

INTERNATIONAL CONFERENCE ON
**INFORMATION SYSTEMS DESIGN
AND INTELLIGENT APPLICATIONS**
— (ICISDA-2026) —

ABSTRACT BOOK

Designing Intelligent Systems for a
Smarter, Sustainable and Inclusive Future

 24 – 25 August, 2026

 Patan, Gujarat, India



Organized by
Sarvasumana Association

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	2	ACS College of Engineering, Bengaluru, India
	3	Cebu Institute of Technology – University, Cebu City, Philippines

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Sarvasumanā Association

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WELCOME

It is my immense pleasure and privilege, on behalf of the **Sarvasumanā Association, Bengaluru**, to extend a warm and heartfelt welcome to all distinguished keynote speakers, researchers, academicians, industry professionals, innovators, scholars, and students to the **International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026)**.



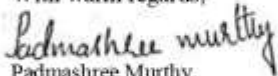
Sarvasumanā Association is a Scientific and Industrial Research Organization (SIRO) recognized by the Department of Scientific and Industrial Research (DSIR), Government of India, and is committed to promoting interdisciplinary research and innovation across science, technology, healthcare, and society. Guided by our vision of fostering knowledge for the betterment of humanity, we strive to create collaborative platforms where ideas transform into impactful solutions. This conference reflects our commitment to advancing cutting-edge research in intelligent systems, computational sciences, artificial intelligence, bioinformatics, data science, cybersecurity, digital healthcare, and emerging technologies through global academic collaboration.

ICISDA-2026 has been conceived as an international forum to bring together leading scientists, engineers, faculty members, research scholars, entrepreneurs, and policymakers to exchange pioneering ideas, present novel research findings, and discuss future directions in information systems and intelligent applications. I sincerely hope that the interactions during these two days will inspire new partnerships, research projects, publications, and technological innovations that contribute to sustainable development and global scientific progress.

I express my heartfelt gratitude to all organizing committee members, advisory board members, technical partners, reviewers, sponsors, collaborating institutions, and volunteers whose dedication and tireless efforts have made ICISDA-2026 possible. I also thank every participant for choosing this conference as a platform to share your valuable research and expertise.

I warmly welcome you to **Patan, Gujarat, India**, and wish you a memorable, intellectually stimulating, and rewarding conference experience. May ICISDA-2026 become a catalyst for new ideas, meaningful collaborations, and transformative innovations.

With warm regards,


Padmashree Murthy.

President
Sarvasumanā Association



"Advancing Knowledge • Inspiring Innovation • Empowering Society"

+91-9448685484
<https://sarvasumana.in>

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From Chairman's Desk

It gives me great pleasure to welcome all delegates, distinguished speakers, researchers, academicians, industry experts, and students to the **International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026)**.

The rapid evolution of intelligent systems, artificial intelligence, data science, bioinformatics, cybersecurity, cloud computing, and digital technologies has transformed the way we address scientific, industrial, and societal challenges. ICISDA-2026 has been envisioned as a global platform where experts from diverse disciplines can come together to exchange innovative ideas, present groundbreaking research, and build meaningful collaborations that will shape the future of intelligent information systems.

As **Conference Chairman**, I am delighted to witness the enthusiastic participation of researchers from India and across the world. The conference has been carefully designed to promote interdisciplinary research through keynote addresses, invited talks, technical paper presentations, workshops, poster sessions, and collaborative discussions. I am confident that these interactions will stimulate new research directions, foster academic excellence, and strengthen partnerships between universities, research organizations, industries, and policymakers.

I sincerely appreciate the efforts of the **Sarvasumanā Association**, the organizing committee, advisory committee, technical program committee, reviewers, collaborating institutions, and volunteers for their unwavering dedication in making this conference a reality. Their commitment to academic quality and professional excellence has laid the foundation for a vibrant and impactful scientific event.

I warmly welcome you to **Patan, Gujarat, India**, and wish you an enriching, productive, and memorable experience at **ICISDA-2026**.

With my best wishes for the grand success of the conference.



Dr. R. Somashekhar
Conference Chairman

**International Conference on Information Systems Design and Intelligent Applications
(ICISDA-2026)**

Vasishth Academy of Advanced Studies & Research [A unit of Sarvasumanā Association® [A DSIR registered SIRO]]

Regd. Office: #168 A, 1st cross, 1st Block, 3rd Phase, Banashankari 3rd stage, Bengaluru-560085, India.

Lab: # 30, 9th Cross, 1st Main, Srinidhi Layout, Churchghatta, 7th Phase, J.P.Nagar, Bengaluru-560062, India.

Website: <https://sarvasumanain.academy.html>; email: info@sarvasumanain.vasishthacademy20@gmail.com



ICISDA-2026

International Conference on Information Systems Design and Intelligent Applications - 24-25 August 2026

Message from the Organizing Secretary

Dear Colleagues, Researchers, and Delegates,

On behalf of the Organizing Committee, it is my privilege to welcome you to the International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026), organized by Sarvasmana Association, Bengaluru, in association with Hemchandracharya North Gujarat University, Patan, ACS College of Engineering, Bengaluru, and Cebu Institute of Technology - University, Cebu City, Philippines.

Theme: "Traditional Knowledge System – The Gen-Next Revolution"

ICISDA-2026 brings together researchers, academicians, and industry professionals on a common platform to explore how advanced technologies such as Artificial Intelligence, Information Systems, and Intelligent Systems can be meaningfully aligned with the principles of Indian Knowledge Systems. The conference encourages interdisciplinary dialogue across computer science, genomics, traditional science, and allied fields, with a shared emphasis on sustainable and ethically grounded innovation.

As Organizing Secretary, I have had the pleasure of coordinating the many moving parts of this conference – from paper submissions and review to logistics and delegate support – alongside a dedicated team of colleagues and volunteers. We have worked to ensure that every participant, whether presenting research or attending as a delegate, finds ICISDA-2026 a smooth, welcoming, and intellectually rewarding experience.

The conference will be held on **24-25 August 2026** at **Hemchandracharya North Gujarat University, Patan, Gujarat, India**, and will feature keynote addresses, paper presentations, and discussions spanning Information Systems Design, Artificial Intelligence, Computational Genomics, and Traditional Knowledge Systems.

I would like to thank our patrons, the Scientific Advisory Committee, co-organizers, and academic partners for their unstinting support, and our authors, speakers, and delegates for their valuable contributions. I look forward to welcoming you all to a productive and memorable ICISDA-2026.

With warm regards,

Dr. Kirthi Kakade
Organizing Secretary, ICISDA-2026



ICISDA-2026

International Conference on Information Systems Design and Intelligent Applications - 24-25 August 2026

Message from the Convener's Desk

Dear Colleagues, Researchers, and Delegates,

It gives me immense pleasure to welcome you to the International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026), jointly organized by Sarvasamana Association, Bengaluru, in association with Hemchandracharya North Gujarat University, Patan, ACS College of Engineering, Bengaluru, and Cebu Institute of Technology - University, Cebu City, Philippines.

Theme: "Traditional Knowledge System - The Gen-Next Revolution"

ICISDA-2026 has been envisioned as a meeting ground where the frontiers of Artificial Intelligence, Information Systems, and Intelligent Applications converge with the enduring wisdom of Indian Knowledge Systems. It invites researchers, academicians, and industry professionals to explore how contemporary computational thinking can draw upon, and breathe new life into, traditional and indigenous knowledge.

The conference is guided by three central objectives: to bring together interdisciplinary perspectives from biology, traditional science, and computational technology in addressing today's complex challenges; to deepen our understanding of large-scale biological data through computational genomics; and to build genuine, lasting bridges between modern and traditional sciences.

To be held on **24-25 August 2026** at **Hemchandracharya North Gujarat University, Patan, Gujarat, India**, the conference will bring together eminent speakers, scholars, and delegates from India and abroad for two days of scholarly exchange, discussion, and collaboration.

I extend my heartfelt gratitude to our patrons, co-organizers, the Scientific Advisory Committee, and all our academic partners for their continued support in shaping this event, and to our esteemed keynote speakers and delegates for choosing to be part of this journey.

I warmly invite you to participate, present your research, and contribute to this unique confluence of technology and tradition. I look forward to your active participation and to a memorable and enriching ICISDA-2026.

With warm regards,

Dr. Mamtaben Soni
Convener, ICISDA-2026

ICISDA

डॉ. आई. बालकृष्ण

संयुक्त निदेशक/वैज्ञानिक

Dr. I Balakrishna

Joint Director/Scientist



इलेक्ट्रॉनिक्स और सूचना प्रौद्योगिकी मंत्रालय
भारत सरकार

Ministry of Electronics and Information Technology
Government of India



Message

Date. 20th Aug 2026

It gives me immense pleasure to extend my warm greetings and best wishes to the **International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026)**.

In an era where **Artificial Intelligence, 5G, 6G, IoT, edge intelligence, and next-generation communication technologies** are reshaping our world, the convergence of technology with **Traditional Knowledge Systems** opens a remarkable pathway toward innovation with cultural roots. The wisdom preserved through generations offers a rich foundation for developing intelligent, sustainable, and socially meaningful technological solutions.

ICISDA-2026 provides a vibrant platform for researchers, academicians, innovators, and industry experts to share pioneering ideas, foster interdisciplinary collaborations, and explore the transformative potential of intelligent information systems. In particular, the integration of **5G/6G-enabled connectivity with AI-driven knowledge systems** can create new possibilities for digitally preserving, enriching, and responsibly disseminating traditional knowledge.

I am confident that the deliberations and scholarly contributions of this conference will inspire **new perspectives, meaningful collaborations, and impactful innovations** at the intersection of heritage and emerging technology.

I sincerely congratulate the organizing committee and all contributors for bringing together this distinguished academic forum. I wish **ICISDA-2026** every success in creating a lasting impact on research, innovation, and society.

With my warmest wishes for a memorable, inspiring, and intellectually enriching conference.

Dr. I BALAKRISHNA, SMIEEE & AP-S, SEMCEI, Life-IETE, ISE & MEMIC

Joint Director/Scientist (Group-A)

ASHOKA AWARDEE 2025, MHA, GoI

National Coordinator, Vidhya Shakti Program, GoI

Ex. CTO, Reliance Jio Pvt. Ltd, Mumbai

Syndicate Member, Anna University & University of Madras

Executive Member, R&D Center for IoT, Anna University

Ministry of Electronics and Information Technology (MeitY),

GOVERNMENT OF INDIA

E-mail: islavath32@gmail.com



CHAROTAR UNIVERSITY OF SCIENCE AND TECHNOLOGY (CHARUSAT)

P. D. Patel Institute of Applied Sciences

Education Campus, Changa – 388421

Ph: 02697 -247500,248133,248202, Fax :02697-247100

website: www.charusat.ac.in Email : gayatridave.bt@charusat.ac.in

MESSAGE

It gives me immense pleasure to extend my warm greetings and best wishes to the organisers, delegates, researchers, academicians and students participating in the International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026), being held at Hemchandracharya North Gujarat University, Patan.

The theme, "Traditional Knowledge System – The Gen-Next Revolution," is both timely and significant. Traditional knowledge represents a vast repository of observations, practices and wisdom developed through generations. The challenge before contemporary science is not merely to preserve this knowledge, but to understand, document, validate and transform it into new scientific possibilities through interdisciplinary approaches.

The convergence of traditional knowledge with information systems, computational biology, artificial intelligence, bioinformatics, systems biology and data-driven approaches offers an exciting pathway towards this transformation. In particular, network pharmacology provides an important framework for exploring the multi-component and multi-target nature of Ayurvedic therapeutics, while emerging technologies such as knowledge graphs, multi-omics and artificial intelligence can further strengthen evidence-based research in traditional medicine.

I believe that conferences such as ICISDA-2026 play a vital role in creating a platform where diverse disciplines can meet, exchange ideas and develop collaborative solutions for the future. The participation of young researchers and students is especially valuable, as they will carry forward the responsibility of connecting our rich traditional knowledge heritage with the scientific and technological possibilities of the next generation.

I congratulate the Sarvasumana Association and Hemchandracharya North Gujarat University for organising this important academic event and wish ICISDA-2026 great success. I hope the deliberations, discussions and collaborations emerging from this conference will contribute meaningfully to the advancement of knowledge and to a scientifically informed Gen-Next vision for traditional knowledge systems.

With my very best wishes for a stimulating, productive and memorable conference.

Dr. Gayatri Dave

Professor & Dean, Faculty of Sciences

P. D. Patel Institute of Applied Sciences (PDPIAS), CHARUSAT

Changa, Gujarat, India



Dr.ACS College of Engineering

(Approved by AICTE, New Delhi, Govt. of Karnataka & Affiliated to Visvesvaraya Technological University, Belgaum)

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It gives me immense pleasure to extend my warmest greetings on the occasion of the **International Conference on Information Systems Design and Intelligent Applications (ICISDA-2026)** and the release of its souvenir.

In an era defined by rapid technological shifts, research must transcend conventional boundaries. ICISDA-2026 stands out by connecting modern computational sciences—such as Artificial Intelligence, Big Data, and Computational Genomics—with the vast, time-tested wisdom of Indian Knowledge Systems (IKS). Bridging these domains opens powerful new pathways for ethical innovation, data-driven biology, and sustainable technology rooted in cultural heritage.

A conference souvenir is more than a commemorative volume; it captures key research insights, collaborative efforts, and the forward-looking vision of its participants. I commend the organizing team, conveners, and faculty for curating a forum that brings together researchers, academicians, and industry leaders to tackle complex global issues through interdisciplinary inquiry.

To all our delegates and researchers: I encourage you to leverage this platform to build cross-disciplinary partnerships, challenge existing paradigms, and translate your research into solutions with real-world impact.

I congratulate the conference committee on bringing this event to fruition and wish ICISDA-2026, along with its souvenir publication, every success.

DR T.Senthil kumaran

Dean (Research)

DR.ACS College of Engineering, Bengaluru

Campus

207, Kambipura, Mysore Road, Bengaluru - 560 074

Ph: 080 - 2974 8222, 2974 8333

E-mail: info@acsce.edu.in, principal@acsce.edu.in

www.acsce.edu.in

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3.	FROM TRADITIONAL WISDOM TO SYSTEMS PHARMACOLOGY: DECODING AYURVEDA THROUGH NETWORK BIOLOGY <i>Dr. Gayatri Dave</i>
4.	AI-ENABLED DRUG RESPONSE PREDICTION: ADVANCING PHARMACOGENOMICS TOWARD CLINICAL PRECISION MEDICINE <i>Assoc. Prof. Dr. Vasudevan Ramachandran</i>
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PLENARY TALKS

**5G/6G-ENABLED INTELLIGENT PLATFORMS FOR DIGITAL
PRESERVATION AND APPLICATIONS OF TRADITIONAL
KNOWLEDGE SYSTEMS**

Dr. I. Balakrishna,
SMIEEE & AP-S, SEMCEI, Life Member-IETE, ISE & MEMIC
Joint Director / Scientist (Group-A)
Electronic Design Center (R&D)
ASHOKA AWARDEE 2025, Ministry of Home Affairs, GoI
National Coordinator, Vidhya Shakti Program, GoI
Ex. CTO, Reliance Jio Pvt. Ltd, Mumbai
Syndicate Member, Anna University & University of Madras |
Executive Member, R&D Center for IoT, Anna University | Ministry of
Electronics and Information Technology (MeitY), GOVERNMENT OF
INDIA.

Traditional Knowledge Systems contain valuable knowledge related to healthcare, agriculture, biodiversity, and sustainable living. However, preserving and sharing this knowledge requires secure, intelligent, and connected digital platforms. This talk explores how 5G and emerging 6G technologies, together with AI, IoT, edge computing, and intelligent information systems, can enable real-time collection, transmission, processing, and preservation of traditional knowledge. The discussion will highlight opportunities for low-latency connectivity, intelligent sensing, edge-AI, and ubiquitous communication in developing smart applications for traditional knowledge, while considering security, privacy, cultural ownership, and ethical use. The talk aims to demonstrate how 5G/6G technologies can bridge traditional wisdom

with next-generation intelligent digital ecosystems. We can explore the very small and create descriptions of the mechanisms that operate at molecular and even at quantum states. But, how do these mechanisms create the conscious experience of the macro world in which we are consciously aware. We will look at some of the effects of epigenome on behaviour and emotional states and also at how our conscious awareness might be connected to activity at the quantum level. How do we sense an odour, how does the European robin find its way during migration and how do specific receptors in the hippocampus impact the chance of depression or suicide? These are not just in our head, they are in our being from the very small to the large, to the spiritual.

FROM TRADITIONAL WISDOM TO SYSTEMS PHARMACOLOGY: DECODING AYURVEDA THROUGH NETWORK BIOLOGY

Dr. Gayatri Dave

**Dean, Faculty of Science Professor, Department of Biological Sciences,
Charotar University of Science and Technology (CHARUSAT), Changa,
Gujarat.**

Ayurveda represents one of the world's oldest systems of knowledge-based healthcare and is characterized by a holistic understanding of health, disease and therapeutic intervention. Unlike the conventional reductionist paradigm of “one drug–one target,” Ayurvedic medicines frequently involve multiple herbs, diverse phytoconstituents and interconnected biological targets. This inherent complexity presents both a challenge and an opportunity for contemporary biomedical research. Network pharmacology provides a systems-level framework for investigating such multi-component, multi-target and multi-pathway therapeutic mechanisms by integrating pharmacology, systems biology, bioinformatics and computational biology.

This keynote will explore the potential of network pharmacology as a bridge between traditional Ayurvedic knowledge and next-generation biomedical science. Using medicinal plants and formulations, including *Ocimum tenuiflorum* (Tulsi), as illustrative examples, the presentation will demonstrate how phytochemical profiling, target prediction, protein–protein interaction networks, pathway enrichment, molecular docking and molecular dynamics can be integrated to generate mechanistic hypotheses. Particular emphasis will be placed on the transition from computational prediction to experimental validation and on the limitations associated with incomplete databases, chemical variability, bioavailability, metabolite-mediated effects and formulation complexity.

Keywords: one-drug-one target, network pharmacology, system biology, computational biology

AI-ENABLED DRUG RESPONSE PREDICTION: ADVANCING PHARMACOGENOMICS TOWARD CLINICAL PRECISION MEDICINE

Assoc. Professor Dr. Vasudevan Ramachandran

Faculty of Health Sciences, MAIWP International University, 68100
Kuala Lumpur, Malaysia.

Precision medicine seeks to improve therapeutic outcomes by considering individual variations in genetic, environmental, and clinical factors. Despite notable progress in pharmacogenomics, predicting drug responses for individual patients remains a significant challenge due to the complex interactions among genomic variants, biological pathways, and treatment protocols. Recent advancements in artificial intelligence (AI) offer promising opportunities to address these challenges by enabling the integration and analysis of extensive multidimensional biomedical data. The impact of AI-driven methods on enhancing drug response prediction and facilitating the application of pharmacogenomic insights in clinical settings is being highlighted here. Techniques such as machine learning and deep learning are increasingly employed to analyze genomic, transcriptomic, proteomic, and electronic health record data, with the aim of identifying patterns associated with therapeutic effectiveness, adverse drug reactions, and personalized drug dosing requirements. By leveraging these diverse datasets, AI models can uncover complex relationships that may be overlooked by traditional statistical approaches. The findings indicate that AI-powered pharmacogenomic systems have the potential to enhance predictive accuracy, improve patient stratification, and support more informed treatment decisions. Furthermore, these methods could help reduce trial-and-error prescribing, decrease drug toxicity, and improve overall health outcomes. However, challenges related to data quality, model interpretability, algorithmic bias, privacy protection, and clinical validation continue to impede the widespread adoption of these technologies. Addressing these challenges will require collaborative efforts among clinicians, data scientists, geneticists, and policymakers. In conclusion, AI-driven drug response prediction represents a transformative approach for pharmacogenomics, paving the way for

more personalized, effective, and equitable healthcare while accelerating the advancement of precision medicine.

Keywords: Artificial Intelligence (AI); Pharmacogenomics; Drug Response Prediction; Precision Medicine

ICSDA-2026

INTELLIGENT INFORMATION SYSTEMS FOR INTEGRATING KNOWLEDGE SYSTEMS WITH MODERN MICROBIOLOGY, BIOTECHNOLOGY, BIOINFORMATICS AND ONE HEALTH

Professor Dr. Noura Karamalla Mohamed Salih
One Health Epidemiology, Faculty of Veterinary Medicine,
University of Bahri-Sudan

The convergence of Intelligent Information Systems (IIS), artificial intelligence, bioinformatics, biotechnology, and traditional knowledge is creating new opportunities for addressing complex challenges in health, agriculture, food security, environmental sustainability, and societal well-being. The Knowledge System, developed through centuries of empirical observation and knowledge transmission, represents a valuable source of information that can complement contemporary scientific approaches when systematically documented, validated, and integrated with modern information technologies.

This keynote will explore the potential of intelligent information systems to capture, organize, analyze, and transform traditional knowledge into scientifically accessible and actionable knowledge resources. Particular emphasis will be placed on the integration of knowledge system with biotechnology, molecular biology, microbiology, bioinformatics, and One Health approaches. Modern computational tools, knowledge graphs, artificial intelligence, machine learning, and bioinformatics can facilitate the identification of relationships between traditional biological resources, medicinal plants, microorganisms, bioactive compounds, ecological systems, and human and animal health. A key focus will be the development of interdisciplinary frameworks that connect traditional knowledge with evidence-based scientific validation while respecting cultural heritage, intellectual property, ethical considerations, and knowledge ownership. Such systems can support the discovery of novel bioactive molecules, sustainable biotechnological applications, microbial resources, natural products, and environmentally responsible solutions.

The keynote will further highlight the importance of developing intelligent, interoperable, and ethically governed knowledge systems that bridge traditional wisdom and contemporary science. By bringing

together KS scholars, biologists, computational scientists, biotechnology researchers, and information-system specialists, we can create knowledge ecosystems capable of supporting innovation while preserving cultural heritage.

Ultimately, the integration of Knowledge Systems with intelligent information technologies offers a powerful pathway toward evidence-based innovation, sustainable development, and a holistic One Health future, demonstrating how ancient knowledge and emerging technologies can work together to address the scientific and societal challenges of the twenty-first century.

From Traditional Knowledge to Intelligent Scientific Innovation

1. Knowledge System (KS)

Traditional knowledge and practices

↓

Medicinal plants • Microorganisms • Food systems • Agriculture •
Environmental knowledge • Traditional health practices

2. Knowledge Digitalization

↓

Documentation • Databases • Ontologies • Knowledge graphs • Data
standardization

3. Intelligent Information Systems

↓

Artificial Intelligence • Machine Learning • Natural Language
Processing • Knowledge Graphs • Predictive Analytics

4. Scientific Validation



Microbiology • Molecular Biology • Genomics • Metagenomics • Bioinformatics
• Experimental validation

5. Biotechnology & Innovation



Bioactive compounds • Novel enzymes • Antimicrobials • Functional foods •
Microbial biotechnology • Sustainable agriculture • Environmental biotechnology

6. One Health Integration



Human Health + Animal Health + Environmental Health

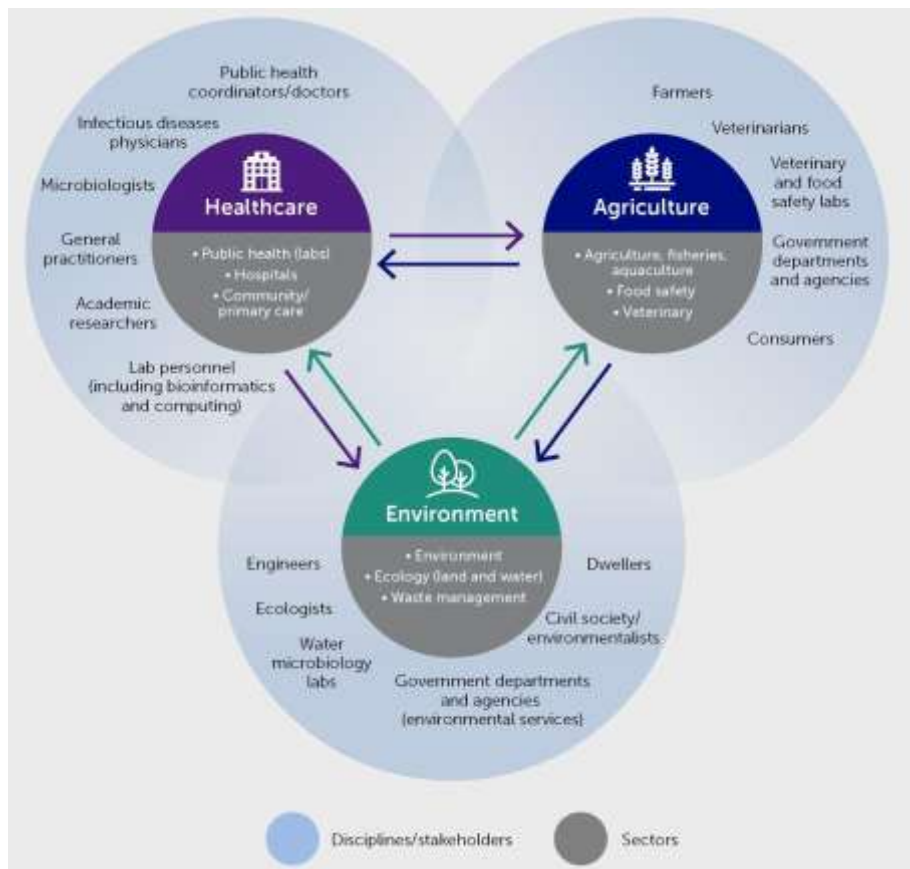
An intelligent system should not simply *store* traditional knowledge. It should help researchers move from:

Traditional claim → Biological hypothesis → Computational analysis → Laboratory validation → Biotechnology application → One Health impact

For example:

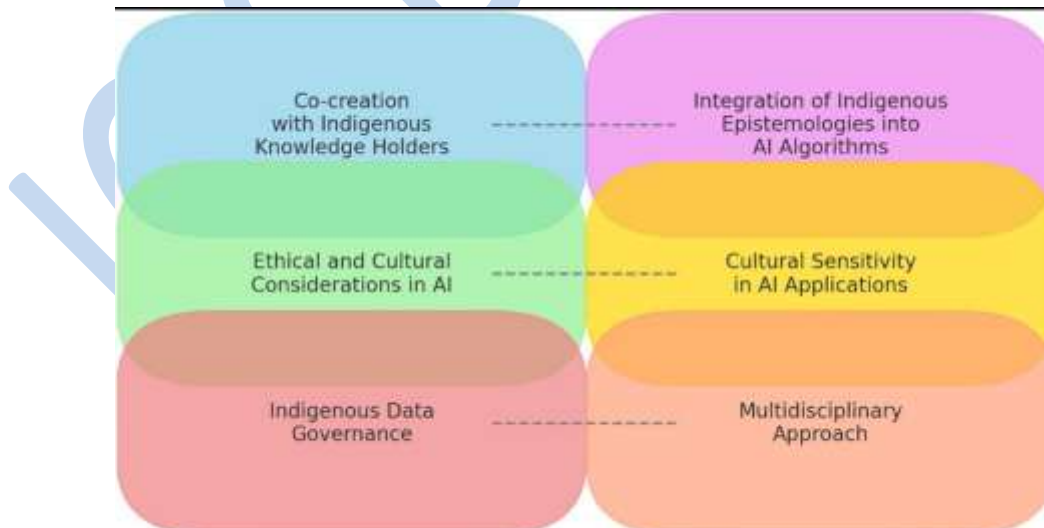
Traditional medicinal plant

- Digital knowledge record
- AI identifies potential bioactive molecules
- Bioinformatics predicts molecular targets
- Microbiological/molecular experiments validate activity
- Biotechnology develops the application
- One Health evaluates effects on humans, animals and the environment.



7. Sustainable & Evidence-Based Innovation

- New scientific discoveries
- Preservation of traditional knowledge
- Sustainable development
- Ethical and responsible innovation



The Central Message

The objective is not to replace traditional knowledge with modern science, but to create intelligent systems that preserve, organize, scientifically validate, and transform valuable traditional knowledge into evidence-based innovation.

CARBON QUANTUM DOTS (CQDS): BRIDGING GREEN CHEMISTRY, INTELLIGENT SENSING, AND SUSTAINABLE TECHNOLOGIES FOR THE GEN-NEXT REVOLUTION

Dr. Kokilaben Parmar, HOD, Department of Chemistry, Hemchandracharya North Gujarat University, Patan

Carbon Quantum Dots (CQDs) are emerging as promising nanomaterials with unique optical, electronic, and surface properties, offering significant potential for sustainable technologies. This talk explores the green synthesis of CQDs from renewable resources such as medicinal plants, agricultural waste, and biomass, providing environmentally friendly alternatives to conventional chemical methods.

The discussion will focus on their applications in intelligent sensing, environmental monitoring, bioimaging, photocatalysis, antimicrobial technologies, energy conversion, and hydrogen production. Integration of CQDs with artificial intelligence, IoT, and portable sensing platforms can enable smart, real-time, and low-cost solutions for environmental and biomedical challenges.

The talk will also address key challenges such as scalability, reproducibility, toxicity, and long-term stability, while highlighting future opportunities for developing multifunctional CQD-based technologies for a greener and smarter future.

Keywords: Carbon Quantum Dots, Green Chemistry, Green Synthesis, Intelligent Sensing, Nanotechnology, Sustainable Technology, AI, IoT.

PRESENTATION

ABSTRACTS

INTEGRATING BLOCKCHAIN AND INTELLIGENT SYSTEMS: A COHESIVE FRAMEWORK FOR CONTEMPORARY BANKING

Trivedi Darshankumar Sureshbhai and Kiritkumar I. Chokhawala
Hemchandracharya North Gujarat University, Patan

The fusion of blockchain technology and artificial intelligence (AI) is profoundly reshaping digital banking, enabling more intelligent, secure, and instantaneous decision-making. As financial institutions transition from outdated legacy systems to agile, data-centric platforms, the demand for robust real-time business intelligence (BI) has become increasingly urgent. Conventional BI solutions, however, often fall short due to fragmented data silos, sluggish processing pipelines, and limited transparency. In contrast, blockchain provides a decentralized, immutable ledger that guarantees exceptional data integrity, traceability, and auditability. When paired with AI's powerful analytical capabilities—such as predictive modeling, anomaly detection, and natural language processing—this combination unlocks transformative potential. The present study explores this promising synergy, proposing a multi-layered architectural framework for real-time BI within digital banking environments. At its foundation, the blockchain layer securely captures, validates, and stores transactional and behavioral data. Layered atop this trustworthy infrastructure, AI modules dynamically analyze the information to generate actionable insights in real time. The framework incorporates supervised learning techniques, including XG Boost and LSTM networks, for tasks such as fraud detection and customer segmentation. Smart contracts automate compliance processes and trigger rule-based alerts, while explainable AI methods like SHAP and LIME ensure transparency, interpretability, and regulatory adherence. Empirical results demonstrate substantial improvements: fraud detection accuracy reaching 96%, near-instantaneous generation of insights with negligible latency, and markedly enhanced stakeholder trust through blockchain's verifiable audit trails. Practical case studies in customer behavior analytics, transaction monitoring, and credit scoring further illustrate how this integrated approach significantly outperforms traditional data infrastructures. The study also candidly addresses key implementation challenges, including interoperability issues, data privacy concerns, computational overhead, and evolving regulatory requirements. Overall, this research contributes a practical, scalable, and ethically grounded blueprint to the ongoing conversation on financial digital transformation—offering a forward-looking model that harnesses the complementary strengths of blockchain and AI to deliver trustworthy, real-time intelligence in next-generation banking systems.

Keywords - Blockchain, Artificial Intelligence, Real-time Business Intelligence, Digital Banking Smart Contracts, Explainable AI, Fraud Detection, Predictive Analytics, Data Security Distributed Ledger Technology (DLT).

**IDENTIFICATION OF SINGLE NUCLEOTIDE POLYMORPHISMS (SNPS)
ASSOCIATED WITH FRUIT SWEETNESS IN DRAGON FRUIT (*HYLOCEREUS*
SPP.)**

Vedaanshi Verma and Preenon Bagchi

School of Life and Basic Sciences, Jaipur National University, Jaipur

Dragon fruit (*Hylocereus* spp.) is an economically important tropical fruit crop whose market value and consumer acceptance are largely determined by fruit sweetness. Understanding the genetic factors associated with sweetness is essential for the development of superior cultivars with improved fruit quality. This study aims to identify Single Nucleotide Polymorphisms (SNPs) associated with fruit sweetness using publicly available next-generation sequencing (NGS) datasets. SNPs were identified through a comprehensive bioinformatics pipeline involving sequence quality assessment, reference genome alignment, variant calling, and functional annotation. The identified SNPs were analyzed to detect genetic variants potentially associated with sweetness-related genes and fruit quality traits. The analysis revealed several candidate SNPs that may contribute to variation in fruit sweetness, providing insights into the genetic mechanisms underlying taste in dragon fruit. The SNP markers identified in this study represent valuable genomic resources for molecular breeding, marker-assisted selection, and the development of sweeter dragon fruit cultivars. This work demonstrates the effectiveness of SNP-based genomic analysis in identifying genetic variants associated with fruit sweetness and provides a foundation for future genetic improvement of dragon fruit.

Keywords: Dragon fruit (*Hylocereus* spp.), Single Nucleotide Polymorphism (SNP), Fruit Sweetness, Whole Genome Sequencing, Variant Calling, Bioinformatics, Genetic Variation

TKS-NGSF: Traditional Knowledge System-Enhanced Neural-Guided Strategy Fusion for Blockchain-Enabled Searchable Encryption in Ayurveda-Informed IIoT Healthcare

Patel Kalpeshkumar Laxmanbhai, Ruchika Dungarani, HardikKumar Bakorbhai Prajapati, Patel Maulikkumar Nareshbha, Patel Dharmikkumar Himmatbhai Swarnnim Startup and Innovation University, Gandhinagar, Gujarat

Abstract—Indian Traditional Knowledge Systems (TKS), and Ayurveda in particular, offer a unique opportunity for personalized and culturally appropriate healthcare when combined with modern digital health technologies. However, digitizing Ayurvedic knowledge introduces serious privacy, security, and operational challenges in Internet-connected healthcare environments. This paper presents TKS-NGSF, a framework that integrates Indian Traditional Knowledge Systems with blockchain-enabled searchable encryption and neural-guided strategy selection for the Industrial Internet of Medical Things (IIoT). TKS-NGSF extends the four-strategy Neural-Guided Strategy Fusion (NGSF) with a fifth strategy, S5 (TKS-Enhanced Ayurvedic Knowledge Retrieval), which provides improved handling of traditional-medicine queries. The framework integrates the IMPPAT (Indian Medicinal Plants, Phytochemistry And Therapeutics) database, supports federated learning for cross-institutional data protection, and employs post-quantum and attribute-based cryptography for enhanced security. Unlike prior simulation-only studies, all detection results are computed on five datasets spanning modern and traditional medical data: Synthetic IoT, the MIMIC-III Clinical Database, CICIoMT2024 IoMT attack traffic, the CERT v6.2 insider-threat corpus, and IMPPAT-TKS Ayurvedic phytochemical data. TKS-NGSF attains an F1-score between 0.99 and 1.00 across all datasets, including a perfect 1.00 on Ayurvedic (TKS) queries, while reducing median search latency below 175 ms and lowering blockchain gas cost by 41.1% relative to a post-quantum baseline, with only 8.4 ms of neural strategy-selection overhead. These results indicate that a learned, culturally-aware strategy selector is effective for secure, auditable, and quantum-resistant healthcare data sharing.

Keywords: Traditional Knowledge Systems, searchable encryption, Ayurveda, IIoT healthcare, blockchain, federated learning, post-quantum cryptography, neural strategy selection, IMPPAT database.

AN AI-DRIVEN ADAPTIVE USER EXPERIENCE FRAMEWORK FOR INTELLIGENT MEDITATION INFORMATION SYSTEMS INTEGRATING INDIAN KNOWLEDGE SYSTEMS

Hinal Prajapati and Nehaben Thakkar
Department of Computer & Information Technology,
HNGU, Patan, Gujarat, India

In today life, because of changing lifestyles, increasing work pressure, and continuous digital engagement, significant global concerns are Mental health disorders, stress, anxiety, and emotional well-being. Many digital meditation applications are available to support above mentioned problem but most existing systems provide generalized recommendations with static user interfaces and limited personalization and they do not integrate Artificial Intelligence (AI), Adaptive User Experience (Adaptive UX), Human–Computer Interaction (HCI), and Indian Knowledge Systems (IKS). Not having above mentioned features, it reduces user engagement and the long-term adoption of digital wellness applications.

To address these challenges, this proposed model - AI-Driven Adaptive User Experience Framework for Intelligent Meditation Information Systems Integrating Indian Knowledge Systems (IKS) is designed. The proposed framework includes behavioural monitoring, AI-driven analytics, adaptive interface design and traditional Indian wellness practices to deliver personalized and culturally relevant meditation experiences. The architecture consists of four interconnected layers: User Layer, AI Business Logic Layer, Personalized Recommendation Layer, and Feedback & Continuous Learning Layer. The User Layer captures profile information and behavioural data, including meditation history, login frequency, session duration, mood assessments, stress levels, and user preferences. By analyzing user behavior, the AI logic layer successfully forecasts wellness requirements. This tracking allows the system to support flexible, adaptive decision-making.

The Adaptive UX Engine changes interface components based on how users behave and what they need. At the same time, the Indian Knowledge Systems Repository provides traditional wellness insights from Yoga, Dhyana, Pranayama, the Bhagavad Gita, Patanjali Yoga Sutras, and Ayurveda. Using these inputs, the Recommendation Layer creates custom meditation sessions, breathing exercises, and tailored layouts.

Finally, a Feedback Layer uses tracking data and user reviews to constantly improve these suggestions.

This framework improves smart information systems by mixing modern AI with traditional Indian wellness concepts under a user-friendly design. Unlike common meditation apps that only provide static content, our setup focuses on active interactions, continuous behavior learning, and cultural practices.

In conclusion, this framework helps build smart wellness apps that focus on user engagement and mental health. It bridges modern digital healthcare with traditional Indian Knowledge Systems. Future work will focus on implementing the framework as an Android-based mobile application and evaluating its effectiveness through usability studies, recommendation accuracy, user satisfaction, and mental wellness outcomes.

Keywords: Artificial Intelligence (AI); Adaptive User Experience (Adaptive UX); Human–Computer Interaction (HCI); Intelligent Information System; Meditation Information System; Indian Knowledge Systems (IKS); Behavioural Analytics; Personalized Recommendation; Digital Healthcare; Mental Well-being.

GRAPHENE-BASED ELEMENT-DOPED CARBON QUANTUM DOTS FOR MULTIFUNCTIONAL APPLICATIONS IN POLYMER NANOCOMPOSITES

Patel Jinal Rajeshbhai

**Shri U.P. Arts, Smt.M.G. Panchal Science & Shri V.L. Shah Commerce College,
Pilvai**

Polymer nanocomposites reinforced with element-doped carbon quantum dots (CQDs) and graphene quantum dots (GQDs) have emerged as an advanced class of multifunctional materials because of their tunable physicochemical and electronic properties. The presence of heteroatoms, such as nitrogen, sulfur, phosphorus and transition metals in CQDs/GQDs, can significantly alter the band structure, surface chemistry and defect states, leading to enhanced photoluminescence, improved charge transport and superior catalytic activity. Embedded in polymer matrices, such as conducting polymers, biodegradable polymers and thermoplastic polymers, these engineered nanodots yield hybrid systems with remarkable enhancements in optical transparency, electrical conductivity, thermal stability and mechanical strength. Crucial for the overall performance of these nanocomposites is the synergistic coupling between doped quantum dots and polymer chains. This review provides a comprehensive overview of synthesis strategies, doping mechanisms and fabrication techniques of CQDs/GQDs based polymer nanocomposites with a special emphasis on the structure property relationships and interface engineering. Moreover, the multifunctional applications of these materials have been critically reviewed including their use in high-performance sensing platforms, energy storage and conversion devices such as supercapacitors and solar cells, and biomedical applications such as bioimaging, drug delivery, and biosensing. Environmental applications such as pollutant detection and degradation are also highlighted. The important potential challenges including scalability, long-term stability, and toxicity are addressed. Future perspectives related to sustainable synthesis, advanced hybrid systems and AI-driven material design for next-generation applications are discussed.

Keywords:

Carbon Quantum Dots (CQDs), Graphene Quantum Dots (GQDs), Polymer Nanocomposites, Elemental Doping, Optoelectronics, Nanotechnology.

ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING FOR HEART DISEASE RISK ASSESSMENT: A SYSTEMATIC REVIEW AND THE CASE FOR AN EXPLAINABLE CLINICAL DECISION SUPPORT SYSTEM

Hiteshkumar Vora and Jignesh Patel

Hemchandrachary North Gujarat University, Patan

Cardiovascular disease continues to be the single largest cause of death worldwide, and despite steady advances in medical treatment, it still claims millions of lives every year. Artificial intelligence (AI), machine learning (ML), and deep learning (DL) have opened new possibilities for detecting cardiac risk earlier and more precisely than conventional methods allow. This paper presents a systematic review of 55 peer-reviewed studies published between 2014 and 2026 that apply AI and ML techniques to the assessment of heart disease risk. Following the PRISMA reporting framework and drawing primarily on the Scopus and Web of Science databases, the review examines how well different models classify risk, how features are selected, how interpretable the resulting models are, how ready they are for clinical use, and what kinds of data underpin them. A bibliometric analysis complements the narrative review by tracing publication trends, the concentration of particular methods, and the geographic spread of research output. The central finding is that most existing models depend on fewer than fifteen clinical variables and rarely bring together structured data, free-text clinical notes, lifestyle information, and laboratory results within a single interpretable system suited to bedside use. In response to this gap, the paper sets out a proposed Clinical Decision Support System (CDSS) that draws on more than twenty variables, blends ensemble and deep learning architectures, and embeds explainability tools such as SHAP and LIME to support physician trust and transparent decision-making. Taken together, the findings make the case for a new generation of cardiac risk tools that are broader in scope, easier to interpret, and more workable in everyday clinical practice.

Keywords: clinical decision support system, heart disease prediction, machine learning, deep learning, natural language processing, electronic health records, cardiovascular risk, explainable AI, systematic literature review

TOWARDS GENERALIZABLE DIABETIC RETINOPATHY GRADING: A MULTI-DATASET CROSS-VALIDATION STUDY USING HYBRID DEEP LEARNING ACROSS APTOS, IDRID, MESSIDOR, AND EYEPACS

Dhumal Surekha Vitthalrao and Mayur Jakhete

Pimpri Chinchwad University Mohitewadi, Pune, Maharashtra, India

A persistent and largely unacknowledged weakness in deep learning-based diabetic retinopathy (DR) grading is the near-universal practice of training and evaluating models on a single benchmark dataset. This creates a dangerous illusion of clinical readiness: a model achieving 99% accuracy on EyePACS may fail substantially when presented with images from an Indian ophthalmology clinic captured under different lighting, on a different camera, with a different patient demographic. This paper directly addresses this generalisation gap by proposing and investigating a hybrid EfficientNet-B4 and Swin Transformer model evaluated under rigorous five-fold cross-validation across four major benchmark datasets: APTOS 2019, IDRiD, Messidor-2, and EyePACS. We systematically analyse the sources of performance variation across these datasets — including domain shift due to imaging device differences, label shift due to differing grading protocols, and prior shift due to class frequency variation — and introduce a domain-agnostic preprocessing pipeline with contrast-limited adaptive histogram equalisation (CLAHE) and standardised resizing to mitigate these effects. We also integrate Grad-CAM++ for cross-dataset explainability analysis. Our experiments demonstrate that models trained and validated on merged multi-dataset splits consistently outperform single-dataset counterparts on unseen clinical data, with average accuracy improvements of 4.2–7.8% on cross-dataset test splits. These findings establish multi-dataset validation as a necessary standard for clinically trustworthy DR grading research.

Keywords—Diabetic Retinopathy, multi-dataset validation, domain generalisation, EfficientNet, Swin Transformer, cross-validation, APTOS, IDRiD, Messidor, EyePACS, domain shift, fundus image analysis, explainable AI

FINITE ELEMENT ANALYSIS AND MODAL CHARACTERISATION OF A TITANIUM 3D-PRINTED SINGLE-AXIS ACCELEROMETER FOR HIGH-G SHOCK APPLICATIONS USING COMSOL MULTIPHYSICS

Maanik Arora and Sukhdeep Singh Dhami

**Department of Mechanical Engineering, National Institute of Technical Teachers
Training & Research, Chandigarh, India**

As technology rapidly advances, there is increasing need for high performance inertial sensing systems that can withstand high shock and vibration conditions, hence alternative materials and fabrication methods to silicon-based MEMS are of interest. The finite element analysis and modal characterisation of a single-axis accelerometer fabricated using 3D printing technology from Titanium (Ti) are presented in this study, with the aim of utilising the accelerometer for high-g sensing applications. The proposed sensor features folded-beam suspension springs and anchor structures around a proof-mass at the center of the sensor die footprint ($2.5 \times 2.5 \text{ mm}^2$). Through Finite Element simulation, which is done in COMSOL Multiphysics v6.3 with Solid Mechanics module, the eigenfrequency analysis is used. A free tetrahedral mesh with 6,132 elements covering the geometry was created to ensure the accuracy of the numerical results. Mesh convergence was checked. A total of 6 modes of structural vibration were obtained, and the most significant was found at 12,001 Hz. The mode shape corresponding to the desired sensing direction had dominant translational motion of the proof-mass along that direction and the higher order modes were well separated so as to reduce modal interference during operation. The theoretical mechanical sensitivity was evaluated to be about 1.725nm/g by the analytical sensitivity evaluation based on the lumped spring–mass model. It was found that when the acceleration was applied to the proof-mass, the predicted proof-mass displacement increased linearly with applied acceleration, up to about 1.725 μm at 1000 g and 17.25 μm at 10,000 g. The result shows that the proposed titanium accelerometer has good dynamics performance for high-g applications and has good mechanical strength compared with the traditional silicon structure, and has the advantages of superior mechanical strength of titanium. The study sets out an inertial sensor design framework based on simulation for additively manufactured inertial sensors and lays the groundwork for future fabrication and experimental validation and optimisation of metallic inertial sensors for aerospace, defence and industrial monitoring applications.

Keywords: MEMS accelerometer, titanium, additive manufacturing, COMSOL Multiphysics, modal analysis, high-g sensing, finite element analysis, inertial sensor

COMPARATIVE IN SILICO ANALYSIS OF ANTHOCYANIN BIOSYNTHETIC ENZYMES REVEALS EVOLUTIONARY CONSERVATION AND FUNCTIONAL DIVERSITY AMONG ORYZA SPECIES

Shravani R, Swathi B, Dhanalakshmi G*

**Department of Biochemistry, Padmashree Institute of Management and Sciences,
Bangalore 560060, Karnataka, India.**

Corresponding author: dhanu.bio@gmail.com

Anthocyanins are important flavonoid pigments that contribute to plant coloration, stress tolerance, and nutritional value. This study comparatively analyzed three key anthocyanin biosynthetic genes—Leucoanthocyanidin dioxygenase 1 (LOD1/ANS), glycosyl transferase, and malonyl transferase—among *Oryza sativa* N22, *O. nivara*, *O. rufipogon*, and *O. punctata*. Multiple sequence alignment and phylogenetic analysis revealed that glycosyl transferase was the most conserved gene (92.08–100% identity), whereas malonyl transferase exhibited the greatest sequence divergence (56.48–95.25%). Physicochemical characterization showed that LOD1 and glycosyl transferase proteins were generally stable and hydrophilic, while malonyl transferase displayed greater variability in stability and isoelectric point. Subcellular localization predicted cytoplasmic localization for LOD1 and malonyl transferase and chloroplast localization for glycosyl transferase across all species. KEGG pathway analysis confirmed the sequential roles of these enzymes in anthocyanin biosynthesis, pigment stabilization, and diversification. The findings demonstrate strong evolutionary conservation of core biosynthetic enzymes and greater diversification of terminal modification enzymes among *Oryza* species.

Keywords: *Oryza Sativa*, anthocyanin biosynthesis, LOD1, glycosyl transferase, malonyl transferase, phylogenetic analysis.

COMPUTATIONAL EVALUATION OF THE ANTI-OBESITY POTENTIAL OF PHYTOCHEMICALS ISOLATED FROM MILLETS USING MOLECULAR DOCKING

Aishwarya G T, Nidhi Shree B, Sneha N, Dhanalakshmi G*

Department of Biochemistry, Padmashree Institute of Management and Sciences,
Bangalore 560060, Karnataka, India.

Corresponding author: dhanu.bio@gmail.com

Kodo millet (*Paspalum scrobiculatum* L.) is a rich source of bioactive phytochemicals with potential anti-obesity and antihypercholesterolemic properties. LC–MS/MS analysis identified major phenolic acids and flavonoids, including hydroxybenzoic acid, ferulic acid, luteolin, apigenin, quercetin, and glycosylated flavones. Lipinski's Rule of Five, ADME properties calculate using SwissADME. Docking analysis was carry out against pancreatic triacylglycerol lipase (PTL) and HMG-CoA reductase using CB-Dock2, with photochemicals of kodo millets Atorvastatin and Orlistat used as positive controls. Apigenin exhibited the strongest binding affinity toward PTL (–9.3 kcal/mol), compared with the Orlistat (–5.7 kcal/mol) it indicate that the compound showed good anti lipase activity, while luteolin showed the highest affinity for HMG-CoA reductase (–9.7 kcal/mol), exceeding Atorvastatin (–8.2 kcal/mol), this speculated that it has excellent anticholesterol controlling capacity. The strong hydrogen-bonding and hydrophobic interactions observed suggest stable ligand–protein complexes. These findings indicate that Kodo millet phytochemicals possess significant potential to regulate lipid metabolism and may provide as promising functional food ingredients or nutraceutical candidates for the management of obesity and hypercholesterolemia. Further in vivo and clinical validation is crucial to establish the formulation of anti obesity drug.

Keywords: Kodo millet (*Paspalum scrobiculatum* L.); Phytochemicals; Functional food; Molecular docking; Hypercholesterolemia; Nutraceuticals.

SUSTAINABLE SYNTHESIS OF BIOCOMPATIBLE HETEROATOM-DOPED CARBON QUANTUM DOTS FROM BIOMASS WASTE FOR BIOMEDICAL AND ENVIRONMENTAL APPLICATIONS

Prajapati Apekshaben Sharadkumar
Department Of Chemistry, Hngu Patan

The increasing demand of sustainable nanomaterials has driven the development of eco-friendly methods for synthesis of carbon quantum dots (CQDs). Heteroatom-doped carbon quantum dots (CQDs) derived from biomass waste have been emerged as promising nanomaterials due to their excellent biocompatibility, low toxicity, tunable fluorescence, chemical stability and the environment friendly nature. This review focuses on the sustainable fabrication of biocompatible heteroatom-doped CQDs from renewable biomass waste such as agricultural residues, fruit peels, food waste, lignocellulosic biomass, algae and other natural carbon sources. The advantages of green synthesis techniques such as hydrothermal, solvothermal, microwave-assisted, pyrolysis and ultrasonic techniques are cost-effectiveness, scalability and less impact on the environment. The doping of heteroatoms such as nitrogen, sulfur, phosphorus, boron and fluorine greatly improves the optical, electrical, catalytic and surface properties of CQDs, thereby enhancing their functional performance in various applications.

Moreover, the review details the physicochemical properties, surface functionalization, photoluminescence mechanisms and characterization techniques of heteroatom-doped CQDs. Their excellent fluorescence behavior and biocompatibility make them have special attention for their biomedical applications such as bioimaging, biosensing, drug delivery, antimicrobial activity, cancer therapy, and tissue engineering. Environmental applications such as pollutant sensing, heavy metal detection, photocatalytic degradation, wastewater treatment and environmental monitoring are discussed in details. Issues concerning large-scale production, reproducibility, toxicity assessment and commercialization are also discussed. In summary, heteroatom-doped CQDs derived from biomass waste represent a sustainable and versatile nanoplatform with immense prospects for advancing green nanotechnology, biomedical innovation, and environmental remediation.

Keywords: Carbon Quantum Dots (CQDs), Biomass Waste Valorization Heteroatom Doping, Green, Nanotechnology, Biomedical and Environmental Applications

ANALYZING FACTORS INFLUENCING STUDENT DROPOUT RATES IN NORTH GUJARAT HIGHER EDUCATION INSTITUTIONS USING THE APRIORI ASSOCIATION RULE MINING ALGORITHM

Het. T. Trivedi and Badal. K. Kothari

Department of Computer Science & IT Hemchandracharya North Gujarat University (HNGU) Patan, Gujarat, India

Student dropout in higher education is a multi-faceted socioeconomic and academic challenge that severely impacts regional human capital development, particularly in developing areas like North Gujarat. This research paper presents an empirical study utilizing the Apriori Association Rule Mining algorithm to identify and analyze hidden patterns, co-dependencies, and root causes behind student dropouts across the five primary districts of North Gujarat: Patan, Mehsana, Banaskantha, Sabarkantha, and Aravalli. A comprehensive dataset consisting of demographic information, socio-economic status, academic history, institutional environment, and geographical constraints was collected from 1,245 dropout and active students affiliated with regional higher education institutions and universities. By applying the Apriori algorithm, we mined statistically significant association rules that highlight combinations of risk factors leading to premature institutional withdrawal. The findings indicate that a low annual family income coupled with a rural commuting distance greater than 15 kilometers, and low parental literacy, yields an association rule with a confidence level of 84.5% and a lift value of 2.1. Additionally, low engagement in foundational first-year IT/Computer application courses was identified as a critical academic pivot point for technical streams. The discovered rules provide actionable, data-driven insights for policymakers, educational administrators, and institutional heads to formulate targeted early-intervention frameworks, optimized transport infrastructure, and financial support schemes tailored specifically to the demographic realities of North Gujarat.

Keywords—Apriori Algorithm, Association Rule Mining, Educational Data Mining (EDM), Student Dropout Ratio, North Gujarat, HNGU, Socio-Economic Factors.

A DESIGN OF AN AI-POWERED PRODUCTIVITY INTELLIGENCE SYSTEM FOR PERSONALIZED WORK OPTIMIZATION

Jayeshkumar Natwarlal Modi

Assistant Professor

Department of Computer and Information Technology.

Hemchandracharya North Gujarat University, PATAN.

In the modern digital era, individuals such as students, researchers, and professionals are required to manage multiple tasks, deadlines, meetings, and large amounts of information simultaneously. Traditional productivity tools such as basic reminder applications and calendar systems provide limited functionality and are unable to intelligently analyze user behavior or prioritize tasks effectively. As a result, users often face challenges such as poor time management, missed deadlines, reduced efficiency, and increased mental workload. Therefore, there is a need for an intelligent system that can assist users in managing their tasks and schedules more efficiently.

The objective of this project is to develop an **AI Personal Productivity Intelligence System** that utilizes artificial intelligence and machine learning techniques to improve personal productivity and time management. The system aims to provide intelligent task scheduling, smart reminders, and personalized productivity insights based on user behavior and activity patterns.

The proposed approach involves designing an intelligent framework that collects user data such as task lists, deadlines, calendar events, and work patterns. Machine learning algorithms will analyze this data to identify user habits, predict optimal task scheduling times, and prioritize tasks based on urgency and importance. The system will also use Natural Language Processing (NLP) to allow users to interact with the platform through simple text or voice commands. Additionally, the system will generate adaptive reminders and productivity analytics to help users organize their activities effectively.

The expected outcome of this research is the development of an intelligent digital productivity assistant that can automatically organize tasks, provide smart recommendations, and improve time management. The system will help users reduce workload stress, increase productivity, and make better decisions in managing daily activities. The proposed framework can be applied in academic, professional, and organizational environments to enhance overall efficiency and productivity.

Keywords : Productivity Optimization, AI Assistant, Natural Language Processing (NLP), Predictive Analytics, Workload Analysis, Productivity Tracking, User Behavior Analysis, Decision Support System, Human-Computer Interaction (HCI), Goal Tracking, Personal Analytics

ICISDA-2026

INTEGRATING TRADITIONAL WATER WISDOM INTO SUSTAINABLE URBAN WATER MANAGEMENT: A CASE STUDY OF INDORE

**Lalitesh Sinha¹, Devaanshi Jagwani¹, Kunal Jetha¹, Archana Keerti Chowdhary¹
and Sandeep M. Narulkar²**

**¹Civil Engineering Department, IPS Academy, Institute of Engineering and Science
Indore, India**

²Civil Engineering & Applied Mechanics Department SGSITS, Indore, India

Rapid urbanization in India has increased groundwater depletion, runoff, flooding, water pollution, and dependence on external water supplies. Traditional systems such as bawdis, wells, tanks, kunds, and linked storage networks offer practical approaches for local retention, recharge, sediment control, and community management. This review examines their relevance to sustainable urban water management in Indore, located on the basaltic Malwa Plateau. Peer-reviewed studies, government reports, and preliminary GPS-based site observations were reviewed. The sites were classified as hydraulic structures, water-related cultural landscapes, or potential water-heritage sites. Their current functions depend on catchment connectivity, structural condition, aquifer characteristics, water quality, sedimentation, ownership, and maintenance. A six-stage framework is proposed for site assessment, functional classification, restoration, and monitoring. Suitable structures may support groundwater recharge, stormwater detention, non-potable storage, ecological improvement, groundwater monitoring, and heritage conservation. The study presents a practical approach for integrating traditional water systems with urban hydrology, groundwater management, and heritage-sensitive planning.

Key words: Traditional water systems, Indian Knowledge System, urban water management.

ENHANCING DISCOURSE COMPETENCE IN L2 ACADEMIC WRITING THROUGH COLLABORATIVE WRITING WITH PANCHATANTRA STORIES AMONG ESL UNDERGRADUATE LEARNERS.

Firdous Fatima, Jawed S. Ahmed

Dept. of English , Aligarh Muslim University

Discourse competence constitutes a fundamental component of L2 academic writing, enabling learners to produce coherent, cohesive, and contextually appropriate texts. However, many ESL undergraduate learners experience persistent difficulties in organizing ideas, maintaining textual cohesion, and constructing academic arguments despite possessing adequate grammatical and lexical knowledge. This study investigates the effectiveness of collaborative writing using Panchatantra stories as a culturally responsive pedagogical intervention to enhance discourse competence in L2 academic writing among ESL undergraduate learners at Aligarh Muslim University. Drawing on sociocultural theory and the principles of collaborative learning, the study conceptualizes writing as a socially mediated process in which learners construct knowledge through interaction, negotiation of meaning, and shared problem-solving. Panchatantra stories provide authentic opportunities for learners to analyse texts, engage in critical discussions, and transform narrative discourse into academic genres, including analytical, argumentative, and expository writing. The collaborative writing tasks are designed to foster coherence, cohesion, logical sequencing, paragraph development, academic vocabulary, and the effective use of discourse markers. The study adopts a mixed-methods research design to examine the impact of this pedagogical approach on learners' discourse competence through writing assessments, classroom observations, and learner perceptions. It is anticipated that collaborative engagement with culturally relevant literary texts will facilitate meaningful language use, promote critical thinking, and improve the overall quality of academic writing. By integrating indigenous literary resources into ESL writing pedagogy, this study contributes to the growing body of research on culturally responsive language teaching and offers practical implications for curriculum designers, teacher educators, and language instructors seeking innovative approaches to developing discourse competence in higher education. The findings are expected to demonstrate the pedagogical value of collaborative writing in fostering academically proficient and culturally grounded L2 writers.

Keywords: Discourse Competence, L2 Academic Writing, Collaborative Writing, Panchatantra Stories, Culturally Responsive Pedagogy.

AUTONOMOUS MULTI-MODEL VISION SYSTEM FOR SITE-SPECIFIC WEED DETECTION AND SELECTIVE SPRAYING IN SMART AGRICULTURE BENCHMARKING YOLOV5 AND MOBILENET-SSD FOR FIELD-DEPLOYABLE CROP-WEED DISCRIMINATION

Sana I. Shaikh and Mayur Jakhete

**Department of Electronics Engineering, School of Engineering & Technology
(SOET), Pimpri Chinchwad University, Pune, Maharashtra, India**

The impact of weed infestation is a serious threat to global food security. Weeds can reduce crop yield by as much as 43%. Mechanical, manual, and chemical methods have been widely used to control weeds. However, the rising costs of labor, the development of herbicide resistance in weeds, and restrictions on chemical warfare are significant concerns for modern agriculture. This article introduces an autonomous, multimodal robotic solution that scans its environment to detect and remove weeds. Initially, we used 3,120 images of crops, weeds, and backgrounds extracted from Internet resources and field photos. These images were annotated, oriented, and resized to 416×416 pixels. Moreover, we applied flips and increased the contrast and exposure to obtain an extended data set. We trained and compared two popular object detectors, including YOLOv5 and MobileNet-SSD, to find the optimal balance between performance and a compact model for further deployment. The mean Average Precision (mAP) of YOLOv5 at 0.5 was approximately 0.86, while the maximum F1-score was 0.83 at a confidence threshold of around 0.49. MobileNet-SSD as a classifier has demonstrated strong performance with an accuracy of 98%. As a result, we also designed and built a mechanical chassis for the robot. Thus, with the obtained results and the analysis of the comparison between the two approaches, we prioritize the following steps for prototype development and field testing.

Keywords: Precision agriculture, weed detection, YOLOv5, MobileNet-SSD, deep learning, robotic weeding, edge AI, smart farming.

CALLUS CULTURE TECHNIQUES IN *CATHARANTHUS ROSEUS* (L.) G. DON: CURRENT ADVANCES, OPTIMIZATION STRATEGIES, AND APPLICATIONS

Kavita Yadav, Anjum Bano, Raghunandan Nathawat, Preenon Bagchi

**School of life and basic sciences, Jaipur national university, Jaipur, Rajasthan,
302017, India**

Catharanthus roseus (L.) G. Don is a medicinally important plant renowned for its ability to synthesize more than 200 bioactive phytochemicals, including the clinically significant terpenoid indole alkaloids vincristine and vinblastine, which are widely used in cancer chemotherapy. However, the naturally low abundance of these metabolites and increasing pharmaceutical demand have necessitated the development of alternative production strategies. Among various biotechnological approaches, callus culture has emerged as a promising in vitro system for plant propagation, germplasm conservation, and enhanced secondary metabolite production. The success of callus culture is governed by several factors, including explant source, culture medium composition, plant growth regulator combinations and environmental conditions. Hormonal interactions play a crucial role in regulating callus induction, proliferation, and morphogenesis, while nutrient availability, pH, light, and incubation conditions significantly influence biomass accumulation and metabolite biosynthesis. This review summarizes the current advances in callus culture of *C. roseus*, with particular emphasis on the principles of callus formation, cellular dedifferentiation and redifferentiation, factors affecting callus initiation and growth, and the characterization of callus cultures. Furthermore, the applications of callus culture in alkaloid production, plant regeneration, and elicitor-mediated enhancement of secondary metabolites are discussed. The review also highlights the major challenges associated with callus culture and outlines future perspectives for improving metabolite production through advanced biotechnological and metabolic engineering approaches. Overall, callus culture represents a valuable platform for the sustainable production of pharmaceutically important compounds in *C. roseus*.

Keywords:

Catharanthus roseus, Callus culture, Plant tissue culture, Terpenoid indole alkaloids, Vincristine, Vinblastine, Secondary metabolites, Plant growth regulators, Explants, Elicitation, Morphogenesis.

GENOMIC AND PHENOTYPIC CHARACTERIZATION OF ANTIFUNGAL RESISTANCE IN CANDIDA AURIS AND NON-ALBICANS CANDIDA SPECIES ISOLATED FROM A TERTIARY-CARE HOSPITAL IN RAJASTHAN, WESTERN INDIA: AN INTEGRATED DRY LAB–WET LAB APPROACH

Suyash Meena and Preenon Bagchi
Jaipur National University, Jaipur

Background: *Candida auris* has emerged as a globally significant multidrug-resistant fungal pathogen, designated by the World Health Organization as a “critical priority” agent within the Fungal Priority Pathogens List (1). Its capacity for nosocomial transmission, biofilm formation, and resistance to multiple antifungal classes poses a substantial threat to intensive care and immunocompromised populations. While genomic surveillance efforts have characterized *C. auris* clades and resistance-associated mutations, notably in *ERG11*, *FKS1*, and *TAC1B* (2–4), across several Indian regions, contemporary epidemiological and genomic data from Western India, particularly Rajasthan, remain sparse (5).

Objective: This study aims to establish an integrated computational–experimental framework for characterizing antifungal resistance among *Candida auris* and non-albicans *Candida* isolates obtained from candidemia and candiduria patients at a tertiary-care hospital in Jaipur, Rajasthan, thereby addressing a regional gap in fungal genomic surveillance.

Methods: Clinical isolates will be prospectively and retrospectively collected from blood and urine cultures, identified via biochemical and MALDI-TOF methods, and subjected to CLSI-based antifungal susceptibility testing across azole, polyene, and echinocandin classes (6). Biofilm-forming capacity will be assessed phenotypically. In parallel, sequencing of resistance-associated loci will inform phylogenetic clade assignment, comparative genomic analysis against global reference isolates, and in silico structural modeling of resistance-conferring mutations to evaluate candidate antifungal–target interactions via molecular docking (7,8).

Expected Outcomes: The study anticipates generating the first genomically resolved resistance profile of *Candida* species from a Rajasthan hospital setting,

correlating phenotypic susceptibility with genotypic markers, and identifying region-specific mutation patterns relevant to local antifungal stewardship.

Significance: Findings will contribute novel regional surveillance data to the sparse literature on Western Indian fungal epidemiology and provide a reproducible dry lab–wet lab pipeline applicable to future rare and emerging pathogen studies.

Keywords: *Candida auris*; antifungal resistance; genomic surveillance; candidemia; Rajasthan; molecular docking; *ERG11*

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DERMAI: A DEEP-LEARNING FRAMEWORK WITH EXPLAINABLE RISK STRATIFICATION AND AGENTIC CARE-JOURNEY ORCHESTRATION FOR AUTOMATED SKIN LESION CLASSIFICATION

Ayan Mohamed and D.Gandhimathi

Department of Computer Science Engineering -Data Science, Dr. ACS college of engineering, Bengaluru, 560074, Karnataka, India.

Skin diseases are one of the most frequent reasons why people go for outpatient care all over the world. Yet, in low-resource areas access to qualified dermatologists remains limited, which often causes a delay in the diagnosis of potentially life-threatening conditions such as melanoma. This paper presents DermAI, a thorough deep-learning framework that integrates dermoscopic image classification, visual explanations, risk assessment, and care management into a single process. Unlike previous studies which have concentrated solely on classification accuracy, DermAI combines the confidence scores from a convolutional neural network (CNN) with Gradient-weighted Class Activation Mapping (Grad-CAM) data and symptoms as reported by the patients, resulting in a combined Risk Fusion Score that is linked to a conversational agent. This agent assists patients in carrying out teleconsultations, booking appointments, and getting medication reminders without having to ask for help. An EfficientNet-B4 backbone was finetuned on the HAM10000 dataset using weighted sampling and a balanced focal loss in order to deal with the severe class imbalance, reaching a top-1 accuracy of 89.4%, a macro F1 score of 0.851, and a melanoma-class recall of 0.86 on a stratified test set – exceeding the 85% accuracy benchmark considered clinically useful for dermatological screening at the triage level. The Grad-CAM visualizations were quantitatively compared to the lesion boundaries annotated by dermatologists using Intersection-over-Union (IoU). As a result, the Risk Fusion Score decreased the number of false reassurances in cases of borderline melanoma when compared to the model's confidence alone. The paper examines the proposed architecture, the deployment strategy, and the practical applications for teledermatology and mobile health, and stresses the ethical and safety measures that are necessary for responsible clinical implementation.

Keywords: Skin lesion classification, EfficientNet, Grad-CAM, explainable AI, risk stratification, teledermatology, conversational agents, HAM10000

DATA ANALYTICS ON HIGHER EDUCATION DATA SET USING PREDICTIVE ANALYTICS

D. Gandhimathi¹ and Jagadeeswari J. M²

¹Department of CSE-Data Science, Dr. ACS College of Engineering, Bengaluru, India

²M.Sc Data Science, Annamalai University, Chidambaram, India

Predictive analytics is a subset of data analytics, used to predict future outcomes by incorporating data with statistical algorithms and modeling techniques. Data analytics is the process of extracting insights from raw data, which supports decision-making across a domain. This chapter focuses on utilizing predictive analytics in higher education to identify the learning interests and behaviour patterns of learners in academics. Through this research, we review how to identify a learner's cognitive level across various aspects of the curriculum. In the digital era, learners gain knowledge through many sources such as tutorials and online courses. Based on a survey collected from undergraduate learners in reputed institutions, we study how learners benefit from offline classroom learning alongside digital education. Academic performance and additional skill sets collected from various sources are summarized, and a predictive analysis model is used to analyze learner performance. The model's performance is compared with related machine learning models, and correlation analysis is performed to examine the relationship between academic performance and additional skill sets acquired by a learner, in order to identify proactive learners.

Keywords: Predictive analytics, Data analytics, Correlation analysis.

PHENOTYPIC AND GENOMIC CHARACTERIZATION OF CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE FROM A TERTIARY-CARE HOSPITAL IN JAIPUR, RAJASTHAN: A COMBINED DRY LAB–WET LAB SURVEILLANCE STUDY

Suyash Meena and Preenon Bagchi

Dept. of Bioinformatics, Jaipur National University, Jaipur, India

Background: Carbapenem-Resistant *Klebsiella pneumoniae* (CRKP) is classified by the World Health Organization as a critical-priority pathogen within its bacterial priority list, owing to its role as a leading cause of untreatable nosocomial bloodstream infections (1). In India, CRKP bloodstream infections have been associated with mortality rates as high as 68%, and the country has been described as an epicentre of carbapenem resistance (2,8). Multicentric Indian genomic surveillance has revealed extensive sequence-type and resistance-gene diversity (2), yet despite this high disease burden, reports characterizing resistance mechanisms remain disproportionately concentrated in southern and northern Indian centres, with molecular data from Rajasthan limited to a single small-scale report of fourteen isolates using PCR-only methodology (3).

Objective: This study proposes an integrated dry lab-wet lab framework to characterize the phenotypic resistance profile, carbapenemase gene content, and genomic context of CRKP isolates collected from a tertiary-care hospital in Jaipur, Rajasthan, extending prior regional work beyond PCR-based detection into whole-genome-informed structural and epidemiological analysis.

Methods: Non-duplicate *K. pneumoniae* isolates will be collected from blood, urine, and respiratory clinical specimens and screened for carbapenem resistance via CLSI-defined disk diffusion and MIC methods (12). Confirmed isolates will undergo carbapenemase detection (modified Carbapenem Inactivation Method, Carba NP test) and multiplex PCR for blaNDM, blaOXA-48-like, blaKPC, and blaVIM genes. Genomic DNA from a representative subset will be whole-genome sequenced to determine sequence type (ST), capsular (K) and O-antigen loci, resistance gene content, and plasmid replicon profiles, benchmarked against existing Indian and global CRKP genomic collections (2,6,7). In silico structural modeling of key resistance enzymes (e.g., NDM-1, OXA-48) and porin loss-of-function variants (OmpK35/36) will support docking-based evaluation of beta-lactamase inhibitor combinations.

Expected Outcomes: The study anticipates producing the first genomically resolved CRKP resistance and lineage dataset from a Jaipur hospital setting, correlating phenotypic resistance with underlying carbapenemase genotype and clonal background, and identifying whether high-risk international clones (e.g., ST231, ST258, ST16) are locally circulating.

Significance: Findings will substantially extend the sole prior Rajasthan-specific report beyond its small-sample, PCR-only scope, contribute to national genomic surveillance networks, and establish a reusable dry lab-wet lab AMR-surveillance pipeline within the Department of Bioinformatics.

Keywords: *Klebsiella pneumoniae; carbapenem resistance; CRKP; genomic surveillance; NDM-1; Rajasthan; antimicrobial resistance*

CRYPTANALYSIS OF BITWISE HILL CRYPTOSYSTEM–A CHOSEN PLAINTEXT ATTACK

Rampaka Manojkumar, M Satish Kumar, Prudhvi Raju Ganasala, Sandi Sridhar Reddy, Macha Pooja and Ravi Shankar Nanduri

Nalla Narasimha Reddy Education Society's Group of Institutions. Hyderabad, India

Abstract. This paper cryptanalyzes a block cipher proposed by Ahmed Desoky et al, which essentially is a variant of the classical Hill Cipher. The researchers have modified the cipher wherein, plaintext is taken in the form of rectangular matrices of size 3×8 in the illustration of the cipher. The claim of the authors is that, since the plaintext is in the form of rectangular matrix, there can be no modular arithmetic inverse for the plaintext. Thus, the cipher overcomes the weakness of the classical Hill Cipher, the known plaintext attack vulnerability. The cipher does show resistance against the known plaintext vulnerability exhibited by the classical Hill Cipher. However, the cryptosystem proposed by the researchers' exhibits weaknesses in the face of the chosen plaintext attack, which is employed in this paper. The cipher is broken with the help of 8 chosen plaintexts.

Keywords: Encryption, Decryption, Modular Arithmetic Inverse, Plaintext, Ciphertext.

CRYPTANALYSIS OF HILL CIPHER MODIFICATION A SIMPLIFIED APPROACH

**Dasari Srivani, Ravula Lavanya, Dheeravath Arundathi, Singireddy Sandyarani,
Netra Nagabhushan, Ravi Shankar Nanduri
Department of CSE (DS)
Nalla Narasimha Reddy Education Society's Group of Institutions, Hyderabad,
India.**

Abstract— This paper cryptanalyzes the Modified Hill Cipher proposed by Jessi R. Paragas et al. The modifications proposed by the researchers do not sufficiently augment the classical Hill Cipher. The cipher is broken with a single chosen ciphertext. This exhibits the short comings of the cipher designed by the researchers. This paper also suggests ways of strengthening the cipher against the attacks such as the one employed in this paper.

Index Terms— Hill Cipher, Modular Arithmetic Inverse, Plaintext, Ciphertext, Radix 64.

DETECTION OF FRAUDULENT DEGREE CERTIFICATES USING HISTOGRAM FEATURES AND AI TECHNIQUES

Sarala M¹, Muralidhara B L², Suresh R³

¹Department of Computer Science(PG), Jyoti Nivas College, Bangalore, India

**²Department of Computer Science and Applications, Bangalore University,
Bangalore, India**

³Department of Statistics, Bangalore University, Bangalore, India

Artificial Intelligence (AI) techniques support detecting fake regions in high-dimensional datasets such as images and videos through fake detection methods. The scope of educational credential forgery is required for authenticating it for admission, and recruitment. In this study, we detected forged educational credentials using machine learning (ML) algorithms such as Support Vector Machine (SVM), NaïveBayes, Logistic Regression, K-Nearest Neighbours (KNN), Random Forest, and Decision Tree. We have collected the primary dataset of degree certificates, and extracted the features using the histogram features (HF): skewness, mean, kurtosis, standard deviation, and entropy from preprocessed certificate images, as structured data is essential for ML models. Further, we conducted a detailed empirical evaluation by fine-tuning the hyperparameters of each model to improve classification performance. Among the algorithms tested, Random Forest attained a good accuracy of 99.4%, surpassing the other methods in detecting fraudulent degree certificates.

Keywords: classification, degree certificate, fraudulent detection, histogram features

SYNTHESIS AND PROPERTY EVOLUTION OF REDUCED GRAPHENE OXIDE FROM NATIVE GRAPHITE

Maitri M Sutariya, Anjali A. Parmar, Sarju Prajapati, K.A. Parmar
Department of Chemistry, Sheth P.T Arts & Science College ,Godhra, Gujrat
***Department of Chemistry, H.N.G.U. University Patan**
E-mail:sutariyamaitri@gmail.com

This work outlines the multi-step conversion of native graphite into reduced graphene oxide (rGO) and evaluates the resulting structural, mechanical, and electrical transformations. Pristine graphite was oxidation-treated using a modified Hummers' method to yield graphene oxide (GO), introducing oxygen-containing functional groups (epoxide, hydroxyl, carboxyl) that disrupted the sp^2 carbon framework and expanded interlayer spacing. Subsequent chemical reduction partially restored the conjugated sp^2 network by removing oxygen moieties. Comprehensive characterization demonstrates significant property shifts across stages: pristine graphite's high initial conductivity collapses upon oxidation into insulating GO, then recovers to orders-of-magnitude higher conductivity in rGO. Additionally, layer exfoliation dramatically increases specific surface area, while defects introduced during oxidation enhance chemical reactivity and dispersibility compared to natural graphite. These property transitions highlight rGO as a versatile candidate for energy storage, catalysis, and nanocomposites.

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