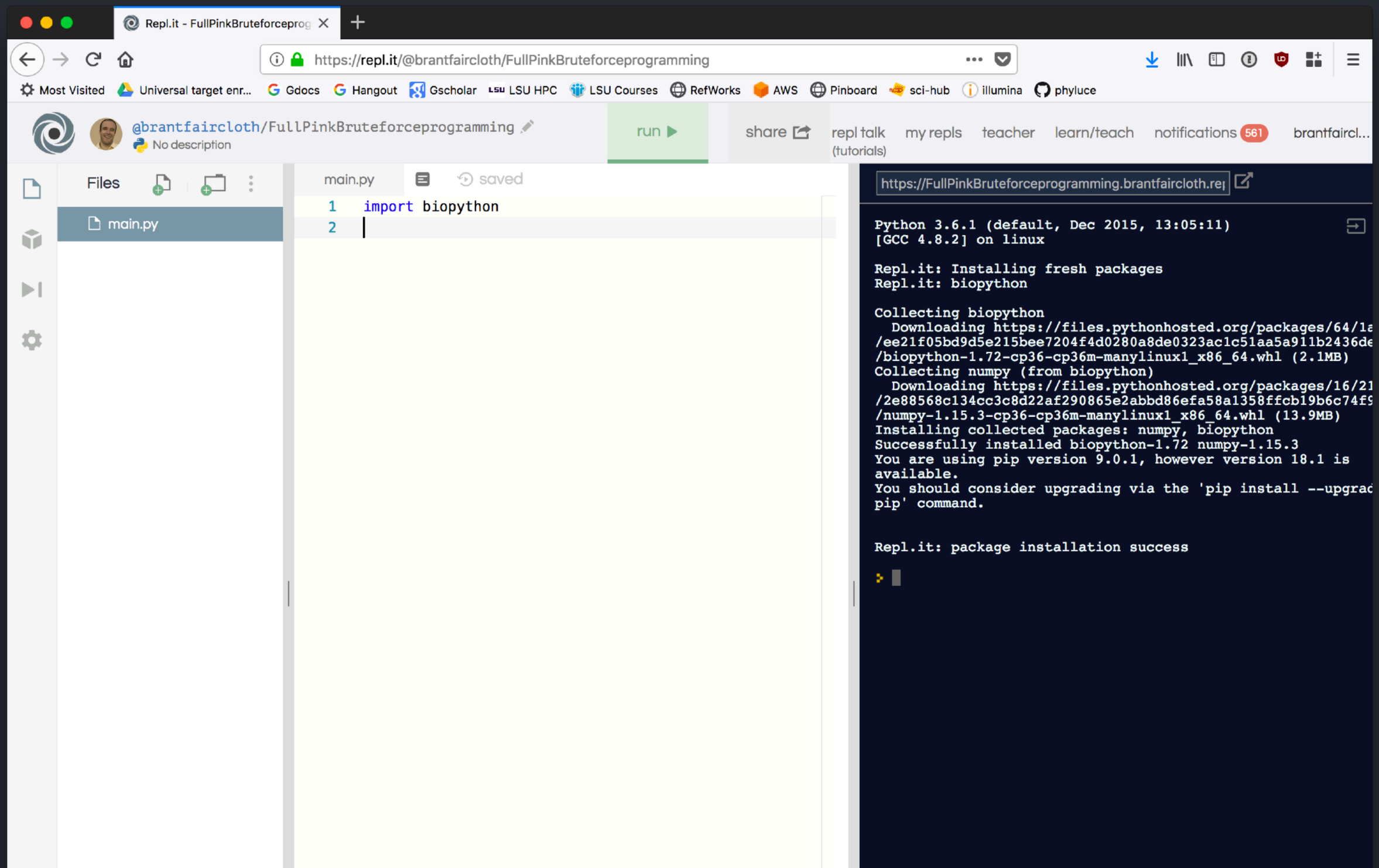
But

BioPython

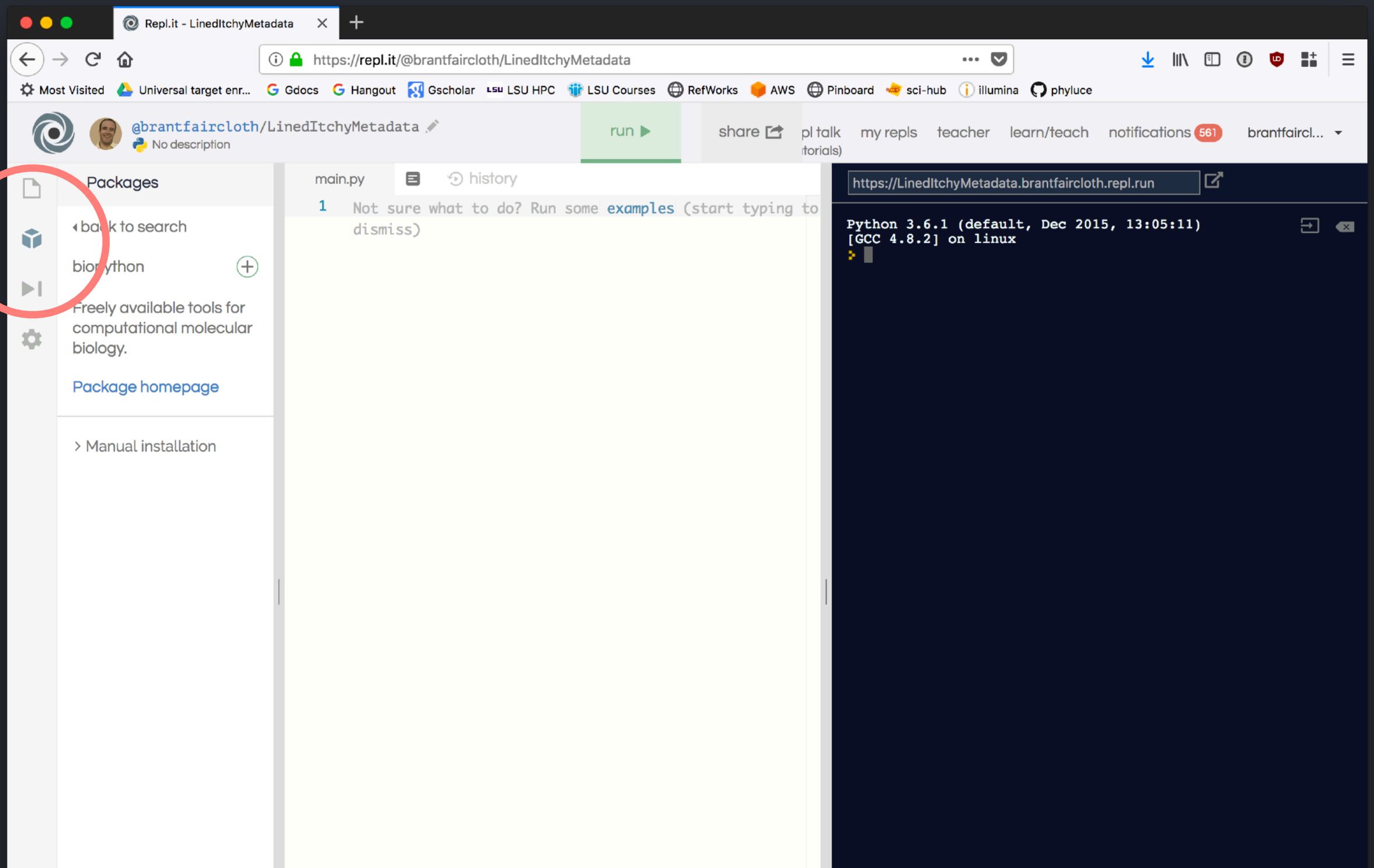
Sequence data
Alignment data
NCBI Interaction

is not one of the pre-installed libraries

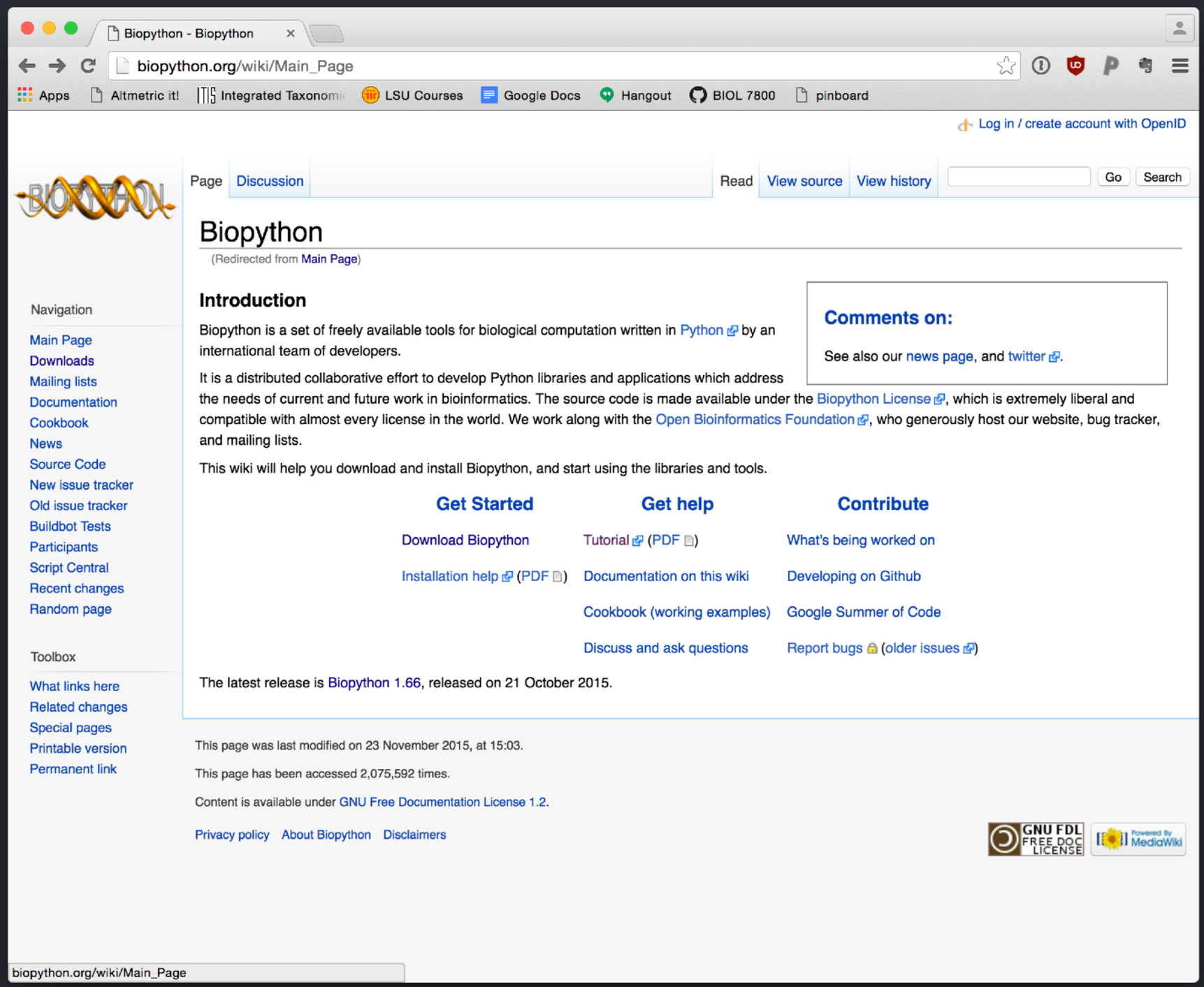
repl.it


Repl.it - FullPinkBruteforceprog
https://repl.it/@brantfaircloth/FullPinkBruteforceprogramming
Most Visited
Universal target enr...
Gdocs
Hangout
Gscholar
LSU HPC
LSU Courses
RefWorks
AWS
Pinboard
sci-hub
illumina
phyluce
@brantfaircloth/FullPinkBruteforceprogramming
No description
run
share
repl talk
(tutorials)
my repls
teacher
learn/teach
notifications 561
brantfaircl...
Files
main.py
saved
1 import biopython
2
https://FullPinkBruteforceprogramming.brantfaircloth.rep
Python 3.6.1 (default, Dec 2015, 13:05:11)
[GCC 4.8.2] on linux
Repl.it: Installing fresh packages
Repl.it: biopython
Collecting biopython
Downloading https://files.pythonhosted.org/packages/64/1a
/ee21f05bd9d5e215bee7204f4d0280a8de0323ac1c51aa5a911b2436de
/biopython-1.72-cp36-cp36m-manylinux1_x86_64.whl (2.1MB)
Collecting numpy (from biopython)
Downloading https://files.pythonhosted.org/packages/16/21
/2e88568c134cc3c8d22af290865e2abbd86efa58a1358ffcb19b6c74f9
/numpy-1.15.3-cp36-cp36m-manylinux1_x86_64.whl (13.9MB)
Installing collected packages: numpy, biopython
Successfully installed biopython-1.72 numpy-1.15.3
You are using pip version 9.0.1, however version 18.1 is
available.
You should consider upgrading via the 'pip install --upgrad
pip' command.
Repl.it: package installation success

repl.it


Repl.it - LinedItchyMetadata
https://repl.it/@brantfaircloth/LinedItchyMetadata
Most Visited
Universal target enr...
Gdocs
Hangout
Gscholar
LSU HPC
LSU Courses
RefWorks
AWS
Pinboard
sci-hub
illumina
phyluce
@brantfaircloth/LinedItchyMetadata
No description
run
share
pl talk
my repls
teacher
learn/teach
notifications 561
brantfaircl...
Packages
back to search
biopython
Freely available tools for computational molecular biology.
Package homepage
Manual installation
main.py
history
1 Not sure what to do? Run some examples (start typing to dismiss)
https://LinedItchyMetadata.brantfaircloth.repl.run
Python 3.6.1 (default, Dec 2015, 13:05:11)
[GCC 4.8.2] on linux

BioPython

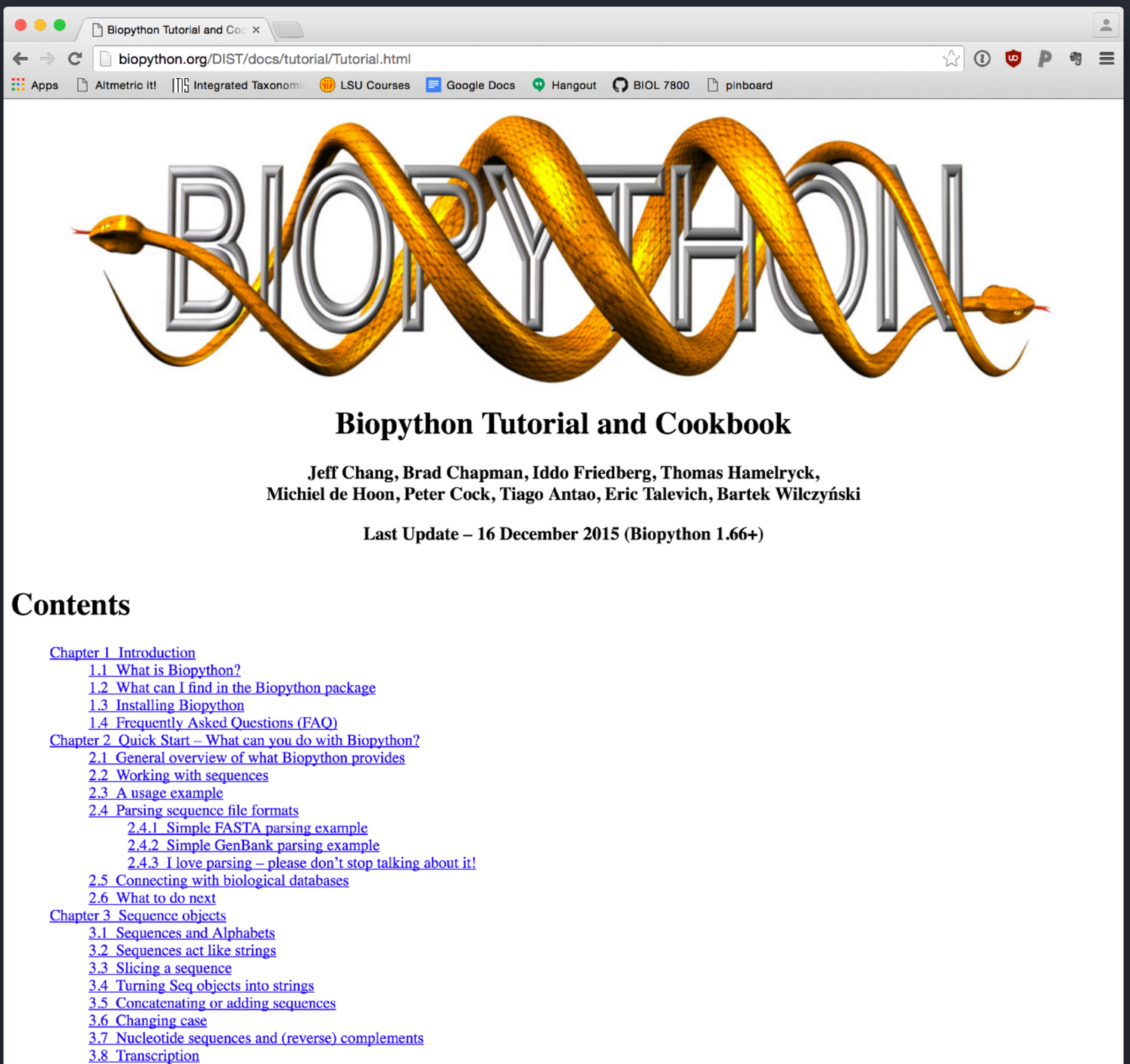


BioPython

Sequence data
Alignment data
NCBI Interaction
(and much more…)

Large library/package with
several submodules
(and sub-sub-modules)

BioPython



One of the most helpful documents is the BioPython Cookbook

BioPython

The primary/main module in BioPython
is the Bio module (and it has many submodules…)

1. zsh

```
bcf at brant-4 in ~
$ ls /Users/bcf/anaconda/envs/py35/lib/python3.5/site-packages/Bio
Affy                            KDTree                          SeqRecord.py
Align                           KEGG                            SeqUtils
AlignIO                         LogisticRegression.py           Sequencing
Alphabet                        MarkovModel.py                  Statistics
Application                     MaxEntropy.py                   SubsMat
Blast                           Medline                         SwissProt
CAPS                            Motif                           TogoWS
Cluster                         NMR                             UniGene
Compass                         NaiveBayes.py                   UniProt
Crystal                         NeuralNetwork                   Wise
Data                            Nexus                           __init__.py
DocSQL.py                       PDB                             __pycache__
Emboss                          ParserSupport.py                _py3k
Entrez                          Pathway                         _utils.py
ExPASy                          Phylo                           bgzf.py
FSSP                            PopGen                          codonalign
File.py                         Restriction                     cpairwise2.cpython-35m-darwin.so
GA                              SCOP                            kNN.py
GenBank                         SVDSuperimposer                 motifs
Geo                             SearchIO                        pairwise2.py
Graphics                        Seq.py                          trie.cpython-35m-darwin.so
HMM                             SeqFeature.py                   triefind.py
Index.py                        SeqIO
```

BioPython

The primary/main module in BioPython
is the `Bio` module (and it has many `submodules`…)

Bio.Seq

Interact with sequence objects
Nucleotide
Protein

Bio.SeqIO

Reading in sequence data
FASTA
FASTQ

Bio.Restriction

Restriction digests of
sequence data

Bio.Align

Interact with alignment objects
Alignment reformatting
Alignment slicing

Bio.AlignIO

Reading in alignment data
Nexus, Phylip, Phylip-relaxed
etc.

Bio.Blast

Interact with BLAST
local or online
parsing BLAST results

Bio.Entrez

Interact with NCBI databases
Taxonomy, Pubmed, etc.

Bio.Seq

```
In:  from Bio import Seq
```
← import Seq submodule from Bio

```
In:  my_seq = Seq.Seq("AGTACACTGGT")
```
← instantiate Seq object (Seq.Seq)

```
In:  my_seq
Out:Seq('AGTACACTGGT', Alphabet())
```
← show object __str__

```
In:  print(my_seq)
Out: AGTACACTGGT
```
← show object __repr__

__str__
Special method
Displays object info

__repr__
Special method
Displays object info from print()

Bio.Seq

```
In:  from Bio import Seq
```
← import Seq submodule from Bio

```
In:  my_seq = Seq.Seq("AGTACACTGGT")
```
← instantiate Seq object (Seq.Seq)

(this is a BioPython sequence object)

```
In:  my_seq
Out:Seq('AGTACACTGGT', Alphabet())
```

What do you think this is?

Bio.Seq

For sequence objects, we can constrain the character set used for sequence to valid characters

```
In:  from Bio import Seq
In:  my_seq = Seq.Seq("AGTACACTGGT")
In:  my_seq
Out:Seq('AGTACACTGGT', Alphabet())
```

```
In:  from Bio.Alphabet import IUPAC
In:  my_seq = Seq.Seq("AGTACACTGGT", IUPAC.unambiguous_dna)
```

Meant to specify sequence alphabet

'ExtendedIUPACDNA',
'ExtendedIUPACProtein',
'IUPACAmbiguousDNA',
'IUPACAmbiguousRNA',
'IUPACData',
'IUPACProtein',
'IUPACUnambiguousDNA',
'IUPACUnambiguousRNA',
'ambiguous_dna',
'ambiguous_rna',
'extended_dna',
'extended_protein',
'protein',
'unambiguous_dna',
'unambiguous_rna'

Bio.Seq

For sequence objects, we can constrain the character set used for sequence to valid characters

```
In:  from Bio import Seq
In:  from Bio.Alphabet import IUPAC
In:  my_seq = Seq.Seq("AGNACACTGGT", IUPAC.unambiguous_dna)
```

What's going to happen here?

Bio.Seq

For sequence objects, we can constrain the character set used for sequence to valid characters

```
In:  from Bio import Seq
In:  from Bio.Alphabet import IUPAC
In:  my_seq = Seq.Seq("AGNACACTGGT", IUPAC.unambiguous_dna)
In:  my_seq
Out:Seq('AGNACACTGGT', IUPACUnambiguousDNA())
```

hmmm....

Bio.Seq

For sequence objects, we can constrain the character set used for sequence to valid characters

```
In:  from Bio import Seq
In:  from Bio.Alphabet import IUPAC
In:  my_seq = Seq.Seq("AGNACACTGGT", IUPAC.unambiguous_dna)
In:  my_seq
Out:Seq('AGNACACTGGT', IUPACUnambiguousDNA())
In:  my_seq_2 = Seq.Seq("NNNNNN", IUPAC.ambiguous_dna)
In:  my_seq + my_seq_2
```

Maybe this won't work?

Bio.Seq

For sequence objects, we can constrain the character set used for sequence to valid characters

```
In:  from Bio import Seq
In:  from Bio.Alphabet import IUPAC
In:  my_seq = Seq.Seq("AGNACACTGGT", IUPAC.unambiguous_dna)
In:  my_seq
Out:Seq('AGNACACTGGT', IUPACUnambiguousDNA())
In:  my_seq_2 = Seq.Seq("NNNNNN", IUPAC.ambiguous_dna)
In:  my_seq + my_seq_2
Out:Seq('AGNACACTGGTNNNNNN', IUPACAmbiguousDNA())
```

Maybe this won't work?

Nope, it works… WTH?

Sequence alphabets are guidelines for type()

not absolutes

Bio.Seq

BioPython sequence objects behave a lot like strings

```
In:  from Bio import Seq
In:  from Bio.Alphabet import IUPAC
In:  my_seq = Seq.Seq("AGNACACTGGT", IUPAC.ambiguous_dna)

In:  len(my_seq)
Out:11
In:  for nucleotide in my_seq:
         print(nucleotide)
A
G
N
A
C
A
C
T
G
G
```

Bio.Seq

BioPython sequence objects behave a lot like strings

```
In:   my_seq = Seq.Seq("AGNACACTGGT", IUPAC.ambiguous_dna)

In:   my_seq[0]
Out:'A'

In:   my_seq[::-1]
Out:Seq('TGGTCACANGA', IUPACAmbiguousDNA())

In:   'ACA' in my_seq
Out:True

In:  my_seq.count('A')
Out:3

In:  my_seq.lower()
Out:Seq('agnacactggt', DNAAlphabet())

In:  my_seq.titlecase()
Out:AttributeError: 'Seq' object has no attribute 'titlecase'
```

(but sequence objects are not strings)

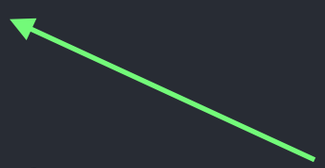
Bio.Seq

BioPython sequence objects behave a lot like strings
(but sequence objects are not strings)

```
In:  my_seq.titlecase()
Out:AttributeError: 'Seq' object has no attribute 'titlecase'
```

We can "stringify" (or cast) sequence objects with/to str()

```
In:  str(my_seq).title()
Out:'Agnacactggt'
```



sequence object cast to str and titlecased

Bio.Seq

Like strings, we can add BioPython sequence objects

```
In:  seq_of_As = Seq.Seq("AAAA", IUPAC.unambiguous_dna)
In:  seq_of_Ts = Seq.Seq("TTTT", IUPAC.unambiguous_dna)

In:  seq_of_As + seq_of_Ts
Out:Seq('AAAATTTT', IUPACUnambiguousDNA())

In:  seq_of_As[:2] + seq_of_Ts [0:2]
Out:Seq('AATT', IUPACUnambiguousDNA())
```

Bio.Seq

Of course sequence objects have their own methods

```
In:   my_seq = Seq.Seq("GGACATTTTCACCGT", IUPAC.ambiguous_dna)
```

```
In:  my_seq.complement()
Out:Seq('CCTGTAAAAGTGGCA', IUPACAmbiguousDNA())
```

complement

```
In:  my_seq.reverse_complement()
Out:Seq('ACGGTGAAAATGTCC', IUPACAmbiguousDNA())
```

rev. complement

```
In:  my_seq.transcribe()
Out:Seq('GGACAUUUUCACCGU', IUPACAmbiguousDNA())
```

transcribe

```
In:  my_seq.translate()
Out:Seq('GHFHR', ExtendedIUPACProtein())
```

translate

Bio.Seq

Of course sequence objects have their own methods

```
In:   my_seq = Seq.Seq("GGACATTTTCACCGT", IUPAC.ambiguous_dna)

In:  my_seq.translate()
Out:Seq('GHFHR', ExtendedIUPACProtein())
```

translate

```
In:  from Bio.Data import CodonTable
Out:standard_table = CodonTable.unambiguous_dna_by_name["Standard"]
```

```
  |  T      |  C      |  A      |  G      |
--+---------+---------+---------+---------+--
T | TTT F   | TCT S   | TAT Y   | TGT C   | T
T | TTC F   | TCC S   | TAC Y   | TGC C   | C
T | TTA L   | TCA S   | TAA Stop| TGA Stop| A
T | TTG L(s)| TCG S   | TAG Stop| TGG W   | G
--+---------+---------+---------+---------+--
C | CTT L   | CCT P   | CAT H   | CGT R   | T
C | CTC L   | CCC P   | CAC H   | CGC R   | C
C | CTA L   | CCA P   | CAA Q   | CGA R   | A
C | CTG L(s)| CCG P   | CAG Q   | CGG R   | G
--+---------+---------+---------+---------+--
A | ATT I   | ACT T   | AAT N   | AGT S   | T
A | ATC I   | ACC T   | AAC N   | AGC S   | C
A | ATA I   | ACA T   | AAA K   | AGA R   | A
A | ATG M(s)| ACG T   | AAG K   | AGG R   | G
--+---------+---------+---------+---------+--
G | GTT V   | GCT A   | GAT D   | GGT G   | T
G | GTC V   | GCC A   | GAC D   | GGC G   | C
G | GTA V   | GCA A   | GAA E   | GGA G   | A
G | GTG V   | GCG A   | GAG E   | GGG G   | G
--+---------+---------+---------+---------+--
```

Standard NCBI translation table

Bio.Seq

Of course sequence objects have their own methods

What if we want a different translation table (e.g. mitochondrial)?

```
In:  my_seq.translate(table="Vertebrate Mitochondrial)
Out:Seq('GHFHR', ExtendedIUPACProtein())
```

translate

```
In:  from Bio.Data import CodonTable
Out:standard_table = CodonTable.unambiguous_dna_by_name["Vertebrate Mitochondrial"]
```

	T	C	A	G	
T	TTT F	TCT S	TAT Y	TGT C	T
T	TTC F	TCC S	TAC Y	TGC C	C
T	TTA L	TCA S	TAA Stop	TGA W	A
T	TTG L	TCG S	TAG Stop	TGG W	G
C	CTT L	CCT P	CAT H	CGT R	T
C	CTC L	CCC P	CAC H	CGC R	C
C	CTA L	CCA P	CAA Q	CGA R	A
C	CTG L	CCG P	CAG Q	CGG R	G
A	ATT I(s)	ACT T	AAT N	AGT S	T
A	ATC I(s)	ACC T	AAC N	AGC S	C
A	ATA M(s)	ACA T	AAA K	AGA Stop	A
A	ATG M(s)	ACG T	AAG K	AGG Stop	G
G	GTT V	GCT A	GAT D	GGT G	T
G	GTC V	GCC A	GAC D	GGC G	C
G	GTA V	GCA A	GAA E	GGA G	A
G	GTG V(s)	GCG A	GAG E	GGG G	G

NCBI mitochondrial translation table

Bio.SeqIO

The BioPython submodule for reading/writing sequence data

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             # do stuff
```

filename/object

file-type

Bio.SeqIO

The BioPython submodule for reading/writing sequence data

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             # do stuff
```

What type of object is this?

Bio.SeqIO

The BioPython submodule for reading/writing sequence data

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             # do stuff
```

What type of object is this? **An iterator.**

Why?

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

Bio.SeqIO

Can return different types of object - some better than others

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             # do stuff
```

We can read entire file at once (< 1 sequence)

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         record = SeqIO.read(infile, 'fasta')
         # do stuff
```

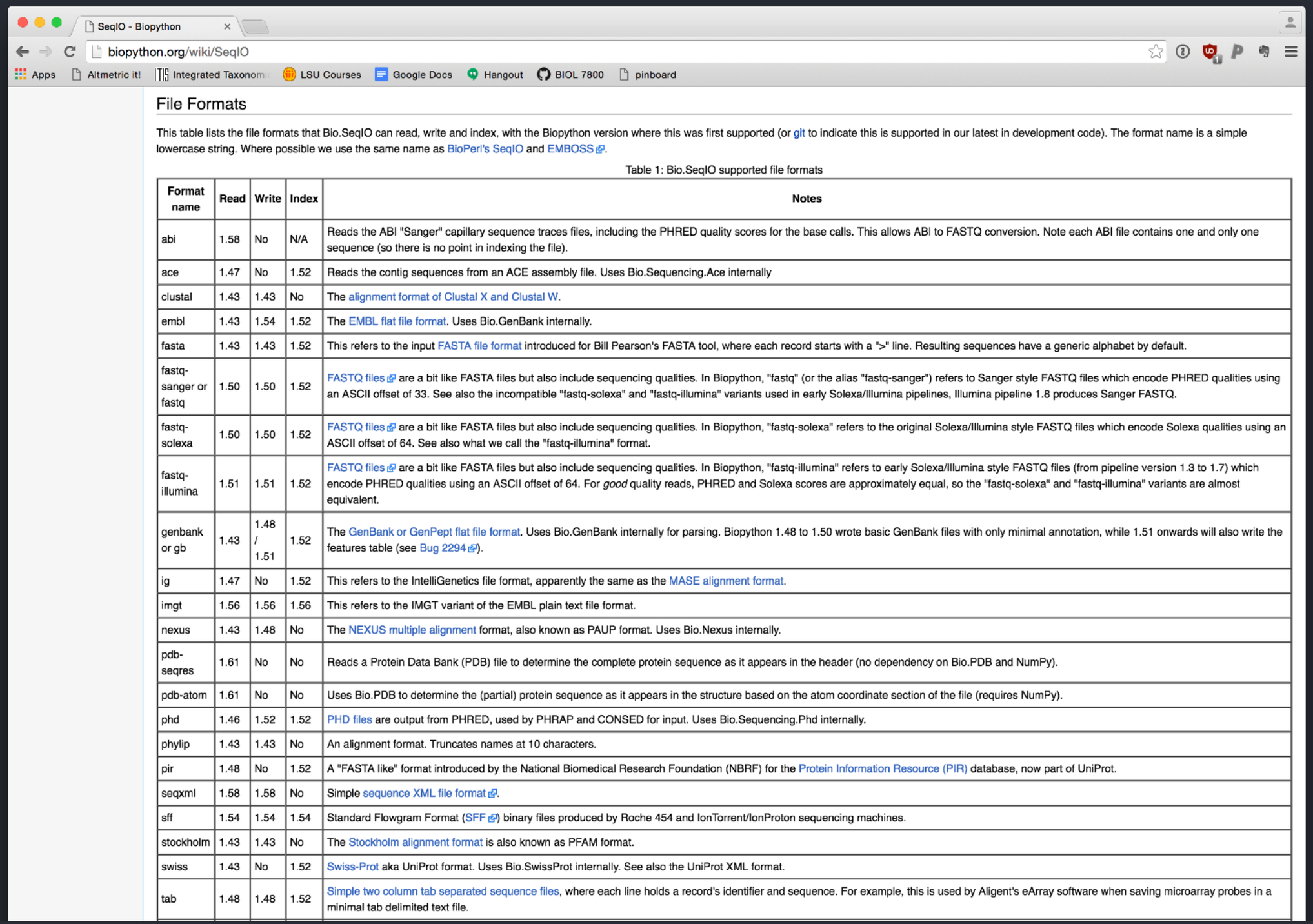
We can also parse entire file and make it a **dict()**

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         records = SeqIO.to_dict(SeqIO.parse(infile, 'fasta'))
         # do stuff
```

Bio.SeqIO

Can parse many, many formats of sequence files



File Formats

This table lists the file formats that Bio.SeqIO can read, write and index, with the Biopython version where this was first supported (or git to indicate this is supported in our latest in development code). The format name is a simple lowercase string. Where possible we use the same name as BioPerl's SeqIO and EMBOSS.

Table 1: Bio.SeqIO supported file formats

Format name	Read	Write	Index	Notes
abi	1.58	No	N/A	Reads the ABI "Sanger" capillary sequence traces files, including the PHRED quality scores for the base calls. This allows ABI to FASTQ conversion. Note each ABI file contains one and only one sequence (so there is no point in indexing the file).
ace	1.47	No	1.52	Reads the contig sequences from an ACE assembly file. Uses Bio.Sequencing.Ace internally
clustal	1.43	1.43	No	The alignment format of Clustal X and Clustal W.
embl	1.43	1.54	1.52	The EMBL flat file format. Uses Bio.GenBank internally.
fasta	1.43	1.43	1.52	This refers to the input FASTA file format introduced for Bill Pearson's FASTA tool, where each record starts with a ">" line. Resulting sequences have a generic alphabet by default.
fastq-sanger or fastq	1.50	1.50	1.52	FASTQ files are a bit like FASTA files but also include sequencing qualities. In Biopython, "fastq" (or the alias "fastq-sanger") refers to Sanger style FASTQ files which encode PHRED qualities using an ASCII offset of 33. See also the incompatible "fastq-solexa" and "fastq-illumina" variants used in early Solexa/Illumina pipelines, Illumina pipeline 1.8 produces Sanger FASTQ.
fastq-solexa	1.50	1.50	1.52	FASTQ files are a bit like FASTA files but also include sequencing qualities. In Biopython, "fastq-solexa" refers to the original Solexa/Illumina style FASTQ files which encode Solexa qualities using an ASCII offset of 64. See also what we call the "fastq-illumina" format.
fastq-illumina	1.51	1.51	1.52	FASTQ files are a bit like FASTA files but also include sequencing qualities. In Biopython, "fastq-illumina" refers to early Solexa/Illumina style FASTQ files (from pipeline version 1.3 to 1.7) which encode PHRED qualities using an ASCII offset of 64. For *good* quality reads, PHRED and Solexa scores are approximately equal, so the "fastq-solexa" and "fastq-illumina" variants are almost equivalent.
genbank or gb	1.43	1.48 / 1.51	1.52	The GenBank or GenPept flat file format. Uses Bio.GenBank internally for parsing. Biopython 1.48 to 1.50 wrote basic GenBank files with only minimal annotation, while 1.51 onwards will also write the features table (see Bug 2294).
ig	1.47	No	1.52	This refers to the IntelliGenetics file format, apparently the same as the MASE alignment format.
imgt	1.56	1.56	1.56	This refers to the IMGT variant of the EMBL plain text file format.
nexus	1.43	1.48	No	The NEXUS multiple alignment format, also known as PAUP format. Uses Bio.Nexus internally.
pdb-seqres	1.61	No	No	Reads a Protein Data Bank (PDB) file to determine the complete protein sequence as it appears in the header (no dependency on Bio.PDB and NumPy).
pdb-atom	1.61	No	No	Uses Bio.PDB to determine the (partial) protein sequence as it appears in the structure based on the atom coordinate section of the file (requires NumPy).
phd	1.46	1.52	1.52	PHD files are output from PHRED, used by PHRAP and CONSED for input. Uses Bio.Sequencing.Phd internally.
phylip	1.43	1.43	No	An alignment format. Truncates names at 10 characters.
pir	1.48	No	1.52	A "FASTA like" format introduced by the National Biomedical Research Foundation (NBRF) for the Protein Information Resource (PIR) database, now part of UniProt.
seqxml	1.58	1.58	No	Simple sequence XML file format.
sff	1.54	1.54	1.54	Standard Flowgram Format (SFF) binary files produced by Roche 454 and IonTorrent/IonProton sequencing machines.
stockholm	1.43	1.43	No	The Stockholm alignment format is also known as PFAM format.
swiss	1.43	No	1.52	Swiss-Prot aka UniProt format. Uses Bio.SwissProt internally. See also the UniProt XML format.
tab	1.48	1.48	1.52	Simple two column tab separated sequence files, where each line holds a record's identifier and sequence. For example, this is used by Aligent's eArray software when saving microarray probes in a minimal tab delimited text file.

Bio.SeqIO

The BioPython submodule for reading/writing sequence data

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             print(record.__str__)
Out:
SeqRecord(seq=Seq('AGCGCGCGCGTGTGT', SingleLetterAlphabet()), id='my_fasta_1', name='my_fasta_1',
description='my_fasta_1', dbxrefs=[])>

SeqRecord(seq=Seq('NNNNNTTTTAAAA', SingleLetterAlphabet()), id='my_fasta_2', name='my_fasta_2',
description='my_fasta_2', dbxrefs=[])>

SeqRecord(seq=Seq('ACACACACACACAC', SingleLetterAlphabet()), id='my_fasta_3', name='my_fasta_3',
description='my_fasta_3', dbxrefs=[])>
```

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

Bio.SeqIO

SeqRecord objects

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             print(record.__str__)
Out:
SeqRecord(seq=Seq('AGCGCGCGCGTGTGT', SingleLetterAlphabet()), id='my_fasta_1', name='my_fasta_1',
description='my_fasta_1', dbxrefs=[])>

...trimmed...
```

Notice here, that we're getting a new class of objects - the SeqRecord

And notice that our Seq object is nested within the SeqRecord object

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

Bio.SeqIO

SeqRecord objects

```
In:  from Bio import SeqIO

In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             print(record.__str__)
Out:
SeqRecord(seq=Seq('AGCGCGCGCGTGTGT', SingleLetterAlphabet()), id='my_fasta_1', name='my_fasta_1',
description='my_fasta_1', dbxrefs=[])>

...trimmed...
```

How do we access the sequence information in this object?

And, what are the other data in the SeqRecord object?

my_file.fasta

```
>my_fasta_1
AGCGCGCGCGTGTGT
>my_fasta_2
NNNNNTTTTAAAA
>my_fasta_3
ACACACACACACAC
```

Bio.SeqIO

SeqRecord objects

```
In:  with open('my_file.fasta', 'r') as infile:
         for record in SeqIO.parse(infile, 'fasta'):
             print(record.__str__)
Out:
SeqRecord(seq=Seq('AGCGCGCGCGTGTGT', SingleLetterAlphabet()), id='my_fasta_1', name='my_fasta_1',
description='my_fasta_1', dbxrefs=[])>
...trimmed...
```

How do we access the sequence information in this object?

```
In:  record.seq
Out: Seq('AGCGCGCGCGTGTGT', SingleLetterAlphabet())
```

And, what are the other data in the SeqRecord object?

```
In:  record.id
Out:'my_fasta_1'
```

```
In:  record.name
Out:'my_fasta_1'
```

```
In:  record.description
Out:'my_fasta_1'
```

Bio.SeqIO

SeqRecord objects

matts_file.fasta

```
>gi|927657366|gb|KT692534.1| Variabilichromis moorii voucher Matthew D. McGee:4237 ultra conserved
element locus uce-505 genomic sequence
AACTCCAGCTCCTGCAGCATCTCGCCCCATCATGACTTTTTCGGCTGATCCCGAGAAGCCAATCCCTTGA
```

```
In:  from Bio import SeqIO
```

```
In:  with open('matts_file.fasta', 'r') as infile:
         matts_seq = SeqIO.read(infile, 'fasta')
```

```
In:   matts_seq.id
Out:'gi|927657366|gb|KT692534.1|'
```

```
In:   matts_seq.name
Out:'gi|927657366|gb|KT692534.1|'
```

```
In:   matts_seq.description
Out: 'gi|927657366|gb|KT692534.1| Variabilichromis moorii voucher Matthew D. McGee:4237 ultra conserved element locus uce-505 genomic sequence'
```

Bio.SeqIO

SeqRecord objects

matts_file.fasta

```
>gi|927657366|gb|KT692534.1| Variabilichromis moorii voucher Matthew D. McGee:4237 ultra conserved
element locus uce-505 genomic sequence
AACTCCAGCTCCTGCAGCATCTCGCCCCATCATGACTTTTTCGGCTGATCCCGAGAAGCCAATCCCTTGA
```

```
In:  from Bio import SeqIO

In:  with open('matts_file.fasta', 'r') as infile:
         matts_seq = SeqIO.read(infile, 'fasta')

In:   matts_seq.id
Out:'gi|927657366|gb|KT692534.1|'

In:   matts_seq.name
Out:'gi|927657366|gb|KT692534.1|'

In:   matts_seq.description
Out 'gi|927657366|gb|KT692534.1| Variabilichromis moorii voucher Matthew D. McGee:4237 ultra conserved element locus uce-505 genomic
sequence'
```

id is header up to 1st space

name is often same

description is **full header**

Bio.SeqIO

SeqRecord objects have a format() method

matts_file.fasta

```
>gi|927657366|gb|KT692534.1| Variabilichromis moorii voucher Matthew D. McGee:4237 ultra conserved
element locus uce-505 genomic sequence
AACTCCAGCTCCTGCAGCATCTCGCCCCATCATGACTTTTTCGGCTGATCCCGAGAAGCCAATCCCTTGA
```

```
In:  from Bio import SeqIO
```

```
In:  with open('matts_file.fasta', 'r') as infile:
         matts_seq = SeqIO.read(infile, 'fasta')
```

```
In:   matts_seq.format('fasta')
```

format() takes desired format as argument

```
Out:">gi|927657366|gb|KT692534.1| Variabilichromis moorii voucher Matthew D. McGee:
4237 ultra conserved element locus uce-505 genomic
sequence\nAACTCCAGCTCCTGCAGCATCTCGCCCCATCATGACTTTTTCGGCTGATCCCGAGAAGCC
\nAATCCCTTGA\n'
```

Bio.SeqIO

SeqIO can process a number of formats

my_file.fastq

```
@NS500216:341:HMVLYBGXX:1:11101:18457:1155 1:N:0:GTCCTTCT+CACTAGCT
CTGCAGAGAGACAAACAGACACACATTTCATTGACAAACAAAAACAGGAGACAGAGAGACATGAACAAAGAAT
+
A/AAAE//EEEEEEEEEEAEEEEEE/AEE/EEAEEEEEEEEEEEEEEAEE<EE/EEAEAEE//EE/EEE//EE
@NS500216:341:HMVLYBGXX:1:11101:17357:1167 1:N:0:GTCCTTCT+CACTAGCT
CACAAATAAGACTTATTCTGATATCCCTGAGTGTATAATCACTTGAATTTTAGTATTGTACCTGCCATAGAAC
+
AAAAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
```

```
In:  from Bio import SeqIO
In:  with open('my_file.fastq', 'r') as infile:
         my_seq = SeqIO.parse(infile, 'fastq')
         fastq = next(my_seq)

In:  fastq.id
Out:'NS500216:341:HMVLYBGXX:1:11101:18457:1155'

In:  fastq.letter_annotations
Out:{'phred_quality': [32,
 14,
 32,
 32,
 32
...
```

← FASTQ here, not FASTA

← Qualities, converted to PHRED

Bio.SeqIO

SeqIO can also write SeqRecords

and **only** SeqRecords!!

```
In:  from Bio import Seq
In:  from Bio.Alphabet import IUPAC
In:  from Bio import SeqRecord
In:  from Bio import SeqIO

In:  seq_string = 'ACGTACGT'
In:  seq_object = Seq.Seq(seq_string, IUPAC.ambiguous_dna)
```

← Create **sequence object** from string

```
In:  seq_record_object = SeqRecord.SeqRecord(
                              seq_object,
                              id="my_first_seq",
                              name=""
                              description=""
                              )
```

← Create **sequence record** from sequence object

```
In:  with open('my_file.fasta', 'w') as outfile:
         SeqIO.write([seq_record_object], outfile, 'fasta')
```

← Write out a **list** of all **sequence records** to a file

Needs to be a list of SequenceObjects to write