

Computer and Mathematical Modeling: Translational Research and Economics in Clinical Diagnostics

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Abstract: The computer and modeling approach has begun to be used extensively in clinical intelligence diagnosis, we have refined the necessary techniques related to intelligence medicine, and we have performed economics-directional analysis of models and structures of artificial intelligence in the translational medicine sense. At the same time, the development of clinical diagnostic techniques is also the result of constant innovation, and we propose the necessary strategy for a cross-disciplinary approach to clinical diagnostics and computer and mathematical modeling, with the authors reporting in conjunction with the results of the study.

Keywords: Computer Mathematics; Clinical Diagnostics; Translational Medicine Economics

1. Research context

Mathematical models and modeling are not only an important part of the scientific theoretical system but also an important tool and method for us to understand the world. The rapid development of computer technology has had a tremendous impact on many disciplines. Computers have made problem solving easier and easier, and the problem area more broadly. For example, computer simulation is often used in mathematical models to find solutions to complex system problems with random factors. In general, computer simulation can effectively solve problems in the following situations: (1) it is difficult to experiment and observe in the physical environment and can only be done by computer simulations, such as the study of space flight; (2) it is necessary to observe the entire process of system development within a short period of time, to estimate the impact of certain parameters on the system change; (3) it is necessary to observe the system over a long period of time, compare operations, and to find optimal solutions from a large number of protocols; (4) it is difficult to interpret the system; and (5) it is too complex analytics, but the process of analysis and calculation can only provide simple and feasible methods by means of computer simulation. Clinical predictive models (also known as clinical prediction rules, predictive models, or risk scores) refer to the use of multivariate models to estimate the probability of having a disease or the probability of an outcome in the future. Methods: Traditional statistical methods: multivariate regression analysis to build a predictive model. Machine-learning methods: machine-learning algorithms such as clustering and classification are used to model predictions. Classification: includes diagnostic and prognostic models. Diagnostic models: based on the clinical symptoms and characteristics of the subjects, the probability of diagnosing a disease at present is more common in cross-sectional studies; prognostic models: the probability of disease recurrence, death, disability, and complications at a certain time in the present disease state is more common in cohort studies. Population selection, prospective cohort study population: best, enhanced to demonstrate the natural course of the disease, and facilitated more planned measures of predictors and outcomes. Patient-control population: absolute risk cannot be calculated, and the overall population of case and control sources is unknown, leaving investigators free to select cases and controls, leading to a predisposition for

bias. Population-based randomized controlled clinical trial population with poor extrinsicity as a result of strict eligibility criteria. If the intervention does not work, the data can be directly combined; if the intervention works, the intervention variable needs to be considered an independent predictor for inclusion in a multivariate model. The sample size estimated that it was possible to overestimate the model's effectiveness when the number of predictors was significantly greater than the number of outcome events. Ideally, a prediction model would require at least a few hundred outcome events, and the literature suggests that a prediction factor of at least ten is a conservative estimate. Choice of predictors and outcome, and of predictors, were screened for sociodemographic characteristics, history, physical examination, disease characteristics, test results, and treatment history. Treatment can be used as a predictor in randomized controlled clinical trials but is not recommended in observational studies. Predictors should have the following characteristics: (1) a test that should have well-defined, standardized, and reproducible predictors, and (2) a method that should be used daily. (3) Predictors should be measurable and readily available. In observational studies, because treatment measures and indications are not uniform, their inclusion as a predictor may introduce bias, and treatment is of little predictive value when compared with age, sex, and disease stage. Outcomes of choice, patient-specific outcome: primary outcome, relapse, mortality, complications, tumor hyperplasia, pain, treatment response, and quality of life. Alternative and intermediate measures: Outcomes are not recommended unless there is a clear causal link between the surrogate or intermediate outcome, such as CD4 cell count and AIDS progression and death, and outcomes should be measured without knowledge of predictors, lest bias be introduced.^{[1][2][3]}

2. Research prospects

One of the most promising applications of machine learning is precision medicine, in which patients receive health care and treatment tailored to their personal characteristics. Accurate oncology, the goal of which is to prescribe cancer treatments based on molecular features of the tumor, is a typical example of the challenges and opportunities that machine learning faces in precision medicine. In current practice, individual molecular markers, such as somatic mutations and gene expression levels, are commonly used to guide treatment choices. However, due to differences in the distribution of other genomic and epigenetic loci and anatomic disease, the patient response is usually highly variable. Complicating precision oncology further, there are hundreds of potential drugs, and not every combination can be tested for each disease. One way that machine learning can help to overcome these challenges is to develop multivariate predictive models of individual diversity. For example, single-use models have been developed to predict functional effects of biological alterations, how gene mutations affect splicing and gene expression, and machine learning models to predict drug responses in cancer cell lines and to shift predictions from cell lines to tumors in patients, and to predict patient responses to treatment based on clinical response data. Accurate future advances in health care may involve modeling on a multiscale basis and serving a variety of purposes. Multiscale modeling will use large biologic data sets to study the growth and development of organisms across discrete spaces. There are computational models for human-viral interactions, cell-cell interactions, and, for example, tumor-immunocyte interactions. Ultimately, we expect to develop the computational models of the organ and the entire individual—the so-called “digital twins”. The goal of digital twins will be multifaceted, such as to predict the efficacy of different combination therapies that have never been used together, and to mimic the effects of disease on different organs. Although multiscale models may become sufficiently accurate that their predictions can be directed to treatment, we envision an intermediate phase in which a machine-learning approach yields a list of recommended therapies that can be used by specially trained physicians to help guide treatment decisions. For example, patient-derived laboratory models can be tested to calculate model predictions and recommend treatment with the best performance predictions. This hybrid approach has several advantages: machine-learning models can significantly reduce the scope for potential therapeutic combinations to consider and identify other combinations that may be overlooked. An experimental validation procedure could be added to provide additional evidence that the predicted treatment may be effective. By using machine learning to automatically tap and search expertise in published literature and patient databases, precision medicine will be further advanced.^{[4][5]}

3. Economic prospects

We should combine mathematical modeling with machine learning with Chinese biomedical science research in the following directions: first, the development of novel and valuable drugs using biotechnology. The most familiar of biotechnology drugs is antibiotics, with annual sales exceeding \$10 billion. Ever since the introduction of growth hormone-releasing inhibitors by E. coli production in the United States in 1977, human efforts to produce new drugs have been continuing. Since biological drugs are more effective than conventional drugs in treating many malignant diseases, the need for biological drugs is growing. Many countries around the world produce genetically engineered drugs, which are used to treat diseases such as cancer, HIV, and dwarfism. The increasing value of biopharmaceuticals produced worldwide using biotechnology has produced huge economic benefits, making the industry's prospects attractive. 2. Using biotechnology to prevent and diagnose diseases, scientists have developed a number of novel vaccines for human testing that effectively control some infectious diseases. The use of cellular engineering technology can produce monoclonal antibodies that can be used both for disease treatment and for disease diagnosis. Microarrays, for example, are one of the new high-throughput, high-specific DNA diagnostic techniques developed in recent years and used in a wide range of applications. iii. The use of biotechnology for gene therapy and the introduction of normal genes for the treatment of diseases caused by genetic defects has been proposed and several therapeutic options, including malignancies and genetic disorders, are being implemented. The Human Genome Project, which uses biotechnology to study the human genome as a whole, will allow insights into the pathogenesis of many of the major diseases afflicting human beings. On the other hand, using biotechnology would solve the energy crisis and combat environmental pollution. It is well known that the world's current energy crisis is pervasive, energy shortages are severe, and our food, clothing, and transportation are inseparable from energy sources, especially oil and coal, which are not renewable. As societies develop, problems that wreak havoc and pollution demand urgent solutions.

3. Conclusion

We conclude that machine learning plays a transformative role in diagnosis and treatment and that it is necessary to develop high-quality, well-planned data sets. Creating high-quality datasets for the use of machine learning in diagnosis and treatment requires technical, legal, and economic problems that often lead to isolated unstandardized biomedical data. To increase the diversity of datasets used for machine learning, data-sharing methods and incentives are also needed. The application of biomedical machine learning requires rigorous evaluation methods, especially in settings that require continuous learning. In our view, the performance of the machine learning system is best measured by the accuracy of its predictions in a prospective setting. Despite the huge challenges ahead, we are optimistic. We believe that all of these efforts are worthwhile, because success implies a rigorous, outcomes-oriented future for medicine, in which detection, diagnosis, and treatment strategies are constantly adapted to individual and environmental differences through machine learning and broad health management.

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