Genome 559
Intro to Statistical and Computational Genomics

Lecture 17b:
Biopython
Larry Ruzzo

Biopython

What is Biopython?

How do I get it to run on my computer?

What can it do?

Biopython

Biopython is tool kit, not a program–a set of Python modules useful in bioinformatics

Features include:

- Sequence class (can transcribe, translate, invert, etc)
- Parsing files in different database formats
- Interfaces to progs/DBs like Blast, Entrez, PubMed
- Code for handling alignments of sequences
- Clustering algorithms, etc, etc.

Useful tutorials at http://biopython.org

Making Biopython available on your computer

Runs on Windows, MaxOSX, and Linux

http://biopython.org/

- Look for download/install instructions
- May require "Admin" privileges

1.53 is latest; works with Python 2.5 -2.6 (not 3?)

Use in the lab

Try

```
import Bio
```

If it fails, try:

```
import sys
for p in sys.path: print p
sys.path.append('/Library/Python/
2.5/site-packages')
import Bio
```

Sequence class

```
>>> from Bio.Seq import Seq # sequence class
>>> myseq = Seq("AGTACACTGGT")
>>> myseq.alphabet
Alphabet()
>>> myseq.tostring()
‘AGTACACTGGT’
```

More functionality than a plain string

```
>>> myseq
Seq('AGTACACTGGT', Alphabet())
>>> myseq.complement()
Seq('TCATGTGACCA', Alphabet())
>>> myseq.reverse_complement()
Seq('ACCAGTGTACT', Alphabet())
```

A sequence in a specified alphabet

```
>>> from Bio.Seq inport Seq
>>> from Bio.Alphabet import IUPAC
>>> myseq=Seq('AGTACACTGGT',IUPAC.unambiguous_dna)
>>> myseq
Seq('AGTACACTGGT', IUPACUnambiguousDNA())
```

Transcribe/Translate

```
>>> from Bio import Transcribe
>>> mydna = Seq("GATCGATGGGCCTATATAGGATCGAAAATCGC",
... IUPAC.unambiguous_dna)
>>> myrna = mydna.transcribe()
>>> print myrna
Seq('GAUCGAUGGGCCUAUAUAGGAUCGAAAAUCGC',IUPACUnambiguousRNA())
>>> myprot = myrna.translate()
Seq('DRWAYIGSKI', ExtendedIUPACProtein())
>>> s2 = Seq("AUGGCCAUUGUAAUGGGCCGCUGAAAGGGUGCCCGAUAG",
... IUPAC.unambiguous_rna)
>>>s2.translate()
Seq('MAIVMGR*KGAR*', HasStopCodon(IUPACProtein(), '*'))
# also possible to reverse transcribe, etc etc
```

Parsing a database format

FASTA database file named "ls_orchid.fasta":

```
>gi|2765658|emb|Z78533.1|CIZ78533 C.irapeanum 5.8S rRNA gene
CGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGATGAGACCGTGGAATAAACGATCGAGTG
AATCCGGAGGACCGGTGTACTCAGCTCACCGGGGGCATTGCTCCCGTGGTGACCCTGATTTGTTGTTGGG
....
from Bio import SeqIO
handle = open("ls_orchid.fasta")
for seqrec in SeqIO.parse(handle, "fasta") :
  print seqrec.id
  print seqrec.seq
  print len(seqrec.seq)
handle.close()

gi|2765658|emb|Z78533.1|CIZ78533
Seq('CGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGATGAGACCGTG ...',
   SingleLetterAlphabet())
740
...
```

Exercise 1

Modify the example above to print the GC% of each sequence, too.

Solution 1

```
from Bio import SeqIO
handle = open("ls_orchid.fasta")
for seqrec in SeqIO.parse(handle, "fasta"):
   print seqrec.id
   s = seqrec.seq
   print s
   print len(s),
   na = s.count('A')
   nc = s.count('C')
   ng = s.count('G')
   nt = s.count('T')
   print "GC%=",(ng+nc)*100.0/(na+nc+ng+nt)
handle.close()
```

Q1: there's also a Biopython func to calc gc%; can you find it?

Q2: Why did I *not* use (G+C)/len(s) ?

Parses GenBank Format, too

```
from Bio import SeqIO
handle = open("ls_orchid.gbk")
for seqrec in SeqIO.parse(handle, "genbank") :
    print seqrec.id
    print repr(seqrec.seq)
    print len(seqrec)
handle.close()
```

This should give:

```
Z78533.1
Seq
('CGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGATGAGACCGTGG.
..CGC', IUPACAmbiguousDNA())
740
...
```

Exercise 2

Change above example to save the records in a list called `seqrecs`

Solution 2

```
from Bio import SeqIO
handle = open("ls_orchid.gbk")
seqrecs = []
for seqrec in SeqIO.parse(handle, "genbank") :
    seqrecs.append(seqrec)
    print seqrec.id
    print repr(seqrec.seq)
    print len(seqrec)
handle.close()
```

This should give:

```
Z78533.1
Seq
('CGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTGATGAGACCGTGG.
..CGC', IUPACAmbiguousDNA())
740
...
```

Feature Tables

```
>>>seqrecs[0]
SeqRecord(seq=Seq('CGTA...CGC', IUPACAmbiguousDNA()),
id='Z78533.1', name='Z78533', description='C.irapeanum
5.8S rRNA gene and ITS1 and ITS2 DNA.', dbxrefs=[])
>>> print seqrecs[0]
ID: Z78533.1
Name: Z78533
Description: C.irapeanum 5.8S rRNA gene and ITS1 and ITS2 DNA.
Number of features: 5
/sequence_version=1
/source=Cypripedium irapeanum
/taxonomy=['Eukaryota', ..., 'Cypripedium']
/keywords=['5.8S ribosomal RNA', ... 'ITS2']
/references=[<Bio.SeqFeature.Reference instance...]
/accessions=['Z78533']
/data_file_division=PLN
/date=30-NOV-2006
/organism=Cypripedium irapeanum
/gi=2765658
Seq('CGTAACAAGGTTTCCGTAGGTGA...CGC', IUPACAmbiguousDNA())
```

Extracting Features

(Lists of objects with dicts of lists of lists of dicts of ...Oh my!)

```
>>> seqrecs[0].annotations
{'sequence_version': 1, 'source': 'Cypripedium
irapeanum', 'taxonomy': ['Eukaryota', ... ... ... ...}

# it's a dictionary!  What keys does it have?

>>> seqrecs[0].annotations.keys()
['sequence_version', 'source', 'taxonomy', 'keywords',
'references', 'accessions', 'data_file_division', 'date',
'organism', 'gi']
# grab one dict entry
>>> seqrecs[0].annotations['keywords']
['5.8S ribosomal RNA', '5.8S rRNA gene', 'internal
transcribed spacer', 'ITS1', 'ITS2']

#It's a list!   We can index into it...

>>> seqrecs[0].annotations['keywords'][1]
'5.8S rRNA gene'
```

Searching GenBank

```
# This example & next require internet access

from Bio import GenBank
gilist = GenBank.search_for("Opuntia AND rpl16")
# (that's RPL-sixteen, not RP-one-one-six)

# gilist will be a list of all of the GenBank
# identifiers that match our query:
print gilist
['6273291', '6273290', '6273289', '6273287',
'6273286', '6273285', '6273284']
```

Searching GenBank

```
ncbidict = GenBank.NCBIDictionary("nucleotide", "genbank")
gbrecord = ncbidict[gilist[0]]
print gbrecord

LOCUS       AF191665 902 bp DNA PLN 07-NOV-1999
DEFINITION Opuntia marenae rpl16 gene; chloroplast gene for
           chloroplast product, partial intron sequence.
ACCESSION  AF191665
VERSION    AF191665.1 GI:6273291
...
```

Exercise 3: What kind of a thing is "gbrecord"? Is there other stuff hidden with it like annotations or feature tables? How do I access it?

Solution 3

```
>>> type(gbrecord)
<type 'str'>

# Aha, it's just a plain string.

>>> gbrecord
'LOCUS       AY851612                892 bp    DNA
linear   PLN 10-APR-2007\nDEFINITION  Opuntia subulata
rpl16 gene, intron; chloroplast.\nACCESSION
AY851612\nVERSION     AY851612.1  GI:
57240072\nKEYWORDS    .\nSOURCE      chloroplast
Austrocylindropuntia subulata\n  ... ... ... ... ... '
```

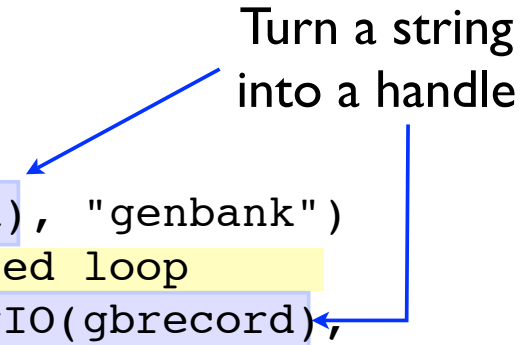
Can we get Biopython to parse it?

To parse a string

```
>>>SeqIO.parse(gbrecord, "genbank")
Traceback (most recent call last): blah blah blah...

# Oops, a string isn't a handle...

>>> import cStringIO
>>> SeqIO.parse(cStringIO.StringIO(gbrecord), "genbank")
<generator object at 0x5254b8>  ## Oops, need loop
>>> for rec in SeqIO.parse(cStringIO.StringIO(gbrecord),
... "genbank"):
...     print rec
...
ID: AY851612.1
Name: AY851612
Description: Opuntia subulata rpl16 gene, intron;
chloroplast.
Number of features: 3
/sequence_version=1
/source=chloroplast Austrocylindropuntia subulata  ...
```



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How would I use Biopython?

Biopython is not a program itself; it's a collection of tools for Python bioinformatics programing

When doing bioinformatics, keep Biopython in mind

Browse the documentation;become familiar with its capabilities

Use help(), type(), dir() & other built-in features to explore

You might prefer it to writing your own code for:

- Defining and handling sequences and alignments
- Parsing database formats
- Interfacing with databases

You don't have to use it all! Pick out one or two elements to learn first

Code re-use

If someone has written solid code that does what you need, use it

Don't "re-invent the wheel" unless you're doing it as a learning project

Python excels as a "glue language" which can stick together other peoples' programs, functions, classes, etc.

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HW notes

```
def func(x):
    handle = open(...)
    ...
    return something
    handle.close()
```

(Some) Other Capabilities

- AlignIO
  - consensus
  - PSSM (weight matrix)
- BLAST
  - both local and internet
- Entrez EUtils
  - including GenBank and PubMed
- Other Databases
  - SwissProt, Prosite, ExPASy, PDB

Exercises

Many!

As one suggestion, look at the "Cookbook" section of the tutorial. Figure out how to read my hem6.txt Phylip alignment & make a WMM from it.

Feel free to do something with one of the other pieces instead.