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Letter to Editor

Bioinformatic materials science reconsidered

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Abstract: Bioinformatic materials science integrates medical science, materials science, informatics, and other disciplines, aiming to maintain the balance of tissues and organs in the human body. This paper explores the relationship between structural information and the structures synthesized through regulated gene expression. Specifically, it describes the transformation of information into substances via biological structural systems, using mathematical formulas to develop bioinformatic materials. These materials have applications in medical treatments, functional foods for preventive healthcare, and cosmetic products for health maintenance. Notably, bioinformatic materials have been applied in treating acromegaly, a rare and life-threatening disease of unknown etiology, and have improved the neurofilament light chain (NFL) index and typical symptoms of Amyotrophic Lateral Sclerosis (ALS). In summary, bioinformatic materials science holds potential for enhancing human health and contributing to advances in medicine.

Keywords: Bioinformatic materialogy, transformation between materials and information, strengthening the body resistance, universal set, subset, Chinese food therapy, amyotrophic lateral sclerosis

Introduction

Bioinformatic materials science integrates medical science, informatics, materials science, and other fields. In the article "A Preliminary Study of Bioinformatics", the author introduces the theory and method of regulating gene expression by recognizing structural information in designed and processed materials [1]. A pressing issue for patients with rare diseases and complex medical conditions is finding effective treatments when the cause is unknown. The development of bioinformatic materials, which can restore the balance of tissues and organs by activating the body's own regulatory functions and achieving self-healing, is key to addressing this challenge. The fundamental approach involves developing bioinformatic materials that can precisely regulate individual structures in the human body to restore balance, ultimately leading to materials that can regulate various tissues and organs.

Transformation between information and materials

The universe consists of matter, energy, and information. Matter forms concrete structures, energy forms abstract structures, and information represents even more abstract structures. The evolution of a structural system involves establishing new dynamic equilibriums based on existing ones. Concrete and abstract structures interact to form dynamic equilibrium systems with self-adaptation, self-organization, and self-regulation capabilities [2]. Bioinformatic materials science aims to explore theories and methods for regulating biological structures through self-adaptation, self-organization, and dynamic equilibrium, ultimately developing functional materials that restore and maintain health. The first step is to create bioinformatic materials that can regulate individual structures within the human body.

The field of Biology recognizes that living organisms are chemical systems capable of maintaining dynamic equilibrium. Not only are their internal structures dynamically adjustable, but they can also produce substances that regulate external structures. The quantity of each structure within an organism's system can increase or decrease as needed to maintain this equilibrium. For instance, assume that a particular structure "a" belongs to the organism's own structural system. Structures either promote or

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inhibit “a”. If the level of “a” is too high, an inhibitory structure reduces it, and if too low, a promoting structure elevates it.

When “a” is an external structure, and the organism recognizes its information, it may not initially have a corresponding inhibitory structure. To maintain dynamic equilibrium, the organism generates an inhibitory structure. For example, when the body recognizes the structural information of an inactivated vaccine, although the vaccine does not attack the body, the organism does not need its structure. Consequently, antibodies are generated as inhibitory structures. Once this structure enters the body, it is regulated to a minimum by these antibodies, maintaining the organism’s equilibrium.

This process can be described mathematically as $r = f(a_i)$, where f represents gene expression, a_i is the structural information of structure “a”, and r denotes the structure synthesized through gene expression f. The gene expression f is influenced by the self-adaptive, self-organizing mechanisms that sustain the dynamic balance of biological systems. The structure r interacts with “a” to regulate its level, thereby preserving the organism’s dynamic balance.

Thus, when an organism encounters a large amount of structural information about “a”, it must upregulate gene expression to produce enough inhibitory structures to constrain “a”. In this context, in the equation $r = f(a_i)$, r is the structure that constrains “a”.

The structural information of “a”, denoted as a_i, can be transformed into the substance r. In turn, the structural information of r can regulate the synthesis of other structures that interact with r, demonstrating that information and material can transform into one another. This represents the transformation between abstract and concrete structures. Due to the inherent self-adaptation, self-organization, and dynamic balance of living organisms, this transformation between information and material can be achieved through the biological structural system, supporting the design goals of bioinformatic materials. Simultaneously, living organisms undergo continuous transformation between abstract and concrete structures, maintaining self-adaptation, self-organization, and dynamic balance.

Bioinformatic materials

Based on various conditions and applications, different bioinformatic materials can be developed using the principle of information-material transformation represented by $r = f(a_i)$.

Development of bioinformatic materials from a disease perspective

When the structure x causing disease is clearly defined, bioinformatic materials can be developed to treat diseases resulting from an imbalance in x. If the disease is caused by an excess of x, and the organism can synthesize the structure that constrains x through gene expression, bioinformatic materials can be created by using x as the raw material. In this case, x corresponds to “a” in the formula $r = f(a_i)$. If the disease is caused by a deficiency of x, and x can be synthesized by the organism, bioinformatic materials can be developed using the structure that constrains x as the raw material. Here, x corresponds to r.

An example of lactose intolerance can illustrate how to develop bioinformatic materials for its treatment based on the two cases discussed earlier. Lactose intolerance is a non-infectious form of diarrhea caused by insufficient secretion of the enzyme lactase, which leads to incomplete digestion of lactose in breast milk or cow’s milk, commonly known as lactase deficiency [3]. Lactase deficiency is a widespread issue globally, frequently causing diarrhea in newborns and infants whose diet is primarily composed of breast milk. Lactose, the main sugar in both breast and cow’s milk, requires lactase for digestion. When lactase secretion is reduced in the apical villi of the small intestine, particularly in the jejunum, lactose remains undigested and passes into the colon. There, intestinal bacteria ferment the lactose into hydrogen, methane, carbon dioxide, and short-chain fatty acids. This fermentation produces gas, leading to symptoms like abdominal distension. The undigested lactose and its fermentation products increase the osmotic pressure in the intestines, drawing water into the intestinal lumen and causing diarrhea, a condition referred to as lactose intolerance [4, 5].

From the perspective of an imbalance caused by excess structures in the biological system, lactose intolerance arises due to an excess of lactose. When the body's structural system recognizes the excessive lactose information, it must increase the production of structures that reduce lactose content to maintain dynamic balance. This involves upregulating genes that lower lactose levels, thereby treating lactose intolerance. In this case, lactose is used to process the bioinformatic material aimed at treating the condition.

From the perspective of a deficient structure causing an imbalance in the biological system, lactose intolerance results from a lack of lactase, preventing the complete digestion of lactose. Lactose is constrained by lactase, so when the body recognizes a large amount of lactose, its structural system increases the expression of genes synthesizing lactase to restore dynamic equilibrium. By using lactose as a bioinformatic material, the expression of lactase genes can be upregulated to treat lactose intolerance. In this case, lactose is used to process bioinformatic materials for lactose intolerance treatment.

In summary, the relationship between r and a in the formula $r = f(a_i)$ is that r constrains "a". An excess of "a" in the biological structural system results from the organism's insufficient production of r. The solution is to upregulate the expression of genes synthesizing r by allowing the organism to recognize the structural information of "a" (a_i).

Development of bioinformatic materials from a health perspective

When multiple structures within a system can cause an imbalance, such as milk containing both lactose (which can cause digestive issues like lactose intolerance) and various proteins (which can cause allergies), different people may experience different diseases due to different imbalances in their structural systems. In such cases, how can bioinformatic materials be developed to restore balance without knowing which specific structures are responsible?

If the structural system is considered a universal set, and the disease-causing structures are subsets, then bioinformatic material development from a health perspective involves addressing the universal set. Taking milk as an example, instead of identifying the exact structure that causes imbalance, the body recognizes the structural information of all components in the milk to restore balance. By treating the entire set, there's no need to pinpoint which specific structure causes which disease, making health maintenance simpler without considering individual differences.

For diseases caused by imbalances in the internal structures of the human body, such as hypertension, diabetes, and other complex conditions with unclear causes, bioinformatic materials can be developed to restore health without needing to identify the exact cause. First, a dynamic balance health model for various tissues and organs can be established by combining the phase theory of traditional Chinese medicine with mathematical modeling.

Assume the structures within a healthy tissue or organ form a universal set, denoted as R, with the structures in R represented as R (y_1, y_2, ..., y_m). The structures that interact with those in the full set R (in terms of generating or inhibiting effects) are computed and denoted as Q, with Q (x_1, x_2, ...). Q (x, x_{ni}) representing the structures in Q. The specific structural information of Q represented as Q_s. By leveraging the body's self-regulation functions to restore balance in the affected tissue or organ, the formula $r = f(a)$ is transformed into $R = F(Q_s)$, and, where F represents the expression of a group of genes that synthesize R.

Different structural imbalances within a tissue or organ result in various diseases, but all imbalanced structures are subsets of the full set R. By developing bioinformatic materials based on the universal set R, and using these materials to regulate the organism, effective treatment can be achieved without needing to pinpoint the exact cause of the disease. This approach focuses on restoring health by regulating the full set, thus establishing a theory and methodology for developing bioinformatic materials for general health applications.

Practical application and summary

To verify the validity of the aforementioned theories and methods, the author used bioinformatic materials developed from a health perspective to observe changes in neurofilament

Table 1. The comparison of the NFL level before and after conditionings in ALS patients

Conditions	The first batch (n = 28)	The second batch	
		The conditionings of central nervous system and immune system (n = 26)	The comprehensive conditionings (n = 28)
Before conditioning NFL (pg/mL)	66.88±42.41	63.66±30.42	55.67±33.90
After conditioning of the first phase NFL (pg/mL)	56.78±33.51	66.27±42.65	46.44±27.29
t value	3.142	-0.627	2.513
P value	0.002	0.538	0.019

Note: NFL: Neurofilament-L; ALS: Amyotrophic lateral sclerosis.

light chain protein (NFL) levels and clinical symptoms in patients with Amyotrophic Lateral Sclerosis (ALS). ALS is a neurodegenerative disorder characterized by the progressive damage and degeneration of motor neurons, resulting in the gradual loss of motor function. The disease is heterogeneous with an unclear pathogenesis, and there is a lack of effective treatments. Typical symptoms of ALS include difficulty speaking, swallowing, choking, and breathing, and patients often die from respiratory muscle paralysis and failure within 3-5 years of onset [6, 7].

Research indicates that ALS is associated with an imbalance in the neuronal environment, disrupting the balance between neuronal death and repair. Neurons require a favorable environment to maintain this balance, and when disrupted, neurodegeneration occurs [8]. NFL is a key biomarker for assessing neuronal damage, with elevated NFL levels indicating neuronal injury and death. Abnormally high NFL levels have been detected in the blood and cerebrospinal fluid of patients with neurodegenerative disorders such as ALS, Alzheimer's disease, Parkinson's disease, and multiple sclerosis [9, 10].

The National Institute of Health Data Science at Nanjing Normal University established the "Traditional Chinese Medicine Dietary Therapy for ALS" research group. This group develops bioinformatic materials designed to support the central nervous system, immune system, heart, liver, spleen, lungs, kidneys, muscles, intestines, and stomach, aiming for a comprehensive treatment approach to ALS. Since October 2023, the group has collected data from 28 ALS patients, with an additional 54 patients enrolled in January 2024. These patients were randomly divided into two groups: an immune + central nervous system conditioning group (26 patients) and a comprehensive conditioning group (28 patients). A contrast method was used to observe changes in NFL levels and symptom improvement before and after treatment in both groups.

As shown in **Table 1**, the results are as follows:

In the first batch of patients, the NFL level was 66.88±42.41 pg/ml before conditioning. After comprehensive conditioning during the first phase, the NFL level dropped to 56.78±33.51 pg/ml, a statistically significant reduction ($P< 0.05$). Despite a recurrence of symptoms after stopping conditioning in phases 2 and 3, the NFL level continued to decline to 51.31±28.02 pg/ml ($P<0.05$). After resuming central nervous system and immune system conditioning in phase 4, symptoms improved further.

In the second batch of patients, the NFL level in the immune + central conditioning group was 63.66±30.42 pg/ml before treatment and 66.27±42.65 pg/ml after the first phase, with no statistically significant difference ($P>0.05$). In the comprehensive conditioning group, the NFL level decreased significantly from 55.67± 33.90 pg/ml before conditioning to 46.44± 27.29 pg/ml after the first phase ($P<0.05$). Symptom improvement between the two groups showed no significant difference.

These results suggest that NFL levels are linked to the neuronal cell environment, and comprehensive conditioning can improve this environment, reduce axonal damage in the central nervous system, and effectively lower NFL levels. The typical symptoms of ALS are associated with neuronal degeneration, and central

nervous system conditioning through bioinformatic materials can help alleviate these symptoms.

In conclusion, the theory, methodology, and preliminary applications of bioinformatic materials have been outlined. Bioinformatic materials hold potential in fields such as medicine, functional foods, and cosmetics, and may extend to everyday products in the future. Their ability to promote life and health could contribute significantly to advancements in medicine and health.

Disclosure of conflict of interest

None.

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References

[1] Wang Y, Ma Q and Huo Z. Identification of hub genes, pathways, and related transcription factors in systemic lupus erythematosus: a preliminary bioinformatics analysis. Medicine (Baltimore) 2021; 100: e26499.

[2] Fang X and Wang J. Nonequilibrium thermodynamics in cell biology: extending equilibrium formalism to cover living systems. Annu Rev Biophys 2020; 49: 227-246.

[3] Jo IH, Paik CN, Kim YJ, Lee JM, Choi SY and Hong KP. Lactase deficiency diagnosed by endoscopic biopsy-based method is associated with positivity to glucose breath test. J Neurogastroenterol Motil 2023; 29: 85-93.

[4] Toca MDC, Fernandez A, Orsi M, Tabacco O and Vinderola G. Lactose intolerance: myths and facts. An update. Arch Argent Pediatr 2022; 120: 59-66.

[5] Catanzaro R, Sciuto M and Marotta F. Lactose intolerance: an update on its pathogenesis, diagnosis, and treatment. Nutr Res 2021; 89: 23-34.

[6] Younger DS and Brown RH Jr. Amyotrophic lateral sclerosis. Handb Clin Neurol 2023; 196: 203-229.

[7] Ralli M, Lambiase A, Artico M, de Vincentiis M and Greco A. Amyotrophic lateral sclerosis: autoimmune pathogenic mechanisms, clinical features, and therapeutic perspectives. Isr Med Assoc J 2019; 21: 438-443.

[8] Ilieva H, Vullaganti M and Kwan J. Advances in molecular pathology, diagnosis, and treatment of amyotrophic lateral sclerosis. BMJ 2023; 383: e075037.

[9] Dreger M, Steinbach R, Gaur N, Metzner K, Stubendorff B, Witte OW and Grosskreutz J. Cerebrospinal fluid neurofilament light chain (NfL) predicts disease aggressiveness in amyotrophic lateral sclerosis: an application of the D50 disease progression model. Front Neurosci 2021; 15: 651651.

[10] Verde F, Otto M and Silani V. Neurofilament light chain as biomarker for amyotrophic lateral sclerosis and frontotemporal dementia. Front Neurosci 2021; 15: 679199.