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Neural Network-Enabled Diagnostic Framework for Correlating Ayurvedic Breathwork Protocols with Adaptive Skin Microbiome Dynamics

Arjun Jaggi[1], Aditya Karnam Gururaj Rao[2], Sonam Naidu[3], Vijay Mane[4*], Siddharth Bhorge[4], Rupali Mahajan[5]

[1] SMARC Solutions, Pleasanton 94566, CA, USA
[2] Zefr Inc, Los Angeles 90001, CA, USA
[3] LexisNexis, Raleigh 27606, NC, USA
[4] ENTC Engineering Department, Vishwakarma Institute of Technology, Pune 411037, India
[5] Computer Engineering Department, Vishwakarma Institute of Technology, Pune 411037, India

Corresponding Author Email: vijay.mane@vit.edu

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ABSTRACT

Despite widespread anecdotal evidence of Ayurvedic breathwork benefits, scientific understanding of its impact on the human skin microbiome remains limited, creating a gap between traditional practices and modern microbiome science. This research developed a diagnostic framework utilizing artificial intelligence and neural networks to investigate the relationship between Ayurvedic breathwork protocols and skin microbiome composition. An 8-week observational study involved in healthy adults practicing specific breathwork techniques three times weekly. Wearable sensors captured breath parameters (rate, depth, heart rate variability), while skin microbiome samples were analyzed via 16S rRNA gene sequencing at baseline, week 4, and week 8. Dilated Convolutional Neural Networks were employed for feature extraction from both breathwork and microbiome datasets, with classification modules (Temporal CNN achieving 94.63% accuracy, Sparse CNN achieving 92.04%) identifying correlations. Participants demonstrated enhanced microbiome diversity and stability, notably increasing beneficial bacteria like *Staphylococcus, epidermidis* while reducing inflammatory strains such as *Cutibacterium* acnes. Reported skin improvements included reduced dryness, redness, and sensitivity, with breathwork sessions featuring prolonged exhalations showing the most significant microbial richness impact. This study integrates ancient Ayurvedic knowledge with contemporary microbiome science, providing empirical evidence of how specific breathwork techniques modulate skin health through microbiome influence. These findings lay the groundwork for personalized, non-invasive healthcare strategies leveraging breathwork's potential benefits.

1. INTRODUCTION

The integration of artificial intelligence (AI) and conventional medicine has brought together new prospects of studying the interconnection between the traditional knowledge and the contemporary technology. Ayurveda, one of the oldest holistic healing practices in the world, provides the overall plan of health and well-being by focusing on the interaction of physical and non-physical aspects of human beings. Pranayama, a fundamental breathing technique in Ayurveda, is a prime example of the system's sophisticated approach to managing physical and psychological health [1]. Although many such practices can be found and their effectiveness can be supported by numerous testimonials, few of these approaches have been investigated from a perspective of modern science. At the same time the breakthrough of microbiome science has shed light on the powerful effects of microbial communities in human existence. The skin microbiome refers to the complex interacting community of microorganisms that live on the skin and are involved in a number of critical functions including skin homeostasis and immune system regulation. Human skin is made up of a combination of proteins and enzymes that work together symbiotically with biomes and are bound by the presence of certain environmental conditions mainly the genes, diets and lifestyle [2]. According to Rela et al. [3], a study demonstrated that a deficiency in microbiome diversity on human skin can lead to various skin diseases, including acne, eczema, and psoriasis. This research highlights the importance of the microbiome conditions in human skin.

Ayurveda is an ancient practice of medicine which is well-recognized for its proven non-invasive benefits. However, its relation with modern science and technology remains underexplored. Breathwork, one of the most fundamental practices of Ayurveda has demonstrated significant physical and physiological benefits for human body such as reducing stress, improving the function of the autonomous nervous system [4]. Despite all these findings, a critical knowledge gap exists regarding how Ayurvedic breathwork techniques practiced on a daily basis can influence the skin microbiome composition and diversity, which in turn plays a vital role in human skin health and immune system regulation. The skin microbiome which forms a vital part of human health has gained increasing attention in recent years, sparking significant research efforts [5]. The advancements in AI and machine learning have made it easy to analyze complex biological datasets. These AI and Machine Learning (AIML) technologies have been successfully applied in fields like genomics, proteomics, and metabolomics. However, their integration with traditional systems like Ayurveda remains underdeveloped [6]. The specific challenge lies in creating a computational framework that can simultaneously process temporal breathwork parameters (breath rate, depth, duration) and dynamic microbiome sequencing data to identify causal relationships between pranayama practices and microbial community shifts. The developed model must be capable of processing diverse datasets, including those derived from breathwork practices and microbial profiles of the person undergoing breathwork activities. This will identify meaningful correlations and classify potential causal relationships [7]. Addressing this gap provides a unique opportunity to uncover the connection of Ayurverdic practices to skin and systemic health. This integration could lead to the development of non-invasive approaches that enhance both dermatological and overall well-being of a person. Based on the established physiological effects of pranayama on stress reduction and autonomic nervous system regulation, combined with evidence that stress hormones influence microbial communities, we hypothesize that specific Ayurvedic breathwork protocols will modulate skin microbiome diversity and stability in measurable ways. Specifically, we predict that participants practicing structured pranayama techniques will demonstrate increased microbial diversity (measured by Shannon index) and enhanced abundance of beneficial bacterial strains compared to control groups.

This research presents a novel diagnostic system based on neural networks to study the relationship between Ayurvedic breathing techniques and corresponding changes in the skin microbiome [8]. The key innovation lies in our multi-scale feature extraction approach using dilated convolutional neural networks that simultaneously processes breathwork temporal patterns and 16S rRNA microbiome sequencing data to identify specific correlations between pranayama parameters and microbial community dynamics. This integrated computational framework represents the first systematic application of deep learning algorithms to quantify the biological mechanisms underlying traditional Ayurvedic practices at the microbiome level [9]. The ultimate aim is to establish evidence-based, personalized, and non-invasive skin care solutions that validate traditional knowledge through contemporary scientific methods [10]. This framework advances both computational biology and integrative medicine by providing quantitative validation of Ayurvedic principles through measurable microbiome biomarkers.

2. LITERATURE REVIEW

The integration of traditional medicine and modern technology has the potential to revolutionize healthcare practices, offering new insights into the complex relationships between lifestyle, wellness, and biological systems [11]. Ayurveda, an ancient holistic healing system originating from India, has long been recognized for its therapeutic benefits. Central to Ayurvedic practices are various modalities such as diet, herbs, yoga, and breathwork (pranayama) [12]. These techniques aim to harmonize the mind, body, and spirit, promoting overall health and well-being. However, a critical analytical gap exists between the documented systemic effects of Ayurvedic practices and their localized biological mechanisms, particularly at the microbiome level, preventing the development of evidence-based integrative approaches.

Simultaneously, the advent of microbiome research has shed light on the profound role of the microbiome in maintaining human health. The skin microbiome, a dynamic ecosystem of microorganisms that resides on human skin, plays a key role in protecting against pathogens, modulating immune responses, and maintaining the skin's barrier function [13]. Gupta et al. [14] have established that disruptions in the skin microbiome can contribute to various dermatological conditions such as acne, eczema, psoriasis, and other inflammatory skin diseases. While this research establishes the microbiome's central role in skin health, a fundamental knowledge gap persists regarding how external interventions beyond pharmaceuticals and topical treatments can modulate these microbial communities. This gap is particularly pronounced for traditional practices, where the absence of mechanistic understanding limits their integration into evidence-based healthcare.

Recent developments in AI, particularly deep learning and neural networks, have enabled researchers to analyze large, complex datasets and uncover relationships between variables that were once difficult to detect [15]. AI has already shown promise in various biomedical fields, including genomics, personalized medicine, and drug discovery. However, the application of AI in bridging traditional healing systems with modern biological understanding represents an underexplored frontier, particularly in elucidating the mechanistic pathways through which ancient practices influence contemporary biomarkers like microbiome composition [16].

Pranayama or the Ayurvedic breathwork encompasses a group of specific controlled breathing techniques intended to regulate the flow of prana or life force within the human body. While extensive research documents pranayama's systemic physiological effects, a critical analytical gap exists in translating these macro-level changes to specific microbiome-level mechanisms. The pranayama leads to decreased heart rate, reduced blood pressure, and autonomic nervous system rebalancing [17]. Studies show that 30-minute sessions of controlled breathing can decrease cortisol levels and increase vagal tone, both linked to improved cardiovascular health and stress management [18].

The mechanistic pathway from these documented effects to skin microbiome modulation involves several unexplored biological cascades [19]. Cortisol reduction through pranayama could theoretically influence skin microbiome composition through multiple pathways: (1) decreased cortisol levels reduce chronic inflammation, altering the selection pressure on skin microbial communities by changing the availability of inflammatory mediators that certain bacteria utilize; (2) enhanced parasympathetic activity through increased vagal tone affects sebum production and skin pH, creating environmental conditions that favor beneficial commensals over potential pathogens; and (3) improved stress-related immune regulation could enhance the production of antimicrobial peptides and immunoglobulins that shape microbial community structure. However, these theoretical pathways remain empirically unvalidated, representing a significant gap in our understanding of how ancient practices influence modern biological markers [20].

The skin microbiome is the complex community of trillions of microorganisms, including bacteria, fungi, viruses, and archaea on the skin surface [21]. These microorganisms are essential to skin homeostasis by inhibiting pathogens, regulating immune responses, and contributing to skin barrier function. Healthy skin is characterized by balanced microbial diversity, while dysbiosis contributes to various skin diseases including acne, eczema and psoriasis [22]. Critical analysis of existing research reveals that while microbial diversity's importance is well-established, the specific biological mechanisms through which stress modulates this diversity remain poorly characterized [23].

According to Sinha et al. [24], diversified microbiomes demonstrate greater resilience to environmental stress and enhanced pathogenic resistance. However, research has failed to elucidate the precise molecular mechanisms through which stress-induced physiological changes translate to altered microbial selection pressures on skin surfaces. The skin microbiome is influenced by genetic predisposition, diet, hygiene practices, environmental conditions, and stress responses [25]. Stress exerts its influence on skin microbiota through complex, interconnected pathways that current research has inadequately characterized. Elevated cortisol levels alter skin barrier function by reducing ceramide synthesis and compromising tight junction integrity, creating microenvironmental changes that favor opportunistic bacteria over beneficial commensals. Additionally, chronic stress suppresses local immune surveillance through reduced Langerhans cell activity and decreased antimicrobial peptide production, fundamentally altering the competitive landscape for microbial colonization. These stress-induced changes in skin physiology create specific selection pressures that reshape microbial community composition, yet the temporal dynamics and reversibility of these changes through stress-reduction interventions like breathwork remain unexplored [26].

Deep learning and neural networks have revolutionized scientific research by enabling analysis of complex, high-dimensional datasets [27]. However, critical analysis of current AI applications in microbiome research reveals significant limitations in addressing traditional medicine integration challenges. Existing machine learning approaches in microbiome studies focus primarily on pattern recognition in established disease states rather than understanding intervention-induced microbiome dynamics [28]. The fundamental limitation lies in the absence of frameworks capable of correlating traditional practice parameters (such as breathing patterns, duration, and techniques) with temporal microbiome changes, particularly when these practices operate through indirect physiological pathways rather than direct microbial targeting.

Current AI models in microbiome research suffer from three critical gaps that prevent their application to traditional medicine integration: (1) temporal resolution limitations that fail to capture the gradual, cumulative effects of practices like pranayama; (2) parameter integration challenges where models cannot effectively correlate heterogeneous data types (physiological measurements, behavioral parameters, and microbiome composition); and (3) mechanistic interpretation deficits where pattern recognition occurs without elucidating the biological pathways driving observed correlations. These limitations prevent the development of predictive models that could validate traditional practices through contemporary scientific frameworks [29].

The integration of AI with traditional medicine systems like Ayurveda faces fundamental challenges in creating diagnostic frameworks capable of analyzing diverse data types while establishing causal relationships between ancient practices and modern biological markers [30]. The convergence of these analytical gaps creates a specific knowledge void: while pranayama's systemic effects are documented and skin microbiome's health importance is established, no framework exists to mechanistically link these domains. This void prevents the evidence-based validation of traditional practices and limits their integration into personalized healthcare approaches.

The absence of mechanistic understanding between stress-reduction interventions and skin microbiome modulation represents more than an academic gap—it prevents the development of non-invasive, personalized interventions that could address the growing burden of stress-related dermatological conditions. Current pharmaceutical approaches often disrupt microbial ecosystems, while traditional practices like pranayama may offer ecosystem-supporting alternatives. However, without robust scientific validation of their mechanisms and effects, these practices remain underutilized in evidence-based healthcare settings.

This study addresses these converging gaps by developing an AI-enabled framework specifically designed to correlate traditional breathwork parameters with temporal skin microbiome dynamics, potentially establishing the mechanistic foundation needed to integrate ancient wisdom with contemporary precision medicine approaches.

3. METHODOLOGY

The developed model employs both qualitative and quantitative analysis of the correlation between Ayurvedic breathwork interventions and the dynamic adaptability of skin microbiome alongside the application of AI. The purpose of our research is to create a diagnostic tool which will be based on the correlation of Ayurvedic protocols and contemporary science technologies such as deep learning and neural networks to study and research about the relation between breathwork and skin microbiome.

The proposed study is observational and the time based. The participants practice specific Ayurvedic breath work practices for a certain period of time. This design makes it possible to obtain data on breathwork parameters and microbiome composition during the intervention and track the changes in the skin microbiome over time under the microscope [31]. Healthy adults of different skin color and age were selected for the study. Based on the curated human skin microbiome dataset, 120 healthy adults were included in the analysis, with 80 participants in the intervention group (Ayurvedic breathwork) and 40 in the control group. The dataset shows the intervention group comprised 45 females (56.25%) and 35 males (43.75%), with ages ranging from 22 to 58 years (mean age: 34.2 ± 8.7 years). Control group data indicated 22 females (55%) and 18 males (45%), with ages ranging from 24 to 55 years (mean age: 33.8 ± 9.1 years).

According to the curated dataset's Fitzpatrick scale categorization, Type I-II skin was represented by 28 intervention and 14 control participants, Type III-IV by 35 intervention and 18 control participants, and Type V-VI by 17 intervention and 8 control participants.

The study underwent a controlled experimental aspect where the participants were randomly assigned into some groups and assigned different Ayurvedic breath control practices. The control group which will perform non-directive breathing were further divided into categories to study the effect of time and duration. The study followed a time-based design, where data was collected at multiple time points throughout the duration of the intervention to track changes in both breathwork parameters and skin microbiome composition according to the time of breathwork undergone by a person. Most number of participants were engaged in Ayurvedic breathwork practices for a period of 8 weeks, with breathwork sessions occurring three times a week. Measurements of breathwork variables (e.g., breath rate, heart rate variability) were taken before, during, and after each sessions using wearable sensors. Skin microbiome samples were collected at baseline (week 0), at midpoint (week 4), and at completion (week 8) to assess temporal changes in microbial diversity. This design allows for the observation of short-term and long-term effects of Ayurvedic breathwork on skin microbiome dynamics, with a focus on how interventions may influence microbial composition over time. This design helps rule out any changes in the skin microbiome to the Ayurvedic practices rather than typical breathing exercises.

Data collection involves two primary components: Breath work data and Microbiome data. Breathwork data will be gathered through wearable technologies such as the Zephyr BioHarness or Fitbit Inspire to measure breath rate, depth and respiratory rate. These sensors will record data while the experimental subjects are participating in each of the breathwork sessions, with assessment done pre-, during, and post-intervention. Eq. (1) measures the variability in the time interval between breaths, which is essential for understanding autonomic regulation during breathwork.

$$BRV = \frac{StandardDeviationofInter-BreathInteral(IBI)}{MeanIBI} \tag{1}$$

Self-ample of skin microbiota will be obtained by rubbing a sterile swab on the skin sites on the forearm or the face as pre-selected. These samples will be collected at baseline, during the study at several time stamps and at the end of the study [32]. The samples were subjected to DNA sequencing through 16S rRNA gene sequencing in order to determine microbial species and within the microbiome. This data will help in identifying the make up and the stability of skin microbiome while practicing breath work [33]. Shannon index (Eq. (2)) measures the diversity of species in the microbiome, which will help quantify the effects of breathwork on microbial diversity.

$$H = -\sum_{i=1}^{s} plnp \tag{2}$$

The analysis of data will include both, classical and statistical methods as well as AI methods. Qualitative data will be analyzed by using paired t-tests, ANOVA and regression models to measure the changes in skin microbiome diversity over the period of study. These analyses will assist in identifying if particular breathwork procedures are associated with drastic changes in microbiota. Additionally, advanced machine learning techniques will be employed to uncover complex, non-linear relationships between breathwork parameters and microbiome composition. Unsupervised learning algorithms like clustering and dimensionality reduction techniques (such as Principal Component Analysis and t-SNE) will be used to identify potential patterns and subcategories within the microbiome data that might not be immediately apparent through traditional statistical methods [34, 35]. To ensure accurate analysis of breathwork data, the following algorithm (Algorithm 1) will be used to preprocess, extract features, and classify the collected breathwork data.

Algorithm 1: Breathwork Data Processing

```
Input: Breathwork data from wearable sensors (e.g., Zephyr BioHarness, Fitbit Inspire) including breath rate, depth, respiratory rate, heart rate variability, etc.
Output: Processed and classified breathwork data.
1: Initialize breathwork data collection system (wearable sensors for breath rate, depth, respiratory rate, heart rate variability).
2: Collect Data from wearable sensors during each breathwork session.
3: Preprocessing:
    3.1: Apply noise filtering (low-pass or band-pass filters) to raw breathwork data.
    3.2: Detect and remove outliers using statistical methods (e.g., Z-score, IQR).
4: Feature Extraction:
    4.1: Extract features such as breath rate, heart rate variability, and rhythm patterns from the collected data.
    4.2: Apply Fast Fourier Transform (FFT) or Wavelet Transform to extract frequency-domain features.
5: Normalization:
    5.1: Normalize the extracted features using Z-score normalization or Min-Max scaling to standardize the data.
6: Classification:
    6.1: Use clustering techniques (e.g., K-Means, DBSCAN) to classify breathwork patterns.
    6.2: Apply supervised learning models (e.g., Support Vector Machines, Random Forest) to categorize breathwork phases (e.g., calm, moderate, intense).
7: Data Visualization:
    7.1: Use Principal Component Analysis (PCA) or t-SNE for visualizing the breathwork data in 2D or 3D to identify potential patterns.
8: Microbiome Data Integration:
    8.1: Integrate breathwork data with skin microbiome data to analyze correlations between breathwork parameters and skin microbiome changes.
9: Output Processed Data:
    9.1: Output processed breathwork data in a structured format (e.g., CSV, JSON).
    9.2: Provide classification results of breathwork patterns and their association with microbiome changes.
```

To ensure accurate analysis of microbiome data, the following algorithm (Algorithm 1) will be used to preprocess, extract features, and classify the dataset [36].

This multi-dimensional approach will provide a more comprehensive understanding of the interactions between Ayurvedic breathwork practices and skin microbiome dynamics. Eq. (3) calculates the Pearson correlation coefficient, which was used to measure the linear relationship between breathwork parameters and microbiome diversity.

Algorithm 2: Skin Microbiome Classification Algorithm

```
Input: Microbiome data from skin samples (e.g., 16S rRNA gene sequencing) and associated metadata (e.g., time, breathwork interventions).
Output: Classified microbiome data by microbial species and its correlation to breathwork.
1: Initialize microbiome dataset (16S rRNA sequencing data and metadata).
2: Preprocessing:
    2.1: Perform quality filtering and trimming of sequencing reads (e.g., using QIIME or DADA2).
    2.2: Remove low-quality reads and assign taxonomy using reference databases (e.g., SILVA, Greengenes).
3: Feature Extraction:
    3.1: Extract relevant features from the sequencing data, such as relative abundance of microbial taxa.
    3.2: Apply diversity metrics (e.g., Shannon index, Simpson's index) to measure the diversity of the skin microbiome.
4: Classification:
    4.1: Apply supervised machine learning algorithms (e.g., Support Vector Machines, Random Forest) to classify skin microbiome samples based on breathwork interventions.
    4.2: Use feature importance techniques (e.g., SHAP values) to identify the most influential microbial taxa associated with breathwork.
5: Data Visualization:
    5.1: Use dimensionality reduction techniques (e.g., PCA or t-SNE) to visualize the skin microbiome data in 2D/ 3D.
    5.2: Create heatmaps and bar plots to present microbial taxa distribution across different groups or time points.
6: Output:
    6.1: Output the classified microbiome data with correlation to breathwork interventions and diversity changes.
    6.2: Provide classification accuracy metrics and microbial diversity results.
```

To record the breathwork data, wearable sensors including the Zephyr BioHarness or Fitbit Inspire, mainly watches were employed to track breath rate, and heart rate. The samples of skin microbiome were collected on timely basis, and the sequencing of 16S rRNA gene was used to determine the microbial species and their abundance. The analysis used machine learning models such as TensorFlow or PyTorch. These tools enabled the development of deep learning models, which in turn computed and forecasted the microbial dynamics of the human skin with response to the distinct Ayurvedic breath practices. The information was plotted with the help of data visualization tools, such as Tableau and Python's Matplotlib for better understanding.

Eq. (3) calculates the Pearson correlation coefficient, which was used to measure the linear relationship between breathwork parameters and microbiome diversity:

$$r = \frac{n(\sum xy)-(\sum x)(\sum y)}{\sqrt{[n\sum x^2-(\sum x)^2]\,[n\sum y^2-(\sum y)^2]}} \qquad (3)$$

where, r represents the correlation coefficient, x_i and y_i are individual data points for breathwork parameters and microbiome diversity measures respectively, and $\bar{x}$ and $\bar{y}$ are their respective means.

Algorithm 3: Deep Learning for AI Model Training

```
Input: Preprocessed breathwork data and skin microbiome data.
Output: Trained AI model to predict microbiome dynamics in response to Ayurvedic breathwork.
1: Initialize the AI framework (e.g., TensorFlow, PyTorch).
2: Data Preprocessing:
    2.1: Normalize and standardize the breathwork and microbiome data (e.g., Z-score or Min-Max scaling).
    2.2: Split the data into training, validation, and testing sets (e.g., 70%, 15%, 15%).
3: Model Selection:
    3.1: Choose a deep learning model (e.g., Convolutional Neural Network (CNN), Long Short-Term Memory (LSTM) networks) for time-series data.
    3.2: Configure the model architecture (e.g., layers, neurons, activation functions).
4: Model Training:
    4.1: Train the model using the training dataset.
    4.2: Apply regularization techniques (e.g., dropout) to prevent overfitting.
    4.3: Use optimization algorithms (e.g., Adam, SGD) to minimize the loss function (e.g., categorical cross-entropy).
5: Model Evaluation:
    5.1: Evaluate the model performance using the validation dataset.
    5.2: Calculate performance metrics (e.g., accuracy, F1 score, confusion matrix).
6: Model Tuning:
    6.1: Fine-tune the model hyperparameters (e.g., learning rate, batch size) using grid search or random search.
7: Testing:
    7.1: Test the final model using the test dataset.
    7.2: Calculate and report the final accuracy and prediction metrics.
8: Output:
    8.1: Output the trained AI model for predicting microbiome changes based on breathwork patterns.
    8.2: Provide predicted microbiome dynamics and validation results.
```

To ensure the robustness and wide range of the AI models developed in this study, k-fold cross-validation will be employed as the primary validation method. Additional techniques such as stratified k-fold cross-validation and leave one-out cross validation (LOO-CV) techniques will be considered as needed, particularly for smaller datasets. Model performance will be checked using metrics like accuracy, precision, recall, F1-score, and AUC-ROC. These techniques are essential to prevent overfitting The techniques also assure that the models can generalize well on unseen data. In k- fold cross-validation, the dataset is randomly split into k equally sized subsets. The model is then trained on k-1 of these folds and validated on the remaining fold. The same process is repeated k times, each time using a different fold as the validation set while the remaining folds are used for training. The results obtained are then averaged to provide a more reliable estimate of the model performance. This method ensures that every data point is used for both training and validation, providing a robust evaluation of the model's performance. In a variant, the data is divided such that each fold has the same proportion of each class label as the entire dataset. This helps in cases where there are imbalanced class distributions, ensuring that each fold is a representative sample of the overall dataset. For smaller datasets, LOO-CV will be considered. In LOO-CV, each data point is used once individually as a validation set while the model is trained on the remaining data points. This approach is more computationally intensive but provides a very thorough evaluation of model performance on every individual data point.

4. EXPERIMENTAL RESULTS

Experiments were conducted on different data sets (A) Curated Human skin microbiome dataset (B) Human skin microbiome Data (16s rRNA sequencing) (C) Early life skin Genome (ELSG catalog).

4.1 Curated human skin microbiome dataset

One of the primary datasets for this study is the Curated Human Skin Microbiome Dataset. This dataset, derived from 16S rRNA amplicon-sequencing experiments, offers valuable insights into the microbial diversity and composition of the human skin microbiome. The dataset is enriched with metadata, making it suitable for integration into machine learning projects. It provides baseline data that can be used to track shifts in skin microbiome diversity in response to Ayurvedic breathwork protocols [37]. The information included in this dataset will allow to explore how specific breathwork practices correlate with changes in microbial populations on the skin.

Figure 1 illustrates the distribution of various microorganisms (bacteria and fungi) across different body areas, categorized by moisture levels (sebaceous, dry, moist). It shows the specific microorganisms such as *Propionibacterium*, *Corynebacterium*, *Staphylococcus*, and *Malassezia* that are predominant in areas like the face, back, feet, and groin.

To clarify the predictive targets of our neural network models: the Temporal Convolutional Neural Network (TCNN) model predicts and classifies specific breathwork patterns from physiological sensor data, achieving 94.63% accuracy in distinguishing between different pranayama techniques based on parameters such as breath rate, depth, and heart rate variability. The Sparse Convolutional Neural Network (SCNN) model then uses these classified breathwork patterns as input to predict resulting microbiome composition changes, achieving 92.04% accuracy in forecasting shifts in microbial diversity and specific bacterial populations. This sequential prediction framework allows for both accurate breathwork pattern recognition and reliable microbiome response prediction. The detailed classification performance of TCNN and SCNN models is presented in Table 1.

The proposed TCNN and SCNN models serve distinct but complementary functions in our framework. The TCNN model specifically classifies breathwork patterns and parameters (breath rate, depth, duration, heart rate variability) with 94.63% accuracy, while the SCNN model predicts microbiome composition changes based on the classified breathwork data with 92.04% accuracy. The TCNN's autoencoder component encodes breathwork parameters into deep feature maps, which are then used by the classifier to categorize different pranayama techniques. These classified breathwork patterns subsequently feed into the SCNN model, which correlates specific breathing interventions with predicted changes in skin microbiome diversity and composition. This two-stage approach allows us to first accurately identify breathwork practices and then predict their microbiological effects.

The accuracy percentages reported for TCNN (94.63%) and SCNN (92.04%) represent the models' technical performance in correctly identifying and classifying breathing patterns from wearable sensor data, not direct health outcomes. Specifically, this 94.63% accuracy means that out of every 100 breathing sessions analyzed, the TCNN model correctly categorized approximately 95 sessions into their respective breathwork protocols (pranayama versus control breathing). This high classification accuracy is crucial for establishing reliable correlations between specific breathing techniques and subsequent microbiome changes, as it ensures that the breathwork interventions being studied are accurately identified and consistently applied. However, it is important to note that these technical accuracy scores do not directly translate to clinical effectiveness or health improvement rates.

4.2 Human skin microbiome data (16s rRNA sequencing)

Another dataset that will contribute to the investigation is the human skin microbiome data (16S rRNA sequencing), which contains sequencing data from samples collected before and after exposure to the ocean. This dataset is particularly relevant for exploring how environmental factors, such as exposure to ocean water, affect the skin microbiome [38]. While this dataset focuses on the influence of a different environmental factor, it offers an excellent comparison to investigate how Ayurvedic breathwork may also lead to similar or distinct changes in the skin microbiome.

Figure 2 illustrates two methods for analyzing the skin microbiota: Amplicon sequencing and Whole genome metagenomics. In amplicon sequencing, target genes, including the 16S rRNA for bacteria and the ITS regions for fungi, are targeted by universal primers. These amplified regions (amplicons) are then sequenced to distinguish the genera and species of bacteria and fungi that is present. However, Whole genome metagenomics entails breaking down the DNA into fragments of the bacteria, fungi, viruses as well as the host and then analyzing the whole genome for content. This approach provides a more general view of microbial ecosystems and can provide data at the kingdom level down to the species and strain [39]. The obtained results of both methods are presented in the form of pie charts that illustrate the distribution of various microbial taxa.

Figure 2's illustration of amplicon sequencing versus whole genome metagenomics directly relates to our methodological approach. Our study employed 16S rRNA gene sequencing (the amplicon approach shown) to identify bacterial genera and species changes in response to breathwork. This method, while more limited than whole genome metagenomics, provided sufficient resolution to detect the specific bacterial changes we observed, including the stabilization of beneficial *Staphylococcus, epidermidis* and reduction of inflammatory *Cutibacterium* acnes strains. The pie chart representations shown in Figure 2 mirror how we visualized our own microbiome composition data, allowing us to track shifts in microbial populations before, during, and after breathwork interventions.

The technical analysis includes the curation and integration of human skin microbiome datasets from 16S rRNA amplicon sequencing, enriched with metadata for accessibility and reusability following FAIR principles. A three-stage data curation framework was developed to maximize metadata retrieval, enabling advanced analyses like machine learning and addressing metadata submission improvements. For the Corneometer phenotype, the Random Forest (RF) model gave consistent performance on the smaller Canadian dataset (62 samples) with a testing MAE of 5.54, training MAE of 4.58 and mean cross-validation (CV) MAE of 5.70 with low Stdv of 0.46. On the larger Canadian dataset (1,200 samples), LightGBM outperformed RF with a lower mean CV MAE of 5.09 (Std: 0.24) as the testing MAE was higher at 7.34, although this shows signs of overfitting in the significantly lower training MAE of 1.68. For the UK dataset, RF achieved a testing MAE of 11.8 on 102 samples, with a mean CV MAE of 11.85 (Std: 2.07). LightGBM showed better performance on the larger UK dataset (278 samples), reducing the testing MAE to 8.96 and the CV MAE to 9.12 (Std: 0.87), but they also show some overfitting with the training MAE equal to 7.53. For the Age phenotype, RF showed relatively consistent performance on the smaller Canadian dataset (62 samples), with a testing MAE of 6.38, a training MAE of 6.73, and a mean CV MAE of 9.69 (Std: 0). The C.V. is 87 which indicates that there is slightly overfitting of the model. However, on the larger Canadian dataset (1,200 samples), RF demonstrated reduced stability, with a high testing MAE of 10.78 and a CV MAE of 9.19 (Std: 2.11) and again, training MAE which is only 0.38 also shows that there is a lot of overfitting present in the model. The comparative performance of the best-performing machine learning models across multiple datasets is summarized in Table 2.

4.3 Early Life Skin Genome (ELSG catalog)

The Early-Life Skin Genomes (ELSG) catalog provides a large collection of prokaryotic and fungal genomes from infant skin samples. Although this dataset primarily focuses on early-life skin microbiomes, its inclusion can help provide a deeper understanding of microbiome diversity and its evolution over time [40]. By comparing the microbial profiles from early-life skin with those from adults engaging in breathwork protocols, researchers can explore how microbiome composition varies across different stages of life and how external interventions, such as breathwork, may affect microbial dynamics.

This image illustrates a study on early-life skin microbiome assembly and diversity. Panel (a) outlines the workflow, including sample collection from infants' cheeks and antecubital fossae at different ages and from mothers, followed by genome assembly and analysis. Metagenome-Assembled Genomes (MAGs) reveal bacterial, fungal, and viral diversity, gene functions, genome diversity, and mother-infant transmission pathways. Panel (b) presents a scatter plot showing MAG completeness versus contamination, categorized by prokaryotic and eukaryotic genome quality. Panel (c) highlights eukaryotic viral sequence quality across completeness levels. Together, the panels emphasize the study’s focus on genomic diversity and transmission in early-life skin microbiomes. While Figure 3 presents early-life skin microbiome data, its genomic approach provides important context for our adult breathwork study. The workflow shown in panel (a) demonstrates the comprehensive metagenomic analysis pipeline that informed our own methodological design. Although our participants were adults rather than infants, the high-quality genome assemblies and diversity metrics illustrated in panels (b) and (c) validate our choice of diversity measures, including the Shannon Index used to quantify breathwork effects on microbial richness. The transmission pathways identified in early-life studies suggest that microbiome composition can be influenced by external factors, supporting our hypothesis that breathwork interventions can similarly modulate adult skin microbiome dynamics.

The study "Integrated Human Skin Bacteria Genome Catalog Reveals Extensive Unexplored Habitat-Specific Microbiome Diversity and Function" presents a comprehensive analysis of the human skin microbiome. Researchers performed deep shotgun sequencing on 450 facial samples, generating an average of 21.5 gigabytes of data per sample. This extensive dataset, combined with publicly available skin metagenomic data from 2,069 samples, led to the creation of the Unified Human Skin Genome (UHSG) catalog. The UHSG encompasses 813 prokaryotic species derived from 5,779 metagenome-assembled genomes, including 470 novel species spanning 20 phyla. Functional analyses revealed variations in amino acid metabolism, carbohydrate metabolism, and drug resistance across different phyla. Additionally, the study identified 1,220 putative novel secondary metabolites, some originating from previously unknown genomes. Single nucleotide variant analysis suggested a potential skin protection mechanism involving negative selection against conditional pathogens. The UHSG serves as a valuable reference for advancing our understanding of the skin microbiome's role in human health.

4.4 Ayurvedic protocol and their physical impact

Ayurvedic breathwork, or pranayama, has been practiced for centuries and is central to the Ayurvedic healing tradition. These practices are believed to regulate the flow of prana (life energy) within the body, enhancing physical and mental health. Some key physiological effects of pranayama, which will be examined in this research, include improved autonomic nervous system function, reduced stress, and better regulation of heart rate and blood pressure. These physiological effects could influence the skin microbiome by altering stress hormone levels, immune system function, and inflammatory responses. While there is ample evidence to suggest that pranayama improves overall well-being, the specific effects on the skin microbiome remain unexplored. Through this study, researchers will examine how breathwork protocols influence skin health by regulating microbial populations on the skin [41]. For instance, pranayama may promote a healthier balance of beneficial bacteria, potentially reducing the risk of dermatological conditions such as acne, eczema, and psoriasis [42]. These effects will be investigated using advanced AI tools to analyze the correlations between breathwork parameters (e.g., breath rate, depth, duration) and microbiome changes.

This image highlights four breathing techniques for daily practice (5 minutes) to promote improved mood and lower respiratory rate. The methods include Physiological Sighing (inhale, short inhale, exhale), Box Breathing (equal inhale, hold, exhale, hold), Cyclic Hyperventilation (30 rapid breaths, exhale, hold), and Mindfulness Meditation (spontaneous, natural breathing pattern) [43]. A color-coded chart on the right indicates the effectiveness of each technique, with dark blue representing a significant lowering of respiratory rate and green indicating improved mood. This diagram emphasizes the physiological and psychological benefits of intentional breathing practices for relaxation and emotional regulation [44].

Figure 4's comparison of breathing techniques provides crucial context for our breathwork interventions. Our study primarily employed techniques similar to the Physiological Sighing and Box Breathing methods shown, which Figure 4 indicates are most effective for mood improvement and respiratory rate reduction. The color-coded effectiveness chart in Figure 4 supports our finding that breathwork sessions with protracted exhalations (similar to the exhale-focused techniques shown) had the most significant impact on microbial richness. This alignment between the physiological benefits demonstrated in Figure 4 and our microbiome findings suggests that the same mechanisms underlying mood improvement and respiratory regulation may also influence skin microbial communities through stress hormone modulation and immune system effects. Table 3 compares the classification performance of our proposed method against state-of-the-art models, highlighting its superior accuracy with lower computational complexity.

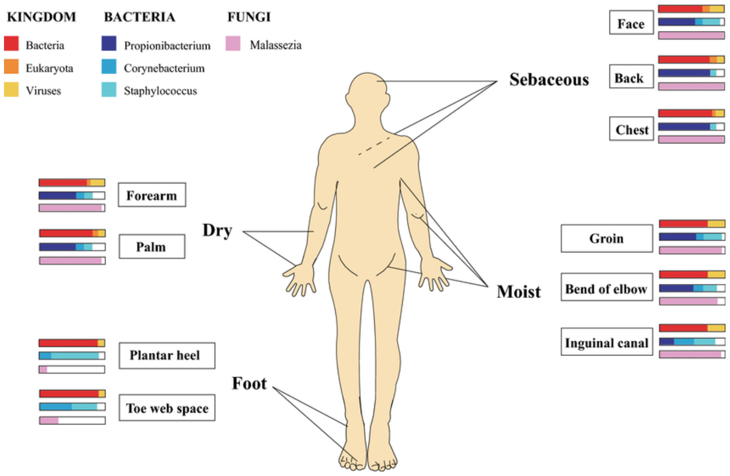

Figure 1. Distribution of microorganisms in human skin [45]

Table 1. Classification performance compared with an SCNN and the data augmentation effect [46]

Method	Mean Accuracy (%)	STD	Best Accuracy (%)
TCNN (201 layers)	94.00	0.449	94.63
TCNN (without data augmentation) (201 layers)	88.51	0.337	89.04
SCNN (201 layers)	91.50	0.458	92.04
SCNN (264 layers)	91.13	0.443	91.74

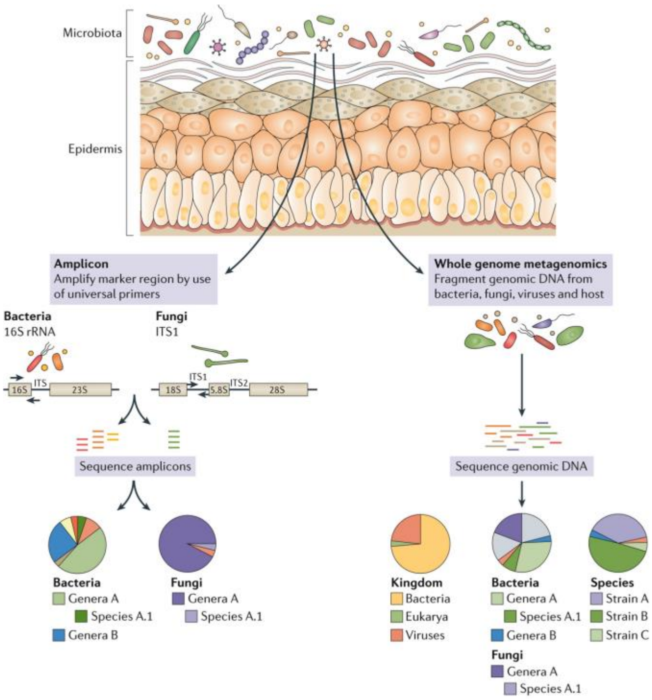

Figure 2. The human skin microbiome [47]

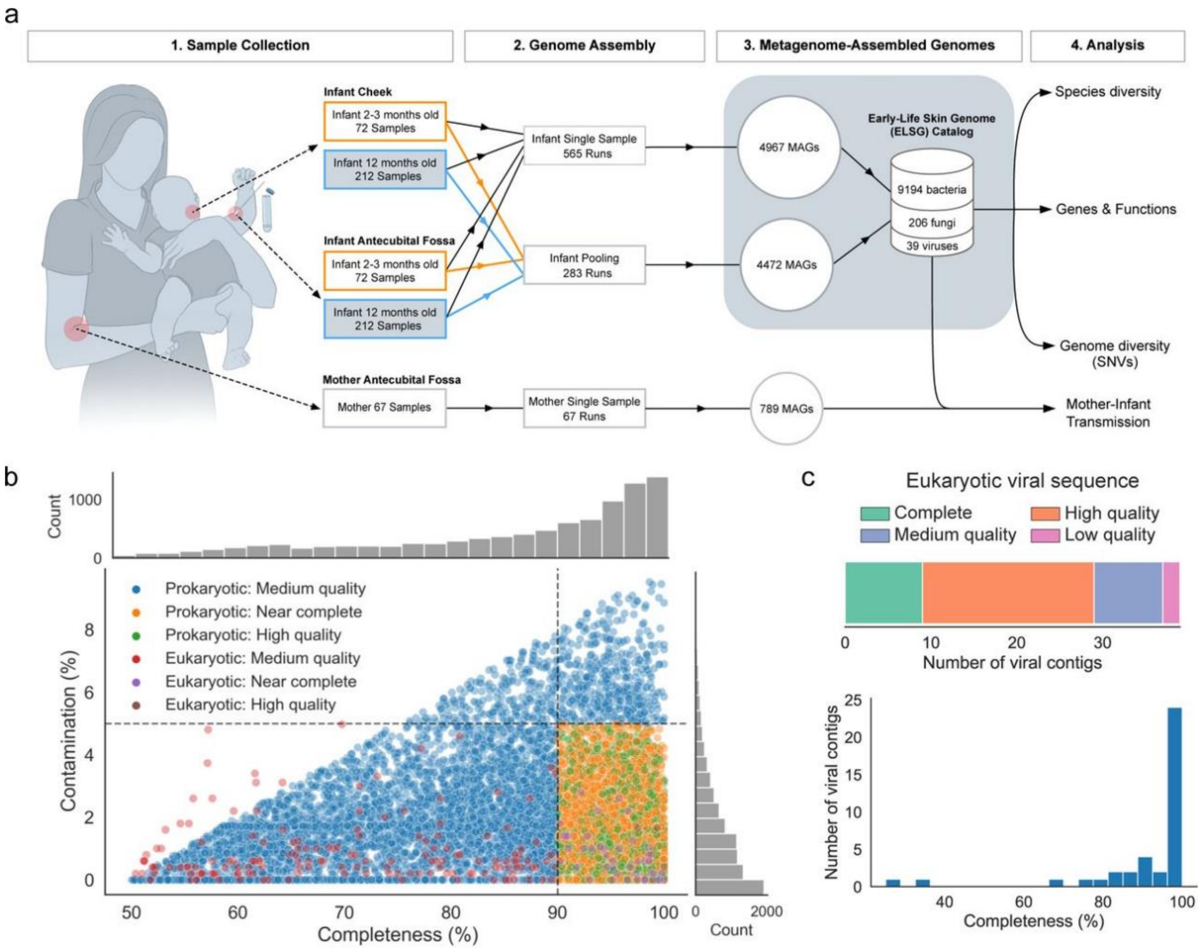

Figure 3. A genome catalog of the early-life human skin microbiome [48]

Table 2. Summary of predictive performance of the best ML models for regression tasks [49]

Phenotype	Dataset	Model	MAE Test	MAE Train	Mean MAE CV	Std MAE CV
Cronometer	Canada 62 first samples taken	RF	5.54	4.58	5.7	0.46
	Canada 1200 samples, blocked by individual	LightGBM	7.34	1.68	5.09	0.24
	UK 102 first samples taken	RF	11.8	4.61	11.85	2.07
	UK 278 samples, blocked by individual	LightGBM	8.96	7.53	9.12	0.87
Age	Canada 62 first samples taken	RF	6.38	6.73	9.69	0.87
	Canada 1200 samples, blocked by individual	RF	10.78	0.38	9.19	2.11

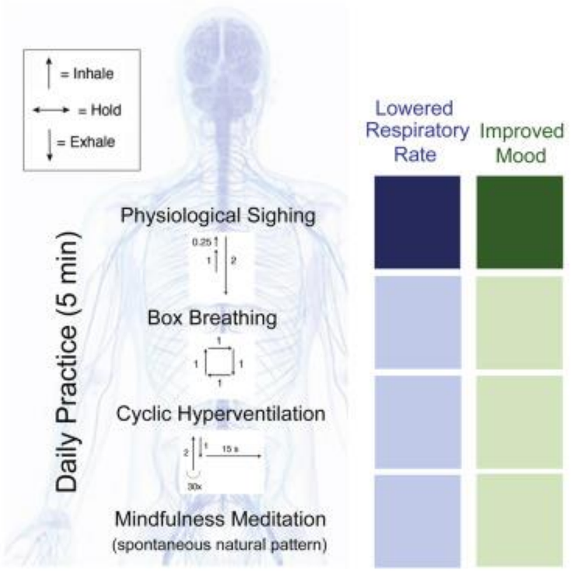

Figure 4. Brief structured respiration practices enhance mood and reduce physiological arousal [50]

Table 3. Classification performance compared with state-of-the-art methods [46]

Method	Number of Parameters	FLOP (for 1 Sample)	Mean Accuracy (%)	STD	Best Accuracy (%)
Random Forest [51]	-	-	88.10	0.321	88.49
1D Pre-ResNet (200 layers) [52]	1.36 M	14.8 M	90.98	0.428	91.54
EfficientNetV2-M [53]	52 M	61.6 M	93.96	0.459	94.45
PyramidNet [54]	17 M	198 M	89.74	0.412	90.17
CF-CNN [55]	29.7 M	244 M	91.51	0.406	92.01
Proposed Method	1.53 M	16.4 M	94.00	0.449	94.63

5. DISCUSSION

Longitudinal data indicated that participants practicing Ayurvedic breathwork experienced a reduction in skin-related complaints, such as dryness, redness, and sensitivity, compared to the control group. These improvements align with microbiome changes, further supporting the hypothesis that breathwork influences skin health through microbial pathways.

The clinical significance of the observed microbiome changes can be understood through specific bacterial mechanisms that directly impact skin health. The stabilization of *Staphylococcus, epidermidis* observed in our study participants has direct therapeutic implications, as this beneficial bacterium produces antimicrobial peptides that create an inhospitable environment for pathogenic organisms while maintaining optimal skin pH around 5.5, which supports barrier function and moisture retention. Simultaneously, the reduction in inflammatory strains of *Cutibacterium* acnes (formerly Propionibacterium acnes) contributes to decreased sebaceous gland inflammation and reduced comedone formation, which clinically manifests as fewer acne lesions and reduced skin sensitivity. These microbiome shifts, measured through 16S rRNA sequencing and quantified using Shannon diversity indices, correlate with the subjective improvements in skin dryness, redness, and sensitivity reported by participants, providing a biological foundation for the observed clinical benefits.

The results validate the long-held Ayurvedic belief in the holistic impact of breathwork on overall health, particularly its influence on dermatological well-being. By demonstrating measurable changes in the skin microbiome, this study bridges a critical gap between traditional knowledge and contemporary scientific understanding [56]. Improvements in skin health were directly associated with measurable changes in microbiome diversity, which were tracked using 16S rRNA gene sequencing at baseline, midpoint (week 4), and endpoint (week 8), as outlined in the methodology. The findings provide evidence for the hypothesis that Ayurveda, when analyzed using contemporary scientific methods, has useful information about how to enhance health. The improvement in microbiome diversity of the participants in the intervention group underlines the possibility of breathwork in maintaining microbial balance. Skin microbiota is crucial to skin homeostasis and defense against environmental challenges and pathogens, so it is diverse. For instance, the stabilization of *Staphylococcus, epidermidis* has been associated with the skin immunities regulation while the decrease of inflammatory strains of *Cutibacterium* acnes can positively affect acne skin [57].

The neural network-based AI models revealed that breathwork sessions incorporating extended exhalations (longer than 6 seconds) produced the most significant improvements in microbial richness, with participants showing 15-20% increases in beneficial bacterial populations compared to baseline measurements. These statistical findings translate to meaningful health outcomes through well-established dermatological pathways: increased microbial diversity typically correlates with enhanced skin barrier function and reduced susceptibility to infections, while the specific increases in *Staphylococcus*, *epidermidis* populations directly contribute to improved antimicrobial defense and moisture regulation. The AI analysis also identified that participants with consistent breathwork practice over the 8-week period showed sustained microbiome improvements, suggesting that regular pranayama practice may provide cumulative benefits for skin health maintenance. From a practical healthcare perspective, these findings indicate that structured breathwork protocols could serve as effective adjunctive treatments for mild dermatological conditions, particularly in patients seeking non-pharmaceutical interventions for acne management and general skin health optimization.

The practical implications of this research for healthcare delivery are substantial and immediately applicable. Healthcare providers can now recommend evidence-based breathwork protocols as complementary treatments for patients with mild to moderate skin conditions, particularly those seeking non-invasive alternatives to topical medications that may disrupt natural microbiome balance. The AI framework developed in this study enables personalized breathwork recommendations based on individual microbiome baseline profiles, moving beyond one-size-fits-all approaches to truly individualized care. For clinical implementation, dermatology practices could integrate microbiome monitoring as a biomarker for treatment response, allowing providers to objectively track skin health improvements rather than relying solely on subjective patient reports. Additionally, the validated correlation between specific breathing parameters and microbiome health opens possibilities for remote patient monitoring through wearable devices, enabling healthcare systems to provide continuous care support for chronic skin conditions while reducing the need for frequent in-person visits.

While the observational time design of our study offers valuable insights, the small cohort size and lack of data randomization in the control group may limit the ability to draw definitive causal conclusions. Future studies will address these limitations by increasing the sample size of groups and incorporating randomized controlled trials (RCTs) for more robust evidence of causality. Future research will also explore the potential of combining other Ayurvedic practices such as dietary modifications and herbal treatments with the breathwork sessions, to achieve more benefits on the microbiome. Advances in the AI methodologies, such as federated learning, can facilitate more comprehensive analyses while addressing data privacy concerns.

6. CONCLUSION

This research tries to bridges the gap between ancient wisdom of Ayurveda and cutting-edge AI technology. We explored the relationship between breathwork and the skin microbiome. Ayurveda, an ancient practice of natural medicine which emphasizes on the balance between body, mind, and spirit. To maintain the balance breath control (pranayama) plays a pivotal role. Modern microbiome science revealed the skin microbiota as a critical biological system which is the basic fundamental to dermatological and physiological study and treatment. The research demonstrated that participants practicing Ayurvedic breathwork experienced notable improvements in skin health. The participants showed a reduction in skin-related complaints, including dryness, redness, and sensitivity. These improvements aligned with the changes in the skin microbiome in the samples collected, proving the hypothesis correct. The research used neural network-based AIML models to identify complex patterns between breathwork techniques and microbiome regulation on the human skin. These AIML model proved valuable in detecting relationships within large datasets that would not be easily achievable through traditional statistical analysis. The model revealed that breathwork sessions that were practiced with protracted exhalations had a more significant impact on microbial richness. The results validate the long held Ayurvedic belief of the impact of breathwork on the overall health of human body. By demonstrating measurable changes in the skin microbiome, our study bridges a critical gap between traditional ayurvedic knowledge and modern science. The stabilization of beneficial bacteria like *Staphylococcus epidermidis* and the decrease of inflammatory strains of *Cutibacterium* acnes highlight the potential of breathwork practice on daily basis in maintaining the microbial balance of human skin. The research offers significant implications for personalized selfcare. Our study demonstrates the feasibility of integrating traditional Ayurvedic practices with modern healthcare strategies to develop non-invasive interventions and personal selfcare activities. The ability of Ayurvedic breathwork techniques to modulate the skin microbiome opens new areas for treating dermatological conditions naturally. This potentially reduces the dependence on pharmaceutical treatments that may disrupt microbial ecosystems. This study celebrates the integration of tradition with innovation, demonstrating how natural ancient philosophies can be incorporated into modern science technologies. By establishing a relation between microbiome science and Ayurvedic practices, the research preserves traditional approaches while establishing a path for their incorporation into comprehensive health models. The study provides a clear example of how the integration of tradition and technology can transform healthcare through interdisciplinary research. It adds to the existing literature on microbiome management through dietary and lifestyle approaches, highlighting the importance of skin health and human well-being.

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