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RADIOGENOMICS IN NEUROLOGICAL DISORDERS: A REVIEW OF IMAGING-GENETIC INTERACTIONS AND IMPLICATIONS FOR PRECISION MEDICINE

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Abstract
Radiogenomics has emerged as an innovative interdisciplinary approach that integrates imaging features with genomic and molecular data to better understand the biological basis of neurological disorders. This approach addresses limitations of conventional diagnostic methods by capturing disease heterogeneity and enabling more precise characterization of complex neurological conditions. This review aims to evaluate the role of radiogenomics in neurological disorders, focusing on imaging-genetic interactions, technological advancements, and implications for precision medicine. A narrative analysis of recent literature was conducted, emphasizing studies on radiomics, imaging genetics, artificial intelligence, and multimodal data integration. Key areas explored include neuro-oncology, neurodegenerative disorders, and psychiatric conditions, along with emerging computational and translational approaches. Radiogenomics demonstrates significant potential in improving early diagnosis, risk prediction, and disease characterization. Integration of artificial intelligence and machine learning enhances predictive modeling, tumor grading, and treatment response evaluation. Multimodal data fusion and systems biology approaches provide deeper insights into disease mechanisms and support biomarker discovery. Applications across glioma, Alzheimer's disease, Parkinson's disease, and psychiatric disorders highlight its versatility and clinical relevance. Radiogenomics represents a powerful tool for advancing precision medicine in neurology. Its ability to combine imaging and genomic data enables personalized treatment strategies, improved prognostic assessment, and non-invasive biomarker development. Continued advancements in computational methods and clinical integration are expected to further enhance its impact on neurological healthcare.

Keywords: Radiogenomics; Neuroimaging; Precision medicine; Artificial intelligence; Neurological disorders; Imaging genetics

1. Introduction

Radiogenomics is an emerging interdisciplinary area, which involves a combination of quantitative imaging characteristics with genomic and molecular data to help explain the biological basis of disease. It extends the larger field of imaging genetics, which aims to determine the relationships between genetic variation and neuroimaging phenotypes, thus allowing a better understanding of disease pathogenesis at multiple biological levels (Mashhour et al., 2025). The last ten years have seen the trajectory of medical imaging be redefined as an information-rich, quantitative science, starting from the conventional radiology and radiomics and then radiogenomics. Radiomics involves high-dimensional extraction of medical images, whereas radiogenomics is an extension of this paradigm that connects this high-dimensional features extraction to genomic signature extraction (Liu et al., 2023).
The abilities are further augmented by the progress in the field of big data analytics and computational modeling, which allows dealing with multimodal datasets. Radiogenomics uses these functions to reveal the hidden patterns that are not easily identified using conventional methods, thus facilitating precision medicine programs (Panayides et al., 2018). In addition, imaging genomics models enable data fusion strategies to integrate imaging biomarkers with genetic data to gain a better understanding of disease heritability and progression (Hartmann et al., 2023).

Neurological disorders are a major and an increasing global health burden and affect millions of people around the world and contribute significantly to morbidity and mortality. Such conditions as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), and other psychiatric disorders are distinguished by complicated etiologies including genetic, environmental, and lifestyle factors. Neuroimaging has been a very important step to further our knowledge about these conditions and specifically in detecting structural and functional changes in the brain.

As an example, neuroimaging studies played a crucial role in explaining the role of cerebral amyloid angiopathy in Alzheimer disease and provided insights into the progression of the disease and its correlation with vascular pathology (Wheeler et al., 2024). In the same way, one of the most common neurodegenerative disorders, Parkinson's disease, has been studied in great detail both in terms of a clinical perspective and an imaging perspective, which emphasizes its progressive nature and a variety of clinical manifestations (Jankovic and Lang, 2021). The historical background of the research of the Parkinson disease highlights the complexity of the neurodegenerative disorders and the necessity of more integrative approaches in order to understand the underlying mechanisms of the neurodegenerative disorders (Przedborski, 2017).

Although dramatic strides have been made in the area of diagnostic imaging and clinical neurology, the conventional techniques of visualizing neurological disorders have often failed in reflecting the heterogeneity of neurological diseases. The differences in the disease patterns and response to treatment of patients with similar clinical presentations can be significantly different, highlighting the limitations of one-size-fits-all diagnostic and treatment plans. Such variability requires considering precision medicine that tries to apply medical interventions according to the specific genetic, molecular, and phenotypic profiles.

The combination of biomolecular data and clinical and imaging data has provided new possibilities of personalized healthcare. Precision medicine models highlight the importance of biologics and molecular biomarkers in enhancing the precision of diagnosis and treatment (Rao, 2022). Moreover, innovations in personalized medicine in different fields of medicine indicate the significance of individualized treatment plans, which can be applied to neurological disorders to improve patient care (Weldy and Ashley, 2021). This combination framework allows determining patterns of complex diseases and facilitates better clinical decision-making.

This review will provide a general overview of the application of radiogenomics in neurological diseases, and in more specific terms, how imaging features and genetic information interact. It investigates the technological and biological basis of radiogenomics, explores its uses in a variety of neurological disorders, and discusses how it might be used to revolutionize precision medicine. The review also notes that translational relevance of radiogenomics to improve early diagnosis, prognostic assessment and individual treatment regimens is also highlighted in the review.

2. Biological and Technological Foundations of Radiogenomics

2.1 Genetic Architecture of Neurological Disorders

The genetic contribution of neurologic diseases is a highly complex polygenic, epigenetic, and gene-environment interaction. Genome-wide association studies (GWAS) have greatly contributed to the discovery of genetic variants related to brain structure and function (Elliott et al., 2018). Recent research also confirms that the structural connectome of the brain is highly genetic, which indicates that neural patterns of connectivity are heritable (Wainberg et al., 2024). Such results highlight the significance of combining genetic information with neuroimaging in achieving a better understanding of disease susceptibility, progression and heterogeneity in neurological disorders.

2.2 Neuroimaging Modalities in Radiogenomics

The neuroimaging modalities are core in radiogenomics as they offer detailed structural and functional information about the brain. Structural MRI (sMRI) allows the examination of the morphology of the brain, whereas functional MRI (fMRI) is able to capture the neural activity and connectivity patterns. More sophisticated methods like dynamic effective connectivity analysis have contributed to a better understanding of the interaction within the brain networks and how it relates with the genetic factors (Park et al., 2018). Diffusion Tensor Imaging (DTI) is used to determine the integrity of the white matter and PET imaging is used to observe the processes of any molecules. But the growing size and complexity of neuroimaging data come with severe statistical and computational challenges that need to be overcome to enable effective integration (Smith and Nichols, 2018).

2.3 Radiomics: Feature Extraction and Quantification

Radiomics is the process of extracting high-dimensional quantitative image features (including texture, shape, and intensity-based features) of medical images. These characteristics can give useful information on the heterogeneity of tumors, as well as the biological processes that underlie them, which can often reveal patterns that are not immediately visible using conventional imaging interpretation. Radiomics has shown great promise in enhancing disease detection and classification, as well as prognostic evaluation (Gillies and Schabath, 2020). Moreover, it has been demonstrated that radiomic features could be associated with molecular and genetic features, thus forming a biological core of imaging phenotypes (Grossmann et al., 2017). This throughput feature generation is useful in creating predictive models in precision medicine. Figure 1 is a graph that shows the radiomics feature extraction process, starting with image acquisition, and continuing with predictive modeling.

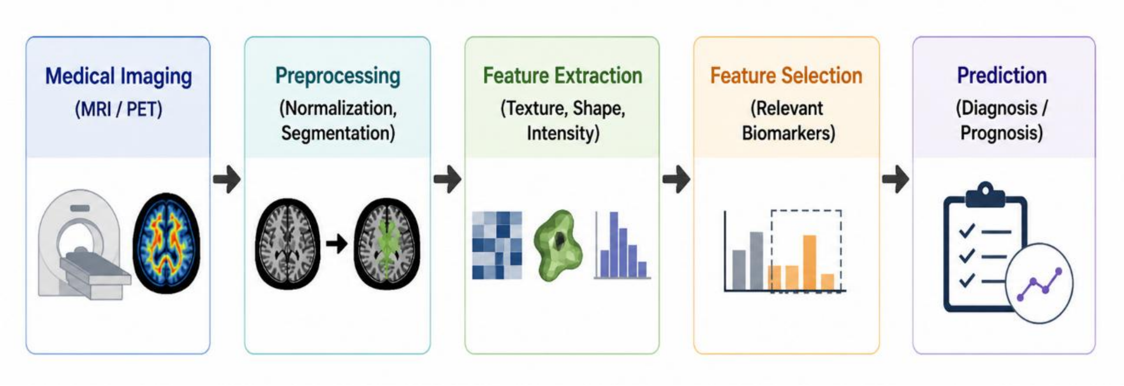

Figure 1. Radiomics Feature Extraction Workflow

In Figure 1, the gradual evolution of the medical imaging data into the quantifiable features that can be incorporated into the predictive models are outlined. This workflow allows clinically relevant biomarkers to be extracted, which aid in improving diagnosis, prognosis, and personalized decision-making in radiogenomics.

2.4 Integration of Genomic and Imaging Data

One of the foundations of radiogenomics is the combination of genomic and imaging data, which can be analyzed using multimodal analysis. Imaging-genetics models integrate neuroimaging characteristics with genetic data to establish significant relationships and biomarkers. State-of-the-art data fusion methods, such as machine learning-based algorithms, can be used to fuse heterogeneous datasets and enhance predictive accuracy (Huang et al., 2022). Also, multi-omics integration strategies use a combination of genomics, transcriptomics, and proteomics data to give a systems-level view of disease processes (Subramanian et al., 2020). They will contribute to the potential to find out more complicated interactions and contribute to the development of a more precise medicine in the neurological disorders.

3. Role of Artificial Intelligence and Machine Learning

3.1 Machine Learning Approaches

Machine learning (ML) can be considered a key component of radiogenomics, as it allows the analysis of high-dimensional imaging and genetic data. Supervised learning algorithms, including support vector machines and random forests, are commonly used to accomplish classification and prediction tasks, and unsupervised learning algorithms help to discover patterns and cluster them in complex data sets. Dimensionality reduction and feature selection are necessary to enhance the level of model performance and minimize overfitting, especially in neuroimaging research with high dimensions. Their applicability to a wide variety of clinical neuroscience problems, such as neuro-oncology and psychiatric disorders, is demonstrated by their ML applications across neurological conditions (English et al., 2021). Moreover, the use of ML has greatly enhanced the grading and diagnostic quality of glioma (Merkaj et al., 2022).

3.2 Deep Learning in Neuroimaging

Neuroimaging Deep learning has transformed neuroimaging, with the ability to automatically extract features and perform sophisticated pattern recognition. Convolutional neural networks (CNNs), recurrent neural networks (RNNs), and transformer-based models are moving towards more medical imaging tasks. These models are good in automatic segmentation, classification and detection of neurological abnormalities. An example is the remarkable success of deep learning in glioma imaging in enhancing tumor detection and characterization (Zlochower et al., 2020). Detailed reviews have shown the intensive developments and wide applicability of deep learning in medical imaging (Zhou et al., 2021). The initial research in the field also highlights the revolutionary effect that deep neural networks have on image analysis (Shen et al., 2017). Table 1 summarizes some of the major artificial intelligence and machine learning algorithms used in radiogenomics.

Table 1. Key Artificial Intelligence and Machine Learning Techniques in Radiogenomics

Method	**Type**	**Application in Radiogenomics**	**Key Advantage**	**Reference**
Support Vector Machine (SVM)	Supervised ML	Tumor classification, disease prediction	High accuracy in small datasets	English et al., 2021
Random Forest	Supervised ML	Feature selection, classification	Handles high-dimensional data	Merkaj et al., 2022
K-means Clustering	Unsupervised ML	Pattern discovery, subgroup identification	No labeled data required	English et al., 2021
Convolutional Neural Network (CNN)	Deep Learning	Image segmentation, tumor detection	Automated feature extraction	Zlochower et al., 2020

Recurrent Neural Network (RNN)	Deep Learning	Temporal imaging data analysis	Captures sequential patterns	Zhou et al., 2021
Transformer Models	Deep Learning	Multimodal data integration	High scalability and performance	Zhou et al., 2021
Explainable AI (XAI)	Interpretability	Model transparency, decision explanation	Enhances clinical trust	Panayides et al., 2020

3.3 Explainable AI (XAI) in Radiogenomics

Although the performance of AI models is impressive, the aspect of black-box nature makes them challenging to adopt by clinical practitioners. Explainable AI (XAI) is a solution to this problem to improve the interpretability of the models used and provide insights into the decision-making processes. In radiogenomics, XAI methods are used to determine the interdependence existing between imaging phenomena and genetic correlates to enhance clinical trust and transparency. The interpretable models are especially significant in the field of healthcare where the decisions made are to be reliable and justifiable. The movement toward introducing explainability into AI systems is gaining momentum, particularly in medical imaging informatics, where transparency is needed to approve the regulatory framework and integrate AI into clinical practice (Panayides et al., 2020).

3.4 Big Data and Computational Challenges

The adoption of AI in radiogenomics is coupled with considerable big data and computational problems. Neuroimaging data are frequently mixed, comprising data provided by numerous sources, modalities and populations. Such variability may affect the generalizability and performance of models. Also, the high-dimensional data predisposes the overfitting effect, especially with the use of small samples. The issue of ensuring reproducibility and robustness of AI models is a key issue in the domain. The statistical issues that are related to large-scale neuroimaging data, such as data standardization and validation, have to be addressed so that reliable results could be obtained (Smith and Nichols, 2018). To accomplish this, it is necessary that the challenges that might be there to overcome are overcome successfully to bring the AI-driven radiogenomics into clinical practice. Nevertheless, even with these developments, the absence of standardized multimodal integration models is still a significant bottleneck to large-scale clinical application.

4. Radiogenomics in Neurological Disorders

4.1 Neuro-Oncology (Glioma, Glioblastoma)

4.1.1 Imaging–Genetic Correlates in Brain Tumors

Radiogenomics has made an important contribution to the comprehension of imaging-genetic relationships in brain tumors, specifically gliomas and glioblastomas. Significant genetic changes have been associated with specific imaging phenotypes including isocitrate dehydrogenase (IDH) mutations and MGMT promoter methylation. Radiomic methods are used to measure tumor heterogeneity as a quantification of spatial variations in imaging features, which represent underlying molecular heterogeneity (Fathi Kazerooni et al., 2021). It has also been demonstrated that imaging can identify genetic heterogeneity within tumors, which can provide information on the aggressiveness of the disease and its resistance to treatments (Chow et al., 2018). Moreover, genomic sequencing technologies are in the process of enhancing the molecular classification of glioblastoma, which helps in precision diagnostics (Jovčevska, 2018).

4.1.2 Radiogenomics for Tumor Grading and Prognosis

Radiogenomics has become an effective instrument in the tumor grading and prognostic evaluation of neuro-oncology. Radiomic features of advanced MRI have been linked to particular changes in chromosome alterations, which allow better stratification of different subtypes of glioblastoma (Min et al., 2021). Machine learning and AI-based methods are additional steps to optimize the forecast of survival and a response to treatment through the combination of imaging and genomic data (Kister et al., 2023). Also, longitudinal imaging studies based on multimodal MRI have made it possible to quantitatively assess the dynamics of tumor growth and provide valuable information on monitoring the progression of the disease and evaluating the effectiveness of therapeutic interventions (Das et al., 2023). All these methods contribute to better clinical decision-making that is more accurate and personalized. Radiogenomics is applied in the most significant neurological disorders, and this is summarized in Figure 2.

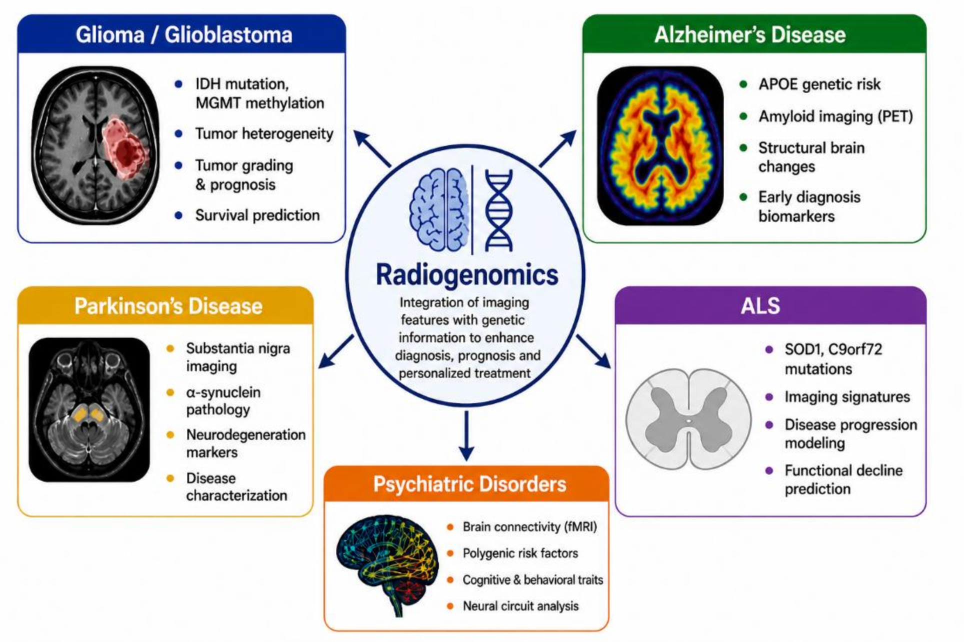

Figure 2. Radiogenomics Applications Across Neurological Disorders

Figure 2 shows the combination of imaging features and genetic markers to support disease characterization, prognosis, and individualized treatment of major neurological and psychiatric diseases.

4.2 Neurodegenerative Disorders

4.2.1 Alzheimer's Disease

Radiogenomics has also been useful in elucidating the Alzheimer disease by demonstrating a connection between imaging biomarkers and genetic risk factors including APOE variants. Neuroimaging, such as MRI and PET, can be used to visualize the amyloid deposition and structural brain alterations related to disease progression. Research in imaging-genetics has revealed the presence of key biomarkers that are associated with cognitive decline and severity of the disease (Chhetri et al., 2024). Additionally, recent studies emphasize the importance of neuroimaging endophenotypes and their role in understanding the genetic mechanisms underlying the Alzheimer disease and other neurological disorders (Wen et al., 2025). Epigenetic changes also play a role in the development of diseases, which is why gene-environment interactions are important in the pathology of Alzheimer (Coppedè, 2023).

4.2.2 Parkinson's Disease

Radiogenomics has also been useful in identifying imaging biomarkers that are linked to neurodegeneration in Parkinson disease. Deep learning techniques have improved structural and functional imaging of the substantia nigra, which is able to detect disease-related changes more precisely (Lillebostad et al., 2025). Also, molecular imaging and other large-scale visualization techniques have given new insights into α-synuclein aggregation, which is one of the main pathological hallmarks of Parkinson disease (Andrews et al., 2025). The above developments underscore the possibility of integrating imaging and genetic information to enhance early diagnosis and characterization of diseases.

4.2.3 Amyotrophic Lateral Sclerosis (ALS)

The radiogenomics strategies used in ALS are aimed at determining the imaging signatures and genetic predictors that are related to the progression of the disease. Probabilistic modeling of predictive trajectories of functional impairment using neuroimaging techniques has been used to provide insights into disease heterogeneity (Tavazzi et al., 2022). Moreover, longitudinal registry-based research has enhanced the knowledge on the survival pattern among patients with ALS, emphasizing the variability of disease outcomes (Vasta et al., 2025). Combining imaging and genetic data will allow more precise prognostic modeling and will help to develop personalized treatment plans in ALS.

4.3 Psychiatric and Cognitive Disorders

4.3.1 Schizophrenia and Mood Disorders

Radiogenomics has helped to understand the biological basis of psychiatric disorders, such as schizophrenia and mood disorders. The study of imaging genetics has revealed that genetic variation can be linked to brain structure, the way it functions, and how it is connected, which can be used to understand disease mechanisms (Bogdan et al., 2017). Large-scale neuroimaging projects have even added to this understanding by combining genetic and imaging data in diverse populations, which then allows identifying reproducible biomarkers (Thompson et al., 2020). These methods enable a better holistic picture of psychiatric conditions other than the use of symptoms in categorizing psychiatric conditions.

4.3.2 Imaging Genetics in Behavioral Phenotypes
The imaging genetics has equally been very instrumental in relating genetic variation with phenotypes with respect to behavior and cognitive traits. Research looking into the genetic architecture of the cerebral cortex has shown that there are significant correlations between genetic and brain morphology, which, in turn, have an effect on cognitive functioning (Grasby et al., 2020). The researchers can be better placed to know the neural circuits of behavior and cognition with the combination of neuroimaging and genomic data. The methodology provided by such a strategy offers an opportunity to investigate the complex characteristics as well as to contribute to the design of individual interventions on the basis of the specific neural pathways. Table 2 provides a comparative summary of radiogenomic applications in the major neurological disorders.

Table 2. Applications of Radiogenomics in Neurological Disorders

Disorder	Imaging Modality	Genetic Marker	Key Application	Key Reference
Glioma / Glioblastoma	MRI	IDH, MGMT	Tumor grading, prognosis	Fathi Kazerooni et al., 2021
Alzheimer's Disease	MRI, PET	APOE	Early detection, biomarker identification	Chhetri et al., 2024
Parkinson's Disease	MRI	α-synuclein (SNCA)	Neurodegeneration assessment	Lillebostad et al., 2025
ALS	MRI	SOD1, C9orf72	Disease progression modeling	Tavazzi et al., 2022
Psychiatric Disorders	fMRI	Polygenic variants	Brain connectivity analysis	Bogdan et al., 2017

5. Multimodal Data Integration and Systems Biology
5.1 Multi-omics Integration
The integration of multi-omics is the core of radiogenomics, in that many neurological diseases cannot be attributed to one particular molecular pathway. Rather, they consist of interactions between genomics, transcriptomics, proteomics, epigenomics, imaging phenotypes, as well as clinical variables. Through their integration, scientists are able to discover disease-specific molecular signatures and relate and associate them with measurable imaging phenomena. Multimodal integration enhances the stratification of patients, predicting their treatment, and biological explanations of disease heterogeneity in precision medicine. Even though much of the best evidence is obtained in the field of oncology, the same principles are becoming equally relevant to neurological disorders, where imaging and omics can collectively explain the complex progression of the disease (Boehm et al., 2022). Integration on a systems level also supports personalized medicine, linking molecular mechanisms and clinical outcomes (Dovrolis et al., 2019).

5.2 Imaging–Omics Fusion Techniques
Imaging–omics fusion techniques aim to combine radiological features with molecular data using data-driven and model-driven approaches. Data based methods are based on machine learning or deep learning in identifying hidden associations between imaging patterns and genomic profiles, where model-based methods use predefined biological assumptions or structured statistical models. Multilevel survival modeling is a technique that can be used in imaging genetics to combine imaging and genetic variables to enhance disease prediction and prognostic estimation (Lu & Colliot, 2021). Fusion strategies have also been expanded by artificial intelligence, which allows the extraction of automated features, risk models, and clinical decision support across workflows based on imaging (Lastrucci et al., 2025). These approaches can be used to convert heterogeneous biomedical data into predictive tools that are clinically relevant.

5.3 Network-Based and Systems Biology Approaches
Systems biology and network-based approaches offer a more comprehensive theory of understanding radiogenomic interactions. These methods do not analyze individual genes or imaging phenotypes but evaluate interconnected pathways, brain networks, molecular circuits, patterns of disease-related interaction and more. The analysis of the brain connectome is especially applicable to neurology since quite a number of disorders involve network dysfunctions across many parts of the brain as opposed to local pathology. Simultaneously, quantitative imaging properties can be affected by technical factors in image acquisition, processing and positioning of the patient making standardization a key to reliable network-based interpretation (Morkup et al., 2019). Imagining frameworks based on AI can also be used to support the systems-level analysis, which involves integrating clinical, imaging, and molecular variables to aid in the characterization of a disease and its treatment planning (Najem et al., 2025). The multimodal radiogenomics data, beginning with acquisition and continuing through clinical application, is shown in Figure 3.

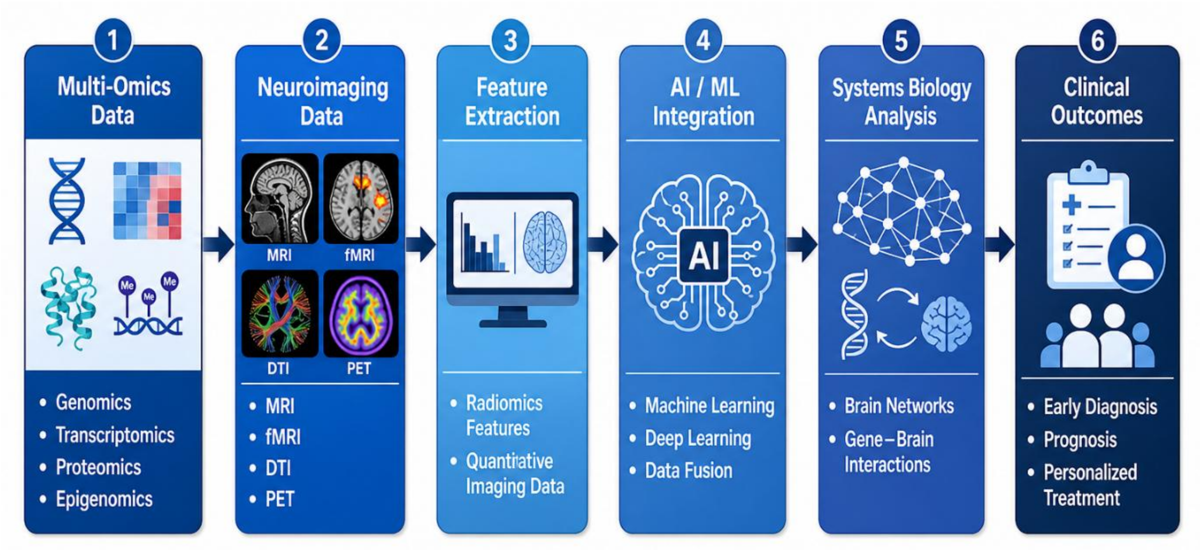

Figure 3. Integrated multi-omics and neuroimaging radiogenomics workflow

Figure 3 demonstrates the radiogenomics workflow that includes multi-omics and neuroimaging data through feature extraction, artificial intelligence-based fusion, and systems biology analysis to produce clinically relevant outputs. This framework facilitates transforming complicated multimodal data into actionable information to aid early diagnosis, prognosis, and personalized treatment in neurological disorders.

6. Clinical Applications and Translational Potential

6.1 Early Diagnosis and Risk Prediction

Radiogenomics can play a major role in providing early diagnosis and predicting risks of neurological disorders by identifying subtle imaging and molecular changes before clinical symptoms occur. Early diagnosis of preclinical diseases is especially relevant in situations where early intervention can make a difference, such as brain tumors and neurodegenerative conditions. The combination of imaging and genomic data into multimodal approaches can significantly help to identify at-risk individuals and patterns of disease onset. Radiogenomic frameworks have been shown to detect early-stage pathological changes to provide more accurate diagnostic conclusions and timely therapeutic responses (Sowmya et al., 2024).

6.2 Personalized Treatment Strategies

Among the most promising ways of using radiogenomics is the creation of new individualized treatment plans. Clinicians can now use imaging features to match therapies with individual patients to enhance the efficacy of therapy and to reduce the adverse effects of therapy. The capability is further improved with multimodal approaches to artificial intelligence that can examine complex datasets to direct focused therapies and precision neuro-oncology interventions (Parvin et al., 2025). Furthermore, the integration of biomolecular knowledge into clinical decision-making helps to develop personalized medicine and allow more accurate therapeutic targeting of the disease based on its particular characteristics (Rao, 2022).

6.3 Prognosis and Disease Monitoring

Radiogenomics is also important in prognosis and monitoring of disease by longitudinal monitoring imaging-genetic tracking. Clinicians can get to know disease progression and response to treatment better by continuously evaluating the changes in the imaging biomarkers and genetic profiles. Developed imaging approaches, such as multimodal MRI, allow tracking the evolution of tumors and their response to therapy in detail. As an example, the imaging-based tumor segmentation methods provide the opportunity to precisely monitor the situation even in those cases when the imaging data is not complete, enhancing the clinical decision-making (Ruffle et al., 2023). Additionally, predicting disease trajectories and patient survival are increased with the integration of imaging datasets and large-scale atlases (Capobianco & Dominietto, 2023).

6.4 Biomarker Development

The development of non-invasive biomarkers is a key translational goal of radiogenomics. Biomarkers derived by imaging when coupled with genomic data are useful insights into the biology of the disease without necessarily having to undergo invasive procedures. These biomarkers are very useful in clinical practice as they can be used in diagnostic settings, prognosis and monitoring of treatment. The combination of the principles of precision medicine into the development of biomarkers further increases their clinical utility by allowing the individual risk assessment and treatment planning (Weldy and Ashley, 2021). Radiogenomics can therefore provide a powerful framework to discover credible, non-invasive biomarkers that will support personalized healthcare and enhance patient outcomes. However, clinical translation is limited by the lack of external validation, heterogeneity of data, and there is no standard of biomarker validation protocols.A summary of key clinical applications of radiogenomics in neurological disorders is presented in Table 3.

Table 3. Clinical Applications of Radiogenomics in Neurology

Application Area	Description	Clinical Benefit	Key Reference
Early Diagnosis & Risk Prediction	Detection of preclinical imaging-genetic alterations	Early intervention and improved outcomes	Sowmya et al., 2024
Personalized Treatment	Integration of imaging and molecular profiles for targeted therapy	Tailored treatment and reduced adverse effects	Parvin et al., 2025
Precision Therapeutics	Use of biomolecular insights for individualized treatment planning	Improved therapeutic efficacy	Rao, 2022
Prognosis & Monitoring	Longitudinal tracking of imaging-genetic biomarkers	Better disease progression assessment	Ruffle et al., 2023
Survival Prediction	Integration of imaging atlases and datasets	Accurate outcome prediction	Capobianco & Dominietto, 2023
Biomarker Development	Identification of non-invasive imaging-genetic biomarkers	Reduced need for invasive procedures	Weldy & Ashley, 2021

7. Challenges and Limitations

7.1 Data-Related Challenges

The availability and quality of data is one of the major challenges in radiogenomics. A good number of studies use rather small sample sizes, thus limiting statistical power and the reliability of predictive models. The problem is especially acute, when it comes to high-dimensional imaging and genomic data, where the number of features can far outnumber the number of samples. Also, due to the variability in imaging protocols, scanner types and acquisition parameters across institutions, inconsistencies in the quality of the data become evident. The absence of standardized data collection and preprocessing approaches only makes integration and comparison across studies more challenging, ultimately impeding large-scale validation and clinical translation.

7.2 Methodological Limitations

The methodological issues are also influential to the development and application of the radiogenomic models. The generalizability of machine learning and deep learning models is one of the biggest limitations because models tend to perform well on training datasets but do not maintain accuracy when applied to independent cohorts. This is often because of overfitting, in which models reflect noise, not meaningful patterns. In addition, the results may be biased by the data selection biases, imbalance in classes, and confounding factors that make the model weaker. The reality that the syntheses of multimodal information are intricate further increases the threat of methodological incompatibilities and it is hard to develop universally applicable analytic schemes.

7.3 Ethical and Legal Concerns

The question of combining the information about genomes and images is a concern in terms of ethics and legal issues. Genetic information is very sensitive and when abused, it can pose a threat of privacy, discrimination and stigmatization. Care should be taken to ensure safe storage, access control and responsible sharing of such information. Furthermore, the informed consent procedures should explicitly provide the way the patient data will be used, especially in the research work with artificial intelligence and data sharing across the institutions. The regulation frameworks also have to transform to reflect the new pressures of data ownership, cross-border data transfer, and ethical use of AI in healthcare.

7.4 Reproducibility and Validation Issues

A significant question in the radiogenomics research is the issue of reproducibility. The majority of the research has not been validated with independent data, decreasing the validity and clinical relevance of their findings. The failure to provide consistency in the results of studies across studies is caused by a variation in the data preprocessing, feature extraction techniques and model development pipelines. Moreover, the absence of certain reporting principles makes the comparisons of results and reproduction of experiments more complicated. These problems can be tackled through incorporation of sound validation practices, clear procedures, and co-operative endeavors to develop standard datasets and benchmarking tools.

8. Future Directions

Future developments in the research discipline of radiogenomics would heavily rely on improvements in artificial intelligence and deep learning. Recent methods like federated learning allow the joint training of models by several institutes without sharing data due to the privacy of patients. Besides that, the development of foundation models, large pre-trained models that can be generalized across different tasks can also help to achieve improved robustness and scalability in medical image analysis. Such a development will result in major breakthroughs in terms of accuracy, generalizability and applicability of radiogenomic models to neuroscience research.

Radiogenomics and digital health technologies are a new trend in the sphere of personalized medicine. Wearables and mobile health systems may also be used to monitor physiological and behavioral parameters to provide timely information that enhanced imaging and genomics. With the help of the integration approach, the opportunity to monitor diseases, detect anomalies, and evaluate risks will be possible. Real-time monitoring in conjunction with radiogenomics will help in making preventive interventions in neurodegenerative and psychiatric diseases where even minor deviations may lead to clinical manifestation.

In order to effectively introduce radiogenomics to the mainstream healthcare setting, adequate regulatory provisions need to be put in place. A standardized technique in getting imaging and data preprocessing and analysis should be used to achieve interoperability and reproducibility. The regulatory authorities should determine the conditions of the validation, clearance, and clinical implementation of AI-powered radiogenomics. Moreover, collaboration among clinical professionals, data scientists, and regulatory bodies would also be crucial in bridging the research and clinical gap to guarantee the safety and effectiveness of the technology.

Radiogenomics as a field will certainly grow and develop in new directions such as precision psychiatry and personalized brain mapping. Precision Psychiatry Precision psychiatry includes the integration of imaging and genomic information into the diagnosis phase, and it might aid in more precise diagnosis and treatment of complicated psychiatric illnesses. The personalized brain mapping can be used to obtain personalized neural signatures that may be used to guide specific therapies. It shows how radiogenomics can be used in the future to promote precision medicine and transform the future of neurological treatment.

9. Conclusion

The concept of radiogenomics is a novel one which attempts to incorporate imaging phenotypes as well as genomic and molecular information in order to better understand neurologic conditions. The review has highlighted how the merging of radiomics with imaging genetics and artificial intelligence has provided deeper insights into the nature of heterogeneity, progression, and biological mechanism associated with diseases. These findings are necessary to demonstrate the utility of using radiogenomics as a non-invasive tool to correlate alterations in the structure and function of the brain with genetic factors in order to improve accuracy and identify early indicators of neurological diseases. With the advent of machine learning techniques, even greater predictive abilities of radiogenomics has been achieved in terms of tumor grading, survival prognosis, and predicting treatment responses. Additionally, the synergy between multimodal data and systems biology approaches has allowed for a deeper insight into the similarity of complex diseases, which may help find robust biomarkers and personalized treatment. It should be mentioned that radiogenomics has been rather effective in providing the opportunity to develop precision medicine by facilitating individual risk profiling, treatment planning, and disease monitoring. Regardless of the challenges that it may face, the continuous development of computational techniques, data fusion strategies, and translational approaches will make radiogenomics an essential component of the future of neurological studies and practices. The connection between molecular biology and medical imaging technologies that this field provides makes radiogenomics an important aspect of the new era of precision neurology.

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