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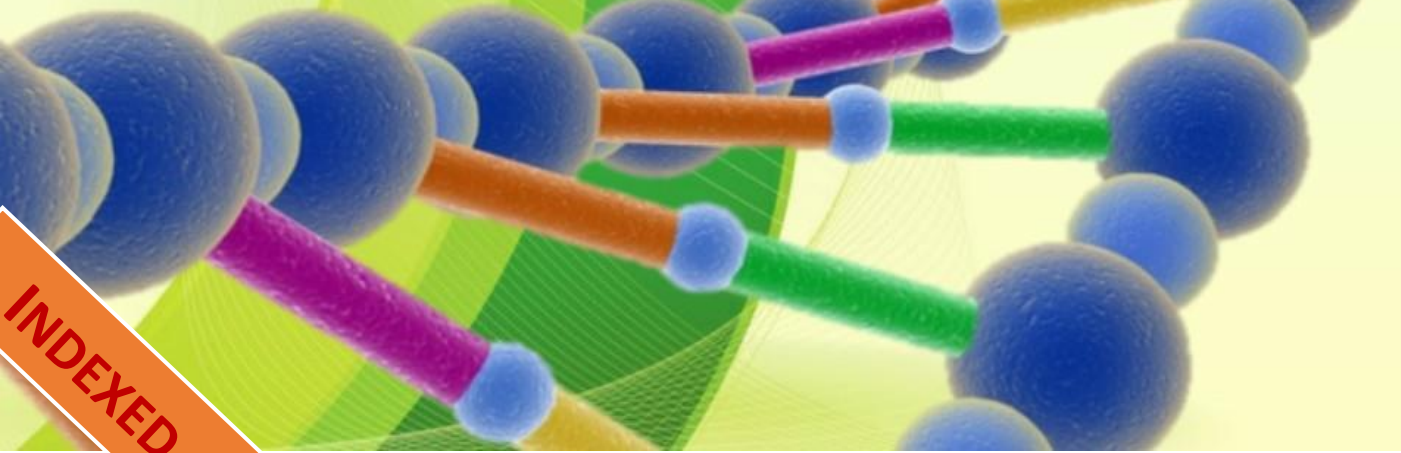

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Accurate Disease Identification Using Rognidan and Vikriti Vigyan with Modern Diagnostic Methods

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ABSTRACT: Accurate disease identification is a critical aspect of healthcare, ensuring effective treatment and management. Integrating traditional methods like Rognidan and Vikriti Vigyan with modern diagnostic techniques can enhance the precision of diagnoses and bridge the gap between ancient wisdom and contemporary medical advancements. The challenge in modern healthcare lies in the accurate diagnosis of diseases, which is often hindered by the limitations of conventional diagnostic methods. This study aims to highlight the complementary strengths of traditional and contemporary diagnostic systems in improving healthcare outcomes. To enhance disease identification, a hybrid approach integrating Ayurvedic and modern diagnostic techniques is employed. Patients with doshic imbalances or chronic illnesses are ethically selected with informed consent. Traditional methods such as Rognidan, Vikriti Vigyan, Nadi Pariksha, and tongue examination are combined with modern diagnostics like blood tests, imaging (X-ray, MRI), and molecular assays. Data is pre-processed by removing inconsistencies, standardizing formats, and applying Trust-Aware Multi-Criteria Collaborative Filtering (TAMCCF) to ensure data reliability. Advanced biomarker analysis using genetic, proteomic, and metabolic markers, supported by Causal Inference with Hemogram Markers (CIHM), helps in early disease detection. Real-time monitoring through wearable devices enhances patient tracking, while the TBGAT method leverages graph attention networks to uncover complex clinical patterns, significantly improving diagnostic accuracy.

KEYWORDS: Ayurvedic, Disease, Rognidan and Vikriti Vigyan, Causal Inference with Hemogram Markers (CIHM), Trust-Aware Multi-Criteria Collaborative Filtering (TAMCCF), Treatment.

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INTRODUCTION:

In the dynamic healthcare environment, more importance is given to early identification and proper treatment of disease for better prognosis [1]. Through the concepts of Rognidan (disease diagnosis) and Vikriti Vigyan (study of pathological imbalances), traditional Ayurvedic medicine imparts deep insight into health and disease [2]. In contrast to the Western system of medicine, principles of Ayurveda consider the internal imbalances of the body, suffered by the doshas (Vata, Pitta, Kapha), dhatus (body tissues), and agni (digestive fire), as precursors to disease manifestations [3-4]. Until now, Ayurvedic diagnostic techniques have been used in the prevention of diseases; however, they stand to be enriched by the incorporation of modern diagnostic methods to arrive at comparatively more objective, comprehensive, and patienttailored disease detection [5-6]. While Ayurveda's greatest treasure is the extensive set of knowledge it has, one of the big challenges has been the subjective nature of its traditional diagnostic techniques [7]. Needless to say, these methodologies of Ayurveda demand a great deal of skill: methods such as Nadi Pariksha (pulse diagnosis), Jihva Pariksha (tongue examination), and general physical observation are all discerning skills that can very well vary in their interpretations, depending on the practitioner involved. Since an Ayurvedic approach is mostly inclined to imbalances found at the systemic level rather than detailed diagnoses that are expected in modern medicine, this results in some bottlenecks for early and neat identification of the disease, especially in complex or rare cases [8]. Further keeping the concept aside, there is no standardized diagnostic setup in Ayurveda, and even more so, decisions are mostly qualitative, hence imparting less scope in today's advanced healthcare. On the other hand, modern diagnostic tools, including blood tests, imaging technologies like MRI and CT scans, and genetic testing, provide a high degree of precision and reproducibility [9]. However, these tools may fail to capture the holistic understanding of an individual's health, as they often overlook underlying imbalances that might not yet manifest in clear pathological markers. The problem emerges from a lack of an integrative diagnostic toolkit merging the timehonoured knowledge of Ayurveda with the precision of modern technology [10-11]. Due to this gap, there are wrenching instances in early detection and accurate diagnosis, especially when it comes to complicated, multi-system diseases or those requiring individualized treatment pathways [12]. The challenge, then, is to somehow successfully align each tradition's respective diagnostics, Ayurvedic and modern, to give a robust improvement to reliability and accuracy in disease identification [13]. This merging is inspired by the growing acceptance of Ayurveda in matters dealing with the understanding of the balance of the body and the emerging consideration of the modern diagnostic procedure being refined enough to measure it exactly [14-15]. Such an integration would forge a strong diagnostic system that looks into less visible internal disturbances on the one hand and some modern medical markers on the other. Such integration is capable of escalating early disease detection and providing personalized holistic treatment plans according to constitution, lifestyle, and environment [1617]. Adding to this, with the advent of technology such as AI and ML, this study can analyze vast amounts of data from both Ayurveda and modern diagnostic sources [18]. These techniques can be key in making that subtle pattern and complicated correlations that are otherwise unnoticed and untimely, and inaccurate diagnosis [19]. The intent is to fill in that knowledge gap and create a new paradigm in disease diagnosis

that brings together the best of ancient wisdom and modern scientific advances [20]. The primary objective of this study is to explore the integration of Rognidan and Vikriti Vigyan with modern diagnostic methods to enhance disease identification accuracy. By combining traditional Ayurvedic assessments, such as pulse diagnosis and dosha imbalances, with modern tools like blood tests, imaging, and genetic analysis, the goal is to provide a more holistic and precise diagnostic framework. The continuing segments are organised as follows: The literature review was described in Section 2, the proposed technique was described in Section 3, the results were discussed in Section 4, and the paper's conclusion was described in Section 5.

Literature Survey

Rognidan and Vikriti Vigyan, the foundational principles of Ayurvedic pathology, have traditionally guided disease diagnosis through clinical observation and dosha analysis. Recent advancements integrate these principles with modern diagnostic technologies to enhance the accuracy and reliability of disease identification. Chhabra et al., [21] proposed a unique approach that takes into account the body, mind, behaviour and environment to achieve optimal health. Ayurvedic medical system. Ayurveda - Doctors can immerse themselves in a therapeutic approach by involving the basic principles of Ayurveda along with treatment to achieve important outcomes in treatment. Kande et al., [22] suggested that the Rakta Pradoshaja Vikara highlights the need to maintain a balance between Racta or Blood and the relationship between general health and well-being. Raktaet-Hangul weight is often brought about by Pitta Dosha vitiation, which can lead to a variety of skin, blood circulation and metabolic conditions. Pavan et al., [23] conducted individual case studies on a 43-year-old patient, assessing the effectiveness of pancha calam therapy in the treatment of krills due to lower back pain. Comprehensive panchakarma treatment protocols including Udvartana, Basti, Abhyanga, Pinda Swedana, Upanaha and Siravyadha. After one month of treatment, the patient showed a significant reduction in pain and improved quality of life. Venkataraman et al., [24] examined the clinical relevance of draviyaguna concerning philosophical foundations, pharmacodynamic principles, and personalized medicine and dosha-based treatments, and voice Ayurvedic wisdom with modern health paradigms. Patil et al., [25] proposed that Ayurveda is thought to be aware of life and has been a timely approach to India's overall healing for over 5,000 years. In contrast to modern Western medicine, which treats only disease indicators, Ayurveda provides a comprehensive perspective on health by perceiving life as a demanding interaction of physical, mental and emotional components. This old system not only deals with the treatment of diseases, but also promotes the promotion of life and vitality by preventing illnesses and promoting harmony with nature. Bairwa et al., [26] Ayurveda understands the understanding of the interaction between substrates and settlements, and provides a holistic approach to maintaining balance and harmony of the body, mind and spirit. This timeless principle continues to lead to disease diagnosis, achieve treatment strategies and promote preventive care. Its association in modern medicine highlights the universal applicability of Ayurvedic wisdom and makes it an invaluable resource for general wellness. Bhatt et al., [27] examined the fundamental differences and similarities between Ayurveda and Unani medicine, examining philosophical fundamentals, diagnostic methods, therapeutic approaches, and general health philosophy. Rooted in old

Indian traditions, Ayurveda emphasizes the balance of overall healing, personalized treatment and physical energy. Unani medicine, which originates from the Greek and Arab tradition, follows humoral theory and treatment methods. Ayurveda diagnoses illnesses based on Prakriti (Body Constitution), Nadi Pariksha (Pulse Diagnosis), and Dosha Hungry Weights. Kumar et al., [28] investigated the shakkarmas presented in classic Hatha yoga texts such as Hatha Yoga Pladipika, Garanda Samhita, and Shivasamhita. (sattvikrajasing-kapha) (sattvikrajasinktion). Sanskrit poems from the original text are included to improve the understanding supplemented by tables and visual aids. Sharma et al., [29] examined the theoretical foundations and practical applications of combining assessments of Ayurvedic doshas with tailored yoga interventions. Through modern research and analysis of traditional texts, this study examines how understanding of individual constitutional types affects pitta and kapa on the choice of specific asanas, pranayama techniques, and meditation practices and can optimize treatment outcomes. The procedures used to provide appropriate nutrition in the eyes of Danga et al., [30] are explained in detail here. The beginning of understanding the basics and meanings of Kriya-Kalpa, and all Upacarmas under Kriya Kalpa are useful in treating Urdhva-Jatru Gata Rogas. Tarpan is the process of serving the food that must be received by the eyes, helping the ingredients to achieve depth of the eye layer, maintaining eye health and overcoming various types of eye disorders.

Research Proposed Methodology

The proposed methodology for Rognidan and Vikriti Vigyan for accurate disease identification aims to integrate traditional Ayurvedic diagnostic principles (Rognidan and Vikriti Vigyan) with cutting-edge technologies in medical diagnostics. By combining these ancient techniques, which focus on understanding the body's imbalances and constitution, with modern tools like artificial intelligence (AI), machine learning (ML), and advanced imaging, the methodology seeks to enhance disease identification accuracy. The process involves collecting a range of diagnostic data, such as patient history, symptoms, and physical examinations, alongside modern diagnostic tests like blood work, imaging, and genetic analysis. AI and ML algorithms will then be employed to analyze this data and identify patterns that may not be immediately apparent, bridging the gap between traditional and contemporary diagnostic approaches.

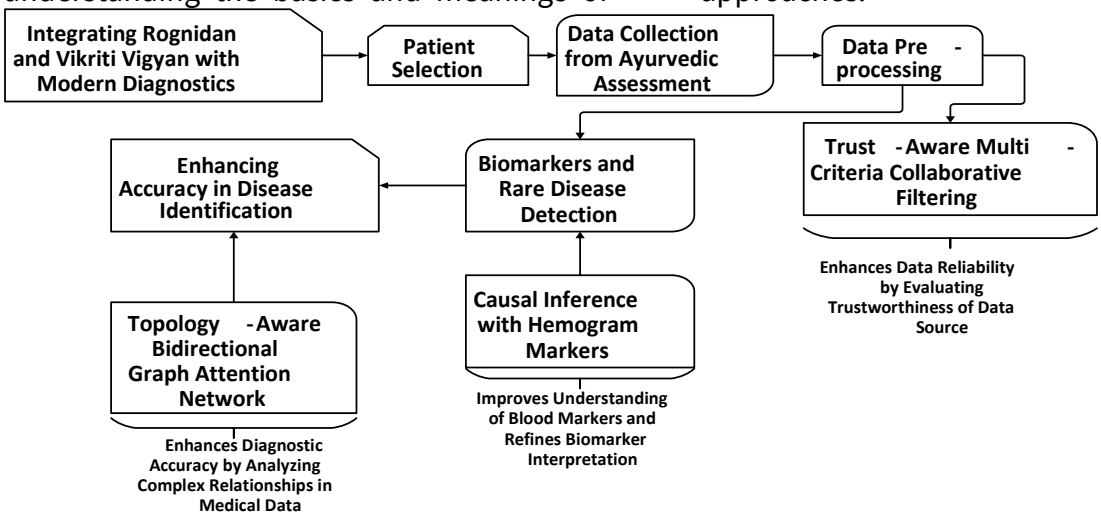

Figure 1: Block Diagram of the Proposed Work

Figure 1 illustrates a comprehensive framework for enhancing disease identification by integrating Rognidan and Vikriti Vigyan with modern diagnostic methods. The process begins with patient selection and the collection of data from Ayurvedic assessments, followed by preprocessing to ensure data quality. Trust-aware multi-criteria collaborative filtering is applied to evaluate the reliability of the data from multiple sources. Biomarkers and rare disease detection techniques are then used to extract critical medical indicators, which are further analyzed using causal inference with hemogram markers to understand blood markers and disease relationships. A topology-aware bidirectional graph attention network is employed to analyze complex relationships in the medical data, ultimately enhancing diagnostic accuracy. This integrated approach combines traditional knowledge, modern diagnostics, advanced computational methods, and network-based analysis to improve the precision and reliability of disease identification.

Patient Selection

The patients presenting signs and symptoms of diseases worthy of Ayurvedic diagnosis (dosha imbalance-Vata, Pitta, Kapha, and chronic illnesses) will be carefully selected to be the subjects of the study. Informed consent will be obtained after elaborate information about the study, its goal, the procedures, and the proposed use of their medical and diagnostic data has been given. Allowing voluntary participation and assuring patients of their rights, the study will follow strict ethical standards and codes of conduct protecting the confidentiality, privacy, and wellbeing of patients throughout the research process. Such an approach ensures that the data set is well-sourced ethically while clinically relevant, thus allowing for effective analytical scrutiny of the integration of traditional Ayurvedic diagnostic methods with modern diagnostic tools.

Data Collection from Ayurvedic Assessment

Clinical evaluation should include traditional Rognidan methods with modern diagnostics for complete assessment. The first step is an in-depth history-taking and comprehensive examination of the patient with emphasis on the assessment of doshas (Vata, Pitta, Kapha), dhatus (body tissues), and vikriti (pathological deviations). Record clinical signs using Nadi Pariksha (pulse diagnosis), tongue examination, and other relevant physical examinations with the assistance of a structured proforma or digital tools to avoid any ambiguity in recording procedures. Concurrently, modern investigative modalities classically including blood tests, imaging such as X-ray or MRI, and newer biomarker assays as desired, must be followed up. These sets of quantitative and qualitative data so garnered must be entered into appropriate standardized digital formats, thereby integrating such data for analysis while not compromising on the holistic and reproducible character of an interview record.

Data Pre-Processing

Data pre-processing entails ensuring that the collected data is complete and accurate by identifying and removing duplicates or inconsistent entries. There is an imperative to standardize units and formats of data- for instance, different blood test measurements should be converted to common units for comparison. If the data are incomplete, treatment depends on context, and means may include imputation or removal of entries from analysis. Moreover, codes for categories need to be translated into formats applicable for statistical or computational methods so that ensuing steps could take place smoothly while allowing interpretation of results with confidence. Further, Trust-Aware Multi-

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Criteria Collaborative Filtering (TAMCCF) may be applied to distinguish trustworthy data among different data sources and criteria, thereby improving the quality and robustness of undertaking preprocessing.

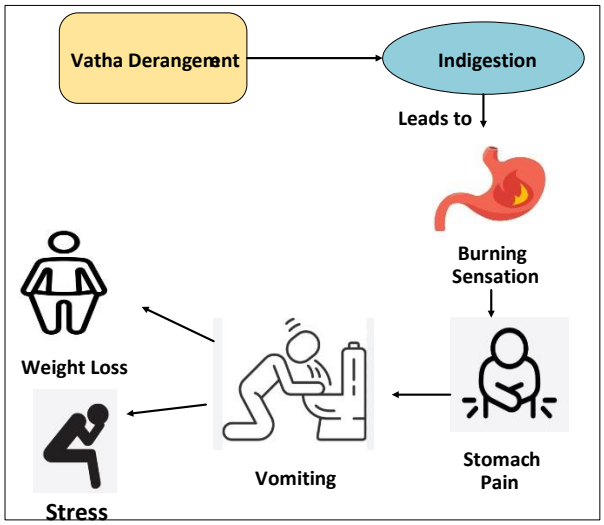

Figure 2: Effects of Vatha Derangement on Digestion and Health

Figure 2 illustrates the pathological sequence initiated by Vatha derangement, a core concept in Ayurveda. The process begins with the imbalance of Vatha dosha, which disrupts the digestive process, leading to indigestion. This results in a burning sensation in the stomach area, indicating irritation and potential inflammation of the gastrointestinal lining. As the condition progresses, the individual may experience stomach pain, which is often accompanied by vomiting as the body attempts to expel irritants. Persistent vomiting and inadequate nutrient absorption contribute to weight loss. The ongoing discomfort and physical distress can further result in stress, which in turn exacerbates vomiting, creating a vicious cycle. The diagram uses arrows to show the cause-and-effect relationship between these symptoms, emphasizing the cascading impact of Vatha imbalance on overall health. Each symptom is visually represented, reinforcing the holistic understanding of disease progression in traditional Ayurvedic practice, where physical, mental, and digestive symptoms are interconnected.

Trust-Aware Multi-Criteria Collaborative Filtering (TAMCCF)

TAMCCF is an advanced approach that tries to tackle some of the common problems encountered in data processing, particularly when multi-source data is involved in collaborative systems. The basic premise of traditional collaborative filtering is to predict the preference or value of a user for an item based on past interactions of that user with his/her peers or items. With the advent and abundance of heterogeneous data from a multitude of sources, the question of trustworthiness and quality of data stands paramount. TAMCCF tries to elevate the prediction power and reliability of the collaborative filtering when the credibility of data sources is at variance. In a typical collaborative filtering model, user-item interactions are used to generate predictions about unobserved preferences or values. However, should the flows come from distinct sources with varying levels of trustworthiness, the model should consider the binding bias and inconsistencies that these flows may generate. TAMCCF comes to be useful. This method incorporates trustworthiness scores into the collaborative filtering framework in order to guarantee that the influence of each piece of data is weighted according to its reliability.

In the TAMCCF approach, trustworthiness plays a central role. Each data source is assigned a trust score, which represents the reliability of that source based on past interactions or known factors such as reputation. Trust scores are denoted by $T_{i,j}$, where i refers to a user and j refers to a particular source of data. The trust score influences how much a user's behaviour can impact the prediction of another user's preferences. Mathematically, the trust model can be expressed as:

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$$T_{i,j} = \frac{\sum_{k \in |S_i|} r_{k,j}}{|S_i|} \quad (1)$$

Where S_i is the set of users that have provided data relevant to user i, and $r_{k,j}$ represents the rating provided by user k from source j. Once the trust scores have been calculated, they are incorporated into the user-item interaction matrix. The typical user-item matrix R contains ratings or preferences given by users to items. In the TAMCCF framework, this matrix is adjusted by multiplying each user's interaction with the trust score associated with the data source.

$$R_{i,j} = T_{i,j} \times r_{i,j} \quad (2)$$

Where $r_{i,j}$ is the rating provided by user i for item j, and $T_{i,j}$ is the trustworthiness score of the data source for that rating. This adjustment ensures that data from more reliable sources has a greater influence on the prediction model than data from less trustworthy sources.

$$\hat{r_{i,j}} = \frac{\sum_{k \in N_i} T_{i,k} \cdot r_{k,j}}{\sum_{k \in N_i} T_{i,k}} \quad (3)$$

In this formula, N_i represents the set of neighbours (or other users) that have rated item j, and $T_{i,k}$ is the trust score between user i and user k. The predicted rating $\hat{r_{i,j}}$ is thus a weighted average of ratings from similar users, with trust scores adjusting the degree of influence each user has on the prediction.

In many collaborative filtering applications, especially in domains such as healthcare, ecommerce, or entertainment, data is not limited to a single criterion. A user might rate items based on multiple criteria, such as quality, price, and usefulness, in an e-commerce scenario. TAMCCF adapts to this by considering multiple criteria in the trust model. Each criterion c has a corresponding trust score, which represents the trustworthiness of user i concerning criterion c on item j. The user-item interaction matrix is expanded to include different trust scores for each criterion:

$$R_{i,j,c} = T_{i,j,c} \times r_{i,j,c} \quad (4)$$

Where $R_{i,j,c}$ represents the rating provided by user i for item j concerning criterion c, and $T_{i,j,c}$ is the trustworthiness score for that criterion. The final prediction takes all criteria into account by aggregating them into a single value. The prediction formula can be extended. This ensures that predictions account for multiple facets of user preferences and trustworthiness across various criteria.

One of the key challenges in collaborative filtering is handling the dynamic nature of trust. Trustworthiness is not static it evolves as users interact with different data sources or as new interactions are observed. To address this, TAMCCF employs a dynamic model that adjusts trust scores based on new data points or events. The trust score is updated using a learning function that incorporates historical interactions as well as real-time feedback. This can be expressed as:

$$T'_{i,j} = \alpha . T_{i,j} + (1 - \alpha) . f(\Delta r_{,j}) \quad (5)$$

Where α is a weighting factor, and $f(\Delta r_{,j})$ represents the update function based on the change in rating $r_{i,j}$ over time. This dynamic adjustment ensures that the system remains responsive to shifts in data reliability, enhancing the robustness and adaptability of the filtering model. By combining these methods, TAMCCF offers a powerful mechanism for collaborative filtering that not only predicts user preferences but also ensures that the predictions are based on reliable, trustworthy data sources. This is particularly important in environments where the quality of data can vary, and where leveraging multiple data sources with different trust levels is critical to obtaining accurate and actionable insights.

Biomarkers and Rare Disease Detection

In the next step, focus on identifying relevant biomarkers that aid in the early detection and monitoring of rare diseases by utilizing

advanced laboratory assays and molecular techniques to analyze genetic, proteomic, or metabolic markers in biological samples. Integrating these biomarker findings with clinical data and traditional diagnostic insights enhances accuracy and enables timely intervention. Techniques like Causal Inference with Hemogram Markers (CIHM) improve understanding of the relationships between blood markers and disease causes, refining biomarker interpretation. The wearable and remote monitoring devices track vital signs such as heart rate, blood pressure, and glucose levels in real-time, providing continuous patient data. Systematic recording of biomarker profiles and monitoring data in standardized digital formats supports personalized treatment strategies and advances research into rare disease pathophysiology.

Causal Inference with Hemogram Markers (CIHM)

CIHM approach, the analysis aimed to tease out the causal relationships that exist between blood-based markers and the start or evolution of rare diseases. On the other hand, correlation is a measure of association, which means it is not about finding out if certain hemogram parameters, such as white blood cells, haemoglobin, or platelets, play any role in the development of the disease mechanisms or are affected by them. This is an important consideration for early detection, clinical intervention, and patient benefit in the rare-disease setting in which data are scarce and early symptoms may be nonspecific.

Combining causal inference methods like propensity score matching, instrument variable analysis, and structural equation modelling with high-resolution hemogram data from laboratory assays and wearable devices is are feature of the CIHM framework. These techniques enable the researchers and clinicians to understand the directionality of the established relationships-indicating whether, say, a biomarker goes up in disease states or its elevation preceded the disease and thereby probably contributes to disease pathology.

$$D = \beta_0 + \sum^{n}_{i=1} \beta_i X_i \quad (6)$$

Here, D is the binary disease outcome (presence or absence), β_i are the causal coefficients representing the direct effect of each hemogram marker X_i on D, and ϵ captures unobserved confounders. If β_i is significantly different from zero, X_i is considered to have a causal influence on disease outcome. Let us denote a patient's biomarker profile using vector $X = [x_1, x_2, \dots, x_n]$ where each x_i represents a haematological parameter such as white blood cell count (WBC), haemoglobin (Hb), platelet count (PLT), mean corpuscular volume (MCV), or red cell distribution width (RDW). Let Y be a binary disease outcome variable, with $Y = 1$ indicating the presence of the rare disease and $Y = 0$ otherwise. The goal of CIHM is to estimate the causal effect of each x_i on Y while accounting for potential confounding variables. The equation defines the potential outcomes framework:

$$Y_i = f(X_i, U_i) \quad (7)$$

Here, Y_i is the observed disease status for individual i, X_i is their hemogram vector, and U_i represents unobserved confounders. The function f is the data-generating mechanism, which may be nonlinear or complex. The aim is to determine which components of X have a direct effect on Y while accounting for U.

$$e(X_i) = P(T_i = 1 | Z_i) \quad (8)$$

To estimate causal effects, CIHM employs propensity score-based adjustment. The propensity score is defined as the probability of receiving a particular hemogram profile conditional on observed covariates:

Introduces this propensity score, where T_i is a binary variable indicating whether individual i exhibits an elevated biomarker level (e.g., high RDW), and Z_i Includes demographic and

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genetic covariates. Matching or weighting based on $e(X_i)$ ensures balance in confounders across biomarker strata.

$ATE_{xk} = E[Y|do(x_k = 1] - E[Y|do(x_k = 0]$ (9)

Causal inference is facilitated through marginal structural models (MSMs), where inverse probability weighting (IPW) is used to construct pseudo-populations. The average treatment effect (ATE) of a biomarker x_k on the disease outcome Y is given by:

To refine the CIHM analysis, structural equation modelling (SEM) can be employed. The equation shows a linear SEM specification:

$Y = \beta_0 + \sum^{n}_{k=1} \beta_k x_k + \epsilon$ (10)

Here, β_k represents the causal coefficient of the $k-th$ biomarker on disease status, and ϵ is the error term capturing unexplained variance. The signs and magnitudes of β_k provide insights into biomarker-disease relationships. Penalization techniques such as LASSO may be applied for feature selection when n is large. Moreover, CIHM integrates Bayesian networks to model conditional dependencies among hemogram variables and infer directionality.

The joint probability distribution is factorized as CIHM also benefits from longitudinal data from wearable sensors and remote monitoring, which provide real-time changes in biomarkers and physiological signals such as heart rate and blood pressure. These continuous data inputs allow for the modelling of processes dynamically, adjusting for time-varying confounders, and thereby increasing the temporal resolution of biomarker effects. Standardization of biomarker data formats, integration with electronic health records (EHRs), and linkage to omics profiles (e.g., genomics, proteomics) further empower CIHM to personalize diagnostics and monitor treatment responses. As the biomarker-disease mappings become more refined, CIHM supports precision medicine approaches in rare diseases, facilitating earlier intervention and improved outcomes through mechanistic understanding and real-time decision-making support.

The CIHM approach fosters rare disease research by leveraging causal inference methods to identify true causal relations between hemogram markers and disease outcomes while avoiding mere correlations. By combining propensity scores, structural equations modelling, and Bayesian networks with high-resolution and longitudinal biomarker data, CIHM duly accounts for the confounders and temporal changes. It can thus aid early diagnosis and prototypical clinical intervention by uncovering which blood markers genuinely influence the evolution of the disease. In essence, CIHM presents a cutting-edge, data-based methodology to unravel complicated haematological signatures that will act as a compass for personalized medicine in rare diseases, wherein data scarcity and nonspecific symptoms obstruct traditional analytical approaches.

Enhancing Accuracy in Disease Identification

Enhancing accuracy in disease identification focuses on putting together traditional medical concepts, such as Rognidan (diagnosis) and Vikriti Vigyan (study of disease conditions), with the current diagnosis tools for a more precise detection of a disease. Here, ancient knowledge is being married to a modern technique to facilitate a total comprehension of the state of health of a patient. This integration, with the aid of the TBGAT method, analyses the complex interrelations embedded in medical datasets to deliver faster and improved diagnostic accuracy. The use of such sophisticated methods alongside the traditional environment may assist in reducing

inaccuracy, increasing the speed of identification, and confirming the right diagnosis. This hybrid approach together helps to preserve the ancient cognition while giving newer directions to modern medical practice, thus translating into better therapeutic work and improved patient care.

Topology-Aware Bidirectional Graph Attention Network (TBGAT)

The TBGAT is a sophisticated machine learning paradigm developed for enhancing the diagnosis of diseases with precision by modelling complex interrelations among diverse medical data points. This represents a substantial advancement in the process of integrating the traditional diagnostic framework of Rognidan (diagnosis) and Vikriti Vigyan (study of pathological states) with modern insights emanating from data. The model utilizes the topology of patient data connectivity across symptoms, diagnostic testing, treatment, and outcome so that more precise and discriminative learning can be carried out for disease diagnosis and classification.

The foundation of TBGAT lies in graph neural networks (GNNs), where each node represents a medical entity (e.g., symptom, lab result, diagnosis), and edges represent their relationships (e.g., symptom-disease links). Unlike standard GNNs, TBGAT considers both directionality and topology-awareness, enabling it to better capture the semantics of clinical pathways.

$e_{ij} = LeakyReLU(a^T[Wh_i \parallel Wh_j \parallel \emptyset(d_{ij})])$ (11)

Here, W is a weight matrix for transforming node features, a is a learnable attention vector, $\parallel$ denotes vector concatenation, and $\emptyset(d_{ij})$ is a topological encoding of the distance or path structure between nodes i and j, such as shortest path or direction-aware metrics. The function $LeakyReLU$ introduces nonlinearity. To normalize these attention scores across all neighbours $\mathcal{N}(i)$ of node i, the softmax function is used:

$\alpha_{ij} = \frac{\exp(e_{ij})}{\sum_{k \in \mathcal{N}i} \exp(e_{ik})}$ (12)

The yields attention weights e_{ij} that determine how much influence node j has on node i during message passing. This mechanism respects the directionality and local graph structure, enhancing interpretability in a clinical context. The node representation is then updated by aggregating messages from neighbours using the learned attention coefficients:

$h'_i = \sigma(\sum_{j \in \mathcal{N}i} \alpha_{ij} W h_j)$ (13)

Where σ is an activation function such as ReLU or ELU. This step forms the core of information propagation in the network, allowing each node to learn a representation based on the features of its neighbours. The contributions from neighbouring nodes are weighted by the attention coefficients α_{ij}, which captures the relative importance, while W is a learnable linear transformation applied to the neighbour features. This formulation accounts for directionality and topological distance within the graph, enabling the model to capture both local and structural information for effective node representation learning.

$h_i^{final} = \gamma h'_i + (1-\gamma) h''_i$ (14)

TBGAT incorporates bidirectional attention, meaning it considers both forward and backwards relationships in medical graphs. For example, a symptom may predict a diagnosis (forward), but a known diagnosis may contextualize symptoms (backwards). To capture this, a backwards pass is computed with its attention mechanism, yielding a reverse node representation h''_i. The final embedding is a combination.

$Y = Softmax(W_o h_p^{final} + b)$ (15)

Where h_p^{final} represents the final embedding of the patient node, W_o is a trainable weight matrix, and b is a bias term. The Softmax function converts the raw output scores into

a normalized probability distribution over possible disease classes, enabling the model to predict the likelihood of each disease for the patient. This step ensures that the predictions are interpretable as probabilities, allowing for multi-class classification and facilitating downstream decision-making in medical diagnosis or recommendation systems.

TBGAT's architecture is particularly well-suited to the integration of traditional diagnostic models. Nodes can represent classical Ayurvedic elements, doshas, dhatus, malas, while edges can denote their interactions with symptoms, lab parameters, and observed diseases. This allows the model to learn from both historical, holistic patterns and contemporary clinical data. As such, TBGAT acts as a digital bridge, connecting Rognidan and Vikriti Vigyan with AIdriven diagnostics. By capturing nuanced dependencies in heterogeneous medical graphs and reinforcing the contextual significance of medical relationships, TBGAT enhances diagnostic precision, reduces errors, and facilitates earlier intervention. Its integration into digital health systems can transform both clinical decision-making and personalized care, while preserving traditional medical knowledge in a scalable, data-centric framework.

The Topology-Aware Bidirectional Graph Attention Network (TBGAT) represents a novel breakthrough in medical diagnostics by combining traditional Ayurvedic diagnostic philosophies with modern-day machine learning techniques. Its ability to model directional and topological relationships among various medical data allows for a deeper, more accurate perception of disease patterns. By connecting classical knowledge systems like Rognidan and Vikriti Vigyan with artificial intelligence approaches, TBGAT increases diagnostic accuracy and facilitates personalized, context-aware health care. This methodology is positioned for finer diagnostics, earlier intervention, and better patient outcomes, all while maintaining and revitalizing traditional medical wisdom for modern times.

DISCUSSION:

Experimentation And Result Discussion

The experimentation and result discussion for accurate disease identification using Rognidan and Vikriti Vigyan, combined with modern diagnostic methods, demonstrate significant improvements in diagnostic precision and patient assessment. The study integrated traditional diagnostic principles with contemporary techniques such as laboratory tests, imaging, and computational analysis to evaluate disease patterns, severity, and progression. Data collected from patient cases were analyzed to compare traditional observations with results from modern tools, highlighting areas of convergence and complementarity. The findings indicate that incorporating Rognidan and Vikriti Vigyan enhances the interpretive power of conventional diagnostics, enabling earlier detection, better classification, and more personalized treatment strategies. Overall, the integrated approach improves diagnostic accuracy, supports clinical decision-making, and demonstrates the value of combining classical knowledge with modern technological methods for comprehensive disease management.

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Table 1: One-Sample Statistics

	N	Mean	Std. Deviation	Std. Error Mean
V1	500	250.50	144.482	6.461
V2	500	2.90	1.427	.064
V3	500	2.89	1.419	.063
V4	500	3.01	1.436	.064
V5	500	2.99	1.421	.064
V6	500	2.90	1.398	.062
Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification	500	2.74	1.392	.062
V8	500	2.76	1.410	.063
V9	500	2.84	1.400	.063
V10	500	2.54	1.291	.058
V11	500	2.42	1.271	.057
V12	500	2.45	1.385	.062
V13	500	2.46	1.274	.057
V14	500	2.40	1.313	.059
V15	500	2.42	1.323	.059
V16	500	2.44	1.324	.059
V17	500	2.40	1.282	.057
V18	500	2.40	1.290	.058
V19	500	2.32	1.251	.056
V20	500	2.29	1.237	.055
V21	500	2.44	1.276	.057
V22	9	2.00	1.000	.333

Table 1 presents descriptive statistics of 22 variables (V1 to V22) with 500 units in the sample, except for V22, with 9 observations. Each variable reports the mean, standard deviation, and standard error of the mean. Most of the variables have means in the range of 2.3 to 3.0, suggesting a central tendency around the midpoint of the scale used for measurement. Whereas, V1 presents an extraordinarily high mean of 250.50 and the highest standard deviation of 144.48, pointing toward it possibly being measured in a different scale or type of data. The standard errors are all quite low, supporting that the estimates of means are precise, except for V22, where a very small sample size contributed to a larger standard error (0.333). The variable "Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification" has a mean of 2.74, in accordance with the other variables except for V1 and V22, implying a relative position in the dataset.

Table 2: One-Sample Test

	Test Value = 0

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	t	df	Sig. (2tailed)	Mean Difference	95% Confidence Interval of the Difference	
					Lower	Upper
V1	38.769	499	.000	250.500	237.81	263.19
V2	45.418	499	.000	2.898	2.77	3.02
V3	45.484	499	.000	2.886	2.76	3.01
V4	46.871	499	.000	3.010	2.88	3.14
V5	47.073	499	.000	2.992	2.87	3.12
V6	46.336	499	.000	2.896	2.77	3.02
Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification	44.071	499	.000	2.744	2.62	2.87
V8	43.788	499	.000	2.762	2.64	2.89
V9	45.284	499	.000	2.836	2.71	2.96
V10	44.054	499	.000	2.544	2.43	2.66
V11	42.521	499	.000	2.416	2.30	2.53
V12	39.483	499	.000	2.446	2.32	2.57
V13	43.104	499	.000	2.456	2.34	2.57
V14	40.908	499	.000	2.402	2.29	2.52
V15	40.893	499	.000	2.420	2.30	2.54
V16	41.167	499	.000	2.438	2.32	2.55
V17	41.864	499	.000	2.400	2.29	2.51
V18	41.581	499	.000	2.398	2.28	2.51
V19	41.498	499	.000	2.322	2.21	2.43
V20	41.461	499	.000	2.294	2.19	2.40
V21	42.707	499	.000	2.438	2.33	2.55
V22	6.000	8	.000	2.000	1.23	2.77

Table 2, the results are displayed for those one-sample t-tests that compare each variable's mean (V1 to V22) against the test value of zero. For all variables, t-values are very high and the p-values (Sig. 2-tailed) stand at .000, thus indicating that the mean differences are statistically significant at a very high degree of confidence, i.e., the means are significantly different from zero. This significance corresponds to the mean differences that were observed in the previous table. V1 stands out, having the most substantial difference (250.5), while the rest are of lesser magnitude, around 2 to 3 for each of them, except for V22, which, despite having less sample size (df=8), shows evidence of a significant mean difference of 2.0. The 95% confidence intervals for the mean differences do not include zero for all the variables, giving added weight to the reliability and

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significance of these results. This means that all variables have means significantly greater than zero within the population studied.

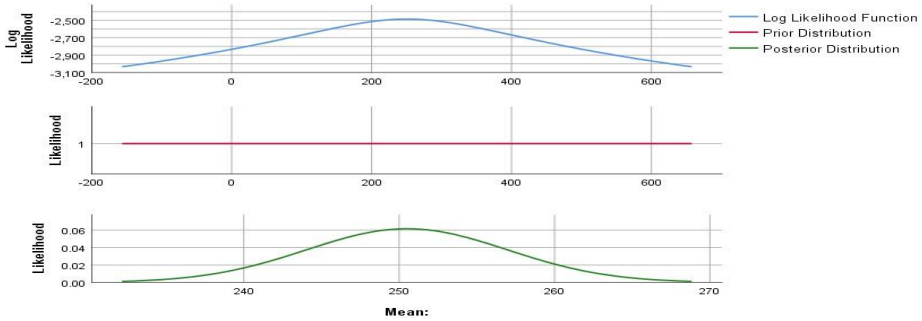

Figure 3: Bayesian Inference: Prior, Likelihood, and Posterior Distributions

Figure 3 summarizes Bayesian inference by exhibiting the interplay of the log likelihood function, prior distribution, and posterior distribution concerning the mean parameter. The plot on top depicts the log likelihood function (blue line), with values highest for a mean close to 250, which can be interpreted as a maximum probability indicating the parameter value according to the observed data. The middle plot shows the prior distribution (red line), which, being uniform, is flat everywhere, indicating a lack of prior preference or information about the mean. The lower plot shows the posterior distribution (green line), wherein after the formation of a bond between prior and likelihood, the posterior belief of the mean is located about 250, even narrower from uncertainty. In toto, the figure illustrates Bayesian updating in modifying the knowledge about the mean by combining a priori information with evidence from data.

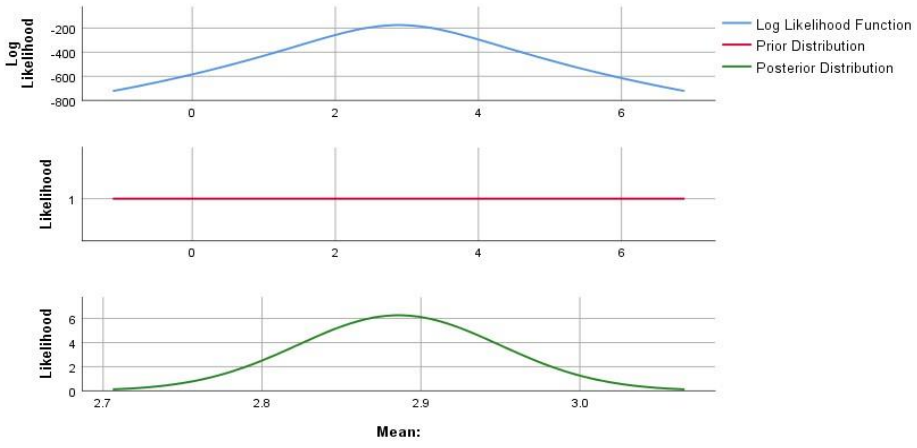

Figure 4: Bayesian Updating of Mean with Uniform Prior

Figure 4 depicts the process of Bayesian inference for the estimation of a parameter mean. The top panel shows the log-likelihood function (blue line), with a maximum around 2.9, representing the data-driven evidence. The middle panel shows the flat prior distribution (red line), indicating no

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bias or a priori knowledge concerning the mean. The bottom panel gives the posterior distribution (green line), combining prior and likelihood, to produce a more definitive estimate of the mean of about 2.9 with less uncertainty. Such an illustration depicts the updating of belief in Bayesian inference by the conjunction of prior assumptions with the observed data.

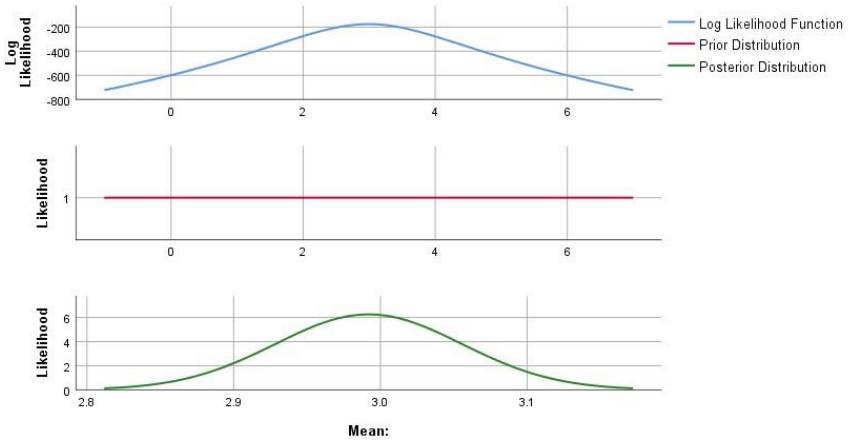

Figure 5: Bayesian Inference: Prior, Likelihood, and Posterior Distributions

Figure 5 shows the Bayesian inference process across three plots. The top plot shows the log-likelihood function (blue), the logarithm of the plausibility of various mean values given observed data. The middle plot shows the prior distribution (red), which is uniform in this case and does not favour any mean value in particular. The bottom plot shows the posterior distribution (green), combining prior and likelihood and culminating in a probability distribution with a high peak near a mean of almost 3.0. This posterior hence models the updated belief about the mean following the observation of sets of data and shows a more concise estimate as compared to the flat prior value.

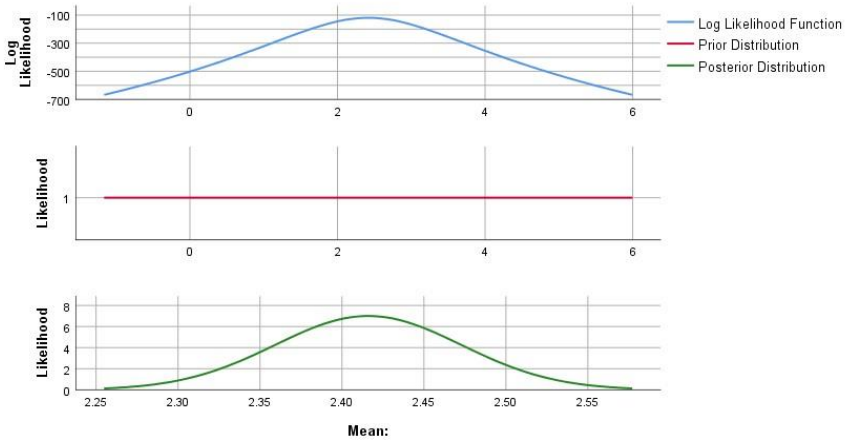

Figure 6: Bayesian Updating: Uniform Prior and Posterior Distribution

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Figures 6 illustrate a Bayesian inference example in three plots. The top plot shows the log likelihood function (blue), which measures how likely each mean value is, having a peak near 2.4 according to the observed data. The middle plot shows the prior (in red), which is uniform, indicating no initial bias toward any mean value. The bottom plot shows the posterior (green), which combines the prior with the likelihood, concentrating the weight around a mean of about 2.4. This posterior represents the updated beliefs about the mean after the given observations, narrowing the estimate when compared to the uniform prior.

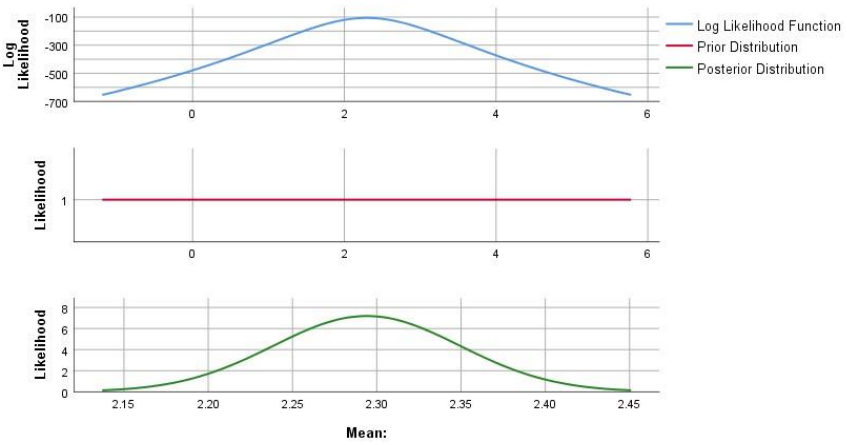

Figure 7: Bayesian Inference with Uniform Prior and Posterior Update

Figure 7 displays three plots relating to Bayesian inference: The likelihood function is plotted at the top (in blue), which is the logarithm of the probability of different mean values conditional on the observed data; it is seen to peak around 2.3. The second plot shows a uniform prior (in red), indicating a state of complete impartiality as to any mean value taken over the range. Construction of the posterior from the likelihood and the prior is plotted at the bottom (in green). The posterior presents a refined estimate of the mean concerning the data, with less uncertainty than the uniform-prior case.

Table 3: Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification

		Frequeny	Percent	Valid Percent	Cumulative Percent
Valid	1	124	24.8	24.8	24.8
	2	122	24.4	24.4	49.2
	3	82	16.4	16.4	65.6
	4	102	20.4	20.4	86.0
	5	70	14.0	14.0	100.0
	Total	500	99.8	100.0	
Missing	System	1	.2		

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Total	501	100.0		

Table 3 shows the frequency distribution of a dataset of 501 observations with values missing, thus, yielding only 500 valid cases. The data have been classified into five groups numbered 1 through 5. Group 1 has the largest number of cases with 124, recording 24.8%, next is Group 2 with 122 cases with 24.4%. Group 4 with 102 cases makes up 20.4%, Group 3 has 82 cases with 16.4%, and Group 5 with 70 cases is 14.0%. Cumulative percentages are, thus, the successive accumulation of valid cases reaching one hundred percent at Group 5. Generally, the table differentiates well into the five categories as to how the observations are shared.

Table 4: ANOVA[a]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	12.889	8	1.611	.	.[b]
	Residual	.000	0	.		
	Total	12.889	8			
a. Dependent Variable: Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification						
b. Predictors: (Constant), V22, V19, V15, V14, V1, V6, V16, V17						

Table 4 shows the regression output of different predictors (V1, V6, V14, V15, V16, V17, V19, and V22) with the dependent variable of "Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification." The total sum of squares that describes the variations in the dependent variable is 12.889, while the residual sum of squares is zero for the remaining variations (variations not explained by the model). The model has 8 degrees of freedom due to the predictors, leading to a mean square of 1.611. F-value and significance values (Sig.) have not been reported, probably because residual degrees of freedom are zero, indicating either a perfect fit of the model to the available data, not customized for the analysis or a problematic specification or sample size.

Table 5: Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.
		B	Std. Error	Beta		
1	(Constant)	9.061	.000		.	.
	V1	-.067	.000	-.145	.	.
	V6	.272	.000	.299	.	.
	V14	.031	.000	.033	.	.
	V15	.526	.000	.359	.	.
	V16	.249	.000	.291	.	.
	V17	-.738	.000	-.878	.	.
	V19	.585	.000	.537	.	.
	V22	-.113	.000	-.089	.	.
a. Dependent Variable: Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification						

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Table 5 displays the coefficients calculated through regression analysis to predict the dependent variable, "Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification," from eight variables (V1, V6, V14, V15, V16, V17, V19, V22). The unstandardized coefficients (B) inform the direction and magnitude of a particular predictor on the dependent variable, with V15 (0.526), V19 (0.585), and V6 (0.272) positively affecting the dependent variable and V1 (-0.067), V17 (-0.738), and V22 (-0.113) negatively affecting it. The Beta, or standardized coefficients, go on to reveal the relative importance of each predictor, with V17 (-0.878) and V19 (0.537) exerting the greatest influence of all predictors considered in the analysis. Standard errors are all zero, and t-values and significance levels are not reported. These might be due to some data or model issues (e.g., perfect multicollinearity, too small a sample size).

Table 6: Descriptive Statistics

	N	Range	Minimum	Maximum	Sum	Mean		Std. Deviation	Variance
	Statistic	Statistic	Statistic	Statistic	Statistic	Statistic	Std. Error	Statistic	Statistic
V1	500	499	1	500	125250	250.50	6.461	144.482	20875.000
V2	500	4	1	5	1449	2.90	.064	1.427	2.036
V3	500	4	1	5	1443	2.89	.063	1.419	2.013
V4	500	4	1	5	1505	3.01	.064	1.436	2.062
V5	500	4	1	5	1496	2.99	.064	1.421	2.020
V6	500	4	1	5	1448	2.90	.062	1.398	1.953
V8	500	4	1	5	1381	2.76	.063	1.410	1.989
V9	500	4	1	5	1418	2.84	.063	1.400	1.961
V10	500	4	1	5	1272	2.54	.058	1.291	1.667
V11	500	4	1	5	1208	2.42	.057	1.271	1.614
V12	500	4	1	5	1223	2.45	.062	1.385	1.919
V13	500	4	1	5	1228	2.46	.057	1.274	1.623
V14	500	4	1	5	1201	2.40	.059	1.313	1.724
V15	500	4	1	5	1210	2.42	.059	1.323	1.751
V16	500	4	1	5	1219	2.44	.059	1.324	1.754
V17	500	4	1	5	1200	2.40	.057	1.282	1.643
V18	500	4	1	5	1199	2.40	.058	1.290	1.663
V19	500	4	1	5	1161	2.32	.056	1.251	1.565
V20	500	4	1	5	1147	2.29	.055	1.237	1.531
V21	500	4	1	5	1219	2.44	.057	1.276	1.629
V22	9	3	1	4	18	2.00	.333	1.000	1.000

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Integrating Ayurvedic and Modern Diagnostics for Accurate	500	4	1	5	1372	2.74	.062	1.392	1.938
Disease Detection									
Valid N (listwise)	9								

Table 6 presents the descriptive statistics of V1 to V22 for a sample of size 500, except V22, which has only 9 valid ones. For each variable, the table displays the range, minimum, maximum, sum, mean, standard error of the mean, standard deviation, and variance. Variable V1 seems to be a sequential or ID variable with values ranging from 1 to 500 and a mean of 250.5, probably used for indexing. Variables V2 to V21 are presumed to contain Likert-scale responses from 1 to 5, with means ranging mostly between 2.29 and 3.01, reflecting slight agreement to neutral responses. The standard deviations of these variables are in the range of 1.2 to 1.4, indicating moderate variability. V22 seems like an outlier with only 9 responses and an average value of 2.00. This data is most likely coming from a pilot study or an incomplete production entry. The last row, "Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification," shows statistical characteristics similar to those of the other Likert scale variables (mean=2.74), giving a clue that it might be another item in the same scale. The "Valid N (listwise)" row confirms the facts, as it shows that only 9 cases had complete data across all variables.

Table 7: Posterior Distribution Characterization for One-Sample Mean

	N	**Posterior**			**95% Credible Interval**	
		Mode	**Mean**	**Variance**	**Lower Bound**	**Upper Bound**
V1	500	250.50	250.50	42.087	237.78	263.22
V2	500	2.90	2.90	.004	2.77	3.02
V3	500	2.89	2.89	.004	2.76	3.01
V4	500	3.01	3.01	.004	2.88	3.14
V5	500	2.99	2.99	.004	2.87	3.12
V6	500	2.90	2.90	.004	2.77	3.02
Integrated Ayurvedic and Modern Diagnostic Methods for Accurate Disease Identification	500	2.74	2.74	.004	2.62	2.87
V8	500	2.76	2.76	.004	2.64	2.89
V9	500	2.84	2.84	.004	2.71	2.96

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V10	500	2.54	2.54	.003	2.43	2.66
V11	500	2.42	2.42	.003	2.30	2.53
V12	500	2.45	2.45	.004	2.32	2.57
V13	500	2.46	2.46	.003	2.34	2.57
V14	500	2.40	2.40	.003	2.29	2.52
V15	500	2.42	2.42	.004	2.30	2.54
V16	500	2.44	2.44	.004	2.32	2.55
V17	500	2.40	2.40	.003	2.29	2.51
V18	500	2.40	2.40	.003	2.28	2.51
V19	500	2.32	2.32	.003	2.21	2.43
V20	500	2.29	2.29	.003	2.19	2.40
V21	500	2.44	2.44	.003	2.33	2.55
V22	9	2.00	2.00	.222	1.06	2.94
Pri	r on Variance: Diffuse. Prior on Mean: Diffuse.					

Table 7 presents Bayesian posteriors for the variables V1 to V22 with respective values for mode, mean, variance, and 95% credible intervals. All variables except V22 have samples of size 500 and generally exhibit posterior means similar to those sample means shown in the foregoing table, signifying stable and consistent estimates under diffuse (non-informative) priors. Posterior variances are contained (mostly about 0.003-0.004), reflecting high precision of the estimated means. The 95% credible intervals for all variables are quite narrow, accentuating the reliability of the estimates. V1, being perhaps an index, had a broader gap for the credibility interval of 237.78 to 263.22 due to its broader range. V22, however, with just 9 observations, provided an estimate with a greater posterior variance of 0.222 and a much wider credible interval of 1.06 to 2.94, hence indicating a considerable degree of uncertainty. Below this, it is specified that diffuse (non-informative) priors were assumed for all parameters; thus, the results are primarily data-driven.

CONCLUSION:

The research concludes that integrating Rognidan and Vikriti Vigyan with modern diagnostic methods significantly enhances the accuracy and reliability of disease identification. By combining classical diagnostic principles with contemporary tools such as laboratory tests, imaging, and computational analysis, the study demonstrates improved detection, classification, and assessment of disease severity. This holistic approach enables earlier intervention, more personalized treatment plans, and better patient outcomes. Furthermore, the findings highlight that traditional knowledge and modern technology complement each other, providing a comprehensive framework for clinical decision-making. Overall, the study underscores the value of integrating ancient diagnostic wisdom with modern methodologies to achieve precise, efficient, and effective healthcare solutions.

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