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Research Article

Data Fusion Model for Muscle Proteomics in Sports Applications

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Proteome is a cell, tissue, or organism to express all the floorboard of the protein; proteomics is the study of proteomics is an emerging discipline; the research on the law of occurrence of sports fatigue and its mechanism is an important and challenging subject in the field of sports medicine. Exercise-induced fatigue refers to the physiological process in which the body's functional ability or work efficiency declines and cannot be maintained at a specific level during exercise. With the improvement of the modern competitive sports level and the increasingly fierce competition, the athletes have to bear more and more loads in sports training, and the probability of sports fatigue is also higher. Appropriate sports fatigue and reasonable recovery methods can promote the improvement of athletes' functional level; on the contrary, excessive fatigue not only affects the training effect but may also cause various dysfunctions, which may damage the athletes' health. Therefore, understanding the mechanism of sports fatigue is of positive significance for accelerating the elimination of sports fatigue. The purpose of this paper is to study the progress of muscle proteomics in sports. Since each athlete has individual differences, different levels of muscle function corresponding to the left lower limb will produce different EMG signals. Static experiments and random visual stimulation evaluation experiments were performed on the left lower limbs of athletes, and they were coordinated with the right lower limbs, and then the left and right lower limbs were compared with the same muscle-weighted RMS (Recipe Management System) and IEMG (Comprehensive electromyography). Experimental results show that using the statistical method of single-factor variance analysis to the same muscles in two states of RMS was analyzed, respectively, under the two states of differences between muscle electromyography IEMG were analyzed, finally, the muscle integral electrical values on the contribution rate of extent of each muscle under the two states are analyzed. For one-way ANOVA, this study defined the significance level of the difference analysis between groups as $P < 0.05$. $P < 0.05$ is a small probability event, indicating that the possibility of an event occurring is very small, so it is considered that the event is unlikely to occur. A low-probability event is an event that has a low probability of occurring. Then, it is almost impossible to happen in one experiment, but it is bound to happen in many repeated experiments. With the continuous improvement of existing technologies and the emergence of more new technologies, proteomics research will make greater contributions to elucidate the mechanism of exercise on skeletal muscle remodeling and its improvement on health.

1. Introduction

With the development of exercise physiology, the understanding of the mechanism of exercise fatigue at home and abroad has evolved from a simple energy consumption or accumulation of metabolites to a multifactor, multilevel, multilink, and comprehensive understanding. Especially with the development of molecular biology technology, the research of fatigue has been developed to the cellular level and molecular level. In the process of to exercise fatigue, there is a complex network regulation, namely, nerve-endocrine-immune-metabolic regulation networks/networked (chain). In this network regulation, the expression of many proteins (enzymes, receptors, cytokines, membrane transport proteins, etc.) changes. Analyzing the changes in protein expression profile during exercise fatigue, it will be

possible to discover new proteins related to exercise fatigue. After the establishment of DNA double helix structure model, the deciphering of human genome sequence, another important milestone in life science research, marks the beginning of life science research into the postgene era. The postgene era, that is, the genome era after the completion of the human genetic map. In the postgene era, the most important task is to understand the structure and function of all protein products of genes. Although gene plays an unshakable role in the field of life science research, it is only the carrier of genetic information, while the real executor of life activities is the expression product of gene—protein. Proteins can more accurately reflect the dynamic changes of cells, tissues, or organisms, and the research focus of life science has gradually shifted from genes to proteins. Therefore, to understand the body's pathophysiological mechanism more deeply, we must start with proteins, and proteomics is the best method to study the activity of proteins.

With the invention and application of mass spectrometry, protein identification becomes more and more convenient, which makes proteomics research develop rapidly. Mass spectrometry has been widely used in the research and development of new molecular structures in industry and related fields. This method, together with NMR, IR, XRD, UV-Vis, and other technologies, has become an indispensable analytical method in research laboratories in the field of organic chemistry. Mass spectrometry is widely used in drugs (drug design, combinatorial chemistry, pharmacokinetics, drug metabolism, etc.), clinical fields (newborn screening, hemoglobin analysis, drug abuse, and stimulants), environmental protection (water quality and food pollution), geological (it has a wide range of uses in many fields such as petroleum components), and biotechnology (proteins, peptides, and hormones). Common techniques used in proteomics research mainly include gel electrophoresis, immunoassay (western blot, enzyme-linked immunoassay, etc.), PCR, 2D-PAGE, Maldli-TOF-MS, and selDI-TOF-MS, which have been developed in recent years, and among them, PCR technology is relatively used and more important [1]. These technologies provide a good technical platform for proteomics research. Because of a powerful technology platform, proteomic research has been into every field of life science research and clinical medical research fields, such as cardiovascular diseases, especially tumor epidemiology, found closely associated with the disease itself and can be used as biological markers of disease proteomics, to clarify disease pathophysiology mechanisms and clinical prevention and treatment of the disease to provide new ideas and methods. However, in the field of sports medicine, proteomics research is still in its infancy, and there are few relevant studies reported at home and abroad. This paper studies the application progress of proteomics in sports kinematics at home and abroad in recent years, so as to provide reference for subsequent studies [2].

The concept of proteome, first proposed by Williams in 1995, can be defined as the entire protein component of a cell, tissue, or entire organism. Proteomics is the study of all proteins in a cell to gain a comprehensive and holistic understanding of the organism [3]. Farrell and his colleagues used two-dimensional gel electrophoresis to map the proteins of E. coli, mice, and guinea pigs, although they were able to separate the different proteins. However, due to the limitation of technical conditions, the isolated proteins could not be identified [4]. Ren et al. introduced a medical migration prediction model based on medical insurance data. However, existing graph neural networks cannot capture time-series relationships between event-type entities. To this end, Ren et al. propose a prediction model based on graph convolutional network (GCN), namely, event-involved GCN (EGCN). The proposed model aggregates traditional entities based on an attention mechanism and event-type entities based on an LSTM-like gating mechanism. Furthermore, skip connections are deployed to obtain the final node representation. To obtain drug-embedding representations based on external information (drug descriptions), an autoencoder capable of embedding drug descriptions is deployed in the proposed model. Finally, extensive experiments are conducted on a real health insurance dataset. Experimental results show that the predictive ability of our model outperforms the state-of-the-art models [5].

In this paper, proteomics techniques can be used to study the skeletal muscle proteome as a whole. Exercise induces an adaptive response in skeletal muscle, and proteomics adjusts accordingly. Different types, intensity, and duration of exercise and muscle fiber types can cause different changes in skeletal muscle proteome. At present, studies on the proteomics of exercise on skeletal muscle remodeling are being carried out, but there are still some technical difficulties. RMS and IEMG were compared after the right and left lower limb muscles were weighted, respectively. The experimental results showed that for one-way ANOVA, the significance level of the difference analysis between groups was defined in this study as $P < 0.05$.

This paper divides the paper into the introduction, the research progress of muscle proteomics in sports, the muscle proteomics in sports, the discussion of muscle proteomics in sports, and the conclusion.

2. The Research Progress of Muscle Proteomics in Sports

2.1. Proteomics Technology. Proteomics techniques can be used to analyze skeletal muscle-related proteins, which can lead to a deeper understanding of muscle function. However, skeletal muscle includes a variety of functional fiber types, which differ in contraction dynamics, bone fibrin subtypes, metabolic enzymes, and mitochondrial density. Skeletal muscle is a type of striated muscle, a muscle attached to the bone, and skeletal muscle is composed of muscle cells arranged in bundles. The length of each cell is different, the cells are closely arranged, the length is complementary, and the outer surface of each cell is covered with a fine mesh membrane. Complex proteomic analysis of skeletal muscle remains a methodological challenge and is complicated by the different characteristics of individual muscles. Skeletal muscle has a high energy requirement, and many proteomics studies focus on mitochondrial-related proteins. At

the same time, skeletal muscle secretory proteome is also an important research object of proteomics for the purpose of discovering the secreted proteins released by muscle which can act on local or systemic proteins. HP protein is a matrix protein, which is a structural protein connecting the viral envelope and the viral core in virology. It has an affinity for the glycoprotein of the host cell wall, and on the other hand, it has an affinity for a variety of ribonucleic acids, which causes it to form a layer of viral nucleoprotein structure under the cell wall. This structure helps the virus mature to encapsulate the RNA and germinate new viruses. The formula for obtaining the HP matrix of protein is as follows:

$$HP(i,j) = [(B(P(i)),j)] \times [(B(P(i)),j)]', \tag{1}$$

$$Q_i = KQ_0U, \tag{2}$$

$$F_i = L_i \times \frac{N_i}{\eta_1}. \tag{3}$$

The structural information of the high-dimensional space is retained in the low-dimensional space and retained as $BP \in \phi^{p\times q}$:

$$BP(p,q) = L(r,p) \times HP(r,c) \times R(c,q), \tag{4}$$

$$N = H - \frac{G(v)}{2}, \tag{5}$$

$$N_1 = \frac{\exp\left(-M^2\right) - v\sqrt{V}(M)}{2v\sqrt{\pi}} V, \tag{6}$$

$$V = \frac{\cot \varphi_i}{\sqrt{2 \times (\beta_1 + \kappa_1 \cos(2\beta))}}. \tag{7}$$

F_W and F_J have the following formulas:

$$F_W = \sum_{I=1}^{K}\sum_{I=1}^{K} L^T(x-m)RR^T, \tag{8}$$

$$F_J = \sum_{I=1}^{J}\sum_{I=1}^{J} L^T(x-L)RR^T. \tag{9}$$

CWT is continuous wavelet transform, which does not involve discrete wavelet transform and does not involve scaling functions; DWT is the discrete Walsh transform, in which the transformation matrix is simple (only 1 and one 1), occupies less storage space, is easy to generate, and has a fast algorithm. It is widely used in image processing problems that require real-time processing of large amounts of data. The CWT formula for feature extraction can be expressed as follows:

$$\mathrm{CWT}(a,b) = \frac{1}{|a|}\int_{-1}^{+1} A(p(t),1)\beta\left(\frac{t+b}{a+b}\right)dt, \tag{10}$$

$$C(a,b) = \mathrm{CWT}(a,b) \times \mathrm{CWT}(a,b)'. \tag{11}$$

The definition of the DWT function is as follows:

$$\mathrm{DWT}(a,b) = \frac{1}{\sqrt{a}}\int f(t)\psi\left(\frac{t-b}{a}\right)dt, \tag{12}$$

$$B^M(R) = -L\chi M(R) - \nabla\beta(R), \tag{13}$$

$$\vec{E} = -JU\vec{A} - \nabla\phi - \frac{1}{\pi}\nabla \times \lambda_\varepsilon, \tag{14}$$

$$\vec{H} = -ML\vec{A}_\varepsilon - \nabla\varphi_m + \frac{1}{\kappa}\nabla \times \gamma. \tag{15}$$

a means scale parameter, and b means translation parameter. First, normalize the features of the monomodal sample:

$$W(i,j) = \exp\left[-\frac{d^2(x_i,x_j)}{\alpha\phi_{i,j}}\right], \tag{16}$$

$$E(L_i) = \frac{1}{N}\sum_{M=1}^{U_s} L_i^n, \tag{17}$$

$$K(p) = \sum_{i=1}^{C_b} -G_i \log(D_i), \tag{18}$$

$$Q_i = \frac{1}{M_s - 1}\sum_{n=1}^{Ns}\left[K_i^n - E(K_i)\right]^2. \tag{19}$$

a is a hyperparameter.

$$\phi_{i,j} = \frac{\mathrm{mean}(d(x_i,k_i)) + \mathrm{mean}\left(d\left(x_i,k_j\right)\right) + \mathrm{mean}\left(d\left(x_j,k_j\right)\right)}{3}, \tag{20}$$

$$P = \beta\left(Di1 - Gi2 + \kappa\sum_j gij\mathrm{Pr}\right), \tag{21}$$

$$\phi = \beta\left(Yi2 - Gi2 + \kappa\sum_j gij\mathrm{Pr}\right). \tag{22}$$

$\mathrm{mean}(d(x_i,k_i))$ represents the average distance between i and its neighbors. Get the final converged network from the original network:

$$L_{t+1}^{(m)} = S_t^{(m)} \times \frac{\sum L_t^{(m)}}{C-1}. \tag{23}$$

Define the probability propagation matrix as

$$T_{ij} = P_t^{(m)} \times \frac{W_{ij}}{\sum w_{kj}}. \tag{24}$$

2.2. Influence of Muscle Fiber Type on Exercise-Induced Proteomic Remodeling. Muscle fiber types also influence the remodeling of exercise-related proteome. According to the contraction speed and metabolic characteristics of muscle

fibers, they can be divided into fast-shrinking-glycolysis type and slow-shrinking-oxidation type. Skeletal muscle fiber is a kind of multinucleated cell, and the number of nuclei varies with the length of the muscle fiber. Shorter ones have fewer nuclei; older ones have 100 to 200 nuclei, which are located below the sarcolemma. The nuclei are oval, lightly stained, and the nucleoli are clear. The size of the muscle fiber area depends on the diameter of the muscle fiber and is affected by age, training, and muscle fiber type. There were differences in protein expression of the two kinds of fibers related to metabolic processes such as glycolysis, free fatty acid metabolism, citric acid cycle, and oxidative phosphorylation. The six proteins, ATP synthase subunit 5B, mitochondrial creatine kinase, myoglobin, glucose phosphate translocation-1, and WD1 repeat protein, were regulated by exercise. However, only mitochondrial NADH dehydrogenase 1 complex 2 and extension factor Tu were differentially expressed in soleus muscle, and both of them were downregulated. It was found that 19 proteins were differently expressed, and 10 and 17 unique secreted proteins were produced in gastrocnemius muscle and soleus muscle after endurance exercise. The dJ-1 protein is more abundant in the gastrector, while the fatty acid-binding protein fabP-3 (FABP-3) is more abundant in the soleus. The authors believe that DJ-1 protein is related to oxidative stress after muscle contraction, while FABP-3 is related to lipid metabolism [6]. The deep polynomial network is shown in Figure 1.

In conclusion, proteomics techniques can be used to study the skeletal muscle proteome as a whole and in depth. Exercise induces an adaptive response in skeletal muscle, and proteomics adjusts accordingly. Different types, intensity, and duration of exercise and muscle fiber types can cause different changes in skeletal muscle proteome. At present, studies on the proteomics of exercise on skeletal muscle remodeling are being carried out, but there are still some technical difficulties. With the continuous improvement of existing technologies and the emergence of more new technologies, proteomics research will make greater contributions to elucidate the mechanism of exercise on skeletal muscle remodeling and its improvement on health [7].

2.3. Application of Myocardial Proteomics in Sports Research. Long-term exercise training can make the heart adapt to change, so that the heart "pump" function increase and the formation of heart self-protection. The increase of cardiac "pump" function is manifested as physiological hypertrophy of the myocardium to enhance the contraction function of myocardium and increase cardiac output to meet the needs of the body. Proteomics is a science that studies the composition of proteins in cells, tissues, or organisms and their changing laws. That is to say, it includes all proteins expressed by a cell or even an organism. Proteomics essentially refers to the study of the characteristics of proteins on a large scale. In order to compare movement mediated myocardial and normal myocardial hypertrophy of proteomics, the study found that 23 movement mediated hypertrophy heart tissue protein point obviously change, and these changes related to mitochondrial oxidative metabolism of protein, such as A statin, malate dehydrogenase, short chains of acetyl-coa dehydrogenase, triose phosphate isomerase, electron transfer flavoprotein beta subunits, ATP synthase alpha, and isocitrate dehydrogenase subunit. In addition, in addition to the upregulation of statin expression in hypertrophic myocardial tissue, there were also upregulation of scaffold, signaling pathway, and proteins related to oxidative stress response. These changes may be related to the enhancement of mitochondrial oxidative metabolism and ATP synthesis ability. Increasing research in sports training rats and intermittent movement training rats cardiac tissue for two-dimensional gel electrophoresis, the results found that 26 protein point difference, 12 of them increasing protein point are only found in sports training in the rat heart tissue, and western blot method confirmed that heat shock protein HSP -20 clear and continue to exist in experimental rat heart tissue. Moreover, hSP-20 expression was upregulated in the myocardium of exercise rats, and phosphorylation of Serine 16 of HSP-20 was found, which was related to the improvement of myocardial contraction and antiapoptosis self-protection [8]. The protein-coding method is shown in Figure 2.

In addition, endurance training is generally considered to enhance myocardial self-protection against ischemia-reperfusion injury-mediated myocardial damage, while the adaptive changes of mitochondria during endurance training play a crucial role in myocardial self-protection. To study the changes of mitochondrial proteins during exercise training [9]. The oprah-way to (be) rats were divided into experimental group and control group in sports training, at the same time, two groups of myocardial mitochondrial protein membrane were isolated and myocardial mitochondrial protein fiber, they are compared, proteomics results identified 222 heart mitochondrial protein, and follow-up study found that the experimental group compared with control group, there are 11 kinds of myocardial fibers mitochondrial protein (cut) expressed in seven kinds of expression, 4 and 2 kinds of myocardial mitochondrial protein membrane (1 kind of express one kind of expression of proteins of) obvious change, and these proteins belong to different functional groups and cardiac protection regulation factor. The mechanism may be the increased expression of antioxidant enzymes and myocardial antiapoptotic proteins (such as HSP-70) mediated by endurance training in mitochondria. These protective factors play an important role in protecting myocardial function against myocardial damage induced by ischemia-reperfusion during exercise [10].

Domestic scholars, respectively, for the movement of atrial and ventricular muscle of rats and the control group differences in proteomics research, cardiac structure, and function of main protein found myosin subtypes: alpha type myocardial myosin heavy chain (alpha MHC) expression in the exercise group rats myocardial cut, this may be related to long-term movement, and energy consumption increase leads to high ATPase activity of alpha MHC shift towards A low beta MHC TPase activity, which can cause the biggest contraction rate of decline. In the study of the changes of ventricular myproteome in rats after exhaustion exercise, it was found that the expression of tropomyosin-1 chain, as an important regulatory protein during muscle contraction,

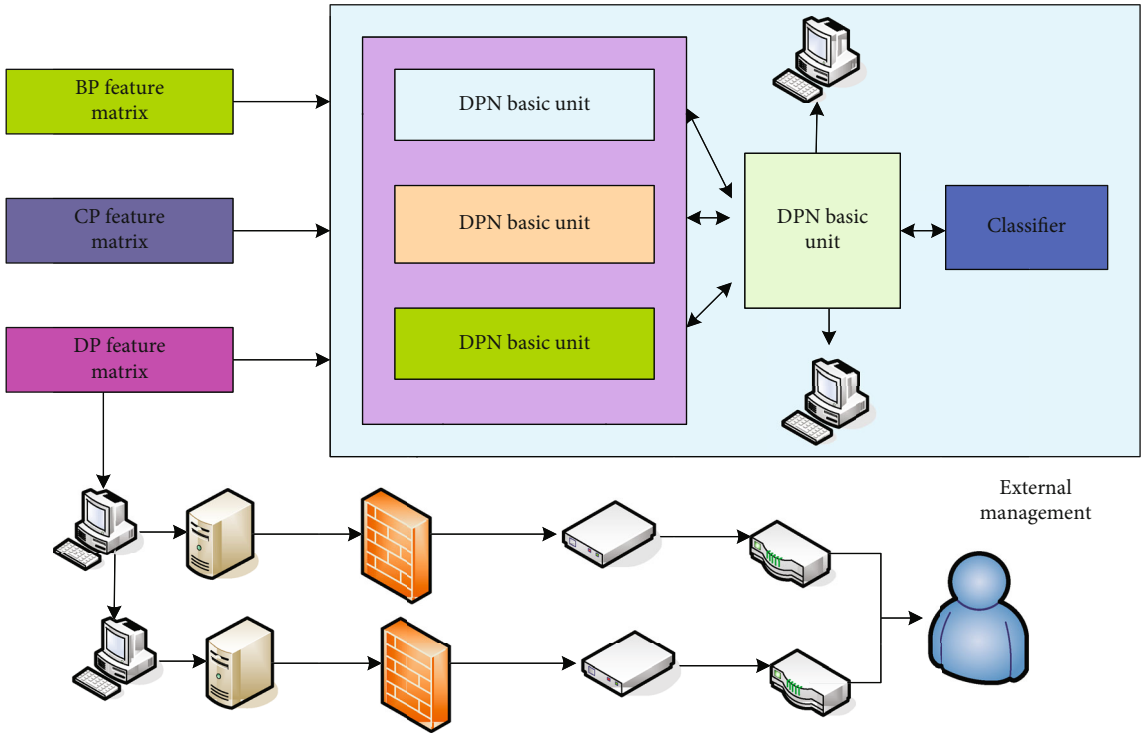

Figure 1: The deep polynomial network.

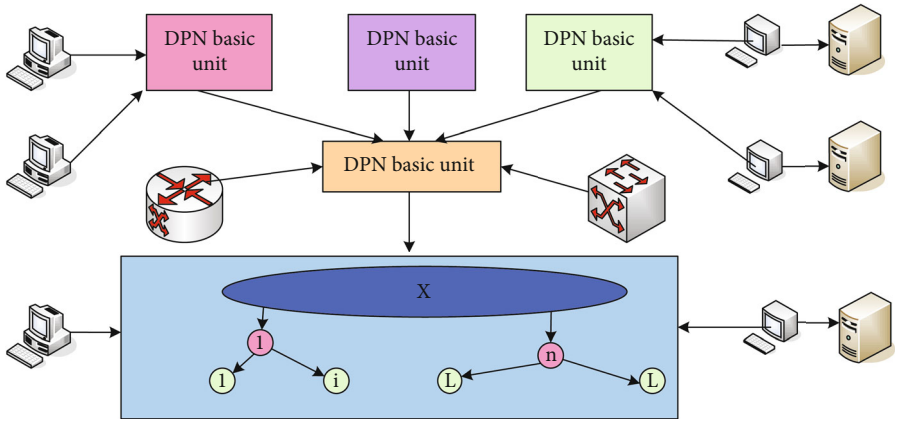

Figure 2: The protein-coding method.

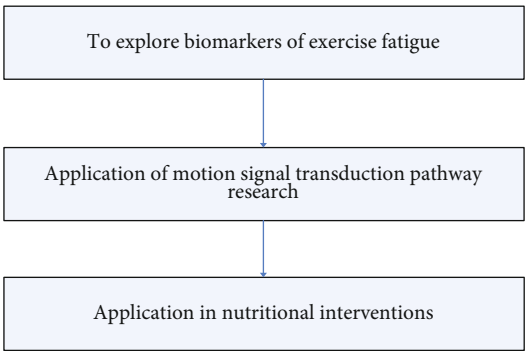

Figure 3: Applied research scope of differential proteomics in sports human science.

Table 1: The isoelectric focusing procedure.

Hydration	50 v	12-16 hours	Active hydration
S1	250 v	30 minutes	Desalination
S2	1000 v	1 hour	Desalination
S3	10000 v	5 hours	Boost
S4	10000 v	60000 volt hours	Focus
S5	500 v	Anytime	Keep

Table 2: The concentration of total RNA and the OD ratio.

Group	1	2	3	4
Sports group	36.2	36.7	90.2	29.5
	1.85	1.81	1.91	1.89
Control group	61.3	53.3	14.1	17.9
	1.89	1.84	1.80	1.86

Table 3: Protein points that disappeared after exercise, and their expression levels were increased by more than twice and decreased to less than below.

SSP number	Mr (KDa) molecular weight	pI isoelectric point	Variation	Fold change range
1251	43	7.93	Up	46.4
1002	66	6.40	Up	13.0
1298	36	8.02	Up	11.7
1025	62	7.27	Up	7.9
1278	39	8.05	Up	7.5

"disappeared" after exhaustion exercise, suggesting that it may be a potential biomarker for the determination of exercise muscle fatigue [11, 12].

2.4. Application of Differential Proteomics in Sports Human Science. Proteins expressed by cells vary in composition and content at specific stages of cell cycle, different stages of differentiation, and different physiological and pathological states. Differential proteomics focuses on such differences, dynamically reflecting the state of the organism, providing accurate molecular description of cells or tissues in a specific state, and more conducive to revealing the essence and laws of life phenomena. Physical exercise changes the physiological environment of human body, such as pH, type and amount of ions, accumulation of metabolic substances, and hormone concentration. Such changes will lead to changes in gene expression and postprocessing modification of protein synthesis, and protein mapping will be different from that under normal physiological conditions [13]. Different exercise mode, exercise intensity, and exercise time have different effects on human physiological function. Different people react differently to the same exercise [14, 15]. Carries on the comparison to the protein mapping between them, we can make a more comprehensive, fully understanding of the different physiological conditions function in the process of life activity metabolism, to reveal the impact of different sports on the body function of biochemical changes in the law, exercise training plan for scientific, medical supervision, and reasonable nutrition intervention to provide theoretical and experimental support, and you can also develop individualized exercise prescription for rehabilitation of patients [16].

(1) Explore the biomarkers of exercise fatigue

In modern sports training theory, without the great physiological load of exercise training, there is no superman, the great physiological load of exercise training inevitably produces exercise fatigue, may even lead to excessive training, cannot be able to eliminate the exercise fatigue again big strength training, and also cannot get good grades, so accurate for diagnosis and effective exercise fatigue of eliminating exercise-induced fatigue is of great significance [17]. Exercise fatigue has always been a practical and challenging topic in the field of sports medicine. The study of exercise fatigue has been going on for a hundred years, ever since digital myography was first used to study the changes in working ability that occur when muscles contract repeatedly. There are many theories about the cause of exercise fatigue, but they all describe one aspect (energy depletion, lactic acid, accumulation of metabolites, etc.). The application of differential proteomics can provide a more comprehensive understanding of the changes of known proteins and some unknown proteins in the process of exercise fatigue. Through comparison, it is possible to find biomarkers that can effectively reflect the generation of exercise fatigue. Thus, it provides a criterion for the diagnosis of the occurrence and development of exercise fatigue. This is of great significance to the development of scientific training plan, effective monitoring of training process, effect evaluation, and prevention of overtraining [18].

(2) Application in the study of motion signal transduction pathways

The changes of body structure and function are realized through a series of motion signal transduction pathways. The signal transduction pathway is composed of a series of proteins. Signal transduction involves protein interactions and posttranslational modifications. At present, in the field of sports medicine, due to the limitations of experimental technology and other factors, the research on the movement signal transduction pathway is still relatively small and shallow. Differential proteomics can identify all proteins that may be involved in signal transduction from the changes of total proteins in cells before and after receptor activation, and start from different protein points to find their upstream and downstream signal transduction molecules. This is a bidirectional or multidirectional method, which can greatly accelerate the research process of signal transduction. By studying the motion signal transduction pathway, we can intervene this process according to different purposes [19, 20].

Table 4: RMS of lower limb muscle surface electromyography in both states.

The experimental project	Shares of rectus muscle	Half tendons	Biceps	Tibialis anterior muscle
Stationary state	4.7 ± 1.8	10.5 ± 5.2	12.8 ± 6.6	4.9 ± 0.9
Random visual excitation	5.2 ± 1.2	31.3 ± 15.2	24.2 ± 10.2	5.6 ± 1.3

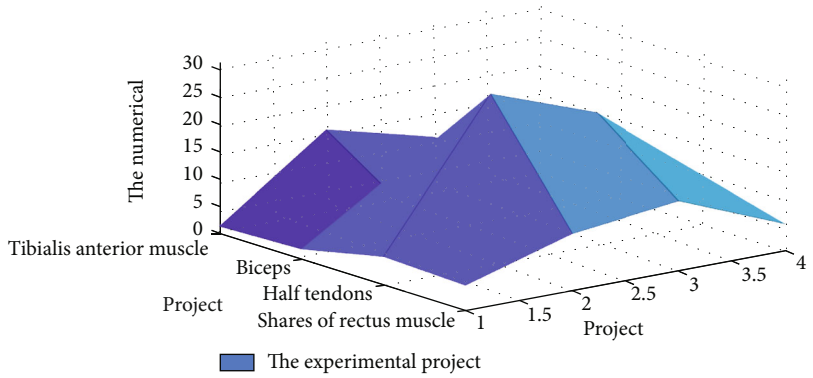

Figure 4: RMS of lower limb muscle surface electromyography in both states.

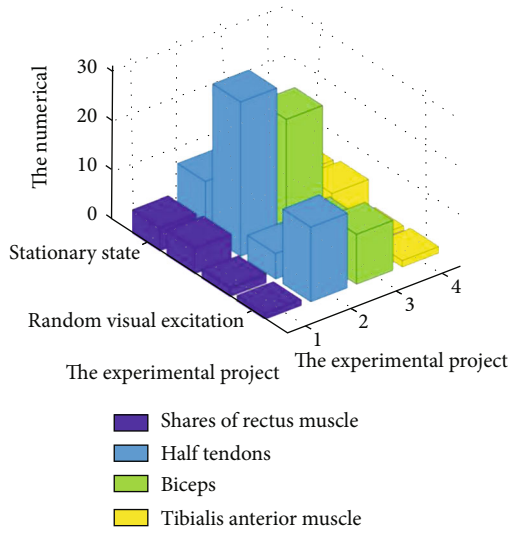

Figure 5: Differences in RMS of the anterior tibia muscle.

(3) Application in nutrition intervention

Lack or excess of nutrients can affect health, physiology, and exercise. Reasonable nutrition supplement for athletes can accelerate the elimination of sports fatigue, enhance immunity, and improve sports ability. Through differential proteomics, new nutritional supplements can be developed, targets of nutritional supplements can be found, mechanism of action and adverse reactions of nutritional supplements can be clarified, and efficacy can be evaluated, so as to improve athletic performance and health. The application and research scopes of differential proteomics in sports human science are shown in Figure 3.

2.5. Development Trend of Proteomics. Proteome research techniques have been applied to various scientific fields, such as cell biology and neurobiology. However, proteome research is still at an early stage of development, and the related technologies and their supporting applications are still very immature. Therefore, the establishment, optimization, and improvement of the technical of proteomics have become one of the main objectives of proteomics research. Proteome technology also has a very attractive prospect in the clinical diagnosis and treatment of major human diseases such as cancer and senile dementia. The focus of future research is to analyze functional proteins and differential proteins. The main technical routes are two-dimensional electrophoresis separation, multidimensional chromatography separation, and mass spectrometry modification analysis of white matter. The main technical routes are enrichment separation and mass spectrometry analysis of modified proteins. Protein complex and protein interaction network analysis are mainly using the existing protein research technology and equipment to carry out the separation and identification of protein complex.

3. Muscle Proteomics Experiments in Sports

3.1. Surface EMG Signal Preprocessing and Feature Extraction. The original EMG signals of the 16 lower limb muscles collected in this paper have not been processed experimentally, and the original signals have a lot of noise, which seriously affects the quality of EMG signals. Therefore, preprocessing and feature extraction of raw EMG signals are required for subsequent muscle activity analysis and nonlinear model of human body dynamic balance. The isoelectric focusing procedure is shown in Table 1.

3.2. Preprocessing of Surface EMG Signals. Based on the nonstationary, nonlinear, amplitude concentration of sEMG signal in 10-10 mV and the main energy concentration in 20-250 Hz frequency, it is extremely easy to be drowned in other noise or interference in the process of signal acquisition. In

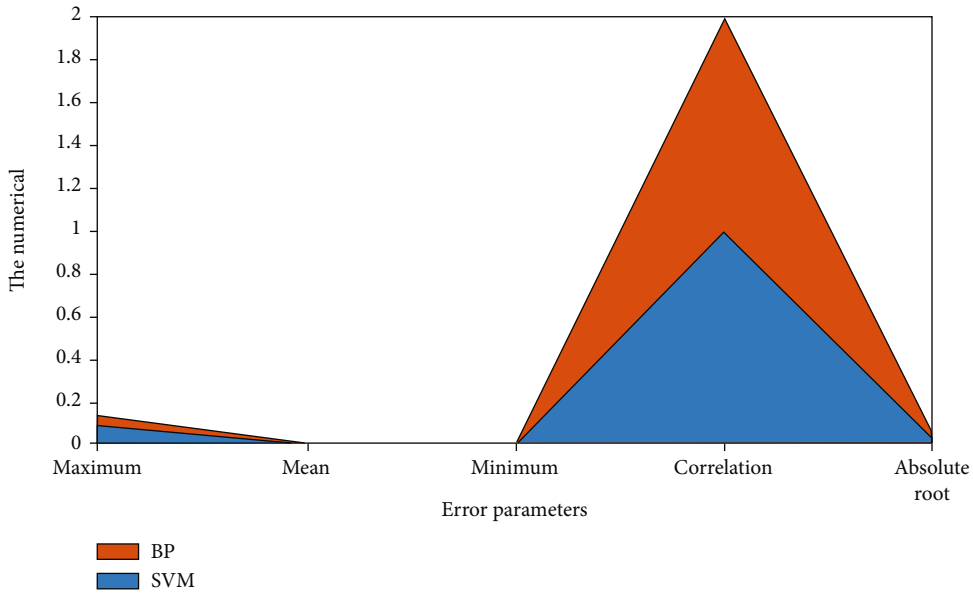

Figure 6: SVM predictive effect data

Table 5: Comparison of BP neural network and SVM prediction results.

Error parameters	BP	SVM
Maximum absolute error	0.0877	0.0467
Mean absolute error	0.00217	0.00182
Minimum absolute error	0.00049	0.00019
Correlation coefficient R	0.9890	0.9922
Absolute root mean square error	0.0275	0.0251

order to reduce the influence of these factors on the subsequent feature extraction and analysis, on the one hand, we should ensure the standard of the experiment during the experiment to overcome some external influences; on the other hand, we should preprocess the signal. In this study, the sEMG signals collected are preprocessed by myoMUSCLE myocle's processing software, and the original EMG signals are filtered by a finite pulse filter at 20-250 Hz. The concentration of total RNA and the OD ratio is shown in Table 2.

3.3. Feature Extraction of Surface EMG Signals. The purpose of this paper is to analyze the activity degree of lower limb EMG signals under stationary state and random visual excitation state and finally use nonlinear identification method to model the nonlinear mapping relationship among surface EMG signals, kinematic data, and dynamic parameters, so as to realize the nonlinear modeling of human dynamic balance. Feature extraction of the task is to determine the activity of muscle data, analyzing the characteristic of the meaningful data as appropriate characteristic parameters extraction is essential to the electromyographic signal analysis, as well as the human body dynamic model of the nonlinear identification provides appropriate input data, on the premise of guarantee of prediction accuracy, keep useful

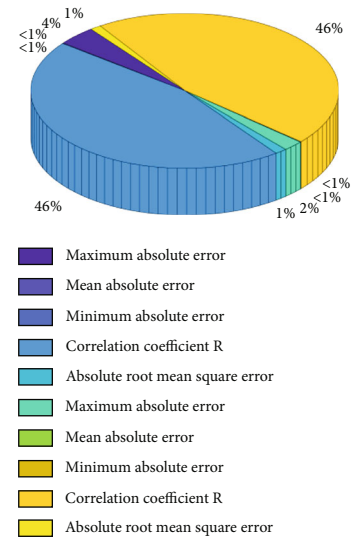

Figure 7: Comparison of BP neural network and SVM prediction results.

information as much as possible, reduce the feature dimension, simplifying the lower limb muscle activity analysis, and speed up the human body dynamic balance of the nonlinear identification process. Table 3 shows the protein points that disappeared after exercise, and their expression levels were increased by more than twice and decreased to less than below.

4. Muscle Proteomics Is Discussed in Sports

4.1. Comparative Analysis of Muscle RMS in the Two States

(1) The experiments using the statistical method of single-factor variance analysis to the same muscles in two states of RMS were analyzed, respectively,

Table 6: Relative net optical density values of the target protein mRNA gel bands in the exercise group and the control group.

Protein name	Changes	Control group ($x \pm s$)	Sports group ($x \pm s$)
Myocardial actin	Upregulate	1.676 ± 0.9683	0.9570 ± 0.6207
Josephin domain protein 1	Upregulate	0.562 ± 0.4207	0.587 ± 0.4338
Adenylate kinase isoenzyme 1	Down	0.859 ± 0.8060	0.714 ± 0.3356
Nucleoside diphosphate kinase B	Down	1.249 ± 0.5923	1.1321 ± 0.3677
Glutathione S-transferase Mu2	Upregulate	0.779 ± 0.3982	0.479 ± 0.1096

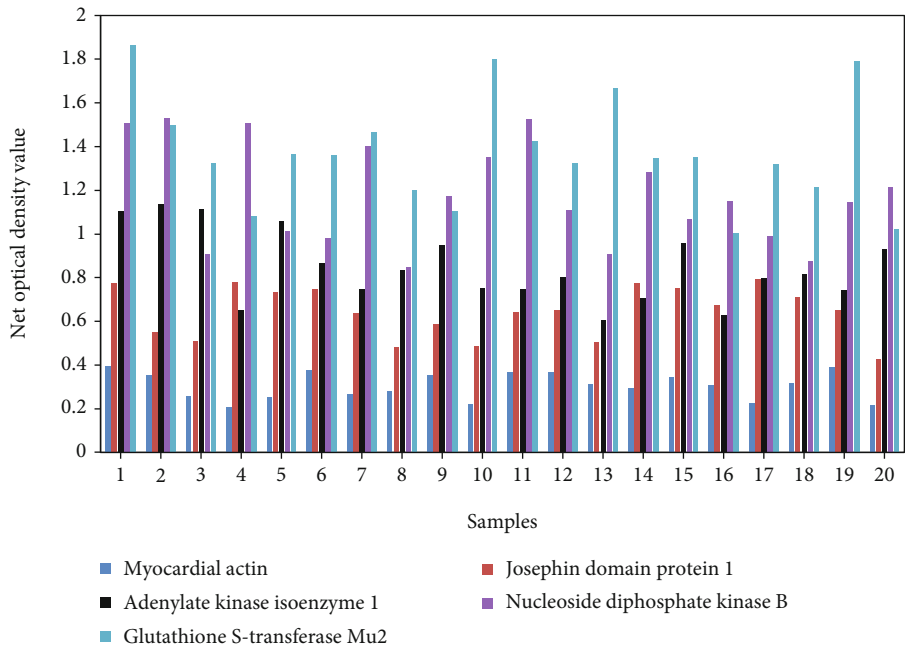

Figure 8: The relative net optical density value of target protein mRNA.

Table 7: The preparation of protein quantification standard curve.

Serial number	Protein content (ug)	Standard solution (5 mg/mlBSA) μL	Double distilled water (μL)	Bradford working fluid (ml)
1	40	8	72	4
2	80	16	64	4
3	120	24	56	4
4	160	32	48	4

under the two states of different between muscle electromyography IEMG were analyzed, finally, the muscle integral electrical values on the contribution rate of extent of each muscle under the two states are analyzed. The protein map basically tells people how to eat, what to eat, and exactly what we need to eat to beat disease. Key levels due to individual differences and two states on the right lower limb corresponding muscles function with the same degree of difference will produce different electromyographic signal, even vary widely, and static experiment and random visual incentive evaluation experiment is done under the left and right side lower limb synergy, and the left and right side lower limb muscles of the same name is adopted, respectively, weighted RMS compared with IEMG later. For one-way ANOVA, this study defined the significance level of the difference analysis between groups as $P < 0.05$. After the stationary experiment and the random visual stimulation experiment, the collected muscles were weighted with the same name, and the statistical results of time-domain eigenvalue-RMS were shown in Table 4 and Figure 4

(2) After one-way ANOVA of RMS of each muscle in the two states, the results showed that the biceps femoris muscle in his half tendons, the lateral gastrocnemius, medial gastrocnemius, long peroneal muscle, and soleus RMS has significant difference ($P < 0.05$), and of the biceps femoris muscle of the lateral sural, soleus RMS difference significantly apparent ($0.01 < P < 0.05$), half tendons, medial gastrocnemius, RMS of long peroneal muscle very significant difference ($P < 0.01$), while rectus, the RMS of the tibialis anterior muscle and no significant

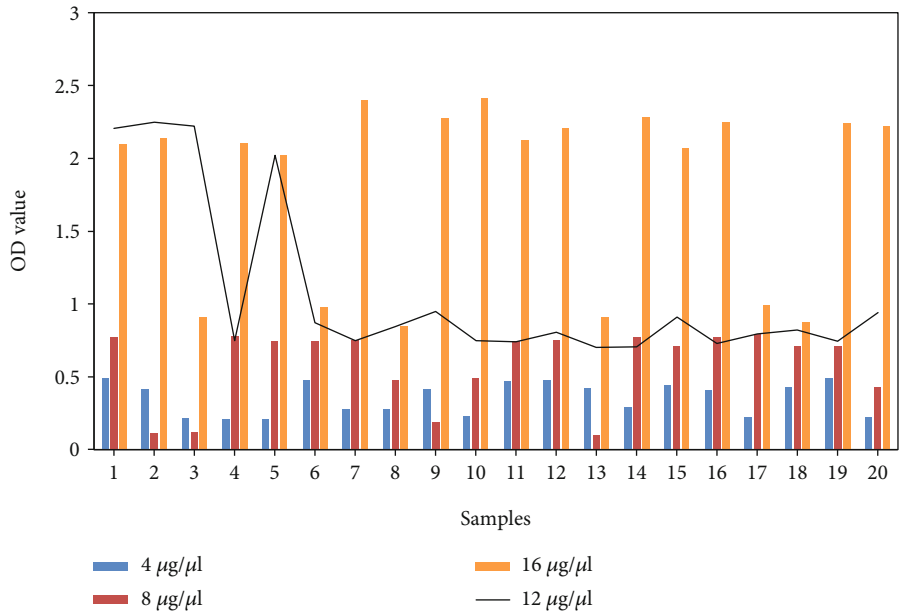

Figure 9: The Bradford quantification standard of atrial muscle extracted protein.

Table 8: The protein spots in the atrial muscle that are upregulated by more than 5 times.

SSP number	Molecular weight (KD)	Isoelectric point (PI)	Increase multiple
1004	20.79	3.89	8.57
1009	21.24	4.62	7.36
1201	30.78	4.92	5.26
1403	38.2	4.56	5.47
2105	55.21	4.77	12.06

Table 9: The protein spots (compared with the control group) that were downregulated by more than 5 times (without the vanishing point) in the atrial muscle.

SSP number	Molecular weight (KD)	Isoelectric point (PI)	Increase multiple
4	22.7	5.48	9.04
201	41.27	4.02	5.52
302	51.51	4.21	0.15
1404	57.05	4.82	9.20
1702	>97	4.68	19.2

Table 10: The protein spots that disappeared in the atrial muscle.

SSP number	Molecular weight (KD)	Isoelectric point (PI)	Increase multiple
4	20.8	3.8	52.8
201	20.77	4.52	202.8
302	55.25	4.86	11.0
1404	>97	5.05	10.4
1702	>97	6.16	17.4

difference ($P > 0.05$), the differences of the RMS of the tibialis anterior muscle as shown in Figure 5

4.2. SVM Prediction Effect

(1) On the basis of previous studies, this study adopts the SVM modeling method to identify the athletes' body dynamic balance nonlinear model. According to the optimized scheme after nonlinear identification, the RMS value of lower limb muscles (lateral gastrocnemius, medial gastrocnemius, peroneus longus, and soleus) and the ankle torque value at the previous moment was input to predict the output value of ankle angle at the next moment. The 5000 sets of data obtained in the experiment were excluded from the data collected at the beginning of discomfort and the data collected when fatigued, and finally 500 sets of data were obtained. The 4500 sets of data in the middle are used for nonlinear recognition of the human dynamics model, the first 4400 sets of data are used as training data, and the last 100 sets ofsamples are used as prediction data. The results show that the SVM predictive output can also approximate the expected output, and the SVM predictive effect is better than that of BP neural network. The SVM predictive effect data are shown in Figure 6

(2) In this paper, a muscle-joint model was established by using SVM, and the predicted output could approach the expected output better. Then compared with the prediction effect of BP neural

Table 11: The differential expression in atrial muscle is predicted.

Serial number	Name	Theoretical molecular weight/isoelectric point	Variety
4	Ferritin light chain 1	(KD/PI)	Down
1009	Tropomyosin beta chain	20.62/5.98	Upregulate
1201	Annexin A5	32. 84/4.66	Upregulate
3102	Glutamine synthetase	35.61/4.93	Down
4506	Transketolase	42.13/6.68	Down

Table 12: The mass spectrometry identification results.

Serial number	Isoelectric point	Points	Variety
1702	5.59	155	Down
1004	4.97	98	Upregulate
6204	6.81	135	Upregulate
2701	5.59	113	Disappear
1705	5.59	132	Down

network, it was found that the correlation between the predicted output of SVM and the expected output was higher than that of BP neural network, and the prediction error was smaller than that of BP neural network. In terms of the prediction effect of athletes' sports dynamic balance, SVM prediction effect was generally superior to BP neural network. The results show that the correlation coefficient between the predicted output and the expected output of SVM is higher than that of BP neural network, and the absolute RMS error between the predicted output and the expected output of SVM model is smaller than that of BP neural network. According to the above analysis, SVM is generally superior to BP neural network in predicting athletes' dynamic balance. The statistical results are shown in Table 5 and Figure 7

Table 6 shows the relative net optical density values of the target protein mRNA gel bands in the exercise group and the control group. As can be seen from the table, the relative net optical density value of cardiac actin mRNA in the control group is 1.676, the exercise group is 0.957, and the exercise group is 0.719 lower than the control group ($P > 0.05$).

Among the 5 target proteins detected, the mRNA expression levels of Josephin domain protein 1, adenylate kinase isoenzyme 1, and nucleoside diphosphate kinase B are consistent with the corresponding protein expression levels. The relative net optical density value of target protein mRNA is shown in Figure 8.

The preparation of protein quantification standard curve is shown in Table 7.

This article carried out three consecutive repetitive electrophoresis and selected a map from the control group and exercise group gel as the reference gel for protein spot matching test, so that the protein spots in each gel correspond to the spots in the reference gel. The Bradford quantification standard of atrial muscle extracted protein is shown in Figure 9.

After exercise, there are 38 protein spots that are reduced by more than 2 times, most of which are concentrated in the molecular weight range of 20-70 KD and the range of 4-8 isoelectric points; among them, 16 protein spots are reduced by more than 5 times (excluding vanishing points) after exercise, and the multiples are reduced. Generally distributed between 5 and 6 times. The protein spots in the atrial muscle that are upregulated by more than 5 times are shown in Table 8.

The protein spots (compared with the control group) that were downregulated by more than 5 times (without the vanishing point) in the atrial muscle are shown in Table 9.

The protein spots that disappeared in the atrial muscle (compared to the control group) are shown in Table 10.

It is inferred that 11 protein spots are differentially expressed more than 5 times after exercise in this study, of which 5 protein spots are upregulated by more than 5 times, and 6 protein spots are downregulated by more than 5 times. The differential expression in atrial muscle is predicted as Table 11 shows.

By comparing the differences in the 2-DE patterns of atrial muscle protein in the exercise group and the control group, the selection prediction is of great significance in sports medicine and clinical medicine. The mass spectrometry identification results are shown in Table 12.

The hydrophobicity of amino acids is one of the factors that affect the stability of protein structure, especially in maintaining and stabilizing protein conformation. The hydrophobicity index of amino acids is shown in Table 13.

Table 13: The hydrophobicity index of amino acids.

Amino acid	A	R	N
Hydrophobicity index	0.61	0.60	0.06
Amino acid	L	K	M
Hydrophobicity index	1.53	1.15	1.18

When $T = 8$, $K = 15$, and $a = 0.4$, the values of ACC, MCC, PE, and SN are 96.71%, 93.61%, 100%, and 93.39%, reaching the peak value. The prediction result of the data set is shown in Figure 10.

One is based on the relative mutation rate of amino acids, using the BLOSUM62 matrix combined with the effective 2DLDA dimensionality reduction method; the other is based on the CWT-based feature extraction of the hydrophobicity of amino acids. The prediction results of the five-fold cross-validation method on the three core data sets are shown in Figure 11.

The average AUC were 97.58%, 95.19%, 95.63%, 97.49%, 96.15%, and 98.43%, and the corresponding standard deviations were 0.28%, 0.73%, 1.02%, 0.46%, 0.24%, and 0.19%. It shows that the average AUC value of the method model TP-

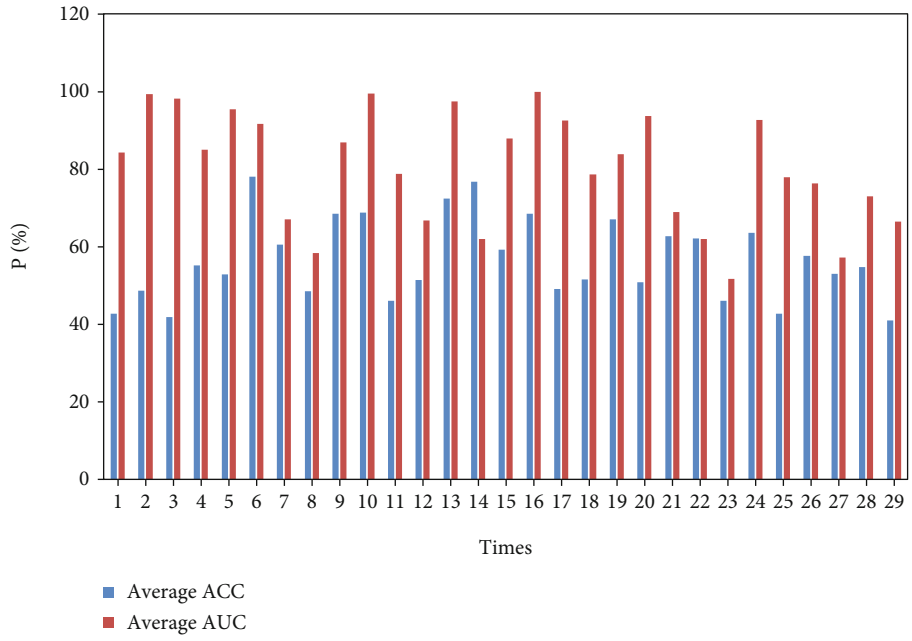

Figure 10: The prediction result of the data set.

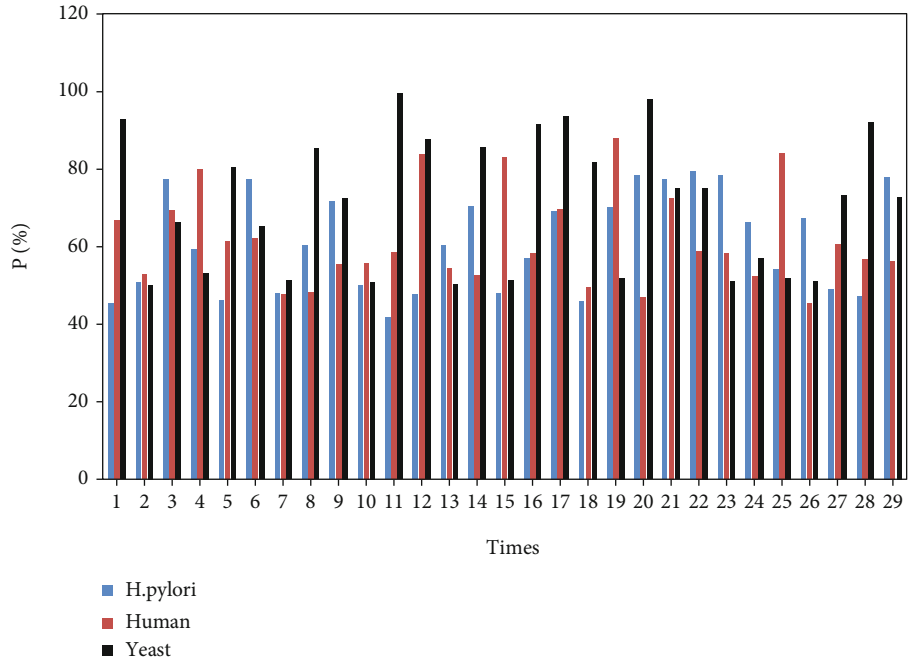

Figure 11: The prediction results of the five-fold cross-validation method on the three core data sets.

SNF-LPA in this paper is increased by at least 0.85%, and the standard deviation is the smallest. The five-fold cross-validation with different other methods on the H. pylori dataset is shown in Figure 12.

The average ACC of the model TP-SNF-LPA in this paper is 94.80%, 97.92%, 94.96%, 97.52%, 98.58% and 99.30%, respectively. The five-fold cross-validation results using other different methods on the Human dataset are shown in Figure 13.

When SVM and LPA are directly used for classification prediction for the same monomodal information, it is obvious that the LPA method has better performance than the

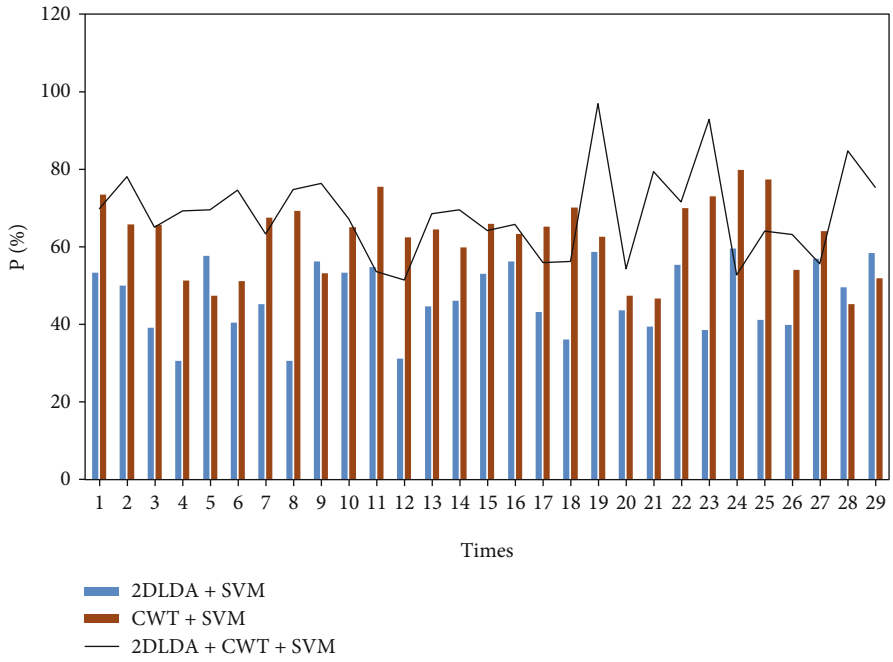

Figure 12: The five-fold cross-validation with different other methods on the H. pylori dataset.

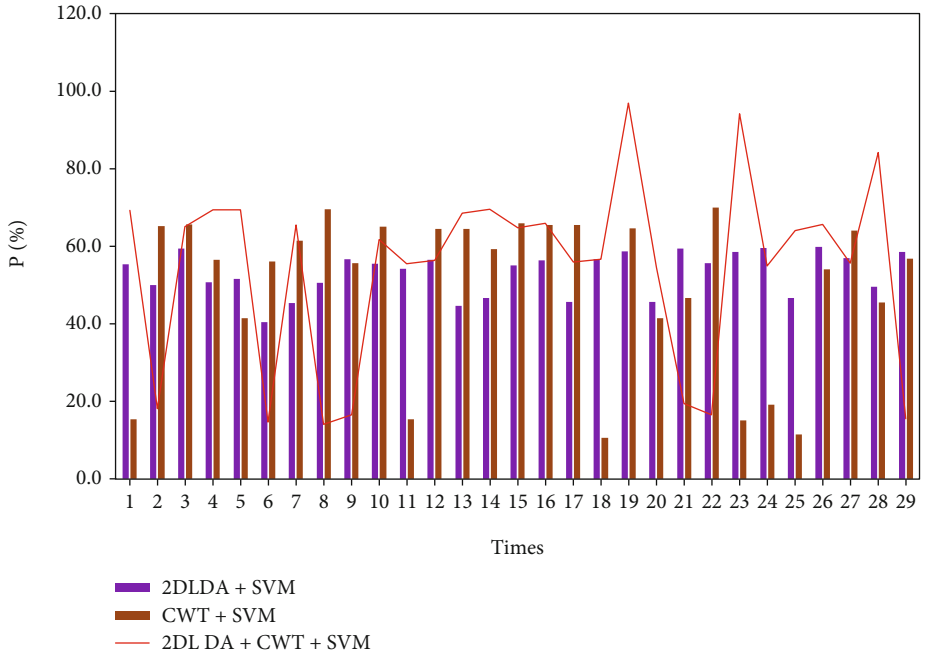

Figure 13: The five-fold cross-validation results with different other methods on the human data set.

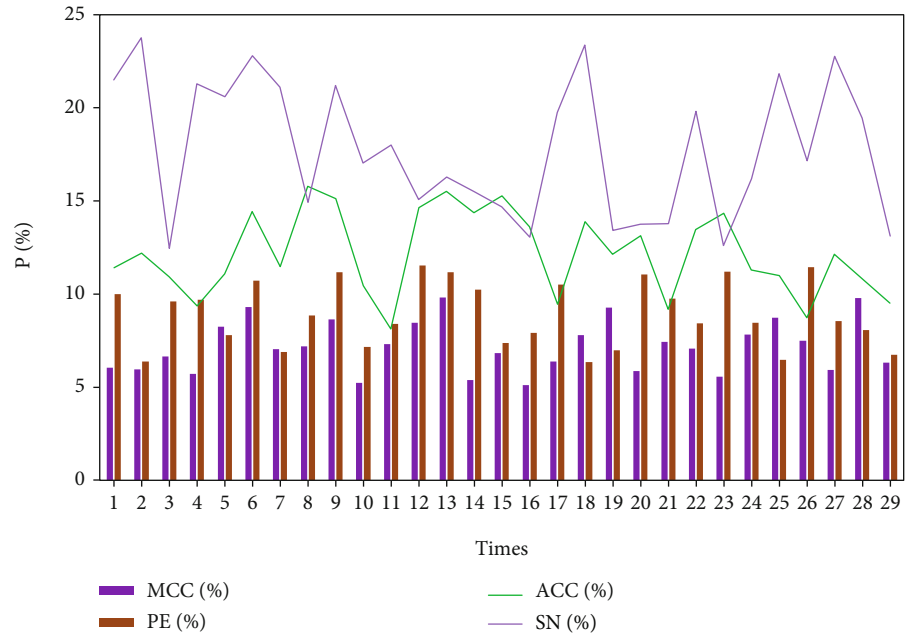

Figure 14: The results of the five-fold cross-validation with different other methods on the yeast dataset.

SVM method. The results of the five-fold cross-validation with different other methods on the yeast dataset are shown in Figure 14.

5. Conclusion

(1) The most direct effect of exercise on the body is to change the shape of skeletal muscles, but the underlying molecular mechanisms are still unknown. Proteomics techniques provide an overview of the molecular pathways that regulate specific stimuli. At present, some progress has been made in the motor mechanism of skeletal muscle remodeling. In this paper, an extensive review and summary analysis of recent proteomics studies on exercise-induced skeletal muscle remodeling is presented. According to the results of this study, protein isolation and protein identification can effectively detect the differentially expressed proteins in skeletal muscles before and after exercise or between exercise and quiet control. Exercise induces an adaptive response in skeletal muscles, so the proteome adjusts accordingly. Different types of exercise, intensity, and duration, and types of muscle fibers lead to different changes in skeletal muscle proteome. With the continuous improvement of existing technologies and the emergence of more and more new technologies, proteomics research will make a great contribution to elucidate skeletal muscle remodeling and improve the movement mechanism of health. Exercise fatigue mainly appears in the early stage-some subjective feelings of discomfort and psychological changes: generally self-feeling tired or even exhausted, poor appetite and sleep, dizziness, dullness, depression, lack of interest and confidence, sensitivity, and irritability wait. Accompanied by the decline in exercise capacity, if the feeling of fatigue develops further without adjustment, there may be slight changes in some objective indicators. Physical functions include weight loss, headache, insomnia, rapid pulse, increased blood pressure, abnormal ECG, decreased hemoglobin, increased white blood cell count, proteinuria, and hematuria. Neurological disorders such as slow response, misjudgment, and inattention. The performance of sports ability is decreased sports quality, fatigue and difficulty in recovery during training, uncoordinated, and inaccurate movements

(2) In sports, muscle proteomics research aimed at understanding sports related to the muscles in the proteome changes, formulate related to sports pathophysiology and molecular mechanism of muscle, to guide and develop scientific and reasonable sports training strategy, and to promote the rapid development of sports undertakings. Although the proteomics research as a whole is still in the preliminary stage, and it is all sorts of deficiencies such as complicated operations, poor experimental requirements, and high sensitivity and accuracy, but as the proteomic technology and the development of genomics and bioinformatics, proteomics will eventually become an optimal approach to study protein expression and functional status. Protein ubiquitously exists in the biological world. It is the material basis of life activities, one of the basic components of organisms, and the most abundant biological macromolecules in organisms. The structure and function of protein are complex, and it is responsible for the tasks of completing various physiological functions in the organism. In terms of material metabolism, body defense, blood coagulation, muscle contraction,

information transmission between cells, individual growth and development, tissue repair, etc., protein plays an irreplaceable role

(3) Muscle tissue is the most abundant tissue in the body of adults. Muscle contraction and relaxation play a very important role in the training of sprinters. The maintenance of various body postures and training movements requires the participation of muscles, which makes the phenomenon of muscle injury become very common. According to the investigation and analysis, muscle injury is a very common training injury among athletes of all ages, which affects the performance and competition ability of athletes, reduces the enthusiasm of athletes to continue to participate in sports training, and may even end their sports career in extremely serious cases. At present, the incidence of muscle injury is increasing year by year, which will affect more athletes and families. Therefore, continuing to study the pathogenesis of muscle injury and exploring more effective treatment methods have become an important research topic in the field of sports medicine. Key levels due to individual differences and two states on the right lower limb corresponding muscles function with the same degree of different will produce different electromyographic signal, even vary widely, and static experiment and random visual incentive evaluation experiment are done under the left and right side lower limb synergy, and the left and right side lower limb muscles of the same name is adopted, respectively, weighted RMS compared with IEMG later. The experimental results showed that for one-way ANOVA, the significance level of the difference analysis between groups was defined in this study as $P < 0.05$

Data Availability

No data were used to support this study.

Conflicts of Interest

The authors state that this article has no conflict of interest.

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