**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

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| **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 \*

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| **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.

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| **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) |