Life Machinery

Lab 2

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» Introduction

Turning Biology into Mathematics

In this lab demonstration we will access the uniprot database and create a new dataset. Our dataset will consist of four thousand proteins, half associated with the keyword antibody and the other half not related to the keyword. The proteins are represented by their primary structure sequence of amino acids, in other words each protein is a string of letters representing each amino acid in the sequence.

» Dataset

The one-letter and three-letter codes for amino acids used in the knowledgebase are those adopted by the commission on Biochemical Nomenclature of the IUPAC-IUB
One-letter code Three-letter code Amino-acid name
A Ala Alanine
R Arg Arginine
N Asn Asparagine
D Asp Aspartic acid
C Cys Cysteine
Q Gln Glutamine
E Glu Glutamic acid
G Gly Glycine
H His Histidine
I Ile Isoleucine
L Leu Leucine
K Lys Lysine

» Dataset cont'd

M Met Methionine
F Phe Phenylalanine
P Pro Proline
S Ser Serine
T Thr Threonine
W Trp Tryptophan
Y Tyr Tyrosine
V Val Valine
O Pyl Pyrrolysine
U Sec Selenocysteine
B Asx Aspartic acid or Asparagine
Z Glx Glutamic acid or Glutamine
X Xaa Any amino acid

Analysis of data using Python Codes


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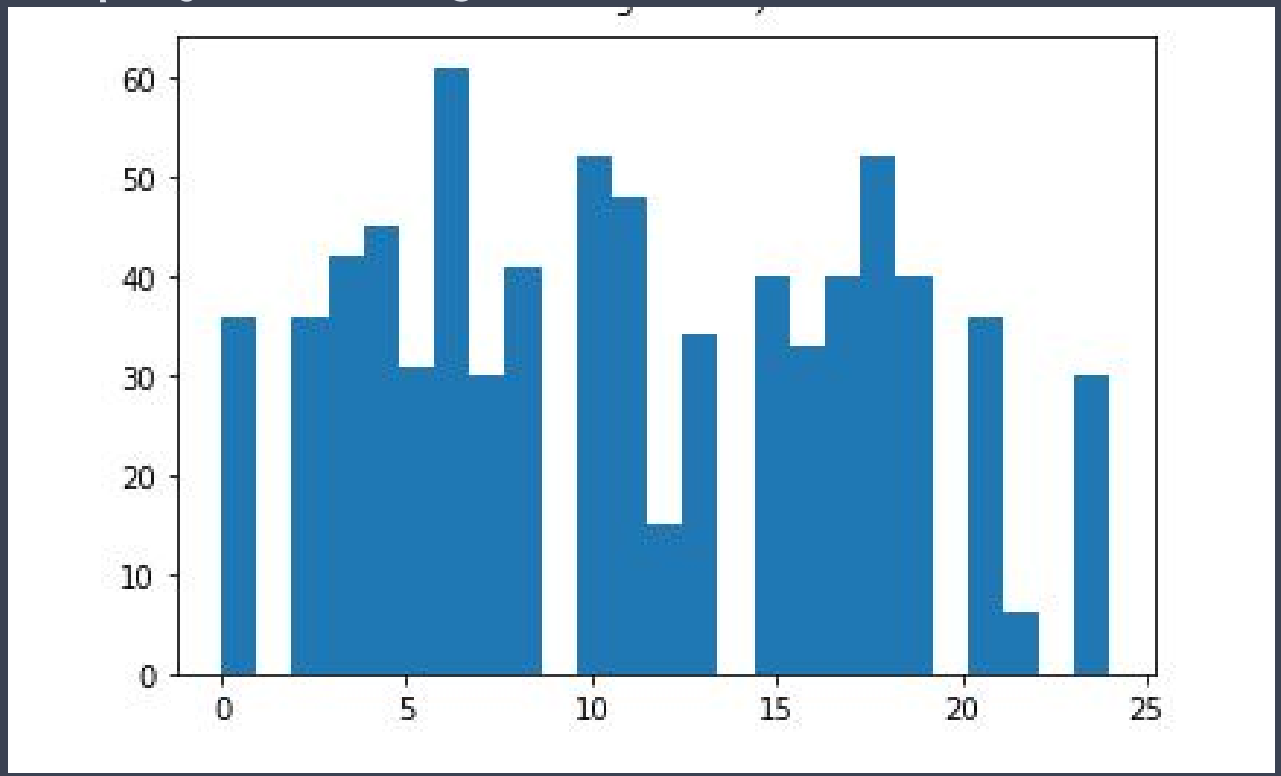
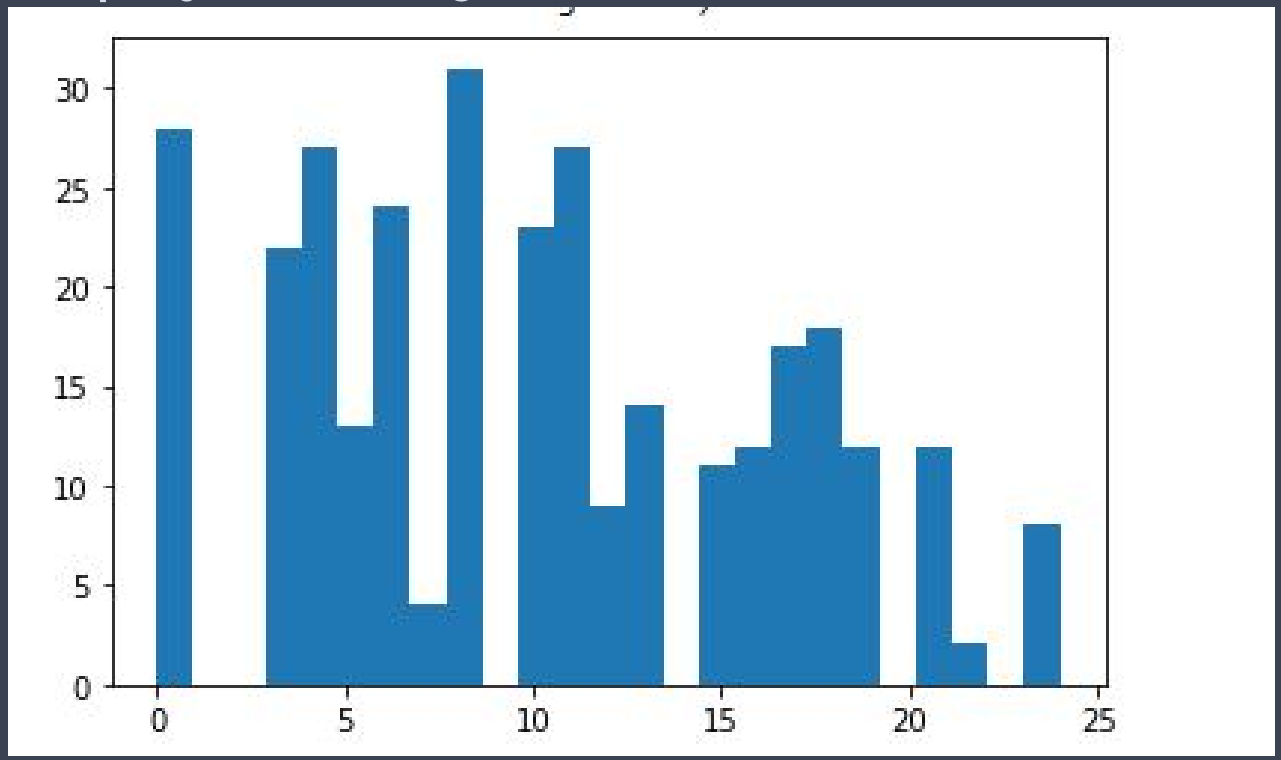
```
!pip install git+https://github.com
/williamedwardhahn/mpcr

# installing pip from instructor's github
from mpcr import *

# This code will create a dataset from the
uniprot database

X, Y = get_uniprot_data('=antibody',
'!antibody', 2000)

# create dataset with 2000 samples

number_X = len(X)
#Assigning name to the length
of X and Y from the dataset
number_Y = len(Y)
```

```
print(len(X[0])),print(len(Y[0]))

#printing out the length of the
1st protein in X (antibodies) and Y (antibodies)
print(len(X[1])),print(len(Y[1]))
print(len(X[2])),print(len(Y[2]))
print(len(X[3])),print(len(Y[3]))
print(len(X[1999])),print(len(Y[1999]))

X[0] #Amino acid sequence of the first protein on t

def process_strings(c):
    '''Takes in a list of sequences 'c' and turns e
       into a list of numbers.'''

    X = []

    for  m, seq in enumerate(c):
        x = []
```

Display of Histogram for X



Display of Histogram for Y



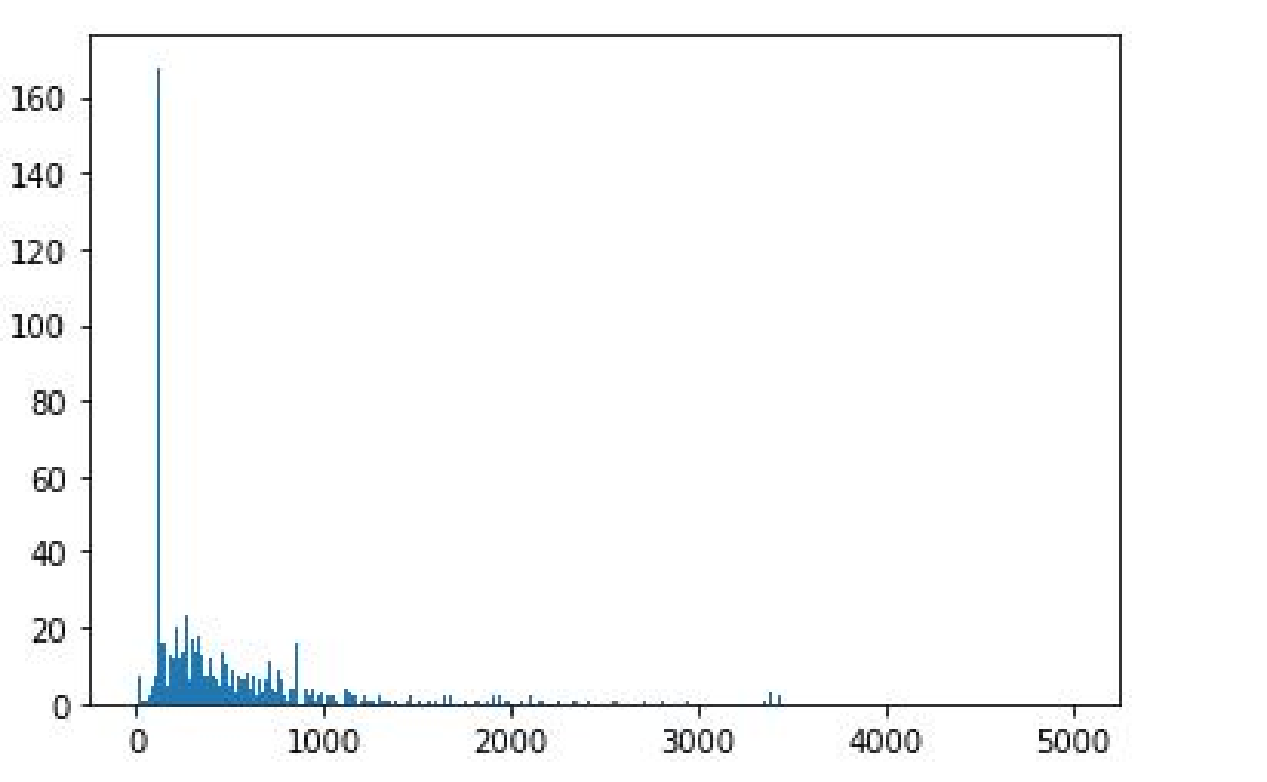
```
np.mean(X[0]),np.std(X[0])
#meaningful? Finding the mean and
standard deviation of the 1st proteins

np.array(X[0]).shape

#size of the first protein in X
```

Find lengths of all proteins:

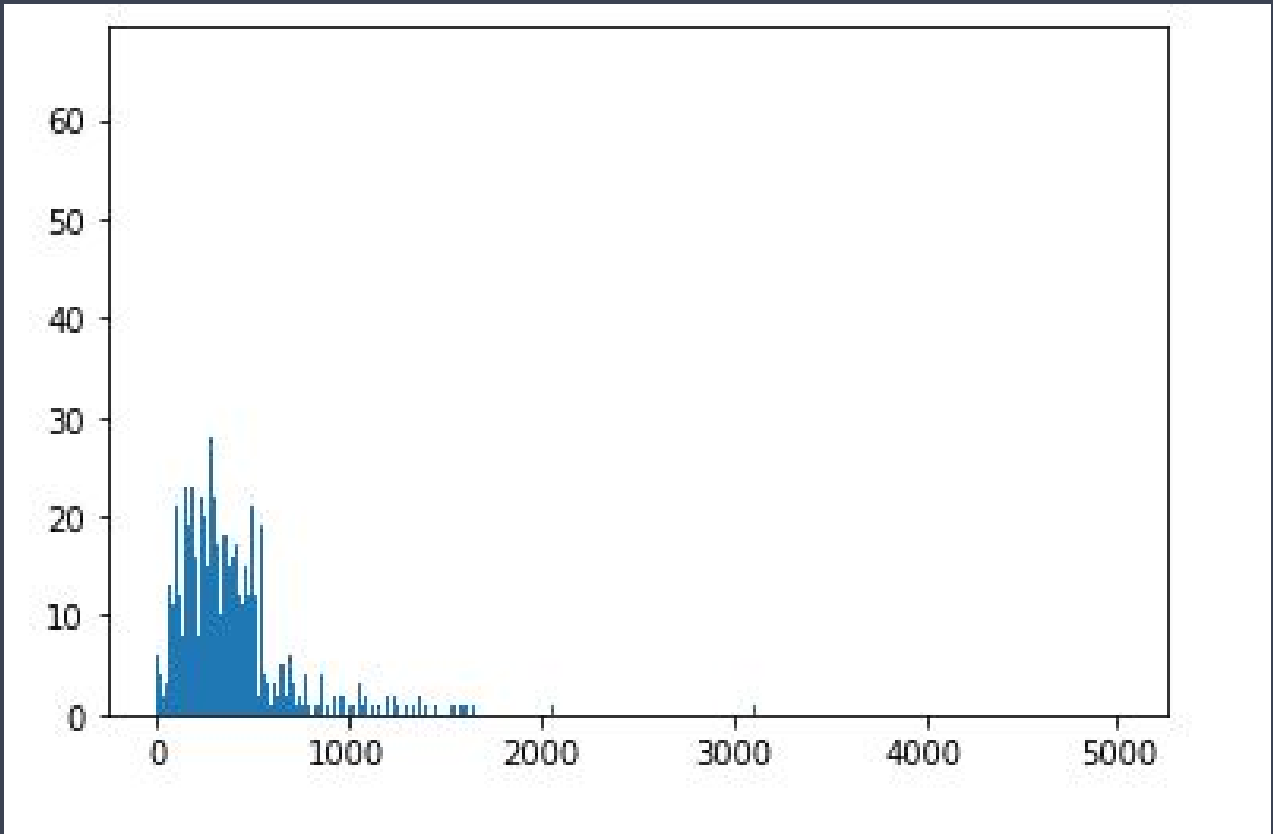
```
X_lengths = [len(s) for s in X]
Y_lengths = [len(s) for s in Y]

np.max(X_lengths)  #Max length in X
np.max(Y_lengths)  #Max length in Y

np.min(X_lengths)  #min length in X
np.min(Y_lengths)  #min length in Y
```

```
plt.hist(X_lengths,bins=1000,range=(0,5000));

#plot a histogram of X lengths
with intervals 1000 from 0–5000}

plt.hist(Y_lengths,bins=1000,range=(0,5000));

#plot a histogram of Y lengths
with intervals 1000 from 0–5000
```

Display of Histogram for X



Display of Histogram for Y



THE END