

Medical Applications of Computational Methods

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Editorial

Academic clinical departments are increasingly required to build expertise in the use of computational and analytical approaches to big "omic" datasets in order to apply "personalised medicine" to the diagnosis and treatment of a wide spectrum of human disorders. With the rapid adoption of novel technologies for generating and analysing genomic datasets, a critical mass of scientists with computational, analytical, and clinical competence became available. Furthermore, current organisational structures both within and outside of the department failed to adequately combine scientific and training possibilities with clinical medicine. Computational modelling can also be used to understand how disease affects the structure and function of living systems, and the insights acquired from modelling can be used to enhance disease diagnostic and treatment procedures.

"Computational medicine" is a new term for an emerging approach. This does not include only molecular network and physiological process models, but Anatomical shapes layered with physiological function are also modelled. Despite the fact that the modelling methodologies employed in each of these fields of computational medicine differ, the use of quantitative data is a common thread. Models to comprehend disease-related changes in structure and function [1,2]. After putting these predictions to the test, models should be tweaked as needed to better reflect the nature of disease.

As we acquire confidence in computer models' ability to forecast human biological processes, they will aid us in navigating the complicated landscape of disease, eventually leading to more effective and reliable disease diagnosis, risk assessment, and therapy strategies. We explain features of computational medicine in this Review, ranging from molecules and networks to highly integrated physiological systems, as well as how models might be applied to improve human health [3,4].

Understanding molecular impression of disease

Data from gene microarrays and other high-throughput technologies can be utilised to establish network-based signatures, which can help with early identification and better prognosis in complicated diseases. The technological, mathematical, and translational constraints to advancement in computational medicine based on statistical learning are the three main ones. To begin, any molecular statistical analysis necessitates high-quality data from a sufficiently big patient cohort to reflect the population. Second, the mathematical difficulties are enormous. Because of the vast number of interacting components, extremely high-dimensional data sets are becoming common in basic biological and engineering research, but they offer technological challenges for statistical learning and inference [5].

Although these prediction criteria may be accurate, interpreting them to get biological insights into why a particular combination of genes is a valuable

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biomarker might be challenging, if not impossible. Easy-to-understand rules based on the expression levels of well-defined gene sets are better for learning since they can be linked more directly to molecular function and, thus, therapy design.

Computational physiological medicine

The traditional experimental and molecule-by-molecule method to biomedical research is not possible for high-throughput assessment of biological complexity due to the large number of interacting components in biological systems. For extracting knowledge from vast arrays of numbers, a principled learning technique has become crucial. This involves discovering and using disease-related information implicitly held in high-dimensional, high-throughput biological data in the case of computational molecular medicine [3].

Physiological function in disease

Cancer: Multiscale tumour growth models, for example, contain signalling events in tumour cells, cell-cell interactions, cell-extracellular matrix interactions, changes in cell environment (for example, oxygen diffusion), and angiogenesis. The model's capacity to forecast the volume of tissue that should be removed would aid surgeons in guiding them through these procedures and may lessen the need for repeat resections.

Diabetes: An insulin infusion pump is connected to a subcutaneous continuous glucose-monitoring sensor, and a control algorithm is utilised to regulate insulin supply based on the recorded glucose level. The development of an adequate method for managing insulin delivery is a major difficulty in these systems.

Heart disease: Cardiac modelling has also advanced to the complete heart level. The use of diffusion tensor MR imaging (DTMRI) to quantify the architecture, fibre, and sheet structure of the heart has been a critical step toward achieving this goal. Whole-heart image-based models are expressed as reaction-diffusion partial differential equations, with the reaction term defined by the system of equations modelling the myocyte and the diffusion term defined by image-based heart anatomy measurements and estimated cell-to-cell coupling via gap junctions.

Computational medicine's future

In the guise of a phone application, CA algorithms have lately been employed directly in the clinic. By mapping an image of the patient's brain and electrode position onto a brain atlas, and then simulating current distribution within the brain given brain structure, electrode placement, and conduction parameters, this programme assists physicians in selecting deep brain stimulation parameters. This enables the user to pick stimulus parameters that direct current to the structures that should be stimulated. Improvements in predictive capacity of these models, as well as ways for restricting models using clinical data, are fast being achieved thanks to breakthroughs in imaging capabilities and ever rising computer power. Each of the computational areas discussed in this overview has the potential for customised medicine application. Because it provides a novel, quantitative method to understanding, identifying, and treating disease at the individual level, computational medicine will continue to flourish as a discipline.

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Conflict of Interest

The authors reported no potential conflict of interest.

References

1. Zhang, Qi, Jianhang Zhou, and Bob Zhang. "Computational traditional Chinese medicine diagnosis: A literature survey." *Comp Bio Med* 133 (2021): 104358
2. Morris, Paul D., Andrew Narracott, Hendrik Von Tengg-Koblighk, Daniel Alejandro Silva Soto, Sarah Hsiao, Angela Lungu, Paul Evans et al. "Computational fluid dynamics modelling in cardiovascular medicine." *Heart* 1 (2016): 18-28.
3. Yang, Sijie, Fei Zhu, Xinghong Ling, Quan Liu, and Peiyao Zhao. "Intelligent health care: Applications of deep learning in computational medicine." *Front Genetics* 12 (2021): 444.
4. Soroushmehr, S.M. Reza, and Kayvan Najarian. "Transforming big data into computational models for personalized medicine and health care." *Dialog Clinic Neurosci* (2022).
5. Collin, Catherine Bjerre, Tom Gebhardt, Martin Golebiewski, Tugce Karaderi, Maximilian Hillemanns, Faiz Muhammad Khan, Ali Salehzadeh-Yazdi et al. "Computational models for clinical applications in personalized Medicine—Guidelines and recommendations for data integration and model validation." *J Personalized Med* 2 (2022): 166.

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