CHEATSHEET PYTHON 5: Biopython

Sequence Input/Output

To read and write sequence or alignment data, import these modules

```
from Bio import SeqIO    # For reading/writing files with sequences
from Bio import AlignIO  # For reading/writing files with alignments
```

Command	Description	Example
`SeqIO.read()`	read a single sequence from file	`SeqIO.read("seq.fasta", "fasta")`
`SeqIO.parse()`	read many sequences from file	`SeqIO.parse("seqs.fasta", "fasta")`
`AlignIO.read()`	read a single alignment from file	`SeqIO.read("align.fasta", "fasta")`
`AlignIO.parse()`	read many alignments from file	`SeqIO.parse("aligns.phy", "phylip")`
`SeqIO.write()`	write sequence(s) to file	`SeqIO.write(seq_record(s), "seq_output.fasta", "fasta")`
`AlignIO.write()`	write alignment(s) to file	`AlignIO.write(aln_record, "align_output.fasta", "fasta")`
`AlignIO.convert()`	Convert alignment file to a different format	`AlignIO.convert("input.fasta", "fasta", "output.phy", "phylip")`

Biopython Seq objects

To use and/or manipulate Seq/SeqRecord objects, import these modules

```
from Bio.Seq import Seq
from Bio.SeqRecord import SeqRecord
from Bio.Alphabet import *
```

Object type	Useful attributes/methods
SeqRecord	`.id, .seq, .description`
Seq	`.transcribe(), .translate(), .complement(), and more!`

Query online databases

To download and parse data from various online databases, import one of these modules

```
from Bio import Entrez     # Query an NCBI database
from Bio import ExPASy     # Query SwissProt/Uniprot
from Bio import SwissProt  # Parse swissprot/uniprot records.
```

Command	Description	Examples

`Entrez.efetch()`	Fetch and parse a record from an NCBI database	`record = Entrez.efetch(id = "NP_000549.1", db = "protein", remode = "text", retype = "gb")`
		
		`record = Entrez.efetch(id = "88758587", db = "nucleotide", remode = "text", retype = "gb")`

1. `ExPASy.get_sprot_raw()` 2. `SwissProt.read()`	Fetch and parse a swissprot record	`handle = ExPASy.get_sprot_raw("A3KFT3") # A3KFT3 is any ID!` `record = SwissProt.read(handle)`