Inter and Intra Organism Patterns in Proteomic Sequences

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1. Methodology

We employed different methodologies for the sub-hypothesis that were defined in previous section.

1. (Hypothesis 1) Reestablishment of Evolutionary Taxonomy

We obtained a sample of 59 organism’s (Eukaryotes) proteome sequences from Ensembl Genome Browser, 17 viral[[1]](#footnote-1) proteome sequences and 18[[2]](#footnote-2) bacterial proteome sequences from Uniprot Catalog. The resulting sequence was pre-processed and the amino acid counts were calculated. We used several statistical tools to establish our hypothesis.

1. Pre-processing:

The proteome sequences for the sample were processed to find out the respective count of each of the 20 (and undetermined 21st) amino acids. We define a count vector that stores this respective count in a 21 dimensional vector.

Further, we scaled the vector to get the relative ratios of each amino acid. This was done due to the fact that the counts of individual amino acids change drastically between different organisms (on the basis of their biological complexity). We define the scaled count vector as:

We use vector for all the statistics under this hypothesis.

1. Plotting the Vectors:

Due to the large dimension (21) of the vector we used the parallel plot technique to obtain the line charts. This was done for a visualization of the relatively high dimensional vectors. The parallel axes were set to a common scale.

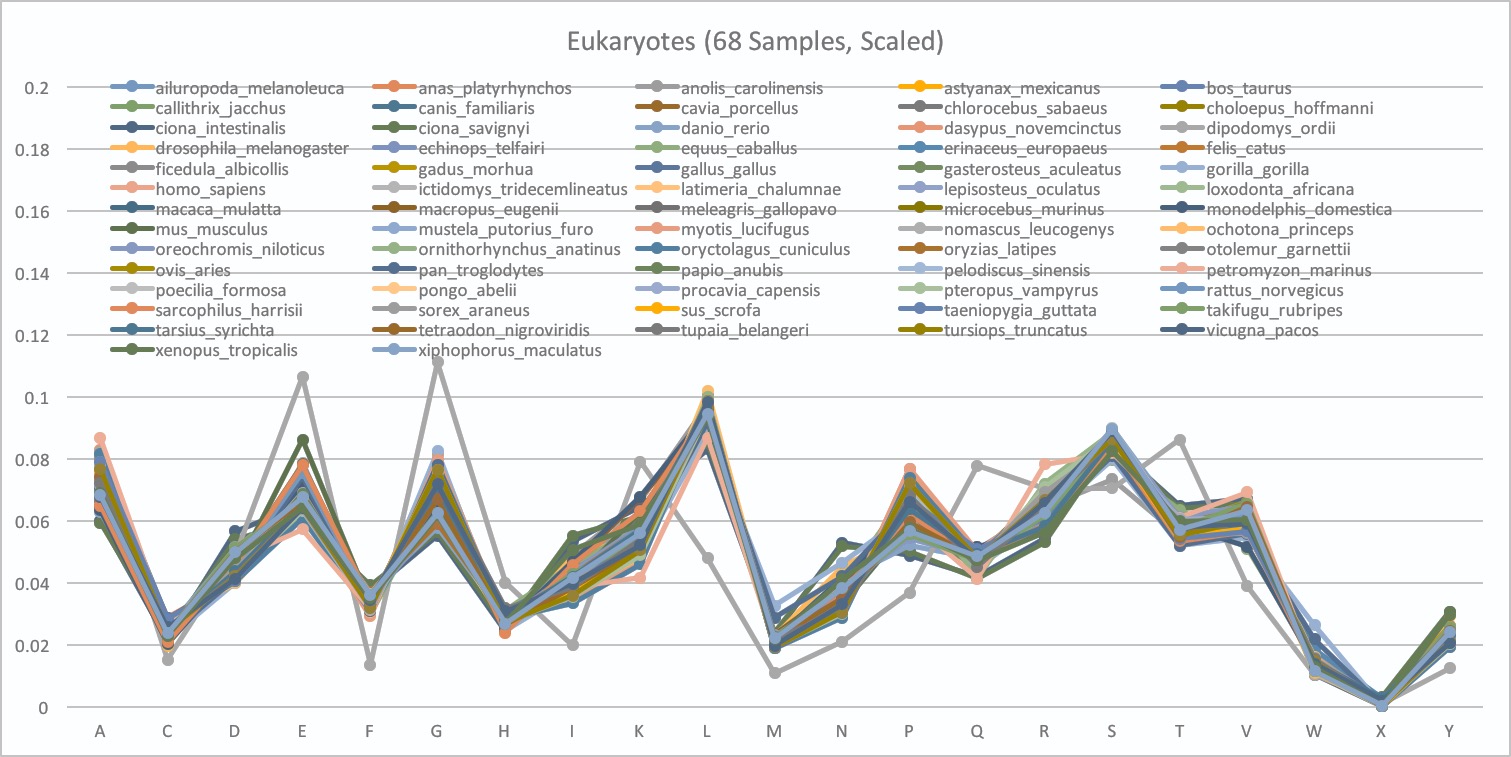
1. Pearson product-moment correlation coefficient:

To quantize the observation in the plots obtained we calculated four sets of correlation coefficients. The sets are:

* Correlation of Eukaryotic Proteome against itself,
* Correlation of Bacterial Proteome against itself,
* Correlation of Viral Proteome against itself, and
* Correlation of Eukaryotic Proteome against Viral and Bacterial Proteome.

Further, the mean of the correlation coefficients obtained was calculated. A higher value of this mean would indicate a greater closeness between the vectors. A lower value of the correlation coefficient, on the other hand, would indicate the inherently distinct behaviour of the data.

1. k-Mean Clustering:



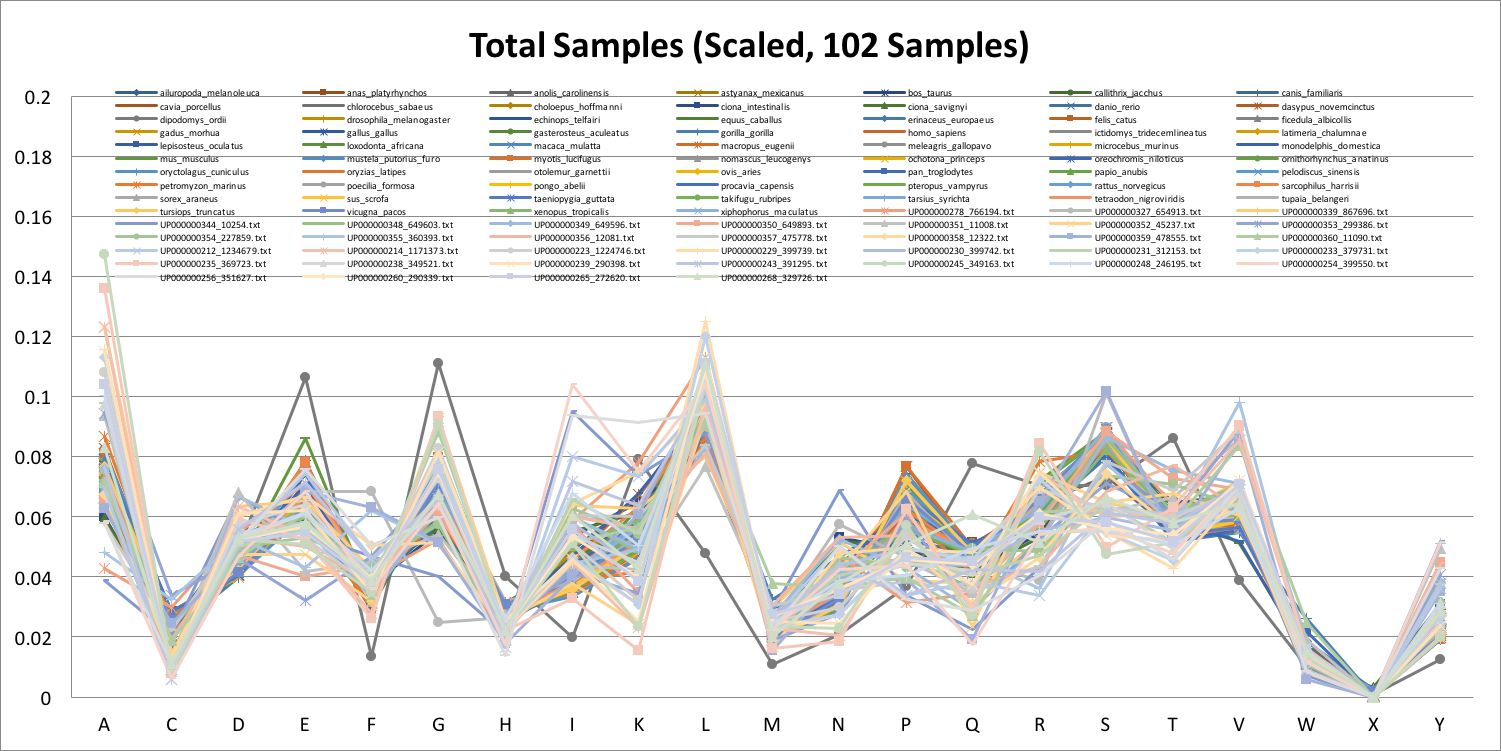


Figure Table s

To further strengthen the closeness between the vectors, we ran a k-mean partitioning with all vector samples. A k-Mean object was trained using the concatenation of Eukaryotic Proteomes. By re-running the samples on the k-mean fitted object and counting the number of respective partitions obtained, we were able to judge the clustering property of the vectors. Lower number of partitions would indicate greater cluster formation.

1. Principle Component Analysis:

We calculated the first two Principal Components of each vector classes separately. Different components for different classes of vectors indicated the data’s dissimilarity or similarity based on the coordinates they clustered at.

## (Hypothesis 2) Bacterial and Viral targets

Viruses cannot survive in isolation; they need a host in which they can survive. The above sample of 429 viruses, obtained for our previous hypothesis, was further tagged according to their hosts. The two subsamples considered were the viruses that attack Bacteria and those that attack *Homo sapiens* (Humans). Alongside, the proteome sequence of *Homo sapiens* and bacteria was taken for comparison. The sample length of bacteria was 250, obtained after random sampling from 692 bacteria.

The pre-processing of the data follows from the previous section.

## (Hypothesis 3)

Past studies have established the generality of this central principle of biochemistry that sequence of amino acids in protein specifies conformation. The dependence of conformation on sequence is significant because of the connection between conformation and function of a protein.

It is seen that residues such as alanine, glutamate, and leucine tend to be present in a helices, whereas valine and isoleucine tend to be present in ß strands. Glycine, asparagine, and proline have a propensity for being in turns.

The proteome data of Mycobacterium Tuberculosis was taken in the FASTA format from UniProt database of proteomes. All the possible amino acids sequences of length five and their respective number of occurrences in the proteome were processed. The sequences were ordered in the decreasing order of their frequencies.

The resulting sequences with highest frequencies were analysed and then compared to known motifs of *Mycobacterium Tuberculosis*.

# Results and Discussion

The following sections summarize the results obtained for the three hypothesis.

1. (Hypothesis 1) Reestablishment of Evolutionary Taxonomy
2. Plots

### Pearson product-moment correlation coefficient:

The value of correlation coefficient is higher for Eukaryotic proteome than the Bacterial and Viral proteome. The following table summarises the result of PPMCC test. An important result here is that the values obtained here conform to the arguments put up from the plots.

TABLE   
Correlation Coefficients and Interpretation

|  |  |  |  |
| --- | --- | --- | --- |
| Candidate | Value | Interpretation | Comments |
| Eukaryotic Proteome against itself | 0.9737 | High correlation (closeness) between the vectors. (Rank 1) | Explains the closeness as obtained in the data. |
| Bacterial Proteome against itself | 0.8813 | Less correlation between the vectors. (Rank 2) | Explains observable irregularities in the plotted vectors. |
| Viral Proteome against itself | 0.8283 | Lesser correlation between the vectors. (Rank 4) | Explains the high irregularities in the vectors. |
| Eukaryotic Proteome against Viral and Bacterial Proteome | 0.8802 | Less correlation between the vectors. (Rank 3) | Explains the irregularities. Strengthens the hypothesis that the vectors are deviating. |

### k-Mean Clustering:

This result indicates that the samples cluster in three distinct partitions.

TABLE II  
Statistics from k-Mean Clustering

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Clustered | Total | Ratio | Interpretations |
| Eukaryotic Proteome | 59 | 59 | 100% | All the sampled Eukaryotic Proteomes clustered in same partition. (Rank 1) |
| Bacterial Proteome | 15 | 17 | 88.2% | Most of the samples clustered in same partition. (Rank 2) |
| Viral Proteome | 14 | 18 | 77.7% | Quite high number of samples clustered. (Rank 3) |

### Principle Component Analysis:

This result indicates that the samples cluster in three distinct partitions.

TABLE III  
Cluster statistics from Principle Component Analysis

|  |  |  |
| --- | --- | --- |
| Sample | Principal Component | Interpretation |
| Eukaryotic Proteome | [0.48020417, 0.29809942] | Three distinct Principal Components imply three distinct classifications of the vectors. |
| Bacterial Proteome | [0.80249911, 0.08815054] |
| Viral Proteome | [0.43344298, 0.15875654] |

### Conclusion for Hypothesis 1:

The results obtained through the said analysis all agrees to our initial hypothesis that the Evolutionary taxonomy, which is based on phylogenetic relationship, can be revalidated through the proteomic sequences. This comes from the result that the proteomes of different classes of organisms and viruses clustered together, leading to a clear distinction between different phylogenetic branches, agreeing to the evolutionary taxonomy.

## (Hypothesis 2)

1. Plots

### k-Mean Clustering:

TABLE IV  
Statistics from k-Mean Clustering (96 samples)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Clustered | Total | Ratio | Interpretations |
| Bacterial Proteome | 33 | 48 | 68.7% | All bacteria do not get clustered in the same partition. |
| Viral Proteome | 32 | 48 | 66.6% | No proper clustering of viruses. |

The above proves that the data is too similar to be divided into two proper classes and hence our hypothesis can be assumed to be true to an accuracy of approximately 32.3%. Hence, there is a probability that we can map a virus to its host by knowing only its proteome sequence up to an accuracy of 32.3%. Increasing the sample length of bacteria to 250, does establish the hypothesis and increases the accuracy to 42%. Further increasing it to 692, an accuracy of 43% can be achieved. The result proves the hypothesis to be wrong and the alternate hypothesis to be correct, which means that one cannot correctly map a virus to its host based only upon the proteome sequence of the two.

TABLE V  
Statistics from k-Mean Clustering (50 samples)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Clustered | Total | Ratio | Interpretations |
| *Homo sapiens* | 1 | 1 | 100% | Expected result for a single point data. |
| Virus that attack Human | 30 | 49 | 61.2% | 28 out of 48 viruses get clustered and tagged into a partition. |

Similar result can be observed here with only 38.78% accuracy in predicting the host of a virus.

TABLE VI  
Statistics from k-Mean Clustering (96 Samples)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Clustered | Total | Ratio | Interpretations |
| Virus that attack Bacteria | 24 | 48 | 50% | No proper clustering. |
| Virus that attack Human | 28 | 48 | 58.3% | 28 out of 48 viruses get clustered and tagged into a partition. |

The above result shows that no clear difference can be established between the viruses that have different hosts. Hence, proteome sequence cannot be the only measure to predict and tag viruses for their hosts.

## (Hypothesis 3)

The average of the number of occurrences of the sequences in the proteome was found out to be 1.91 and its variance to be 12.85. This suggested that there could be some sequences that occurred multiple times. Following were the sequences with highest frequency of occurrences in descending order:

Trying to find the presence of these sequences in known motifs of Mycobacterium Tuberculosis could not produce any concrete result. Though, looking at the above table we can conclude that the sequences are Glycine (G) rich. Referring to the paper we can see that these Glycine rich proteins are in fact important as they regulate the cell outer structure (antigen) of this particular bacteria.

Moreover, by table, relative frequency of Glycine in secondary structures infer that it is predominantly found in turns, suggesting, Glycine must be an important amino acid which modulates the structure of the proteins in *Mycobacterium Tuberculosis*.

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gv_figure_4

Fig. 1 A sample line graph using colors which contrast well both on screen and on a black-and-white hardcopy

Fig. 2 shows an example of a low-resolution image which would not be acceptable, whereas Fig. 3 shows an example of an image with adequate resolution. Check that the resolution is adequate to reveal the important detail in the figure.

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Fig. 2 Example of an unacceptable low-resolution image



Fig. 3 Example of an image with acceptable resolution

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* example of a book in [1]
* example of a book in a series in [2]
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* example of a standard in [12]

1. Conclusions

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Causal Productions wishes to acknowledge Michael Shell and other contributors for developing and maintaining the IEEE LaTeX style files which have been used in the preparation of this template. To see the list of contributors, please refer to the top of file IEEETran.cls in the IEEE LaTeX distribution.

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1. 17 viruses sampled randomly from 429 Viruses. [↑](#footnote-ref-1)
2. 18 bacteria, sampled randomly from 629 Bacteria. [↑](#footnote-ref-2)