



THE UNIVERSITY *of* EDINBURGH  
School of Biological Sciences

# **Assignment 1**

## **Practical Systems Biology**

Student Exam Number: B161216

```
In [1]: import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
```

## Probability

```
In [2]: dna1 = str(np.load('dna1.npy'))
dna2 = str(np.load('dna2.npy'))
```

### Question 1.1

```
In [3]: #define a function that reports the probability of finding a base (b) in a sequence (seq)
def base_prob(seq, b, seq_name):
    i = 0
    for n in seq:
        if n == b:
            i += 1
    prob = i/len(seq)
    print ("The probability of finding {} in {} is {}".format(b, seq_name, prob))
```

```
In [4]: #call probability reporter for each base and each sequence
bases = "ACTG"
for base in bases:
    base_prob(dna1, base, "dna1")
print()
for base in bases:
    base_prob(dna2, base, "dna2")
```

The probability of finding A in dna1 is 0.308125  
The probability of finding C in dna1 is 0.223625  
The probability of finding T in dna1 is 0.29925  
The probability of finding G in dna1 is 0.169

The probability of finding A in dna2 is 0.30875  
The probability of finding C in dna2 is 0.217  
The probability of finding T in dna2 is 0.3105  
The probability of finding G in dna2 is 0.16375

### Question 1.2

```
In [5]: #define a function that reports the probability of finding a fragment(f) in a sequence (seq)
def base_prob2(seq, f, seq_name):
    exp = len(seq)/4**len(f)
    i = 0
    c = 0
    #test every position of the sequence
    for n in range(len(seq)):
        #doesn't matter the number of bases being surveyed because this adapts to f's length
        if seq[c:c+len(f)] == f:
            i += 1
        c += 1
    prob = i/len(seq)
    print ("The probability of finding '{}' in {} is {}".format(f, seq_name, prob))
```

```
In [6]: #define fragment to search for
fragment = "TTTT"

#search for fragment's sequence in each
base_prob2(dna1, fragment, "dna1")
base_prob2(dna2, fragment, "dna2")
```

The probability of finding 'TTTT' in dna1 is 0.009875  
The probability of finding 'TTTT' in dna2 is 0.02775

Considering that the probability of finding a given sequence of base pairs in another random sequence (each base is independent from the rest of the sequence) is  $(1/4)^n$ , where  $n$  is the given sequence's length, the probability of finding a 4-base long sequence (in this case TTTT) would be  $(1/4)^4$ , or 0.00390625. This probability is closer to the one found in dna1, so this must be the synthetic sequence and dna2 must be the natural one.

## Entropy

### Question 2.1

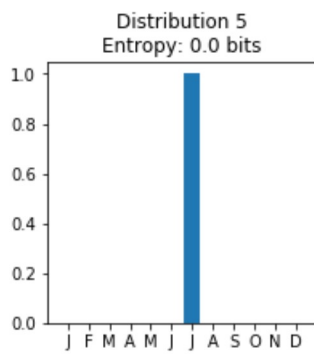
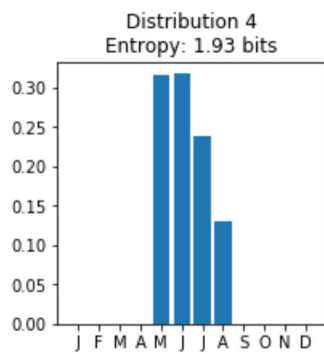
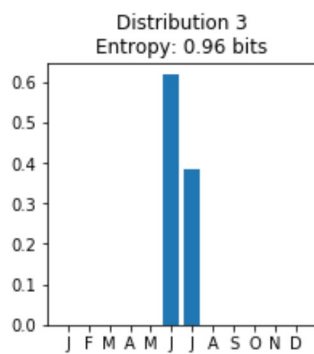
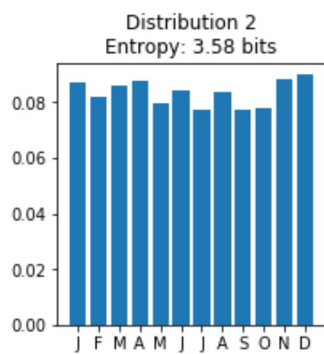
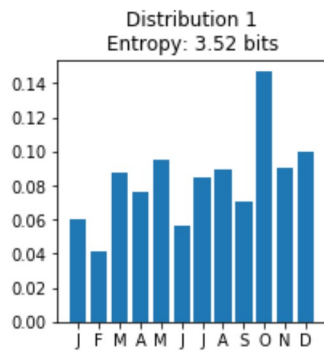
```
In [7]: #calculate the entropy of a variable given its probability distribution
#pd is a list of probabilities for each state of a variable
def entropy(pd):
    total = 0
    for n in pd:
        if n != 0:
            total -= n*np.log2(n)
    return total
```

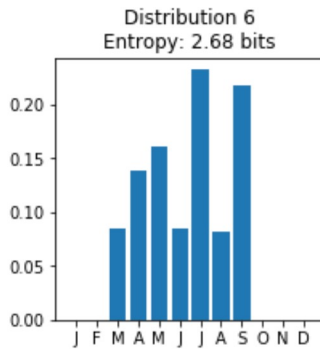
### Question 2.2

```
In [8]: d1= np.load('annualprobs.npy')

#set the x-axis labels for figures
months = ["J", "F", "M", "A", "M", "J", "J", "A", "S", "O", "N", "D"]
x_axis = np.linspace(0, len(months)-1, len(months))

#for each distribution (dist) 1 to 6, calculate its entropy and plot it
for dist in range(len(d1)):
    #rounding entropy values to 2 decimal places
    ent = round(entropy(d1[dist]), 2)
    plt.figure(figsize = (3,3))
    plt.title("Distribution {} \nEntropy: {} bits".format(dist+1, ent))
    plt.bar(x_axis, d1[dist])
    plt.xticks(x_axis, months)
    plt.show()
```





The entropy seems to be higher if the probabilities are similar for each state of the distribution, as best represented in Distribution 2 (with the highest entropy).

If there is a strong bias to one or some of the states (probability is concentrated in a few states), as in Distributions 5 or 3, respectively, the entropy is lower. This makes sense with the definition of entropy as "a measure of how disorganized something is".

## Measuring the dependance between two random variables

```
In [9]: d2 = np.load('XandY.npy')
```

### Question 3.1

```
In [10]: def correlation(x, y):
    #get means for each list
    mx = np.mean(x)
    my = np.mean(y)

    #variables to store each sum in the correlation
    sum_x2 = 0
    sum_y2 = 0
    sum_xy = 0

    #get values for every sum
    for n in x:
        sum_x2 += (n - mx)**2
    for n in y:
        sum_y2 += (n - my)**2
    for c in range(len(x)): #x and y need to have the same amount of elements
        sum_xy += (x[c] - mx) * (y[c] - my)

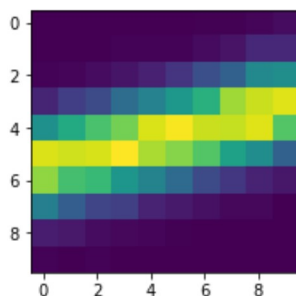
    #return the final calculation of the correlation
    return sum_xy / (sum_x2 * sum_y2) ** (1/2)
```

### Question 3.2

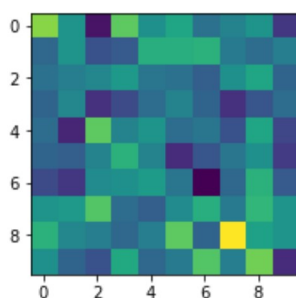
Plotting for every dataset instead of just one

```
In [11]: for set in range(0, len(d2), 2):
          hist, xedges, yedges = np.histogram2d(d2[set], d2[set+1], bins = 10)
          hist = np.rot90(hist)
          print("Dataset", int(1+set/2))
          plt.figure(figsize = (3,3))
          plt.imshow(hist, aspect = 'auto')
          plt.show()
```

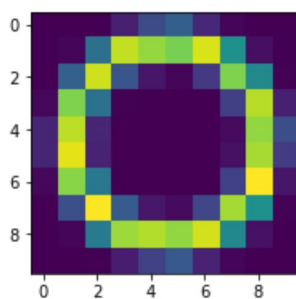
Dataset 1



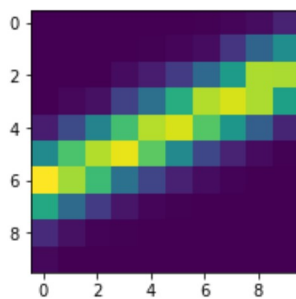
Dataset 2



Dataset 3



Dataset 4



### Question 3.3

The number of events is the length of each dataset.

The probability that an event falls into a bin should then be equal to the number of events in that bin divided by the total number of events

```
In [12]: #this function returns the mutual information between x and y, normalized by the entropy of y
def normalized_mutual_information(x, y):
    hist, xedges, yedges = np.histogram2d(x, y, bins = 10)
    hist_norm = hist/np.sum(hist) #normalize the histogram to get the bins probability distribution

    #calculate conditional entropy of y given x
    cond_ent = 0
    for x_val in hist_norm:
        x_prob = np.sum(x_val)
        for y_val in x_val:
            if y_val != 0:
                cond_ent += y_val*np.log2(x_prob/y_val)

    #calculate y entropy and normalized mutual information
    y_probs = np.sum(hist_norm, axis = 0)
    y_ent = entropy(y_probs)
    nmi = (y_ent-cond_ent)/y_ent

    return nmi
```

```
In [13]: #approximating final results to 2 decimal points
cor = round(correlation(d2[0], d2[1]), 2)
nmi = round(normalized_mutual_information(d2[0], d2[1]), 2)
print("Dataset 1")
print("Correlation:", cor)
print("Normalized Mutual Information:", nmi)
```

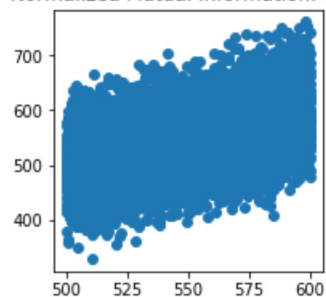
```
Dataset 1
Correlation: 0.52
Normalized Mutual Information: 0.09
```

## Question 3.4

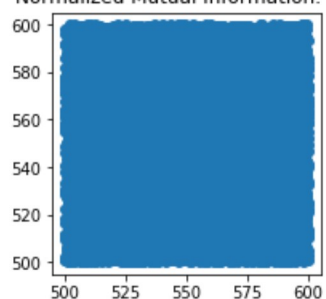


```
In [14]: for set in range(0, len(d2), 2):  
          #approximating final results to 2 decimal points  
          cor = round(correlation(d2[set], d2[set+1]), 2)  
          nmi = round(normalized_mutual_information(d2[set], d2[set+1]), 2)  
          plt.figure(figsize = (3,3))  
          plt.scatter(d2[set], d2[set+1])  
          plt.title("Dataset {} \nCorrelation Coefficient: {} \nNormalized Mutual Information: {}"  
                    .format(int(1+set/2), cor, nmi))  
          plt.show()
```

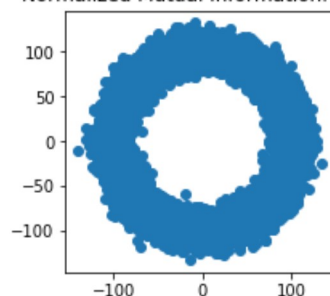
Dataset 1  
Correlation Coefficient: 0.52  
Normalized Mutual Information: 0.09



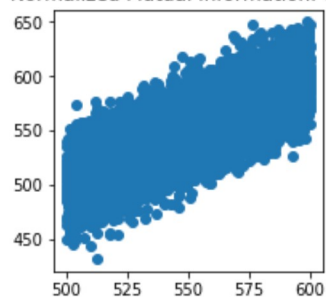
Dataset 2  
Correlation Coefficient: -0.01  
Normalized Mutual Information: 0.0



Dataset 3  
Correlation Coefficient: -0.0  
Normalized Mutual Information: 0.25



Dataset 4  
Correlation Coefficient: 0.82  
Normalized Mutual Information: 0.27



While correlation and mutual information have some measure of dependance between  $x$  and  $y$ , they behave differently.

Correlation appears to be high only if there is a linear approximation to the relation between  $x$  and  $y$ , as seen in datasets 1 and 4. As there is no linear correlation between  $x$  and  $y$  in datasets 2 and 3, the correlation coefficient nears 0.

The normalized mutual information, in the other hand, still has distinguishable values for datasets 1 and 4, but now also for dataset 3. Visually, dataset 3 seems relatively "organized". We can know a lot about  $y$  if we know  $x$ , even if they do not correlate linearly, and that is why the normalized mutual information nears the one seen in dataset 4. As the probabilities are still concentrated in a few positions of the probability-space, the entropy is reduced. If we know the values for  $x$ . For example, if we know that  $x$  is a middle-value in dataset 3, we would certainly know that  $y$  would have an extreme value.