Biopython

from Bio import SeqIO # SeqIO used to read sequence files

from Bio.Align import MultipleSeqAlignment #import MultipleSeqAlignment module

#create a list of filenames

files = ['your\_sequence\_file1.fasta', 'your\_sequence\_file2.fasta', ...]

#create a list of sequences

records = []

for f in files:

for record in SeqIO.parse(f, format='fasta'):

records.append(record)

#align all the sequences in the file

align = MultipleSeqAlignment(records)

Numpy

* Working with arrays
* basic linear algebra
* basic statistical operations
* random simulation