



Editorial

Applications of artificial intelligence, mathematical modeling and simulation in medical biophysics

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Mathematical modeling and simulation have been used for years to solve various problems in medical biophysics, such as computational methods incorporating biomedical knowledge and automate reasoning. Recently, we are witnessing the renaissance of artificial intelligence (AI), accentuated by the rapid advances of internet-based computing technologies, namely, big data analytics and cloud computing [1]. Nobel laureate George Bernard Shaw said: “Progress is impossible without change, and those who cannot change their minds cannot change anything.” [2]. AI brought about sweeping changes in recent years and accounted for a large number of incredible progress in medical biophysics such as cancer therapy, nanotechnology and drug delivery [3]. AI also changed the way people think, and played key roles in decision making and problem solving.

Just imagine how a machine having “human” intelligence can help you complete a task. The process is basically done by machine learning, a specific AI algorithm capable of computing large datasets, while recognizing the complexity within the detailed patterns [4]. Using a computing system of artificial neural networks which consist of the input, output and hidden layers, a model built by machine learning can answer complex question. To date, AI takes advantage of the big data cloud advancement because of the huge amount of data acquired for machine training [1]. By using the pay-as-you-go approach, appropriate amount of computing resources such as CPU time, storage and software can be purchased from the service provider to finish the job. This flexible approach makes data transfer, storage and processing flexible as it takes place in a remote cloud, in which software updates can take place quickly.

However, despite the recent positive advancements enabling AI algorithms to solve problems in medical biophysics, not all problems can be solved. This is because to do that, it will need an artful blend of AI and human intelligence as well as a suitable amount of emotional intelligence from human being. In addition, the implementation of this digital tool in medical biophysics should not give an impression to the researchers/clinicians that AI will eventually replace them. By maintaining the authority of final decision making in setting up AI as a digital assistant, a competent researcher/clinician who uses AI to solve problems in medical biophysics, soon replace others who neglect this digital tool [5].

Although AI can reduce human error, working continuously without any need for rest, and providing faster decision making, it has issues regarding machine training data privacy and security, complexity of artificial neural network, and lack of personnel who know both AI and medical biophysics. Therefore, traditional mathematical modeling and simulation are still popular means to work out solutions in the field.

Generally, in medical biophysics modeling, a problem is converted to mathematical expressions or formulas with variables: the factors affecting the phenomenon or experimental results in the study. These mathematical formulas can be linear or nonlinear functions, which are usually optimized to determine different conditions as some variables have achieved the maximum or minimum values. It is necessary to verify the model by comparing the deviation between the actual and predicted data in order to reduce the deviation to an acceptable level. Sometimes, simulation is used to predict result based on the verified model. Some simulation methods such as Monte Carlo [6,7], based on repeated random sampling, can help to predict numerical result when it is difficult for traditional mathematical method to find out the absolute solution of a problem. This can save a lot of human resource.

The articles in this special issue cover a wide range of medical biophysics applications using modeling. These include investigating the hydro-dynamical problem of flow in proximal renal tubule using the steam function, based on a system of ordinary differential equations; and the study of moisturizing effect of cream on human skin using the Cole model with data acquired from measurement of the bioimpedance. For the studies on COVID-19 pandemic, Monte Carlo simulation is carried out to study the thermal-induced folding of a nucleocapsid COVN protein. Moreover, the charged amino acids in the spike protein of SARS-CoV-2 are investigated, focusing on their electrostatic characteristics, which facilitate the COVID-19 infection of the cell.

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