



## EDITORIAL: Bio-CAD

Wei Sun

Drexel University, [sunwei@drexel.edu](mailto:sunwei@drexel.edu)

CAD has been traditionally used to assist in engineering design and modeling for representation, analysis and manufacturing. Advances in Information Technology and in Biomedicine have created new uses for CAD with many novel and important biomedical applications. Such applications can be found, for example, in the design and modeling of orthopedics, medical implants, and tissue modeling in which CAD can be used to describe the morphology, heterogeneity, and organizational structure of tissue and anatomy. CAD has also played an important role in computer-aided tissue engineering for biomimetic design, analysis, simulation and freeform fabrication of tissue scaffolds and substitutes. This special issue selected 6 referred papers as an introduction to recent technical advances, research and developments, and novel applications on using CAD modeling, design, analysis, and freeform fabrication for biomedical and tissue engineering.

A biomodeling approach to compute accurate contours from non-invasive medical imaging data using B-spline curve approximation was introduced in the first paper. The approach and the visualization were conducted primarily based on the voxel and facet (triangle) based model representation. The NURBS, the *de facto* standard to represent geometry in CAD systems, was used in the reported work to perform a critical task for bio-fabrication of human bone and head. The modeling accuracy and shape fidelity were commented in the report.

The second paper reported a Kinematics Differential Evolution (kDE) approach to model flexible biological molecules of different type, size and shape through the rapid identification of low-energy molecular conformations. One of the main benefits of the proposed methodology was that a population of alternative low-energy solutions could be provided for each tested molecular structure compared with a single low-energy solution usually obtained by traditional molecular modeling approaches. This population includes a number of different molecular conformations that attain the same low energy value and hence correspond to an energetic state with high probability of occurrence. Results presented in the paper show that the kDE model provided a set of molecular structures similar to those obtained by traditional molecular dynamics.

An interactive application tool for creating 3D models of anatomical organs and other biological structures from 2D medical imaging data was presented in the third paper. 3D models were generated by using reverse engineering algorithm and Planar Contour method by SolidWorks developed in Visual Basic Language. The reported work included transferring Computed Tomography (CT) and Magnetic Resonance Imaging (MRI) images into digital matrixes, entering digital matrixes into SolidWorks environment, building feature library for 3D reconstruction, creating medical rapid prototyping models. 3D reconstruction is created by edge configuration generation and triangulated cube configuration generation in capturing section contour points from medical image per slice, creating B-

spline curve with the control points in each layer, and producing solid model construction in Planar Contours method. Applications to medical rapid prototyping models were shown in SolidWorks, including the work of developing image processing 3D visualization in SolidWorks and its Application Programming Interface (API) using Visual Basic Language. The results revealed that the accuracy of 3D reconstruction by using SolidWorks was acceptable.

A new multi-function based modeling of 3D heterogeneous porous wound scaffolds to improve wound healing process for complex deep acute or chronic wounds was reported in the fourth paper. The imaging-based approach was developed to extract 3D wound geometry and recognize wound features. Linear healing fashion of the wound margin towards the wound center was mimicked. Blending process was applied to the extracted geometry to partition the scaffold into a number of uniformly gradient healing regions. Computer models of 3D engineered porous wound scaffolds were then developed for solid freeform modeling and fabrication. Spatial variation over biomaterial and loaded bio-molecule concentration was developed based on wound healing requirements. Release of bio-molecules over the uniform healing regions is controlled by varying their amount and entrapping biomaterial concentration. A prototype multi-syringe single nozzle deposition system was used to fabricate a sample scaffold.

Paper 5 revealed the basement membrane, a specialized connective tissue structure found in all tissue systems, as a framework in an adaptive computer aided design (CAD) strategy for the reverse engineering of 3 dimensional (3D) tissue structures. The reported approach to the creation of functional 3D tissue structures was centered on authors' previous models of vascular supply systems which included complete and accurate replications of capillary bed systems, the circulatory interface necessary to sustain 3D tissue structures. By using the basement membrane as a guide, design models for the reverse engineering of the other extracellular connective tissue structures and their matrix elements were sought. The paper demonstrated the basement membrane as a platform for the design and engineering of tissue scaffolding for vascularized alveolar systems in the lung and for the vascularized dermal skin layer.

In last paper presented an approach for symmetry line recognition, from 3D scanned data of a subject's back. This method was validated by comparison with traditional techniques based on cutaneous marking. For this purpose, the upright standing and sitting postures of a sample of 75 subjects, who usually perform different sports activities, were analysed. Error in symmetry line detection was measured as the distance between the estimated symmetry line and the position of the markers. The proposed method was compared with the openly reported approach results were analysed and discussed.

I hope that the selected papers are of interest to you, and can encourage and stimulate further research in Bio-CAD. I also would like to take this opportunity to thank all contributors and reviewers, and thank Prof. Piegl, the Editor of CAD, for asking me to put the papers together.