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Research Article

Evolutionary Insights in Ontology: A Bibliometric Analysis of Cognitive Computing Applications in Cancer Research

Samuel-Soma Mofoluwa Ajibade[1,2,*], Gloria Nnadwa Alhassan[3,4], Muhammed Basheer Jasser[2], Ghassan Saleh ALDharhani[5,6], Ismail Ahmed Al-Qasem Al-Hadi[5]

[1]Department of Computer Engineering, Istanbul Ticaret University, Istanbul, TURKEY.
[2]Department of Computing and Information Systems, School of Engineering and Technology, Sunway University, Petaling Jaya, Selangor, MALAYSIA.
[3]Department of Clinical Pharmacy, Faculty of Pharmacy, Cyprus International University, North Cyprus, TURKEY.
[4]Western Caspian University, Baku, AZERBAIJAN.
[5]Institute of Computer Science and Digital Innovation, UCSI University, Kuala Lumpur, MALAYSIA.
[6]Faculty of Information Science and Technology, UKM University, Bangi, Selangor, MALAYSIA.

ABSTRACT

The research landscape on cognitive computing algorithms, such as Genetic Algorithms (GA), in Cancer/Tumor and Oncological (CTO) research from 2003 to 2022 was examined using Scopus-indexed publications. Bibliometric analysis was employed to assess social networks and thematic areas of GACTO research. The analysis revealed that researchers published 114 articles and 92 conference papers, representing 55.34% and 44.66% of the total publications (TP=206), respectively. Of these, 129 publications were open access, distributed across Gold, Hybrid Gold, Bronze, and Green mediums. Researchers showed a preference for articles over conference papers. Stakeholder analysis highlighted a robust number of active authors, affiliations, and countries involved in GACTO research. Top performers included Zuherman Rustam (TP=5), Universitas Indonesia (TP=6), and India. Productivity was attributed to the availability of resources such as financial support, with top funders being Universitas Indonesia, the National Natural Science Foundation of China, and Brazil's Conselho Nacional de Desenvolvimento Científico e Tecnológico. Social network analysis indicated a low rate of co-authorship at 18.18%, suggesting limited collaboration at the author level. However, at the national level, collaborative links were stronger, with the largest cluster comprising India, Iran, and the United States, and the smallest including Turkey and the United Kingdom. This reflects better access to resources, funding, and infrastructure at the national level. Hotspot analysis identified three major keywords: genetic algorithms, diseases, and feature extraction. Cluster analysis revealed three focus areas: Precision Health Analytics, Genomic Cancer Profiling, and Integrated AI Diagnosis. In conclusion, the GACTO research landscape actively engages in socially impactful and scientific themes, utilizing computational tools to address challenges posed by cancer and other oncological diseases.

Keywords: Oncology, Tumors, Cognitive Computing, Genetic Algorithm, Computational Tools, Cancer Research, Bibliometric Analysis.

Correspondence:
Samuel-Soma M. Ajibade
[1]Department of Computer Engineering, Istanbul Ticaret University, Istanbul, TURKEY
[2]Department of Computing and Information Systems, School of Engineering and Technology, Sunway University, Petaling Jaya, Selangor-47500, MALAYSIA.
Email: asamuel@ticaret.edu.tr
ORCID: 0000-0002-3452-1889

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INTRODUCTION

The history of mankind and diseases has been an intricate relationship with historical, social, and scientific dimensions.[1] Over time, diseases have etched an enduring impression on civilizations, thereby influencing socioeconomic structures and global demographics.[2,3] The quest for a better understanding of infectious diseases has fuelled public health programs,[4] which have in turn produced medical advances such as antibiotics and vaccinations.[5,6] However, the growing challenge posed by recent diseases such as the recent scourge of diseases such as Ebola, HIV/AIDS, and Coronaviruses like SARS-CoV-2 (COVID-19), and MERS-CoV (Middle East Respiratory Syndrome)[7] among others, remain an ever-present challenge. Likewise, lifestyle-related non-communicable diseases such as Cancers have become a major concern,[8] owing to their tremendous impacts on the socio-economic levels of societies around the globe.

Cancer is a multifaceted set of disorders defined by aberrant cells increasing uncontrollably and developing into tumors that can infect nearby tissues and perhaps spread to other areas of the body.[9,10] It is considered a complex disease caused by genetic mutations typically initiated by genetic susceptibility and environmental stressors among others,[11,12] which play a crucial part in its development in patients. Due to its impact on

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modern society, significant resources have been dedicated to understanding, managing, and treating this menacing disease. The successful treatment of cancer requires early detection with various treatment modalities varying based on the stage of the disease in patients.[13,14] On the other hand, prevention strategies include leading a healthy lifestyle, regular screenings, and avoiding environmental triggers.[15-17]

Despite progress, cancer remains a global health concern. Consequently, there is a growing need to develop, highlight, and implement multidimensional strategies such as education, awareness, research, and development to help in the fight against the menace of cancer worldwide. Owing to its adaptableness and divergency, cancer requires creative methods for deciphering its fundamental mechanics,[18,19] which are critical to formulating successful treatment plans. One such approach is the use of computational tools in the diagnosis, prognosis, and treatment of cancer.[20-22] As such as it is, there is growing belief that the fusion/utilisation of state-of-the-art computational techniques such as Artificial Intelligence (AI), genomics, and Genetic Algorithms (GA) will be critical to not only understanding cancer but also combatting this complex disease.

The concept of GA is motivated by natural selection which is aptly suited to providing a novel computational framework for navigating the complex genomic maze of cancer biology.[23,24] GA, also known as genetic search and optimization algorithms, are derived from natural selection and genetics.[25,26] GA mimics the evolutionary process by creating a random population of viable solutions and choosing the most suitable individuals through crossover and mutations for reproduction. GAs finds applications in computational biology, machine learning, and optimization because they perform well in broad search domains. Their applicability across a variety of disciplines is increased by variations and additions. Due to its inherent nature, GA is considered an important computational technique for identifying and interpreting the complexities in the genomic landscapes of Cancers, Tumors, and Oncological (CTO) research.[20,27,28]

With the ever-growing use of GA and other computational methods in cancer research, it is necessary to conduct a comprehensive analysis of its current applications and potential implications. To better understand the application of GAs in Cancer/Tumour and Oncological (hereafter termed GACTO) research, this study has been undertaken to examine the research landscape, scientific growth, and technological developments in the sector over the last 20 years. Therefore, Bibliometric Analysis (BA) was adopted to provide readers with evolutionary insights into the GACTO research landscape with a special emphasis on identifying the patterns and trends that have shaped the field from 2003 to 2022. Hence, the research objectives are: to present the current status and publication patterns from 2003 to 2022 in the field of cognitive computing in cancer/tumour and oncological research. This includes categorizing topic areas and analysing various indicators such as publication counts, citations, and research directions to provide a comprehensive overview of the field's evolution. Secondly, to analyse collaborations at multiple levels, including countries, authorship, and institutions. This involves visualizing collaboration networks through network visualization maps for co-authorship and collaborating countries on cognitive computing in cancer/tumour and oncological research. The aim is to identify key collaborative relationships and patterns within the research community, and the third objective is to aggregate the themes of all publications and identify the top influential journals in the field through author-keywords analysis.[29,30] By doing so, it aims to provide insights into the hotspots and focus areas within cognitive computing in cancer/tumour and oncological research, facilitating a better understanding of the research landscape.

The concept has been successfully utilised to examine the research landscape in various fields such as healthcare,[31,32] Coronavirus pandemic,[33,34] healthcare facilities,[35,36] as well as non-health or medical sectors such as waste management,[37,38] greenhouse gas emissions,[39,40] plastic pollution[41,42] food safety[43,44] and energy efficiency.[45,46] The robustness, versatility, and applicability of the technique, which utilises statistical methods for comprehensive publications data analysis, has informed its choice for this study. It is envisaged that this BA study will provide readers with a comprehensive on the applications of GA in CTO research by revealing key trends, emerging themes, and influential contributors driving the evolution of this interdisciplinary field.

Therefore, the contributions of this research are highlighted below:

The current status is presented, along with the publication patterns from 2003 to 2022, as well as the topic area categories, which include the general analysis and fundamental features that are provided include the following: several viewpoints on types and research directions, as well as significant indicators at the levels of countries, institutions, and funding organizations. Furthermore, this study presents the varying number of highest publications and citations within the past two decades (2003-2022).

Analysing the collaborations at the level of countries, authorship and institutions, the corresponding networks are demonstrated by network visualisation map for co-authorship on GACTO research, network visualisation map for collaborating countries on GACTO research.

The themes of all publications and the top influential journals are aggregated based on the author-keywords analysis aimed to help researchers understand the hotspots and focus.

Ultimately, the study seeks to add impetus to the current discourse surrounding the growth of Cognitive Computing in cancer/tumour and oncological research, nurturing a greater comprehension of its transformative prospects as well as challenges that require tackling to harness its complete benefits.

According to all the analyses and visualisation maps, it is also envisaged that the insights garnered from the study will avail academics, politicians, and medical practitioners with critical insights that could stimulate pioneering research initiatives and novel collaborations.

The rest of this research article is organized as follows: Section 2 presents the review of existing literature on GACTO research; while section 3 discusses the methodology of this research and section 4 presents the result and discussion which includes the publication trends analysis, stakeholders profile analysis, social network analysis, highly cited publications, prolific researchers, institutions and countries, funding organizations and thematic hotspots. Section 5 discusses the conclusion of this research work.

LITERATURE REVIEW

The literature review of the benchmark publications on GACTO research was performed. Table 1 presents the studies and their major findings over the last 20 years examined in this study.

METHODOLOGY

Web of Science (WoS) and Scopus are the most extensive integrated academic information resources worldwide, offering comprehensive scholarly information across a wide range of fields.[65,66] However, in the paper the data source is Scopus. We chose the Scopus database for the following reasons:[67] Scopus offers a more extensive selection of indicators for assessing the impact of research compared to the Web of Science. Scopus offers a greater range of collaboration capabilities compared to Web of Science, including author profiles and a collaboration network.

Table 1: Literature review of the major studies and their findings on GACTO research.

References	Study objectives	Major findings
Peng, Xu[47]	The study focuses on the use of genetic algorithms and support vector machines for the molecular classification of cancer types from microarray data.	This study combines genetic algorithms and paired support vector machines for multiclass cancer identification, achieving accuracies of 87.93% for eight-class and 85.19% for fourteen-class classifications, outperforming previous methods.
Petrovskib, Sudha.[48]	The study focuses on the use of particle swarm optimisation and genetic algorithms for optimising cancer chemotherapy.	This paper explores the use of Particle Swarm Optimization as an alternative optimization technique in cancer treatment, comparing its efficacy with genetic algorithms, to help identify the best chemotherapeutic treatments.
Paul and Iba.[49]	The study examines the use of a probabilistic model-building genetic algorithm for classifying cancers and gene selection.	This paper presents a PMBGA-based technique for extracting informative genes from microarray data, demonstrating higher classification accuracy in binary and multi-type tumors, potentially optimizing chemotherapy for cancer patients.
Dolled-Filhart, Rydén.[50]	To examine the process of breast cancer classification using tissue microarrays and genetic algorithms.	The demonstrated the potential for breast cancer mRNA profiling and identification using gene sets correlated with outcome, which requires specialized technologies. Results showed that the AQUA-based quantitative analysis of tissue microarrays identified minimal markers with maximal prognostic value.
Lollini, Motta.[51]	The study focused on the development of cancer immunization regimens using an agent-based simulator and a genetic algorithm.	The authors developed a GA-based minimal search approach for determining the most effective vaccination timeframe for preventing cancers. The results showed that a 40% reduction in vaccinations can accomplish maximum protection.
Shah and Kusiak.[52]	The study examined the application of data mining and GA for detecting cancer-related genes.	This study proposed an integrated gene-search algorithm for the early detection and classification of lung, prostate, and ovarian cancers using gene expression data. Results showed that the GA-based algorithm was also able to enhance drug development and treatment options.

References	Study objectives	Major findings
Tseng and Liao.[53]	Examined the use of GA and DNA viruses to diagnose breast tumors.	In this work, information measurement techniques such as ANOVA were used to explore the bioinformatics of DNA viruses and breast tumors. Results showed that the HHV-8 produced less accurate results.
Petrovic, Morshed.[54]	The study examined the use of multi-objective GA for radiotherapy treatment scheduling in cancer patients.	Results showed that multi-objective optimization model and algorithms can be used to schedule radiotherapy treatments for cancer patients, by considering real-life constraints like doctor rota and machine availability.
Moriyama, Meng.[55]	To examine the use of GA and a forward-backwards time-stepping technique detecting breast cancers.	Results showed that microwave imaging, a hybrid approach that combines a forward-backward time-stepping algorithm and genetic algorithm can be used to detect breast cancer.
Wu, Lin.[56]	To classify ultrasound images of breast tumors using a GA and SVM.	This work proposed a feature selection and parameter-setting computer-aided diagnosis system for ultrasound breast tumors. Results showed that the system shortens the time required for feature extraction with a high accuracy of 95.24%.
Daliri.[57]	The study examined a hybrid automatic system that uses fuzzy extreme learning machines and GA to diagnose lung cancer.	Results showed that the proposed automatic diagnosis system using extreme learning machines and GA could be used to diagnose lung cancer.
Zadeh, Haddadnia.[58]	Examined the use of medical infra-red thermal imaging combined with GA and ANN for the diagnosis of breast cancers.	This study demonstrated the potential for using quantitative and qualitative data to diagnose breast cancer using medical infrared imaging. Results showed that 8 diagnostic parameters were extracted from 200 people's thermal images using the combinatorial model at 50% sensitivity, 70% accuracy, and 75% specificity.
Yang, Lin.[59]	The study focused on the examination and application of improved GA to create genotype SNP barcodes for the diagnosis of breast cancer.	Results showed that GA can identify the genes causing complex diseases. In addition, the reliability of the approach was improved with IGA.
Belciug and Gorunescu.[60]	The study examined a hybrid NN/GA for detecting the existence and or recurrence of breast cancers.	The results showed that breast cancer detection and recurrence can be accomplished with the evolutionary training of a feedforward Neural Network (NN) and Multi-Layer Perceptron (MLP) designed with a GA routine and implemented with Java.
Pereira, Ramos.[61]	To examine the combined impact of wavelet analysis and GA in the detection and segmentation of breast cancers in mammograms.	The study demonstrated that a computer-aided detection and diagnosis system can be developed to effectively detect and classify cases annually. Although the authors highlighted the need for improved methods, it showed that computational tools could be efficiently employed segmentation and detection of mammograms with masses'.
Lu, Zhu.[62]	The study examined a novel GA-based feature selection technique for lung cancer diagnosis.	This work presents a new feature selection algorithm that is based on the genetic algorithm and makes use of a mutual information matrix and a trace-based separability criterion. A dataset of lung cancer experiments demonstrates good diagnosis performance.
Li, Li.[63]	To examine the use of GA and serum surface-based Raman spectroscopy for the characterization and non-invasive diagnosis of Bladder cancer.	The results showed that GA and (LDA) linear discriminate analysis can be applied to classify the spectra from serum Surface-based Raman Spectroscopy (SERS) in patients experiencing bladder cancer.

References	Study objectives	Major findings
Nguyen, Nahavandi.[64]	The study investigated the use of GA combined with mass spectrometry and Haar wavelets to classify cancer-based data.	The results showed that the selected hybrid feature extraction method based on Haar wavelets and GA was highly robust and capable of classifying cancers.
Aalaei, Shahraki.[65]	The study adopted GA to carry out feature selection and examination of distinct datasets for the diagnosis of breast cancer in patients.	The findings indicate that feature selection enhances classifiers' sensitivity, specificity, and accuracy like other models on Wisconsin breast cancer datasets.
Kavitha and Chellamuthu.[66]	The authors proposed the use of a Seeded Modified Region Growing (GFSMRG), GA and fuzzy initialization technique to segment a brain tumour from an MRI image during cancer diagnosis and treatment.	The results showed that the novel GA can enhance the detection and segmentation accuracies of detecting tumor in medical image processing.
Paul, Su.[67]	The study examined the application of feature selection in predicting the outcomes of oesophageal cancer through the use of GA and RFC (random forest classifiers).	The findings showed that the proposed novel feature selection strategy successfully predicted and analysed outcomes and prognoses of cancer patients using PET images and clinical data.
Motieghader, Najafi.[68]	The study developed a hybrid gene selection algorithm called GALA that integrates GA and learning automata for application in the classification of cancer microarrays.	The findings showed that the hybrid meta-heuristic algorithm successfully assessed and classified the cancer datasets with acceptable accuracy and temporal complexity.
Sharma and Rani.[69]	The study examined the application of GA and DL (deep learning) in the classification of cancers.	Results showed that the use of the GA-DL algorithm was effective in classifying and by so doing providing an effective framework for analysing cancer and gene expression data.
Bahadure, Ray.[70]	The study proposed a comparative method for the classification and segmentation of brain tumors using GA and MRI data.	The study demonstrated the efficacy of using computer-aided technology in detecting and classifying brain tumors. The proposed method adopted an automatic classification system based on GA in comparison with various segmentation methods.
Hou, Bing.[71]	The study developed an ANN (Artificial Neural Network) and GA Optimization approach for the diagnosis and prognosis of prostate cancers.	Findings showed that the diagnostic prediction model successfully detected Prostate Cancer (PCa) using Differentially Expressed Genes (DEGs) from publicly available microarray data.
Kabir Anaraki, Ayati.[72]	The study examined the use of GA and Convolutional Neural Networks (CNN) for the classification and grading of brain tumors.	The results showed that the proposed GA-CNN technique is an effective non-invasive pathway for classifying various grades of gliomas using MRI.
Sayed, Nassef.[73]	To examine the application of Nested GA feature selection of high-dimensional cancer microarray data sets.	The results showed that the ensemble feature selection method lowered the high-dimensionality of Microarray datasets for cancer research by utilizing the t-test and the genetic algorithm Nested-GA. By merging information from two distinct datasets, the method achieved 99.9% classification accuracy.

References	Study objectives	Major findings
Jansi Rani and Devaraj.[74]	The study proposed a two-step hybrid gene selection technique comprising GA and Mutual Information for classifying cancer data.	The findings showed that the MI-GA gene selection algorithm was successful in classifying cancer data through the selection of informative genes.
Pan, Zhang.[75]	The study showed the potential of optimized NNs and Probabilistic GA (PGA) in predicting the prognosis of oral tongue cancer among patients.	The study developed ML-NN methods for predicting the survival rate of patients. Among the three trained NNs, the PGA-BP model demonstrated the highest level of predictive accuracy and when combined with the t-SNE dimensionality reduction algorithm, patient survival intervals were predicted with accuracy.
Maleki, Zeinali.[76]	A k-NN method for lung cancer prognosis with the use of a genetic algorithm for feature selection.	The k-nearest-neighbours technique for lung cancer diagnosis is presented in this paper. It achieves 100% accuracy on a lung cancer database, indicating the method's potential for effective data mining.
Peng, Wu.[28]	The study examined the classification of Cancer using EGA (Embedded Genetic Algorithms) and MGRFE (Multilayer Recursive Feature Elimination).	The findings showed that the MGRFE outperformed other feature selection algorithms in terms of gene number selection and accuracy during the classification of cancers.
Deng, Li.[77]	The study aimed to investigate a novel hybrid gene selection strategy for the classification of cancer using a multi-objective GA and XGBoost.	The results showed that the two-stage gene selection strategy that combines XGBoost and a multi-objective optimization genetic algorithm was effective in the classification of cancer microarray datasets.
Fekri-Ershad and Ramakrishnan.[78]	The objective was to examine the capability of feed-forward multilayer networks optimized by GA and modified uniform local ternary patterns for the diagnosis of cervical cancer.	The findings showed that the proposed approach has a low run time and higher detection accuracy when tested on the Herlev database, which makes it suitable for online problems and deep networks.
Balaha, Saif.[27]	The diagnosis of breast cancer in early ultrasound was examined using a hybrid deep learning and genetic algorithms (HMB-DLGAHA) proposed and developed in the study for breast cancer diagnosis.	The study findings showed that the proposed hybrid deep learning and GA approach which incorporates an abstract CNN architecture could be used for breast cancer research.
Dweekat and Lam.[79]	The study aimed to examine the potential application of an Integrated System of Multilayer Perceptrons (MP), GA, and Principal Component Analysis (PCA) in the identification of cervical cancer.	Results showed that the integrated (MP-GA-PCA) system performs better than currently available techniques whilst obtaining the highest accuracy in Hinselmann, Biopsy, and Cytology diagnosis.

Scopus contains a greater amount of open-access material compared to Web of Science.[68]

Bibliometric analysis is effective for evaluating the merits of a given discipline.[69,70] Hence, in this study, the research landscape on the utilisation of genetic algorithms to unearth the evolutionary insights in Cancer, Tumours, and Oncology (GACTO) research was critically examined. The methodology involved a three-stage process of identifying, screening, and examining related publications on GACTO research based on publications in the Elsevier Scopus database and the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) approach. Scopus is considered the most comprehensive abstract and citation database in the world, which is the most suitable database for identifying and selecting related publications on wide-ranging topics.[80] The PRISMA approach is widely used to identify and screen related publications on any given field of research or topic with the view to elucidate the current scientific growth and technological developments[81] as shown in Figure 1.

The first step involved the design of a search string based on important topical-related keywords for execution in Scopus.

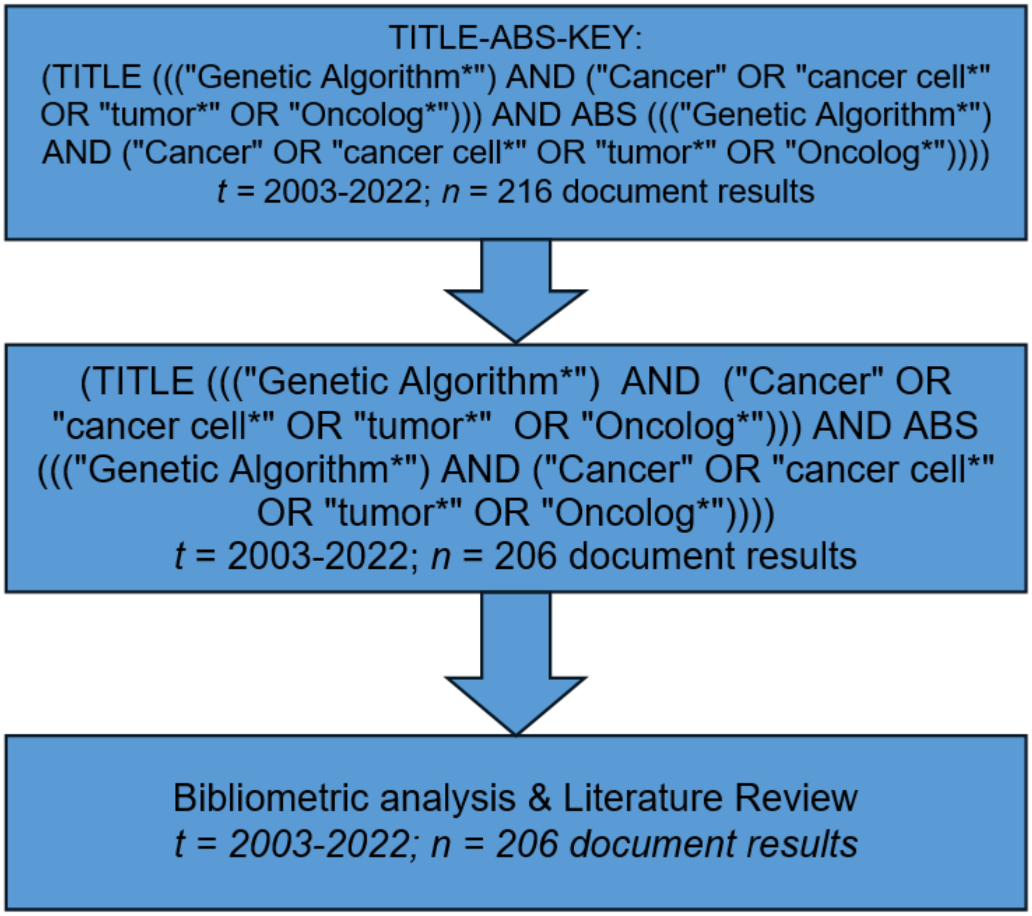


Figure 1: PRISMA flowchart methodology for analysing GACTO research landscape.

The following search string was executed (TITLE ((("Genetic Algorithm*") AND ("Cancer" OR "cancer cell*" OR "tumor*" OR "Oncolog*"))) AND ABS ((("Genetic Algorithm*") AND ("Cancer" OR "cancer cell*" OR "tumor*" OR "Oncolog*")))). The search recovered a total of 216 documents comprising various document types, source types, and languages published and indexed in the Scopus database from 2003 to 2022.

The second stage involved screening the recovered publications to remove irrelevant documents using the LIMIT-TO and EXCLUDE functionalities of the Scopus database. The selected screening string query was (TITLE ((("Genetic Algorithm*") AND ("Cancer" OR "cancer cell*" OR "tumor*" OR "Oncolog*"))) AND ABS ((("Genetic Algorithm*") AND ("Cancer" OR "cancer cell*" OR "tumor*" OR "Oncolog*")))). The screening process resulted in 206 documents comprising only English language-based articles and conference proceedings published over the last 20 years from 2003 to 2022.

The third stage involved analysing the publication trends, social networks, and hotspot/thematic areas on GACTO research using Bibliometric Analysis (BA). The BA of the recovered publications was conducted using VOSviewer (version 1.6.20). The technique has been widely used to map and analyse the research landscape of numerous fields.[32,82] Notable examples of such fields or areas of research include computer sciences,[83] renewable energy,[84] climate change,[85] food products,[44] waste management,[86] greenhouse gas emissions,[40] safety management,[87] healthcare and medical research,[88] among others. Lastly, a review of the literature of GACTO research publications, as well as the identification of research gaps, and future research areas was conducted in the study.

RESULTS

Publication Trends Analysis

Figure 2 shows the growth trajectory of yearly publications on GACTO research. As can be observed, the total number of publications increased steadily from 4 to 26 (or an average of 10.3 per year) publications from 2003 to 2021 before dropping marginally to 23 in 2022. The highest number of publications[26] were observed in 2012 indicating this was the most productive year for researchers on the topic worldwide. This observation along with the growth trajectory of publications shows that there is growing interest among researchers in the topic across the globe. The high research output and researchers' interest is an indication of the active exploration, scholarly commitment, and potential impact of any given topic. However, the quality of the research, the diversity of viewpoints, the practical application,

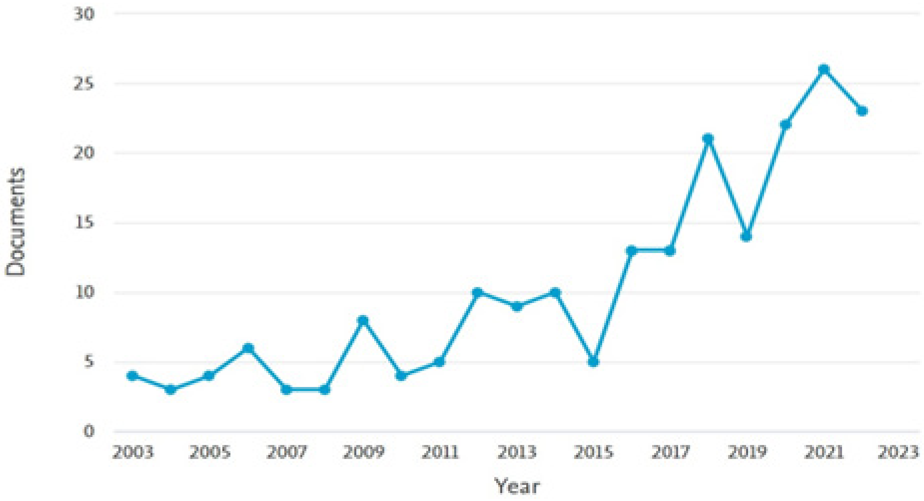


Figure 2: Publications growth trajectory for GACTO research landscape.

Table 2: Top 10 most cited publications on GACTO Research.

References	Title	Source Title	Cited by
Kabir Anaraki, Ayati.[72]	Magnetic resonance imaging-based brain tumor grades classification and grading via convolutional neural networks and genetic algorithms.	Biocybernetics and Biomedical Engineering.	332
Peng, Xu.[47]	Molecular classification of cancer types from microarray data using the combination of genetic algorithms and support vector machines.	FEBS Letters.	193
Pereira, Ramo.[61]	Segmentation and detection of breast cancer in mammograms combining wavelet analysis and genetic algorithm.	Computer Methods and Programs in Biomedicine.	160
Sayed, Nassef.[73]	A Nested Genetic Algorithm for feature selection in high-dimensional cancer Microarray datasets.	Expert Systems with Applications.	145
Maleki, Zeinali.[76]	A k-NN method for lung cancer prognosis with the use of a genetic algorithm for feature selection.	Expert Systems with Applications.	117
Shah and Kusiak.[52]	Cancer gene search with data-mining and genetic algorithms.	Computers in Biology and Medicine.	116
Aalaei, Shahraki.[65]	Feature selection using genetic algorithm for breast cancer diagnosis: Experiment on three different datasets.	Iranian Journal of Basic Medical Sciences.	109
Bahadure, Ray[70]	Comparative Approach of MRI-Based Brain Tumor Segmentation and Classification Using Genetic Algorithm.	Journal of Digital Imaging.	98
Paul, Su.[67]	Feature selection for outcome prediction in oesophageal cancer using genetic algorithm and random forest classifier.	Computerized Medical Imaging and Graphics.	97
Motieghader, Najafi.[68]	A hybrid gene selection algorithm for microarray cancer classification using genetic algorithm and learning automata.	Informatics in Medicine Unlocked.	94

and interdisciplinary collaboration are some of the variables that determine the genuine impact of any research area.

Publications growth trajectory for GACTO research landscape.

The diverse, extremely specialized, and broadly themed nature of GACTO research has also resulted in Highly Cited Publications (HCP). Table 2 shows the Top 10 most cited publications on GACTO research in the Scopus database. The data analysis shows that have gained Total Citations (TC) ranging from 94 to 1461 or an average of 344.38 over the years. Various studies have revealed that HCPs provide critical insights into the degree of visibility, recognition, and impact on any given field of research.[89] Likewise, such publications could also influence education and policy, which is not only critical to the creation of novel standards but also to directing research in the future. Furthermore, HCPs can help researchers and institutions attract much-needed financing and collaborations.

Table 3: Top 5 journal sources for GACTO research.

Source Title	TP	%TP	Source Type
Advances In Intelligent Systems And Computing.	10	4.63	Journal
Lecture Notes In Computer Science Including Subseries Lecture Notes In Artificial Intelligence And Lecture Notes In Bioinformatics.	10	4.63	Conference Proceedings
Neural Computing And Applications.	6	2.78	Journal
Communications In Computer And Information Science.	4	1.85	Conference Proceedings
Expert Systems With Applications.	3	1.38	Journal

TP: Total publications; **%TP:** Percentage total publications.

Table 4: Key subject areas of GACTO research landscape.

Subject area	TP	%TP
Computer Science	146	33.5
Engineering	92	21.1
Mathematics	58	13.3
Medicine	42	9.6
Biochemistry, Genetics and Molecular Biology	25	5.7
Physics and Astronomy	22	5.0
Decision Science	14	3.20
Health Professions	9	2.1
Material Sciences	9	2.1
Chemistry	6	1.4

TP: Total Publications, %TP: percentage Total Publications.

Source Title and Subject area

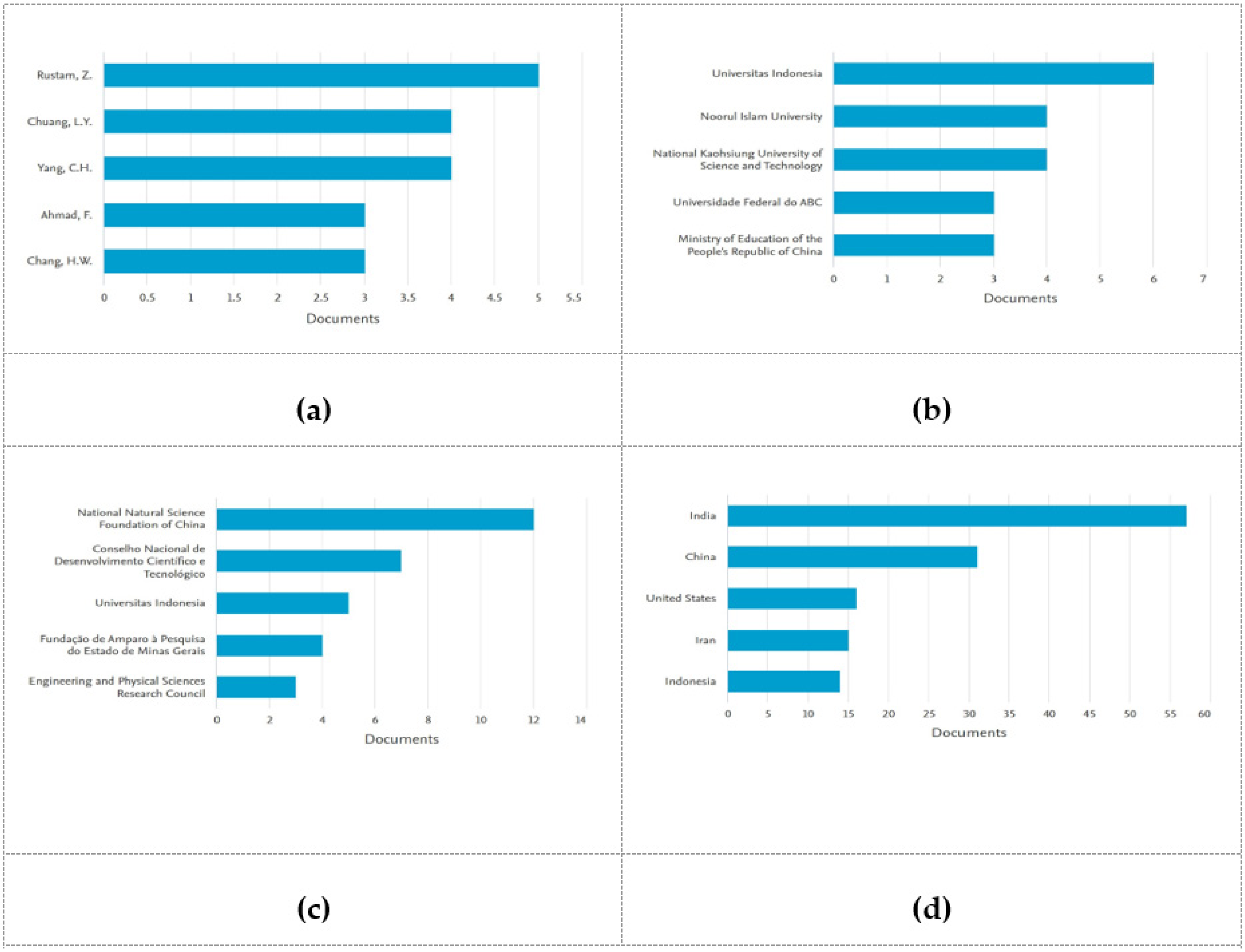
According to Table 3, the top 5 source titles have published 33 documents, or 15.3% of the TP on the topic. Based on the findings, Advances In Intelligent Systems And Computing, Neural Computing And Applications, and Expert Systems With Applications are the top journals, while Lecture Notes In Computer Science Including Subseries Lecture Notes In Artificial Intelligence And Lecture Notes In Bioinformatics and Communications In Computer And Information Science are the top conference proceedings in the field of GACTO. The nature and productivity of the journals and conference proceedings may be due to the nature, impact, and reputation of the journals. Another critical factor may be the subject area and theme of the journals, which attracts researchers in the field. To further examined this submission, a critical analysis of the subject area and scope of the GACTO research landscape was carried out using data from Scopus. Table 4 presents the key subject areas of the GACTO research landscape. The data shows that GACTO publications in the Scopus database are classified into 22 subject areas. The top 10 presented in the table show that the GACTO research landscape is broadly themed with multiple disciplines majorly from STEM (science, technology, engineering, and mathematics). Further analysis shows that *Computer Science, Engineering,* and *Mathematics* are the core themes based on the Bradfords Law (Chaturbhuj *et al*. 2020). The rule stipulates that sources or titles that account for 33.33% or more of the total publications on any given topic are considered the most prominent.

Stakeholders' Profiles Analysis

The analysis of stakeholder profiles is another critical aspect of bibliometric analysis. The proper understanding of research stakeholders' dynamics is crucial for resource allocation, resource management, policy formulation, and competitiveness, promoting collaboration and impactful research projects.[85,87] In this study, the stakeholders selected for analysis include authors, affiliations, countries, and funding organisations. Figure 3(a, b, c and d) show the top 5 actors in each stakeholder category examined in this study. As observed in Figure 2(a) the top 5 authors have published between 3 and 5 publications each (TP=19; Average=3.8). The most prolific researcher on GACTO research is Zuherman Rustam who has 5 publications, which is 1 more than the second-placed top authors Liyeh Chuang (4) and Cheng H. Yang (4). Furthermore, the most prolific research affiliation is Universitas Indonesia (UI) based at Depok in Indonesia. The productivity of UI is largely due to the work of Zuherman Rustam and colleagues such as Velery V. P. Wibowo, Vabiyana S. Desdhanty, among others. In second and third places are Noorul Islam University (India) and the National Kaohsiung University of Science and Technology of Taiwan.

As shown in Figure 3(c), the funders with the most publications (number of publications in brackets) on the topic are the National Natural Science Foundation (NSFC) of China (12), Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) of Brazil (7) and Universitas Indonesia (5). The publication's output indicates these funders have been cited in the acknowledgement as a testament to their financial or material contributions to the studies.

Figure 3(d) shows the top 5 most prolific nations on GACTO research. As observed, India is the leading nation based on the publications output data from Scopus, followed by China, the US, Iran, and Indonesia.



(a)

(b)

(c)

(d)

Figure 3: Top 5 stakeholders on GACTO research (a) Authors, (b) Affiliations, (c) Funding agencies, (d) Countries.

Social Network Analysis

Social network analysis enhances BA by mapping collaboration networks, identifying key players, measuring social capital, detecting research communities, understanding knowledge diffusion, and improving information flow analysis. In this study, VOSviewer software was used to map the network of collaborators among researchers and nations actively engaged in GACTO research. Figure 4 (a and b) shows the network visualisation maps for co-authorships at the author and country levels.

Figure 4 (a) shows the network visualisation maps for co-authorships at the author. As observed, the map shows 3 clusters of 3-4 authors comprising the 55 authors that have published 2 or more publications on the topic. The highest number of publications was observed for Z Rustam (5), as earlier stated, whereas the Citations (CT)(165) and Total Link Strength (TLS)(12) were observed for the trio MZ Do Nascimento, AS Martins, and LA Neves. Based on the findings, the most prolific researcher is Z Rustam, whereas the trio are the most influential on the topic. In addition, the data shows that there are a total of 16 links, which have a TLS of 23. However, it was also observed that only 10 authors out of the 55 have co-authored or co-published together. This finding indicates that the rate of co-authorship is a mere 18.18% for the research landscape. As such, it can be reasonably inferred that the rate of collaborations is low at the author level.

Figure 4 (b) shows the network visualisation maps for co-authorships at the country levels. As observed, the map shows 3 clusters with 7 links and a TLS of 10. The largest cluster comprises India, Iran, and the United States, whereas the smallest is made up of Turkey, and the United Kingdom. Additional examination shows that 13 countries out of the possible 37 have published 5 or more documents on GACTO research over the years. As earlier stated, the highest number of publications is credited to India (57), whereas Iran has the highest citations (822), and lastly, China has the highest TLS (5).

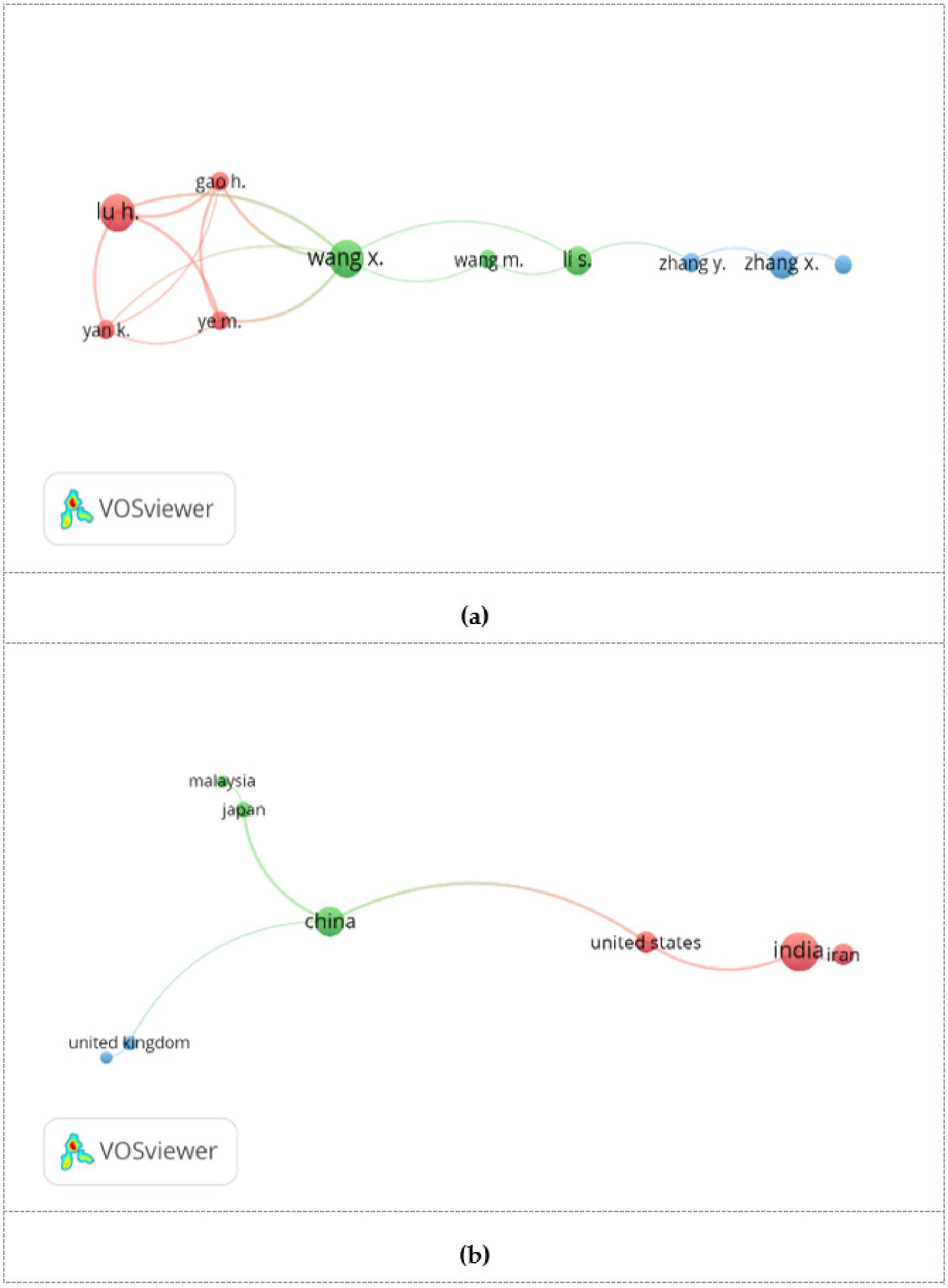


Figure 4: Network visualisation maps for co-authorships at (a) author level (b) country levels.

Hotspot/Thematic Area analysis

The examination of the hotspots or thematic focus area in any field of study provides critical insights into its current state of research and development. This analysis can be accomplished by examining the co-occurrence of major keywords indexed by researchers in various scientific databases. In this study, VOSviewer was employed to examine the major keywords on GACTO research. Figure 5 shows the network visualisation and overlay visualisation maps for the major occurring keywords (minimum occurrence, n=20) for GACTO research.

The results show that 21 of the 2037 possible keywords appeared at least 20 times during the analysis. The top 3 keywords (occurrences in brackets) are genetic algorithms (150), diseases (95), and feature extraction (48), whereas TLS were observed for genetic algorithm (641), diseases (454), and feature extraction (298). The strongest link was observed between GA and diseases, which indicates that there is currently an emphasis on the application of GA in the

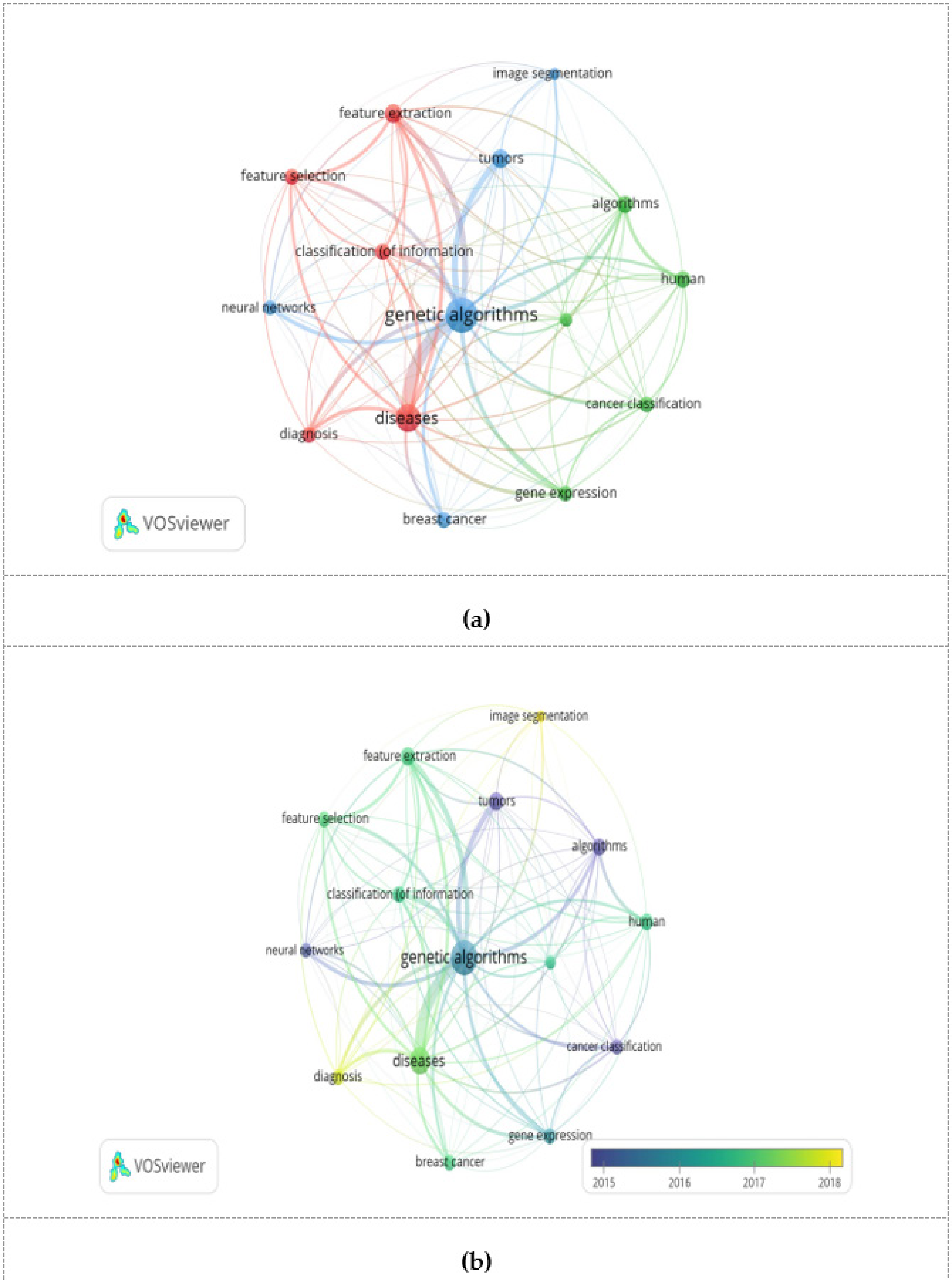


Figure 5: Keywords co-occurrence maps for GACTO research (a) Network visualisation (b) Overlay visualisation.

selection or extraction of pertinent features from disease-related datasets. The use of GA supports feature selection, simplifies data, and improves treatment approaches. It can also help to detect biomarkers and enhance models for predicting cancer during research. This strategy eventually advances cancer biology and personalized medicine by ensuring robust, repeatable research, bolstering diagnostic instruments, and facilitating multi-omics data integration.

The network visualisation and overlay visualisation maps in Figure 5 also show that there are 3 major clusters for the co-occurrent keywords on GACTO research. Cluster 1 comprises the keywords classification of information, diagnosis, diseases, feature extraction, and feature selection. On the other hand, cluster 2 consists of algorithms, cancer classification, gene expression, human, and support vector machines. Lastly, cluster 3 includes breast cancer, genetic algorithms, image segmentation, neural networks, and tumors. Based on the keywords in each cluster (C1, C2, and C3), the hotspots on the GACTO research can be categorised into three major/key areas namely;

Precision Health Analytics (C1),

Genomic Cancer Profiling (C2) and,

Integrated AI Diagnosis (C3).

Precision Health Analytics (PHA)

This describes the methodical application of data analytics, cutting-edge technologies, and algorithms such as GA to precisely analyze and interpret health-related or disease (e.g., cancers and tumors) datasets. Such datasets include the patient's environment, lifestyle, genetic composition, and other personal health information to customize medical decisions, interventions, and treatments.

Genomic Cancer Profiling (GCP)

GCP refers to the process of methodically examining a patient's cancer from a genomic perspective. The process typically involves the use of GA, mutation analysis, and other molecular features unique to the patient's tumor for profiling purposes. GCP has the potential to help clinicians modify treatment plans (e.g., immunotherapies or targeted therapies) to target the particular genetic characteristics and distinct genomic profiles of cancers.

Integrated AI Diagnosis (AID)

This refers to the all-encompassing approach of diagnosing diseases through the use of combinatory Artificial Intelligence (AI) methods (e.g., genetic algorithms) and feature selection techniques to diagnose cancer. It also involves optimizing the selection of pertinent features from genetic data using GA and other sophisticated AI algorithms.

DISCUSSION

There has been a significant increase in the growth trajectory and publication trends of GACTO research throughout the years. The observed growth in both publication output and total citations can be linked to several factors. The growth trajectory and publication trends on GACTO research were further examined based on the document types, source titles and subject areas. The analysis was conducted to gauge researchers' preference for the dissemination of their research findings and the impact of such metrics on the publication's output and trends in GACTO research. Based on data in Scopus, the distribution of document types on the research landscape shows that researchers have published 114 article s and 92 conference papers, which account for 55.34% and 44.66% of the Total Publications (TP=206), respectively. It was also observed that 129 out of the TP were published on Open Access (OA) comprising Gold, Hybrid Gold, Bronze, and Green mediums. This finding indicates that 62.62% of the TP have been published in OA journals. According to various researchers in the literature, research output is positively impacted by publication in open-access journals or source titles.[90,91] This observation is largely because it fosters more visibility, accessibility, and teamwork. Furthermore, freely available research attracts larger audiences, which in turn encourages wider participation that could advance the field in the scientific community. Similarly, open-access publications frequently have more citations, which suggests a greater influence.[92,93] Overall, the OA publishing model improves information diffusion, and increases the applicability and influence of research, especially in gold and green open-access formats, albeit the impact differs depending on the discipline. Based on the aforementioned, it can be reasonably inferred that the publications output observed in this study, is due to various factors including researchers' productivity, open-access publishing, and research impact of GACTO research across the globe.

The preferred source titles for researchers on GACTO research were also examined in this study. The data shows that the top 5 titles (TP) are Advances In Intelligent Systems And Computing (10), Lecture Notes In Computer Science Including Subseries Lecture Notes In Artificial Intelligence And Lecture Notes In Bioinformatics (10), Neural Computing And Applications (6), Communications In Computer And Information Science (4), and Expert Systems With Applications (3). Additional analysis shows that 3 out of the top 5 source titles are Journals whereas 2 are Conference Proceedings. The plausible explanation for researchers' preference for Journals may be due to in-depth investigation, coverage, and synthesis of specialized topic research typically found in the former over the latter. The structure of Journals is the product of teamwork among experts in a field and this is well suited for specific audiences.

On the other hand, the analysis of the subject areas in any given field can be an effective tool for tracking research trends and allocating resources.[94,95] It can also help in fostering specialization, spotting interdisciplinary links, and assisting with strategic planning all depending on the analysis of subject areas within a field.[96,97] Lastly, the process can help researchers effectively search for and attract research financing, as well as identify publication methods, which can enhance the entire body of knowledge, influence, and relevance.[45] In this study, the top subject areas (TP) are Computer Science, Engineering, Mathematics, Medicine, Biochemistry Genetics and Molecular

Biology, Physics and Astronomy, Decision Sciences, Health Professions, Materials Science, Chemistry. The top three subject areas are Computer Science (30.61%), Engineering (18.82%), and Mathematics (12.7%) of the TP on GACTO research.

Based on the outlined, it can be inferred that the GACTO research landscape is largely characterised by STEM-based subject areas. Critical assessment further reveals that progress in the study of cancer is collectively advanced by Computer Science, Engineering, and Mathematics. The influence of the outlined subject areas is ascribed to their capacity to employ computational tools such as imaging technology, mathematical models, genomic analysis, and clinical trials to comprehend the biomarkers and dynamics of tumours or cancers to discover, design and develop targeted medicines. This interdisciplinary partnership has also helped in developing diagnosis, therapy, and care approaches for cancer patients. Overall, the subject area analysis shows that GACTO research is a thematically broad, highly specialized, and multidisciplinary field of research with significant potential for human development.

Furthermore, investigating the Highest Cited Publication (HCP), In the GACTO research landscape, the most HCP publication is "Magnetic resonance imaging-based brain tumor grades classification and grading via convolutional neural networks and genetic algorithms" by Kabir Anaraki, Ayati[72] which has been cited a total of 332 times by date. Published in the "*Biocybernetics and Biomedical Engineering*", the highly cited paper presented an innovative, flexible, and practical approach to categorize different grades of *glioma* (which is the most common primary brain tumor in adults) using Convolutional Neural Networks (CNNs), Genetic Algorithms (GA), and Magnetic Resonance Imaging (MRI). Similarly, Peng, Xu[47] published "Molecular classification of cancer types from microarray data using the combination of genetic algorithms and support vector machines" which at 193 citations ranks as the second most HCP in GACTO research. The study which was published in the "*FEBS Letters*" demonstrated the potential for integrating GA and SVM (support vector machines) as an important tool or approach for categorising various types of tumours in microarray-based diagnosis of cancers and tumors. On the other hand, Pereira *et al.* (16) published the third most HCP on GACTO "Segmentation and detection of breast cancer in mammograms combining wavelet analysis and genetic algorithm" which has 160 citations.

Other HCPs on GACTO research have examined additional areas on the application of GA in cancer research. For example, Sayed, Nassef[73] examined a nested GA equipped with an optimizing feature selection for application in high-dimensional cancer microarray datasets. Maleki, Zeinali[76] developed an innovative GA that enhances the k-nearest neighbours method used for performing prognosis on lung cancer patients. Shah and Kusiak[52] examined the use of genetic algorithms and data mining to identify cancer genes. Aalaei, Shahraki[65] investigated the diagnosis of breast cancer using a GA to select features from various datasets. Bahadure, Ray[70] evaluated the potential of various methods for brain tumor segmentation using MRI and GA. Paul, Su[67] examined the use of a genetic algorithm, random forest classifier, and their intrinsic features for predicting the outcome of oesophageal cancer. Lastly, the study by Motieghader, Najafi[68] presented a hybrid gene selection system that combines GA and learning automata for classifying microarray cancer. Overall, the studies showed that the use of GA and related algorithms is an important approach for identifying, predicting, classifying, and diagnosing various cancers, along with their related genes and biomarkers from large datasets.

The productivity of stakeholders in any research landscape is typically ascribed to various factors including but not limited to research funding and research policies/priorities of nations across the globe. In this study, the top funders of GACTO research were examined based on data retrieved from the Scopus database. While the NSFC and CNPq have funded a vast number of researchers, the UI funds have been directed at only a handful of researchers who have dominated the research landscape. Hence, it is logical to surmise that UI is the most influential research funder, whereas NSFC and CNPq are the most prolific.

In terms of topmost prolific countries, the dominance of India in the top 5 could be ascribed to various factors. The prolific publications on the applications of GA to cancer research in India can be attributed to the nation's strategic focus on medical and biotechnological research and development initiatives. Evidence suggests that India has over the years invested significantly in infrastructure and training talent for multidisciplinary research in computer science and biomedical fields.[98] In addition, the nation's dominance could be ascribed to various government initiatives. Typically, government initiatives support cancer research, which helps to foster collaborations and exchange of knowledge. Lastly, India's diverse patient data and international recognition have helped to drive innovative GA applications in cancer studies. The impact of collaborations at the author and national levels is examined in the next section of the paper. Furthermore, based on the Total Link Strength (TLS) and Citation (CT), China and Iran are the most influential countries in GACTO research whereas India is the most prolific. Cluster analysis revealed that 8 countries out of the 13 with 5 or more publications are linked, which indicates a co-authorship rate of 61.54%. This finding shows that the rate of collaborations is higher than earlier reported for the author level, in the context of GACTO research. The plausible reason for this is that research challenges are global and as such countries as opposed to individual researchers can pool and share resources/ funding, specialized expertise, and infrastructure. More so, nations have more comprehensive international initiatives, cultural exchange, and diplomatic considerations that greatly foster research and development through open scientific exchanges and create multinational research teams or knowledge clusters. As a result, nations have a higher rate of collaboration than among individual authors.

CONCLUSION

This study examined the landscape of genetic algorithm research in cancer, tumor, and oncology over the past two decades, using Scopus articles from 2003 to 2022. The analysis revealed a significant increase in publications, highlighting growing interest and advancements in the field. Stakeholders from various countries, particularly in Asia, have contributed extensively, with major involvement from India, China, Iran, Universitas Indonesia, and Noorul Islam University. Funding from Asian institutions like NSFC (China) and Universitas Indonesia has been pivotal in advancing this research. Social network analysis emphasized the importance of co-authorship and international collaborations, which enhance research impact by providing greater access to resources, funding, and infrastructure. Hotspot analysis identified three major focus areas: Precision Health Analytics (PHA), Genomic Cancer Profiling (GCP), and Integrated AI Diagnosis. These areas reflect the integration of computational tools in cancer detection, diagnosis, and treatment, underscoring the current priorities in GACTO research. Future research should explore the intersection of AI and genetics, focusing on how these synergies can improve cancer diagnosis, treatment, and personalized medicine. Despite significant advancements, gaps in understanding cancer mechanisms remain. Continued investigation into the impact of cognitive computing on clinical decision-making and patient outcomes is essential. Interdisciplinary collaboration among computer scientists, oncologists, geneticists, and bioinformaticians will be crucial for accelerating progress. Researchers should also explore novel cognitive computing algorithms beyond genetic algorithms, such as deep learning, reinforcement learning, and hybrid approaches, to enhance predictive models. As AI technologies evolve, addressing ethical considerations like bias, interpretability, and privacy is paramount. Integrating ethical frameworks and regulatory guidelines into research and development will ensure the appropriate and unbiased deployment of AI technologies in oncology and healthcare. In conclusion, the ongoing evolution of GACTO research, driven by interdisciplinary collaboration and ethical considerations, is essential for advancing cancer treatment and personalized medicine, ultimately improving patient outcomes and the field of oncology.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ABBREVIATIONS

GACTO: Genetic Algorithms (GA) in Cancer/Tumor and Oncological; **CTO:** Cancer/Tumor and Oncological; **BA:** Bibliometric Analysis; **WoS:** Web of Science; **SVM:** Support Vector Machine; **NN:** Neural Network; **MLP:** Multi-Layer Perceptron; **DL:** Deep learning; **ANN:** Artificial Neural Network; **LDA:** Linear discriminate analysis; **SERS:** Surface-based Raman Spectroscopy; **PCa:** Prostate Cancer; **DEGs:** Differentially Expressed Genes; **EGA:** Embedded Genetic Algorithms; **MGRFE:** Multilayer Recursive Feature Elimination; **PRISMA:** Preferred Reporting Items for Systematic Reviews and Meta-Analyses; **HCP:** Highly Cited Publications; **TC:** Total Citations; **NSFC:** National Natural Science Foundation; **CT:** Citations; **TLS:** Total Link Strength; **AI:** Artificial Intelligence; **STEM:** Science, Technology, Engineering, and Mathematics; **PHA:** Precision Health Analytics; **GCP:** Genomic Cancer Profiling; **AID:** Integrated AI Diagnosis.

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