Inter and Intra Organism Patterns in Proteomic Sequences

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1. Introduction

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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:

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

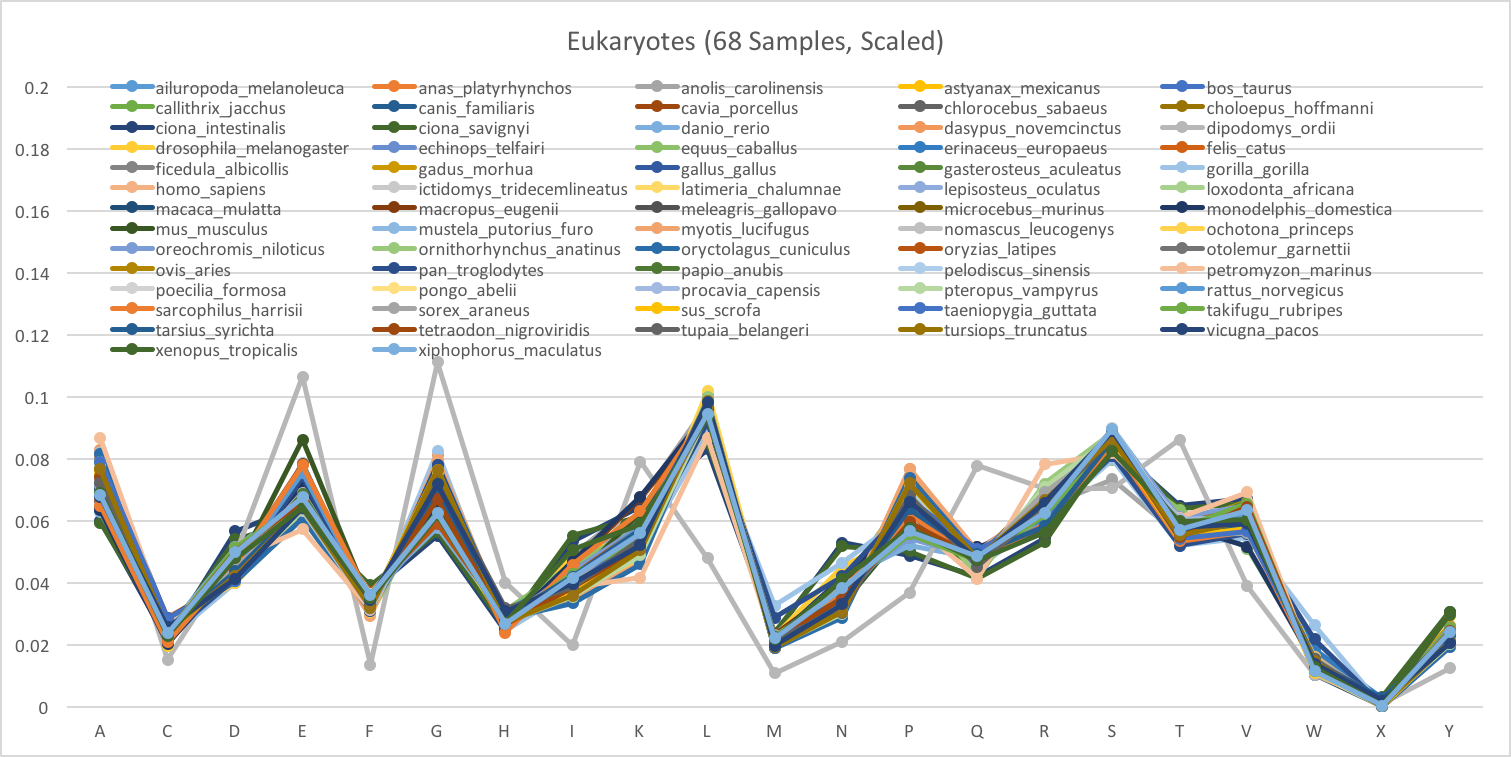


TABLE   
Font Sizes for Papers

|  |  |  |  |
| --- | --- | --- | --- |
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| 8 | table caption (in Small Caps),  figure caption,  reference item |  | reference item (partial) |
| 9 | author email address (in Courier),  cell in a table | abstract body | abstract heading (also in Bold) |
| 10 | level-1 heading (in Small Caps),  paragraph |  | level-2 heading,  level-3 heading,  author affiliation |
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Figures and tables must be centered in the column. Large figures and tables may span across both columns. Any table or figure that takes up more than 1 column width must be positioned either at the top or at the bottom of the page.

Graphics may be full color. All colors will be retained on the CDROM. Graphics must not use stipple fill patterns because they may not be reproduced properly. Please use only *SOLID FILL* colors which contrast well both on screen and on a black-and-white hardcopy, as shown in Fig. 1.

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



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* example of a technical report in [11]
* example of a standard in [12]

1. Conclusions

The version of this template is V2. Most of the formatting instructions in this document have been compiled by Causal Productions from the IEEE LaTeX style files. Causal Productions offers both A4 templates and US Letter templates for LaTeX and Microsoft Word. The LaTeX templates depend on the official IEEEtran.cls and IEEEtran.bst files, whereas the Microsoft Word templates are self-contained. Causal Productions has used its best efforts to ensure that the templates have the same appearance.

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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)