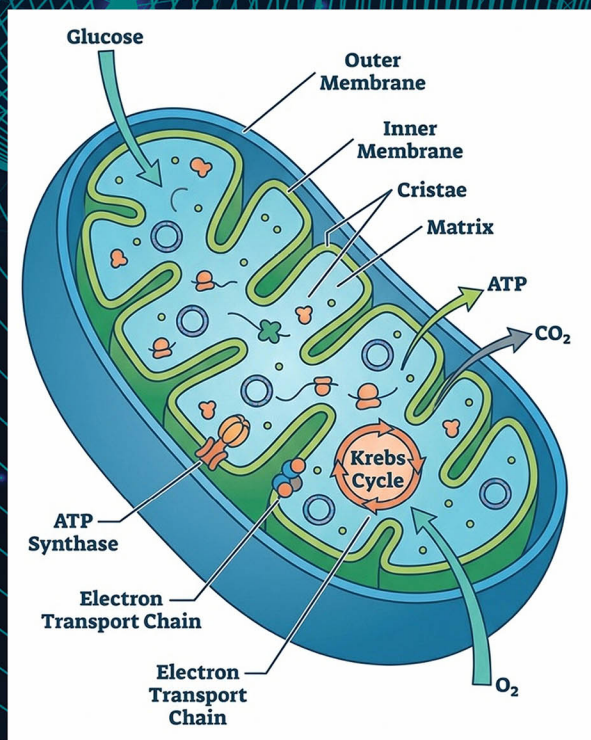


Computational Intelligence in Epigenetics, Cellular and Mitochondrial Functions



EDITED BY

**Saurav Mallik, Zhongming Zhao, Namrata Tomar,
Soumita Seth, Saiyed Umer, Tapas Bhadra,
and Ranjeet Kumar Rout**



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Computational Intelligence in Epigenetics, Cellular and Mitochondrial Functions

This book analyzes the integrated model of artificial intelligence, deep learning, and cloud computing for various bioinformatic problems, including gene signature discovery, rare cell detection, disease classification, and rare disease detection. It discusses biomedical image processing and deep learning integrated tools for the stage detection of critical diseases like cancer.

This book:

- Presents a comparative study of gradient-boosted classifier and deep learning classifier for disease classification of multi-omics sequencing data.
- Showcases biomarker discovery and differential expression analysis in single-cell RNA sequencing data through the integrated model of data imputation, feature selection, and cell clustering.
- Explains artificial intelligence, machine learning, and integrated models for DNA methylation and gene expression data analysis and disease classification.
- Covers the fundamentals of artificial intelligence, machine learning, deep learning, and cloud computing tools in bioinformatics.
- Explores rare cell detection and transcriptomic analysis in single-cell RNA sequencing.

It is primarily written for senior undergraduates, graduate students, and academic researchers in electrical engineering, electronics and communications engineering, computer science and engineering, and biomedical engineering.



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Preface

Recent advances in high-throughput omics technologies have transformed our ability to explore the molecular mechanisms that govern cellular behavior, aging, and disease. Epigenetic regulation, cellular dynamics, and mitochondrial function have emerged as central determinants of health and pathological progression, yet their inherent complexity demands analytical frameworks that go beyond traditional statistical approaches. Harnessing computational intelligence (CI)—including machine learning (ML), data-driven modeling, and integrative analytics—has become indispensable for extracting meaningful biological insights from large-scale, heterogeneous datasets. This book is conceived at the intersection of computational science and molecular biology, aiming to provide a coherent platform for understanding how intelligent computational methods can decode epigenetic modifications, cellular state transitions, and mitochondrial dysfunction in both normal and diseased systems.

Chapter 1 discusses cancer diagnosis, which is also a crucial task nowadays. The integration of biomedical image processing and deep learning showed a good result for cancer diagnosis. This chapter discusses an overview of the integration of biomedical image processing and deep learning techniques for accurate cancer detection. We discuss the latest research work, different biomedical image processing techniques, and deep learning techniques.

Chapter 2 introduces deep learning (DL), which has revolutionized cancer detection by utilizing advanced biomedical imaging techniques, greatly improving diagnostic accuracy, efficiency, and patient outcomes. Given that cancer continues to be a major global cause of death, the importance of early detection in enhancing survival rates cannot be overstated. Conventional diagnostic approaches, although useful, frequently fall short in terms of accuracy and the ability to scale. DL models, particularly convolutional neural networks (CNNs) and innovative architectures such as Vision Transformers (ViT) and ensemble learning, have the capability to autonomously organize and categorize medical images from magnetic resonance imaging (MRI), CT, PET, and histopathology. This investigation

presents an innovative approach to detecting lung and colon cancer, integrating the Tuna Swarm Algorithm with GhostNet-based feature extraction. This approach demonstrates a high level of precision, achieving a score of 99.33%. DL encompasses a broader range of functions beyond merely categorizing items into groups. This approach accelerates processes, reduces the time required for interpretation, and promotes the analysis of medical data across various formats, utilizing tools like natural language processing (NLP) and imaging genomics. Even with notable progress, obstacles remain in areas such as data diversity, understanding model outputs, and adhering to regulations. Overcoming these challenges through collaborative efforts across disciplines and the use of standardized datasets will enable smooth integration into clinical practice. With advancements in DL, its applications extend beyond mere diagnosis. This technology can facilitate the development of intelligent healthcare settings featuring automated decision support systems, tailored treatment plans, and enhanced patient monitoring. This study highlights the transformative impact of DL on biomedical imaging, paving the way for a future where AI-driven cancer diagnostics become a fundamental component of precision medicine.

Chapter 3 explores a broad spectrum of neurological disorders, emphasizing that accurate brain lesion segmentation plays a critical role in clinical diagnosis, treatment planning, and ongoing disease monitoring. The need for accurate and automatic lesion delineation approaches has increased significantly since nuclear MRI has become the dominant imaging modality due to its non-invasive nature and superior soft-tissue contrast. With a focus on the intricate morphological features of pathological tissues and the computational challenges brought on by their spatial variability, intensity inhomogeneity, and deformable anatomical structure, this chapter provides a thorough examination of brain lesion segmentation in MRI. Modern deep learning techniques, such as CNNs and augmented attention-based U-Net variants, are discussed in addition to more conventional morphological segmentation techniques. Particular attention is paid to how data-driven representations and anatomical priors work together to improve segmentation accuracy. This chapter also covers crucial preprocessing methods, such as spatial normalization, bias field correction, and skull stripping, which enhance image fidelity and lesion detectability. A comparative morphological examination is provided for several lesion groups, including gliomas, ischemic stroke lesions, and demyelinating plaques associated with multiple sclerosis. This demonstrates how different diseases and imaging modalities can have different lesion characteristics. This chapter also looks at well-known public datasets like ISLES and BraTS and uses standard evaluation measures like the Hausdorff Distance, Dice Similarity Coefficient, and volumetric overlap assessments to assess algorithmic effectiveness. This chapter concludes with an overview of key advancements that will impact the future of brain lesion segmentation, including the

incorporation of multimodal imaging, the application of explainable artificial intelligence (XAI) to facilitate comprehensible clinical decision support, and federated learning for safe distributed analysis.

Chapter 4 shifts the focus to Alzheimer's disease (AD), a relentlessly progressive neurodegenerative disorder, and continues to constitute a formidable challenge in clinical diagnostics due to its insidious onset and multifactorial pathology. Conventional unimodal diagnostic paradigms—whether based on structural neuroimaging, molecular assays, or neurocognitive testing—frequently exhibit limited discriminative capacity, particularly in the prodromal stages of the disease. To address these shortcomings, this study advances a multimodal artificial intelligence (AI) diagnostic architecture that amalgamates structural MRI morphometrics, cerebrospinal fluid (CSF) biomarkers, cognitive indices, and epigenomic-mitochondrial signatures within an ensemble computational framework. Methodologically, the system leverages heterogeneous ML pipelines—CNNs for neuroimaging, support vector machines (SVMs) for epigenetic features, and gradient boosting ensembles for fluid and cognitive markers. While unimodal models attained accuracies ranging from 80% (epigenetics) to 87% (CSF and cognition), their integrative deployment culminated in a multimodal ensemble that achieved 94.1% diagnostic accuracy, with 93% precision, 92% recall, and an F1-score of 92%. Furthermore, the final classifier exhibited an exceptional discriminative capacity (97.5% accuracy; AUC=0.999), thereby eclipsing existing benchmarks reported in prior literature. Crucially, statistical interrogation via ANOVA identified MMSE scores, hippocampal volume reduction, and CSF tau elevation as the most salient predictors, reaffirming the model's biological plausibility and clinical interpretability. By fusing molecular, neuroanatomical, and cognitive dimensions into a unified computational substrate, this framework transcends traditional siloed methodologies and demonstrates the viability of AI-enabled multimodal integration as a transformative pathway for early detection, staging, and precision-guided therapeutic planning in AD.

Following this, Chapter 5 aimed to develop a sophisticated computational framework for detecting deoxyribonucleic acid (DNA) mutations and modeling clustered regularly interspaced short palindromic repeats-associated protein 9 (CRISPR-Cas9) gene editing. To categorize DNA sequences altered via one-hot encoding, a hybrid deep learning model including CNNs and bidirectional long short-term memory layers was used. A novel dual-chain visualization technique was developed to compare nucleotide variations between reference and patient sequences, and a detailed simulation of the CRISPR-Cas9 workflow was created to depict key steps such as guide ribonucleic acid (gRNA) matching, protospacer adjacent motif identification, cleavage, and homology-directed repair. The model performed satisfactorily, with a precision of 95.42%, recall of 99.81%, specificity of 95.16%, and an F1-score of 97.57%, indicating that it can reliably differentiate mutations. Furthermore, it achieved a Matthews correlation coefficient

(MCC) of 0.95 and an area under the receiver operating characteristic curve (AUC) of 0.99, demonstrating its outstanding classification performance. The CRISPR-Cas9 simulation successfully demonstrated the gene-editing process, offering valuable insights into targeted genomic alterations. Finally, the integrated approach successfully solved challenges in genomic data processing and mutation identification, indicating the promising prospects for precision medicine and targeted genetic therapeutics.

Chapter 6 highlights that cancer is a complex and highly diverse disease, which makes personalized medicine crucial for improving patient outcomes. One of the key molecular mechanisms influencing tumor development and progression is the methylome—the complete set of DNA methylation modifications. These modifications play a vital role in gene regulation, epigenetic reprogramming, and tumor’s response to treatment. DNA methylation serves as a unique epigenetic signature, and computational approaches enhance our understanding of DNA methylation regulation and its role in cancer progression. By leveraging these technologies, we can develop more accurate and data-driven strategies for personalized cancer treatment. Additionally, we highlight real-world case studies, demonstrating how AI and ML are being used in methylation—reflecting various aspects of a cell’s state, including its lineage identity, transcriptional activity, mitotic history, and proliferative potential. Because of its significance, methylation profiling has emerged as a promising approach for cancer diagnosis and therapy. With the rapid advancements in AI and ML, researchers can now analyze the methylome with greater precision, uncovering cancer biomarkers, classifying tumor subtypes, and predicting treatment responses. In this chapter, we explore how AI- and ML-driven approaches enable early cancer detection, prognosis prediction, and therapeutic decision-making. Despite these advancements, challenges such as data variability, the “black box” nature of AI models, data bias, and difficulties in integrating data across different platforms remain significant hurdles. Therefore, there is still much to explore in this rapidly evolving field. This chapter also discusses how addressing these challenges and refining AI-driven strategies could shape the future of methylation-based personalized medicine, ultimately leading to more effective cancer diagnostics, improved treatment outcomes, and better patient care.

Building on the evolving role of AI in healthcare, Chapter 7 examines cancer as a complex and highly heterogeneous disease driven by intricate molecular interactions across diverse biological processes. Due to this complexity, relying on a single type of biological data—known as a “single-omics” approach—is often insufficient to fully understand how cancer develops or how it may respond to treatment. This chapter provides a comprehensive overview of integrating multi-omics data using CI techniques to enhance cancer diagnosis, prognosis, and treatment planning. This chapter focuses on the critical roles of epigenetic regulation, cellular dynamics, and mitochondrial function, which collectively influence tumor development

and treatment response. We will discuss how AI, ML, and network-based methods facilitate the integration of high-dimensional omics data. These integrated data analyses support the identification of biomarkers, classification of disease subtypes, and discovery of drug response patterns. Special emphasis will be given to the following areas: epigenomic modeling (e.g., DNA methylation and histone modification) for early detection, single-cell and spatial transcriptomics to decode the tumor microenvironment and track cell state transitions, and mitochondrial multi-omics to uncover metabolic dependencies and mechanisms of treatment resistance.

Chapter 8 highlights that understanding how genes regulate each other is central to modern biology as these interactions control everything from cellular growth to disease progression. Reconstructing gene regulatory networks (GRNs) from time-series expression data remains a major challenge because the datasets are often short in length and noisy, while the number of genes involved is typically very large. In this work, we explore the scope of GRN modeling through recurrent neural networks trained with evolutionary optimization strategies. Beyond presenting one specific method, we critically discuss alternative approaches such as Boolean networks, Bayesian frameworks, and particle swarm optimization, highlighting their strengths and limitations in comparison to recurrent models. We further expand the application landscape of GRN inference, showing its relevance in personalized medicine, synthetic biology, drug resistance studies, and agricultural biotechnology. Using simulated and benchmark datasets, we demonstrate the ability of recurrent evolutionary models to capture hidden interactions with competitive accuracy, while also reflecting on the computational cost and scalability issues that remain open. The insights gained underline both the progress achieved and the need for hybrid, interpretable, and computationally efficient solutions for large-scale biological systems.

Chapter 9 explores single-cell RNA sequencing (scRNA-seq), which has revolutionized biology by enabling the transcriptomic profiling of individual cells, offering unprecedented resolution into cellular heterogeneity. However, the inherent characteristics of scRNA-seq data—namely high dimensionality, pervasive sparsity due to dropout events, and significant technical noise—present formidable computational challenges. Standard analytical pipelines address these challenges through a sequence of discrete steps, including data imputation, feature selection, and cell clustering. This review posits that the sequential and often independent application of these methods can propagate and amplify biases, compromising the reliability of downstream biological interpretation. We argue for an integrated analytical framework where the synergistic and often conflicting effects of these crucial preprocessing stages are considered jointly. This review critically evaluates the major classes of algorithms for data imputation, from model-based and diffusion-based methods to advanced deep learning paradigms; for feature selection, including variance-based, model-based, and correlation-aware approaches; and for cell clustering, with a focus on prevalent graph-based

community detection methods. We dissect the profound interdependencies among these steps, demonstrating how choices in one stage fundamentally alter the data landscape for all subsequent analyses. Through a synthesis of extensive benchmarking studies and methodological critiques, we highlight a critical dilemma: many data correction techniques, while seemingly improving data quality by superficial metrics, fail to enhance, and may even degrade, the performance of downstream tasks such as cell type identification and trajectory inference. This observation motivates the exploration of joint-learning models that simultaneously optimize imputation, feature selection, and clustering within a unified framework. By examining the impact of this integrated approach on differential expression (DE) analysis and biomarker discovery, we provide a comprehensive guide to navigating the complexities of scRNA-seq data. We conclude with a forward-looking perspective on best practices, remaining challenges such as scalability and the need for gold-standard benchmarks, and the future trajectory of the field toward multi-omics and spatially resolved analyses.

Chapter 10 addresses recent advances in high-throughput biological technologies, such as next-generation sequencing, DNA methylation profiling, and mitochondrial functional assays, which have enabled the generation of large-scale epigenetic and cellular datasets. While these data provide valuable opportunities to investigate disease mechanisms, aging, and cellular health, their high dimensionality and complexity pose significant analytical challenges. CI, combined with business analytics methodologies, offers effective tools for transforming complex biological data into interpretable and actionable insights. This chapter presents a structured analytical framework for interpreting epigenetic, cellular, and mitochondrial data using techniques familiar to business analytics, including data pre-processing, feature selection, predictive modeling, and performance evaluation. Emphasis is placed on system-level interpretation, predictive analytics for disease risk assessment, and the use of XAI to enhance transparency and trust in analytical outcomes. This chapter also discusses decision support mechanisms that translate analytical results into actionable insights for healthcare and biotechnology applications. By integrating CI with business analytics, this chapter aims to equip students and practitioners with practical approaches for applying analytical thinking to biomedical data and supporting informed decision-making in healthcare analytics, precision medicine, and biotechnology management.

Chapter 11 explores the application of modern technologies—including AI, ML, deep learning, and cloud computing—in bioinformatics. Special attention is given to the development of efficient multi-agent systems (MAS) based on large language models (LLMs) and their adaptation to the processing of multimodal biometric data. MAS consist of several specialized agents capable of learning independently and exchanging information while coordinating their actions through shared databases (RAG) or communication protocols (MCP, ACP, A2A, etc.). This approach enables the

effective resolution of complex tasks in dynamic environments with heterogeneous data. In the context of biometric systems, an example is presented of a multimodal multi-agent architecture in which each agent specializes in a specific type of biometrics, such as DNA analysis, facial and iris recognition, fingerprint analysis, voice, signature handwriting, gait dynamics, and other parameters. The facial recognition agent employs deep learning algorithms for the analysis of 2D and 3D images, the DNA analysis agent focuses on genetic sequence research, and the iris and fingerprint analysis agents apply high-precision algorithms for extracting unique patterns and computer vision methods. A distinctive feature of the described system is the use of the Mixture of Nested Experts (MoNE) concept, which enables the optimization of biometric data processing through dynamic allocation of computational resources among agents. This allows the system to remain efficient even under limited computational resources, maintaining a balance between operational speed and identification accuracy. Integration of the outputs of individual agents into a unified multimodal system is essential, enabling cross-verification, identification of interdependencies among biometric parameters, and improvement of reliability and identification precision. Ensemble methods, Bayesian networks, and dedicated integration algorithms are utilized for this purpose. Particular attention is paid to data security through the implementation of agents specializing in encryption, threat detection, and cyberattack countermeasures, particularly the imitation of biometric markers. Neural network models such as WaveNet and Tacotron are also considered for voice synthesis, Translatotron for real-time speech generation, as well as deepfake technologies for video identification. The mentioned multi-agent services can be developed further using cloud technologies to ensure the scalability of biometric systems and the deployment of additional agent monitoring and self-learning mechanisms. An important direction includes the enhancement of algorithms for integrating heterogeneous biometric data, the development of new encryption methods, and information protection solutions, which will significantly increase system efficiency and security. The multimodal multi-agent architecture proposed in this section represents a promising solution for the development of highly efficient and reliable biometric systems across various domains—from security to medicine. This approach offers broad possibilities for adaptive learning and the integration of diverse data while ensuring a high level of information protection.

Chapter 12 highlights the accurate prediction of protein structures, a fundamental challenge in bioinformatics that is essential for understanding protein function, interactions, and therapeutic applications. The relationships between protein structure and sequence are explored in this paper utilizing Artificial Neural Networks (ANNs) and Hidden Markov Models. Two Hidden Markov Models were explored, embodying different modeling strategies: one approach modeled protein secondary structures as latent states and viewed amino acid sequences as the emitted observable data,

whereas the alternative model regarded the sequences as hidden states and the structural conformations as observations. Efficiencies of both HMMs are calculated and compared, with the results cross-validated using ANNs, aiming to identify key hidden factors influencing observed amino acid sequences.

Chapter 13 explores the rising demand for sustainable agriculture and the need to tackle global food security issues, which has intensified the focus on enhancing crop performance using sophisticated biotechnology methods. Integrative computational models using multi-omics data, including genomes, epigenomics, transcriptomics, proteomics, and metabolomics, have arisen as potent instruments for forecasting intricate crop characteristics. These models amalgamate diverse biological data to provide complete insights at the genetic, molecular, and physiological levels on agricultural attributes, including yield, disease resistance, stress tolerance, and nutritional value. This study aims to update current trends in computational methods for integrating multi-omics data, with a primary emphasis on ML, deep learning, and network-based modeling techniques. We examine their applications in trait prediction, emphasizing significant research that demonstrates the potential of these models to enhance crop breeding tactics. Additionally, we outline the constraints and limits of multi-omics data integration, including data heterogeneity, computational complexity, and the need for strong validation procedures. We suggest a direction for future research to enhance these models for improved application in precision agriculture and the production of high-yield, climate-resilient crop varieties.

Chapter 14 embarks on how nanotechnology has emerged as a transformative approach in cancer management, enabling advances in diagnosis, biomarker discovery, and therapy. Unique nanoscale properties—such as high surface reactivity, tunable optical and magnetic behavior, and functionalization flexibility—allow precise interactions with biological systems. These capabilities enhance early detection through nano-enabled biosensors and imaging agents, support sensitive biomarker profiling, and improve drug delivery via targeted, controlled-release nanocarriers. In addition, nanotechnology strengthens immunotherapy strategies and addresses emerging challenges in cardio-brain oncology, including blood–brain barrier penetration and therapy-induced cardiotoxicity. Integration with cancer signaling pathway analysis, omics platforms, and AI-driven design is shaping next-generation precision nanomedicine. While regulatory, safety, and clinical translation challenges remain, nanotechnology offers significant promise for earlier diagnosis, improved therapeutic efficacy, and personalized cancer care.

Following this, Chapter 15 examines how electrochemical signaling—encompassing ion channels, transporters, and membrane voltage dynamics—profoundly influences the malignant behavior of cancer cells. This chapter delineates the interdependence of membrane potential, ion movement, and

intracellular signaling, as well as explains how their disruption sustains canonical cancer traits, including unchecked proliferation, metastasis, and metabolic rewiring. We review core signaling hubs such as voltage-gated and ligand-gated channels, transient receptor potential (TRP) channels, store-operated calcium channels (SOCs), and ion pumps, emphasizing their rising prominence as actionable therapeutic targets. A cardio-brain oncology lens is applied to show how bioelectric cues fuel tumor growth, shape neuron–tumor interactions in brain malignancies, and contribute to therapy-related cardiotoxicity. This chapter further integrates electrochemical biology with omics-enabled precision oncology, highlighting diagnostic and prognostic applications. We critically appraise therapeutic strategies—from pharmacologic modulators to advanced non-pharmacologic modalities and rational combinations designed for synergistic control of bioelectric signaling. Finally, we discuss practical barriers to clinical translation and outline future directions for embedding these pathways into precision oncology.

By bringing together diverse perspectives, methodologies, and application-driven studies, this volume seeks to bridge the gap between biological theory and computational practice. These chapters collectively emphasize interpretability, robustness, and translational relevance, highlighting how CI can support predictive modeling, biomarker discovery, and decision-making in biomedical and biotechnological contexts. We hope this book will serve as a valuable resource for researchers, clinicians, data scientists, and advanced students, fostering interdisciplinary collaboration and inspiring future innovations in the study of epigenetics, cellular dynamics, and mitochondrial function.

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Biomedical image processing meets deep learning

A review of current trends in cancer stage detection

Radha Krishna Jana, Atanu Kotal, Sujoy Hazra, and Soutik Pattanayek

1.1 INTRODUCTION

Cancer remains a leading cause of illness and death globally, with millions of new cases diagnosed annually. Early detection is crucial for improving survival rates, but traditional diagnostic methods can be subjective and prone to human error, leading to misdiagnosis or delayed treatment [1]. Recent AI advancements, particularly deep learning, have shown promise in overcoming cancer diagnosis challenges. Deep learning algorithms use neural networks to analyze complex image data[59], providing more accurate and consistent interpretations than traditional methods [2,63]. Convolutional neural networks (CNNs) have been successfully applied to various imaging techniques, outperforming traditional methods in tumor detection, segmentation, and classification tasks [3]. Deep learning combined with biomedical image processing enhances disease detection accuracy and streamlines clinical workflows. AI-assisted systems support radiologists by reducing workload and improving diagnostic efficiency, ultimately leading to better patient care [4,64]. Deep learning models can learn from large datasets, making them highly effective in oncology. Trained on diverse datasets, they generalize well across populations and imaging conditions, enabling robust diagnostic tools for various clinical settings [5,65]. A major challenge with deep learning in cancer detection is the lack of transparency in AI models, making it hard to understand their decision-making process, which can limit their clinical adoption [6,66]. Researchers are working to improve AI model interpretability using techniques like attention mechanisms and saliency maps, which highlight key features in input images, hence increasing trust in AI-driven cancer detection [7]. A key challenge is securing high-quality annotated datasets for training deep learning models, which is time-consuming and costly [67]. Researchers are exploring semi-supervised and unsupervised learning techniques to leverage unannotated data, addressing this limitation [8]. Integrating deep learning tools into clinical workflows raises ethical and regulatory concerns, requiring careful consideration of patient privacy, data security, and regulatory compliance to ensure safe and effective clinical use [9,68]. This work discussed on application of machine

learning algorithm on different health related data [10,72]. In this work, Genetic algorithm is applied for a healthcare dataset [11,73]. The authors discussed the protein–protein interaction in this work [12,74]. This study discussed the progression prediction of Alzheimer’s Disease using different machine learning model [13,75].

1.2 BACKGROUND AND MOTIVATION

Through deep learning techniques and biomedical image processing integration, just to name a few, the diagnostic field has been totally transformed [69]. Detection, treatment, and staging of serious diseases are just an example of advancements brought about by biomedical image processing and deep learning techniques [70]. Detection at the earliest stage is vital, as it has a significant influence on treatment decisions and hence on patient prognosis. Traditional cancer diagnosis procedures are largely characterized by a reliance on invasive operations, subjective assessments, and the proficiency of radiologists or pathologists, which could lead to different results and slow diagnoses [14].

1.2.1 Advancements in imaging techniques

New improvements in imaging technologies, such as MRI, CT, and PET, have largely enhanced our ability to visualize and evaluate tumors. The problem is that the amount of imaging data generated can be so high that it is difficult for even the most trained staff to manage it. It is very important that these images are interpreted correctly and quickly in order to treat cancer efficiently, especially in its late stages where treatment possibilities are few [2].

1.2.2 The role of deep learning

Deep learning, which is one of the artificial intelligence (AI) methods, has set a goal to grant itself as little human intervention as possible in the process of data preparation. Deep learning, a branch of AI, has become popular mainly because it can do feature extractions (FEs) by itself from complicated datasets, and its results are better than those of standard techniques. CNNs, in particular, have shown remarkable success in image classification tasks, thereby making it possible to develop the reliable models that can accurately stage tumors. These models can learn the hierarchical nature of the data, thus allowing them to uncover very small features that even an expert may not be able to notice [15]. This work analyzed the protein–protein interactions to identify critical molecular partners. This study also included the cancer-related computational analysis [12].

1.2.3 Integration of image processing techniques

Biomedical image processing that uses traditional methods of image segmentation, enhancement of images, FE, and machine-learning-based techniques can greatly assist in cancer detection and staging [60]. Noise removal and brightness enhancement as a preprocessing method [71] can become one of those methods that will enable CNNs to work better and, therefore, prediction of cancer will be more reliable [14].

1.2.4 Motivation for research

This research project aims to develop deep-learning-based tools for efficient cancer detection and staging, alleviating the workload of medical practitioners and improving patient treatment by integrating image analysis and process optimization for real-time diagnosis [15].

1.3 OVERVIEW OF CANCER STAGING

Accurate cancer staging is crucial for clinical decision-making, treatment planning, and prognostication, as it determines the extent of cancer spread, guiding healthcare professionals to develop personalized treatment plans and adjust therapies accordingly [16].

1.3.1 TNM classification system

TNM system is the main classification standard for cancer stages [17].

- **T (Tumor):** The primary tumor's dimensions and extent.
- **N (Nodes):** The condition of the local lymph nodes.
- **M (Metastasis):** The absence or presence of metastases that were not close to the tumor.

1.3.2 Stage groups

Cancer stages are often divided into categories, from Stage 0 (carcinoma in situ) through Stage IV (aggressive tumor), with the latter implying not only local but distant spreading of cancer [18].

1.3.3 Goal of correct staging

Correct staging has a big influence on treatment and on patients' eligibility for clinical trials, and it also provides essential prognostic data. The accurate staging is essential for selecting the right treatments including surgery, chemotherapy, radiotherapy, and immunotherapy [19].

1.3.4 Old staging techniques

Diagnostic imaging (MRI, CT scans, and PET scans) and tissue biopsies are always at the forefront of cancer diagnostics [20].

1.3.5 Biomedical image processing and deep learning integration

The use of biomedical image processing and deep learning technologies has been on the rise in recent times, and these changes have led to improved staging accuracy of cancer. These technologies have many benefits [14].

1.3.6 Automated image analysis

Deep learning architectures, especially CNNs, are capable of processing a large volume of medical images to spot tumors, to evaluate histopathological features, and to find lymph node met with amazing precision [14].

1.3.7 Feature extraction and classification

Deep learning can be a powerful tool for the detection of subtle changes in images that are not easily recognizable by human experts. As a result, the sensitivity and specificity of staging-related are significantly enhanced [21].

1.3.8 Predictive modeling

Developing machine learning models that can be provided with patient's health histories data to predict the outcomes of the patients based on their images would lead to more accurate stages and better treatment choices [22].

1.3.9 Integration with clinical data

The integration of imaging with clinical data, such as genetic markers and patient history, leads to a more comprehensive evaluation of cancer stage and may be a better predictor of treatment response [23].

1.3.10 Online feedback

The incorporation of these capabilities into clinical workflows can lead to online assessment of patient management schedule, which may allow for prompt interventions [24].

1.4 BIOMEDICAL IMAGE PROCESSING TECHNIQUES

1.4.1 Overview

Image processing techniques extract valuable information from biomedical images, enabling analysis of organs and structural characteristics. Key methods include preprocessing, FE, and segmentation, which yield bounding boxes or masks of identified objects, thereby facilitating cancer detection. Preprocessing improves biomedical image quality by reducing noise and enhancing information content, which is crucial for accurate segmentation and FE. Techniques like filtering and symmetrized Gauss filtering are used, while FE identifies regions of interest using edges, corners, and other local characteristics [25]. The primary goal is to isolate candidate regions for further processing, hence improving system efficiency by preselecting areas for detailed analysis. Techniques like SIFT and SURF are used to detect local patterns and dense regions, aiding cancer stage prediction [26]. Image segmentation identifies meaningful regions or object boundaries, which helps in detecting suspicious areas and informing classifier decisions. Initial approaches often involve partitioning images into significant regions to narrow down the search space for tumors or lesions [15].

1.4.2 Image preprocessing methods

Image preprocessing is a foundational phase of the overall section Image Processing Techniques. Medical image data are sometimes noisy, which can arise due to various factors—for instance, when a breast ultrasound image is taken by a doctor for interpreting and predicting cancer stage. If the doctor machine is not well enhanced or the ultrasound system encounters multifarious sides, then, at the time of image acquisition, the image may possess different noises. These types of noises continuously reduce the image quality; therefore, the cancer symbols become confusing like non-smooth ones, hairy or fuzzy images, or even the denotation of the tumor region can be in doubt. These noises in the image cause obstacle for the local entangled attributes of the tumor, essentially the tumor margin on the skin. These limited image features, when used as input attributes, neither effectively enable the activation of the deep CNN nor identify a tumor. DATA-augmentation image processing is an essential segment of the neural network because it amplifies the dataset through a set of transformations such as flipping, rotation, schlieren, and cropping [16]. Before a picture is taken into the neural network, it is often squashed into a 224×224 -sized image, leading to the loss of intrinsic characteristics. This notion does not apply to breast ultrasound images, as signal brightness and boundary clarity of an organizational image vary when the image is rotated, flip-changed, or transformed. Preprocessing is the process that highlights each image's

characteristics and supplies the network with the best network dataset so that classifiers may operate even more efficiently for FE. Past Deep Learning Techniques detail the application of deep learning algorithms that perform automatic FE from processed breast cancer images [18].

1.4.3 Feature extraction techniques

FE techniques play a vital role in the classification and diagnosis of diseases, providing a condensed and representative subset of image data to various classifiers [28]. Images must be converted into feature descriptors to extract their primary information, a task that requires an elevated level of experience [17]. In the field of medical automatism, such as breast cancer detection on histopathological images, adequate methods of FE allow the differentiation of benign and malignant tumors. They are critical for locating lesions and extracting feature values [19]. The major forms of FE can be split into three primary categories: frequency domain, spatial domain, and color FE [27]. Frequency domain descriptors transform the image signal into the frequency domain to access pertinent details concerning the relevant content or the image's nature. In the approximation of these types of descriptors, the extraction method is based on finding frequencies within the normal comprehension range that describe or characterize the image itself. Popular algorithms include the Fourier transform, curvelet transform, and the Gabor filter, often employed with the latter bearing the ability to digitize the texture of the image space at various scales. Spatial domain descriptors extract information usually by measuring the local variations in intensity for each region or subregion. Consequently, the extraction of such descriptors accepts the principle of transforming the pixels into specific quantities representing the statistical or the structural properties of the image. This kind of extraction includes popular methods such as texture, morphological, and edge-based extraction, and it must be noted that many methods belonging to this classification extract textures through statistics. This particular feature was applied to various studies. Color FE estimates the distribution of the color within the image and may be defined based on models that use the coordinate systems of RGB, HSV, YCbCr and CIE $L^*a^*b^*$ to transform the image information and calculate the relevant color histograms, mean and variance [29]. Color is considered as a pertinent property when targeting the classification of particular images.

1.4.4 Image segmentation approaches

Tumor boundary delineation is essential for image-guided tasks [11]. Based on application and algorithms, segmentation approaches include thresholding, region-based, edge-based, fuzzy, neural-network-based, probabilistic, and machine learning techniques. Comprehensive medical-image-segmentation

overviews outline classical, machine learning, and deep learning methods and offer guidelines for selecting breast cancer segmentation methods. Thresholding assigns pixels to backgrounds or targets based on intensity-level thresholds. Adaptive thresholding considers local or global image intensities. Region-based techniques utilize intensity, texture homogeneity, and spatial similarity, leading to algorithms such as region growing, splitting and merging, clustering, and watershed. Edge-based methods detect boundaries via gradients and Laplacians; however, hybrid techniques combining spatial–intensity and contours often yield superior results. As manual design and parameter tuning are labor-intensive, fuzzy, neural network, probabilistic, and machine learning techniques address the segmentation problem in progressive steps.

Fuzzy-segmentation methods—including fuzzy c-means and atlas-based techniques—manage image vagueness, improve accuracy, and reduce time. Neural network approaches focus on self-learning: Adaptive Resonance Theory (ART)-based classification and hybrid networks target FE and classification, whereas convolutional (CNN), fully convolutional (FCN, U-Net), and semi-supervised networks perform pixel-level analyses [30]. Probabilistic-segmentation techniques employ Markov random field (MRF) and level-set models. Machine learning methods encompass support vector machine (SVM) frameworks alongside supervised, unsupervised, semi-supervised, and deep learning algorithms [31]. Given the small size and complex boundaries of medical-image targets, no single segmentation technique universally outperforms others for all cancer types, underscoring the continuing relevance of thresholding, region-based methods, hybrid models, and neural networks.

1.5 DEEP LEARNING FUNDAMENTALS

Deep learning is the major source of change that has been recognized in the field of biomedical image processing, with the most remarkable application being the detection and diagnosis of the most severe diseases like cancer. This part explains the basics of deep learning with an emphasis on the related concepts that have contributed to recent breakthroughs in medical image processing, i.e., neural networks and CNNs, which are the main architectures used in today’s image analysis systems [32].

1.5.1 Introduction to neural networks

Neural networks belong to the category of machine learning models that take the human brain as a model with regard to their architecture and function. They consist of nodes (neurons) that are interconnected by layers

- **Input Layer:** This layer represents the characteristics of the given dataset (e.g., pixel brightness values in an image).
- **Hidden Layers:** Via the propagation of the inputs through weighted links and activation functions, the inputs are completely transformed. The networks' ability to unravel complex patterns is depending on the complexity and depth of such layers.
- **Output Layer:** Based on the inputs, the output layer produces either estimations or categorizations.

1.5.2 Principle concepts

- **Activation Functions:** They explain the process of output of the weighted sum of inputs through the given function. Among the mentioned functions are ReLU (Rectified Linear Unit), sigmoid, and softmax.
- **Backpropagation:** An important algorithm, which is working backwards, makes the process of the adjustment of weights more efficient by lessening the loss function—a function that measures the difference between the predicted and actual values.

Applications in Cancer Detection: Neural networks can acquire knowledge from histopathological images, where they can track the faintest differences between cancerous and non-cancerous tissues.

1.5.3 Convolutional neural networks (CNNs)

CNNs are one category of neural networks that are built specifically for working with images or other structured grid data. They employ spatial hierarchies to increase the success greatly in visual tasks:

- **Convolutional Layers:** They employ convolutional filters to take features from input images. Each filter takes different features (edges, textures, etc.) at different places.
- **Pooling Layers:** They reduce the dimensionality of feature maps, while they retain the most important features. Max pooling and average pooling are common techniques.
- **Fully Connected Layers:** In these layers, every neuron of one layer is connected to every neuron of the next layer; usually, it is done just before the output layer for classification tasks.

1.5.4 Benefits of CNNs

- Less number of parameters because of weight sharing and local connectivity.

- Better resistance to translation, scaling, and other distortions in images.
- The capability to automatically extract the features, which leads to the elimination of manual FE.

1.5.5 Applications in cancer detection

CNNs are allowed to interpret visual data such as mammograms, MRIs, and even microscopic pictures, enabling them to mark the stages accurately and to make diagnostics reliable.

1.5.6 Deep learning models

Deep learning model training is a multi-step procedure that has a direct effect on the models' performance and their ability to generalize [29]:

Gathering and Preparing Data: Properly annotated datasets of good quality are a must for an efficient training. The diversity of datasets can be boosted by using the technique of augmentation (e.g., rotation and flipping).

Loss Function: This function is used for a model's performance.

Optimizer: Adam, SGD, and RMSprop help to lower loss functions by changing weights during training.

Problems and Thoughts: The model may overfit, performing well on training data but poorly on new data. Techniques like dropout and early stopping can help mitigate this risk.

Transfer Learning: Using pre-trained models (e.g., ImageNet) and fine-tuning them for specific tasks saves time, reduces effort, and often boosts accuracy.

1.5.7 Implementations

Tools such as Tensor Flow and PyTorch give us instruments and libraries for the whole process of the training as well as for visualizing the network during training and evaluation [30].

1.6 INTEGRATION OF IMAGE PROCESSING AND DEEP LEARNING

The linking of image processing techniques with deep learning models means an impressive leap in the field of biomedical image analysis, especially in the area of core disease detection such as cancer.

This part illustrates the main steps.

1.6.1 Data preparation

Data preparation is the most vital part in creating a successful deep learning model for biomedical image processing. It includes a few major sub-steps:

Image Acquisition: Collecting data by different methods of imaging (e.g., MRI, CT, and histology images). Each modality may require different preprocessing techniques due to resolution, contrast, and noise characteristics [33].

1.6.2 Image preprocessing

Normalization: Equalizes intensity values from different images so that a standard intensity is applied. This standardization will help improve model convergence.

Resizing: To meet the required input size of the neural network, images may need to be resized to be of the same size.

Augmentation: To get more varied training data, several methods of augmentation like rotation, flipping, and contrast adjustment are used. This is especially effective in preventing overfitting.

Segmentation: Locating the ROIs within the image to identify those parts that are showing cancerous growths. Techniques can include simple ones like thresholding or region growing and more complex ones like U-Net

Labeling: Proper labeling of data is the foundation of it all. It can comprise expert annotations (e.g., radiologists marking tumors) or the use of weakly supervised learning methods if there is little labeled data available.

Splitting the Dataset: The dataset is divided into three parts: training, validation, and test sets for model training and evaluation.

1.6.3 Model development

This point refers to choosing and training of deep learning structures depending on the task of cancer detection [34].

1.6.4 Model architecture selection

- **Convolutional Neural Networks (CNNs):** These are the most common networks used for image-related tasks. We can build a network from scratch or utilize transfer learning (e.g., taking pre-trained models like VGG16, ResNet, and InceptionV3 as the starting point) [35].
- **Generative Adversarial Networks (GANs):** These networks can be used to create more data for training or to synthesize new images so that a model becomes more robust.
- **Hybrid Models:** Merging CNNs with RNNs (recurrent neural networks) to deal with sequence data (such as video imaging in cancer diagnoses).

1.6.5 Training techniques

- **Backpropagation:** The process that trains the model by reducing the chosen loss function, which is most often Binary Cross-Entropy or Categorical Cross-Entropy.
- **Regularization:** The user can install dropout, L1/L2 regularization, and other techniques to help fight overfitting.
- **Fine-Tuning:** Improving model performance by adjusting hyperparameters and training strategies.
- **Implementation Frameworks:** The use of libraries like TensorFlow, PyTorch, or Keras that have extensive support in the creation and training of deep learning models [36].

1.6.6 Evaluation metrics

Model performance evaluation is a must in confirming model effectiveness in clinical applications. The following metrics are the ones without which it is hard to assess the model quality:

Accuracy: A measure that shows how many instances the model correctly predicts out of all the instances. Although it is a straightforward measure, it might not reflect the real situation in the case of highly unbalanced datasets.

1.6.7 Precision and recall

Precision (Positive Predictive Value): Among all positive predictions, the fraction of true positives. The higher the precision is, the lower the false positive rate will be.

F1-Score: The harmonic mean of precision and recall, thus creating a single metric that reflects the balance between the two, especially in the case of imbalanced datasets.

ROC–AUC (Receiver Operating Characteristic–Area Under Curve): This is a measure for distinguishing the model's capacity between classes at all threshold settings. AUC figures can take values starting from 0 up to 1, with 1 being an ideal classification.

Confusion Matrix: A classification matrix giving the count of true positive, true negative, false positive, and false negative observations.

1.7 CASE STUDIES

In this chapter, we will focus on how biomedical image processing and deep learning have been implemented to the detection of different types of cancers, namely breast, lung, and prostate cancers. Each case provides not only the insight into what has been done methodologically, but also

the significance of these techniques and the achieved outcomes in terms of accuracy and diagnosis improvement [37].

1.7.1 Techniques utilized

- **3D CNNs:** 3D CNNs are very suitable for CT scan data taking voluminous data as the manner in which they can reveal the spatial hierarchy in three dimensions [38].
- **Radiomics:** This method is about deriving a large number of features from medical images and employing machine learning algorithms to link these features with clinical outcomes [39].
- **Nodules Detection Algorithms:** Specific models, such as “DeepLung”, are created to identify and categorize pulmonary nodules from CT scans and are good at upgrading the radiological pre-assessment [40].

The latest works demonstrate the great metrics of future such as precision and recall by especially coalescing CNNs with other machine learning algorithms. Prostate cancer detection, typically relying on mpMRI, is benefiting from AI-powered imaging analysis, significantly boosting detection rates, especially for clinically significant lesions [14].

The evidence of deep learning models can be found in the results of their identification of prostate cancer lesions, which are highly sensitive and specific, thus reducing the false-positive rates as compared to the interpretations of traditional imaging [41].

1.8 CHALLENGES IN IMPLEMENTATION

On top of these technical improvements and the high hopes of deep learning, the stage recognition of cancer via deep learning and biomedical image processing is still quite far from being used practically[42]. Such challenges can affect models up to inaccuracies, their applicative potential in clinical settings, and, finally, their extent in patient care. This part of the paper will give a brief overview of three main issues: the quality and availability of data, the adaptability of the model, and understanding the result [43].

1.8.1 Data quality and availability

Data quality and availability are the focal points of many problems related to the building of deep learning models that accurately detect cancer. In fact, properly annotated datasets of high quality are indispensable for training effective models as they practically depend on large datasets for the learning process. The following features make the domain complicated [44].

1.8.1.1 Limited access to diverse datasets

Sometimes, medical imaging datasets may be private properties of certain institutions or may have been collected in specific institutional settings and thus be less diverse and representative. The lack of generality in the models could potentially lead to biases and poor performance with populations and kinds of imaging equipment that are different from those on which the models were trained.

1.8.1.2 Imbalanced datasets

Most of the cancer datasets mainly consist of images with fewer tumors in certain stages of cancer, thus leading to datasets in which one class dominates, and it is quite a challenge to train machine learning models properly. Such imbalance can make these models weak in recognizing stages with fewer instances [62].

1.8.1.3 Variability in imaging techniques

Just different imaging procedures (e.g., MRI, CT, and PET) and operational protocols can be a source of data variability that makes it hard for models to be general across different data acquisition conditions [45].

1.8.1.4 Annotation quality

The experience and knowledge of the annotating radiologists or pathologists can lead to variability in the annotated datasets. Such variability changes the scenarios of training and testing deep learning algorithms and thus their performance and stability.

1.8.2 Model generalization

Generalization is a model's capability to perform well on data that it hasn't seen before and hence is not part of the training set. Accurate cancer stage prediction is crucial across diverse patient populations and clinical settings, ensuring effective treatment and improved outcomes. Here are some challenges [46].

1.8.2.1 Overfitting

Deep learning models often struggle with generalizability, memorizing training data rather than extracting features, leading to poor performance on new data. This is particularly problematic in medical imaging due to patient-image variability.

1.8.2.2 Domain adaptation

Domain shifts due to variability in imaging protocols, equipment, and patient demographics can significantly degrade deep learning model performance on new, unseen data. One of the major challenges is to make sure that the models are able to adapt to these differences without going through a lengthy retraining process.

1.8.2.3 Integration of multimodal data

The detection of cancer is, most of the time, a procedure that requires the use of different types of data (e.g., histopathological images, genetic data, and clinical data). It is quite a difficult task to develop models that effectively use this multimodal information while remaining generalizable [47].

1.8.3 Interpretability of results

The interpretability of deep learning models, in particular, when these models are regarded as “black boxes”, is among the issues that have been raised with regard to their use in clinics. It is very important for healthcare professionals to accept and trust models only when they know how models arrive at their decisions. The following are some of the challenges [48].

1.8.3.1 Lack of transparency

Most of the deep learning models do not disclose the exact step-by-step process through which a decision is arrived at. Such non-disclosure can make acceptance by clinicians difficult as they really require the logic of the diagnosis or stage detection in the clinical setting, which is very important.

1.8.3.2 Need for visual explanations

Most of the time, healthcare professionals require model predictions put in the spotlight visually along with the support. One of the frontier research areas is building methods that can deliver interpretable and clinically relevant visualizations (e.g., heatmaps and saliency maps).

1.8.3.3 Validation and trust

Clinicians will not easily rely on automated systems that are not sufficiently validated against traditional diagnostic methods. Apart from high accuracy, building trust in the use of AI requires allowing professionals to make meaningful interpretations of model outputs that conform to their professional knowledge and clinical experience [49].

1.9 FUTURE DIRECTIONS IN BIOMEDICAL IMAGE PROCESSING AND DEEP LEARNING FOR STAGE DETECTION OF CRITICAL DISEASES

The hybrid of deep learning and biomedical image processing techniques has significantly altered the identification and staging of the most critical diseases, especially cancer [58]. The current section is intended to trace the future moves of an extremely volatile work domain, indicating technological progress and possibly new areas of research.

1.9.1 Advancements in technology

Multimodal imaging, where information from different imaging methods will be combined to enhance detection accuracy, is the future of biomedical image processing. In this manner, a deeper understanding of the tumor's properties could be achieved, thus its stage could be determined more accurately [14].

The authors proposed YOLOv8 deep learning model for brain tumor detection from MRI images [50,76].

- a. **Real-time Processing and Edge Computing:** The innovation of edge computing will allow for real-time processing of imaging data, thus allowing diagnoses and treatment plans to be made in a shorter time. This will indeed be a great opportunity in less privileged areas where there is a shortage of expert radiologists and hence immediate access is not always possible.
- b. **Explainable AI (XAI):** With the increasing complexity of deep learning models, it is harder for humans to comprehend them, and this is the main reason why their interpretability is very important for clinical acceptance. The main purpose of future developments in XAI is to build models that can provide very clear reasons for their predictions, which will at last result in the formation of trust between medical professionals and patients [43].
- c. **Integration of Artificial Intelligence with Genomics and Liquid Biopsy:** Incorporating imaging data, genomic information, and liquid biopsy can depict a more complete picture of cancer progression. The future work could be about discovering ways of combining these different types of data simultaneously to achieve more accurate staging and personalized treatment strategies [61].
- d. **Federated Learning:** Federated learning is a method where the models are trained in multiple locations, without moving or sharing the data, thus ensuring the privacy of the patients [57]. Institutions may hence collaborate on building the models without exchanging confidential patient data, which not only keeps it safe but also makes it possible

for the models to become better trained as they have access to a more diverse range of datasets [58].

1.9.2 Potential research areas

Longitudinal studies with imaging data and clinical outcomes are needed to enhance predictive modeling. Comprehensive datasets mirroring tumor progression and treatment response can improve model training, enabling better prediction of cancer outcomes [28]. Ethical AI development requires addressing bias and ensuring fairness for diverse populations. Future research should focus on identifying and mitigating AI bias, creating methods that promote fairness and equity for all demographic groups [51]. Future studies will integrate patient-reported outcomes, clinical findings, and imaging to personalize therapy, considering both disease metrics and patient quality of life, enabling more holistic and effective treatment approaches [52].

1.10 ETHICAL CONSIDERATIONS

Ethical considerations are significant when biomedical image processing is involved, and deep learning techniques have evolved to the point where they can identify critical diseases automatically. These technologies are still being implemented in daily clinics, but it is necessary to keep in mind the ethical issues that may arise. This chapter will be concerned with only two main ethical issues relating AI technologies in medicine, that is, confidentiality and bias [53].

1.10.1 Patient privacy

Healthcare confidentiality is a major moral problem in the healthcare system, especially when it comes to very sensitive data such as health images. Most deployments of deep learning algorithms usually call for numerous datasets of patient images, which can contain personally identifiable information (PII) [54]. The trust relationship between patients and healthcare providers can only be maintained if the confidentiality and security of this data are assured.

Among the aspects of patient privacy that need consideration are:

Data Anonymization: The precondition for the use of medical images for AI training is that the data has been anonymized so as not to have any identifier of the patient.

Informed Consent: Informed consent is essential for AI research using patient data, respecting patient autonomy and meeting legal requirements. Patients should be informed about data usage, including AI research, to ensure transparency and trust.

Data Security: There should be very strict security measures to guard against illegal access to or security breaches of patient data. This could be by using encryption, secure storage, and conducting data access audits regularly.

Compliance with Regulations: In addition to this, it is crucial that the existing law regulating HIPAA in the USA or the GDPR in Europe is followed as the only way to guarantee patient privacy and their rights to it [55].

Bias in AI Models: Bias in AI models is a significant ethical issue that can result in health disparities. Models may not perform well for specific demographic groups and eventually lead to misdiagnosis and undertreatment if the data to train deep learning algorithms do not reflect the diversity of the patient population [56].

1.11 CONCLUSION

This study discussed the different steps of biomedical image processing and different techniques of deep learning to detect cancer. On a side note, applying image processing operations like segmentation, FE, and enhancement is basically a prerequisite for preparing data for deep learning models. Techniques such as histogram equalization, morphological operations, and edge detection implemented for images could be a key to higher efficiency of the following deep learning algorithms. The synthesis of these technologies not only enables the proper staging of cancer but additionally makes it possible to a patient-specific therapy by shedding light on tumor features and activities. In addition, transfer learning is highly beneficial as it allows pre-trained models to be customized for a particular kind of tumor, thus reducing the need for several labeled datasets and shortening the time for clinical deployment. The issues, notwithstanding, are still many. The problems range from data security to the need for very large labeled datasets and the difficulty in interpreting deep learning models that slow down safe and effective use of this technology in the healthcare.

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Biomedical image processing meets deep learning

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AI-driven classification and biomarker discovery in Alzheimer's disease

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