


Chapter 1


A Decade of Progress: Artificial Intelligence in Multiple Sclerosis (2015–2025) – Diagnostic Innovations, Prognostic Modeling, and Future Pathways

Jyoti Kumari

 <https://orcid.org/0009-0005-4853-8963>

Veer Surendra Sai University of Technology, India

Santi Kumari Behera

 <https://orcid.org/0000-0003-4857-7821>

Veer Surendra Sai University of Technology, India

Prabira Kumar Sethy

 <https://orcid.org/0000-0003-3477-6715>

Sambalpur University, India

ABSTRACT

Over the past decade, AI has transformed multiple sclerosis (MS) research and care, enhancing diagnosis, prognosis, and disease monitoring. From 2015 to 2025, AI evolved from basic image classification to advanced multi-modal models predicting disease progression and treatment response. Deep learning improved lesion detection and brain atrophy assessment via MRI, while machine learning enabled MS subtype identification and prognostic modeling. Researchers leveraged diverse datasets—MRI repositories, clinical trials, and EHRs—to train CNNs, RNNs, ensembles, and transformers. These advances improved diagnostic precision and supported disease trajectory prediction. AI tools now aid radiologists in tailoring

DOI: 10.4018/979-8-3373-2706-8.ch001

treatments, though challenges like model generalizability, data harmonization, and regulatory approval persist. The future lies in federated learning, explainable AI, and real-time decision support to realize precision medicine in MS care.

1. INTRODUCTION

Multiple Sclerosis (MS) is an immune-mediated, chronic neurodegenerative condition of the central nervous system (CNS) that strikes millions of people across the globe. MS is marked by inflammation, demyelination, and neurodegeneration, resulting in numerous physical and cognitive disabilities (Ramaglia et al., 2021). Primary progressive MS (PPMS), secondary progressive MS (SPMS), and relapsing remitting MS (RRMS) are some of the other forms of MS, which have their own respective clinical issues and disease courses. Treatment at an early stage for the delay of the course of the disease is dependent on early and proper diagnosis, but MS remains difficult to diagnose because of its heterogeneity, symptom variability, and requirement for proper integration of clinical, radiological, and laboratory evaluations (Ghasemi et al., 2016). Challenges in discrimination between multiple sclerosis and other neuroinflammatory diseases, discrimination of disease subtypes, prediction of long-term outcomes, and assessment of response to therapy remain undeterred notwithstanding advances in clinical and radiological assessment, including magnetic resonance imaging (MRI) (Rose et al., 2021). Because of their deep dependence on experienced doctors, classical diagnostic and prognosis methods impose subjectivity, inter-observer variability, and time lag in decision-making. Exploration into advanced technology, particularly artificial intelligence (AI), has been motivated by the growing complexity in MS diagnosis and treatment. AI has the potential to tackle grand challenges in MS clinical practice by enhancing disease stratification, enhancing diagnostic precision, and providing predictive value (Nabizadeh et al., 2022). AI has the ability to assist doctors in identifying patterns that may be difficult for human vision to detect using vast amounts of clinical and imaging information. This can assist in the detection of early MS, accurate subtype classification, and prediction of disease progression. This decade review strives to present the key advances in AI applications in MS research during the period 2015-2025. Besides predicting the future direction and emerging trends, this research tries to evaluate the impact of these advances in MS diagnostics, prognostics, and clinical management. This review is targeted at presenting a systematic understanding of the progress in application of AI in MS by integrating the current status of integration of AI in MS and indicating any loopholes and areas where research can be extended. An extensive literature search was conducted to identify relevant studies that were published between 2015 and 2025. A PRISMA-type architecture guided

20 more pages are available in the full version of this document, which may be purchased using the "Add to Cart" button on the publisher's webpage: www.igi-global.com/chapter/a-decade-of-progress/396965

Related Content

T-Scan 8 Recording Dynamics, System Features, and Clinician User Skills

Robert B. Kerstein, DMD and Robert Anselmi (2017). *Medical Imaging: Concepts, Methodologies, Tools, and Applications* (pp. 1771-1829).

www.irma-international.org/chapter/t-scan-8-recording-dynamics-system-features-and-clinician-user-skills/159786

Application of Kirlian Captures and Statistical Analysis of Human Bioelectricity and Energy of Different Organs: Observations and Graphical Notations

Rohit Rastogi, Mamta Saxena, Devendra K. Chaturvedi, Mayank Gupta, Neha Gupta, Deepanshu Rustagi, Sunny Yadav and Pranav Sharma (2021). *International Journal of Health Systems and Translational Medicine* (pp. 10-32).

www.irma-international.org/article/application-of-kirlian-captures-and-statistical-analysis-of-human-bioelectricity-and-energy-of-different-organs/277367

The Power of Data: Leveraging Machine Learning for Parkinson's Disease Diagnosis

Vipasha Abrol, Hina Gupta and Aditya Shukla (2024). *Intelligent Technologies and Parkinson's Disease: Prediction and Diagnosis* (pp. 1-19).

www.irma-international.org/chapter/the-power-of-data/338814

Exploring Telemedicine Scope: A Deep Dive Into Malaysia's Landscape

Faerozh Bin Madli, Shaierah Binti Gulabdin, Yun Wong Sing and Ismail Abdul Jabbar (2025). *Digitalization and the Transformation of the Healthcare Sector* (pp. 437-462).

www.irma-international.org/chapter/exploring-telemedicine-scope/362465

Computational Inference of Gene Regulation from Whole-Transcriptome Analysis of Early Embryos

Sung-Joon Park and Kenta Nakai (2016). *Emerging Research in the Analysis and Modeling of Gene Regulatory Networks* (pp. 241-279).

www.irma-international.org/chapter/computational-inference-of-gene-regulation-from-whole-transcriptome-analysis-of-early-embryos/155031