Knowledge structure and emerging trends in the application of deep learning in genetics research: A bibliometric analysis [2000–2021]

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Introduction: Deep learning technology has been widely used in genetic research because of its characteristics of computability, statistical analysis, and predictability. Herein, we aimed to summarize standardized knowledge and potentially innovative approaches for deep learning applications of genetics by evaluating publications to encourage more research.

Methods: The Science Citation Index Expanded ™ (SCIE) database was searched for deep learning applications for genomics-related publications. Original articles and reviews were considered. In this study, we derived a clustered network from 69,806 references that were cited by the 1,754 related manuscripts identified. We used CiteSpace and VOSviewer to identify countries, institutions, journals, co-cited references, keywords, subject evolution, path, current characteristics, and emerging topics.

Results: We assessed the rapidly increasing publications concerned about deep learning applications of genomics approaches and identified 1,754 articles that were cited by the 1,754 related manuscripts identified. We used CiteSpace and VOSviewer to identify countries, institutions, journals, co-cited references, keywords, subject evolution, path, current characteristics, and emerging topics.

Conclusion: Here, we summarized the current literature related to the status of deep learning for genetics applications and analyzed the current research characteristics and future trajectories in this field. This work aims to provide
resources for possible further intensive exploration and encourages more researchers to overcome the research of deep learning applications in genetics.

KEYWORDS

deep learning, machine learning, genetics, bibliometric, knowledge graph

1 Introduction

Deep learning (DL) is a subfield of machine learning (ML) that aims to avoid extensive manual processing in traditional methods Wu et al., (2020). Different from machine learning, deep learning is a form of representation learning in which a machine is fed with raw data and develops its own representations needed for pattern recognition—which is composed of multiple layers of representations Esteva et al., (2019). The application of DL in medical healthcare has been widely reported. For example, DL has been reported to be successful in identifying a variety of histopathological features and detecting the biomarkers (Berrar and Dubitzky, 2021). DL has also been applied to predict diagnosis, prognosis, and treatment response in certain cancers Tran et al., (2021). This information could prove valuable in clinical decision-making for cancer treatment and triage for in-depth sequencing.

Genomic data had served as a biomarker for the onset and progression of the disease. Various deep learning applications in genomics had been reported, such as predicting gene expression from genotype data and studying the splicing-code model and the identification of long noncoding RNAs (Tripathi et al., 2016; Xie et al., 2017; Vellido, 2020; Tang et al., 2021). Recent advances in deep learning have emerged in several applications, ranging from natural language to vision processing Zou et al., (2019). Bibliometric approaches have generated a considerable impact on the deep learning research field, such as providing an overview of the application of DL in genomics research. Information on the following topics was collected: title, abstract, authors, institution, country/region, journal, keywords, and references. Articles were indexed in the WoSCC and excluded meeting articles, repeated articles, proceedings articles, book chapters, and unpublished documents without enough information for further analysis at the same time.

We described publication characteristics, including institutes, countries, journals, and keywords. The Journal of Citation Reports (JCR, 2021 version) was accessed to identify impact factors that reflected the scientific value of research (Eyre-Walker and Stoletzki, 2013). Retrieved data were analyzed in VOS viewer (Leiden University, Leiden, Holland) and CiteSpace V (Drexel University, Philadelphia, Pennsylvania).

2 Materials and methods

On 22 December 2021, we downloaded data from the Web of Science Core Collection (WoSCC); two authors independently verified citations and retrieved studies. The WoSCC is a frequently used authoritative database for scientific information, from which we generated a clustered network of 69,806 references cited by 1,754 studies. Between the publication years 2000 and 2021, literature searches were performed using the search terms: [TS = (“deep learning” OR “machine learning” OR “convolutional neural network*” OR CNN* OR RNN OR “Recurrent neural network*” OR “Fully Convolutional Network*” OR FCN*)], and The literature type = “Article OR Review OR Opening Online”, WoS category = Genetic heredity. Information on the following topics was collected: title, abstract, authors, institution, country/region, journal, keywords, and references. Articles were indexed in the WoSCC and excluded meeting articles, repeated articles, proceedings articles, book chapters, and unpublished documents without enough information for further analysis at the same time.

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PA, United States), which facilitated collaborative network analyses connecting different publication characteristics (Chen, 2006; Chen, 2017). From the analysis and measures above, we obtain the current characteristics, research hotspot, subject evolution path, and future trajectories in deep learning applications of genetics.

3 Results

3.1 Distribution of articles by publication years

A total of 1,754 articles from 2000 to 2021 were published. As shown in Figure 1, the line with points denoted by square shows

| Rank | Country | Count | H-index | Institution | Count | H-index | Cited journal | Count | If (2021) |
|------|---------|-------|---------|-------------|-------|---------|---------------|-------|-----------|
| 1    | United States | 728   | 65      | Chinese Academy of Sciences | 41    | 13      | BIOINFORMATICS | 1,175 | 6.93      |
| 2    | CHINA   | 407   | 35      | Harvard Medical School | 37    | 12      | NATURE         | 1,082 | 49.96     |
| 3    | GERMANY | 118   | 33      | Stanford University | 29    | 18      | NUCLEIC ACIDS RES | 1,075 | 16.97     |
| 4    | ENGLAND | 101   | 35      | University of Pennsylvania | 28    | 11      | P NATL ACAD SCI United States | 868   | 11.20     |
| 5    | CANADA  | 92    | 22      | Harvard University | 26    | 25      | PLOS ONE       | 856   | 3.24      |
| 6    | AUSTRALIA | 54    | 19      | University of Toronto | 25    | 12      | SCIENCE        | 780   | 47.72     |
| 7    | INDIA   | 48    | 11      | Columbia University | 25    | 11      | BMC BIOINFORMATICS | 764   | 3.16      |
| 8    | FRANCE  | 43    | 16      | Yale University | 24    | 14      | NAT GENET      | 734   | 38.33     |
| 9    | ITALY   | 41    | 15      | University of Washington | 24    | 13      | CELL           | 683   | 41.58     |
| 10   | JAPAN   | 41    | 16      | Shanghai Jiao Tong University | 22    | 9       | GENOME BIOL    | 622   | 13.58     |
the trend of publications from 2000 to 2021, and the line with points denoted by circles shows the number of articles published each year. The number of published articles showed a rapid increase since 2018, and more than 70% of the total articles were published in the last 4 years. This suggests that the studies of deep learning applied in genetics research were new research hot points in recent years.

3.2 Analysis of countries, institutions and journals

A total of 101 countries and 2,487 institutes contributed publications. The top 10 countries, institutions, and cited journals are listed in Table 1. 728 (41.5%) articles published in the United States ranked first place, which was 18.3% higher than those in China, whose publication number was 407 (23.2%), thereby ranking second. However, it is worth noting that the research institution with the largest number (41 articles) of published articles was the Chinese Academy of Sciences, which indicated this institution had powerful scientific research ability in the field of deep learning application in genetics research. The collaborations between different countries and institutions are shown in Figures 2, 3. The bigger size of the circle represents the larger number of articles published by this country. The shorter the distance between two circles, the better the cooperation between the two countries. As shown in Figure 2, the biggest circle belongs to the United States of America which had close cooperation with Germany, England, and France. Although the Chinese Academy of Sciences published the largest number of articles, it was lack of cooperation with other institutions. Harvard Medical School was in a key position in this study field, which kept close cooperation with multiple institutions, such as Columbia University and Stanford University (shown in Figure 3).

3.3 Journal analysis

A total of 151 cited journals published publications related to deep learning in genetics research. The top 10 cited journals are presented in Table 1 (with green background). The highest cited count belonged to the BIOINFORMATICS (1,175 times), followed by NATURE (1,082 times). Among
these journals, NATURE had the highest impact factor (49.962). Collaborations among these cited journals are shown in Figure 4.

In academic journals, referential relationships facilitate knowledge exchange within the research field, where citing articles form the knowledge frontier and cited articles form the knowledge base. A journal dual-map overlay is shown in Figure 5. The cluster analysis of citing articles (the left side) belongs to journals focusing on the field of molecular/biology/immunology research. Also, the cluster analysis of cited articles (the right side) belongs to journals focusing on the field of molecular/biology/genetics research. The primary
citation path colored orange represents the citation relationship between the two clusters, which indicated that based on genetics research, deep learning tends to be applied to immunology.

3.4 Reference analyses

References are key bibliometric indicators as frequently cited documents can greatly influence their research areas (Table 2). The article was published on Nature which was cited 89 times, ranking first. Summarizing the highly cited topics, the result indicated that deep learning methods such as deep convolutional nets and recurrent nets have dramatically improved drug discovery and genomics research.

In network research, betweenness centrality is a major indicator to determine the importance of nodes in the network, and a higher betweenness centrality means that the literature is more important Synnestvedt et al., (2005). Table 2 also shows the betweenness centrality of these works of literature.

In this article, a co-cited document-based clustering analysis can be used to generate sub-fields and connect nodes in the research. We constructed a network of co-cited references to test the scientific relevance of related publications (Figure 6). Cluster setting parameters were

| Rank | DOI                  | Title of cited reference                                                                                                           | Count | Centrality | Interpretation of the findings                                                                 | Year  |
|------|----------------------|-------------------------------------------------------------------------------------------------------------------------------------|-------|------------|-------------------------------------------------------------------------------------------------|-------|
| 1    | 10.1038/nature14539 | Deep learning                                                                                                                     | 89    | 0.01       | This article discussed deep learning methods such as deep convolutional nets and recurrent nets that have dramatically improved speech and visual recognition. Other domains such as drug discovery and genomics brought about breakthroughs | 2015  |
| 2    | 10.1038/nbt.3300    | Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning                                           | 77    | 0.08       | This study built a stand-alone software by using a diverse array of experimental data and evaluation metrics ascertained sequence specificities that is essential for identifying causal disease variants | 2015  |
| 3    | 10.1038/nmeth.3547  | Predicting effects of noncoding variants with a deep learning-based sequence model                                                | 65    | 0.07       | This document developed a deep learning-based algorithmic framework that enables the prediction of noncoding variants | 2015  |
| 4    | 10.1145/2939672.2939785 | Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining                                  | 54    | 0          | This study described a highly effective scalable tree boosting machine learning method and proposes a novel sparsity-aware algorithm for sparse data and weighted quantile sketch for approximate tree learning | 2016  |
| 5    | 10.1101/gr.200535.115 | Basset: learning the regulatory code of the accessible genome with deep convolutional neural networks                             | 47    | 0.1        | This study offered a powerful computational approach to annotating and interpreting the noncoding genome. Researchers perform a single sequencing by CNN’s assay to annotate every mutation in the genome with its influence on present accessibility and latent potential for accessibility | 2016  |
| 6    | 10.1038/nature19057 | Analysis of protein-coding genetic variation in 60,706 humans                                                                      | 44    | 0.01       | This study analysis protein-coding genetic variation in 60,706 humans, and it can efficiently filtering of candidate disease-causing variants and discover human ‘knockout’ variants in protein-coding genes | 2016  |
| 7    | 10.1093/nat/gkw226 | DanQ: a hybrid convolutional and recurrent deep neural network for quantifying the function of DNA sequences                         | 36    | 0.05       | This study proposed a novel hybrid convolutional and bi-directional long short-term memory recurrent neural network framework for predicting non-coding function de novo from the sequence | 2014  |
| 8    | 10.1038/nature14248 | Integrative analysis of 111 reference human epigenomes                                                                           | 36    | 0.08       | The article described the integrative analysis of 111 reference human epigenomes generated and profiled for histone modification patterns, DNA accessibility, DNA methylation, and RNA expression | 2015  |
| 9    | 10.15252/msh.20156651 | Deep learning for computational biology                                                                                           | 34    | 0.03       | This study reviewed the applications of this new breed of analysis approaches in regulatory genomics and cellular imaging | 2014  |
| 10   | 10.1038/ng.2892    | A general framework for estimating the relative pathogenicity of human genetic variants                                            | 34    | 0.05       | This study discussed a framework that objectively integrates many diverse annotations into a single, quantitative score to differentiate 14.7 million simulated variants | 2015  |
Top N% = 0.5, #Years Per Slice = 3, and the pruning algorithm was chosen. The Modularity Q score = 0.7197, which was > 0.5, indicated the network adopted loosely coupled clusters. The Weighted Mean silhouette score = 0.9185, which was > 0.5, indicated acceptable cluster homogeneity. From the literature, we used index items as cluster markers (#0 – #6); the largest cluster (#0) was “deep learning”, #1 was “logic regression”, #2 was “variant prioritization”, #3 was “random forests”, #4 was “scRNA-seq”, #5 was “genomic regulation”, and #6 was “recombination”.

3.5 Co-occurrence and burst keyword analyses

We extracted and analyzed keyword co-occurrence in related publications. The top 20, with highly linked strengths, are shown in Table 3. The co-occurrence of any two terms indicates their presence in the same publication. While identifying thesematics in research areas, keyword analyses of articles 1754) identified 27 keywords with a minimum of 40 occurrences (Figure 7). The co-occurrence analysis based on author keywords was built with occurrence times as a threshold. There are several distinct
FIGURE 7
Network map of keywords is divided into 6 clusters.

FIGURE 8
Keywords with the strongest citation bursts of publications from 2000 to 2021.
clusters with different colors. The co-occurrence network map of keywords is shown in Figure 7, given that the larger the size of the circle, the higher the co-occurrence of keywords. Furthermore, having closer keywords together shows a stronger relationship. The average year of publication of the keywords was determined using colors. Machine learning, deep learning, and genetics constitute the largest circle of all keywords that are identified through co-occurrence analysis. Our study also investigated temporal trends in hotspot shifts using the top 19 keywords having the strongest citation bursts. These included prediction (2016–2021), sequence (2017–2021), mutation (2017–2021), and cancer (2019-2021) (Figure 8).

4 Discussion

4.1 General data

Between the publication years 2000–2021, we selected and investigated 1754 SCIE articles related to deep learning in genetics. Since 2015 with the development of gene sequencing technology, biological genetic data have exploded. The number of published articles showed a rapid increase. Another growth time node is 2018, more than 70% of the total articles were published in the last 4 years. This suggests that as deep learning technology enters its mature stage, it has attracted widespread attention. The highest number of studies (728) was generated by the United States, with China in second place at 407. The top ten institutions included seven in the United States and two in China. According to our data, most of the research in deep learning in genetics was produced by institutions and countries in developed countries, such as the United States, Germany, and France. The reason for this trend is that better socioeconomic development can be the premise of ensuring adequate funding, resources, and human input to explore brand new scientific research. Socioeconomic factors such as GDP, GDP per capita, research and development funding, number of researchers, number of physicians, or international collaboration are important decisive factors of scientific productivity. There are many reasons for this trend, such as GDP level Nature Genetics was the most frequently used publishing journal; therefore, it significantly contributed to research in this area. Additionally, we investigated the top 10 cited publications; the top-cited article was published by Lec et al. on Nature and was cited 89 times. These high cited articles will shed some light to this research field.

4.2 The knowledge base and current research characteristics

In previous studies, different deep learning research applications have been investigated in genetics and generated significant results. As indicated (Figure 6), after clustering co-cited references, key clustering nodes successfully identified knowledge bases, namely: #0 “deep learning”, #1 “logic regression”, #2 was marked as “variant prioritization”, #3 was marked as “random forests”, cluster #4 was marked as “scRNA-seq”, cluster #5 was marked as “genomic regulation”, and cluster #6 was marked as “recombination”. We described the knowledge base according to different clusters with time characteristics.

In the #0 “deep learning” cluster, applications of deep learning methods show cutting-edge performance in a variety of complex prediction tasks and large datasets in natural images. Scientists propose a deep-learning framework for genetic research events, e.g., distant metastasis in cancer, protein subcellular localization, genome recombination map of African Drosophila melanogaster, and DNA transcription factor binding; the abovementioned aspects show the advantages (Xiao et al., 2019; Adrion et al., 2020; Zhang et al., 2021a; Chereda et al., 2021).

In the #1 “logic regression” cluster, Liu et al. proposed a logic regression-based approach that was used to analyze the gene–gene interaction of eight genes involved in cell adhesion in 806 NSCL/P Chinese case-parent triad recruited to explore the risk of non-syndromic cleft lip Liu et al., (2019). Nicodemus KK’s team tested and discussed the interactions between these susceptibility genes using four machine learning algorithms (including random forest, generalized enhanced regression, and Monte Carlo logistic regression) in a case-control study of schizophrenia Nicodemus et al., (2010). Dasgupta et al. reviewed machine learning and regression-based methods in 200 common or rare genetic variants from exome sequencing data and discussed cross-validation for model assessment and selection Dasgupta et al., (2011).

In the #2 “variant prioritization” cluster, key challenges in genomics research are variant prioritization methods. Huang et al. identified a deep learning framework, which was evolution-based, for unified variant and gene prioritization. The authors integrated constraints predicting missense variants and protein-coding genes associated with dominant disorders and estimated fitness effects for potential single-nucleotide variants, which outperformed current methods Huang, (2020). Zhang et al. formulated a disease-specific variant classifier that assessed discriminate pathogenic variants from benign variants and prioritized disease-associated variants Zhang et al., (2021b). In their study, Mattia et al. proposed an automated computational framework that identified causal genetic variants (small insertions and deletions and coding/splicing single-nucleotide variants) to improve causal variant prioritization methods and variant pathogenicity classifications Bosio et al., (2019).

For the #3 “random forest” cluster, as a standard regression model, which has been widely used in the machine learning (ML) application, Jian Y’s team applied a random forest machine learning algorithm to purity pediatric children central nervous system tumor analysis, which helps with the clinical management
of pediatrics Yang et al., (2021). Chen Z constructed a deep learning network model based on the random forest classifier, and it can easily identify malonylation sites, for predicting sites shows high confidence Chen et al., (2018). Nicholls et al. reviewed ML model (gradient boosting and random forests) applications, dissected variant and gene signal heterogeneity, prioritized complex disease-associated loci, and critically evaluated prioritization issues for genome-wide association studies Nicholls et al., (2020).

For the #4 “scRNA-seq” cluster, as single-cell RNA-sequencing (scRNA-seq) is used to analyze gene expression with high resolution, scientists have comprehensively exploited this area to dissect individual cell types in several diseases. For example, Carlos et al. generated a Deep Neural Network (DNN) model which quantified immune infiltration levels in breast and colorectal cancer bulk RNA-seq samples and identified improved and accurate survival prediction and quantification data (Torroja and Sanchez-CaboDigitalsorter, 2019). Cédric et al., in an effort to accommodate increasing levels of scRNA-seq data, designed a deep neural network-based imputation algorithm that is more suitable for the ever-increasing scRNA-seq data (Arisdalessian et al., 2019). Additionally, Yao and Nelson’s teams generated unsupervised deep learning methods for improved data integration which showed improved performances in scRNA-seq datasets (Johansen and Quon, 2019; He et al., 2020).

For the #5 “gene regulation” cluster, an ML modality was adapted by Colbran et al. to impute gene regulation information from genotyped data and investigate 490 ancient Eurasian human DNA samples and explore divergent gene regulation mechanisms which contributed to skin pigmentation and metabolic and immune functions. The authors identified gene regulation roles in adaptation and associations between complex traits and genetic diversity Colbran et al., (2021). Atak et al. devised a deep learning approach and integrative genomics strategy to analyze functional enhancer mutations with allelic imbalance of gene expression and chromatin accessibility and successfully interpreted and predicted the impact of a mutation on gene regulation Atak et al., (2021). Godwin et al. devised a deep learning-based model to predict the gene regulatory effects of low-molecular-weight compounds; the model potentially identified drug candidates inducing particular gene responses, without prior interactional information on protein targets Woo et al., (2020).

For the #6 “recombination” cluster, a central tenet of genomics is the accurate assessment of genome-wide recombination rates in natural populations. Andrew et al. used ML algorithms to examine if DNA motifs across the genome could be used to predict crossover variation and identify genetic factors influencing variation in recombination rates Adrian et al., (2016). Kha F proposed a DL intelligent computational predictor based on the deep neural network (DNN) as a classification engine for the identification of recombination spots through an experimental benchmark dataset with 10-fold cross-validation which achieved the 95.81% highest accuracy Khan et al., (2020).

4.3 Hotspots and frontiers in research

Keywords concentrate on contemporary research issues or concepts, while burst keywords represent emerging trends and frontiers in research. In our work, we used CiteSpace to capture burst keywords, and four related research frontiers were identified: four keywords with the strongest citation bursts, such as prediction (2016–2021), sequence (2017–2021), mutation (2017–2021), cancer (2019–2021), and these key words cover the research frontier of the current topic.

4.3.1 Sequence (2017–2021)

Large-scale genetic datasets and deep-learning approaches are increasingly exploited by bioinformatics approaches to model protein structures and complexes. Zhao et al., using sequence information, devised a deep forest-based protein location algorithm to accurately predict protein subcellular locations using only protein sequences, which outperformed contemporary state-of-art algorithms Zhao et al., (2018). Cui et al. analyzed the main methods used to represent protein sequence data, theoretically reviewed the architecture of different embedding models, and investigated the development of these sequence-embedding approaches Cui et al., (2021). Braberg et al. analyzed the emergence of large-scale genetic datasets and deep learning approaches which modeled protein structures and associated interactions (deep mutational scanning, genome-scale genetic or chemical-genetic interaction mapping, and coevolution) and discussed structural data integration from different sources Braberg et al., (2022).

4.3.2 Cancer (2019–2021)

Originally used for image processing and pattern recognition methods, deep learning models are now used to detect genetic alterations in cancer and determine cancer patient prognoses. The framework by Mallik et al. integrated linear regression, differential expression, and deep learning and facilitated the robust interpretation of DNA methylation signatures and gene expression data for cervical cancer Mallik et al., (2020). Poirion et al., using multi-omics data, established a deep learning ensemble network that predicted patient survival subtypes Poirion et al., (2021) In order to predict survival outcomes in cancer patients, Huang et al. broadly analyzed The Cancer Genome Atlas cancers using several deep learning-based models Huang et al., (2020). Tran et al. reviewed emerging deep learning approaches and how they were applied to precision oncology. The authors not only exemplified how deep learning was used for cancer diagnostics, prognostics, and treatment management strategies, but they also reviewed
the current limitations and challenges of deep learning in this area Vaernet, (1972).

4.3.3 Mutation (2017–2021)

With considerable high-throughput technology advancements, somatic mutations in their millions have been reported, but critically, the identification of specific driver genes expressing oncogenic mutations is highly challenging and complex. In their study, Luo et al. used “deep drive” to predict driver genes by combining similarity networks with features that characterize the functional impact of mutations. They use AUC scores to evaluate predictive efficiency. DeepDriver achieved AUC scores of 0.984 and 0.976 on breast cancer and colorectal cancer, respectively, which were better than those of the competing algorithms. Luo et al., (2019) Sahraeian et al. inaugurated a deep convolutional neural network–based somatic mutation detection strategy using high-confidence somatic mutations in a cancer cell line. The authors generated comprehensive models using multiple datasets and highly robust and significantly superior methods when compared with traditional detection strategies Sahraeian et al., (2022).

4.3.4 Prediction (2016–2021)

Ding YL provided a comprehensive review of ML-based approaches for predicting disease–biomolecule associations with multi-view data sources. They discussed feature representation methods and provided some perspectives for further improving biomolecule-disease prediction methods (Ding et al., 2021). Groschel MI presented a translational genomics platform for tuberculosis application to predict antibiotic resistance from next-generation sequence data. After benchmarking, it can rapidly and accurately predict resistance to anti-tuberculosis drugs Gröschel et al., (2021). Majumdar A et al. developed a novelty ensemble support vector regression to predict each drug response value for a single patient based on cell-line gene expression data. This can be used to develop a robust drug response prediction system for cancer patients using cancer cell lines guidance and multi-omics data (Majumdar et al., 2021).

5 Limitations

Our study still has some limitations to be addressed. First, we choose the SCIE database as the collection, while a few studies not included in the core collection were missed. Second, this study includes two types of publication (article and review), and the uneven quality of the collected publications may reduce the credibility of the mapping analysis. However, the visualized analysis based on bibliometric analysis undoubtedly lays a foundation for readers to quickly understand the research subjects, hotspots, and development trends in an unfamiliar research field.

6 Conclusions

Using bibliometrics, we systematically, comprehensively, and objectively investigated the literature related to deep learning applications in genetics research. Importantly, we identified research bases, current hotspots, and future trends in this area. The knowledge bases were “deep learning,” logic regression,” “variant prioritization,” “random forests,” “scRNA-seq,” “genomic regulation,” and “recombination”. We also provided hotspot and frontier guidance for researchers wishing to conduct advanced genetics research in the future. We identified research frontiers and emerging trends topics that incorporated prediction, sequence, mutation, and cancer. Finally, some studies selected for this research were not comprehensive and may have generated publication bias, thereby potentially affecting the study outcomes of this bibliometric review.

Data availability statement

The original contributions presented in the study are included in the article/Supplementary Material; further inquiries can be directed to the corresponding author.

Author contributions

Author TF and BZ make the conception and design of this work. Author BZ was responsible for making the acquisition, analysis, interpretation of the data, and drafting the manuscript. TF designed the study and revised the article. All the authors read and approved the final manuscript.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.
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