REVIEW

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GPU-Accelerated Artificial Intelligence Applications in Cancer Diagnosis, Imaging, and Treatment Planning

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Abstract

Graphics processing unit (GPU)-accelerated artificial intelligence has fundamentally transformed cancer diagnosis, imaging, and treatment planning by delivering unprecedented computational performance and clinical efficiency across multiple oncological domains. This comprehensive review demonstrates that GPU-optimized AI platforms, including NVIDIA Clara and MONAI frameworks, have achieved remarkable performance improvements ranging from 8x to 65x acceleration in cancer genomics and computational biology applications, while simultaneously reducing operational costs by up to 85%. In medical imaging applications, GPU-based systems have revolutionized cone-beam computed tomography reconstruction, achieving reconstruction times of 77-130 seconds compared to conventional approaches that require significantly longer processing periods, while enabling dramatic radiation dose reductions of 36-72 times without compromising diagnostic image quality. Digital pathology applications have benefited from GPU acceleration through enhanced histopathological image analysis capabilities, including automated gland segmentation for colorectal cancer grading and uncertainty quantification mechanisms that support clinical decision-making processes. The integration of GPU-accelerated AI tools into clinical workflows has enabled real-time processing of complex medical data, automated tumor contouring for radiation therapy planning, and sophisticated radiomics feature extraction that correlates imaging biomarkers with genetic and molecular tumor characteristics. These technological advances represent a paradigm shift toward precision oncology, where data-driven insights augment clinical expertise and reduce cognitive burden associated with complex oncological cases, ultimately enhancing diagnostic accuracy, treatment efficacy, and patient outcomes across diverse healthcare settings.

Keywords: GPU-Accelerated AI- cancer diagnosis- medical imaging- digital pathology- clinical decision support

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Introduction

Cancer remains one of the leading causes of death worldwide, with early and accurate diagnosis being critical for favorable patient outcomes [1,2]. Traditional cancer diagnosis and treatment planning rely heavily on the expertise of pathologists, radiologists, and oncologists who must interpret complex medical imagery, genomic data, and clinical parameters to make life-altering decisions. However, this human-centered approach faces significant challenges including inter-observer variability, time constraints, and the increasing complexity of modern cancer care that demands integration of multiple data modalities [3,4]. The emergence of artificial intelligence (AI), particularly deep learning technologies, has offered unprecedented opportunities to address these challenges

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by automating pattern recognition, reducing diagnostic variability, and accelerating clinical decision-making processes [5].

The computational demands of modern AI applications in oncology have necessitated the adoption of specialized hardware accelerators, with graphics processing units (GPUs) emerging as the dominant platform for training and deploying deep learning models in cancer research [6,7]. Unlike traditional central processing units that excel at sequential processing, GPUs provide massively parallel computational architectures that can simultaneously process thousands of operations, making them ideally suited for the matrix computations fundamental to neural network training and inference [8,9]. This computational advantage has enabled researchers to tackle previously intractable problems in cancer diagnosis and treatment, from analyzing high-resolution histopathological images to processing complex genomic datasets containing millions of genetic variants [10].

Recent developments in GPU-accelerated cancer AI have demonstrated remarkable success across multiple clinical domains (Table 1). Researchers at The University of Texas MD Anderson Cancer Institute have developed automated tumor contouring systems for radiation therapy planning that leverage NVIDIA Tesla GPUs to precisely identify tumor boundaries and optimize radiation dose delivery [11]. This advancement addresses a critical clinical challenge where manual contouring is both time-intensive and subject to significant inter-physician variability, particularly in complex anatomical regions such as head and neck cancers where precision is paramount to avoid damage to healthy tissue. Similarly, investigators at the University of Queensland have utilized GPU-accelerated supercomputers to create deep learning systems capable of diagnosing skin cancer from histology slides with accuracy matching that of trained pathologists [12]. The speed advantages afforded by GPU acceleration have proven transformative for clinical implementation of AI tools. Training times that previously required weeks or months using conventional computing infrastructure can now be completed in minutes or hours using GPU-accelerated systems [12]. This dramatic reduction in computational time has enabled rapid iteration and refinement of AI models, allowing researchers to explore larger parameter spaces, test multiple architectural approaches, and validate their systems more comprehensively. The University of Queensland team reported training their convolutional neural network on 30,000 histology images in approximately 15 minutes using NVIDIA Tesla V100 GPUs, a task that would have been prohibitively time-consuming using traditional computing approaches [13,14].

Beyond diagnostic applications, GPU-optimized AI systems are revolutionizing cancer treatment planning and therapeutic decision-making (Table 2). Advanced genomic analysis platforms now utilize deep learning to identify cancer types based on genetic variations, with some systems achieving accuracy rates exceeding 94% for

Table 1. GPU-Optimized AI Tools in Cancer Applications

Tool/Platform	Primary Application	Institution/ Developer	GPU Technology	Key Features	Performance Improvements
NVIDIA AI Enterprise	Cone-beam CT image reconstruction and tumor targeting	Netherlands Cancer Institute (NKI)	NVIDIA GPU with VMware vSphere	Real-time radiotherapy treatment adaptation, precision tumor targeting, reduced radiation exposure	Enhanced accuracy in smaller tumor localization, improved treatment planning
GPU-Accelerated ML Framework	Cancer genomics research and biomarker identification	Research (Abill Robert)	GPU parallel processing	Large-scale genomic data analysis, genetic mutation identification, predictive modeling	Significantly expedited genomic data processing, improved prediction accuracy
CUDA-Enabled Registration Algorithm	Real-time lung tumor tracking for MRI	Clinical research	NVIDIA Tesla K40c GPU	Automated radiation therapy, mobile tumor boundary tracking	5x computational acceleration over CPU, average Dice score of 0.87
NVIDIA Clara Platform	Comprehensive healthcare AI applications	NVIDIA	NVIDIA GPU acceleration	Medical imaging, genomics, NLP, drug discovery, smart hospitals	Accelerated AI development across multiple medical domains
MONAI Core/ Label	Medical imaging AI development	NVIDIA Clara ecosystem	NVIDIA GPU	15 pre-trained models for CT, MR, Pathology, Endoscopy	Streamlined AI model development and deployment
NVIDIA BioNeMo	Drug discovery and molecular modeling	NVIDIA	Multi-GPU scaling (1000s of GPUs)	Generative AI, Large Language Models for drug discovery	Optimized scaling for biomolecular data processing
QuPath with DJL	Digital pathology image analysis	Open-source community	NVIDIA GPU (Windows/ Linux)	Deep learning for pathology image analysis	Enhanced performance for pathology workflows
PathAI Platform	AI-powered pathology diagnosis	PathAI	HPC GPU infrastructure	Objective pathology analysis, data-driven diagnostics	3-4x processing speed increase, reduced operating costs

AI, Artificial Intelligence; CT, Computed Tomography; DJL, Deep Java Library; GPU, Graphics Processing Unit; HPC, High-Performance Computing; ML, Machine Learning; MONAI, Medical Open Network for AI; MRI, Magnetic Resonance Imaging; NLP, Natural Language Processing; NKI, Netherlands Cancer Institute.

Table 2. Performance Improvements in Cancer Research Applications Using GPU-Accelerated AI Systems

Application Area	Performance Improvement	Specific Metrics
Cancer Genomics and Computational Biology	8x to 65x speed improvement	Processing acceleration over traditional methods
Medical Imaging Reconstruction	Up to 100x faster processing	Compared to CPU-based systems
Cone-Beam CT Reconstruction	77-130 seconds	Using NVIDIA Tesla C1060 GPU
System Delay Optimization (90 frames)	26% improvement	Overall system performance
System Delay Optimization (120 frames)	39% improvement	Scaled performance gains
Reconstruction Delay (90 frames)	2.1x improvement	Processing time reduction
Reconstruction Delay (120 frames)	3.3x improvement	Enhanced processing efficiency
Maximum Reconstruction Improvement	Up to 66x faster	When projection acquisition delay dominates

distinguishing between multiple cancer types and healthy tissues [15]. These genomic deep learning approaches analyze complex patterns of mutations across oncogenes and tumor suppressor genes, providing insights that could enable earlier detection through circulating tumor DNA monitoring and more precise therapeutic targeting [16,17]. The integration of GPU-accelerated AI tools into clinical workflows represents a paradigm shift toward precision oncology, where treatment decisions are increasingly informed by data-driven insights rather than solely relying on subjective clinical assessment [18]. Modern multidisciplinary cancer conferences are beginning to incorporate AI-generated treatment recommendations that consider comprehensive patient data including histopathological features, genomic profiles, and clinical parameters [19,20]. These systems demonstrate the potential for AI to serve not as a replacement for clinical expertise but as a powerful augmentation tool that enhances physician decision-making capabilities and reduces the cognitive burden associated with complex oncological cases.

This review aims to provide a comprehensive analysis of the current state and future potential of GPU-optimized AI tools in cancer research and clinical practice, examining their applications across the entire cancer care continuum from early detection through treatment planning and outcome prediction. We systematically evaluate the computational advantages of GPU acceleration in enabling real-time processing of complex medical data, assess the clinical performance and validation status of existing AI systems, and identify key challenges and opportunities for expanding the adoption of these technologies in routine oncological practice. Additionally, this review synthesizes emerging trends in AI-driven cancer care, including the integration of multi-modal data sources, the development of explainable AI systems for clinical decision support, and the potential for GPU-accelerated platforms to democratize access to advanced diagnostic capabilities across diverse healthcare settings.

Medical Imaging and Radiological Applications

Advanced Imaging Analysis and Cone-Beam Computed Tomography for Tumor Detection

GPU-accelerated AI has revolutionized medical imaging analysis in oncology, particularly in areas requiring rapid processing of high-resolution image data [21]. The Netherlands Cancer Institute has pioneered the use of NVIDIA AI Enterprise software for enhancing cone-beam computed tomography (CBCT) imaging in radiation therapy applications. This implementation addresses the critical need for precise tumor targeting during radiotherapy by enabling real-time adaptation of treatment plans to account for anatomical changes that occur between treatment sessions. Unlike traditional CT scanners that capture data in slices, CBCT systems use cone-shaped X-ray beams to generate comprehensive three-dimensional images, which require substantial computational resources for accurate reconstruction and analysis [5,22,23].

The computational demands of modern medical imaging have driven widespread adoption of GPU-based processing systems. Groundbreaking research has demonstrated that GPU-based fast cone beam CT reconstruction algorithms can achieve reconstruction times ranging from 77 to 130 seconds on an NVIDIA Tesla C1060 GPU card, representing approximately 100 times faster processing compared to similar iterative reconstruction approaches. These performance improvements enable clinical implementation of advanced reconstruction techniques that were previously computationally prohibitive in real-time clinical environments. The reconstruction efficiency extends beyond speed improvements to encompass significant dose reduction capabilities. As shown in Table 3, advanced GPU algorithms have proven that as few as 20-40 x-ray projections are sufficient to reconstruct images with satisfactory quality for image-guided radiation therapy (IGRT), compared to conventional protocols requiring approximately 360 projections. Furthermore, these systems can operate effectively under scanning

Table 3. Radiation Dose Reduction and Clinical Safety Improvements with GPU-Optimized Protocols

Imaging Parameter	Traditional Protocol	GPU-Optimized Protocol	Reduction Factor
X-ray Projections Required	360 projections	20-40 projections	9x to 18x reduction
Radiation Exposure	0.4 mA s/projection	0.1 mA s/projection	4x dose reduction
Overall Dose Reduction	Baseline	Optimized protocol	36-72x reduction
Cost Reduction	Baseline	GPU implementation	Up to 85% savings

protocols with radiation exposure as low as 0.1 mA s/projection, compared to the current widely used full-fan head and neck scanning protocol of approximately 0.4 mA s/projection [24,25]. This represents an overall dose reduction of 36-72 times while maintaining diagnostic image quality.

Performance Optimization and System Integration

Advanced GPU parallel acceleration techniques have enabled further optimization of medical imaging workflows through sophisticated system architectures [26–28]. Research demonstrates that when 90 frames of projections are utilized for reconstruction, GPU-based systems achieve a 26% improvement in overall system delay and a 2.1-fold improvement in reconstruction delay. When the number of projection frames increases to 120, these improvements scale to 39% and 3.3 times respectively. In scenarios where projection acquisition delay dominates the imaging chain, reconstruction processes can be almost completely hidden, yielding reconstruction delay improvements of up to 66 times. The filtered back projection (FDK) algorithm implementation with GPU parallel acceleration has proven particularly effective for real-time clinical 3D imaging acquisition. These systems utilize distributed architectures connected via TCP/IP protocols, making full use of projection acquisition consumption to hide reconstruction delays and further improve overall system performance. The geometric symmetry optimization within GPU implementations enhances computational efficiency while maintaining reconstruction accuracy [29,30].

Histopathological Image Analysis and Deep Learning Applications

Gland Segmentation and Cancer Grading

The application of GPU-accelerated deep learning in histopathological image analysis has achieved significant breakthroughs in cancer diagnosis and grading. The GlaS@MICCAI’2015 Gland Segmentation dataset, which serves as a benchmark for automated cancer detection systems, consists of 165 images containing 1,530 labeled glandular objects derived from 16 H&E-stained histological sections of stage T3 or T4 colorectal adenocarcinoma. These sections represent samples from different patients processed on various occasions, ensuring high inter-subject variability in both stain distribution and tissue architecture. The digitization process for these histological samples utilizes high-resolution Zeiss MIRAX MIDI Slide Scanners with initial pixel resolution of 0.465μm, subsequently rescaled to 0.620μm (equivalent to 20× objective magnification). A total of 52 visual fields from both malignant and benign areas across the entire set of whole-slide images were selected to cover the widest possible variety of tissue architectures. Expert pathologists grade each visual field as either benign or malignant according to overall glandular architecture, providing ground truth annotations for automatic segmentation algorithms [31]. GPU-based deep learning networks for gland segmentation incorporate minimal information loss (MIL) units that retain maximal information essential for accurate boundary delineation. These networks utilize dilated convolution techniques combined with atrous spatial pyramid pooling for multi-level aggregation, enabling effective segmentation of glands displaying varying shapes and sizes across different cancer grades. The high-resolution processing requirements necessitate substantial GPU memory resources, as dilated convolution over original image sizes requires significantly more parameters compared to down-sampled implementations [32].

Uncertainty Quantification and Clinical Decision Support

Advanced GPU-accelerated systems incorporate uncertainty quantification mechanisms that apply random transformations to input images for generating predictive distributions4. This approach yields superior segmentation results while enabling identification of areas with high uncertainty, such as regions with dense nuclei or imaging artifacts, which can be clinically informative for pathologists4. The uncertainty measures are utilized to rank images requiring prioritized pathologist annotation, optimizing workflow efficiency in clinical settings [32].

Radiomics and Radiogenomics Integration

Quantitative Feature Extraction and Analysis

The emerging fields of radiomics and radiogenomics represent a paradigm shift in cancer imaging, leveraging GPU-powered AI systems to extract quantitative features from medical images that correlate with genetic and molecular characteristics of tumors [33–35]. These approaches enable the identification of imaging biomarkers that can inform treatment decisions and predict patient outcomes. GPU-based systems excel in this domain due to their ability to process the massive datasets required for extracting and analyzing hundreds of quantitative features from each medical image [22]. Modern GPU implementations in radiomics applications utilize advanced hardware specifications including NVIDIA A100 GPUs with up to 80GB memory capacity and 624 TFLOPS FP16 Tensor Core performance [36]. Professional-grade workstation cards such as the NVIDIA RTX A6000 provide 10,752 CUDA cores with 48GB GDDR6 memory and 768GB/sec memory bandwidth, enabling comprehensive analysis of high-resolution medical imaging datasets. These hardware specifications support the sophisticated parallel processing requirements for radiomics feature extraction, which can involve analyzing thousands of quantitative parameters simultaneously across multiple image modalities [37,38]. The cuRadiomics framework exemplifies GPU-accelerated radiomic feature extraction platforms that leverage CUDA parallel processing for enhanced computational efficiency. These systems enable extraction of texture, shape, and intensity-based features from medical images at unprecedented scales, supporting the development of predictive models for cancer diagnosis, prognosis, and treatment response. The parallel processing capabilities of modern graphics processors allow researchers to perform complex mathematical operations on large image datasets simultaneously, significantly reducing the time required for comprehensive radiomics analyses [39,40].

Table 4. Digital Pathology Market Size and Growth Projections

Metric	2021	2024	2028	2029	Growth Rate
Market Value (Primary Projection)	-	$990 million	-	$1.94 billion	14% annually
Market Value (Alternative Projection)	$740.26 million	-	$1738.82 million	-	Variable
Year-over-Year Growth Rate	-	37.3%	31.4%	27.3%	Decreasing trend

Digital Pathology and Histological Analysis

As shown in Table 4, the digital pathology sector has emerged as a rapidly expanding market driven by technological advancements and increasing demand for precision diagnostics [41–43]. Current market analysis indicates the global digital pathology market reached approximately $990 million in 2024, with projections showing continued robust growth at 14% annually over the next five years, expected to reach $1.94 billion by 2029. This growth trajectory represents a significant acceleration from previous estimates, with alternative projections suggesting the market will expand from $740.26 million in 2021 to $1738.82 million by 2028 [44–46]. The market has demonstrated remarkable year-over-year growth rates of 37.3%, 31.4%, and 27.3% over three consecutive recent years, indicating sustained momentum in adoption across healthcare institutions.

Market Dynamics and Institutional Adoption

Digital pathology represents one of the most computationally intensive applications of GPU-accelerated AI in cancer research, requiring substantial storage infrastructure and processing capabilities to handle the enormous datasets generated by modern pathology scanners [47]. As shown in Table 5, the institutional adoption landscape reveals that hospitals lead the market with 36.5% of digital pathology equipment utilization, followed by diagnostic laboratories, biotechnology companies, and academic institutions [48–50]. This distribution reflects the primary clinical applications driving market expansion, particularly in environments where high-volume diagnostic workflows demand enhanced efficiency and accuracy. As shown in Table 6, a typical implementation for a large pathology facility includes approximately 25 pathologists working with 9 high-throughput scanners that generate around 1,800 slides per day, resulting in approximately 1.1 petabytes of data annually [50,51]. Each individual slide scan averages 2.5 gigabytes in size and must be retained for extended periods, often seven years or more, necessitating sophisticated data management and tiered storage solutions [50,52]. The scale of data generation becomes even more pronounced when considering that a single square centimeter of tissue requires 2.7 gigabytes for the base image at 20x optical magnification with 0.33 micrometers per pixel resolution. When accounting for the pyramid file structure used in digital pathology systems, this increases to approximately 3.5 gigabytes per square centimeter of tissue [50, 53, 54].

Technical Infrastructure and Processing Requirements

The computational demands of digital pathology extend beyond storage to encompass significant processing capabilities [55–57]. The AI inference process for digital pathology analysis requires over 100 gigabytes of GPU memory, typically necessitating multi-GPU systems to handle the computational load effectively. These systems perform automated detection and analysis of various cancer types, including breast cancer, gastric cancer, and lymph node metastasis detection. The technical specifications reveal that with 40x magnification and five focal planes, a single pathology case can generate up to one terabyte of data [48]. However, advanced compression techniques using JPG2000 can achieve approximately 30:1 compression ratios, reducing storage requirements

Table 5. Institutional Adoption Distribution in Digital Pathology

Institution Type	Market Share	Primary Applications
Hospitals	36.5%	High-volume diagnostic workflows
Diagnostic Laboratories	Second largest	Specialized testing services
Biotechnology Companies	Third largest	Research and development
Academic Institutions	Fourth largest	Research and education

Table 6. Digital Pathology Data Storage Requirements

Parameter	Measurement	Scale	Annual Requirements
Pathologists per Facility	25	Large facility	-
High-throughput Scanners	9	Per facility	-
Daily Slide Processing	1,800 slides	Per day	-
Annual Data Generation	1.1 petabytes	Per facility	Continuous growth
Average Slide Size	2.5 gigabytes	Per slide	Standard resolution
Data per Square Centimeter (20x)	2.7 gigabytes	Base image	High resolution
Data with Pyramid Structure	3.5 gigabytes	Per square centimeter	Complete file structure

Table 7. Large-Scale Implementation Requirements for Digital Pathology

Implementation Scale	Data Volume	Storage Needs	Processing Requirements
Single Pathology Case (40x, 5 focal planes)	Up to 1 terabyte	High-performance storage	Multi-GPU systems
Major Medical Center (80,000 cases/year)	138 terabytes annually	Tiered storage architecture	Over 100GB GPU memory
Compression Efficiency (JPG2000)	30:1 ratio	Reduced storage requirements	Maintained diagnostic quality
Data Retention Period	7+ years	Long-term storage	Regulatory compliance

to more manageable levels while maintaining diagnostic quality [58, 59]. Large-scale implementations demonstrate the infrastructure requirements necessary for clinical deployment. For example, a major medical center processing approximately 80,000 cases annually require 138 terabytes of storage capacity per year (Table 7) [60, 61]. This massive data volume necessitates sophisticated tiered storage architectures where older scans are migrated to lower-cost, lower-performance storage systems as retention requirements extend over multiple years. The data management strategy must account for regulatory compliance, with typical retention periods of seven years or more for pathological specimens [59, 61, 62].

Efficiency Gains and Cost-Benefit Analysis

The economic advantages of digital pathology implementation extend beyond initial technological investments to encompass significant operational improvements. AI-driven analyzers have demonstrated the capability to reduce analytical turnaround time by up to 89%, dramatically improving laboratory efficiency and patient care delivery [63]. This reduction in processing time directly translates to enhanced pathologist productivity and faster patient diagnosis, which is particularly critical in cancer care where early detection significantly impacts survival rates. Financial analysis reveals that digital pathology systems can generate cost savings of $1.3 million over a five-year implementation period2. These savings result from multiple factors including reduced administrative work, enhanced workflow efficiency, improved remote collaboration capabilities, and decreased need for physical slide management and storage [64]. The efficiency improvements are particularly pronounced in high-volume laboratories where automated analysis can prioritize cases requiring immediate attention while routing routine cases through streamlined digital workflows.

Research Foundation and Validation

The statistical foundation supporting digital pathology adoption derives from comprehensive research methodologies combining both secondary and primary data sources [65, 66]. Recent market analysis incorporated 35 interviews with digital pathology stakeholders from hospitals, academia, biopharmaceutical companies, and contract research organizations, alongside survey responses from 100 clinical pathology laboratories and 40 biopharmaceutical survey respondents. This extensive research foundation provides robust validation for market projections and adoption trends across diverse healthcare sectors. The GPU-accelerated processing enables pathologists to focus their attention on areas of highest concern identified by the AI system, potentially improving diagnostic accuracy while reducing the time required for comprehensive tissue analysis [51]. This technology is particularly valuable in scenarios where early detection can significantly impact patient outcomes, as faster and more accurate pathological analysis directly correlates with improved survival rates. The integration of AI with traditional pathological workflows represents a paradigm shift toward precision medicine, where computational power enhances human expertise rather than replacing it [51, 67].

Cancer Genomics and Computational Biology

The integration of GPU technology in cancer genomics and computational biology has fundamentally transformed the landscape of genetic research and clinical diagnostics. Recent advances demonstrate remarkable performance improvements across multiple genomic analysis tasks, with GPU-accelerated systems achieving speedups ranging from 8× to 65× compared to traditional CPU-based methods, while simultaneously reducing costs by up to 85% and energy consumption by similar margins. These technological advances have made comprehensive genomic analysis feasible for routine clinical implementation, enabling real-time genetic profiling that can directly inform personalized treatment decisions in cancer care [68, 69].

Genomic Sequence Analysis and Variant Detection

Performance Breakthroughs in Sequence Alignment

The application of GPU-enhanced computational models in cancer genomics has created new possibilities for analyzing complex genetic data with unprecedented speed and accuracy. Modern cancer genomics research generates massive datasets requiring sophisticated computational approaches for sequence alignment, variant calling, and gene expression analysis. Recent benchmarking studies reveal that GPU-accelerated algorithms demonstrate significant performance improvements over traditional CPU-based methods across all critical analytical tasks, with sequence alignment showing particularly dramatic improvements [70]. The AGAThA (Accelerated GPU Alignment) platform represents a breakthrough in guided sequence alignment for long read mapping, achieving an 18.8× speedup against CPU-based baselines and a 9.6× improvement over the best existing GPU-based approaches [71]. This system addresses the computational challenges of aligning increasingly longer DNA sequences to reference genomes, a process that previously required tens or hundreds of hours but can now be completed in a fraction of the time [70]. The parallel processing architecture of graphics processors is particularly well-suited for genomic applications, where multiple sequences can be processed simultaneously, dramatically reducing the time required for comprehensive genetic analysis.

Variant Calling Acceleration and Clinical Impact

NVIDIA Clara Parabricks represents a significant advancement in cancer genome sequencing analysis, providing GPU-accelerated tools for variant annotation and genomic data processing. This platform has demonstrated remarkable performance improvements, achieving up to 65× acceleration with germline variant callers and bringing HaplotypeCaller runtimes down from 36 hours to just 33 minutes on AWS, 35 minutes on Google Cloud Platform, and 24 minutes on NVIDIA DGX systems [72]. The system's ability to process whole genome sequences rapidly has particular importance in clinical settings where timely genetic analysis can inform treatment decisions. Comparative analysis across different genomic analysis tasks reveals consistent performance advantages for GPU implementations. Variant calling tasks that previously required 3,600 seconds on CPU systems now complete in just 450 seconds on GPU platforms, representing an 8× speedup [8,72]. The DeepVariant algorithm, when GPU-accelerated through Parabricks, can complete 30× whole genome sequencing analysis in 25 minutes instead of hours, while whole exome analysis runtime has been reduced from over 3 hours to as little as 11 minutes, achieving a 17× improvement in processing speed [72,73].

Cost-Effectiveness and Energy Efficiency

The economic implications of GPU acceleration in genomics extend beyond simple performance improvements to encompass substantial cost and energy savings. Comprehensive cost analysis demonstrates that variant calling expenses drop from \$2.50 per run on CPU systems to just \$0.35 per run on GPU platforms, representing an 86% cost reduction [72]. Similarly, gene expression analysis costs decrease from \$2.00 to \$0.30 per run, maintaining the same dramatic cost savings pattern. Energy consumption analysis reveals even more striking improvements, with GPU systems consuming approximately 85% less energy than CPU equivalents for the same genomic analysis tasks [74]. The integration of GPU processing in genomic workflows has made it feasible to perform comprehensive genetic analysis as part of routine clinical care, moving beyond research applications to practical diagnostic implementations. Whole exome analysis using GPU-accelerated pipelines achieves cost reductions of up to 70% while maintaining accuracy standards required for clinical diagnostics [73]. This cost-effectiveness has democratized access to advanced genomic analysis capabilities, enabling smaller research institutions and clinical facilities to implement state-of-the-art genomic analysis pipelines that were previously economically prohibitive [72, 75].

Deep Learning Applications in Genetic Analysis

Advanced Pattern Recognition in Genomic Data

The integration of deep learning models with GPU platforms has enhanced predictive capabilities for cancer prognosis and treatment response based on genomic data [76,77]. These advanced computational models can identify complex patterns in genetic information that may not be apparent through traditional analytical approaches. Recent studies demonstrate that AI-powered diagnostic systems can achieve higher accuracy than specialized physicians in cancer prognosis, with neural networks trained on NVIDIA P100 GPUs using cuDNN-accelerated TensorFlow frameworks showing superior performance in brain cancer outcome prediction [78]. GPU acceleration enables the training of sophisticated neural networks on large genomic datasets, facilitating the discovery of novel genetic biomarkers and therapeutic targets. The enhanced processing capabilities have also accelerated the development of personalized medicine approaches by enabling real-time analysis of patient genetic profiles to inform treatment selection. Brain cancer prognosis models, for instance, require analysis of microscopic images containing billions of pixels, necessitating substantial computational power for processing thousands of predictions to help pathologists visualize single tissue samples [79,80].

Transcriptome Analysis and Single-Cell Genomics

RNA sequencing analysis has experienced transformational improvements through GPU acceleration, with differential gene expression analysis showing remarkable speedup ratios [81]. The GPU-accelerated DESeq2 pipeline can process large datasets of 1,000 samples in approximately 1 hour compared to 10 hours required by CPU-based methods, representing a 10-fold reduction in processing time. Similarly, the edgeR algorithm demonstrates comparable improvements, with GPU-accelerated versions completing analysis in 1.5 hours versus 12 hours for CPU-based implementations. Single-cell RNA sequencing (scRNA-seq) applications have particularly benefited from GPU acceleration, addressing the computational challenges of analyzing gene expression at individual cell resolution [82]. Preprocessing tasks for datasets comprising 50,000 cells now complete in 1.5 hours compared to 8 hours using traditional methods. Clustering algorithms for the same dataset size finish in less than 2 hours versus over 12 hours with CPU-based approaches, enabling researchers to explore cellular heterogeneity with unprecedented efficiency [83].

Multi-Dimensional Genomic Integration

The transformative potential of GPU technology in cancer genomics extends beyond basic sequence analysis to encompass complex multi-dimensional genetic analyses that integrate various types of biological data [8,84]. Modern GPU-enhanced systems can simultaneously process genetic sequences, gene expression profiles, and epigenetic modifications to provide comprehensive molecular characterizations of cancer patients. Gene expression analysis using GPU platforms completes RNA-Seq data processing in 400 seconds compared to 3,000 seconds on CPU systems, achieving an 8-9× speedup that enables real-time integration of multiple data types [74]. This integrated approach has proven particularly valuable in identifying patient subgroups that may respond differently to specific therapeutic interventions, advancing the goal of precision oncology.

The Genomics-GPU benchmark suite, comprising ten widely-used genomic analysis applications, demonstrates the broad applicability of GPU acceleration across diverse genomic tasks including genome comparison, matching, and clustering for both DNA and RNA analyses [85]. These comprehensive analytical capabilities support the development of sophisticated computational models that can predict treatment responses and identify novel therapeutic targets through parallel processing of multiple genomic data streams simultaneously.

GPU-Optimized AI Platforms and Development Frameworks in Cancer Research

The intersection of AI and cancer research has been revolutionized by GPU-optimized platforms and development frameworks, creating unprecedented opportunities for diagnostic precision, therapeutic discovery, and personalized treatment approaches [9]. This comprehensive review examines the current landscape of GPU-accelerated AI technologies specifically applied to oncology, spanning from foundational computing frameworks to specialized cancer-focused platforms. The analysis reveals that modern cancer AI research relies heavily on NVIDIA's CUDA-X ecosystem, with platforms like PyTorch, TensorFlow, and JAX serving as primary development environments [86]. Cloud-based solutions including Google Compute Engine, Azure N Series, and specialized providers like Lambda Labs have democratized access to high-performance computing resources [87]. Emerging specialized platforms such as AI-powered pathology systems for lung cancer diagnostics and drug discovery frameworks like NVIDIA BioNeMo are demonstrating remarkable clinical translation potential, with some AI-discovered cancer therapeutics already advancing to Phase 1 clinical trials [88].

Foundational GPU Computing Frameworks for Cancer AI

NVIDIA CUDA-X AI Ecosystem

The backbone of modern cancer AI research rests on NVIDIA's CUDA-X AI platform, which provides a comprehensive deep learning software stack specifically designed for researchers and software developers building high-performance GPU-accelerated applications in conversational AI, recommendation systems, and computer vision [89]. This unified programming model enables researchers to develop cancer-focused applications across diverse deployment environments, from desktop workstations to data centers, and even resource-constrained IoT devices with minimal code modifications. The CUDA-X AI libraries consistently deliver world-leading performance for both training and inference across industry benchmarks such as MLPerf, making them particularly valuable for computationally intensive cancer research applications that require processing large-scale genomic data, medical imaging, and multi-omics datasets [86]. The flexibility offered by GPU-optimized CUDA-X AI libraries has proven instrumental for framework developers and researchers seeking to accelerate new architectures specifically designed for cancer applications [90, 91]. This adaptability is particularly crucial in oncology research, where novel neural network architectures must be continuously developed to address the unique challenges of cancer heterogeneity, treatment resistance patterns, and the integration of multi-modal data sources including histopathology images, genomic sequences, and clinical records1. The NVIDIA NGC catalog further supports this ecosystem by providing over a hundred repositories covering products, demonstrations, samples, and tutorials specifically designed to help researchers get started with cancer-focused AI applications [86].

Core Deep Learning Frameworks

Cancer AI research predominantly relies on three major deep learning frameworks that have been extensively optimized for GPU acceleration: PyTorch, TensorFlow, and JAX. These frameworks offer essential building blocks for designing, training, and validating deep neural networks through high-level programming interfaces that are particularly well-suited for the complex modeling requirements of cancer research [86]. Each framework leverages GPU-accelerated libraries such as cuDNN and TensorRT to deliver high-performance training and inference capabilities essential for processing the massive datasets typical in cancer research, including whole-slide histopathology images, genomic sequencing data, and longitudinal patient records. The containerized versions of these frameworks available through NGC provide additional advantages for cancer researchers by offering the latest GPU optimizations integrated with CUDA libraries and drivers [86,90]. These containerized frameworks undergo monthly verification and testing to ensure optimal performance across multiple edge and cloud platforms, which is particularly important for cancer research applications that may need to be deployed in diverse clinical environments [92]. The integration of these frameworks with specialized cancer research workflows has enabled the development of sophisticated AI models capable of tasks ranging from automated pathology analysis to drug discovery and treatment response prediction.

Cloud-Based GPU Platforms for Cancer Research

Major Cloud Infrastructure Providers

The democratization of GPU computing for cancer research has been significantly advanced through cloud-based platforms that provide scalable access to high-performance computing resources without requiring substantial upfront infrastructure investments [82, 93]. Major cloud providers including Google Compute Engine, Microsoft Azure N Series, and Oracle Cloud Infrastructure have developed specialized GPU offerings that cater to the computational demands of cancer AI research. These platforms are particularly valuable for cancer research because they can accommodate the variable computational loads typical of research projects, from intensive model training phases requiring multiple GPUs to inference deployment that may need different resource configurations. The efficiency gains provided by GPU computing are especially pronounced in cancer research applications due to the resource-intensive nature of training AI models on medical data. Dense operations that might require 50 minutes on a CPU can be completed in approximately one minute on even low-end GPUs, making it economically feasible for research institutions to conduct large-scale studies that would otherwise be prohibitively expensive [87]. This dramatic improvement in computational efficiency has enabled cancer researchers to explore more complex models, larger datasets, and more sophisticated validation approaches that were previously impractical.

Specialized Cloud GPU Providers

Beyond the major cloud infrastructure providers, specialized platforms such as Lambda Labs Cloud, IBM Cloud GPU, and Vast AI have emerged to serve the specific needs of AI researchers working on cancer applications [12]. These platforms often provide more flexible pricing models, specialized hardware configurations, and research-focused support services that are particularly valuable for academic cancer research institutions with limited budgets. The ability of GPUs to execute multiple tensor operations simultaneously, combined with their higher memory bandwidth compared to CPUs, makes them ideally suited for the sort of large-scale input data and deep networks that characterize modern cancer AI projects [15]. The numerous cores available in GPU architectures enable parallel processing of the extensive matrix operations required for cancer AI applications, including convolutional operations for medical image analysis, dense layer computations for genomic data processing, and attention mechanisms for multi-modal data integration. This parallel processing capability is particularly crucial for cancer research, where models must often process high-resolution histopathology images containing millions of pixels, genomic datasets with hundreds of thousands of features, and clinical datasets with complex temporal relationships [87].

Specialized Cancer AI Platforms and Applications

AI-Powered Cancer Diagnostics Platforms

Recent developments in specialized cancer AI platforms have demonstrated remarkable potential for clinical translation, particularly in the area of automated pathology analysis. A cutting-edge example is the AI-powered pathology platform developed by researchers at the University of Cologne, which provides fully automated and in-depth analysis of benign and cancerous tissues for faster and more personalized lung cancer treatment [48, 94]. This platform addresses critical limitations in traditional cancer diagnosis, where oncologists must manually examine tissue samples under microscopes in a process that is time-consuming, subjective, and prone to variability that can lead to misdiagnosis. The deep-learning-based multi-class tissue segmentation platform automatically analyzes digitized lung tissue samples, screening for cancer while providing detailed cellular analysis of the affected regions. The AI model was trained and validated on an extensive dataset from six institutions, encompassing 4,097 annotated slides from 1,527 patients, demonstrating the scale of data required for robust cancer AI applications. According to the study's senior author, the algorithm can differentiate between 11 distinct tissue types, ranging from tumor tissue to tumor-associated classes such as tumor stroma, necrotic debris, and mucin, as well as normal tissues like cartilage and lymphatic tissue, achieving an impressive average Dice Score of 0.893 for pixel-wise accuracy. The computational infrastructure supporting this cancer AI platform utilized a sophisticated array of NVIDIA GPUs, including 12 NVIDIA V100 GPUs on the University of Cologne's high-performance computing cluster, four NVIDIA A100 GPUs on the pathology institute's AI server, and PC stations equipped with NVIDIA GeForce RTX 3090 and NVIDIA RTX 4090 GPUs. This setup enables rapid analysis of entire slide images, processing whole-slide images ranging from 200 to 2000 MB in approximately 1 to 5 minutes [95]. The platform's ability to reveal detailed characteristics of tumor and immune cells within the cellular environment provides insights into how cancer interacts within the body, potentially informing more precise and effective treatments and offering valuable predictions about patient responses to specific cancer therapies [96–98].

AI-Driven Drug Discovery Platforms

The application of GPU-optimized AI platforms to cancer drug discovery represents one of the most promising developments in computational oncology. Iambic's AI-driven drug discovery platform, built in collaboration with NVIDIA, exemplifies the potential of generative AI to rapidly develop new therapeutic candidates for cancer patients. The platform has successfully identified IAM1363, a selective and brain-penetrant inhibitor of HER2 signaling designed for treating HER2-driven breast, lung, and colon cancers, which has now advanced to Phase 1 clinical trials. IAM1363 demonstrates the sophisticated capabilities of modern AI-driven drug discovery platforms, as it was specifically designed to reach metastatic tumors throughout the body, including the challenging brain environment, while maintaining a greater therapeutic index than current therapies in its class and avoiding associated toxicity. The integration of NVIDIA BioNeMo and other emerging NVIDIA technologies into Iambic's platform has accelerated the creation of this oncology candidate, showcasing how specialized AI frameworks can compress traditional drug discovery timelines from decades to years [88]. This rapid progression from computational discovery to clinical testing represents a paradigm shift in cancer drug development, where AI platforms can now identify, optimize, and validate therapeutic candidates with unprecedented speed and precision [99-101].

Hardware Considerations and Infrastructure Requirements

GPU Selection for Cancer AI Applications

The selection of appropriate GPU hardware for cancer AI applications requires careful consideration of the specific computational demands, data characteristics, and deployment requirements of different oncological research areas [102]. The University of Cologne's cancer diagnostics platform demonstrates the diversity of GPU requirements, utilizing everything from high-end data center GPUs like the NVIDIA V100 and A100 for large-scale model training to consumer-grade RTX 3090 and RTX 4090 cards for development and inference tasks. This heterogeneous approach reflects the varied computational needs across different phases of cancer AI research, from initial model development to large-scale validation studies. The choice of GPU architecture significantly impacts the feasibility and efficiency of different cancer AI applications. High-memory GPUs like the A100 are particularly valuable for processing large histopathology images or genomic datasets that exceed the memory capacity of smaller GPUs, while the RTX series cards offer excellent price-performance ratios for development work and smaller-scale studies [96]. The computational requirements for cancer AI are often unpredictable, as model complexity and dataset size can vary dramatically between different research questions, making flexible infrastructure arrangements particularly important [103–106].

Performance Optimization and Scaling

The optimization of GPU performance for cancer AI applications involves careful consideration of both hardware configuration and software implementation strategies. The CUDA-X AI libraries provide optimized implementations of common operations used in cancer AI, including convolutions for image analysis, matrix operations for genomic data processing, and attention mechanisms for multi-modal data integration [90]. These optimized libraries ensure that cancer researchers can achieve maximum performance from their GPU investments without requiring deep expertise in low-level GPU programming. Scaling considerations are particularly important for cancer AI applications due to the large datasets and complex models typically involved. The ability to scale from single GPU configurations to multi-GPU and multi-node setups enables researchers to tackle increasingly ambitious projects, from analyzing entire patient cohorts to training foundation models on multi-institutional datasets [8]. The unified programming model provided by CUDA-X ensures that cancer AI applications can be developed on desktop systems and deployed to data center environments with minimal code modifications, facilitating the translation of research prototypes to clinical applications [86].

Recent Developments and Future Directions

Emerging GPU Technologies for Cancer AI

Recent announcements regarding NVIDIA's RTX 50 series, codenamed "Blackwell," indicate significant advances in AI-optimized GPU technologies that will likely impact cancer research applications. These new GPUs are expected to feature advanced DLSS technology with improved algorithms for higher frame rates and more detailed rendering, which could be particularly valuable for cancer imaging applications requiring high-resolution visualization of cellular structures. Enhanced ray tracing capabilities and improved RT cores for more realistic lighting and shadow effects may enable more sophisticated 3D visualization of tumor environments and cellular interactions. The introduction of neural rendering techniques based on AI represents a potentially transformative development for cancer visualization and analysis. These AI-accelerated graphics performance optimizations could enable new approaches to visualizing complex cancer data, from molecular interactions to tumor growth patterns. More efficient energy use through AI-based optimization of energy consumption and temperature control will be particularly valuable for large-scale cancer research projects that require sustained computational workloads. Improved AI upscaling processes could benefit cancer researchers working with medical imaging by enabling higher quality enhancement of low-resolution historical data or real-time imaging streams.

Integration with Emerging AI Paradigms

The integration of cancer AI platforms with emerging paradigms such as generative AI represents a significant frontier in computational oncology. Generative AI acceleration capabilities in new GPU architectures will likely enable more sophisticated approaches to cancer drug discovery, treatment optimization, and biomarker identification. The success of platforms like Iambic's drug discovery system demonstrates the potential for generative AI to revolutionize cancer therapeutics development by enabling rapid exploration of vast chemical spaces and identification of novel therapeutic targets. Advanced features such as improved AI upscaling processes and neural rendering could transform how cancer researchers visualize and interpret complex biological data. These technologies may enable new forms of interactive analysis where researchers can explore high-dimensional cancer datasets through AI-enhanced visualization interfaces. The continued development of AI-based optimization techniques for energy consumption and performance will make large-scale cancer AI projects more accessible to resource-constrained institutions, potentially democratizing access to advanced computational oncology tools.

Current Challenges and Future Directions

Technical and Regulatory Challenges

Despite the significant advances in GPU-accelerated AI for cancer applications, several challenges remain that must be addressed to realize the full potential of these technologies. Regulatory approval processes for AI-assisted medical devices and diagnostic tools continue to evolve, with agencies working to establish appropriate frameworks for evaluating the safety and efficacy of AI-powered healthcare applications. The complexity of validating AI systems across diverse patient populations and clinical scenarios presents ongoing challenges for developers and regulators alike. Data standardization and interoperability represent additional significant challenges in the widespread adoption of GPU-accelerated AI tools in cancer care. Healthcare systems often employ different imaging protocols, data formats, and electronic health record systems, making it difficult to develop AI tools that can function effectively across diverse clinical environments. The development of standardized data formats and interfaces will be crucial for enabling broader deployment of AI-assisted cancer care tools.

Emerging Applications and Research Directions

The future of GPU-accelerated AI in cancer research and clinical practice is likely to encompass increasingly sophisticated applications that integrate multiple data modalities and analytical approaches. Emerging research directions include the development of foundation models for medical imaging that can be adapted for specific cancer types and clinical scenarios. These large-scale models, trained on diverse medical datasets, could provide a foundation for developing specialized applications with reduced training data requirements and improved generalization capabilities. Real-time genomic analysis represents another promising frontier for GPU-accelerated cancer care applications. As sequencing technologies continue to improve and costs decrease, the ability to perform comprehensive genetic analysis during patient encounters could become routine clinical practice. GPU-accelerated processing will be essential for enabling this transition, as current genomic analysis workflows often require hours or days to complete, limiting their utility for immediate clinical decision-making.

In conclusion, the convergence of GPU acceleration and AI has established a transformative foundation for modern cancer care, demonstrating that computational advances can directly translate into improved patient outcomes through enhanced diagnostic precision, reduced treatment times, and democratized access to sophisticated analytical capabilities. The documented performance improvements, including 100-fold acceleration in medical image reconstruction, 66-fold improvements in processing delays, and substantial radiation dose reductions while maintaining diagnostic quality, illustrate the profound clinical impact achievable through GPU-optimized AI implementations. As cancer incidence continues to rise globally and diagnostic complexity increases with the integration of multi-modal data sources, GPU-accelerated AI platforms position healthcare institutions to meet these challenges through scalable, efficient, and accurate diagnostic and treatment planning systems. The demonstrated success across diverse applications from real-time cone-beam CT reconstruction and automated histopathological analysis to genomic variant classification and radiomics feature extraction indicates that GPU-accelerated AI has matured beyond experimental implementation to become an essential component of comprehensive cancer care. Future developments in this field promise continued expansion of AI capabilities, integration of explainable AI systems for enhanced clinical decision support, and broader accessibility of advanced diagnostic tools across varied healthcare environments, ultimately contributing to the evolution of precision oncology and improved cancer patient outcomes worldwide.

Author Contribution Statement

FM and BM contributed to the conceptualization, methodology, and literature review. NN and RN developed the framework and study design. AN and AS drafted sections of the manuscript and participated in discussions. FJ and AN conducted the statistical analysis and supported the literature review. AR and AM assisted in data synthesis and methodological evaluation. MD and KA played key roles in manuscript preparation and oversaw the research process. HN and AM read and approved the final manuscript.

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Ethics Approval

This article does not involve studies with human participants or animals.

Competing Interests

The authors declare no conflicts of interest.

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