Metaheuristic Optimization in Cancer Detection: A Comprehensive Literature Review

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Abstract

This paper presents a comprehensive synthesis of recent advancements in the application of metaheuristic optimization algorithms for cancer detection, classification, and prediction. Drawing from a curated collection of studies spanning diverse cancer types including breast, lung, skin, cervical, oral, thyroid, and brain cancers, the work emphasizes how metaheuristics address challenges inherent to biomedical data, such as high dimensionality, noise, and limited sample sizes. A methodology table was developed to categorize each study by cancer domain, optimization method, and specific research task, enabling a comparative analysis of algorithmic patterns and hybridization strategies. The synthesis reveals that no single metaheuristic algorithm consistently outperforms others; instead, success depends on aligning algorithmic strengths with the characteristics of the diagnostic task and data. The discussion highlights the dominance of hybrid approaches, the emerging role of multi-objective optimization, the potential for cross-domain adaptation, and the necessity of addressing ethical, reproducibility, and clinical integration challenges. This work contributes both a structured reference and a roadmap for future research aimed at advancing computational oncology through strategic algorithm selection and design.

Keywords: Metaheuristic Optimization; Feature Selection; Cancer Detection; Computational Oncology; Diagnostic Systems

1. Introduction

Cancer remains one of the most formidable challenges in modern medicine, both in its biological complexity and in the computational demands of its study. Current projections estimate that the global cancer burden will surpass twenty-eight million new cases annually by the year 2040, with mortality rates disproportionately concentrated in low- and middle-income countries due to persistent inequalities in healthcare infrastructure, diagnostic capabilities, and access to advanced therapies [1, 2]. The disease encompasses a wide array of pathological conditions that differ not only by tissue of origin but also by molecular and genetic profiles, tumor microenvironment characteristics, and the adaptive capacity of malignant cells to survive under therapeutic pressure [3,4]. This heterogeneity represents a major obstacle in the development of universally effective treatments and necessitates computational approaches capable of handling high-dimensional, dynamic, and often incomplete biomedical data.

In recent years, the integration of high-throughput genomic, transcriptomic, proteomic, metabolomic, and radiomic technologies has led to an unprecedented expansion of available data. While these datasets enable highly granular characterizations of tumor biology, they also introduce new analytical complexities. Many critical decision-making tasks in oncology, such as designing optimal treatment schedules, selecting relevant biomarkers, configuring radiotherapy beams, or choosing drug combinations, are inherently combinatorial in nature. In computational terms, these tasks belong to a category of problems that become exponentially

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more challenging as their scale increases, rendering exhaustive search or traditional deterministic algorithms impractical for clinical timeframes [5].

To address these challenges, metaheuristic optimization techniques have gained substantial attention. Metaheuristics represent a family of adaptive, stochastic algorithms designed to efficiently explore vast and complex search spaces without requiring gradient information or strict mathematical assumptions about the shape of the solution landscape [6]. Their design philosophy emphasizes a balance between exploration, which seeks new and potentially better regions of the search space, and exploitation, which focuses on refining promising solutions. This dual capacity makes them particularly suitable for biomedical problems where the objective space is multi-modal, noisy, and shaped by competing clinical goals.

The historical progression of metaheuristics in oncology reflects both advances in algorithmic innovation and the evolution of available computational resources. In the 1970s and 1980s, early work on genetic algorithms applied the principles of evolutionary biology to optimize radiotherapy dose distributions. By the 1990s, particle swarm optimization and ant colony optimization, inspired by collective animal behaviors, were being adapted for clustering genomic data and feature selection in cancer diagnostics. The early 2000s introduced artificial bee colony algorithms, differential evolution, and firefly algorithms to handle multi-objective treatment planning scenarios. Over the last decade, hybrid frameworks that integrate metaheuristics with deep learning, reinforcement learning, and even quantum-inspired search methods have emerged, enabling applications in highly complex and data-rich oncology contexts [7–10]. The impact of metaheuristics in cancer research is best illustrated through domain-specific case studies. In breast cancer diagnosis, for instance, metaheuristic-driven feature selection from mammographic images has enhanced classification accuracy by systematically eliminating redundant or irrelevant variables [1]. In lung cancer treatment planning, multi-objective genetic algorithms have been successfully used to optimize stereotactic body radiotherapy beam arrangements, improving tumor targeting while reducing collateral exposure to healthy tissues [2]. For advanced-stage cancers, hybrid particle swarm optimization combined with deep learning has been employed to integrate multi-omics datasets into prognostic models, enabling better stratification of patients into treatment groups [3]. Similarly, ant colony optimization has proven effective in clustering large-scale transcriptomic profiles for tumor subtype characterization, demonstrating robustness in the presence of data noise and variability [4]. In histopathology image classification, deep learning architectures tuned by metaheuristics have achieved notable performance improvements [7, 8], while quantum-inspired metaheuristics have been explored for rapidly identifying effective multi-drug combinations in chemotherapy-resistant cancers [10].

Conceptually, the application of metaheuristics in oncology follows a systematic workflow. First, diverse datasets from omics technologies, medical imaging, and clinical records are collected and preprocessed to ensure compatibility and quality. These datasets are then subjected to feature engineering or dimensionality reduction to highlight the most informative variables. The metaheuristic algorithm acts as the central optimization engine, searching for solutions that balance multiple clinical objectives, such as maximizing therapeutic efficacy, minimizing toxicity, and optimizing resource utilization. The outputs are evaluated through predictive modeling or simulation and validated against retrospective or prospective patient data, with the ultimate goal of integrating the findings into clinical decision support systems. [10]

Despite their promise, metaheuristics are not without limitations. Their stochastic nature can lead to variability in results across runs, and without careful parameter tuning, they may converge prematurely to suboptimal solutions. Moreover, while they can provide high-quality approximations, they generally lack formal guarantees of global optimality. These limitations have motivated research into adaptive parameter control, hybridization with exact algorithms, and biologically inspired modifications that better align with the hierarchical and adaptive nature of cancer biology. This work is situated at the intersection of computational intelligence, oncology, and optimization theory. It aims to systematically explore, evaluate, and extend metaheuristic methods for diverse cancer-related applications, with a focus on algorithmic innovation, computational efficiency, and translational potential. By uniting advanced computational frameworks with domain-specific biological insights, this study aspires to contribute to the emerging paradigm of computational oncology, where optimization-driven strategies accelerate the development and delivery of personalized, effective cancer treatments. [7, 8]

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The rapid advancement of high-throughput technologies such as genomics, transcriptomics, proteomics, and metabolomics has transformed the ability of researchers and clinicians to characterize tumors with unprecedented detail. These molecular-level insights are complemented by advanced imaging techniques, including MRI, PET, CT, and high-resolution digital histopathology, as well as emerging liquid biopsy approaches capable of detecting tumor-derived biomarkers in blood samples. Such technologies generate vast, multidimensional datasets that not only provide static views of tumor states but also track their evolution across time and under therapeutic pressure. However, these data bring new analytical challenges: the number of variables frequently exceeds the number of patient samples by several orders of magnitude; the relationships between variables are nonlinear, context-specific, and often obscured by noise; and missing or incomplete data are common. Cancer is also inherently dynamic — gene expression patterns, tumor composition, and cellular phenotypes shift in response to both disease progression and applied treatments. Addressing these challenges requires computational strategies that are not only powerful but also flexible, capable of integrating diverse data types and accommodating change over time. Many of the most critical tasks in oncology, such as designing optimal treatment schedules, identifying biomarker panels, configuring radiotherapy beams, or finding effective drug combinations, are combinatorial in nature and scale in difficulty so rapidly that exhaustive search methods become impractical. It is within this computationally challenging landscape that metaheuristic optimization has proven increasingly valuable. Metaheuristics form a diverse family of adaptive, stochastic algorithms designed to efficiently search large and complex solution spaces without the limitations imposed by gradient-based or deterministic approaches. They are characterized by their ability to balance exploration — seeking new and potentially better regions of the search space — with exploitation — refining known high-performing solutions. This capacity is especially important in biomedical contexts where the optimization landscape is rugged, discontinuous, and multi-modal, and where the available data may be incomplete or uncertain. Additionally, metaheuristics handle multiple objectives naturally, making them ideal for medical problems where several competing clinical goals must be satisfied simultaneously, such as maximizing tumor control, minimizing side effects, and conserving resources. as evolved alongside both algorithmic innovation and advances in computational resources. Early applications in the 1970s and 1980s employed genetic algorithms, inspired by Darwinian evolution, to optimize radiotherapy dose distributions. In the 1990s, swarm intelligence methods such as particle swarm optimization and ant colony optimization were introduced, allowing researchers to tackle clustering of genomic data and feature selection tasks for cancer diagnostics. By the early 2000s, artificial bee colony optimization, differential evolution, firefly algorithms, and harmony search had been adapted for complex multi-objective treatment planning scenarios. Over the past decade, hybrid models have emerged that combine multiple metaheuristics or integrate them with deep learning, reinforcement learning, Bayesian inference, and quantum-inspired computation to address increasingly complex, high-dimensional problems in oncology.

Concrete examples highlight their impact. In breast cancer diagnostics, metaheuristic-driven feature selection applied to mammographic data has improved classification accuracy while reducing the dimensionality of the dataset. In lung cancer radiotherapy, multi-objective genetic algorithms have been used to optimize stereotactic body radiotherapy beam arrangements, improving tumor coverage while reducing radiation exposure to surrounding healthy tissue. For advanced-stage cancers, hybrid particle swarm optimization combined with deep learning has integrated diverse omics datasets into unified prognostic models, enabling more precise patient stratification and personalized treatment planning. Ant colony optimization has been applied to classify tumor subtypes from noisy transcriptomic datasets, demonstrating robustness despite biological and technical variability. In histopathology image analysis, deep learning architectures fine-tuned by metaheuristic algorithms have achieved significant improvements in predictive accuracy. More recently, quantum-inspired metaheuristic methods have been explored for rapid identification of optimal multi-drug combinations in chemotherapy-resistant cancers, drastically reducing computational time while maintaining solution quality. Despite their versatility and demonstrated successes, metaheuristics are not without limitations. Their stochastic nature means that outcomes can vary between runs, and without effective parameter tuning, there is a risk of prematurely converging to suboptimal solutions. While these algorithms can reliably produce high-quality approximations, they generally do not offer guarantees of finding a true global optimum. These challenges have driven research into adaptive parameter control strategies, the design of hybrid frameworks that combine metaheuristics with exact optimization methods, and the incorporation of biologically inspired mechanisms that more closely emulate the dynamic, hierarchical structure of cancer biology. Looking ahead, as both the scale and complexity of biomedical data continue to grow, the refinement of metaheuristic techniques to ensure scalability, reproducibility, and clinical reliability will be critical. [3] This study is positioned at the intersection of computational intelligence, oncology, and optimization science. Its goal is to systematically explore, adapt, and evaluate metaheuristic approaches for a wide range of cancer-related applications, emphasizing methodological innovation, computational efficiency, and translational potential. By combining advanced optimization strategies with a deep understanding of cancer biology, this work aims to contribute to the growing field of computational oncology, where algorithmically derived insights have the potential to directly inform and accelerate the development of personalized, effective therapeutic interventions.

The integration of metaheuristic optimization into oncology research has undergone a remarkable and deliberate evolution, progressing from isolated computational experiments into a sophisticated, multi-disciplinary research domain that now actively influences both theoretical developments and clinical applications. This transformation has been neither abrupt nor accidental; rather, it has been shaped by decades of iterative progress, the maturation of computational intelligence methodologies, the exponential growth of biomedical data resources, and the steadily intensifying demand for decision-support frameworks capable of addressing the highly combinatorial, multi-objective, and dynamic nature of cancer-related challenges. Across this timeline, each generation of algorithms and computational strategies has built upon the conceptual and technical foundations laid by its predecessors, resulting in an increasingly rich ecosystem of methods that can be adapted to a wide spectrum of oncological problems.

The earliest documented explorations into metaheuristic principles for cancer-related problems can be traced to the pioneering adoption of genetic algorithms in the 1970s and 1980s. These algorithms, drawing directly from Darwinian evolutionary theory and incorporating mechanisms such as selection, mutation, and crossover, offered a radically new perspective on solving optimization problems. In the specific context of radiotherapy treatment planning, the challenge of delivering an effective, tumor-eradicating dose of radiation while simultaneously preserving the integrity and function of surrounding healthy tissues had long been recognized as an inherently multi-objective problem. Traditional deterministic or gradient-based optimization techniques, while valuable for well-behaved mathematical models, were frequently constrained by oversimplifying assumptions that stripped away clinically relevant complexity. Genetic algorithms circumvented these limitations by adopting a population-based search strategy capable of exploring diverse regions of the solution space in parallel, thereby enhancing the likelihood of identifying treatment configurations that achieved more favorable trade-offs between tumor control probability and normal tissue complication probability. Although the computational infrastructure of that era imposed limitations on population size, iteration depth, and problem dimensionality, these early successes provided compelling proof-of-concept demonstrations that inspired subsequent decades of research. The 1990s witnessed a pronounced broadening in the range of metaheuristic paradigms available to biomedical researchers, particularly with the introduction and adoption of swarm intelligence models. Particle swarm optimization (PSO), inspired by the coordinated movement patterns observed in bird flocks and fish schools, brought with it a dynamic balance between individual-level exploration and collective convergence toward promising regions of the search space. In oncology, PSO was adapted to the clustering and classification of complex, high-dimensional datasets such as microarray-derived gene expression profiles. By enabling the identification of coherent clusters of co-expressed genes, PSO facilitated the discovery of novel biomarkers and the delineation of molecular subtypes with potential diagnostic or prognostic value. Ant colony optimization (ACO), drawing upon the pheromone-mediated foraging behaviors of

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real ant colonies, offered a complementary set of capabilities for discrete combinatorial problems. In cancer research, ACO proved adept at tasks such as determining optimal delivery paths in brachytherapy, refining fractionation schedules, and selecting minimal yet highly informative sets of molecular features for inclusion in diagnostic algorithms.

The early 2000s marked a period of diversification in the metaheuristic landscape, as researchers began to explore an expanding set of nature-inspired algorithms beyond the established evolutionary and swarm-based families. Artificial bee colony (ABC) optimization, emulating the foraging and communication patterns of honeybee swarms, was applied to multi-objective drug scheduling problems, enabling the identification of dosing regimens that maximized therapeutic impact while minimizing toxicity, side effects, and the emergence of drug resistance. Differential evolution (DE), with its emphasis on perturbing and recombining candidate solutions in a continuous search space, demonstrated robust performance in the parameter optimization of predictive models for tumor growth kinetics and treatment response forecasting. Firefly algorithms (FA), based on the concept of attractiveness proportional to perceived brightness, were employed for high-dimensional feature selection, often leading to tangible improvements in the accuracy and robustness of cancer classification models. Harmony search (HS), inspired by the improvisation process of musicians, was explored for its flexibility in both discrete and continuous optimization problems in oncology, particularly in adaptive radiotherapy planning where rapid re-optimization was required in response to changes in tumor volume or patient anatomy. The past decade has been characterized by the emergence and rapid expansion of hybrid metaheuristic approaches, in which the strengths of multiple algorithms are combined or in which metaheuristics are integrated with advanced machine learning and statistical methods. Deep learning architectures, renowned for their capacity to learn rich, hierarchical representations directly from raw data, have been coupled with metaheuristic search processes to optimize network topologies, activation functions, learning rates, and regularization parameters for cancer classification and segmentation tasks. Reinforcement learning frameworks have been combined with metaheuristics to enable adaptive treatment planning systems that can iteratively refine their strategies based on simulated or real patient responses. Quantum-inspired metaheuristics, informed by principles of quantum mechanics such as superposition and entanglement, have begun to demonstrate their potential in accelerating convergence and diversifying solution populations, particularly in constrained optimization scenarios such as the identification of synergistic multi-drug regimens for therapy-resistant cancers.

A review of specific case studies illustrates the versatility and adaptability of metaheuristic approaches in oncology. In breast cancer research, the use of metaheuristic-driven feature selection on mammographic imaging datasets has not only reduced dimensionality but has also enhanced the performance of diagnostic classifiers, enabling more reliable early detection. In lung cancer radiotherapy, multi-objective evolutionary algorithms have optimized beam configurations by simultaneously considering factors such as dose homogeneity, conformity indices, and organ-at-risk sparing, resulting in treatment plans that outperform those derived from conventional planning systems. In the management of advanced-stage cancers, hybrid particle swarm optimization–deep learning models have successfully integrated diverse datasets spanning genomics, transcriptomics, proteomics, and clinical records, producing prognostic models with higher predictive accuracy and better generalization across patient cohorts. Ant colony optimization has been employed to robustly identify molecular subtypes from noisy transcriptomic datasets, a task complicated by high biological variability and technical artifacts. In histopathology image analysis, convolutional neural networks fine-tuned through metaheuristic optimization have yielded measurable gains in classification performance across multiple cancer types. Quantum-inspired metaheuristics have further accelerated the process of discovering optimal drug combinations, reducing computational time requirements from days to hours without sacrificing solution quality. Despite the successes documented in the literature, several persistent methodological and practical challenges remain. The performance of metaheuristic algorithms is often highly sensitive to the selection of control parameters such as population size, mutation rate, or pheromone evaporation coefficient. Inappropriate parameter settings can lead to premature convergence, where exploration of the search space halts too soon, or to excessive exploration, where the algorithm fails to sufficiently refine high-potential solutions. The inherent stochasticity of metaheuristics means that repeated executions can yield different outcomes, complicating efforts to ensure reproducibility in clinical contexts where decision-making must be consistent and defensible. Additionally, while metaheuristics are adept at producing high-quality approximations to optimal solutions, they do not generally provide formal guarantees of global optimality, a fact that must be carefully communicated to practitioners and stakeholders in the clinical decision-making process.

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2. Literature Review

The integration of metaheuristic optimization into oncology research has undergone a remarkable and deliberate evolution, progressing from isolated computational experiments into a sophisticated, multi-disciplinary research domain that now actively influences both theoretical developments and clinical applications. This transformation has been neither abrupt nor accidental; rather, it has been shaped by decades of iterative progress, the maturation of computational intelligence methodologies, the exponential growth of biomedical data resources, and the steadily intensifying demand for decision-support frameworks capable of addressing the highly combinatorial, multi-objective, and dynamic nature of cancer-related challenges. Across this timeline, each generation of algorithms and computational strategies has built upon the conceptual and technical foundations laid by its predecessors, resulting in an increasingly rich ecosystem of methods that can be adapted to a wide spectrum of oncological problems. Building on this historical progression, the contemporary landscape of metaheuristic optimization in oncology has matured into a multidisciplinary environment where algorithm design, biomedical data analysis, and clinical problem-solving intersect in increasingly sophisticated ways. The breadth of applications now spans the entire cancer care continuum, from early detection and diagnosis to prognosis estimation, treatment planning, and post-therapy monitoring. This evolution has been driven not only by advances in algorithmic innovation but also by the parallel growth of biomedical data repositories, imaging technologies, and molecular profiling capabilities that generate the complex, high-dimensional datasets ideally suited to metaheuristic approaches. One significant driver of methodological innovation has been the recognition that cancer-related data often combine features of both continuous and discrete optimization problems. Imaging-derived metrics, for example, may be continuous-valued, capturing pixel intensities, shape descriptors, and textural features, while genomic or proteomic datasets may present binary or categorical variables indicating the presence or absence of specific molecular markers. Metaheuristic algorithms excel in such hybrid spaces, capable of simultaneously navigating discrete decision variables and continuous parameter landscapes. This capacity has opened the door to joint optimization tasks—such as simultaneously selecting the most informative features and tuning the parameters of a classification model—thereby streamlining the diagnostic pipeline and reducing the risk of overfitting.

Another defining characteristic of modern research in this domain is the shift from purely accuracy-driven goals toward multi-criteria optimization objectives that better reflect the realities of clinical practice. For example, in radiotherapy treatment planning, the best plan is not necessarily the one with the absolute highest tumor control probability; it is the one that balances tumor eradication with minimal damage to healthy tissues, meets time constraints for delivery, and respects patient-specific anatomical and physiological constraints. Multi-objective metaheuristic algorithms, which maintain a diverse set of Pareto-optimal solutions rather than a single "best" outcome, have become increasingly prominent in such contexts. This allows clinicians to choose among equally optimal plans based on qualitative factors or patient preferences, aligning computational outputs with personalized medicine goals. In parallel, the integration of metaheuristics with deep learning has emerged as a particularly fruitful avenue for innovation. Deep neural networks, while powerful, are notoriously sensitive to hyperparameter settings such as learning rate, network depth, and regularization parameters. Metaheuristics can systematically explore the vast and irregular hyperparameter search space, identifying configurations that significantly enhance predictive performance while reducing the manual trial-and-error process. Beyond hyperparameter tuning, metaheuristics have been applied to structural optimization—selecting the optimal number of neurons in each layer, pruning redundant connections, and even evolving entirely novel network topologies tailored to the unique characteristics of cancer-related datasets. These approaches have shown promise in both imaging tasks, such as histopathology slide analysis, and non-imaging contexts, such as predicting treatment response from genomic signatures. One emerging trend within the literature is the development of hybrid pipelines that integrate metaheuristics at multiple stages of the analytical process. In such frameworks, metaheuristics might first be employed to select a minimal yet highly informative set of input features from a large dataset. The reduced dataset can then be passed to a metaheuristic-tuned machine learning model, and finally, optimization algorithms can be used again to refine output decision thresholds or risk stratification criteria. This layered integration allows each stage to benefit from the exploratory and adaptive strengths of metaheuristics while maintaining computational efficiency by progressively narrowing the search space.

Recent years have also seen the application of metaheuristic optimization to increasingly complex multimodal datasets. Modern oncology research often involves integrating data from multiple sources: radiological images, histopathology slides, molecular profiles, clinical records, and even wearable device outputs that track physiological parameters over time. Each modality brings its own noise characteristics, feature distributions, and missing data patterns, making direct integration challenging. Metaheuristics can play a central role in this integration process by optimizing the weights or fusion strategies that combine these modalities into a unified predictive framework. This has particular relevance for personalized treatment planning, where the optimal therapeutic strategy may depend on a nuanced combination of imaging-based tumor characteristics, molecular subtype information, and patient comorbidity profiles. A further methodological advance has been the exploration of constrained metaheuristic optimization in oncology. While unconstrained optimization allows free exploration of the search space, many real-world clinical problems come with strict feasibility constraints: radiation doses must remain within safety limits, chemotherapy regimens must respect toxicity thresholds, and diagnostic tests must stay within budgetary or logistical boundaries. Incorporating these constraints directly into the metaheuristic search process ensures that candidate solutions are clinically viable from the outset, reducing the need for post-optimization adjustments. This has led to the development of custom constraint-handling mechanisms within popular algorithms, allowing them to navigate feasible regions of highly complex search spaces without sacrificing convergence performance.

The literature also reflects growing interest in adaptive and self-tuning metaheuristic algorithms. Traditional implementations require manual specification of key parameters—population size, mutation rates, inertia weights, and so forth—which can greatly influence performance. Adaptive variants monitor search progress in real time and adjust these parameters dynamically, shifting the balance between exploration and exploitation as needed. This self-regulating behavior is especially valuable in oncology applications, where the landscape of the optimization problem may shift abruptly due to the discovery of new biomarkers, the introduction of novel imaging modalities, or changes in treatment protocols. In terms of problem domains, the range of applications continues to expand beyond diagnosis and treatment planning. Prognostic modeling, for instance, benefits from metaheuristic-driven feature selection and model tuning to identify patients at high risk of recurrence or adverse treatment outcomes. Metaheuristics have also been applied to optimize screening strategies at the population level, determining the optimal allocation of limited screening resources to maximize early detection rates while minimizing unnecessary testing. In surgical oncology, optimization algorithms have been used to plan resection strategies that maximize tumor removal while preserving functional tissue, particularly in delicate anatomical regions such as the brain or liver. A recurring theme in this body of work is the need for robustness. In the inherently noisy and variable environment of clinical data, models must maintain stable performance even when faced with incomplete or imperfect inputs. Robust metaheuristic optimization strategies incorporate mechanisms to handle missing data gracefully, resist overfitting to small datasets, and maintain solution quality under perturbations to the input distribution. These capabilities are particularly critical in settings where retraining or recalibrating the model is costly or infeasible, such as in resource-limited healthcare systems or in applications involving rare cancer types. The literature also documents an increasing emphasis on interpretability. While metaheuristics are primarily optimization tools rather than interpretable models in themselves, their influence over model parameters, feature selection, and decision boundaries can be leveraged to improve transparency. For example, if a metaheuristic consistently selects a small subset of features as most informative for a classification task, this subset can be analyzed for biological relevance, potentially revealing new biomarkers or confirming the clinical importance of known ones. Similarly, the evolution of decision boundaries during the optimization process can offer insights into how different patient subgroups are separated in the feature space, aiding in hypothesis generation and validation. Technological advances have played a crucial enabling role in this field's expansion. High-performance computing, parallel processing, and distributed architectures have significantly reduced the time required to evaluate large populations of candidate solutions. Cloud-based infrastructures allow research groups without extensive local hardware resources to run computationally demanding metaheuristic experiments, democratizing access to these techniques. Additionally, the rise of open-source software libraries for metaheuristic optimization has lowered the barrier to entry for new researchers, facilitating broader experimentation and cross-disciplinary collaboration.

One of the more recent and exciting developments is the application of metaheuristic optimization in the context of adaptive clinical trials. Traditional trials are rigidly structured, but adaptive designs allow for modifications to patient allocation, dosage, or even treatment arms based on interim results. Metaheuristics can be employed to optimize these adaptations in real time, balancing the competing objectives of maximizing trial efficiency, ensuring patient safety, and preserving statistical validity. This represents a convergence of optimization, statistical design, and ethical oversight, underscoring the broad applicability of these algorithms in the healthcare domain. Looking ahead, the trajectory suggested by the literature points toward even deeper integration of metaheuristics with other computational paradigms. For instance, coupling metaheuristic optimization with reinforcement learning could produce treatment recommendation systems that not only search for optimal strategies in a static dataset but also learn and adapt based on ongoing patient responses. Similarly, combining metaheuristics with causal inference frameworks could help distinguish between correlations and genuine cause-effect relationships in observational cancer datasets, leading to more reliable clinical recommendations. The diversity of algorithmic strategies documented—from genetic algorithms and particle swarm optimization to more recent quantum-inspired techniques—demonstrates the field's openness to innovation. Each class of algorithm brings its own balance of exploration and exploitation, susceptibility to local minima, and computational demands, allowing researchers to tailor their choice to the specific contours of the problem at hand. As the complexity of oncology datasets continues to grow, so too will the need for hybrid approaches that combine the strengths of multiple metaheuristic families, perhaps augmented by problem-specific heuristics or domain knowledge.

The sustained and deliberate evolution of this field underscores an important reality: metaheuristic optimization in oncology is not a passing trend but a robust methodological paradigm with the flexibility to adapt to new challenges. From the early proof-of-concept studies on limited datasets to the sophisticated, multi-modal, and clinically integrated systems of today, the literature tells a story of continuous refinement, expansion, and interdisciplinary collaboration. This trajectory suggests that as both computational and biomedical sciences continue to advance, metaheuristic optimization will remain at the forefront of innovation in precision cancer care.

The earliest documented explorations into metaheuristic principles for cancer-related problems can be traced to the pioneering adoption of genetic algorithms in the 1970s and 1980s. These algorithms, drawing directly from Darwinian evolutionary theory and incorporating mechanisms such as selection, mutation, and crossover, offered a radically new perspective on solving optimization problems. In the specific context of radiotherapy treatment planning, the challenge of delivering an effective, tumor-eradicating dose of radiation while simultaneously preserving the integrity and function of surrounding healthy tissues had long been recognized as an inherently multi-objective problem. Early works, even with limited computational resources, demonstrated the capacity of population-based searches to produce competitive solutions compared to conventional deterministic techniques, thereby laying the groundwork for methods such as the improved marine predators algorithm in breast cancer analysis [11] and optimization-based feature pruning for mammogram classification [12]. The 1990s witnessed a pronounced broadening in the range of metaheuristic paradigms available to biomedical researchers, particularly with the introduction and adoption of swarm intelligence models. Particle swarm optimization (PSO), inspired by the coordinated movement patterns observed in bird flocks and fish schools, brought with it a dynamic balance between individual-level exploration and collective convergence toward promising regions of the search space. In oncology, PSO found application in clustering and classification tasks for microarray-derived gene expression data, enabling the identification of coherent biomarker clusters. Parallel developments in ant colony optimization (ACO) provided complementary strengths for discrete combinatorial problems, such as feature subset selection in diagnostic models and optimization of brachytherapy seed placement. The adaptability of these paradigms to diverse oncological contexts foreshadowed later innovations such as the application of crow search algorithms for predictive modeling in brain cancer [13] and hybrid coot-based CNN models for thyroid cancer detection [14].

The early 2000s marked a period of diversification in the metaheuristic landscape, as researchers began to explore a growing set of nature-inspired algorithms beyond the evolutionary and swarm-based families. Artificial bee colony optimization was applied to multi-objective chemotherapy scheduling, differential evolution demonstrated robustness in tumor growth modeling, and firefly algorithms excelled in high-dimensional feature selection. Harmony search was used in adaptive radiotherapy re-optimization workflows. These developments set the stage for more integrated frameworks in the following decades, as evidenced by more recent approaches such as hybrid PSO–ACO for lung cancer imaging [15] and optimized deep CNN architectures for skin lesion detection [16].

The past decade has been characterized by the rapid emergence of hybrid metaheuristic approaches, often in combination with machine learning and deep neural networks. These systems leverage the global exploration capacity of metaheuristics to fine-tune parameters in complex models, yielding substantial gains in accuracy

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and robustness. Examples include breast cancer molecular subtype detection frameworks combining radiomics and metaheuristics [17], lung cancer segmentation using metaheuristic-driven region extraction [18], and skin cancer classification pipelines employing hyperparameter optimization for CNNs [19]. Recent years have also seen the expansion of multi-objective optimization strategies, acknowledging the inherently multi-criteria nature of oncology decision-making. Studies have optimized treatment plans by balancing accuracy, computational time, and interpretability, as in melanoma detection frameworks integrating multi-objective metaheuristics with CNN tuning [20], and breast cancer prediction models using feature-selected gradient boosting optimized by metaheuristics [21]. These works demonstrate that the strategic integration of metaheuristics continues to push the frontier of computational oncology, enhancing both methodological sophistication and clinical applicability. Taken collectively, these additional case studies confirm that the field has moved beyond isolated algorithmic experiments into a mature and rapidly evolving discipline. The incorporation of metaheuristic optimization into diverse data modalities, problem scales, and cancer types suggests not only its current effectiveness but also its potential to serve as a foundational tool for the next generation of precision oncology systems.

Table 1: Methodology summary of metaheuristic optimization studies not used in the introduction.

Reference	**Cancer Domain**	**Metaheuristic Method**	**Task**
[22]	Skin Cancer	Metaheuristic or Hybrid Optimization	Classification
[23]	Oral Cancer	Metaheuristic or Hybrid Optimization	Classification
[24]	Cervical Cancer	Metaheuristic or Hybrid Optimization	Classification
[25]	Cervical Cancer	Metaheuristic or Hybrid Optimization	Classification
[26]	Breast Cancer	Cuckoo Search	Image Enhancement
[27]	Cross-Cancer / General	Metaheuristic or Hybrid Optimization	Feature Selection
[28]	Cross-Cancer / General	Metaheuristic or Hybrid Optimization	Hyperparameter Optimization
[29]	Brain Cancer	Firefly; Cuckoo; Lion; Bat Optimization	Detection
[30]	Breast Cancer	Metaheuristic or Hybrid Optimization	Prediction
[31]	Breast Cancer	Metaheuristic or Hybrid Optimization	Clustering
[32]	Lung Cancer	Beetle Swarm Optimization	Detection
[33]	Lung Cancer	Crow Search	Prediction
[34]	Skin Cancer	Neural Network Optimization Algorithm	Detection
[35]	Breast Cancer	Differential Evolution	Classification
[36]	Lung Cancer	Bat Algorithm	Prediction
[37]	Cross-Cancer / General	Metaheuristic or Hybrid Optimization	Feature Selection
[38]	Skin Cancer	Metaheuristic or Hybrid Optimization	Classification / Prediction
[39]	Cross-Cancer / General	Cuckoo Search	Classification
[40]	Breast Cancer	Whale Optimization Algorithm	Detection

The presented methodology table offers a structured synthesis of a wide spectrum of contemporary studies applying metaheuristic optimization algorithms to cancer detection, classification, prediction, and diagnosis tasks. It serves as both a classification tool and a meta-analysis reference framework, consolidating information from diverse publication venues and spanning multiple cancer domains. By organizing each study according to its bibliographic reference, targeted cancer domain, applied metaheuristic method, and specific research task, the table forms a high-resolution mapping of methodological diversity in the field. The purpose of this table is not merely to list references, but to systematically organize the methodological approaches adopted in each cited work. It distinguishes between the cancer domain, specifying whether a study targets a single cancer type or adopts a cross-cancer or multi-cancer perspective, the metaheuristic method, identifying the primary optimization strategy or strategies applied in the study, whether single-algorithm or hybridized frameworks, and the title or task, providing a concise but accurate description of the research problem and scope of the study. This classification allows the reader to navigate quickly through a complex and heterogeneous literature landscape and identify patterns of methodological alignment or divergence across cancer research domains. From an analytical perspective, the cancer domain column reveals a striking degree of specialization among researchers. A significant portion of the studies focus on breast cancer, reflecting its high global prevalence, the availability of benchmark mammographic datasets, and the urgent clinical need for improved early detection methods. Breast cancer entries in the table span a variety of metaheuristics, including marine predators algorithm, whale optimization algorithm, and cuckoo search, demonstrating both methodological diversity and experimentation with nature-inspired strategies. Lung cancer also remains a major focus of research due to its high lethality and the challenges posed by its imaging characteristics. Studies targeting lung cancer employ butterfly optimization, crow search, bat algorithm, and hybrid metaheuristics, illustrating that multiple optimization paradigms are actively compared in this domain to address noise, occlusion, and morphological variability. Skin cancer, including melanoma, is another domain where metaheuristic integration is prominent, particularly in dermoscopic image analysis. Many skin cancer studies in the table use optimization algorithms to improve feature selection, hyperparameter tuning, or segmentation, and multi-objective metaheuristics have been explored to balance competing criteria such as accuracy and computational efficiency. Other cancers such as cervical, thyroid, oral, brain, and prostate cancer appear less frequently but demonstrate that metaheuristics are being adapted to diverse medical contexts. These cases often present unique imaging modalities and clinical constraints that influence algorithm choice and configuration. Cross-cancer or general oncology studies are also present, representing works that propose adaptable frameworks rather than disease-specific solutions.

The table's explicit labeling of metaheuristic methods allows immediate assessment of algorithmic trends. Many works refine or apply a single metaheuristic such as cuckoo search, whale optimization algorithm, crow search, or marine predators algorithm. This is common when the goal is to benchmark a specific method against state-of-the-art baselines. Hybrid algorithms appear frequently, combining, for example, genetic algorithms with particle swarm optimization or integrating whale optimization with deep neural networks. Hybridization aims to exploit complementary strengths, improve convergence rates, and avoid premature stagnation. Multi-objective optimization appears in specialized contexts, notably melanoma detection, where maximizing sensitivity while controlling false positives is critical. Some methods are inspired by specific biological or ecological processes, such as beetle swarm optimization, bat-inspired search, coot-based optimization, and marine predator behaviors. These novel algorithms often bring unique exploration–exploitation trade-offs to the problem domain. The task descriptions in the table reveal considerable diversity beyond classification. Image segmentation is a major category, especially in lung and skin cancer, where isolating tumor regions from imaging data is a prerequisite for downstream analysis. Metaheuristic-tuned clustering, thresholding, and feature extraction methods are used to improve segmentation accuracy and robustness. Feature selection and dimensionality reduction are also frequent applications, particularly for high-dimensional biomedical data such as gene expression profiles or radiomic feature sets. Algorithms like ant colony optimization, genetic algorithms, and differential evolution are employed to identify minimal yet informative feature subsets, thereby enhancing classifier performance while reducing overfitting risk. Hyperparameter optimization for deep learning models is another key application, with metaheuristics used to tune CNN architectures, learning rates, and regularization strategies. This is especially prominent in skin cancer and breast cancer studies where deep learning has already shown strong performance, but manual hyperparameter tuning is time-consuming and suboptimal. Some works integrate metaheuristics into multi-stage pipelines, combining preprocessing, segmentation, feature extraction, and classification into an end-to-end framework. These integrated systems often aim for full automation of diagnostic tasks.

A holistic reading of the table reveals several patterns and research gaps. Certain algorithms, such as whale optimization and cuckoo search, appear across multiple cancer types, suggesting they have broad applicability, while others, such as beetle swarm optimization, remain niche and tied to specific problems. Hybrid

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approaches are particularly common in cancers with complex imaging data, like lung and brain cancer, likely due to the difficulty of modeling such data with a single algorithm. However, multi-objective optimization remains relatively underused despite its potential advantages for balancing competing clinical and computational objectives. Furthermore, some cancers, such as pancreatic, liver, and colorectal cancer, are absent, indicating opportunities for further research. The cross-domain adaptation of algorithms—applying methods developed for one cancer type to another—also appears limited, suggesting a direction for expanding methodological impact. The placement of this table within the methodology section, using a non-floating longtable environment, ensures that it appears exactly where intended in the document, maintaining narrative continuity. This design choice prevents displacement that can occur with floating tables and allows for seamless integration into the text. Researchers consulting this table can quickly identify dominant and emerging metaheuristic approaches for a given cancer type, benchmark against similar studies, discover underexplored algorithm–cancer combinations, and observe hybridization patterns that have led to performance improvements. The structured representation transforms the table into more than a reference list; it becomes a decision-support tool for designing new experiments and selecting optimization strategies aligned with the unique challenges of specific cancer detection and classification problems. By systematically cataloging the interplay between cancer domain, metaheuristic method, and specific research task, this table provides an organized knowledge base that reflects the methodological state of the art. Its value lies both in the breadth of studies covered and in the precision of its classification, enabling informed methodological choices in future work. The patterns and gaps identified through this synthesis underscore the dynamic nature of metaheuristic applications in oncology and point toward both promising directions for innovation and areas where methodological diversity could be expanded.

Table 2: Comprehensive Summary of Metaheuristic Optimization Studies in Cancer Domains Not Used in the Introduction

Reference	**Metaheuristic Method**	**Task**	**Methodology**	**Key Findings / Results**
			Breast Cancer	
[26]	Cuckoo Search	Image Enhancement	Applied brightness-preserving cuckoo search to optimize histogram equalization of mammograms	Improved image contrast while preserving brightness, enhancing visibility of lesions
[30]	Metaheuristic or Hybrid Optimization	Prediction	Developed metaheuristic-driven ensemble learning framework using clinical and imaging features	Achieved higher predictive accuracy compared to conventional ensemble methods
[31]	Metaheuristic or Hybrid Optimization	Clustering	Utilized metaheuristic-based clustering for early-stage breast cancer patient grouping	Identified meaningful patient clusters that correlated with disease stage
[35]	Differential Evolution	Classification	Designed bio-inspired CNN optimized with differential evolution for RNA-seq gene data	Outperformed baseline CNNs in classification accuracy on gene expression datasets
[40]	Whale Optimization Algorithm	Detection	Integrated WOA into neural network training for mammography mass detection	Increased detection rate and reduced false positives compared to standard MLP
			Lung Cancer	
[32]	Beetle Swarm Optimization	Detection	Optimized SVM parameters via improved weight-based beetle swarm optimization	Enhanced detection accuracy and reduced computational cost
[33]	Crow Search	Prediction	Applied crow search for feature selection in lung cancer prediction models	Improved prediction performance with reduced feature dimensionality
[36]	Bat Algorithm	Prediction	Used bat-inspired metaheuristic to optimize CNN for CAD-based lung cancer prediction	Achieved better accuracy and robustness compared to non-optimized CNN
			Skin Cancer	
[22]	Metaheuristic or Hybrid Optimization	Classification	Combined deep training with metaheuristic optimization for dermoscopy images	Improved classification accuracy for malignant vs. benign skin lesions
[34]	Neural Network Optimization Algorithm	Detection	Used kernel fuzzy C-means and improved neural network optimization for lesion detection	Increased detection sensitivity and specificity in challenging image conditions
[38]	Metaheuristic or Hybrid Optimization	Classification / Prediction	Reviewed multiple metaheuristics for skin lesion classification and prognosis	Highlighted superior performance of hybrid optimization strategies
			Oral Cancer	
[23]	Metaheuristic or Hybrid Optimization	Classification	Applied deep feature selection via metaheuristic optimization for oral cancer images	Achieved improved classification accuracy by selecting most relevant features
			Cervical Cancer	
[24]	Metaheuristic or Hybrid Optimization	Classification	Built deep learning model optimized by metaheuristics for smear image classification	Enhanced sensitivity and specificity in cervical cancer detection
[25]	Metaheuristic or Hybrid Optimization	Classification	Developed lightweight deep network (MLNet) optimized for cervical cancer diagnosis	Reduced computational load while maintaining high diagnostic accuracy
			Brain Cancer	
[29]	Firefly; Cuckoo; Lion; Bat Optimization	Detection	Applied multiple metaheuristics for MRI preprocessing, feature extraction, and classification	Improved detection accuracy and reduced noise in brain tumor imaging
			Thyroid Cancer	
[14]	Metaheuristic or Hybrid Optimization	Detection	Used hybrid coot-based CNN for thyroid nodule detection in ultrasound images	Achieved high detection precision and robustness across imaging variations
			Cross-Cancer / General Oncology	
[27]	Metaheuristic or Hybrid Optimization	Feature Selection	Comprehensive review of metaheuristic feature selection methods in disease diagnosis	Identified common trends and best practices for multi-domain datasets
[28]	Metaheuristic or Hybrid Optimization	Hyperparameter Optimization	Reviewed CNN hyperparameter tuning via metaheuristics for medical imaging	Highlighted efficiency gains and accuracy improvements across tasks
[37]	Metaheuristic or Hybrid Optimization	Feature Selection	Applied advanced metaheuristics for medical dataset classification and selection	Improved classification metrics across multiple datasets
[39]	Cuckoo Search	Classification	Hybrid cuckoo search for cancer classification tasks	Outperformed baseline classifiers in accuracy and stability

The compiled table presents a broad survey of metaheuristic optimization research across diverse cancer domains, providing a structured comparison of algorithms, tasks, methodologies, and reported results. By grouping studies according to cancer type, it becomes easier to identify domain-specific trends while also recognizing cross-cutting themes that span multiple application areas. In the **Breast Cancer** section, algorithmic diversity is evident, with Cuckoo Search, Whale Optimization Algorithm, Differential Evolution, and hybrid metaheuristics all represented. Methodologies range from low-level image enhancement—where optimization adjusts histogram equalization parameters—to high-level predictive modeling using clinical and imaging data. These studies consistently report improved diagnostic accuracy, reduced false positives, and better interpretability compared with non-optimized baselines. Clustering methods, in particular, highlight the role of unsupervised learning in uncovering latent subtypes, while predictive frameworks demonstrate the value of metaheuristics in refining model parameters for complex, multi-modal datasets. The **Lung Cancer** studies emphasize detection and prediction tasks, employing Beetle Swarm Optimization, Crow Search, and Bat Algorithm. These algorithms are well-suited to the high-dimensional, noisy nature of lung cancer datasets derived from CT imaging. Methodologies typically integrate metaheuristics with SVM or CNN classifiers for feature selection and parameter tuning. The results show that such optimization can lead to more efficient models with higher accuracy, an essential requirement given the often late-stage diagnosis of lung cancer. In **Skin Cancer**, the primary focus is on classification in challenging imaging conditions. Metaheuristic methods are applied either directly to improve segmentation accuracy or indirectly through deep network optimization. Examples include kernel fuzzy C-means with neural network optimization and hybrid metaheuristic-deep learning approaches for dermoscopy images. Across studies, sensitivity and specificity improvements are consistently reported, indicating strong potential for enhancing automated dermatological screening. The **Oral Cancer** entry, while singular, is significant in demonstrating the use of metaheuristic-driven deep feature selection. This approach reduces input dimensionality and focuses learning on diagnostically relevant features, improving classification accuracy in a domain characterized by image heterogeneity. The two **Cervical Cancer** studies apply metaheuristics to optimize deep learning frameworks, with an emphasis on lightweight architectures like MLNet. Such designs are crucial for deployment in low-resource settings where computational efficiency is as important as accuracy. Results confirm that carefully tuned lightweight networks can achieve high sensitivity and specificity with minimal computational overhead. For **Brain Cancer**, a multi-algorithm approach combining Firefly, Cuckoo, Lion, and Bat Optimization is notable. This diversity reflects the recognition that no single algorithm dominates all problem types. The methodology spans MRI preprocessing, feature extraction, and classification, yielding improved detection accuracy and robustness to noise—critical for treatment planning. In **Thyroid Cancer**, a hybrid coot-based CNN is optimized for ultrasound imaging, addressing challenges of low contrast and artifacts. The reported improvements in detection precision and robustness underscore the value of metaheuristic tuning for subtle pattern recognition tasks. The **Cross-Cancer / General Oncology** section illustrates the adaptability of metaheuristics to multi-domain applications. Tasks range from feature selection to CNN hyperparameter optimization, with consistent findings of reduced training time, improved accuracy, and enhanced generalization. The presence of general-purpose algorithms like Cuckoo Search across multiple cancer types suggests strong potential for cross-domain transferability. Several broader trends emerge from the table. Classification is the most common task, followed by detection, with prediction and clustering filling niche but important roles. Metaheuristics are rarely used in isolation; instead, they function as optimization layers on top of machine learning or deep learning models. Hybridization—either between multiple metaheuristics or between metaheuristics and other AI paradigms—is a recurring theme, reflecting a desire to combine complementary strengths and mitigate individual weaknesses.

From a methodological perspective, metaheuristics excel in handling high-dimensional, noisy, and heterogeneous data, enabling effective feature selection and hyperparameter tuning. These capabilities address two of the biggest challenges in biomedical AI: the curse of dimensionality and the sensitivity of model performance to parameter settings. The performance gains reported—higher accuracy, better sensitivity and specificity, and in some cases reduced computation—demonstrate that well-tuned metaheuristics can offer tangible improvements over conventional search or default parameter configurations. In sum, the table serves as both a catalog of current research and an indicator of the evolving role of metaheuristics in computational oncology. It highlights their broad applicability, adaptability to domain constraints, and capacity to improve clinical decision-support systems. As algorithmic innovation continues and biomedical datasets grow in scale and complexity, metaheuristic optimization is poised to remain a core enabler of high-performance, clinically relevant AI systems in cancer research and care. 2

3. Discussion

The integration of metaheuristic optimization algorithms into cancer research, as reflected in the methodology table, reveals a dynamic and maturing field where these algorithms are becoming central components of high-performance diagnostic, prognostic, and therapeutic decision-support pipelines. The diversity of cancer types, optimization strategies, and tasks covered illustrates both methodological adaptability and a willingness to experiment with novel algorithmic paradigms to improve clinical outcomes. A key observation is the dominance of breast, lung, and skin cancer in current applications. Breast cancer studies leverage the abundance of high-quality annotated imaging datasets and genomic profiles, applying a variety of metaheuristics such as whale optimization, cuckoo search, and marine predators algorithm. No single method emerges as universally superior; rather, the diversity suggests that algorithm choice is driven by the balance between exploration, exploitation, convergence speed, and computational efficiency. Lung cancer research frequently adopts hybrid approaches—e.g., PSO–ACO combinations—addressing challenges in CT imaging segmentation and classification where anatomical variability and low tissue contrast demand robust search strategies. Skin cancer applications emphasize hyperparameter tuning for CNNs in dermoscopic analysis, aiming to balance classification accuracy with computational efficiency for teledermatology and portable diagnostics. Less represented domains—cervical, thyroid, oral, and brain cancers—demonstrate innovative, disease-specific applications. For example, cervical cancer models employ lightweight deep networks optimized for low-resource settings, brain cancer MRI pipelines combine multiple metaheuristics for robust tumor detection, and thyroid cancer ultrasound systems use hybrid CNN–metaheuristic frameworks to address low-contrast imaging challenges. These studies show that even in data-scarce domains, metaheuristics can be tailored to the nuances of specific imaging or molecular datasets. Across all cancer types, metaheuristics serve multiple roles: feature selection to reduce dimensionality in genomic datasets, hyperparameter tuning for deep architectures, segmentation and clustering for medical images, and preprocessing to enhance data quality prior to classification. Methodological specialization often aligns with cancer type—for example, whale optimization is prevalent in breast and skin cancer imaging, while cuckoo search appears in cross-cancer classification, and crow search is favored in multimodal MRI contexts. The table also highlights methodological diversity, from established algorithms like genetic algorithms and PSO to newer ones like beetle swarm optimization and bat algorithm. The repeated use of hybrid and multi-objective variants reflects a recognition that no single approach dominates across all scenarios and that trade-offs among accuracy, sensitivity, specificity, and computational efficiency are inherent to clinical optimization problems. Several gaps are evident. Certain high-burden cancers—pancreatic, gastric, colorectal—are absent, suggesting data availability or modality complexity as barriers. Multi-objective optimization is underutilized despite its clear alignment with the multi-criteria nature of clinical decision-making. Cross-domain adaptation is rare, though segmentation or feature selection pipelines developed for one cancer could often be transferred to others with minimal modification. Standardizing evaluation protocols, datasets, and metrics could enable more meaningful algorithm comparisons and accelerate best-practice identification. Implementation-aware optimization remains an unmet need. Gains in statistical accuracy do not automatically translate to improved patient outcomes unless models integrate seamlessly into clinical workflows, maintaining interpretability and trust. Adaptability to evolving datasets is also critical; most studies assume static data, leaving models vulnerable to performance degradation due to hardware changes, protocol shifts, or patient population differences. Online or incremental metaheuristic variants could address such data drift. Scalability is another concern. Deep architectures tuned by metaheuristics can be computationally intensive, limiting adoption in low-resource settings. Strategies such as parallelized search, surrogate modeling, and heuristic-informed initialization could reduce computation without sacrificing performance. Additionally, interpretability remains essential; integrating transparency mechanisms such as feature attribution or rule extraction can enhance clinician trust. Equity considerations demand diverse, representative training datasets to prevent performance disparities across demographic groups. Fairness constraints embedded within optimization objectives can help ensure equitable model performance. Future directions point toward integrated optimization ecosystems, where metaheuristics operate at multiple levels—feature selection, model tuning, treatment planning—within adaptive, learning healthcare systems.

In summary, the methodology table serves as both a record of progress and a roadmap for future research. It reflects a field marked by diversity of approach, adaptability to domain-specific challenges, and growing methodological sophistication, while also identifying opportunities for expansion into underrepresented cancers, broader use of multi-objective frameworks, improved scalability, and stronger integration with clinical realities.

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4. Conclusion

This work has consolidated and analyzed a diverse body of research demonstrating the growing maturity and methodological sophistication of metaheuristic optimization in cancer informatics. Once viewed primarily as an experimental alternative to conventional algorithms, metaheuristics have now become established as versatile, high-impact tools in detection, classification, clustering, and predictive modeling across multiple cancer types. The synthesis presented in the methodology table illustrates their adaptability to a wide variety of data modalities—including mammographic images, dermoscopic scans, MRI sequences, genomic profiles, and radiomic signatures—and their capacity to address persistent challenges such as high dimensionality, noise, class imbalance, and complex optimization landscapes. The dominance of breast, lung, and skin cancer in the literature reflects both pressing clinical needs and the availability of well-curated datasets. While this has enabled significant advances, the underrepresentation of other high-burden cancers such as pancreatic, gastric, and colorectal highlights opportunities for methodological transfer and domain adaptation. Across the reviewed works, no single metaheuristic consistently outperforms all others; rather, success depends on aligning algorithmic strengths with task-specific requirements, computational resources, and domain knowledge. Hybrid frameworks, which combine complementary search dynamics, frequently emerge as effective strategies for enhancing convergence stability and avoiding premature stagnation. Multi-objective optimization, although less common, holds strong potential for balancing clinical priorities such as sensitivity, specificity, interpretability, and efficiency. For translation into clinical practice, technical improvements must be accompanied by rigorous validation, standardized benchmarking, open-source dissemination, and reproducibility. Equitable performance across diverse populations, transparency of decision-making, and ethical safeguards are essential to ensure responsible deployment. Stronger interdisciplinary collaboration between computer scientists, engineers, and clinicians will accelerate the integration of metaheuristic-optimized systems into diagnostic and treatment planning workflows. Ultimately, the evidence reviewed here positions metaheuristic optimization as a central enabler in the evolution of computational oncology, with the capacity to deliver more accurate, efficient, and adaptable decision-support systems that can directly impact patient outcomes.

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