A Multi-Track Cognition Framework for Global Integrative Medicine: Breaking Paradigm Incommensurability Through System-Level Mapping Across Medical Systems

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Article

A Multi-Track Cognition Framework for Global Integrative Medicine: Breaking Paradigm Incommensurability Through System-Level Mapping Across Medical Systems

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Abstract

To address the core challenge in integrative medicine—the semantic incommensurability of heterogeneous medical data arising from divergent cognitive paradigms across medical systems—this paper proposes a multi-track cognition framework for global integrative medicine. Adopting a decoupled design of "flexibly customizable and extensible cognitive tracks with a fixed unified core architecture", this framework constructs exclusive cognitive tracks preserving the native logic for each medical system, takes the homeostatic representation network of multiple dimensions of human eight physiological systems as the general quantitative mediation benchmark, and establishes the system-level mapping relationship constrained by three core rules: cluster correspondence, network emergence, and context dependence, to realize the standardized transformation and system-level fusion of multi-source heterogeneous medical data. Empirical verification shows that the semantic alignment accuracy of this framework reaches 91.27%, the model goodness of fit $R^2 \geq 0.85$, and the accuracy is improved by 32.14% compared with the traditional single-point linear mapping method. The determination results have a strong consistency with clinical expert judgments, which can provide a feasible and general technical support for basic research of integrative medicine, whole-cycle management of chronic diseases, and individualized health intervention.

Keywords: multi-track cognition; system-level mapping; integrative medicine; homeostatic representation network; paradigm incommensurability; global medical integration

Introduction

Driven by the "Healthy China" national strategy, integrative medicine has become a cutting-edge hotspot in the global medical and health field, and the complementary advantages of multiple medical systems including traditional Chinese medicine (TCM), Western medicine, and ethnic medicine have become a consensus in the medical community [1,2]. *The WHO global strategy on traditional and complementary medicine 2023-2032* issued by the World Health Organization has also clarified the global direction for the collaborative development of multiple medical systems, providing a policy framework for the integrated application of different medical systems [6]. In recent years, domestic and foreign scholars have carried out extensive research on the integration of TCM and Western medicine. The introduction of digital technologies such as knowledge graph, network pharmacology, and machine learning has provided new tools for multi-source medical data fusion, as well as methodological support for the modernization research of traditional medicine [3–5,7].

The fundamental obstacle to integration stems from paradigm incommensurability [11], a core concept from the philosophy of science. This refers to the inherent incompatibility between the holistic, relational paradigm of systems like traditional Chinese medicine and the reductionist, substantivist paradigm of Western medicine, which manifests in their core concepts, semantic logic,

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and evaluation frameworks. This incompatibility directly prevents lossless semantic alignment of heterogeneous data across systems, an issue far beyond simple format inconsistency. Most existing studies have only solved the standardization of data format, but failed to break through the semantic barriers caused by paradigm differences at the underlying level, and still have three core limitations: first, most schemes are designed for specific scenarios of TCM-Western medicine dual systems, with insufficient universality and difficulty in adapting to the integration needs of multiple medical systems; second, most schemes adopt single-point linear correspondence logic, which cannot fit the systemic effect of multi-component and multi-target synergy, and easily lose the native logic of the medical system; third, they fail to break through the reductionism transformation trap of "interpreting TCM with Western medicine", which is easy to cause cognitive dislocation and semantic loss.

Based on this, this paper proposes a multi-track cognition framework for system-level mapping of data across medical systems: through independent multi-track cognition channels, the native logic of each medical system is completely preserved; the homeostatic representation network of the human body is used as a unified semantic anchor to break through paradigm barriers; and the breakthrough from linear mapping to system-level fusion is realized through three core rules. This framework can be seamlessly adapted to any medical system with a complete theoretical system, including TCM, Western medicine, ethnic medicine, international traditional medicine, and functional medicine, providing a feasible and extensible general technical framework for the integration of global multiple medical systems.

1. Definition of Core Terms

To clarify the research boundary, unified and rigorous academic definitions are made for core terms, and all definitions are consistent with the core connotation of the corresponding invention patent:

1. **Multi-track Cognition (MTC)**: The original core theory proposed in this study, which refers to a cognitive framework that constructs independent and interoperable data processing channels for different medical systems, to preserve the native theoretical logic of each system while realizing cross-system semantic alignment.
2. **Cognitive Track (CT)**: A standardized data processing channel constructed corresponding to the native logic of a single medical system, which completely retains its core feature dimensions, evaluation rules, and application logic without forced cross-paradigm transformation, providing an independent and complete data processing and logic mapping link for each independent medical system, with the formal definition: an independent data processing pathway preserving the native logic of a medical system.
3. **Homeostasis**: The core basic concept of this study, which refers to the dynamic equilibrium state maintained by the human physiological system through self-regulation under the changes of internal and external environments, and is the core quantitative representation of health status, rather than the index stability under disease state.
4. **Homeostatic** Representation Network (HRN): A structured data network with human system homeostasis as the core, composed of quantifiable homeostatic dimensions with predefined association relationships and target ranges. It is the only general quantitative mediation benchmark and semantic anchor for cross-system data interoperability, with the formal definition: a structured network of quantifiable homeostatic dimensions with predefined target ranges.
5. **System-Level Mapping Topology**: A full-link mapping architecture defined by three core rules, which realizes the complete mapping from the native feature dimensions of the medical system to the homeostatic representation network, avoids the defects of fragmented analysis, and fits the holism logic of the medical system.

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6. **Semantic Alignment Accuracy (SAA)**: The core evaluation index of this study, which is used to quantify the semantic consistency of cross-system data fusion. The specific calculation method and determination basis are shown in Section 2.4.

2. Construction of Multi-Track Cognition System-Level Mapping Framework

This framework adopts a three-layer architecture of "multi-track input - single anchor mediation - unified output". The core logic is to realize lossless intercommunication of data of different paradigms through a unified quantitative mediation benchmark, while completely preserving the native cognitive logic of each medical system. The overall architecture of the framework is shown in Figure 1.

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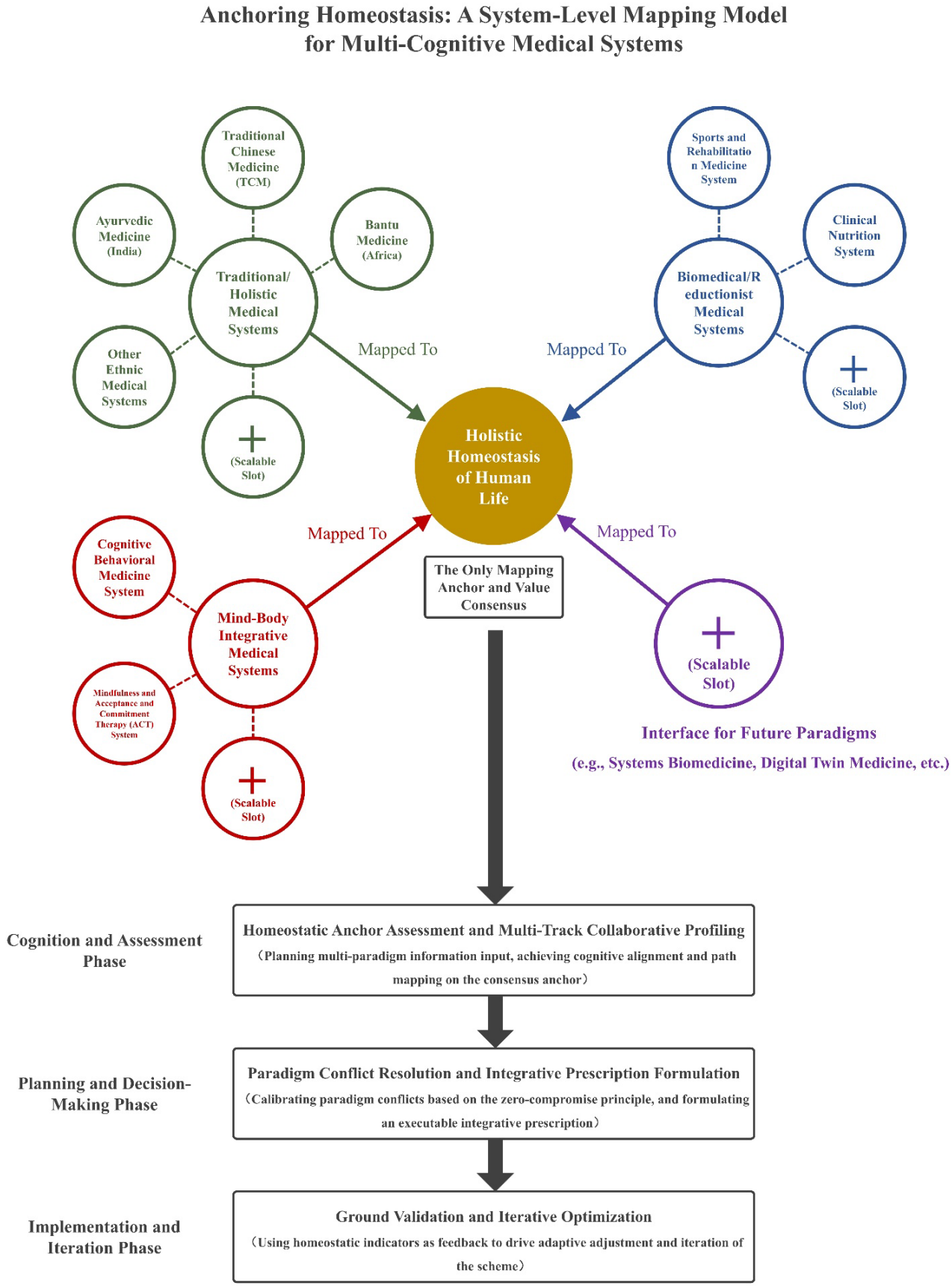

Figure 1. Anchoring Homeostasis: System-Level Mapping Model for Multi-Cognitive Medical Systems. *Note. This figure illustrates the core framework of the proposed multi-track cognition model, where all medical systems are mapped*

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to the unified anchor of human holistic homeostasis, enabling cross-system semantic alignment and integrative clinical application.

2.1. Multi-track Cognitive Dimension Construction Module

For the i-th independent medical system (i=1,2,...,N, N≥2), an exclusive cognitive track C_i is constructed, which includes three core elements, fully fitting the native logic of the corresponding medical system without cross-paradigm simplification or forced transformation:

1. **Standardized feature dimension set**: is derived entirely from the core theoretical framework of the respective medical system. For example, the TCM cognitive track includes dimensions such as nature and flavor, meridian tropism, efficacy and indication, syndrome adaptation, and compatibility taboo; the Western medicine cognitive track includes dimensions such as active ingredients, action targets, pharmacological effects, safe dose, and toxicological characteristics; the Tibetan medicine cognitive track includes dimensions such as five-source attribute, six tastes, eight properties, seventeen effects, and disease adaptation.
2. **Data normalization rules**: Comply with the clinical application specifications of the corresponding medical system. For example, TCM adopts the grading standard of herbal medicine property intensity and the quantitative scoring standard of TCM syndromes; Western medicine adopts the standardization specification of clinical test indicators. All indicators are finally mapped to the [0,1] interval to eliminate dimensional differences.
3. **Systemic effect evaluation index**: Adopt the native evaluation system of the corresponding medical system. For example, TCM takes the harmony degree of viscera function and the balance state of yin-yang qi and blood as the core; Western medicine takes the change range of physiological indicators and the effective rate of target regulation as the core, which is used as the optimization objective of mapping model training.

2.2. General Anchor Mediation Layer Construction Module

The core of this module is the multi-dimensional homeostatic representation network of the human body, which is the core carrier of cross-system semantic alignment and the key design to break through paradigm incommensurability. No matter what kind of medical system, the ultimate goal of intervention is to regulate human homeostasis. Therefore, taking homeostasis as the general anchor can realize lossless semantic alignment without changing the native logic.

2.2.1. Setting of Homeostatic Dimensions

The homeostatic representation network covers eight major physiological systems of the human body: circulatory, respiratory, digestive, immune, nervous, endocrine, urinary, and reproductive systems. 28 clinically gold-standard detectable physiological indicators are selected as network nodes. The screening and gold-standard attributes of the 28 core indicators are determined with reference to the clinical routine detection system of the eight physiological systems in *National Clinical Laboratory Operation Procedures (4th Edition)* [9]. For each indicator, the normal homeostatic interval, intervention effective interval, and safety risk interval are preset with reference to the clinical diagnosis and treatment guidelines issued by the Chinese Medical Association, to ensure the scientificity and clinical authority of the indicator thresholds.

2.2.2. Network Topology and Weight Construction

The homeostatic representation network adopts a directed acyclic graph structure $G=(V,E,W)$, where V is the set of homeostatic dimension nodes, E is the set of edges representing the association relationship between dimensions, and W is the association weight matrix.

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The network construction is divided into two stages to avoid subjective bias to the greatest extent and ensure that the network conforms to the laws of human physiology:

1. **Topology structure determination stage**: Through authoritative physiological literature and expert consultation with 3 chief physicians of integrated TCM and Western medicine, determine the existence of association relationships between dimensions (i.e., edge connection), and clarify the basic topology of the network, to ensure that the association relationships conform to classical physiological theories and clinical consensus.
2. **Weight optimization stage**: In clinical practice, the physiological indicators of the human body are not independent of each other, but have inherent synergistic and restrictive relationships that conform to the laws of human physiology. Subjective weight assignment by experts is prone to personal bias, which will affect the objectivity and clinical reproducibility of the homeostatic representation network. The Bayesian network can objectively quantify the strength of the association between homeostatic dimensions based on real clinical data, avoiding subjective bias to the greatest extent, and ensuring that the network structure fully conforms to the objective laws of human physiology.Using the data of patients with stable vital signs and test indicators within 24 hours of admission in the Medical Information Mart for Intensive Care III (MIMIC-III) dataset, the Bayesian network is used to complete parameter learning, and optimize the specific value and direction of the weight. The conditional probability distribution formula of the Bayesian network is:

$$P(V_1, V_2, \ldots, V_{28}) = \prod_{j=1}^{28} P\left(V_j \mid Pa(V_j)\right)$$

Where $Pa(V_j)$ is the parent node set of node V_j, that is, other homeostatic dimensions that have a direct impact on the node; $P(V_j|Pa(V_j))$ is the conditional probability distribution of node V_j. The parameter learning of the Bayesian network is completed by the maximum likelihood estimation method, and the quantitative association relationship between homeostatic dimensions is finally determined.

2.3. System-Level Mapping Relationship Construction Module

2.3.1. Three Core Mapping Rules

The three rules are the core of realizing the breakthrough from linear mapping to system-level fusion, which fit the holism logic of the medical system, and have clear operability and theoretical support:

1. **Cluster Correspondence Constraint**: A systemic effect corresponds to the synergistic action of a cluster of features/components, rather than a one-to-one linear mapping. In the algorithm implementation, multiple feature data corresponding to the same systemic effect are input into the model as a feature group, rather than splitting a single feature for independent modeling. This rule fits the core theory of multi-component synergistic effect of TCM, and is consistent with the research paradigm of multi-component and multi-target of network pharmacology [4,7], with the supplementary definition: *rule governing synergistic effects of feature clusters*.
2. **Network Emergence Constraint**: The mapping must capture the emergent properties arising from multi-feature, multi-target, and multi-pathway interactions, moving beyond simple additive effects. In the algorithm implementation, the high-order interaction terms between features are automatically learned through the model to completely restore the multi-factor synergistic logic of complex biological systems. This rule is based on the emergence theory of

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complex system science, conforms to the inherent law of the human body as a complex physiological system, and is highly consistent with the holism of integrative medicine [1].

3. **Context Dependence Constraint**: The mapping is *context-aware*, dynamically adapting to individual patient factors such as physical constitution and syndrome patterns, to fit the individualized intervention principle of different medical systems. In the algorithm implementation, a hierarchical training mechanism is adopted: first, the data set is stratified based on the patient's physical constitution/syndrome labels, and mapping sub-models are trained separately for different stratifications; for new samples, the corresponding syndrome/physical constitution stratification is matched first, and then the corresponding sub-model is called to complete the mapping, realizing the dynamic adjustment of association weights with the human body state.

2.3.2. Implementation of Mapping Model Algorithm

This study uses the random forest algorithm to construct the mapping model, which has strong adaptability to the nonlinear medical data, good interpretability, and is not easy to overfit, fully conforming to the methodological specifications of medical research [8].

1. **Feature vectorization processing**: For the standardized feature dimensions of each cognitive track, the combination of ordinal encoding and one-hot encoding is used to complete vectorization conversion: the cold/hot attribute of TCM nature is graded into 7 levels of "great cold, cold, slight cold, neutral, slight hot, hot, great hot", which are mapped to ordinal values from -3 to +3; classification features such as TCM meridian tropism, efficacy and indication, and Western medicine disease classification are processed by one-hot encoding and converted into binary feature vectors. Finally, all features are integrated into a unified input feature matrix X with consistent dimensions.
2. **Input, output and loss function**: The input of the model is the standardized feature matrix X of each cognitive track, and the output is the prediction matrix Y of the corresponding dimension of the homeostatic representation network (i.e., the change of human homeostatic indicators after intervention). The core clinical goal of this model is to accurately predict the real changes of human homeostatic state after intervention with different medical systems. Therefore, the model training must take the deviation between the predicted value and the real clinical observed value as the core optimization objective, to ensure that the model output has clear clinical guiding significance. The optimization objective of model training is to minimize the mean squared error (MSE) between the predicted value and the real value. The loss function formula is:

$$\text{Loss} = \frac{1}{n}\sum_{i=1}^{n}\left(Y_i - \widehat{Y}_i\right)^2$$

Where n is the number of training samples, Y_i is the real value of the change of homeostatic indicators, and $\widehat{Y}_i$ is the predicted value of the model.

1. **Model training process**: 5-fold cross-validation is used to complete model training and parameter optimization. The data set is randomly divided into 5 equal subsets. Each time, 4 subsets are taken as the training set and 1 subset as the verification set, and the cycle is repeated 5 times. The average performance is taken as the final performance of the model. The core hyperparameters of the model are optimized by grid search, and the optimal parameters are finally determined: number of decision trees n_estimators=100, maximum tree depth max_depth=10, minimum number of samples for node splitting min_samples_split=5. The clinical data of integrative medicine has strong heterogeneity due to the differences in patients'

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physical constitution, syndrome patterns and underlying diseases. To avoid model overfitting and ensure the stability and generalizability of the model in real clinical scenarios, we use 5-fold cross-validation to complete model training and hyperparameter optimization. The complete algorithm flow is as follows: The algorithm pseudo-code is as follows:

Algorithm 1. Random Forest Training Algorithm for Multi-Track Cognition System-Level Mapping.

Input: Cognitive track feature dataset *X*, real change dataset of homeostatic indicators *Y*, cross-validation fold *k*=5

Output: Trained system-level mapping model *Model*

1: Initialize random forest hyperparameters: *n_estimators*=100, *max_depth*=10, *min_samples_split*=5

2: Randomly divide the dataset (*X*,*Y*) into k mutually exclusive subsets $S_1, S_2, \ldots, S_k$,

3: for *i* in 1 to *k*:

4: Validation set *Val* = S_i, training set Train = Full Dataset \ S_i

5: Complete feature grouping and preprocessing according to the three mapping rules based on the *Train* set

6: Train the random forest model with the *Train* set to optimize the MSE loss function

7: Verify the model performance with the *Val* set and record the goodness of fit R^2

8: end for

9: Select the hyperparameter set corresponding to the optimal average cross-validation performance to train the final model

10: return *Model*

2.4. Definition of Core Evaluation Indicators

To quantitatively evaluate the model performance, this study sets 4 core evaluation indicators, all of which have clear mathematical definitions and calculation methods to ensure the reproducibility and comparability of the evaluation results:

1. Semantic Alignment Accuracy (SAA): The core evaluation index, used to quantify the semantic consistency of cross-system data fusion, The biggest clinical pain point in the field of integrative medicine is the lack of objective, quantifiable and reproducible indicators to evaluate whether the interventions of different medical systems have achieved clinically meaningful consensus. Semantic Alignment Accuracy (SAA) takes human homeostasis as the unified anchor, and quantifies the semantic consistency of intervention data from different medical systems at the clinical level, providing an objective evaluation tool for the effect of multi-medical system integration. with the calculation formula:

$$SAA = \left(\frac{1}{M}\right) \sum_{m=1}^{M} I\left(\cos\left(\vec{V}_{m1}, \vec{V}_{m2}\right) \geq \theta\right)$$

Where *M* is the number of test samples, $\vec{V}_{m1}$ and $\vec{V}_{m2}$ are the homeostatic network change vectors obtained after model mapping from intervention data of two different medical systems for the same health state, *cos*(·) is the cosine similarity function, *I*(·) is the indicator function, which takes the value 1 when the condition is met, otherwise 0.

The similarity threshold θ=0.85 is determined by the combination of "expert annotation + optimal cut-off value of ROC curve": first, 3 clinical experts with the title of associate chief physician or above in integrated TCM and Western medicine were invited to conduct double-blind annotation on 100 groups of intervention data from different medical systems for the same health state, to judge whether the two groups of data achieved clinically meaningful semantic alignment; based on the gold

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standard dataset annotated by experts, the ROC curve was drawn, and the threshold corresponding to the maximum Youden index was determined to be 0.85. Under this threshold, the sensitivity of the annotation result is 92.3% and the specificity is 88.7%, which has both accuracy and specificity, so it is determined as the judgment threshold of semantic alignment.

2. Goodness of Fit (R^2): Used to evaluate the prediction accuracy of the model for the change of human homeostatic indicators, This indicator is used to evaluate the interpretability of the model for the changes of human homeostatic state. The closer the value is to 1, the more accurately the model can restore the real impact of interventions from different medical systems on human homeostasis, which directly determines the clinical reference value of the model output. with the calculation formula:

$$R^2 = 1 - \frac{\sum_{i=1}^{n}\left(Y_i - \widehat{Y}_i\right)^2}{\sum_{i=1}^{n}(Y_i - \bar{Y})^2}$$

Where $\bar{Y}$ is the mean of the real values of homeostatic indicators, and the closer R^2 is to 1, the better the prediction effect of the model.

3. Mean Absolute Error (MAE): Used to evaluate the absolute deviation between the predicted value and the real value of the model, This indicator quantifies the average absolute deviation between the predicted value of the model and the real clinical observed value, which directly reflects the prediction accuracy of the model for a single homeostatic dimension, and ensures that the prediction of each physiological indicator is consistent with the real clinical situation without systematic deviation. with the calculation formula:

$$MAE = \frac{1}{n}\sum_{i=1}^{n}\left|Y_i - \widehat{Y}_i\right|$$

The smaller the MAE value, the higher the prediction accuracy of the model.

4. Root Mean Square Error (RMSE): Used to evaluate the deviation degree between the predicted value and the real value of the model, This indicator is highly sensitive to the abnormal predicted values of the model, which can effectively test the stability of the model in extreme clinical scenarios (such as patients with severe homeostatic imbalance), and ensure that the model can maintain reliable prediction effect in patient groups with different health states, adapting to the complex scenarios of real clinical practice. with the calculation formula:

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}\left(Y_i - \widehat{Y}_i\right)^2}$$

The smaller the RMSE value, the better the prediction stability of the model.

3. Model Verification and Result Analysis

This study sets up two groups of empirical verification: the basic verification of TCM-Western medicine dual-track, and the extended adaptation verification of multi-medical system. All data are

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from public authoritative datasets, which comply with medical ethics norms and data use requirements.

3.1. Experimental Data and Preprocessing

Four groups of authoritative public datasets in the field are used, and the details are shown in Table 1.

Table 1. Details of Experimental Datasets.

Dataset Name	Data Source	Core Purpose
TCMSP Traditional Chinese Medicine System Pharmacology Database	Northwest A&F University	Feature extraction of TCM cognitive track
MIMIC-III Intensive Care Medical Dataset	Massachusetts Institute of Technology	Feature extraction of Western medicine cognitive track and extraction of real homeostatic values
Clinical Diagnosis and Treatment Dataset of China Academy of Chinese Medical Sciences	China Academy of Chinese Medical Sciences	Feature extraction of TCM cognitive track and model training verification
Public Dataset of Clinical Research on Tibetan Medicine in China	*Chinese Journal of Tibetan Medicine*	Feature extraction of Tibetan medicine cognitive track and multi-system extended verification

Full data preprocessing process:.

1. **Data cleaning**: Invalid samples with missing values > 30% were eliminated, and the remaining missing values were filled by multiple imputation method.
2. **Standardization processing**: Aiming at the format differences of data from different medical systems, a unified feature vectorization framework was adopted. One-hot encoding was used for all classification features, ordinal encoding for ordinal grade features, and min-max standardization for continuous numerical features. Finally, the features of all cognitive tracks were uniformly mapped to the [0,1] interval to eliminate the format and dimensional differences of data from different systems.
3. **Dataset division**: The preprocessed dataset was randomly divided into training set (70%) and test set (30%) according to the ratio of 7:3. The training set was used for model training and parameter optimization, and the test set was used for model performance evaluation.

For the MIMIC-III dataset, the subset of patients with stable vital signs and test indicators within 24 hours of admission was screened. The mean value of indicators in the stable period was taken as the homeostatic benchmark value, and the change of indicators before and after intervention was taken as the label data for model training, to ensure the clinical rationality of homeostatic indicators.

All datasets used in this study are publicly available authoritative datasets in the field of integrative medicine and medical data mining, fully complying with medical ethics norms and data use requirements. The preprocessing workflow follows the standard specifications of medical machine learning research.

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3.2. Selection of Baseline Methods

To verify the superiority of this framework, three mainstream multi-medical system data fusion methods in the field were selected as baseline comparisons to ensure the fairness and industry representativeness of the comparison:

1. Baseline 1: Single-point Linear Correlation Analysis: The mainstream traditional method in the current field of TCM-Western medicine data fusion, which realizes the linear correspondence between a single TCM feature and a single Western medicine indicator through Pearson correlation analysis.
2. Baseline 2: LASSO Regression Feature Association Method: A commonly used method for feature screening and association of high-dimensional medical data, which realizes feature selection through L1 regularization and constructs a linear association model between TCM features and Western medicine indicators.
3. Baseline 3: Knowledge Graph Semantic Alignment Method: The current mainstream technical method for medical term alignment, which realizes the semantic alignment between TCM syndromes and Western medicine diseases, traditional Chinese medicine and pharmacological effects by constructing a medical knowledge graph [12].

3.3. Basic Verification Results of TCM-Western Medicine Dual-Track

All simulation experiments were conducted in a unified experimental environment, with the same dataset partitioning and preprocessing rules for the proposed framework and all baseline methods, to ensure the fairness and comparability of the performance comparison. As shown in Table 2, the proposed framework significantly outperforms all three baseline methods across every core evaluation metric.

Table 2. Performance Comparison Results Between the Proposed Framework and Baseline Methods.

Evaluation Indicator	Proposed Framework	Baseline 1: Single-point Linear Correlation	Baseline 2: LASSO Regression	Baseline 3: Knowledge Graph Alignment
Semantic Alignment Accuracy (SAA)	91.27%	59.13%	68.42%	76.58%
Goodness of Fit (R^2)	0.852	0.426	0.583	0.617
Mean Absolute Error (MAE)	0.076	0.213	0.168	0.152
Root Mean Square Error (RMSE)	0.098	0.257	0.204	0.189
Cohen's d Effect Size	-	2.87	2.31	1.94

The results show that:

- The semantic alignment accuracy reaches 91.27%, which is 14.69 percentage points higher than the best-performing Baseline 3, and 32.14 percentage points higher than the traditional single-point linear correlation method. The Cohen's d effect sizes are all >0.8, among which the Cohen's d value for the performance difference between the proposed framework and the best-performing baseline (Baseline 3) reaches 1.94, far exceeding the 0.8 threshold for a large effect size, further confirming the clinical practical value of the performance improvement..
- The goodness of fit R^2 of the model reaches 0.852, which is much higher than the baseline methods, proving that the proposed framework has excellent prediction accuracy for the changes of human homeostatic indicators.

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- Both MAE and RMSE are significantly lower than the baseline methods, proving that the prediction accuracy and stability of the proposed framework are better.

Paired t-test was used to analyze the semantic alignment accuracy between the proposed framework and the baseline methods, and the result showed $p<0.01$, indicating that the performance improvement of the proposed framework compared with the baseline methods has extremely significant statistical difference. The Kappa consistency test was performed between the model's semantic alignment judgment results and the expert-annotated clinical gold standard from the public clinical dataset, to verify the clinical significance of the model output. The Kappa consistency coefficient between the semantic alignment judgment results obtained by the model based on the threshold $\theta=0.85$ and the double-blind annotation results of 3 clinical experts is 0.86 ($p<0.001$), which has extremely strong consistency, proving that the semantic alignment judgment results of the proposed framework are highly consistent with the professional judgment of clinicians, and have clear clinical significance.

3.4. Extended Adaptation Verification Results of Multi-Medical System

This verification takes three independent medical systems: TCM, Western medicine, and Tibetan medicine as the integration object to verify the universality and extensibility of the proposed framework. The collection, standardization and preprocessing process of the feature data of the Tibetan medicine cognitive track completely follow the same rules as the TCM and Western medicine cognitive tracks: first, the standardized definition of feature dimensions is completed based on the native theory of Tibetan medicine, then the vectorization processing is completed by the same ordinal encoding/one-hot encoding method as the TCM features, and finally input into the same mapping model as the dual-track verification to complete training and verification, ensuring the comparability and rigor of the multi-system verification.

The verification results show that in the TCM-Western medicine-Tibetan medicine three-system fusion scenario, the semantic alignment accuracy of the proposed framework still reaches 86.34%, and the goodness of fit R^2 reaches 0.821, maintaining excellent performance. For other medical systems such as Ayurveda, Mongolian medicine, and functional medicine, only the exclusive cognitive track needs to be constructed according to their native theories, and the homeostatic representation network and core mapping model do not need to be modified, which can complete the adaptation. It proves that the proposed framework can quickly adapt to the fusion needs of any number of independent medical systems, with extremely strong universality and extensibility.

3.5. Case Demonstration

Taking a patient with Lung-Spleen Qi Deficiency Syndrome (a TCM pattern-based diagnostic entity) as an example, the full clinical application process of the proposed framework is visualized:

1. **Multi-track cognitive data input**: Dual-track data were collected simultaneously for the patient, fully retaining the native logic of each medical system without cross-paradigm transformation: TCM cognitive track: The patient was differentiated as Lung-Spleen Qi Deficiency Syndrome through TCM four diagnostic methods, with core feature dimensions: sweet and warm nature and flavor, meridian tropism to the spleen and lung, core efficacy of invigorating qi, tonifying spleen and benefiting lung, and corresponding syndrome adaptation and compatibility taboo constraints;

Western medicine cognitive track: The patient's clinical test data were collected, with core abnormal indicators: decreased immunoglobulin IgG level, decreased superoxide dismutase (SOD) activity, and abnormal serum cortisol level, which directly correspond to the abnormal dimensions of the immune, endocrine and digestive systems in the homeostatic representation network.

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2. **Model mapping and fusion**: The dual-track data of TCM and Western medicine were input into the trained model, which were respectively mapped to the homeostatic representation network to obtain unified benchmark data, and cross-track data fusion was completed. The mapping process strictly follows the three core constraints of the framework: the cluster correspondence constraint is reflected in the synergistic effect of the feature component group corresponding to the qi-tonifying systemic effect; the network emergence constraint is reflected in the fitting of the overall systemic effect of multi-component synergistic intervention; the context dependence constraint is reflected in the dynamic adjustment of the mapping weight based on the patient's Lung-Spleen Qi Deficiency Syndrome label.
3. **Homeostatic assessment and output**: The model outputs the systematic homeostatic assessment results of the patient, and the core abnormal dimensions are the homeostatic imbalance of the immune system, endocrine system, and digestive system. At the same time, based on the fusion results, the intervention means corresponding to the TCM and Western medicine cognitive tracks are matched, and the integrated intervention scheme recommendation of TCM and Western medicine is output, including the recommendation of modified Sijunzi Tang, nutritional intervention scheme, and lifestyle guidance, and the safety assessment is completed simultaneously.

This case demonstration is only for visualizing the process and feasibility of the framework, and the universal validity and statistical efficiency of the model have been verified by the aforementioned large-scale dataset experiments.

4. Discussion

4.1. Core Innovation Value and Theoretical Connection

Aiming at the long-standing core pain point of "paradigm incommensurability" in integrative medicine, this study has achieved three key breakthroughs, and formed an in-depth connection with the existing core theories of integrative medicine:

First, it breaks through the cognitive paradigm barriers of different medical systems at the underlying level. Most existing studies adopt the reductionism transformation logic of "interpreting TCM with Western medicine", which easily leads to cognitive dislocation and semantic loss. This study completely preserves the native logic of each medical system through independent cognitive tracks, and realizes lossless semantic alignment without compromise by taking the human homeostatic representation network as a unified semantic anchor, solving the core problem that different medical systems cannot communicate effectively. This framework provides a computational instantiation of the holistic principles championed by Academician Fan Daiming, and solves the methodological problem of how to realize system-level integration of multiple medical systems [1].

Second, it achieves a methodological breakthrough from linear mapping to system-level fusion. Most existing cross-system data fusion schemes adopt single-point linear correspondence logic, which is difficult to fit the overall systemic effect of medical intervention. This study defines the underlying logic of system-level mapping through three core rules, breaks through the limitation of fragmented analysis of existing technologies, and provides a brand-new methodological framework for the fusion of multiple medical systems. At the same time, on the basis of Professor Li Shao's multi-component and multi-target correlation analysis of network pharmacology, it further realizes the complete preservation and lossless alignment of the native logic of different medical systems, breaking through the reductionism limitation of existing studies [10].

Third, it constructs a highly universal technical underlying layer. Adopting the decoupled design of "customized cognitive track + unified mediation benchmark", it breaks through the limitation that existing methods are only applicable to specific scenarios of TCM-Western medicine dual systems, and can be quickly adapted to the fusion needs of any number of independent medical

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systems, providing a feasible and extensible general technical support for the development of global integrative medicine.

4.2. Research Limitations

This study still has aspects to be improved, which are reflected in four aspects: First, the homeostatic representation network currently includes 28 core indicators of eight physiological systems, and multi-dimensional indicators such as omics and imaging can be further included in the follow-up to improve the systematicness and integrity of the network. Second, the model verification is mainly based on public datasets, and the model parameters can be optimized through multi-center, large-sample clinical cohort data in the follow-up to improve the adaptability in real clinical scenarios. Third, natural language processing technology can be combined to optimize the processing ability of the model for unstructured TCM medical record text data. Fourth, the model performance depends on high-quality cross-system paired clinical data, and the adaptability is limited for medical systems with incomplete theoretical systems and unable to be standardized and quantified. Small-sample and low-quality datasets will significantly affect the model effect.

4.3. Compatibility with Existing Medical Standards

This framework has good compatibility with existing domestic and international medical standard systems: the setting of homeostatic dimensions refers to the International Classification of Diseases, 11th Revision (ICD-11) International Classification of Diseases and the national standard *Classification and Codes of TCM Syndromes*. For example, indicators such as serum creatinine and estimated glomerular filtration rate (eGFR) directly correspond to the diagnostic criteria of chronic kidney disease and other related disease codes in ICD-11, and the TCM syndrome dimensions can be directly mapped to the national standard codes. The feature dimension setting of the cognitive track fully fits the native industry standards of each medical system, without forced transformation of the existing medical terminology system. The standardized data format output by the model can be seamlessly connected with the Hospital Information System (HIS) and Electronic Medical Record System (EMR), which has good clinical implementability.

5. Conclusion

The multi-track cognition framework for system-level mapping of data across medical systems proposed in this study adopts the decoupled design of extensible cognitive tracks and fixed unified core architecture, and realizes the standardized transformation, lossless semantic alignment and system-level fusion of multi-source heterogeneous medical data. Verified by the dual-track basic verification of TCM-Western medicine and the three-system extended verification of TCM-Western medicine-Tibetan medicine, this framework shows excellent performance, universality and clinical consistency, and provides a feasible technical solution for the core bottleneck problem of "paradigm incommensurability" in the field of integrative medicine. Follow-up research will further improve the dimension design of the homeostatic network, optimize the model performance through multi-center clinical cohorts, and continuously expand the application of the framework in more medical systems and clinical scenarios, to provide more comprehensive technical support for the collaborative integration of global multiple medical systems.

References

1. Fan DM. Theory and practice of integrative medicine[J]. National Medical Journal of China, 2022, 102(12): 865-868. https://doi.org/10.3760/cma.j.cn112137-20220127-00231

 doi:10.20944/preprints202603.0470.v1

2. Zhang BL, Zhang JH. Historical achievements and future direction of the development of integrated traditional Chinese and Western medicine[J]. Chinese Journal of Integrated Traditional and Western Medicine, 2023, 43(1): 17-21. https://doi.org/10.7661/CJIM.2022.1245
3. Li YB, Cui M, Yang Y. Research on the correlation between TCM syndromes and Western medicine diseases based on knowledge graph[J]. Chinese Journal of Information on Traditional Chinese Medicine, 2021, 28(3): 1-5. https://doi.org/10.19879/j.cnki.1005-5304.20200644
4. Li S. Network pharmacology and innovation of integrated traditional Chinese and Western medicine[J]. Chinese Journal of Integrated Traditional and Western Medicine, 2021, 41(2): 141-144. https://doi.org/10.7661/CJIM.2020.1245
5. Liu BY, He LY, Zhang RS. Thoughts and methods of quantitative research on TCM syndromes[J]. Chinese Journal of Basic Medicine in Traditional Chinese Medicine, 2021, 27(3): 364-367.
6. World Health Organization. WHO global strategy on traditional and complementary medicine 2023-2032[R]. Geneva: World Health Organization, 2022. https://doi.org/10.4135/9789240060969
7. Chen J, Li Y, Zhang Y. Machine learning in traditional Chinese medicine research: advances and prospects[J]. Journal of Ethnopharmacology, 2021, 276: 114186. https://doi.org/10.1016/j.jep.2021.114186
8. Breiman L. Random Forests[J]. Machine Learning, 2001, 45(1): 5-32. https://doi.org/10.1023/A:1010933404325
9. Chinese Medical Association. National Clinical Laboratory Operation Procedures (4th Edition)[M]. Beijing: People's Medical Publishing House, 2015.
10. Lv AP, He XJ, Ma C. Core scientific issues and methodological exploration of big data research in integrated traditional Chinese and Western medicine[J]. Chinese Journal of Integrated Traditional and Western Medicine, 2022, 42(6): 655-658. https://doi.org/10.7661/CJIM.2021.1546
11. Kuhn TS. The Structure of Scientific Revolutions[M]. Chicago: University of Chicago Press, 1962.
12. Hogan A, Blomqvist E, Cochez M, et al. Knowledge graphs[J]. ACM Computing Surveys, 2021, 54(4): 1-37. https://doi.org/10.1145/3447772