The field of biomedicine: a systematic review and meta-analysis

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Abstract
This article introduces the mathematical modeling method and its important role in the field of biomedicine. Combining practical problems such as DNA sequence classification and infectious diseases, it explains the establishment and application of mathematical models, and introduces the specific steps of mathematical modeling in biomedicine. It also specifically introduces: DNA sequence classification model, infectious disease model, curative effect evaluation model, deterministic model and randomness model, and promotes in-depth research on biomedical mathematical modeling methodology.

Keywords: mathematical modeling; biomedicine; application

1. Introduction

Mathematics is a highly abstract art. It is precisely its high abstraction that determines its wide application. In particular, with the development of science and technology and the application and popularization of electronic computers, mathematical methods are used in agriculture, forestry, medicine, and economics. Energy, transportation and other fields occupy more and more important positions. This also validates Marx’s words: “A science can only be considered perfect when it successfully uses mathematics.” In fact, the application of mathematics in the field of biomedicine can be traced back to the 17th century, when the “blood circulation system ‘Existing problems’ and "blood flow problems" are outstanding examples of applying mathematical methods to study life science problems. However, the great potential of mathematics in the field of biomedicine was only realized in the middle and late 20th century: British physiologists, biophysicists Hodgkin and Huxley applied differential equations to describe the transmission of nerve fibers and nerve impulses, and thus gained The Nobel Prize in Medicine and Biology in 1963; American scientist Cormac created the CT theory using the two-dimensional Radon transform and won the Nobel Prize in Medicine and Physiology in 1979; the Danish scientist Jerne K applied mathematical principles to study immune network theory, He won the 1984 Nobel Prize in Medicine and Biology [1]. All these awards strongly prove the role and influence of mathematics in the field of biomedicine.

2. The process of mathematical modeling

Biomedicine is a cross-edge discipline. It combines the methods and theories of medicine, biology and engineering. It mainly uses engineering techniques to study and solve life sciences, especially related problems in medicine. Of course, mathematics is also indispensable. Methods. There are two types of mathematical methods often used in the research of medical problems in biomedicine: statistical analysis and mathematical modeling. Statistical analysis methods are one of the most widely used, direct, and effective mathematical methods used in medicine at this stage. They are mostly used for medical problems that require clinical trials, such as: the efficacy of drugs and the detection rate of medical instruments. For medical problems that require mechanism analysis, mathematical modeling methods are used more often, and the effect is better, which is also easy to guide the practical application.

The so-called mathematical modeling refers to the use of mathematical symbols, expressions, programs, graphics, etc. to describe the essential attributes of real problems or practical topics. It is required that such characterization should be as accurate and concise as possible, and the mathematical solutions obtained by the model must be able to Reasonable interpretation of objective phenomena may predict future development trends. The specific modeling process is as follows:

2.1 Model preparation

First of all, we must understand the actual background, look for the internal laws, form a relatively clear outline, and ask questions.

2.2 Model assumption

On the basis of clarifying the purpose and grasping the information, grasp the essence of the problem, discard the secondary factors, and make reasonable simplifying assumptions on the actual problem.

2.3 Model establishment

Under the assumptions made, appropriate mathematical methods are
used to characterize the relationship between variables, and a
mathematical structure is obtained, that is, a mathematical model. In
principle, on the basis of being able to achieve the desired effect, the
mathematical method chosen should be as simple as possible.

2.4 Model solution

After modeling, the model must be analyzed and solved. The solution
involves different mathematical methods such as graphical solutions,
proofs of theorems, and solving equations. Sometimes, it is necessary
to use a computer to find numerical solutions.

2.5 Model analysis, inspection and application

The results of the model should be able to explain the existing
phenomena, and the processing method should be the optimal
decision-making and control scheme. Therefore, the solution of the
model needs to be analyzed and tested. Return the obtained
mathematical result to the actual problem and test its rationality. If the
theoretical result is in line with the actual situation, then it can be used
to guide practice, otherwise it is necessary to put forward hypothesis,
modeling, and solution again, and the actual application cannot be
carried out until the model result is consistent with the actual.

In short, mathematical modeling is a creative work, it is impossible to
use some rules and regulations to stipulate very rigid, as long as it can
achieve comprehensive consideration, can grasp the essence of the
problem, and the final test result is a good mathematical model.

3. Application of mathematical modeling in biomedicine

3.1 DNA sequence classification model

DNA molecules are the basic unit of genetic information storage, and
many major problems in life sciences rely on in-depth understanding
of this particular molecule. Therefore, the question of DNA molecular
structure and function has become one of the most important topics in
the 21st century. The problem of DNA sequence classification is the
basis for studying the molecular structure of DNA, and its commonly
used method is cluster analysis [4]. Cluster analysis is a method of
simplifying data using data modeling. It divides the data into different
classes or clusters. The data in the same cluster has great homogeneity,
while the data in different clusters has great data. Dissimilarity. When
classifying DNA sequences, you need to first introduce sample
variables, such as the abundance of a single base, the ratio of
abundance of two bases, etc.; then calculate the sample variable value
of each DNA sequence and store it in a vector; Finally, according to
the principle of similarity measurement, the Lance and Williams
distance between all sequences are calculated, and the classification is
based on the distance. For the quality of the model, the DNA sequence
of the known classification can be selected for testing. If the
classification made according to the model is consistent with the
known classification, the model is preferable. Otherwise, the sample
variables need to be debugged until a satisfactory result is obtained.

3.2 Infectious Disease Model

In order to quantitatively study the spread of infectious diseases,
people have established various types of models to predict and control
the occurrence and development of diseases, for example, SI model
(for difficult to cure after disease), SIS model (for disease The
patient does not have immunity after being cured), SIR model (applies to
the patient with lifelong immunity after being cured), SIRS model (applies
to the patient with temporary immunity after being cured), etc. Here,
the SIR model is used as an example for specific explanation.

Assuming that factors such as birth, death, and migration of the
population are not taken into
consideration, let the total population always maintain a constantN, the
number of susceptible persons, infected persons and recovered persons
at time t are S(t), i(t) and r(t) respectively, then the following three-
bedroom model can be established:

\[ \frac{di}{dt} = ksi - li \cdot dr = lis(t) + i(t) + r(t) = N \]
\[ i(0) = i_0, r(0) = 0 \]

Among them, k is the infection intensity of the disease in the area, l is
the recovery coefficient of the disease in the area.

Solved by:

\[ i(t) = i_0 + s_0 - s(t) + p(\ln(s(t)/s_0)) \]

with \( p = 1/k \)

From the above solution, it can be seen that if \( S0 \leq \rho \), then \( i(t) \)
will monotonically decrease to 0, that is, the infectious disease will not
spread; if \( S0 > \rho \), then \( i(t) \) will increase monotonously, that is, the
infectious disease will spread, but in As \( i(t) \) increases, \( s(t) \) will decrease
monotonically. When \( s(t) \) decreases to less than or equal to \( \rho \), \( i(t) \) stops
increasing and begins to decrease until the disease disappears in the
area. Therefore, in order not to spread the disease, it is necessary to
increase \( \rho \) and reduce \( S0 \) as much as possible. Common methods are
to reduce the contact rate with infected persons, improve the health
level, improve the medical level, and increase the group immunity.

3.3 Efficacy evaluation model

For the same disease, doctors often formulate different treatment plans
based on their different experiences, and each plan has different
economic costs and will produce different degrees of side effects.
Therefore, it is of great significance to reasonably evaluate its efficacy.
The commonly used curative effect evaluation models include multiple
nonlinear regression models, fuzzy evaluation models, gray correlation
models, and BP neural network models. No matter which model you
need to determine the evaluation parameters first, the so-called
evaluation parameters refer to what measures the efficacy. For example,
in the evaluation of AIDS efficacy, CD4 concentration, HIV
concentration, or the ratio of CD4 to HIV concentration can be used to
measure the efficacy Good or bad [6]. When selecting a model, as long as
it can objectively and truly reflect the comprehensive efficacy of the
sample, it is effective.

3.4 Deterministic model and random model

Mathematical models in biomedicine can be divided into two main
types: deterministic and random. For the deterministic model, given
the initial conditions, there is a completely definite solution. On the
contrary, both the stochastic model and its solution involve
probabilistic conditions and use probabilities to describe what
happens. Deterministic models are widely used in biomedicine. Most
tracer applications are based on deterministic models. Model,
hydrodynamic model of circulatory system, etc.

Generally it is deterministic. But many aspects of biomedicine use
random models. For example, the biostatistical model is random,
and today's popular disease simulation method and electrocardiogram
analysis also include random elements. In short, in biomedicine, both
deterministic models and more and more random models are used.
Although the model is divided into deterministic and random types,
although it is simple and clear, in practice, this division is not too
simple. All deterministic models used to represent realistic measurable
quantities are limited by the accuracy of the measurement, and these
limitations cause uncertainty, so that the probabilistic elements must
be introduced into the initial conditions of the model and the quantities
predicted by the model. In some cases, the stochastic model may also
be reduced to a deterministic model.

4. Conclusion

Mathematical modeling plays an important role in research in the field of biomedicine, especially higher-level medical research often depends on the establishment of reasonable mathematical models. Therefore, to train high-level medical researchers, it is necessary to strengthen mathematical modeling Position in teaching in higher medical colleges. At present, the importance of mathematics teaching in higher medical colleges is far from enough. Whether it is the content of mathematics teaching or the setting of the curriculum system, it needs urgent reform.

Conflict of interest

We have no conflict of interests to disclose and the manuscript has been read and approved by all named authors.

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