CARBON CONTENTS OF H1N1 PROTEINS

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Abstract— **Carbon is the single most elements that dominate the hydrophobic interactions in proteins. Proteins evolve based on this carbon content. Though all proteins use 20 naturally occurring amino acids, it differs in arrangements. How to capture this difference? To address this happening at atom level the work has been taken up here. The protein sequences of influenza A virus H1N1 has been chosen as case study. That is the carbon distribution in all 11 proteins are analysed. The analysis uses scale of carbon content of 31.45% for measurement. Our program called CARBANA has been used for this purpose. Our results reveal that the carbon content and distribution along the sequences is vital for protein's function. The carbon distributions in viral proteins are different from the normal proteins. Either the carbon content is different or the distribution is not uniform. The difference in carbon distribution causes disease. The carbon distribution study along the protein chain is the most significant step towards understanding the biological reactions. The natural way of adding different sequences during development and evolution is better understood based on carbon content. Appropriate improvement in carbon content and distribution in viral proteins might help in functionality.**

Keywords- Carbon distribution, H1N1, influenza A, sequence analysis, swine flu

I. INTRODUCTION

Carbon is the only element that contributes towards the dominant force, hydrophobic interaction in proteins. Protein's carbon content evolves in response to its stability and activity. This carbon content and distribution in viral proteins are expectedly different from normal one because the organization of amino acids in viral proteins is different though use same 20 naturally occurring amino acids. It is reported that proteins prefers to have 31.45% carbon for its stability [1]. This fraction of carbon content can be used as standard of carbon content measurement and comparison [2]. The difference in carbon distribution in viral proteins is the focus of this work by taking H1N1 as case study. The carbon distribution along these viral proteins are investigated and reported.

II. METHODOLOGY

The genomic and protein sequences of influenza A virus H1N1 are collected from the NCBI. The nucleotide contents are counted as shown in the table. The amino acid compositions in 11 different proteins are calculated and tabled. The carbon distributions in these 11 proteins are computed using our CARANA program available online which uses the principle of 31.45% of carbon. The results on carbon percentage versus atomic positions are plotted as shown in figure.

III. RESULTS AND DISCUSSION

The influenza A virus H1N1 genome contains 11 genes with eight segments of RNAs, encoding for 11 proteins namely Hemagglutinin (HA), Neuraminidase (NA), Nucleoprotein (NP), PA, PB1, PB1-F2, PB2, NS1, NS2, M1 and M2. Out of these 11 proteins, PB1-F2 and M2 are very small proteins which are not taken into account here for carbon distribution study. The results on the other 9 proteins are shown in figure 1.

The two membrane proteins (HA and NA) clearly show the rich of carbon contents all along the sequences. Normally a threshold value of 31.45% is expected along the sequences. NP is a nucleoprotein which wrap around genomic RNA forming a ribonucleoprotein complex. This protein contains a mix of both hydrophobic and hydrophilic regions along the sequence. The PA, PB1 and PB2 are viral RNA polymerase proteins which show a normal carbon distribution. PA protein has slightly higher carbon content. There is a dip in carbon content at position around 3000 in PB1 protein shows a hydrophilic region. Any further rise in carbon content at this point might improve the activity of this protein. The two small non-structural proteins, NS1 and NS2 are shown with normal carbon content which are not significant. The matrix protein, M1 has less amount carbon content. There are regions of hydrophilic in nature.

The carbon based study reveals the hydrophobic regions more successfully than the other methods like hydropathy plot.

IV. CONCLUSION

The carbon distribution studies on viral proteins reveal that the carbon content and distribution along the sequences is vital for its function. A difference in carbon distribution is noticed in most of the H1N1 proteins. The distribution is not normal. The difference in carbon distribution in proteins causes diseases. The carbon distribution study along the protein chain is the most significant step towards

understanding the biological reactions. In fact carbon based method

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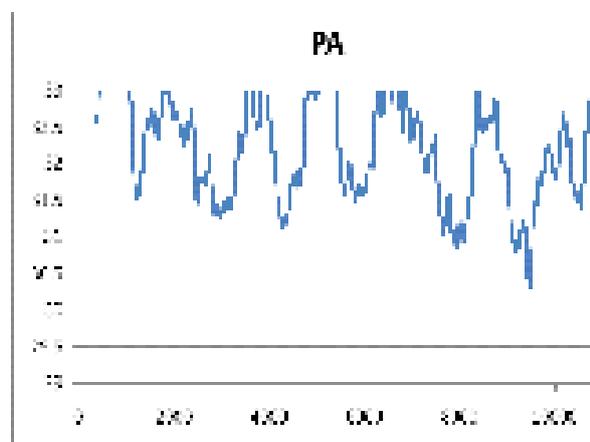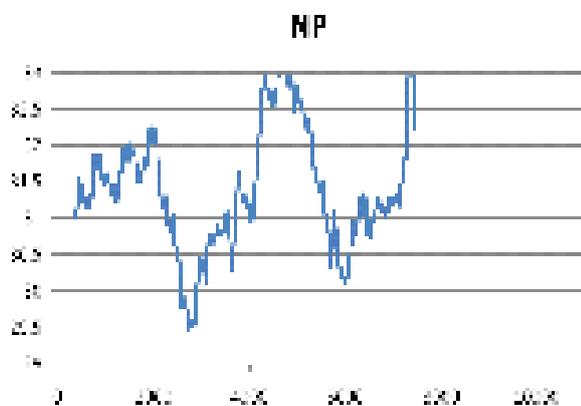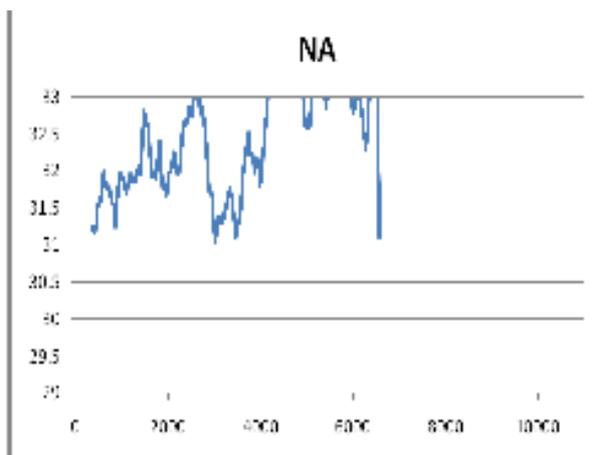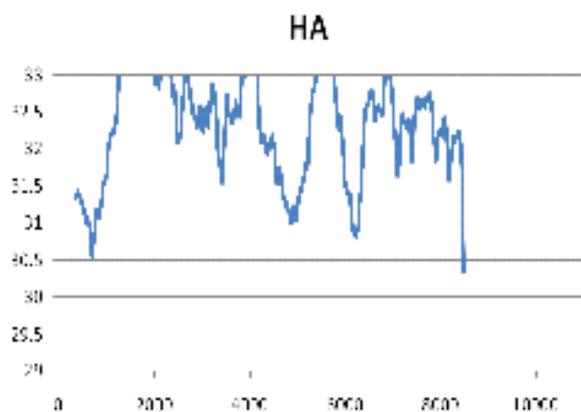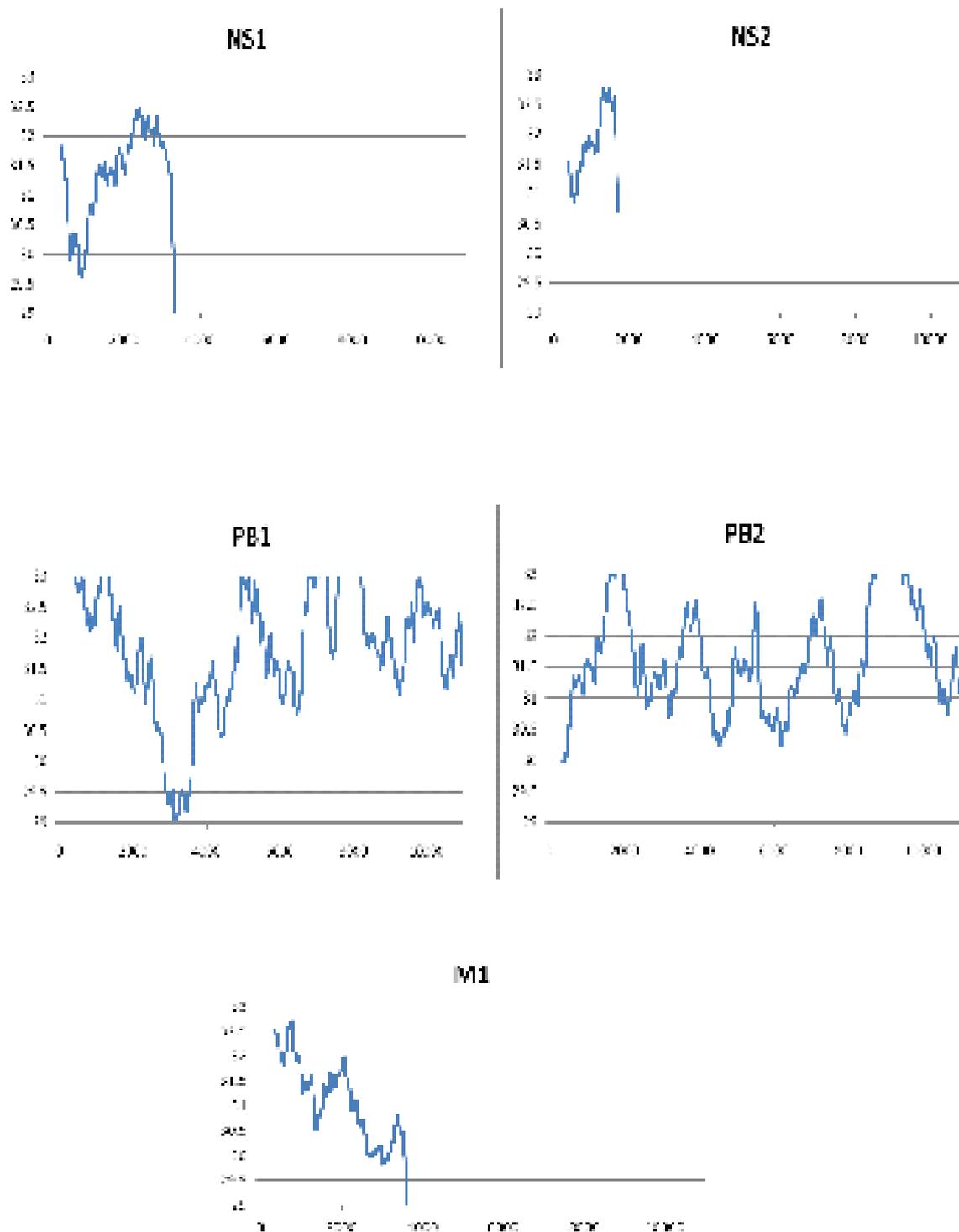
Figure 1.   Carbon percentage at different atomic position in HA, NA, NP, PA, NS1, NS2, PB1, PB2 and M1 proteins of H1N1.