Biopython

What is biopython?

Biopython is a collection of python modules that contain code for manipulating biological data. Many handle sequence data and common analysis and processing of the data including reading and writing all common file formats. Biopython will also run blast for you and parse the output into objects inside your script. This requires just a few lines of code.

Installing Biopython

This is very straightforward once you have anaconda or minconda installed. I use miniconda because it's smaller. We are going to use `sudo`, because this will give us permission to install in the 'correct' directory python is expecting to find the modules. Other users will be able to use it too. Using `sudo` can cause problems, but it's ok here. You will need the administrator password for the machine. If you don't have this, ask the person who does administration on your machine.

```
% mamba create --name bio
% mamba activate bio
(bio)% mamba install --channel conda-forge --channel bioconda biopython
bioconda/noarch                                             Using cache
bioconda/osx-64                                             Using cache
conda-forge/noarch                                          Using cache
conda-forge/osx-64                                          Using cache

Transaction

  Prefix: /Users/pfb2024/mamba/envs/bio

  Updating specs:

   - biopython


  Package              Version  Build                            Channel           Size
─────────────────────────────────────────────────────────────────────────────────────────
  Install:
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  + biopython             1.70  np112py36_1                      bioconda           3MB
  + blas                   1.1  openblas                         conda-forge        1kB
  + ca-certificates  2024.8.30  h8857fd0_0                       conda-forge     Cached
  + freetype            2.12.1  h60636b9_2                       conda-forge     Cached
  + jpeg                    9e  hb7f2c08_3                       conda-forge      232kB
  + lcms2                 2.12  h577c468_0                       conda-forge      414kB
  + lerc                   3.0  he49afe7_0                       conda-forge      175kB
  + libcxx              19.1.2  hf95d169_0                       conda-forge     Cached
  + libdeflate            1.10  h0d85af4_0                       conda-forge       80kB
  + libffi               3.4.2  h0d85af4_5                       conda-forge     Cached
  + libgfortran          3.0.1  0                                conda-forge      507kB
  + libpng              1.6.43  h92b6c6a_0                       conda-forge      269kB
  + libsqlite           3.46.0  h1b8f9f3_0                       conda-forge      909kB
  + libtiff              4.3.0  hfca7e8f_4                       conda-forge      597kB
  + libwebp-base         1.4.0  h10d778d_0                       conda-forge     Cached
  + libzlib             1.2.13  h87427d6_6                       conda-forge       57kB
  + mmtf-python          1.1.3  pyhd8ed1ab_0                     conda-forge       26kB
  + msgpack-python       1.0.2  py36hc61eee1_1                   conda-forge       82kB
  + ncurses                6.5  hf036a51_1                       conda-forge     Cached
  + numpy               1.12.1  py36_blas_openblash4251c03_1001  conda-forge        4MB
  + olefile               0.46  pyh9f0ad1d_1                     conda-forge       33kB
  + openblas             0.3.3  hdc02c5d_1001                    conda-forge       18MB
  + openjpeg             2.5.0  h69f46e4_0                       conda-forge      541kB
  + openssl             1.1.1w  h8a1eda9_0                       conda-forge        2MB
  + pillow               8.3.2  py36h950f3bb_0                   conda-forge      665kB
  + pip                 21.3.1  pyhd8ed1ab_0                     conda-forge        1MB
  + python              3.6.15  haf480d7_0_cpython               conda-forge       22MB
  + python_abi             3.6  2_cp36m                          conda-forge        4kB
  + readline               8.2  h9e318b2_1                       conda-forge     Cached
  + reportlab           3.5.68  py36h92d37d9_0                   conda-forge        3MB
  + setuptools          58.0.4  py36h79c6626_2                   conda-forge      983kB
  + sqlite              3.46.0  h28673e1_0                       conda-forge      912kB
  + tk                  8.6.13  h1abcd95_1                       conda-forge     Cached
  + wheel               0.37.1  pyhd8ed1ab_0                     conda-forge       32kB
  + xz                   5.2.6  h775f41a_0                       conda-forge     Cached
  + zlib                1.2.13  h87427d6_6                       conda-forge       89kB
  + zstd                 1.5.6  h915ae27_0                       conda-forge     Cached

  Summary:

  Install: 37 packages

  Total download: 59MB

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Confirm changes: [Y/n] Y

Transaction starting
reportlab                                            2.6MB @  11.5MB/s  0.2s
openssl                                              1.7MB @  11.7MB/s  0.1s
numpy                                                3.9MB @  11.4MB/s  0.3s
biopython                                            2.5MB @   7.0MB/s  0.3s
pip                                                  1.3MB @   5.4MB/s  0.1s
```

```
libsqlite                                          908.6kB @   1.9MB/s  0.1s
sqlite                                             912.4kB @   4.9MB/s  0.1s
setuptools                                         983.0kB @   3.1MB/s  0.3s
pillow                                             665.5kB @   2.6MB/s  0.2s
libtiff                                            596.9kB @ 972.2kB/s  0.2s
python                                              21.6MB @  29.4MB/s  0.7s
lcms2                                              413.9kB @   5.8MB/s  0.1s
openjpeg                                           540.8kB @  ??.?MB/s  0.1s
libgfortran                                        507.0kB @   3.1MB/s  0.1s
lerc                                               174.5kB @  ??.?MB/s  0.0s
zlib                                                88.7kB @  ??.?MB/s  0.0s
libpng                                             268.5kB @   1.9MB/s  0.1s
jpeg                                               231.8kB @  66.6kB/s  0.1s
msgpack-python                                      82.4kB @ 756.4kB/s  0.1s
libdeflate                                          80.0kB @ 761.1kB/s  0.1s
libzlib                                             57.4kB @ 556.3kB/s  0.1s
olefile                                             33.1kB @ 371.6kB/s  0.1s
wheel                                               32.0kB @  ??.?MB/s  0.0s
python_abi                                           4.0kB @  ??.?MB/s  0.0s
openblas                                            18.4MB @  18.8MB/s  0.9s
mmtf-python                                         26.0kB @ 415.9kB/s  0.1s
blas                                                 1.3kB @  20.7kB/s  0.1s
Linking libgfortran-3.0.1-0
Linking libcxx-19.1.2-hf95d169_0
Linking libzlib-1.2.13-h87427d6_6
Linking ncurses-6.5-hf036a51_1
Linking libffi-3.4.2-h0d85af4_5
Linking xz-5.2.6-h775f41a_0
Linking jpeg-9e-hb7f2c08_3
Linking libdeflate-1.10-h0d85af4_0
Linking libwebp-base-1.4.0-h10d778d_0
Linking ca-certificates-2024.8.30-h8857fd0_0
Linking openblas-0.3.3-hdc02c5d_1001
Linking lerc-3.0-he49afe7_0
Linking zstd-1.5.6-h915ae27_0
Linking tk-8.6.13-h1abcd95_1
Linking libsqlite-3.46.0-h1b8f9f3_0
Linking zlib-1.2.13-h87427d6_6
Linking libpng-1.6.43-h92b6c6a_0
Linking readline-8.2-h9e318b2_1
Linking openssl-1.1.1w-h8a1eda9_0
Linking blas-1.1-openblas
Linking libtiff-4.3.0-hfca7e8f_4
Linking freetype-2.12.1-h60636b9_2
Linking sqlite-3.46.0-h28673e1_0
Linking openjpeg-2.5.0-h69f46e4_0
Linking lcms2-2.12-h577c468_0
Linking python-3.6.15-haf480d7_0_cpython
Linking python_abi-3.6-2_cp36m
Linking setuptools-58.0.4-py36h79c6626_2
Linking wheel-0.37.1-pyhd8ed1ab_0
Linking pip-21.3.1-pyhd8ed1ab_0
Linking olefile-0.46-pyh9f0ad1d_1
Linking msgpack-python-1.0.2-py36hc61eee1_1
Linking numpy-1.12.1-py36_blas_openblash4251c03_1001
Linking pillow-8.3.2-py36h950f3bb_0
Linking reportlab-3.5.68-py36h92d37d9_0
Linking mmtf-python-1.1.3-pyhd8ed1ab_0
Linking biopython-1.70-np112py36_1

Transaction finished
```

See if the install worked

```
python3
>>> import Bio
>>> print(Bio.__version__)
1.70
```

If we get no errors, biopython is installed correctly.

Biopython documentation

Biopython wiki page

Getting started

Biopython tutorial

Complete tree of Biopython Classes

Working with DNA and protein sequences

This is the core of biopython. And uses the Seq object. Seq is part of Bio. This is denoted Bio.Seq

```
#!/usr/bin/env python3
import Bio.Seq
seqobj = Bio.Seq.Seq('ATGCGATCGAGC')
print(f"{seqobj} has {len(seqobj)} nucleotides")
```

> Note: Sometimes you might have to convert an object to string to get sequence `seq_str = str(seqobj)`. The Seq Object predicts that if a user writes `print(seqobj)` they will want to print the sequence string not the entire Seq Object. Likewise, the Seq Object predicts that if a user writes `len(seqobj)` they will want to caluculate the length of the sequence not the length of the entire Seq Object

produces

```
ATGCGATCGAGC has 12 nucleotides
```

From ... import ...

Another way to import modules is with `from ... import ...` . This saves typing the Class name every time. Bio.Seq is the class name. Bio is the superclass. Seq is a subclass inside Bio. It's written Bio.Seq. Seq has several different subclasses, of which one is called Seq. So we have Bio.Seq.Seq. To make the creation simpler, we call Seq() after we import with `from ... import ...` like this

```
#!/usr/bin/env python3
from Bio.Seq import Seq
seqobj=Seq('ATGCGATCGAGC')
protein = seqobj.translate()
print(f'{seqobj} translates to {protein}')
```

produces

```
ATGCGATCGAGC translates to MRSS
```

Extracting a subsequence

You can use a range [0:3] to get the first codon

Visit biopython.org to read about [Slicing a sequence]

```
>>> seqobj=Seq('ATGCGATCGAGC')
>>> seqobj[0:3]
Seq('ATG', Alphabet())
>>> print(seqobj[0:3])
ATG
```

Let's use Regular expressions in conjunction with BioPython to get every codon

```
>>> seqobj=Seq('ATGCGATCGAGC')
>>> import re
>>> for codon in re.findall(r"(.{3})",str(seqobj)):
...   print(codon)
...
ATG
CGA
TCG
AGC
>>>
```

> The Seq Object has not predicted that if we use seqobj as input to `findall()` that we want to search just the sequence. But it has predicted that if we use the `str()` we want to return the sequence that is contained within our object.

Data types

The Seq Object predicts that we want a string when we `print()` our seqobj or if we try to caculate `len()` or if we try to take a substr `seqobj[0:3]` of our seqobj. The authors have coded this functionality into the Class rules. They did not predict, or write into the Class rules that if we use `findall()` that we want to search just the sequence. The Class does not know how to handle this. But it has predicted that if we use the `str()` we want to return the sequence that is contained within our object.

```
>>> seqobj=Seq('ATGCGATCGAGC')
>>> type(seqobj)
<class 'Bio.Seq.Seq'>
>>> seqobj
Seq('ATGCGATCGAGC', Alphabet())
>>> str(seqobj)
'ATGCGATCGAGC'
>>> type(str(seqobj))
<class 'str'>
```

Read a FASTA file

Earlier in the course were learning how to read a fasta file line by line. We are going to go over the BioPython way to do this. `SeqIO.parse()` is the main method for reading from almost any file format. The examples will use seq.nt.fa:

```
>seq1
AAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGCCACCAATTATGGTGTATGAGTGAATCTCTGGTCCG
AGATTCA
CTGAGTAACTGCTGTACACAGTAGTAACACGTGGAGATCCCATAAGCTTCACGTGTGGTCCAATAAAACACTCCGTTGGTCAAC
>seq2
GCCACAGAGCCTAGGACCCCAACCTAACCTAACCTAACCTAACCTACAGTTTGATCTTAACCATGAGGCTGAGAAGCGATGTCCTGACC
GGCCTGT
CCTAACCGCCCTGACCTAACCGGCTTGACCTAACCGCCCTGACCTAACCAGGCTAACCTAACCAAACCGTGAAAAAAGGAATCT
>seq3
ATGAAAGTTACATAAAGACTATTCGATGCATAAATAGTTCAGTTTTGAAAACTTACATTTTGTTAAAGTCAGGTACTTGTGTATAATAT
CAACTAA
AT
>seq4
ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAAACAACATGCCAAATAGAAACGATCAATTCGGCGAT
GGAAATC
AGAACAACGATCAGTTTGGAAATCAAAATAGAAATAACGGGAACGATCAGTTTAATAACATGATGCAGAATAAAGGGAATAATCAATTT
AATCCAG
GTAATCAGAACAGAGGT
```

Get help on the parse() method with

```
>>> from Bio import SeqIO
>>> help(SeqIO.parse)

Help on function parse in module Bio.SeqIO:

parse(handle, format, alphabet=None)
    Turns a sequence file into an iterator returning SeqRecords.

        - handle   - handle to the file, or the filename as a string
          (note older versions of Biopython only took a handle).
        - format   - lower case string describing the file format.
        - alphabet - optional Alphabet object, useful when the sequence type
          cannot be automatically inferred from the file itself
          (e.g. format="fasta" or "tab")

...
```

Here's a script to read fasta records and print out some information

```
#!/usr/bin/env python3
from Bio import SeqIO
for seq_record in SeqIO.parse("../files/seq.nt.fa", "fasta"):   # give filename and format
  print('ID',seq_record.id)
  print('Sequence',seq_record.seq)
  print('Length',len(seq_record))
```

Prints this output

```
ID seq1
Sequence
AAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGCCACCAATTATGGTGTATGAGTGAATCTCTGGTCCG
AGATTCACTGAGTAACTGCTGTACACAGTAGTAACACGTGGAGATCCCATAAGCTTCACGTGTGGTCCAATAAAACACTCCGTTGGTCA
AC
Length 180
ID seq2
Sequence
GCCACAGAGCCTAGGACCCCAACCTAACCTAACCTAACCTAACCTACAGTTTGATCTTAACCATGAGGCTGAGAAGCGATGTCCTGACC
GGCCTGTCCTAACCGCCCTGACCTAACCGGCTTGACCTAACCGCCCTGACCTAACCAGGCTAACCTAACCAAACCGTGAAAAAAGGAAT
CT
Length 180
ID seq3
Sequence
ATGAAAGTTACATAAAGACTATTCGATGCATAAATAGTTCAGTTTTGAAAACTTACATTTTGTTAAAGTCAGGTACTTGTGTATAATAT
CAACTAAAT
Length 98
ID seq4
Sequence
ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAAACAACATGCCAAATAGAAACGATCAATTCGGCGAT
GGAAATCAGAACAACGATCAGTTTGGAAATCAAAATAGAAATAACGGGAACGATCAGTTTAATAACATGATGCAGAATAAAGGGAATAA
TCAATTTAATCCAGGTAATCAGAACAGAGGT
Length 209
```

How do you know what methods and attributes are available?

In the last example we used the `id()` and `seq()`. How do we find out that we could use these or what are other options are?

You can use option+tab in the interpreter to find out. Type the object then a '.' then option+tab. You will get a list of attributes and methods you can use with this specific object.

```
>>> from Bio import SeqIO
>>> for seq_record in SeqIO.parse("../files/seq.nt.fa", "fasta"):
...   print(seq_record.
seq_record.annotations          seq_record.id                   seq_record.seq
seq_record.dbxrefs              seq_record.letter_annotations   seq_record.translate(
seq_record.description          seq_record.lower(               seq_record.upper(
seq_record.features             seq_record.name
seq_record.format(              seq_record.reverse_complement(
...   print(seq_record.
```

Seq Object vs SeqRecord Object

The Seq Object and the SeqRecord Object two Objects are not the same. As you have seen we can directly print the sequence that is stored within a `Seq` Object. But this is not possible with `SeqRecord`. You need to use the `seq()` method to retrieve just the sequence bit of the `SeqRecord` Object.

```
>>> from Bio.Seq import Seq
>>> seqobj=Seq('ATGCGATCGAGC')
>>> print(seqobj)
ATGCGATCGAGC
>>>
>>> type(seqobj)
<class 'Bio.Seq.Seq'>
>>>
>>> from Bio import SeqIO
>>> filename = "../files/seq.nt.fa"
>>> for seq_record in SeqIO.parse(filename, "fasta"):
...   type(seq_record)
...   print(seq_record.seq)
...   print(seq_record)
...
<class 'Bio.SeqRecord.SeqRecord'>
AAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGCCACCAATTATGGTGTATGAGTGAATCTCTGGTCCG
AGATTCACTGAGTAACTGCTGTACACAGTAGTAACACGTGGAGATCCCATAAGCTTCACGTGTGGTCCAATAAAACACTCCGTTGGTCA
AC
ID: seq1
Name: seq1
Description: seq1
Number of features: 0
Seq('AAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGC...AAC')
<class 'Bio.SeqRecord.SeqRecord'>
GCCACAGAGCCTAGGACCCCAACCTAACCTAACCTAACCTAACCTACAGTTTGATCTTAACCATGAGGCTGAGAAGCGATGTCCTGACC
GGCCTGTCCTAACCGCCCTGACCTAACCGGCTTGACCTAACCGCCCTGACCTAACCAGGCTAACCTAACCAAACCGTGAAAAAAGGAAT
CT
```

```
# ... etc
```

Here is another example of opening a FASTA file, retrieving each sequence record, and doing something the data. We are going to translate each sequence record

```
#!/usr/bin/env python3
from Bio import SeqIO
filename = "../files/seq.nt.fa"
for seq_record in SeqIO.parse(filename, "fasta"):
  print('ID',seq_record.id)
  print(f'len {len(seq_record)}')
  print(f'translation {seq_record.seq.translate(to_stop=False)}')
```

> We added the translation of the DNA sequence into protein
> Output:

```
ID seq1
len 180
translation KSSSR*CDRWR*SKCPMGHQLWCMSESLVRDSLSNCCTQ**HVEIP*ASRVVQ*NTPLVN
ID seq2
len 180
translation ATEPRTPT*PNLT*PTV*S*P*G*EAMS*PACPNRPDLTGLT*PP*PNQANLTKP*KKES
ID seq3
len 98
translation MKVT*RLFDA*IVQF*KLTFC*SQVLVYNIN*
ID seq4
len 209
translation MLTKVSVRTCR*ATLKKETTCQIETINSAMEIRTTISLEIKIEITGTISLIT*CRIKGIINLIQVIRTE
```

Because one of our sample sequences is not a complete CDS we will get this message from biopython

```
/Users/pfb2024/mamba/envs/biopython/lib/python3.6/site-packages/Bio/Seq.py:2309:
BiopythonWarning: Partial codon, len(sequence) not a multiple of three. Explicitly trim
the sequence or add trailing N before translation. This may become an error in future.
  BiopythonWarning)
```

This is displayed to standard error and not standard out, and therefore will not affect the contents if redirected from standard out into a file.

```
% python3 biopython_translate.py > tmp
/Users/smr/opt/anaconda3/lib/python3.9/site-packages/Bio/Seq.py:2334: BiopythonWarning:
Partial codon, len(sequence) not a multiple of three. Explicitly trim the sequence or add
trailing N before translation. This may become an error in future.
  warnings.warn(
% cat tmp
ID seq1
len 180
translation KSSSR*CDRWR*SKCPMGHQLWCMSESLVRDSLSNCCTQ**HVEIP*ASRVVQ*NTPLVN
ID seq2
len 180
translation ATEPRTPT*PNLT*PTV*S*P*G*EAMS*PACPNRPDLTGLT*PP*PNQANLTKP*KKES
ID seq3
len 98
translation MKVT*RLFDA*IVQF*KLTFC*SQVLVYNIN*
ID seq4
len 209
translation MLTKVSVRTCR*ATLKKETTCQIETINSAMEIRTTISLEIKIEITGTISLIT*CRIKGIINLIQVIRTE
```

Convert FASTA file to Python dictionary in one line

`Bio.SeqIO.to_dict()` reads the entire FASTA file into memory and stores the contents in a dictionary.

```
>>> from Bio import SeqIO
>>> id_dict = SeqIO.to_dict(SeqIO.parse('../files/seq.nt.fa', 'fasta'))
>>> id_dict
{'seq1':
SeqRecord(seq=Seq('AAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGC...AAC',
SingleLetterAlphabet()), id='seq1', name='seq1', description='seq1', dbxrefs=[]), 'seq2':
SeqRecord(seq=Seq('GCCACAGAGCCTAGGACCCCAACCTAACCTAACCTAACCTAACCTACAGTTTGA...TCT',
SingleLetterAlphabet()), id='seq2', name='seq2', description='seq2', dbxrefs=[]), 'seq3':
SeqRecord(seq=Seq('ATGAAAGTTACATAAAGACTATTCGATGCATAAATAGTTCAGTTTTGAAAACTT...AAT',
SingleLetterAlphabet()), id='seq3', name='seq3', description='seq3', dbxrefs=[]), 'seq4':
SeqRecord(seq=Seq('ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAA...GGT',
SingleLetterAlphabet()), id='seq4', name='seq4', description='seq4', dbxrefs=[])}
```

Let's retrieve some info from our new dictionary

```
>>> id_dict['seq4']
SeqRecord(seq=Seq('ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAA...GGT',
SingleLetterAlphabet()), id='seq4', name='seq4', description='seq4', dbxrefs=[])
>>> id_dict['seq4'].seq
Seq('ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAA...GGT',
SingleLetterAlphabet())
>>> str(id_dict['seq4'].seq)
'ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAAACAACATGCCAAATAGAAACGATCAATTCGGCGA
TGGAAATCAGAACAACGATCAGTTTGGAAATCAAAATAGAAATAACGGGAACGATCAGTTTAATAACATGATGCAGAATAAAGGGAATA
ATCAATTTAATCCAGGTAATCAGAACAGAGGT
>>>
```

> need to use this format to get the string of the sequence: `str(id_dict['seq4'].seq)`

Seq methods

Visit biopython.org to read how Sequences act like strings

```
from Bio.Seq import Seq
seqobj.count("A")  # counts how many As are in sequence
seqobj.find("ATG") # find coordinate of ATG (-1 for not found)
```

OR, as mentioned earlier in the interpreter you can use tab to find out what methods are available:

```
>>> from Bio.Seq import Seq
>>> seqobj=Seq('ATGCGATCGAGC')
>>> seqobj.
seqobj.alphabet             seqobj.find(                seqobj.rstrip(
 seqobj.transcribe(
seqobj.back_transcribe(     seqobj.lower(               seqobj.split(
seqobj.translate(
seqobj.complement(          seqobj.lstrip(              seqobj.startswith(
 seqobj.ungap(
seqobj.count(               seqobj.reverse_complement(  seqobj.strip(
seqobj.upper(
seqobj.count_overlap(       seqobj.rfind(               seqobj.tomutable(
seqobj.endswith(            seqobj.rsplit(              seqobj.tostring(
>>> seqobj.
```

AND, you can use the help() in the interpreter to find out more:

```
>>> help(seqobj.count_overlap)
Help on method count_overlap in module Bio.Seq:

count_overlap(sub, start=0, end=9223372036854775807) method of Bio.Seq.Seq instance
    Return an overlapping count.

    For a non-overlapping search use the count() method.

    Returns an integer, the number of occurrences of substring
    argument sub in the (sub)sequence given by [start:end].
    Optional arguments start and end are interpreted as in slice
    notation.

    Arguments:
     - sub - a string or another Seq object to look for
     - start - optional integer, slice start
```

```
      - end - optional integer, slice end

    e.g.

    >>> from Bio.Seq import Seq
    >>> print(Seq("AAAA").count_overlap("AA"))
    3
    >>> print(Seq("ATATATATA").count_overlap("ATA"))
    4
    >>> print(Seq("ATATATATA").count_overlap("ATA", 3, -1))
    1

    Where substrings do not overlap, should behave the same as
    the count() method:
:
```

SeqRecord objects

SeqIO.Parse generates Bio.SeqRecord.SeqRecord objects. These are annotated Bio.Seq.Seq objects.

Main attributes:

- id - Identifier such as a locus tag (string)
- seq - The sequence itself (Seq object or similar)

Access these with `sr.id` and `sr.seq`. `str(sr.seq)` gets the actual sequence string.

Additional attributes:

- name - Sequence name, e.g. gene name (string)
- description - Additional text (string)
- dbxrefs - List of database cross references (list of strings)
- features - Any (sub)features defined (list of SeqFeature objects)
- annotations - Further information about the whole sequence (dictionary). Most entries are strings, or lists of strings.
- letter_annotations - Per letter/symbol annotation (restricted dictionary). This holds Python sequences (lists, strings or tuples) whose length matches that of the sequence. A typical use would be to hold a list of integers representing sequencing quality scores, or a string representing the secondary structure.

SeqRecord objects have .format() to convert to a string in various formats

```
>>> for seq_record in SeqIO.parse("../files/seq.nt.fa", "fasta"):
...   seq_record.format('fasta')
...
'>seq1\nAAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGCCACCAA\nTTATGGTGTATGAGTGAATCTCTGGTCCGAGATTCACTGAGTAACTGCTGTACACAGTAG\nTAACACGTGGAGATCCCATAAGCTTCACGTGTGGTCCAATAAAACACTCCGTTGGTCAAC\n'
```

In the interpreter:

```
...   seq_record.
seq_record.annotations          seq_record.id                   seq_record.seq
seq_record.dbxrefs              seq_record.letter_annotations   seq_record.translate(
seq_record.description          seq_record.lower(               seq_record.upper(
seq_record.features             seq_record.name
seq_record.format(              seq_record.reverse_complement(
```

Retrieving annotations from GenBank file

To read sequences from a genbank file instead, not much changes.

```
#!/usr/bin/env python3
from Bio import SeqIO
for seq_record in SeqIO.parse("../files/sequence.gb", "genbank"):
  print('ID',seq_record.id)
  print('Sequence',str(seq_record.seq)[0:60],'...')
  print('Length',len(seq_record))
```

Output:

```
ID NM_204156.1
Sequence GGCCCCGGCCGGTGGGGCGGGTTGCGTTGCGCTGCGCGGCGGTAGGGTCTGCGGCCGTGG ...
Length 3193
```

File Format Conversions

Many are straightforward, others are a little more complicated because the alphabet can't be determined from the data. It's usually easier to go from richer formats to simpler ones.

```
#!/usr/bin/env python3
from Bio import SeqIO
fasta_records = SeqIO.parse("../files/seq.nt.fa", "fasta")
count = SeqIO.write(fasta_records , '../files/seqs.tab' , 'tab')
```

Produces

```
% more seqs.tab
seq1
AAGAGCAGCTCGCGCTAATGTGATAGATGGCGGTAAAGTAAATGTCCTATGGGCCACCAATTATGGTGTATGAGTGAATCTCTGGTCCG
AGATTCACTGAGTAACTGCTGTACACAGTAGTAACACGTGGAGATCCCATAAGCTTCACGTGTGGTCCAATAAAACACTCCGTTGGTCA
AC
seq2
GCCACAGAGCCTAGGACCCCAACCTAACCTAACCTAACCTAACCTACAGTTTGATCTTAACCATGAGGCTGAGAAGCGATGTCCTGACC
GGCCTGTCCTAACCGCCCTGACCTAACCGGCTTGACCTAACCGCCCTGACCTAACCAGGCTAACCTAACCAAACCGTGAAAAAAGGAAT
CT
seq3
ATGAAAGTTACATAAAGACTATTCGATGCATAAATAGTTCAGTTTTGAAAACTTACATTTTGTTAAAGTCAGGTACTTGTGTATAATAT
CAACTAAAT
seq4
ATGCTAACCAAAGTTTCAGTTCGGACGTGTCGATGAGCGACGCTCAAAAAGGAAACAACATGCCAAATAGAAACGATCAATTCGGCGAT
GGAAATCAGAACAACGATCAGTTTGGAAATCAAAATAGAAATAACGGGAACGATCAGTTTAATAACATGATGCAGAATAAAGGGAATAA
TCAATTTAATCCAGGTAATCAGAACAGAGGT
```

Here it is again in one step using the convert() method. Let's try FASTQ to FASTA.

```
#!/usr/bin/env python3
from Bio import SeqIO
count = SeqIO.convert('../files/pfb.fastq', 'fastq', '../files/pfb.converted.fa',
'fasta')
```

Was that easy or what??!??!!?

Parsing BLAST output

For simple parsing, or non BioPython parsing of NCBI BLAST results, use output formated in tab-separated columns (`-outfmt 6` or `-outfmt 7`) Both these formats are customizable when running the BLAST locally.

If you want to parse the full output of BLAST with biopython, it's necessary work with **XML** formatted BLAST output `-outfmt 5`.

You can get biopython to run the blast for you too. See `Bio.NCBIWWW`

To parse the output, you'll write something like this

```
#!/usr/bin/env python3
from Bio.Blast import NCBIXML
result_handle = open("../files/UTKBKAM5014-Alignment.xml")
blast_records = NCBIXML.parse(result_handle)
for blast_record in blast_records:
   query_id = blast_record.query_id
   for alignment in blast_record.alignments:
     for hsp in alignment.hsps:
        if hsp.expect < 1e-10:
           print(f'qid: {query_id} hit_id: {alignment.title} E: {hsp.expect}' )
           # print(query_id, alignment.title, hsp.expect, sep="\t" ) # print tab
delimited results table
```

Output:

```
qid: Query_26141 hit_id: sp|Q13547.1| RecName: Full=Histone deacetylase 1; Short=HD1
[Homo sapiens] >sp|Q5RAG0.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Pongo
abelii] E: 0.0
... etc
```

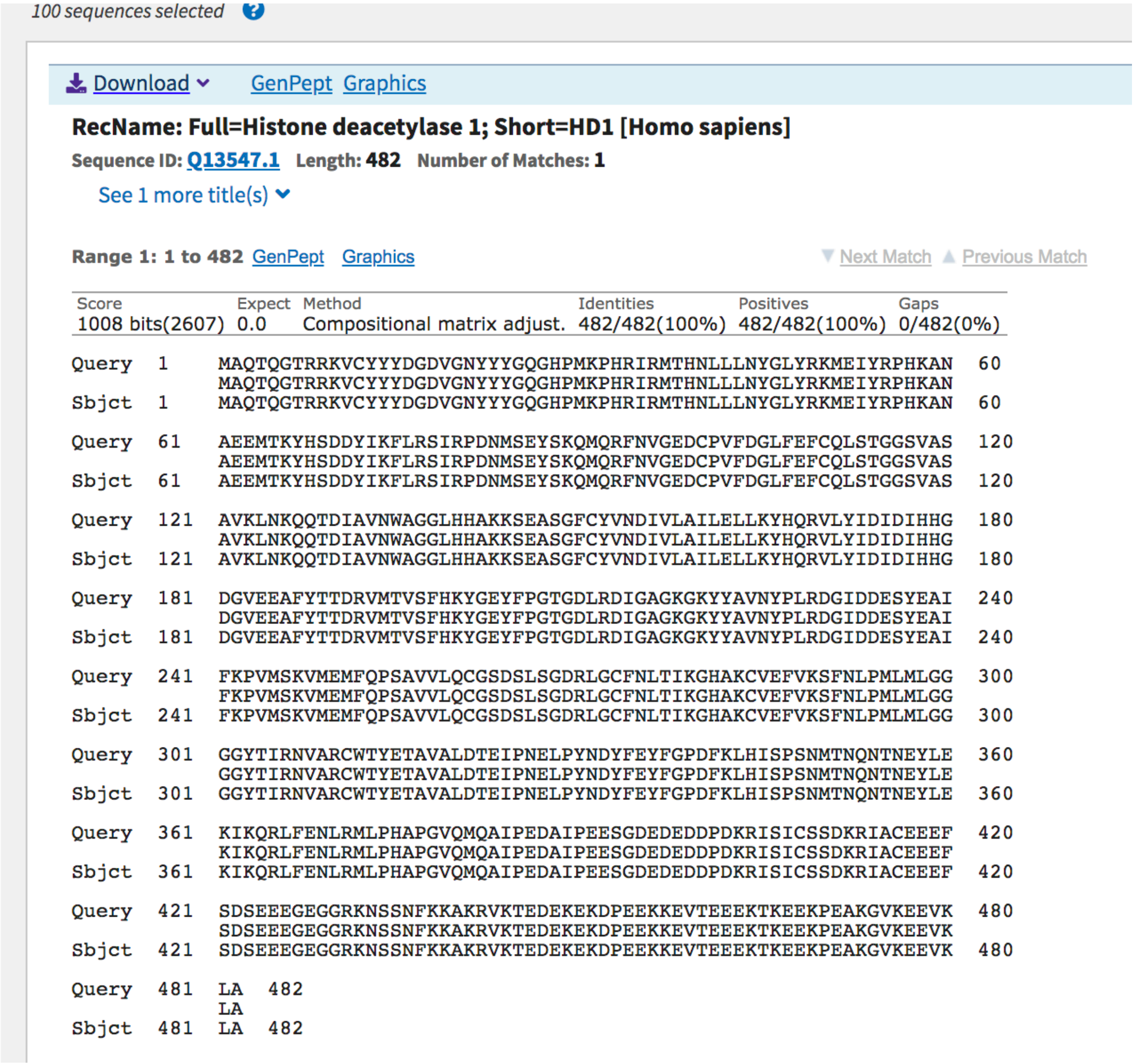
tab-delimited print output (`print(query_id, alignment.title, hsp.expect, sep="\t"`)

```
Query_26141 sp|Q13547.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Homo sapiens]
>sp|Q5RAG0.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Pongo abelii]  0.0
Query_26141 sp|O09106.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Mus musculus]
0.0
Query_26141 sp|Q4QQW4.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Rattus
norvegicus] 0.0
Query_26141 sp|Q32PJ8.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Bos taurus]  0.0
Query_26141 sp|P56517.1| RecName: Full=Histone deacetylase 1; Short=HD1 [Gallus gallus]
0.0
Query_26141 sp|O42227.1| RecName: Full=Probable histone deacetylase 1-B; Short=HD1-B;
AltName: Full=RPD3 homolog [Xenopus laevis] 0.0
... etc
```

About BLAST Search Report and BioPython:

- `blast_records` (type <class 'generator'>) can contain handle multiple queries (the sequence you are using as input)
- The results for each query are considered a `blast_record` ()
- Each `blast_record` will have info about the query, like blast_record.query_id
- Each `blast_record` will have information about each hit.
- A Hit is considered an `alignment` (<class 'Bio.Blast.Record.Alignment'>)

- An `alignment` has the following info: alignment.accession, alignment.hit_id, alignment.length, alignment.hit_def, alignment.hsps, alignment.title
- Each `alignment` will have 1 or more `hsp` (<class 'Bio.Blast.Record.HSP'>).
- An HSP is a "high scoring pair" or a series of smaller alignments that make up the complete alignment.
- `hsp` have the following info: hsp.align_length, hsp.frame, hsp.match, hsp.query, hsp.sbjct, hsp.score, hsp.bits hsp.gaps, hsp.num_alignments, hsp.query_end, hsp.sbjct_end, hsp.strand, hsp.expect, hsp.identities, hsp.positives, hsp.query_start, hsp.sbjct_start



RecName: Full=Histone deacetylase 1; Short=HD1 [Homo sapiens]

Sequence ID: Q13547.1 **Length:** 482 **Number of Matches:** 1

Range 1: 1 to 482 GenPept Graphics

Score	Expect	Method	Identities	Positives	Gaps
1008 bits(2607)	0.0	Compositional matrix adjust.	482/482(100%)	482/482(100%)	0/482(0%)

```
Query  1    MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKAN  60
            MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKAN
Sbjct  1    MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKAN  60

Query  61   AEEMTKYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVAS  120
            AEEMTKYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVAS
Sbjct  61   AEEMTKYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVAS  120

Query  121  AVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHG  180
            AVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHG
Sbjct  121  AVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHG  180

Query  181  DGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAI  240
            DGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAI
Sbjct  181  DGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAI  240

Query  241  FKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG  300
            FKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG
Sbjct  241  FKPVMSKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGG  300

Query  301  GGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLE  360
            GGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLE
Sbjct  301  GGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLE  360

Query  361  KIKQRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEF  420
            KIKQRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEF
Sbjct  361  KIKQRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEF  420

Query  421  SDSEEEGEGGRKNSSNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVK  480
            SDSEEEGEGGRKNSSNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVK
Sbjct  421  SDSEEEGEGGRKNSSNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVK  480

Query  481  LA  482
            LA
Sbjct  481  LA  482
```

Sample of BLAST XML output:

```
<Iteration>
  <Iteration_iter-num>1</Iteration_iter-num>
  <Iteration_query-ID>Query_26141</Iteration_query-ID>
  <Iteration_query-def>CAG46518.1 HDAC1 [Homo sapiens]</Iteration_query-def>
  <Iteration_query-len>482</Iteration_query-len>
<Iteration_hits>
<Hit>
  <Hit_num>1</Hit_num>
  <Hit_id>sp|Q13547.1|</Hit_id>
  <Hit_def>RecName: Full=Histone deacetylase 1; Short=HD1 [Homo sapiens] &gt;sp|Q5RAG0.1|
RecName: Full=Histone deacetylase 1; Short=HD1 [Pongo abelii]</Hit_def>
  <Hit_accession>Q13547</Hit_accession>
  <Hit_len>482</Hit_len>
  <Hit_hsps>
    <Hsp>
      <Hsp_num>1</Hsp_num>
      <Hsp_bit-score>1008.82</Hsp_bit-score>
      <Hsp_score>2607</Hsp_score>
      <Hsp_evalue>0</Hsp_evalue>
      <Hsp_query-from>1</Hsp_query-from>
      <Hsp_query-to>482</Hsp_query-to>
      <Hsp_hit-from>1</Hsp_hit-from>
      <Hsp_hit-to>482</Hsp_hit-to>
      <Hsp_query-frame>0</Hsp_query-frame>
      <Hsp_hit-frame>0</Hsp_hit-frame>
      <Hsp_identity>482</Hsp_identity>
      <Hsp_positive>482</Hsp_positive>
      <Hsp_gaps>0</Hsp_gaps>
      <Hsp_align-len>482</Hsp_align-len>

 <Hsp_qseq>MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKFLRS
IRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYH
QRVLYIDIDIHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKPVMSKVMEMFQPSA
VVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHI
SPSNMTNQNTNEYLEKIKQRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEEEGEGGRKNS
SNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA</Hsp_qseq>

 <Hsp_hseq>MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKFLRS
IRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYH
QRVLYIDIDIHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKPVMSKVMEMFQPSA
VVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHI
SPSNMTNQNTNEYLEKIKQRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEEEGEGGRKNS
SNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA</Hsp_hseq>

 <Hsp_midline>MAQTQGTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMTKYHSDDYIKF
LRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELL
KYHQRVLYIDIDIHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKPVMSKVMEMFQ
PSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGYTIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFK
LHISPSNMTNQNTNEYLEKIKQRLFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEEEGEGGR
KNSSNFKKAKRVKTEDEKEKDPEEKKEVTEEEKTKEEKPEAKGVKEEVKLA</Hsp_midline>
```

```
    </Hsp>
  </Hit_hsps>
</Hit>
<Hit>
  <Hit_num>2</Hit_num>
  <Hit_id>sp|O09106.1|</Hit_id>
  <Hit_def>RecName: Full=Histone deacetylase 1; Short=HD1 [Mus musculus]</Hit_def>
  <Hit_accession>O09106</Hit_accession>
  <Hit_len>482</Hit_len>
  <Hit_hsps>
    <Hsp>
      <Hsp_num>1</Hsp_num>
  ...
```

There are many other uses for Biopython

- reading multiple sequence alignments
- searching on remote biological sequence databases
- working with protein structure (requires numpy to be installed)
- biochemical pathways (KEGG)
- drawing pictures of genome and sequence features
- population genetics

Why use biopython

Massive time saver once you know your way around the classes.

Reuse someone else's code. Very quick parsing of many common file formats.

Clean code.