Editorial

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Biographical notes: Perambur Neelakanta is Professor in the Department of Computer and Electrical Engineering and Computer Science (CEECS), at Florida Atlantic University (FAU), Boca Raton, Florida, USA. His current research area includes Bioinformatics. He has supervised 20 PhD dissertations and several MS theses. He has authored six books and is currently writing a book tentatively entitled *Introduction to Bioinformatics*: *Algorithms and Computational Methods.* He has published over 125 journal papers plus several conference papers. He is a Chartered Engineer (UK) and a Fellow of IEE (UK), (now known as IET). He has 43 years of academic plus corporate experience.

Mirjana Pavlovic is a Research and Adjunct Professor in the CEECS Department/Bioengineering Program, FAU, Boca Raton, Florida, USA. Her teaching interests include Introduction to Bioengineering and Tissue Engineering courses. Her research and clinical experience have rendered an excess of 120 papers and abstracts. Target interest includes translating laboratory data to clinical arena. Her efforts are directed toward autoimmune diseases and stem cells (fundamental, research, computational approach and clinical applications). For 10 years, work on lupus anti-DNA antibodies structural, functional and pathogenic features including mechanisms of DNA hydrolysis/cytotoxicity) has been her research direction.

Hanqi Zhuang is currently Professor in the CEECS Department at FAU, Boca Raton, Florida, USA. His research interests include computer vision, robotics and biometrics. He has published 100+ refereed papers and co-authored two books. He has guided more than 10 PhD and 17 MS theses. His recent research includes DoD DIS sponsored project on secure telecommunication using face and speaker recognition techniques. He was earlier an Associate Editor of IEEE Transactions on Robotics and Automation and now is an Associate Editor of *International Journal of Computer Applications*. Also, he serves on the Editorial Board of *International Journal of Biometrics*.

It is imperative that diagnostic and therapeutic options in modern medical science emphasise on strategies that facilitate control and curative measures across innumerable diseases that prevail in the society. In the sphere of grossly pervading but immensely

agonising disease processes, the human exercise has been not only to find therapeutics toward cures but also (if possible) seek strategies for effective disease-control and prevention techniques. In this venture, a vital consideration has been on finding the pathogens that cause adverse effects on living systems and formulating methods of preventive schedules toward adverse influences from the universe of germs.

In the aforesaid context, the underlying prospects in vogue cater for and comprehensively include rigorous efforts of developing vaccines and relevant state-of-the-art comprehensively support schemes to realise rational vaccine designs that carry the visions of Pasteur and dreams of Pauling in nourishing the hopes of millions of patients.

The tale of such vaccine designs has a genesis borne by the efforts of Louis Pasteur, who ranks on the top as the greatest benefactors of humanity. He solved the mysteries of rabies, anthrax, chicken cholera and silkworm diseases and contributed to the development of the first vaccine. While Pasteur sought and paved the way of knowing the germs and vaccination technique, Linus Carl Pauling explained through mathematical analysis of protein molecules, the structure of antibodies and the nature of serological reactions – the gist of knowledge that enable modern researchers to formulate rational vaccine designs.

This Special Issue on 'Viral DNA analysis and rational vaccine design' was conceived to gather details on new research considerations that exist in understanding and designing vaccines in the context of modern wet-lab data and computational facility available in analysing genomic and proteomic information pertinent to invading germs and host receptacles. Hence, papers in bioinformatic applications *vis-à-vis* vaccine design considerations and virus-related analysis were collected, peer-reviewed and offered to readers through this Special Issue.

Concepts of rational vaccine design are reviewed comprehensively in the first paper entitled 'From Pauling's abzyme concept to the new era of hydrolytic anti-DNA autoantibodies: a link to rational vaccine design? – A review'. Essentially, it speaks of specific entities of naturally occurring DNA hydrolytic and cytotoxic anti-DNA antibodies/abzymes that are linked to autoimmune and lymphoproliferative disorders. It traces relevant aspects of the origin of antibodies that are still unknown with corresponding immunogens remaining to be identified. It is suggested that anti-DNA antibodies with DNA hydrolytic/cytotoxic capacity could be the organism's immune response to microbial attack or specific genes within the microbial DNA sequence are targeted for neutralisation. It is surmised that multi-functional antibodies with characteristic structure, function and pathogenicity when studied through wet-lab procedures and bioinformatic methods could lead to the new concepts of rational vaccine designs.

In the second paper on 'Computation of entropy and energetics profiles of a single-stranded viral DNA', the bioinformatic aspects of computing entropy and energetic profiles associated with a viral single-stranded DNA (ssDNA) are addressed. Determining the structural (stem and loop) features, identifying the CpG motifs and delineating the boundaries of Codon DNA Segments (CDS) along a test viral (B19) ssDNA are done *via* analytical modelling and computational efforts that conform to Shannon entropy and thermodynamic kinetics of the test genome. Pertinent details are viewed in the context of their possible uses in rational vaccine designs.

The third paper, 'CDS identification in a viral single-strand DNA (ssDNA) using Fisher linear discriminant' applies the concept of Fisher linear discriminant that enables

distinguishing the features of Codon DNA Segments (CDS) in a DNA sequence consistent with the underlying stochastic attributes. It is specifically applied to a viral ssDNA. Inferences as regard to CDS regions present in the test sequence are made indicating possible fuzzy transitions of codon/non-codon sections. Such fuzzy details could differentiate different strains of a virus toward appropriate vaccine designs.

In the fourth paper entitled, 'Virus infection on brain white matter: statistical analysis of DT MRI scans', the textural variations in brain white matter specific to a set of control images vs. images of a HIV+ subject are assayed *via* an algorithm based on the so-called grey level co-occurrence matrix (GLCM), and the associated Haralick features are extracted from the GLCM to characterise the test (clinical) images gathered from diffusion tensor magnetic resonance imaging (DT MRI).

Described under the title, 'B- and T-cell epitope mapping of human sapovirus capsid protein: an immunomics approach' is the fifth paper that attempts to define and predict the immunogenic epitopes of sapovirus using the tools of immunoinformatics. Relevantly mapped T- and B-cell epitopes are subjected to a conservation analysis in a set of genotypes of sapovirus leading to the prediction of certain epitopes useful for designing peptide-based subunit vaccine to confer humoral as well as cell-mediated immunity.

Lastly, the sixth paper, 'Computer-aided vaccine design for liver cancer using HBx protein epitopes isolated from HBV substrains' addresses the context of Hepatitis B virus-encoding HBx, which is considered as being responsible for virus infection in mammals; and, this HBx interacts with the transcription factors affecting transcription activation (thereby, modulating the signal transduction pathways of etiological (molecular) factors of significance in establishing the liver cancer). To predict epitopes from a set of three HBx proteins (for vaccine designs), use of certain computational tools is indicated in the study. Results obtained *via* modelling and pattern search show presence of helix, sheets and turns that contain the predicted epitopes. Relevant patterns presumably characterise the possible biological activity of the vaccine of interest.

Thanks to the efforts of a number of reviewers, a total of six papers of good quality have been finally shortlisted and presented in this Special Issue. This collection of papers governs the general theme of bioinformatics and emphasises the analyses of viral structures and rational design prospects of vaccines. New methodologies and techniques form the overall scope of these peer-reviewed papers.

It is our pleasure and privilege to take this opportunity to thank all the authors, who contributed to this Special Issue, and deeply appreciate the efforts of all the reviewers for their invaluable comments and constructive criticisms making the reviewing process diligently successful. We also extend our heartfelt appreciation, profuse thanks and deep regards to Prof. Yi Pan, the Editor-in-Chief of IJBRA for his untiring encouragement and support. The opportunity to organise this Special Issue as extended by the Editor-in-Chief and by the Inderscience is deeply recognised and appreciated.