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Perceptions of forensic scientists on statistical models, sequence data, and ethical implications for DNA evidence evaluations: A qualitative assessment

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ABSTRACT

With the introduction of next generation sequencing (NGS) technology in the forensic field, it will be of interest to assess if forensic scientists feel equipped to interpret and present DNA evidence for sequence data. Here, we describe perceptions of sixteen U.S.-based forensic scientists on statistical models, sequence data, and ethical implications for DNA evidence evaluations.

To get an in-depth understanding of the current situation, we used a qualitative research approach with a cross-sectional study design. Semi-structured interviews ($N = 16$) were conducted with U.S. forensic scientists working with DNA evidence. Open-ended interview questions were used to explore participants' views and needs surrounding the use of statistical models and sequence data for forensic purposes. We conducted a conventional content analysis using ATLAS. ti software and employed a second coder to ensure reliability of our results.

Eleven themes emerged: 1) a statistical model that maximizes the value of the evidence is preferred; 2) a high-level understanding of the statistical model used is generally sufficient; 3) transparency is key in minimizing the risk of creating black boxes; 4) training and education should be an ongoing effort; 5) the effectiveness of presenting results in court can be improved; 6) NGS has the potential to become revolutionary; 7) some hesitations surrounding the use of sequence data remain; 8) there is a need for a concrete plan to alleviate barriers to the implementation of sequencing techniques; 9) ethics plays a major part in the role of a forensic scientist; 10) ethical barriers for sequence data depend on the application; 11) DNA evidence has its limitations.

The results of this study give insight into the perceptions of forensic scientists regarding the use of statistical models and sequence data, providing valuable information in the move towards implementing sequencing methods for DNA evidence evaluations.

1. Introduction

DNA typing is a mature field and overwhelmingly seen as the gold standard in forensic evidence. The interpretation of DNA evidence, however, is far from straightforward and challenges arise when evaluating complex profiles and assessing the statistical weight of the evidence. Accurate representation of forensic evidence in court is crucial to avoid misinterpretations and, ultimately, to reduce the possibility of a miscarriage of justice. This not only requires sensible models that can handle the complexity associated with DNA profiles, but also an understanding of the methods used by forensic scientists who will be writing the reports and potentially serving as expert witnesses in court.

In general, when reporting an inclusion, admissible DNA evidence in court needs to be accompanied by a quantitative statement. The forensic scientist is often requested to provide additional meaning to these results. Although the scientific evidence is restricted to the DNA profile, the trier of fact needs to incorporate this to decide on the ultimate issue of guilt. This requires additional links between the evidence and an inference of contact with the crime scene as well as an association with the crime, while also incorporating all other relevant information available. Correct presentation of the DNA results by the forensic expert is crucial to ensure that statements are related only to probabilities regarding the DNA evidence.

Valid probabilistic reasoning is not easy and numerous studies have been conducted showing the occurrence of fallacies manifesting within the forensic community [1–4]. Over the years, mitigation strategies have been proposed to reduce the effect of bias in forensic decision-making [5,6]. To increase our understanding of how forensic scientists feel

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about interpreting and presenting DNA evidence, it will be valuable to obtain direct input from this group. Such studies have the potential to illuminate the barriers faced by these professionals and can serve as guidance for the implementation of statistical models for new techniques and applications. This is especially timely in light of the transformation of current approaches to the incorporation of next generation sequencing (NGS) technology.

Early research has focused on the perceptions of sequencing technologies within the field through surveys and highlighted opinions on current use, future views, and challenges in forensics [7]. To get a more in-depth understanding of the current situation, we conducted a qualitative study involving interviews with U.S. forensic scientists working with DNA evidence. The objective of this study was to describe the views and needs of these professionals surrounding the use of statistical models and sequence data for forensic purposes.

2. Methods

2.1. Study design

We conducted a cross-sectional study involving forensic scientists based in the U.S. and working with DNA evidence. Semi-structured interviews were used to explore the views and needs of this group of professionals over three domains. The first two domains focused on the application of statistical models and use of sequence data in forensic DNA evidence evaluations, respectively. The final part assessed some ethical topics concerning these concepts. An interview guide was developed with open-ended questions over the three domains and subsequently refined using a key informant (see Appendix I). A mock interview was conducted before proceeding with official interviews. All study activities were reviewed and approved by the University of Washington Human Subjects Division.

2.2. Recruitment

We reached out to the organization behind the International Symposium on Human Identification (ISHI) for recruitment purposes. ISHI is the largest symposium focusing solely on DNA forensics with about 1000 forensic experts from around the world attending their yearly event [8]. They agreed to use their network to reach out to 90 individuals who previously attended NGS-based workshops. Initial emails sent out by the organization contained a study description and a link to an external form where people could indicate their interest in participating in the study and leave their contact information. We followed up with those individuals who expressed interest in participating with a second email asking for more background information to confirm eligibility and to set up a time for an interview. To increase response rates, a second batch of recruitment took place by reaching out to our own contacts.

Individuals were eligible if they were employed by a U.S. forensic laboratory at the time of the study and they worked with DNA evidence. Eligible candidates were invited to participate in a one-time ~45-min confidential interview over Zoom. A modest incentive in the form of a $25 gift card was offered in return for their participation, although not all participants could accept this incentive. During recruitment, we collected background information on the size of the workplace, number of years in the field, and whether or not the participant had experience with court testimony. Our goal was to recruit individuals with different work experiences to gather a range of perspectives. Recruitment took place over two months and resulted in 24 completed recruitment forms. A total of 16 individuals were successfully contacted and interviewed. Of the remaining eight individuals, six did not respond to our follow-up emails and two had to drop out due to personal circumstances.

2.3. Data collection

Data collection was performed over a period of three months (April–June 2022). Zoom interviews were scheduled at a time convenient to the interviewee. All interviews were conducted in English and digitally recorded. Verbal consent was obtained from each of the participants at the beginning of the interview and included permission to record the interview. The automatically generated audio transcription files of completed recordings were manually curated to remove errors and to anonymize the data. The resulting transcripts were assigned a unique identifier to ensure confidentiality.

2.4. Data analysis

ATLAS.ti v.9 [9] was used to support coding, analysis, and data management. Transcripts were subjected to a conventional content analysis using a mixed approach of top-down and open coding until code saturation was reached [10,11]. A subset of transcripts was independently coded and reviewed by a second coder. Coding differences were resolved through discussion. We collapsed the final codes into initial themes and translated these into underlying concepts as they emerged from the data. During the late-stage analysis, we used groundedness (total occurrence of a code) and pervasiveness (occurrence over unique transcripts) metrics to maximize our ability to identify all relevant themes.

3. Results

3.1. Participant characteristics

The participants of our study represented twelve different states from around the U.S.[1] Their educational background included degrees in chemistry, biology, genetics, and forensic science. Work experience with DNA evidence ranged from less than a year to over 33 years (median of 13 years). The majority of interviewees indicated using probabilistic genotyping (PG) software as part of their jobs and a handful described having been actively involved in the validation process. Except for early-career scientists, almost every participant had experience with expert testimony in a court setting. Most participants reported that their workplaces did not use sequence data at the time of the interview and thus had no practical experience working with it. Four participants reported to be in the validation process of a sequencing technique or had recently completed validation and were working on implementation. Participant characteristics are summarized in Table 1.

Table 1
Participant characteristics.

Characteristic – *N* (%)	*N* = 16
Work experience	
≤5 years	5 (31.3%)
>5 years	11 (68.7%)
Experience with court testimony	
No	4 (25.0%)
Yes	12 (75.0%)
Use of statistical software	
STRmix	11 (68.7%)
TrueAllele	2 (12.5%)
None or other (e.g., Popstats)	3 (18.8%)
Experience with sequence data	
No	10 (62.5%)
Yes	2 (12.5%)
In validation/implementation	4 (25.0%)

[1] The following states are represented in this study: Arizona, California, Colorado, Florida, Louisiana, Minnesota, Nebraska, New York, North Carolina, Oklahoma, South Carolina, Washington.

3.2. Theme identification

Nine main themes emerged describing participants' views and needs concerning the application of statistical models and sequence data for forensic DNA evidence evaluations. Two additional themes came up while exploring some ethical topics related to these concepts. The themes are graphically illustrated in Fig. 1 over the three domains.

3.3. Theme 1: A statistical model that maximizes the value of the evidence is preferred

Participants expressed their support for probabilistic genotyping software and generally preferred a statistical model that uses as much data as possible. Although there was agreement that such models can be more difficult to understand, most (81%) noted that this should not be a reason for resorting to more simplistic approaches.

> *"I wouldn't think: 'Oh it's too difficult, I wish we didn't have to do this'. If that's the best way to do it, then that's the way we do it." (P9)*

> *"[F]or me it is 100% worth it to have a more complicated model in order to be able to generate more accurate results, whether it's an inclusion or an exclusion." (P7)*

Others mentioned the need to find a middle ground between model complexity and an analyst's needs. These participants highlighted the importance of keeping in mind the question being asked, the quality of the data, and whether results can be explained well in court.

> *"I feel like it's just this middle ground that we have to find where an analyst does feel comfortable enough to talk about it and then understand what [the statistical models] are saying." (P2)*

Overall, participants valued consistency and being able to use the same software for all cases. They were looking for something they can trust and that is easy to use. Moreover, the forensic scientists included in this study wanted to make sure that they are maximizing the value of the evidence, which was considered most fair to all parties involved.

3.4. Theme 2: A high-level understanding of the statistical model used is generally sufficient

While it may be preferred to have a full understanding of the models used during an analysis, participants overwhelmingly agreed that this is not realistic or even needed in most settings. Multiple participants used an analogy to describe their views on this topic:

> *"One analogy that I thought of is: I've taken a class on how to use a graphing calculator. I can use a lot of functions on it, but do I know the programming that went into it, to be able to do these things … ?" (P8)*

> *"You have this analogy; it is so simple. I drive a car. I know how to drive the car, but do I have to know how the engine works from top to bottom? Absolutely not. I don't know how to do that, nor do I want to learn." (P12)*

We noted though that participants did feel responsible to not "just plug in data" and have at least a high-level understanding of the statistical models used. This holds especially in light of being able to adequately present results in court. Although a simplified explanation is often preferred in a court setting, participants acknowledged that this required a strong foundational knowledge of the statistical model.

> *"It's not just about I press go, and then accept everything that comes out. […] I really need to understand how it's working in order to present to court that I have some confidence, that I trust what it's doing." (P13)*

Furthermore, the required level of proficiency may also depend on the maturity of the technology.

> *"At the beginning of the technology, as it's being introduced, yeah, you have to have a really good understanding of it to be able to present it in court for the first time. And then, as it gets more routine, I think it's less important that you have a deep dive understanding of it." (P14)*

3.5. Theme 3: Transparency is key in minimizing the risk of creating black boxes

PG software has been criticized in the literature due to its perceived black box nature [12] and the use of sophisticated modeling techniques has been the subject of several discussions within the forensic science community [13–17]. Participants understood the sentiment and agreed that, from the outside, PG software can look like a "black box", especially in light of the underlying code not being readily accessible. However, this was not necessarily seen as a problem or even a relevant issue. Participants highlighted the amount of research, training, and validation that goes into setting up PG software for DNA casework. They expressed trust in the software used within their labs, provided that the developers remain transparent about their work.

> *"I don't love [the black box] part of it. I think it simplifies how much work goes into understanding how it works within your lab setting, and how much work goes into all the validation that has to happen before we start using it." (P16)*

Furthermore, a recurring thought amongst participants was that the "black box issue" was not a relevant point of concern and mainly used as a Defense tactic.

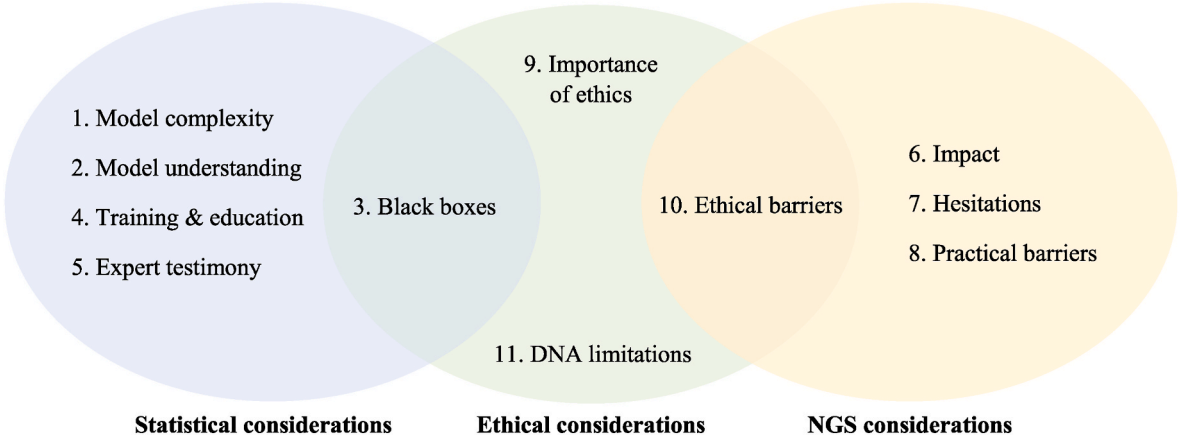

Fig. 1. Graphical illustration of the identified themes within each of three domains and areas of overlap.

"[I]t's part of the game, I guess, that they're going to challenge. They want to see what they can't see and as soon as you let them see it then it's not a big issue." (P14)

3.6. Theme 4: Training and education should be an ongoing effort

When asked about their needs with respect to statistical modeling for DNA evidence evaluations, participants noted that they can never have enough training. While extensive training occurs in certain situations, such as for new hires and with the introduction of a new technique or software, participants expressed interest in having ongoing training opportunities as well. Training courses are seen as most useful when they provide hands-on experience and are adapted to deal with different learning needs and levels. It may also be helpful to focus on new scientific developments as participants reported struggling to keep up with relevant papers.

"I know people learn differently, but when it comes to [PG software] I think you need to do it to learn it. […] I think the biggest thing is training. […] And definitely even continued training." (P2)

"I think probably the biggest challenge would be the continuing education of keeping up to date with whatever the current model is, because it is easy in school to learn what the most cutting-edge technique is, but then that only stays cutting edge for so long." (P9)

That being said, it is important to be mindful about time constraints as forensic scientists may experience work pressure and are not always able to make education a priority.

3.7. Theme 5: The effectiveness of presenting results in court can be improved

Participants felt a huge responsibility when it comes to effectively explaining DNA analysis results in court. One difficulty brought up was finding a balance between explaining results thoroughly but not too complicated.

"That's always one of the challenges, to explain our results, and one of the downsides to using [PG software] is that it is hard to explain and that a [random match probability] is much easier to explain. […] It falls on us to explain that, as best as we can." (P1)

"I'm always seeking what's the best … simplest explanation that I can provide somebody to help them understand something that they perceive as being super complicated." (P3)

Participants also expressed frustrations in dealing with lawyers, especially in case of fallacies or a (deliberate) misdirection.

"No matter how we explain it, [lawyers] are going to interpret [the likelihood ratio] in a different way. They are going to interpret it as the transposed conditional most of the time. […] That part is difficult." (P10)

"I guess really the thing that's hardest with the statistics right now is just different defense experts come forward and, generally speaking, bring up something that really does not matter. […] It makes you have to jump through a whole bunch of more hoops." (P7)

Notably, one participant mentioned that well-intentioned efforts from the field to create awareness regarding fallacies may lead to more paranoia among forensic scientists. The result may be a rigid approach with statements being made solely for the transcript instead of focusing on the people in court. Multiple participants were proponents of offering training courses to justice officials, especially for the Defense. Others also suggested creating handouts or videos for juries.

"It's tough because at the end of the day you got to explain it to the jury. The jury won't have that background in statistics. But it will definitely be helpful if at least the lawyers will have them." (P15)

3.8. Theme 6: NGS has the potential to become revolutionary

Participants expressed their excitement when talking about the potential of NGS techniques in a forensic setting.

"I think this is one of the most exciting things that's come about in forensic DNA probably since STRs." (P3)

"I feel it's going to be revolutionary. […] There have been tremendous changes and I'll just say … the opportunity now is greater than any time that I've seen." (P6)

Numerous applications for sequence data were brought up, including but not limited to unidentified human remains, cold cases, investigative genetic genealogy (IGG), forensic phenotyping and ancestry inference, and mixture and low-level contributor deconvolution. Having a technique that provides access to all the data at once was seen as the main benefit. Participants thought that NGS techniques will initially be employed for lead-generating approaches, such as IGG, noting that it would be relatively easy to implement and has already proven to be successful. Most agreed that we are still a long way out until sequence data will be fully incorporated into forensic casework. Some envisioned sequencing techniques to become the standard, while more than half of the participants (63%) saw the use of these as a specialized application with short tandem repeat (STR) typing through capillary electrophoresis (CE) remaining the default approach.

"I think, in my opinion, it would just take over the whole platform. No capillary electrophoresis, it would spit out the STR, Y, and the SNP at the same time and you're good." (P15)

"If the technology gets robust enough that we can convert it, all of our STR profiles, to be compatible with that, I could see it replacing it entirely. But I think that would be a very long way out." (P8)

"I don't think it will ever outpace CE because that workflow is very straightforward and reasonably … it's still expensive but it's just a lot fewer steps and it's so much easier to analyze than [NGS] data." (P11)

3.9. Theme 7: Some hesitations surrounding the use of sequence data remain

Despite the enthusiasm among participants about NGS techniques, there also exist concerns. Participants acknowledged that there are still a lot of uncertainties surrounding the application of sequence data and it is not always clear what the added value exactly is. It was also noted that there may be a reluctance within the community to accept new technologies, partly because of a fear of change and (public) misconceptions. Some expressed worries that this may lead to sequence data not reaching their potential.

"I have a hard time convincing myself that the extra information is worth it, given the current statistics that we get. Is ten to the 30^{th} not high enough?" (P10)

"I think there's so much potential, and I think people have hesitated. Probably because there's certain things that weren't there, but it has kind of become like this chicken or egg thing." (P16)

Participants noted that such concerns are always an issue with the introduction of new technologies, and it takes time to get over the acceptance hump. Promotions and a push from high up are believed to be beneficial to overcoming existing hesitations.

"We are all human beings, so you do have to get over the little bit of personal fear. People don't like change. Sell me on it a little bit. Help me become part of the change." (P6)

3.10. Theme 8: There is a need for a concrete plan to alleviate barriers to the implementation of sequencing techniques

When asked about specific barriers surrounding sequence data, participants brought up numerous practical issues. First, it was noted that the implementation of sequencing techniques requires a massive investment from a laboratory. The need for money, time, training, and staff was brought up numerous times. Moreover, participants acknowledged that the decision-making was mostly out of their hands, and it could well be that priority was given to other applications.

"[Laboratories] don't want to train their whole staff all over. Maybe they don't have time to do the validation work and to do research for it." (P5)

"I feel the sale is there, […] so you have the industry's interest and now it's a matter of working to reduce the barriers through training, technology, business case, all of those things." (P6)

Second, participants experienced a lack of data and resources. This includes the need for sequence-based databases, samples to be used for validation purposes, and the need for reliable software. Specifically, participants noted that they do not want to change PG software and were hoping for an update that could accommodate sequence data if their labs decided to proceed in that direction. At the time of writing, the developers of the PG software STRmix just released a paper introducing their newest software for sequence data [18].

"[T]here's no autosomal sequence data that exists in a database that we can search the same way that we can search STRs." (P9)

"The amount of data being generated from [NGS technology] is huge. How to deal with that is going to be another problem." (P4)

"We definitely need a probabilistic genotyping tool to be able to incorporate [sequence] data. […] I don't think I would want to go back to a different model, or to a different kind of statistical tool." (P16)

Overall, participants expressed a need for a concrete plan. This includes guidance on preparing a laboratory for the implementation of sequencing technology to ultimately running an analysis and presenting results when applied to casework.

3.11. Theme 9: Ethics plays a major part in the role of a forensic scientist

Participants described ethics as playing a major daily role in their jobs. Responses indicated that the topic was seen as extremely important, with a need for continuous promotion and requiring yearly training. Some participants brought up the potential of bias creeping in during an investigation and valued a work environment that promotes open discussions to minimize such risks. While a forensic scientist may strive towards objectivity, a few participants noted that they are not operating in a vacuum. There exists an added complexity in being linked to law enforcement. This may lead to misconceptions that forensic scientists work for one side only. One participant also expressed frustration in dealing with pressure coming from investigators.

"Everybody has conspiracy theories, like the labs are in cahoots with the prosecution, which is totally wrong. […] I'm for the truth, for the evidence." (P13)

"[Investigators] come in guns blazing and want us to start working. […] Not that they are asking us to be unethical, […] they just want it done now. And our stance at the laboratory has always been quality over quantity, all day long." (P12)

3.12. Theme 10: Ethical barriers for sequence data depend on the application

The majority of the participants (75%) indicated not seeing any potential harm for sequence data obtained from STR regions. Responses also showed that using NGS techniques for investigative leads was seen as unproblematic. Participants were more hesitant when it comes to novel sequencing techniques and data outside of the standard STR regions, including phenotyping, ancestry-related information, and single nucleotide polymorphism (SNP) data that may inadvertently reveal medical information.

"When you think about the traditional analysis of STRs, I don't think that [potential harms are] too much of a problem. The things that concern me are some of the newer marker types like ancestry estimation." (P11)

That being said, many noted that law enforcement is held to high standards and that forensic laboratories are used to having tremendous checks and balances in place. Nevertheless, some participants acknowledged that having safeguards in place never completely takes away all risks and there always exists a potential of misuse.

"I don't think there could be any harm in [DNA sequence] information if the information is interpreted or looked at in an appropriate way. Everybody has the ability to spin things, or make things look worse than they are, or not in the right context." (P12)

While privacy concerns and the risk of misuse and misinterpretation should be reasons for thoroughly vetting the use of sequence data, participants said that they should not be a reason to discontinue NGS techniques. Others mentioned the existence of misconceptions from the public and how time and information would likely overcome fears.

When talking about the use of whole genome sequence (WGS) data, participants were more divided in their opinions. About a third saw this as a next step and great opportunity to get even more data, while others were more hesitant and saw no direct need for such data for forensic purposes.

"I think that [using WGS data] is our next step." (P3)

"I don't see why we need to move to [WGS data] into the future. […] I think it seems a bit excessive and probably an unnecessary amount of information, but how the future moves forward, I don't know." (P4)

"Let's do the information we need. Let's not do it all, because we can do it all." (P2)

3.13. Theme 11: DNA evidence has its limitations

Interestingly, multiple participants brought up situations where DNA evidence may be of limited value. One observation was that participants experienced a shift in the court room from source level to activity level, something that has been noted in the literature as well [19–21]. Furthermore, while the increase in sensitivity of technologies may help deconvolute complex mixtures involving low contributors, participants noted that there exists a line between pushing the limits and getting unreliable results. This may point towards concerns about an over-reliance on DNA evidence, an issue that was also reported in a worldwide survey of forensic scientists [22]. This notion can also be problematic when dealing with extreme statistics that may become overwhelming.

"[I]n the big scheme of things: what is the difference between one in a billion and one in 10 billion?" (P5)

"We've worked so hard at getting to sensitivity levels where we can detect so little DNA. I don't necessarily think it's bad, but I think that sometimes DNA is not the answer to the question. Sometimes DNA doesn't help at all." (P1)

4. Discussion

Our findings describe several factors contributing to the perceptions of forensic scientists surrounding the use of statistical models and

sequence data for DNA evidence evaluations. Although our study results are limited to a small set of professionals and are therefore not readily generalizable, we can frame our findings in a broader context by drawing from existing literature. With respect to statistical modeling, participants noted that forensic scientists are generally not experts in statistics and that this holds even more true for legal practitioners and jurors in a court setting. Yet, the forensic scientist is tasked with the difficult job of presenting the statistical weight of DNA evidence during expert testimony. The occurrence of themes relating to the need for training and education, and the improvement of presenting results in court, was therefore unsurprising. Similar observations are described in the literature. Eldridge suggests that it is apparent that improvements should be made when it comes to expert testimony, noting that juries do generally not interpret results as intended [23]. Unfortunately, it is less clear how such changes will look, and the forensic community is still in search of the most desirable way to present evidence, if it even exists [23]. In terms of providing handouts to juries, as suggested by one participant of our study, focusing on visual aids may be helpful [23]. Still, there will always exist factors that complicate expert testimony for DNA evidence due to the nature of the criminal justice setting. While frustrations in dealing with such difficulties situations, as brought up by some of our participants, may be valid, it has also been noted that it is precisely the defense lawyer's job to create doubt [24].

While participants acknowledged the increased level of complexity involved in PG software, we noticed high levels of support for such models. Even though it may complicate the presentation of results as compared to resorting to more simplistic approaches, this was not seen as a reason to oppose the use of PG software. This sentiment is echoed by other key criminal justice stakeholders, as described in a recent qualitative study on probabilistic reporting in forensic science [24]. These different stakeholder groups, including judges, prosecutors, and defense attorneys, highlighted the need for forensic scientists to "accurately and impartially convey their findings" and for investments in training and education on the use of statistical models [24]. A big aspect in creating comfort surrounding the use of statistical models is having validations in place, something that was brought up by our participants but is also pointed out in the aforementioned study [24]. Validations can help alleviate concerns and show that results are accurate and trustworthy. In addition, transparency is invaluable in creating trust. This may include having access to a good support team from software developers and being aware of the workings and limitations of the model. While disclosure of the source code may also be helpful in establishing trust, opinions among different stakeholder groups seem to differ on the necessity of providing such access by default [24].

When it comes to sequence data participants saw huge potential for numerous applications, with a primary initial use case for SNP data in investigative leads. The NGS applications brought up during the interviews have been well-described in the literature [25,26]. Participants' opinions differed on the future of forensic DNA typing, with some seeing sequencing techniques as an addition to the current workflow while others saw it replacing CE-based STR technology entirely. Whatever the situation, all participants agreed that a shift will take years, potentially ranging from about 5 to 10, or even 20 years. Several factors play a role in these beliefs. First and foremost, participants noted that practical barriers currently prohibit the implementation of sequencing techniques for routine casework. Over the years, studies have published guidelines as well as sequence-based data necessary for NGS-based DNA evidence evaluations [27–30]. Despite these developments, technical barriers still remain, and the issues noted by our participants reflect findings from other publications [7,31,32]. In addition to practical barriers, participants advocated for the consideration of perceptual and ethical barriers. While some participants expressed interest in wanting to be at the forefront of new developments, others would rather wait until all the kinks have been worked out. Participants also expressed concern about the (lack of) added value of sequence data. Opinions on ethical implications seem to differ based on the application. While the use of the standard forensic STR markers is seen as unproblematic among our participants, potential harm from sequence data was deemed more likely to occur for other marker systems.

Our work has both strengths and limitations. Our background in forensic statistics put us in a great position to carry out this work. However, we are aware of the possibility of our work being biased. To minimize the risk of results being influenced by personal views, we deliberately opted for a largely open coding approach to let the data guide our analysis. Our second coder was less familiar with the topic, which provided a unique perspective and maximized our ability to identify relevant themes. As with most qualitative studies, this work may suffer from self-selection bias. Specifically, our sample consists of individuals who expressed interest in NGS technology and had previously attended NGS-based workshops, which may have led to biased opinions in favor of NGS applications. Furthermore, due to the limited sample size and way of sampling, our findings are not representative of the forensic community in general. Nevertheless, we believe our data provides a rich set of perspectives on the topics of interest.

5. Conclusion

In this paper, we highlighted important themes concerning statistical concepts, sequence data, ethical implications, and their interactions within the field of forensic DNA evidence evaluations based on in-depth interviews with sixteen U.S. forensic scientists. We showed to what extent they felt the need to have an understanding of the statistical models used to be able to perform their work and what aspects they valued in such models and PG software. We also identified experienced barriers and needs in light of feeling better prepared to work with statistical models, as well as to present such results in a court setting. Finally, we discussed the perceived impact of sequence data on the forensic field and revealed practical barriers and ethical considerations to take into account for such new technologies. While the perceptions of forensic scientists with respect to these topics provide valuable input, it is important to remember that they are part of a larger system. On the one hand, barriers need to be addressed from a scientific standpoint, including the creation of databases and PG software for sequence data. On the other hand, the business side requires consideration of higher-level organizational issues, including funding and management needs. We believe both perspectives need to be taken into account in our journey towards successfully implementing sequencing methods for DNA evidence evaluations.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix I. - Interview Guide

Part/Domain	Activities/Questions
I. Introduction	Provide general study background Describe interview process Obtain consent Start recording Verify participant background Q1. Can you tell me more about your job and what you do at work?
II. Content	Q1. What is your personal experience working with statistical concepts and modeling in a forensic setting?
Statistical considerations	Q2. How comfortable do you feel with concepts like the random match probability, the likelihood ratio, and probabilistic genotyping? Q3. To what extent do you feel you need to be proficient in statistics to perform your work? Q4. To what extent can or should we ask for proficiency in statistics of lawyers and judges? Q5. For probabilistic genotyping software, to what extent do you feel you need to understand the underlying modeling concepts? Q6. Do you think using the most sophisticated statistical model is always the best option? Q7. Are there any barriers related to this topic you are facing in your work? Q8. Do you feel you have adequate access to training opportunities? Q9. What would you need to feel better equipped to work with statistical models for DNA evidence? Q10. What would you need to feel better equipped to present such evidence to a jury/in court?
NGS considerations	Q1. What is your personal experience working with sequence data in a forensic setting? Q2. How comfortable do you currently feel working with sequence data? Q3. How do you think sequence data will change what forensic scientists do? Q4. Do you think sequencing technologies will take over STR CE typing completely? Q5. What would you need to feel better equipped/prepared to work with sequence data?
Ethical considerations	Q1. How do you feel about the term “black boxes”, which is sometimes used to describe probabilistic genotyping software? Q2. Do you think the introduction of sequence data will be beneficial to the forensic community? Q3. Do you foresee potential harm with the introduction of sequence data for forensic purposes? Q4. How do you feel about the use of whole genome sequence data for forensic purposes? Q5. Are there any ethical issues you are dealing/struggling with in regard to your work as a forensic scientist?
III. Conclusion	Q1. Is there anything else you would like to add? Stop recording Describe follow-up process

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