Biomedical System Importance

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Editorial

Biomedical system is an up-and-coming discipline at the convergence of computing and the life sciences aimed at the development of technologies for extracting, storing, visualizing, analysing and interpreting biological information, which is really an interconnected field. Not only have advances in computing assisted the increase in the speed of the process of data generation, but the need to process and analyse this immense amount of information has led to advances in both software technologies such as visualization and hardware architectures. Furthermore, there is significant interest in Bioinformatics from researchers in medicine. Recent developments in Biomedical Visualization have led to an explosive growth in biological information. Biomedical Visualization is being generated faster than it can be analysed and utilized. This special issue of the International Journal of Visual Languages and Computing highlights recent research results in this field of Biomedical Visualization. The visualization techniques related to bioinformatics range from methods of generating 3D renderings of protein structures to creating maps of the physical location of genes. For example, for the visualization of nucleotide sequence data and protein structure data, these techniques can make Bioinformatics applications more easily understood and learnt. Visualization is one of the most active areas of research and development in Bioinformatics, in particular, Biomedical Visualization. The aim of the Asia-Pacific Bioinformatics Conference is to provide an international forum for researchers, professionals and industrial practitioners to share their knowledge of how to surf this tidal wave of information and data. The Asia-Pacific Bioinformatics Conference series is intended to be an annual forum for exploring research, development and novel applications in Bio medical systems.

In response to the First Asia-Pacific Bioinformatics conference Call for Papers, which was disseminated globally, we received 61 papers from 20 countries in Asia (Armenia, China, Hong Kong, India, Japan, Korea, Singapore, Taiwan and Thailand), America (USA, Canada), Europe (France, Germany, Ireland, Italy, Sweden and UK), New Zealand and Australia. The papers contained in this special issue were selected from among the papers presented at the First Asia-Pacific Bioinformatics conference. All the papers are revised and extended versions of those presented and have been reviewed again through rigorous peer review process for this special issue. The paper entitled "The Visualization and Measurement of Left Ventricular Deformation using Finite Element Models" applied to the visualization technique that is used in solid mechanics and fluid dynamics to two biomedical data sets. It can obtain a new insight into the mechanics of the healthy and diseased left ventricle. This also facilitates the understandings of the complex deformation of the heart muscle. The use of tensor ellipsoids, streamlines and hyper streamlines make it possible to visualize complex deformation behaviour in a single image. Line integral convolution uncovers the presence of degenerate points at which the principal strains suddenly change direction. Further investigations are necessary to find the relationship between degenerate points, fibre structure and the ventricular anatomy. Furthermore, authors explore their significance for diagnosing heart diseases. Visualizing a ventricle with dilated cardiomyopathy showed that the deformation of the lateral wall resembles most closely the expected motion, whereas the septal wall behaved almost contrary to the expected deformation. The combined effect of these deformations seems to be a pumping action by shape deformation rather than by contraction. The visualizations and measurement performed in this paper demonstrated the usefulness of their visualization toolkit for exploring biomedical models.

This article explains techniques for visualizing and evaluating biomedical finite element models and demonstrates their application to biomedical data sets by using an example of two models of a healthy and a diseased human left ventricle. The paper entitled "Visual Comparison of Metabolic Pathways" discussed how the visual comparison of pathways across different species can be very useful for scientists by offering new insight into the different metabolic processes. However, visual interfaces to databases do not support such tasks very well. Authors have presented a new approach for the visual comparison of pathways which uses a graph drawing algorithm. Using horizontal constraints, identical parts of similar pathways in different species are placed on the same horizontal layers, thereby highlighting similarities and differences between these pathways. This visualization method has been tested with data obtained from the Bio Path system and the KEGG database. The presented approach supports different drawing styles and offers a user-friendly [1-5].

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