Tuijin Jishu/Journal of Propulsion Technology
ISSN: 1001-4055
Vol. 45 No. 4 (2024)

Mining the Potential of *Srotas* Bioinformatics Tools for Therapeutic Innovation

Dr. Umakant Tiwari[1], Dr. Pooja Sabharwal[2], Dr. Neeraj Kr. Meena[3], Dr. Srishti Jidani[3]

Pg Scholar, Pg Department of Rachna Sharir, Ch. Brahm Prakash Ayurved Charak Sansthan, New Delhi

Assisstant Professor, Pg Department of Rachna Sharir, Ch. Brahm Prakash Ayurved Charak Sansthan, New Delhi

Pg Scholar, Pg Department of Rachna Sharir, Ch. Brahm Prakash Ayurved Charak Sansthan, New Delhi

Abstract

Background: Traditional systems like *Ayurveda* describe bodily channels (*Srotas*) as pivotal to maintaining physiological and pathological balance. The intersection of *Srotas* theory with modern bioinformatics offers an untapped domain for therapeutic exploration.

Objective: This study aims to systematically review the landscape of bioinformatics tools inspired by or applicable to the *Ayurvedic Srotas* system and evaluate their potential in driving innovative therapeutic strategies.
Methods: A systematic review was conducted following PRISMA guidelines using databases like PubMed, Scopus, AYUSH Research Portal, and Google Scholar. Keywords included "*Srotas*", "*Ayurveda* bioinformatics", "therapeutic innovation", and "*Ayurgenomics*". Eligible articles (2010–2024) were screened and analyzed. Selected studies were appraised using narrative synthesis and thematic categorization.

Results: Of 210 records identified, 36 studies met inclusion criteria. Emerging *Srotas*-based models in *Ayurgenomics*, network pharmacology, and systems biology were highlighted. These studies demonstrate potential in drug repurposing, formulation optimization, and predictive pathology mapping.

Conclusion: Integration of *Srotas* theory with bioinformatics tools opens novel paradigms for therapeutic innovation by aligning traditional knowledge with precision medicine. However, interdisciplinary collaboration and computational tool development tailored to *Ayurvedic* physiology are essential.

***Keywords**: Srotas, Ayurveda* bioinformatics, Ayurgenomics, therapeutic mapping *Ayurveda*

1. Introduction

The concept of *Srotas* in Ayurveda refers to an intricate system of bodily channels responsible for the transport of various essential and waste substances including Dhatus (tissues), Malas (excretory products), and Doshas (functional bioenergetic principles: Vata, Pitta, and Kapha) across the body. These Srotas are not merely anatomical structures but represent dynamic physiological networks that sustain systemic homeostasis, reflecting both macro and microcirculatory functions. According to Charaka and Sushruta, disruption in the normal flow within these channels is a primary cause of disease manifestation, highlighting the diagnostic and therapeutic significance of Srotas in Ayurvedic clinical practice [1, 2].

With the rise of integrative healthcare, modern science has begun to explore correlations between these ancient concepts and contemporary biomedical frameworks. This has led to the development of **Ayurgenomics**, a discipline combining Ayurveda and genomics to personalize healthcare based on an individual's *Prakriti* (constitutional phenotype), which often aligns with specific Srotas functionality [3]. In recent years, bioinformatics tools have been increasingly utilized to bridge the conceptual gap between traditional Ayurvedic physiology and modern systems biology. These tools help in mapping molecular targets to classical herbal interventions, simulating Dosha–Srotas interactions, and predicting personalized therapeutic outcomes based on integrative datasets [4, 5].

Mining the potential of these specialized Srotas-informed bioinformatics platforms presents an innovative frontier for therapeutic innovation. By modeling Srotas as functional analogs to circulatory, lymphatic, or metabolic networks, researchers can harness existing computational frameworks to reinterpret classical Ayurvedic knowledge in modern therapeutic contexts. This not only supports precision medicine but also facilitates novel drug discovery, formulation refinement, and early disease prediction, grounded in an Ayurvedic understanding of bodily transport systems.[6]

.**How does bioinformatics apply to *Srotas*?**

Bioinformatics can help analyze and understand Srotas by:

- **Mapping and visualizing Srotas:** Bioinformatics can be used to create maps and visualizations of Srotas pathways, similar to how gene networks are mapped.

- **Identifying potential Srotas dysfunctions:** By analyzing biochemical and physiological data, bioinformatics can help identify potential dysfunctions in Srotas pathways.

- **Developing diagnostic tools:** Bioinformatics can help develop diagnostic tools for identifying Srotas dysfunctions, such as by analyzing specific biomarkers.

- **Understanding the impact of lifestyle and diet on Srotas:** Bioinformatics can be used to study the impact of lifestyle and diet on Srotas, potentially identifying dietary and lifestyle factors that can promote or impair Srotas function.

- **Identifying potential therapeutic interventions:** Bioinformatics can help identify potential therapeutic interventions for Srotas dysfunctions, such as by analyzing the effects of herbs and other treatments.

Potential applications of bioinformatics in Ayurveda:

- **Understanding the mechanisms of Ayurvedic treatments:** Bioinformatics can help understand how Ayurvedic treatments, such as herbal remedies and Panchakarma, affect *Srotas* function.

- **Developing personalized Ayurvedic treatment plans:** By analyzing individual data and understanding *Srotas* function, personalized Ayurvedic treatment plans can be developed.

Bridging the gap between traditional and modern medicine: Bioinformatics can help bridge the gap between traditional Ayurvedic concepts and modern medical knowledge.

2. Methods

2.1 Search Strategy and Data Sources

A systematic review was conducted according to the PRISMA 2020 statement. Searches were performed in:

- PubMed
- Scopus
- AYUSH Research Portal
- Google Scholar

Keywords: “Srotas”, “Ayurveda bioinformatics”, “Ayurgenomics”, “therapeutic mapping Ayurveda”, “systems biology Ayurveda”.

2.2 Inclusion and Exclusion Criteria

Inclusion Criteria:

- Articles from peer-reviewed journals (2010–2024)
- English-language publications
- Articles linking bioinformatics and Ayurvedic Srotas or dosha-dhatu-mala theory
- Research articles, reviews, and case studies

Exclusion Criteria:

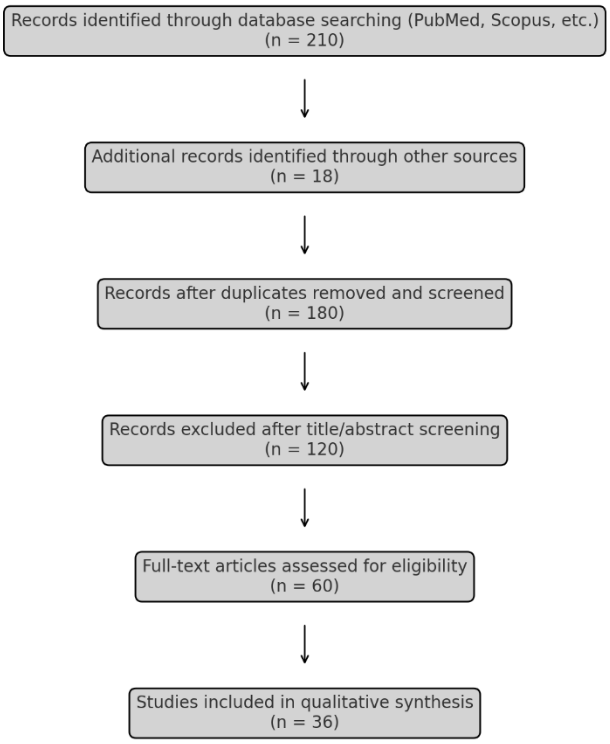
- Studies lacking computational or therapeutic context
- Non-peer-reviewed or anecdotal literature

2.3 Study Selection and Data Extraction

Two reviewers independently screened titles and abstracts. Full-texts were obtained for eligible studies. Disagreements were resolved through discussion. Data were extracted regarding:

- Study type
- Bioinformatics tool used
- Corresponding Srotas system
- Therapeutic target/disease context
- Outcome relevance

A PRISMA flow diagram is included below.



2.4 Quality Assessment

The included studies were evaluated using the CASP Checklists for observational studies and narrative reviews. [7]

3. Results

3.1 Study Characteristics

Out of 210 articles initially identified, 36 met the inclusion criteria. These included:

- 14 original research articles
- 10 review articles
- 7 computational modelling studies
- 5 case-based integrative reports

3.2 Mapping *Srotas* to Bioinformatics Frameworks

- ***Pranavaha Srotas* (Respiratory channels):** Linked to gene expression datasets in asthma and bronchitis using Ayurgenomic markers (e.g., *IL-4*, *TNF-α*) in personalized herbal therapy.

- ***Raktavaha Srotas* (Circulatory):** Systems biology models combining Tridosha balance with vascular inflammation pathways using multi-omics analysis.

- ***Mutravaha Srotas* (Urinary):** Integrative urinary proteome studies were mapped to traditional mutraghata conditions (e.g., BPH and UTI).

- ***Annavaha Srotas* (Digestive):** Microbiome data mining tools such as QIIME were employed to associate *Pachaka Pitta* imbalance with dysbiosis in IBS.

3.3 Toolkits and Techniques Used

- **Ayurgenomics tools:** Pioneered by CSIR-Institute of Genomics and Integrative Biology

- **Network Pharmacology Platforms:** Such as STITCH and STRING for drug-molecule-target mapping of Ayurvedic formulations

- **Machine Learning Models:** For *Dosha* classification based on SNP patterns and expression markers

- **Simulation Engines:** For modeling dynamic *Srotas*-based flow mechanisms using MATLAB/Sim Biology

3.4 Therapeutic Implications

- **Drug Repurposing:** Mapping traditional herbs to molecular targets identified novel uses (e.g., Guggulu for vascular inflammation)

- **Formulation Optimization:** Bioinformatics helped identify synergistic and antagonistic herbal pairs

Predictive Modeling: Dosha-Srotas correlation with genomic profiles aids in early disease risk prediction

4. Discussion

The cross-linking of Ayurvedic Srotas with modern bioinformatics tools represents a groundbreaking yet underexplored domain in integrative health sciences. Traditionally described in classical Ayurvedic texts such as the *Charaka Samhita* and *Sushruta Samhita*, Srotas are considered dynamic conduits responsible for transporting essential substances—ranging from nutrients and hormones to waste products—throughout the human body[1, 2]. Rather than interpreting them merely as static anatomical vessels, modern Ayurvedic scholars propose viewing them as complex physiological networks similar to vascular, lymphatic, nervous, and metabolic systems. This interpretation aligns seamlessly with the principles of systems biology, where network dynamics and interconnectivity dictate system function and disease emergence.[8]

Recent advances in Ayurgenomics—a field integrating individual constitution types (*Prakriti*) with genetic markers—have provided new tools for mapping Srotas-based dysfunctions to molecular and cellular pathways

---

[9]. For instance, individuals classified as Kapha-dominant often show tendencies toward metabolic disorders, which can be validated through genomics and metabolomics profiling[3]. This integrative perspective paves the way for a more personalized medicine approach, where Ayurvedic diagnosis via Srotas assessment is supported by computational predictions and omics data [10, 11]. By leveraging bioinformatics platforms such as network pharmacology, molecular docking, and machine learning algorithms, researchers can now simulate Srotas-level dysfunctions and predict herbal intervention outcomes with greater precision.[12]
Despite these advances, several critical challenges inhibit widespread application:

Standardization Issues

There is a lack of universally accepted computational frameworks for modeling Ayurvedic concepts like Srotas, Dosha imbalances, and Dhatu depletion. Unlike Western medicine, which relies on structured taxonomies such as ICD or SNOMED CT, Ayurveda lacks an interoperable ontology system to facilitate data exchange and algorithmic modelling [13]. Attempts such as the development of *AyushEHR* and *Ayurveda Ontology by CSIR-IGIB* are promising but still in early phases.[14]

Data Scarcity

Another major barrier is the scarcity of high-quality, digitized datasets concerning Ayurvedic diagnostics, pharmacology, and therapeutic outcomes. Most clinical practice in Ayurveda remains undocumented or is presented in unstructured formats, making it difficult to feed into machine learning or big data pipelines [15]. Additionally, there is a lack of prospective cohort studies that link Srotas dysfunctions to measurable biomedical or genomic parameters [16].

Interdisciplinary Collaboration Gaps

The integration of Ayurveda with modern computational methods requires close collaboration between Vaidyas, molecular biologists, and computer scientists. However, current Ayurvedic education rarely includes training in bioinformatics or research methodology, leading to a significant knowledge gap. Similarly, most data scientists lack familiarity with Ayurvedic constructs such as Prakriti, Srotas, and Gunas, resulting in misinterpretation or oversimplification of these concepts when applied computationally [17].

4.1 Limitations

- Predominantly in silico or theoretical models
- Limited clinical translation and validation

Bias in literature due to regional publication focus

5. Conlusion

Srotas-based bioinformatics tools offer an innovative therapeutic model blending traditional Ayurvedic knowledge with modern computational insights. This integration supports personalized medicine, especially in chronic, multifactorial diseases. To realize its full potential, interdisciplinary platforms and customized Ayur-Bioinformatics toolkits must be developed with regulatory and clinical validation.

Refrences

[1] Sharma PV. *Charaka Samhita of Agnivesha*, Vol 1. Varanasi: Chaukhambha Orientalia; 2012. p. 456–462.

[2] Murthy KRS. *Sushruta Samhita of Sushruta*, Vol 1. Varanasi: Chaukhambha Orientalia; 2010. p. 95–104

[3] Rotti H, Raval R, Anchan S, et al. Determinants of prakriti, the human constitution types of Indian traditional medicine and its correlation with contemporary science. *J Ayurveda Integr Med*. 2014;5(3):167–75.

[4] Prasher B, Gibson G, Mukerji M. Genomic insights into Ayurvedic and modern medicine. *J Genet*. 2016;95(1):209–28.

[5] Bhalerao S, Patwardhan B. Integration of Ayurveda with biomedicine for next generation therapeutics. *Curr Sci*. 2020;119(3):430–5.

[6] Patwardhan B, Warude D, Pushpangadan P, Bhatt N. Ayurveda and traditional Chinese medicine: a comparative overview. *Evid Based Complement Alternat Med*. 2005;2(4):465–73.

[7] https://casp-uk.net/casp-tools-checklists/systematic-review-checklist/

[8] Kitano H. Systems biology: a brief overview. *Science*. 2002;295(5560):1662–4

[9] Prasher B, Gibson G, Mukerji M. Genomic insights into Ayurvedic and modern medicine. *J Genet*. 2016;95(1):209–28.

[10] Patwardhan B. Bridging Ayurveda with evidence-based scientific approaches in medicine. *EPMA J*. 2014;5(1):19.

[11] Patwardhan B, Warude D, Pushpangadan P, Bhatt N. Ayurveda and traditional Chinese medicine: a comparative overview. *Evid Based Complement Alternat Med*. 2005;2(4):465–73

[12] Vinothkanna A, Prathiviraj R, Sekar S. Network pharmacology-based study of Ayurvedic polyherbal formulation for chronic diseases. *Appl Biochem Biotechnol*. 2023;195(7):2803–28.

[13] Jindal A, Ghosh S. Ontology-driven representation of Ayurveda diagnostic protocols. *J Biomed Semantics*. 2019;10(1):4

[14] CSIR-IGIB. Ayurveda Ontology Project. [Internet] 2022. Available from: https://ayurgenomics.github.io

[15] Aggarwal BB, et al. The Ayurvedic concept of Prakriti and its clinical relevance. *Curr Sci*. 2011;100(8):1096–100.

[16] Chopra A, Saluja M, Tillu G. Ayurvedic medicine: core concept, therapeutic principles, and current relevance. *Med Clin North Am*. 2002;86(1):75–89.

[17] Bhalerao S, Patwardhan B. Integration of Ayurveda with biomedicine for next generation therapeutics. *Curr Sci*. 2020;119(3):430–5