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Review

Artificial Intelligence and Forensic Genetics: Current Applications and Future Perspectives

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Abstract: The term artificial intelligence (AI) was coined in the 1950s and it has successfully made its way into different fields of medicine. Forensic sciences and AI are increasingly intersecting fields that hold tremendous potential for solving complex criminal investigations. Considering the great evolution in the technologies applied to forensic genetics, this literature review aims to explore the existing body of research that investigates the application of AI in the field of forensic genetics. Scopus and Web of Science were searched: after an accurate evaluation, 12 articles were included in the present systematic review. The application of AI in the field of forensic genetics has predominantly focused on two aspects. Firstly, several studies have investigated the use of AI in haplogroup analysis to enhance and expedite the classification process of DNA samples. Secondly, other research groups have utilized AI to analyze short tandem repeat (STR) profiles, thereby minimizing the risk of misinterpretation. While AI has proven to be highly useful in forensic genetics, further improvements are needed before using these applications in real cases. The main challenge lies in the communication gap between forensic experts: as AI continues to advance, the collaboration between forensic sciences and AI presents immense potential for transforming investigative practices, enabling quicker and more precise case resolutions.

Keywords: artificial intelligence (AI); forensic sciences; forensic genetics; forensic implication; STR interpretation

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1. Introduction

Although the term artificial intelligence (AI) was coined in the 1950s by McCarthy et al. [1], other important concepts, such as neural networks, were defined in the 1940s [2]. Based on the definition of McCarthy, AI represents the science and engineering of making intelligent machines, especially intelligent computer programs [2]. The most significant developments in the last sixty years have been in search and machine learning (ML) algorithms, as well as in the integration of statistical analysis, and applying this knowledge in covering different important aspects of healthcare [3]. Forensic sciences and AI are increasingly intersecting fields that hold tremendous potential in solving complex criminal investigations [4–6]. AI technologies, such as ML and computer vision, have improved how forensic evidence is analyzed and interpreted. AI is the study of creating computer systems that are capable of activities like pattern recognition, problem-solving, and decision-making that normally require human intellect [7]. In the last decade, there has been a surge of interest surrounding the domain of AI due to the availability of various open-source module packages such as TensorFlow, Keras, and PyTorch, as well as commercial software such as PLS_Toolbox and Solo 9.0 [8].

Most of the research investigating the role of AI in forensic sciences has focused on areas such as sex and age estimation [9–18], physical attributes, and in forensic odontology and anthropology for human identification purposes [12,19–26]. Furthermore, AI could be very helpful in the evaluation of DNA methylation-based age prediction. Specifically, Thong et al. showed that an artificial neural network (ANN) had a higher accuracy in age prediction than a regression model, even though regression models are commonly used to estimate age [27]. Other experimental papers have explored the challenging field of definition of the cause of death: in rare cases, it can be difficult to define the manner of death and AI could be helpful. For example, in cases of drowning, several research papers have focused on the application of AI in automating diatom testing, with the aim of achieving higher levels of efficiency and accuracy in the definition of the exact cause of death [11,28–33]. Other authors have tried to apply AI in the evaluation of firearm lesions, demonstrating that digitizing and analyzing the fired projectile specimens could be used for firearm identification [34]. At the same time, AI systems could be applied in order to identify gun-shot entrance/exit wounds [35]. Several applications have been used to perform biomechanical studies on patterns of cranial bone fracture [36]. Furthermore, other papers have focused on the application of AI for the definition of the post-mortem interval (PMI) [37]. Finally, in medico-legal sciences, AI could play a pivotal role in the management of medical liability [38,39].

The integration of AI algorithms and forensic genetics has the potential to enhance the accuracy, efficiency, and reliability of forensic investigations, ultimately leading to better outcomes in solving crimes and identifying perpetrators [40]. The seminal paper that focused on the application of AI to forensic genetics was published in 2008 [41]. In that article, the authors discussed the application of multiple independent ML methods to develop formal classification functions, resulting in an integrated high-throughput analysis system for cost-effective and accurate classification of large numbers of samples into haplogroups. Moreover, AI tools are applied to a wide range of genetic and genomic analyses, such as the creation of genomic annotations, the identification of functional genomic components, and the comprehension of gene expression mechanisms [42].

Forensic science is defined as multidisciplinary, considering the wide range of disciplines integrated into this field. For this reason, to solve a crime, it could be necessary to analyze different biological data. In this context, the intricacy and richness of biological data (DNA, RNA, protein, and epigenetic markers), as well as the differentiation between human and non-human evidence, make this endeavor difficult [43]. Complex analyses are needed for the processing of generated data, and these tasks cannot be completed without computational support [44]. Current applications of ML in forensic biology can be divided into three categories: applications related to human identification, applications related to forensic intelligence, and applications related to increasing the evidential value of DNA evidence [40].

Forensic anthropology, forensic odontology, forensic pathology, forensic genetics, and other forensic fields are among the five subsections into which one group of authors separated their findings [4]. The keywords they used to analyze the implications between AI and forensic genetics were, however, too limited, as we discovered after closely examining their use of the following terms: “artificial intelligence”, “deep learning”, “forensic”, “medicolegal”, “forensic anthropology”, “forensic odontology”, “forensic pathology”, “forensic genetics”, “forensic radiology”, “forensic medicine”, “forensic entomology”, “ballistics”, “traffic medicine”, “death”, “postmortem interval”, “DNA”, and “ethics”.

Moreover, considering the great evolution in the technologies applied to forensic genetics, this literature review aims to explore the existing body of research that investigates the application of AI in the field of forensic genetics. Analyzing the published articles, the goal of this review is to provide a comprehensive overview and potential future directions in this interdisciplinary domain.

2. Materials and Methods

A systematic review was conducted according to the PRISMA guidelines [45].

Scopus and WOS databases were used as the search engines from 1 January 1980 to 3 December 2023. The following keywords were used: (artificial intelligence) AND (Forensic genetics)—21; (artificial intelligence) AND (DNA mixture profiling)—10; (artificial intelligence) AND (forensic biological evidence)—7; (artificial intelligence) AND (forensic human identification)—98; (artificial intelligence) AND (NGS forensic analysis)—1; (artificial intelligence) AND (forensic genetics laboratory)—4; (artificial intelligence) AND (massively parallel sequencing)—11; (artificial intelligence) AND (forensic DNA typing)—2; (artificial intelligence) AND (Y AND X chromosome STR)—1; (artificial intelligence) AND (STR typing)—1; (artificial intelligence) AND (STRs)—5.

2.1. Inclusion and Exclusion Criteria

The following exclusion criteria were used: articles not in English (12), conference papers (25), reviews (20), book chapters (3), books (2), conference reviews (2), short surveys (2), editorials (1), and notes (1). The inclusion criteria were as follows: original articles, articles in English.

2.2. Quality Assessment and Data Extraction

F.S first assessed all the articles by evaluating their titles, abstracts, and the entire text. Subsequently, M.S. conducted an independent reanalysis of the selected articles. If there were any conflicting opinions among the articles, they were referred to C.P. for further evaluation.

2.3. Characteristics of Eligible Studies

Out of a pool of 161 articles, 16 duplicates were eliminated, and 68 studies were excluded because of specific criteria. The remaining 77 articles (reported in the Supplementary Materials Table) were first evaluated based on the abstract content: the 36 articles marked in red in the Supplementary Materials Table were removed after abstract evaluation. Forty-one full-text papers were further analyzed, excluding 29 articles (marked in yellow in the Supplementary Materials Table) and including 12 articles (marked in green in the Supplementary Materials Table). Finally, the systematic review included a total of 12 articles (Figure 1).

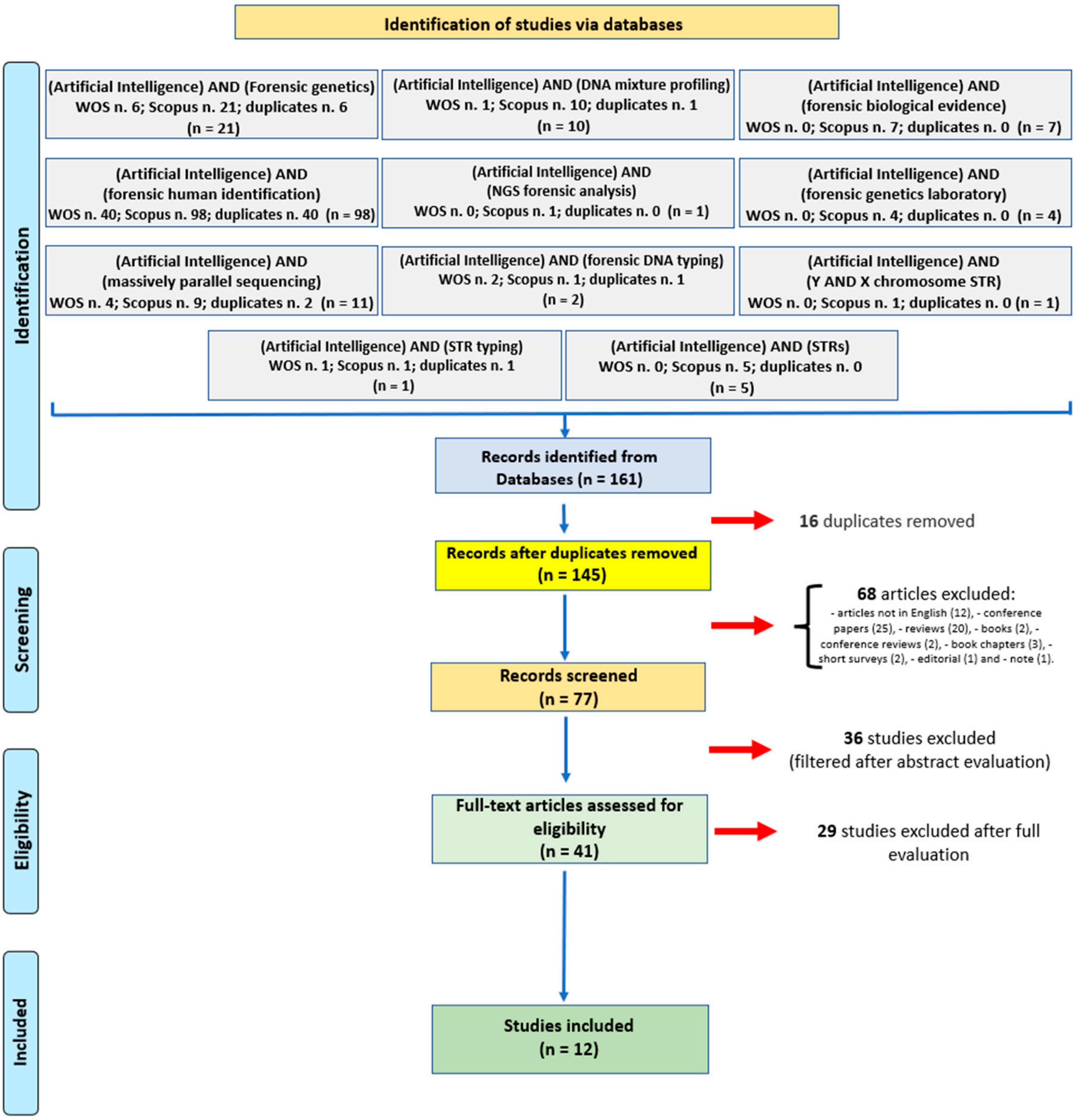

Figure 1. Flow diagram illustrating included and excluded studies in this systematic review.

3. Results

According to the assessment of the first author, the selected articles were contributed by research groups from various countries including the United States (3), Australia (2), China (2), India (1), Netherlands (1), Poland (1), Portugal (1), and the United Kingdom (1). When examining the distribution of articles based on the year of publication, the earliest relevant paper to our research topic was published in 2008. Notably, a significant number of studies were conducted in the last three years. This review included publications in 2008 (1), 2011 (1), 2014 (1), 2016 (1), 2018 (1), 2019 (1), 2020 (1), 2021 (2), 2022 (1), and 2023 (2).

The application of AI in the field of forensic genetics has predominantly focused on two aspects. Firstly, several studies have investigated the use of AI in haplogroup analysis to enhance and expedite the classification process of DNA samples. Secondly, other research groups have used AI to analyze STR profiles, thereby minimizing the risk of misinterpretation. Information about each publication (first author, year, and nationality), the AI application used in the study, and the main findings are reported in Table 1.

Table 1. The AI applications used in each included study, and the main findings.

First Author, Year, and Nationality	Article Title	AI Application	Main Findings
Schlecht et al., 2008, U.S.A. [41]	Machine-learning approaches for classifying haplogroup from Y chromosome STR data	The authors report ML approaches for classifying the haplogroup from Y chromosome STR data.	The authors introduce a novel alternative using modern ML algorithms to infer Y chromosome haplogroups with high accuracy by scoring a relatively small number of Y-linked short tandem repeats (STRs). The authors demonstrate that the application of MLA represents an integrated high-throughput analysis system for cost-effective and accurate classification of large numbers of samples into haplogroups.
Pereira et al., 2011, Portugal [46]	PopAffiliator: online calculator for individual affiliation to a major population group based on 17 autosomal short tandem repeat genotype profile	The authors employ an ML model constructed from a dataset of approximately fifteen thousand individuals to identify individual population affiliation.	The authors introduce a free online calculator called PopAffiliator, (when checked it was not accessible at the link reported in the paper—http://cracs.fc.up.pt/popaffiliator, accessed on 27 February 2024), designed for individual population affiliation in three main population groups: Eurasian, East Asian, and sub-Saharan African.
Mukunthan and Nagaveni, 2014, India [47]	Identification of unique repeated patterns, location of mutation in DNA finger printing using artificial intelligence technique	Artificial neural network techniques were applied to DNA profiling and sequencing.	The authors discuss the challenges in genetic engineering and forensic identification using conventional techniques and algorithms for analyzing DNA profiles. The authors demonstrate that these methods involve complex computational steps and mathematical formulas could be useful in forensic identification.
Taylor and Powers, 2016, Australia [48]	Teaching artificial intelligence to read electropherograms	The authors apply artificial neural networks (ANN) in order to recognize different aspects of an electropherogram.	The work demonstrates the application of an artificial neural network trained to interpret electropherograms, showcasing its ability to generalize to unseen profiles.
Alfieri et al., 2018, United Kingdom [49]	DNA methylation-based age prediction using massively parallel sequencing data and multiple machine learning models	AI was applied to extract information from DNA evidence using a DNA methylation quantification assay for chronological age estimation.	The authors demonstrate the importance of AI in the analysis of data obtained through massively parallel sequencing (MPS).
Adelman et al., 2019, USA [50]	Automated detection and removal of capillary electrophoresis artifacts due to spectral overlap	The authors apply an AI model (a series of mathematical models, created using symbolic regression achieved through genetic programming) in order to improve electropherogram analysis.	The authors conclude that by employing models in combination with a dynamic threshold, the presence of pull-up peaks within true alleles can be effectively addressed, resulting in the elimination of artefactual pull-up peaks and accurate peak height corrections, improving the interpretation of STR analysis
Siino and Sears, 2020, USA [51]	Artificially intelligent scoring and classification engine for forensic identification	The authors enhance the Elston–Stewart algorithm to create a groundbreaking method for matching individuals with pedigrees based on likelihood ratio. This AI model incorporates a prediction cascade that utilizes gradient descent logistic regression, enabling iterative solutions for scenarios involving multiple missing persons.	The described innovative approach enhances the balance between sensitivity and specificity, improving the conventional kinship analysis tools.

Table 1. *Cont.*

First Author, Year, and Nationality	Article Title	AI Application	Main Findings
Li et al., 2021, China [52]	Validation studies of the ParaDNA® Intelligence System with artificial evidence items	The authors test a reliable STR profiling platform known as the ParaDNA Intelligence Test System. This innovative system enables investigators to obtain early tactical intelligence and make informed decisions regarding sample prioritization for detection.	The ParaDNA intelligence test is highly effective in producing valuable DNA profiles, particularly in cases involving blood, saliva, and semen samples that contain abundant DNA.
Volgin et al., 2021, Australia [53]	Validation of a neural network approach for STR typing to replace human reading	The authors test an ML tool known as an artificial neural network (ANN), which can perform the same task as a human profile reader to interpret STR capillary electrophoresis profile data.	The tool's accuracy in detecting allele peaks in reference profiles was found to be 99.7%, which was considered sufficiently high.
Veldhuis et al., 2022, Netherlands [54]	Explainable artificial intelligence in forensics: Realistic explanations for number of contributor predictions of DNA profiles	The authors apply an ML approach to achieve impressive accuracy in determining the number of contributors (NOC) in short tandem repeat (STR) mixture DNA profiles.	The described tool can be used for the prediction of the number of contributors in a mixture profile.
Chen et al., 2023, China [55]	Comprehensive evaluations of individual discrimination, kinship analysis, genetic relationship exploration and biogeographic origin prediction in Chinese Dongxiang group by a 60-plex DIP panel	In this study, the authors apply four AI algorithms and four biogeographic origin inference models in order to predict the biogeographic origins of individuals based on the results obtained through amplification and genotyping with the 60-plex panel.	The AI models applied to their data demonstrated that the biogeographic origin prediction model could be predicted accurately in 99.7% of biogeographic origin models based on three continents; this value decreased to 90.59% on a model based on five continents.
Klosa et al., 2023, Poland [56]	A Machine-Learning-Based Approach to prediction of biogeographic ancestry within Europe	The authors apply three classifiers (Random Forest, Support Vector Machine (SVM), and XGBoost) to the prediction of biogeographic ancestry within Europe, in order to classify DNA samples from Slavic and non-Slavic individuals.	The best results were obtained using SVM that demonstrated an accuracy of 99.9% and F1-scores of 0.9846–1.000 for all classes.

In the field of AI, researchers have harnessed its power to improve various aspects of forensic genetics, including haplogroup classification. Haplogroups are groups of individuals who share a common ancestor through their maternal or paternal lineage. These groups can be distinguished by specific variations in their mitochondrial DNA (mtDNA) or on the Y chromosome in males. Forensic geneticists often use haplogroup classification to determine the ancestral origins of unidentified remains or individuals in criminal investigations. By understanding a person's haplogroup, it becomes easier to narrow down potential geographic origins and genetic relationships. AI can significantly enhance the efficiency and accuracy of haplogroup classification in forensic genetics: using the traditional approach, haplogroup classification required experts to manually analyze genetic data, which was a time-consuming and labor-intensive process. AI algorithms can automate this classification process, greatly reducing the time and effort required. Furthermore, AI systems can learn from large datasets and adapt to new information [41,46,51,55,57].

Analyzing the application of AI in the interpretation of STRs, these tools could be very useful in the creation of automated DNA profile interpretation systems. These systems use ML algorithms to analyze DNA profiles generated from STR typing, analyzing a vast amount of data and identifying patterns that may not be easily recognizable by human examiners. In this way, it is possible to reduce the risk of human error, enhancing the speed and accuracy of DNA matching in forensic genetics. By comparing an individual's DNA profile to a massive DNA database, AI algorithms can quickly identify potential matches. This process, known as DNA fingerprinting, has been instrumental in solving cold cases and exonerating wrongfully convicted individuals [47,48,50,56].

Although AI has brought several benefits to STR interpretation in forensic genetics, challenges still exist. Ensuring the transparency and interpretability of AI models is crucial to gaining the trust of forensic examiners and legal professionals. Additionally, the ethical implications of AI in forensic genetics, such as privacy concerns and potential misuse of technology, must be carefully addressed. The ethical issues and challenges of using AI in forensic science focused on criminal cases: there is a need for a comprehensive definition of AI systems, accountability, and legal procedures, emphasizing the application of these tools under human control [58].

4. Discussion

AI techniques, such as ML, data mining, and pattern recognition, can be effectively employed to analyze genetic data and facilitate the identification of suspects. These technologies enable forensic experts to process and obtain valuable results from vast amounts of data, including fingerprints, DNA samples, and surveillance footage, facilitating faster and more accurate identification of suspects [40]. Moreover, AI-driven facial recognition systems assist in identifying criminals from images or videos, assisting law enforcement agencies in solving crimes and bringing justice to victims [40]. There are limitations and potential biases that may arise when utilizing AI algorithms in forensic genetics, and, as such, emphasis must be placed on the importance of transparency, interpretability, and fairness in algorithmic decision making [59]. To reduce AI bias, several strategies could be applied, such as robust data augmentation for each algorithm used, the application of counterfactual fairness, and the imperative for diverse, representative datasets alongside unbiased data collection methods [60]. Moreover, each tool must report its known limitations. As previously described, an important step is represented by the definition of ML algorithms. In this sense, ANNs are networks that, by employing a condensed set of ideas from biological neural systems, mimic a biological neural network. ANNs simulate the electrical activity of the brain and nervous system: there are neurodes arranged as a layer or vector: each output represents an input for the following layers. To date, in the forensic context, ANN applications have been useful in criminal detection through the comparison of faces [61]. Another algorithm is the Random Forest which operates by constructing a multitude of decision trees based on samples, their variables, and their class. An example of its application is the age estimation of bloodstains based on temporal colorimetric analysis. The SVM is an ML algorithm that determines boundaries between data points based on predefined classes, labels, or outputs [62]. It uses supervised learning models to solve complex problems related to classification, regression, and outlier detection. In forensic sciences, it is frequently used in anthropology studies [63]. Another algorithm that could be used for ML is XGBoost; it belongs to the ensemble learning category, specifically the gradient boosting framework, using decision trees as base learners and employing regularization techniques to enhance model generalization. This algorithm could be used in a forensic context to evaluate biogeographic ancestry [56].

A fundamental step is the evaluation of the algorithm used for the ML. For example, the classification accuracy represents the ratio of the total number of input samples to the number of accurate predictions; it is used to evaluate the accuracy. Another method used for algorithm evaluation is the Area Under Curve (AUC). It is used for binary classification problems: the likelihood that a randomly selected positive example will be ranked higher than a randomly selected negative example is known as the AUC of a classifier. The F1 Score represents the harmonic mean of memory and accuracy. The F1 Score is used to provide two key performance indicators and it has a range of (0, 1). The indicators are the number of examples that the classifier properly classifies (its precision) and the number of instances that it does not miss (its robustness) [64,65].

Different genomics and genetics issues have been addressed by ML techniques, such as functional gene annotations, pattern recognition in DNA sequences, and annotation of genomic sequence elements. Histone modification, transcription factor (TF) binding ChIP-seq data, chromatin accessibility assays, microarray or RNA-seq expression data, and other genomic assay data can all be fed into ML. Gene expression data can be utilized to find potentially useful illness biomarkers and differentiate between various disease characteristics. It may be possible to identify new types of functional elements by using chromatin data to annotate the genome in an "unsupervised" manner [40].

In order to comprehend the mechanics underlying gene expression, ML techniques have also been applied. While some methods take into account TF binding profiles at the gene promoter region or ChIP-seq histone modification, others predict gene expression only based on the DNA sequence. By developing a network model, more advanced techniques try to jointly model the expression of every gene in a cell [66].

ML researchers have a history of concentrating on a subset of statistical problems and placing a strong emphasis on the analysis of big, diverse data sets. The ML literature generally lacks basic statistical notions like power calculations, statistical confidence estimation, and likelihood estimate calibration [67].

Due to their complexity and diversity, the detection of genetic markers employed for forensic DNA typing necessitates a substantial amount of data, which may make manual implementation challenging [68]. In addition, handling such data, interpreting it, and comparing it by hand is difficult, labor-intensive, and prone to inaccuracy, despite it occurring rarely [69]. Therefore, analyzing and interpreting such a large amount of data may be made easier by artificial intelligence, which has access to bioinformatic techniques, mathematical algorithms, and statistical computations. Based on the data obtained through this literature review, to date the application of AI in the field of the forensic genetics is limited to two main fields: haplogroup classification and STR electropherogram interpretation.

From a practical standpoint, AI can expedite the forensic investigation process, helping forensic geneticists and law enforcement agencies identify human remains or unknown individuals more efficiently. This is particularly relevant in cases involving missing persons or mass disasters, where the identification process can be challenging, considering the great amount of data that could be handled. The application of AI algorithms in haplogroup classification can streamline and improve the accuracy of this process, benefiting forensic investigations and scientific research alike. With further advancements and continued collaboration between these fields, AI can revolutionize the way forensic genetics and haplogroup classification are conducted, enabling faster and more accurate analyses of genetic data [5].

In the same manner, AI has transformed the field of forensic genetics, especially in the interpretation of STRs. The interpretation of DNA profiling is related to the peak height intensities expressed in relative fluorescence units (RFU), which are shown on an electropherogram (EPG), a graph of fluorescence vs. time. Allelic peak heights for a perfect PCR process are correlated with the amounts that come from the contributing individuals. These peak heights, however, are random and will differ between PCR procedures, particularly in cases where there is little DNA or when there is degradation or allelic drop-out—a result of low template and/or damaged DNA that leads to incomplete DNA profiles, stutter, or artifacts [70,71]. Due to these factors, forensic genetic analyses may complicate the manual interpretation of mixed DNA profiles, and STRs in particular may be amplified and then sequenced [72]. These restrictions are removed and the full potential of the DNA typing data is realized by statistical software packages that integrate probabilistic interpretation models [73,74]. Fully continuous DNA mixture interpretation software, such as STRmixTM, has been extensively tested and used in forensic DNA labs to analyze STR data [75]. STRmixTM determines the probability of the profile given all potential genotype combinations by utilizing quantitative data from an EPG, such as peak heights. We give the normalized probability density a number, or weight. The likelihood of the EPG given each potential genotype combination at a locus is given a relative weight by STRmixTM [70]. Therefore, using probabilistic genotyping software facilitates the control of imported trace samples, particularly those with damaged DNA [75,76]. It also enables the comparison of the presence or absence of alleles in the reference profile and the trace sample directly. Additionally, the availability of software tools reduces analysis time and human weariness [77]. Prior to interpretation, the electropherogram must be inspected to confirm if the profile is indicative of a DNA component or an artifact. There are two ways to go about this phase. When done by hand, it takes a while and can produce different results depending on the analyst reading the layout. To get around this restriction, an analytical threshold—below which the data are discarded—or a double reading method by two separate analysts is used. However, these methods may squander a significant amount of genetic material and require an unnecessary amount of analytical time. However, sophisticated EPG scanning systems like GeneMarker, OSIRIS, and Genemapper may be able to automatically eliminate artifacts. Even with this capability, a lot of artifacts still need to be manually removed before the EPG can be utilized for criminal investigations, which prolongs the reading process. These days, ANNs could be used to create an expert EPG reading system that can discriminate between alleles and artifact, reducing the amount of manual control that is required [48].

Moreover, the application of the latest techniques in forensic DNA profiling that have been established in the last few years employing MPS, also known as NGS, is another crucial question regarding the mixed profile [78]. These techniques can simultaneously identify SNPs, STRs, and in/del (insertions and deletions). Using spatially separated and clonally amplified DNA templates, MPS is related to a range of high-speed sequencing platforms (sometimes referred to as "second generation" or "next generation") that share a common technical approach to sequence many fragments in parallel [79]. These methods include multiple steps, including library construction, enrichment, and bridge amplification or emulsion PCR. STRs may be amplified and then sequenced; this method allows nucleotide variations found in the flanking regions and repeat motifs of interest to be analyzed. The data produced by these new methods are compatible with previously archived data [80]. Moving forward with MPS will allow the forensic community to continue using millions of DNA profiles that are currently stored in DNA databases, while also expanding its use of forensic DNA typing with increased genetic diversity in STR and SNP. Continued advances in AI are likely to play a crucial role in solving crimes and promoting justice in the future [40,81].

Great progress has been made in other fields of forensic sciences such as forensic odontology. One of the first applications was reported by Chen et al. [19], who described a dental biometric system for human identification using dental radiographs. The described system is based on two main stages: feature extraction and matching. Tooth correspondences between postmortem and antemortem radiographs are established, and a distance based on corresponding teeth measures similarity. The potential applications of artificial intelligence technology in forensic odontology can be categorized into four areas: analysis of human bite marks, identification of sex determination, age estimation, and dental comparison [82]. For example, considering the international migration scenario that is considered a present concern worldwide, determining a minor's age represents an important goal for upholding the rights of all minors [83]. Methods should be replicable, accurate, and objective: in this regard, the use of new AI tools is necessary to guarantee a trustworthy procedure.

Patil and Ingle [84] analyzed the possibility of applying an algorithm to fingerprint patterns, which are determined by a combination of genetic and environmental factors, to determine gender and age group, and in predicting blood group and classifying common clinical diseases that have a genetic basis, including hypertension, type-2 diabetes, and arthritis. After all, electronic fingerprint recognition has been commercially applied with identification purposes and could be translated to the forensic field [85]. Indeed, to date, the use of fingerprints for identification purposes in the forensic field is one of the more affordable methods, even though recognizing fragmented fingerprints is a difficulty for forensic experts; in this way, the development of AI represents an important tool [86]. Moreover, in a recent study the main goal of the authors was to calculate the sexual dimorphism in unfused or disarticulated hyoids, using ML methods [87].

AI and forensic genetics have emerged as two rapidly evolving fields that are revolutionizing the way investigations are conducted in various domains, especially in the field of criminal justice. Considering the paucity of research, to improve the AI application in forensic genetics, there is a need for interdisciplinary collaboration between AI researchers, forensic scientists, and legal experts to ensure the responsible and ethical implementation of these technologies in the criminal justice system. AI may improve the accuracy of DNA profiling, predicting physical traits and ancestry from DNA samples, and identifying potential familial relationships among individuals [88]. Interestingly, there is a possibility of exploring the use of AI in data interpretation in the field of DNA transfer. DNA transfer in forensic investigation is a crucial process: the sensitivity and specificity of DNA analysis techniques have greatly improved over the years, allowing investigators to detect and analyze even the smallest traces of DNA that could be transferred in a direct/indirect manner [89–93]. The ability to transfer DNA from one surface to another unintentionally, referred to as secondary or indirect transfer, can occur through a variety of mechanisms, such as direct contact or environmental factors [94,95]. Forensic investigators must carefully consider the context of DNA findings, evaluating the likelihood of direct or indirect transfer, and cross-checking various pieces of evidence to ensure accuracy in their conclusions [96]. Of particular interest is indirect transfer that occurs when DNA is transferred between individuals or objects indirectly, often through third-party or environmental factors. One common example is the transfer of DNA from an object to a person and then onto another object [97–99]. Factors such as the duration of contact, intensity of contact, and the nature of the surface can affect the presence and persistence of DNA [100,101]. For instance, if an individual handles a weapon that is later used in a crime, their DNA may be transferred from the weapon onto the perpetrator, providing a link between the suspect and the crime scene. DNA can be carried through the air by particles such as dust, dander, or skin cells, settling onto surfaces and ultimately being transferred to other objects or individuals [102]. It is crucial for forensic investigators to consider these mechanisms and recognize potential sources of indirect transfer when analyzing DNA evidence. Understanding the principles of DNA transfer (i.e., transfer, persistence, prevalence and recovery of DNA) is essential for forensic investigators to accurately interpret DNA evidence and present reliable conclusions in a court of law [100,103]. The Bayesian model has become widely used in evaluating indirect DNA transfer in the forensic field, providing a statistical framework for assessing the likelihood of such transfers. One key aspect of the Bayesian model is the use of prior probabilities: these represent the initial beliefs about the likelihood of different scenarios.

In this context, the application of AI tools for the analysis of the activity level could help the investigator to evaluate the weight of evidence in the worked case. However, it is important to note that the Bayesian model is dependent on the input data and assumptions made. Biases or inaccuracies in the data or incorrect assumptions can impact the validity of the results [104–106].

AI could be helpful in the prediction of physical traits and ancestry from DNA samples. By training machine learning models on extensive genetic databases, researchers have developed algorithms that can accurately predict a person's physical characteristics, such as eye or hair color, improving so-called forensic DNA phenotyping. Additionally, AI can provide insights into a person's ancestry or geographical origin by analyzing STRs and other genetic markers, such as SNPs; to date, it is possible to use a set of ancestry informative markers to determine the ancestry of an individual [88,107]. While the simultaneous analysis of hundreds of DNA predictors with targeted MPS can be valuable in criminal investigations, particularly in the identification of the suspect or the identity of unknown human remains, it should be desirable to conduct further studies to achieve the forensic validation of these tools [108].

5. Conclusions

AI algorithms are playing a crucial role in revolutionizing forensic investigations on a global scale. The fields of AI and forensic genetics are rapidly evolving, particularly within the criminal justice domain. While AI has proven to be highly useful in interpreting STR profiles and conducting haplotype analysis, further improvements are needed before deploying these applications in real cases. The main challenge lies in the communication gap between forensic experts, crime investigators, and lawyers, causing statistical evidence to be misunderstood and misinterpreted in court, leading to erroneous decisions. Thus, there is a pressing need to develop methods that facilitate effective communication and act as a bridge to address these issues. As AI continues to advance, the collaboration between forensic sciences and AI presents immense potential for transforming investigative practices, enabling quicker and more precise case resolutions. However, it is important to acknowledge that although AI has benefited forensic genetics, considering the variability of forensic samples, it is difficult to expect AI tools to effectively understand, analyze, and interpret genetic data as efficiently as human forensic experts, scientists, and investigators. AI can be seen as a valuable aid, but it should never replace the essential role of human expertise.

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