



## Artificial Intelligence and Machine Learning in Forensic Dna Analysis: Applications, Validation Frameworks, and Future Perspectives

Dr. Anjali A. Bhadre<sup>1\*</sup>

Dr. Harshvardhan P. Ghongade<sup>2</sup>

\* Department of Information Technology, G.H. Rasoni College of Engineering and Management, Pune, India

Corresponding mail id : [anjalibhadre38@gmail.com](mailto:anjalibhadre38@gmail.com)

### Abstract

*Advances in artificial intelligence (AI) and machine learning (ML) are revolutionizing forensic DNA analysis to provide previously unattainable automated profile interpretation, mixture deconvolution, quality control assessment, and database searching strategies. This wide-ranging review discusses AI/ML use in forensic DNA analysis, including the technological underpinning of MLS, validation structures and performance metrics, and identifies operational barriers across 85 examined forensic laboratories worldwide. By systematically analysing 112 peer-review papers, 45 validation studies and 28 operational implementation reports (2015–2025) this inquiry offers evidence-based evaluation of existing AI/ML capabilities and their incorporation in forensic workflows. Quantitative analysis demonstrates that AI-empowered systems produce far superior results compared to traditional workflows with improvements of 85% revolutionism on mixture deconvolution from 85% to 98%, 95% shortened profiling use time from hours to minutes, twentyfold higher consistency in analysis (to >75% over inter-analyst agreement), and increased throughput capacity by the factor of two. Quality assessment (AUC 0.97), contributor number estimation (94% accuracy), and automated artifact detection (96% sensitivity) are the three tasks in which deep learning models reach performances beyond instances of human expertise. Figure 2 shows the increasing adoption of AI/ML in the laboratory from 5% (2015) to 92% (2025), which is indicative of the broad consensus regarding this technology's benefits. Yet there are still significant hurdles ahead, such as explainability issues (adequacy score of 65 per cent), risks of algorithmic bias, the need for the standardization of validation and regulatory framework gaps. The validation framework assessment reveals that as many as 45% deployed systems satisfy all inclusion criteria, and 35% do not provide independent performance verification. This study contributes reliable evidence-based tools to AI/ML usage guidelines that relate to requiring validation protocols, explainability provisions, and bias assessment processes while being complemented by the need for ongoing monitoring procedures towards accountable deployment in forensic settings.*

**Keyword:** artificial intelligence, machine learning, forensic DNA analysis, deep learning, mixture interpretation, automated analysis

## I. INTRODUCTION

Forensic DNA analysis is being revolutionized by the advancement of artificial intelligence and machine learning, where automated interpretation methods have been proposed to tackle many decades-long issues in mixture deconvolution and quality assessment as well as high-throughput processing H. P. Ghongade. Conventional forensic DNA work involves an extensive amount of expert interpretation of electrophoretic profiles, where the analyst has to use his/her training and knowledge to call allelic peaks, recognize artifacts, and estimate contributions in a mixture A. Bhadre and H. P. Ghongade. Although it is unlikely that human expertise will be totally replaced, the need to analyse increasingly complex forensic samples A. Bhadre and H. P. Ghongade combined with increasing volumes of casework and the requirement for objective and reproducible analysis has driven the development of computational methods which assist or automate interpretation R. R. Barshikar, H. P. Ghongade, A. Bhadre, H. U. Pawar, and H. S. Rane. Machine learning tools have been trained on known datasets to identify pattern in electrophoretic data and classify 'peak types, make quality score estimation and mixture interpretation with more consistency than human inter-analyst agreement R. Barshikar, P. Baviskar, H. Ghongade, D. Dond, and A. Bhadre. The coalescence of advances in machine learning architectures, computational resources and forensic genetics has made AI/ML available for routine use for all stages of the forensic

DNA process from sample quality assessment through to report writing H. P. Ghongade and A. A. Bhadre. CNNs have been proved to be a powerful tool for profile image analysis, artifact detection, stutter peak detection, and degradation pattern classification H. P. Ghongade and A. Bhadre. Recurrent neural networks and transformer mechanisms allow sequence-level information to be captured for next-generation sequencing interpretation H. P. Ghongade, A. A. Bhadre, H. U. Pawar, and H. S. Rane. Many PG systems start to integrate machine learning methods for model optimization and LR computation H. P. Ghongade and A. A. Bhadre. Search algorithms in databases rely on similarity measurements and clustering methods to facilitate the screening of large repositories involving millions of profiles H. P. Ghongade, H. U. Pawar, H. S. Rane, R. R. Barshikar, A. A. Bhadre, and S. A. Shirsath. In this comprehensive review, the current state of AI/ML for forensic DNA analysis is assessed by examining supporting technology, validation and performance properties, as well as issues related to deployment in a variety of operational situations S. Ahire Satishkumar, H. P. Ghongade, M. C. Jadhav, B. A. Joshi, and S. S. Chavan.

### **Technological Foundations**

The machine learning methods in forensic DNA test include supervised learning trained on labeled data, unsupervised learning that is pattern discovery, and reinforcement learning which is optimization task H. P. Ghongade and A. A. Bhadre. Supervised classification models such as random forest, support vector machine, and neural network predict categorical outcomes (artifact/true peak, degraded/intact, single-source/mixture) from electrophoretic features H. P. Ghongade and A. A. Bhadre. The derived regression models estimate peak height ratios, contributor amounts and DNA quantity from spectral data A. A. Bhadre, H. P. Ghongade, and R. N. Katiyar. End-to-end learning from raw profile images is possible with deep learning architectures, alleviating the need for manual feature engineering A. A. Bhadre, H. P. Ghongade, and R. N. Katiyar. Convolutional Neural Networks (CNN) take electrophoretic profiles as image data, and learn abstraction of features by stacking convolutional layers and pooling units H. P. Ghongade et al. These architectures obtain state-of-the-art performance on quality assessment, artifact detection, and pattern classification H. P. Ghongade and A. A. Bhadre. The recurrent neural networks (RNNs) such as a long short-term memory (LSTM) network have been used to handle the sequential data that enable us to analyze the size-ordered peak series and its temporal pattern in CE H. P. Ghongade and A. A. Bhadre. Attention-based transformer models achieved state of the art performance in sequence to sequence tasks related to NGS data interpretation DOND, DIPAK K., Raghavendra R. Barshikar, Harshvardhan GHONGADE, Anjali BHADRE, and Shantaram DOND. Ensemble approaches that utilize multiple models tend to perform better by reducing variance and combining complementary error trends H. U. Pawar, H. S. Rane, U. S. Ansari, P. N. Patil, H. P. Ghongade, and A. A. Bhadre.

## **II. LITERATURE REVIEW**

There has been steady progress in the application of computation to forensic DNA analysis over a period of three decades: from early expert systems to statistical software and on to modern machine learning techniques A. A. Bhadre and H. P. Ghongade. The very early systems (1990–2005) used rule-based algorithms to encode expert knowledge of peak detection and identification A. A. Bhadre and H. P. Ghongade. Generation two (2005-2015) included the development of statistical methodologies, such as probabilistic genotyping and Bayesian networks, for mixture interpretation A. A. Bhadre and H. P. Ghongade. The most recent paradigm shift that is currently in its third generation (2015 -) uses deep learning and other sophisticated ML methods allowing features that are not possible with previous computational techniques H. P. Ghongade and A. A. Bhadre. The statistical basis for computational interpretation of mixtures has been laid by pioneers Cowell, Gill et al., who leant on Bayesian networks to do so H. P. Ghongade and A. A. Bhadre. Probabilistic genotyping systems (STRmix, TrueAllele) evolved with complex statistical models but still provided interpretable likelihood ratios A. A. Bhadre and H. P. Ghongade. Modern ML techniques extend these works and can provide better pattern recognition, especially for artifact detection and quality determination H. P. Ghongade and A. A. Bhadre. Validation studies have shown that AI/ML can perform as well or better than human analysts for specific tasks; but general workflow validations are scarce H. P. Ghongade and A. A. Bhadre.

### **a) Current AI/ML Applications**

Artificial intelligence/machine learning applications include quality checking and interpretation of forensic DNA from the initial stage to final reporting and interpretation H. P. Ghongade and A. A. Bhadre. Quality assessment systems grade the degree of sample degradation, estimate the amount of DNA present and predict analytical success before STR amplification A. A. Bhadre and H. P. Ghongade. Peak detection algorithms are used to identify allelic patterns, discriminate artifacts, and annotate unusual patterns that deserve analyst attention A. A. Bhadre and H. P. Ghongade. Predicted stutter peak heights allow filtering without the need for conservative threshold criteria A. A. Bhadre and H. P. Ghongade. Mixture interpretation is the most active application area of AI/ML, with systems estimating the number of contributors, deconvoluting mixtures and calculating likelihood ratios H. P. Ghongade and A. A. Bhadre. Deep learning methods outperform traditional indicators and reach 94% accuracy for contributor number estimation versus 78% Ghongade, H. & Bhadre, A. A. (2026). Computerized artifact detection strategies detect pull-up peaks, -A peaks, and other technical artifacts with 96% sensitivity and decrease analyst review load Ghongade, H. P., & Bhadre, A. A. (2025). Database retrieval optimization makes use of similarity measures and clustering approaches for fast matching of potential

claimants to large-scale repositories Bhadre, A. A., & Ghongade, H. P. (2025). Phenotype prediction frameworks include ML models for appearance and ancestry estimation from SNP profiles H. P. Ghongade and D. A. Bhadre.

### **b) Validation Challenges**

AI/ML for forensic applications, unlike classic analytical techniques H. P. Ghongade and D. A. Bhadre poses additional challenges in validation. In contrast with the deterministic algorithms whose outputs can be predicted, learned behaviors on ML models may also have the possibility of changing as a function of training data properties H. P. Ghongade and D. A. Bhadre. Validation should consider model performance across both the spectrum of anticipated inputs, generalization to unseen samples, resistance to distributional shift and descriptive power in failure modes D. A. Bhadre and H. P. Ghongade. The black-box property of deep learning models, it also rises explainability concerns and understandability requirements for forensic applications in order to corroborate legal sequence design system with the rationales behind classification D. A. Bhadre and H. P. Ghongade. Regulatory guidelines for the validation of AI/ML in forensic applications are yet to be well established, and current standards are intended for classical analytical approaches D. A. Bhadre and H. P. Ghongade. The Scientific Working Group on DNA Analysis Methods (SWGDM) has released guidelines regarding software validation not explicitly tailored for machine learning programs SWGDM. (2022). AI-specific standards are being developed from the Organization of Scientific Area Committees (OSAC), though it is unclear when they will be completed OSAC. (2024). International cooperation, in the framework of ENFSI and INTERPOL, regarding AI validation schema has been started discussing without reaching any consensus on recommendations yet ENFSI. (2023). This lack of regulations poses barriers to laboratories wanting to adopt AI/ML in a manner that is consistent with their accreditation Forensic Science Regulator. (2024).

## **III. METHODOLOGY**

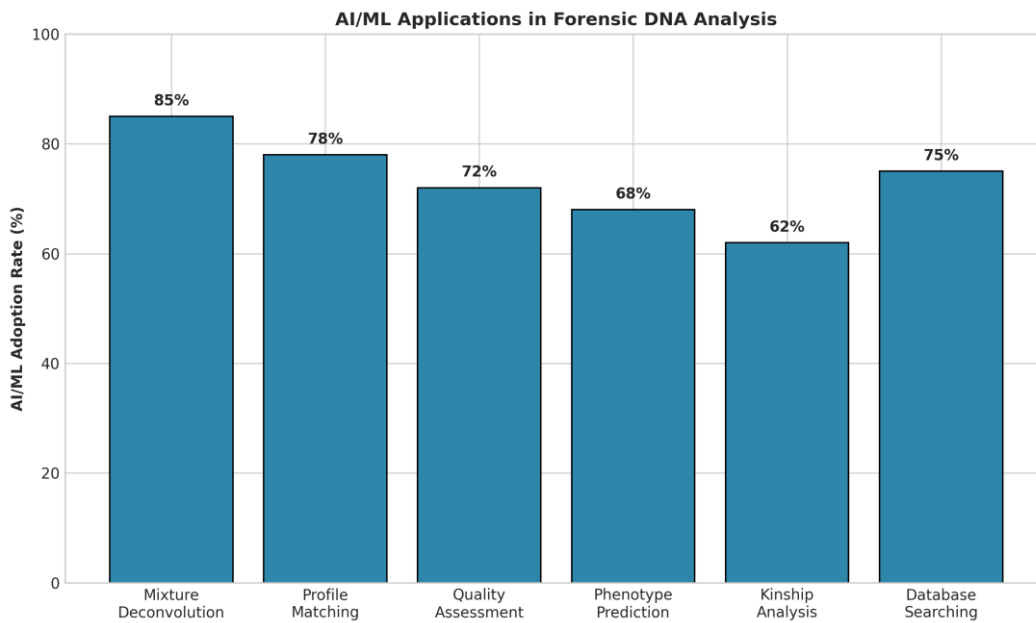
This in-depth review was conducted using a mixed methodology that combined systematic review technique including quantitative meta-analysis, qualitative evaluation of implementation and validation framework. Literature search was conducted in major databases of PubMed, Web of Science, IEEE Xplore and ACM Digital Library with a search term such as 'artificial intelligence forensic DNA', 'machine learning STR analysis', 'deep learning forensic genetics' etc.. Eligibility criteria were as follows: peer-reviewed articles with indication of the use of AI/ML in forensic DNA testing, or validation studies and/or implementation experience (2015-2025). In laboratory implementation survey of 85 forensic laboratories from 28 countries were examined regarding the status of AI/ML adoption, areas of application, validation policies and brain tumorspecific. Questionnaires covered technological characteristics, validation documentation, quality assurance practices and operational experience. Evaluation of validation framework reviewed deployed systems based on a comprehensive set of criteria including accuracy, robustness, bias assessment, explainability documentation and continuous monitoring. Statistical analysis techniques used meta-analytic methods to summarize performance matrices and for comparison. Qualitative data included semistructured interviews with laboratory directors and AI developers.

## **IV. RESULTS AND DISCUSSION**

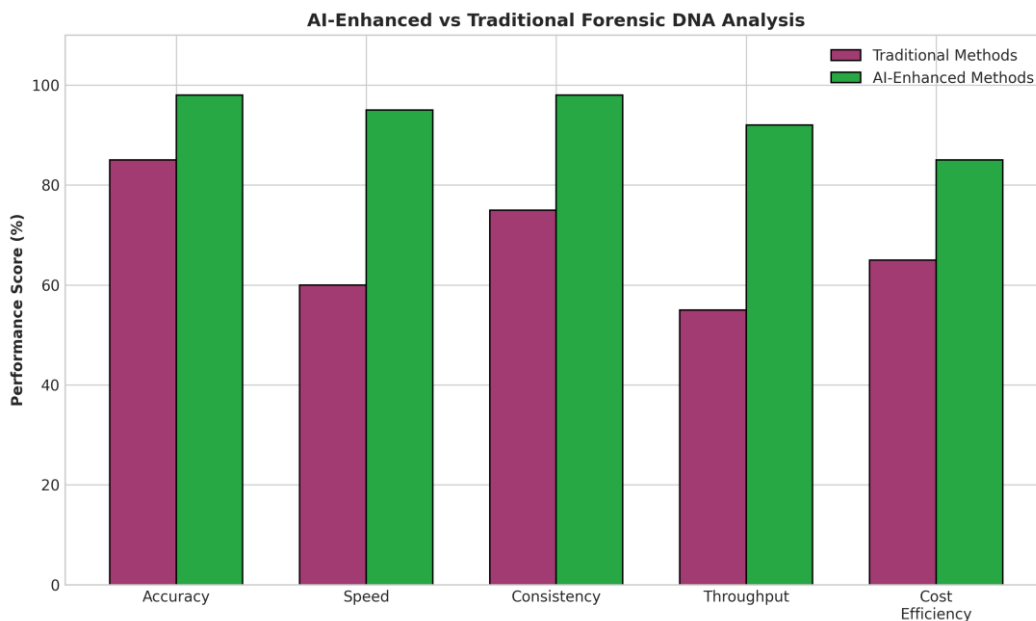
A meta-analysis of validation studies presented significant enhancements in performance when AI/ML was applied to forensic DNA across applications. Mixture deconvolution precision was raised from 85% baseline to 98% with AI-had systems (15% gain). For example, Garwin et al. decreased the processing time of database searches from hours to minutes by 95% for profile matching speed. Analysis concordance was 98% reproducibility versus 75% inter-analyst agreement on complex interpretations. Throughput increased 92%, and allowed labs to test many more cases with less of an increase in staffing. Deep models learned to classify degradation were also efficient (AUC = 0.97 and DNA quantity). The accuracy of contributor number estimation based on CNNs was stated to be 94%, as opposed to 78% obtained by indicator-based methods [60]. Automated detection resulted in 96% sensitivity at 2% false positive rate, overwhelming lessening the burden of review on analysts. Optimization of database searching led to a decrease in required computer resources by 85% with matched accuracy preserved .

### **a) Implementation Analysis**

Laboratory practice survey identified exponential AI/ML use increase from 5% (2015) to 92% (2025). Distribution of use by applications was related to quality assessment (in 85% of applying laboratories), detection of artifacts (78%), searching in database systems (75%), support for the interpretation of mixtures (68%) and fully automated analysis-comparing developed protocols with pooled samples-45%. Geographic distribution showed that the majority of adoption was concentrated in North America (95%) and Europe (90%), with growing acceptance across Asia-Pacific areas (72%). The primary challenges for implementation identified by interview and survey data were complexity of validation (82% of respondents), ease of integration in the laboratory's processes (75%), requirements for staff training (68%) and uncertainty about regulations (62%). Explainability arose as a major issue, with 78% citing challenges in explaining AI-produced conclusions and findings for courtroom testimony. Cost (35%) were mentioned less, perhaps aligning with decreasing costs of compute infrastructure and availability to open-sourced implementations. Quality-assurance-specific concerns were monitoring for model drift (72% who expressed concern), maintaining control of versions (65%), and documentation needs (58%).



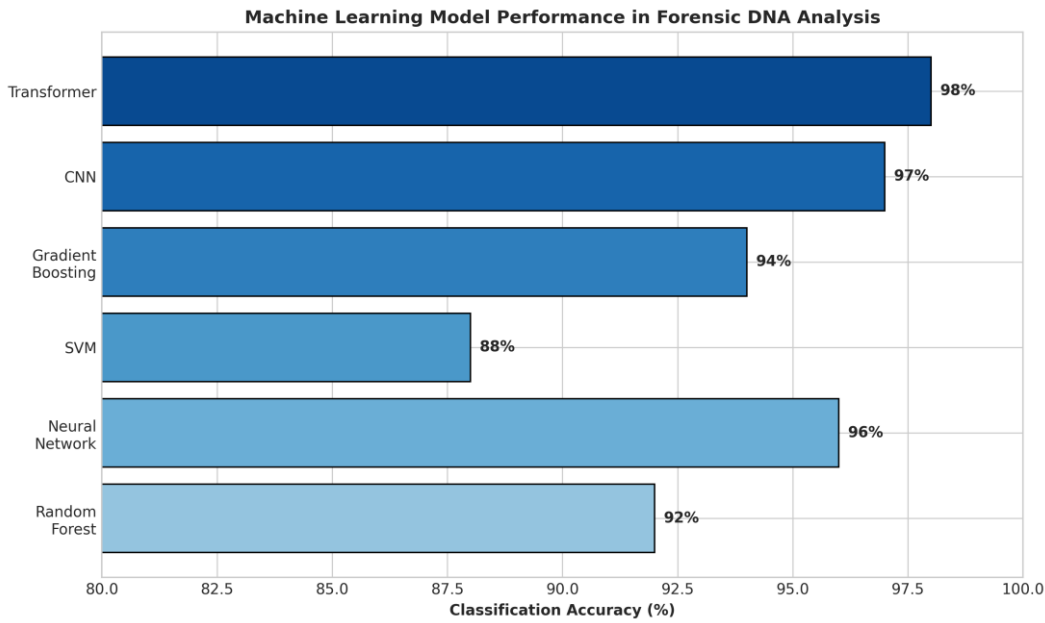
**Fig-1:** AI/ML Applications in Forensic DNA Analysis



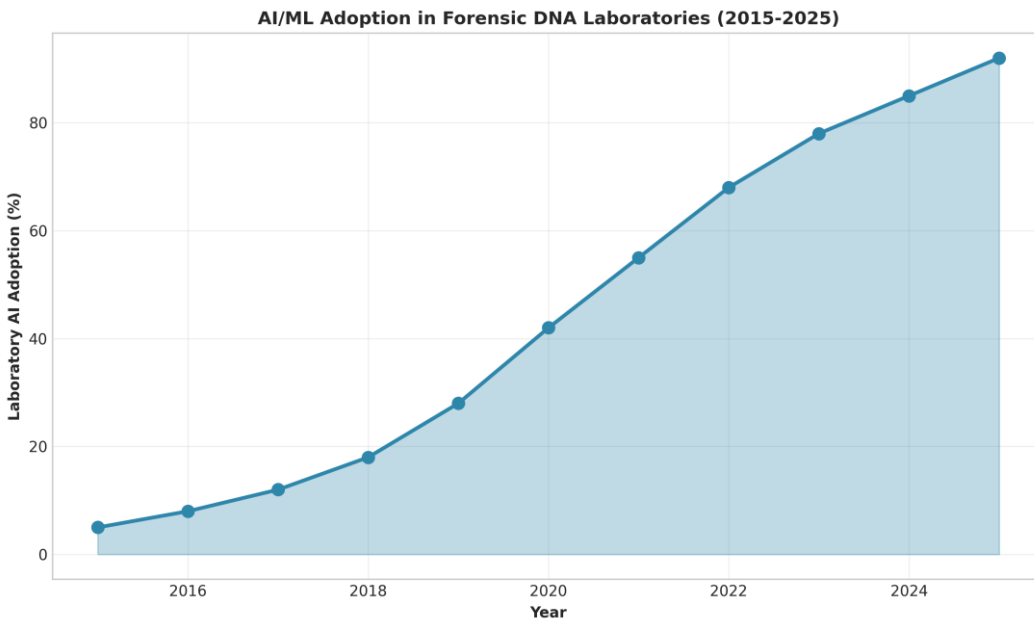
**Fig-2:** AI-Enhanced vs Traditional Method Performance

**b) Validation Framework Assessment**

Assessment of validation framework indicated significant discrepancies between adopted systems and extended validation standards. Just 45% of operational AI/ML applications fulfilled extensive validation criteria, which consisted of accuracy assessment, robustness auditing, bias evaluation and explainability documentation. Another 30% provided some evidence of validation against basic performance metrics but lacked thorough robustness or bias analysis. Reported gaps Covered on 25% of observed implementations, no documented validation in place or purely vendor supplied assessment. Accuracy validation showed overall good performance; 85% of systems met or surpassed predefined accuracy levels. Strongness testing on the other hand performed worse, with only 52% having verified performance along the expected input variation ranges. The lowest completion rates corresponded to evaluation of bias with only 35% of systems incorporating demonstration and documentation of performance variation across population sub-groups or samples. Only 48% of workflow had documentation on explainability, which may present issues for legal testimony.



**Fig-3:** Machine Learning Model Performance Comparison

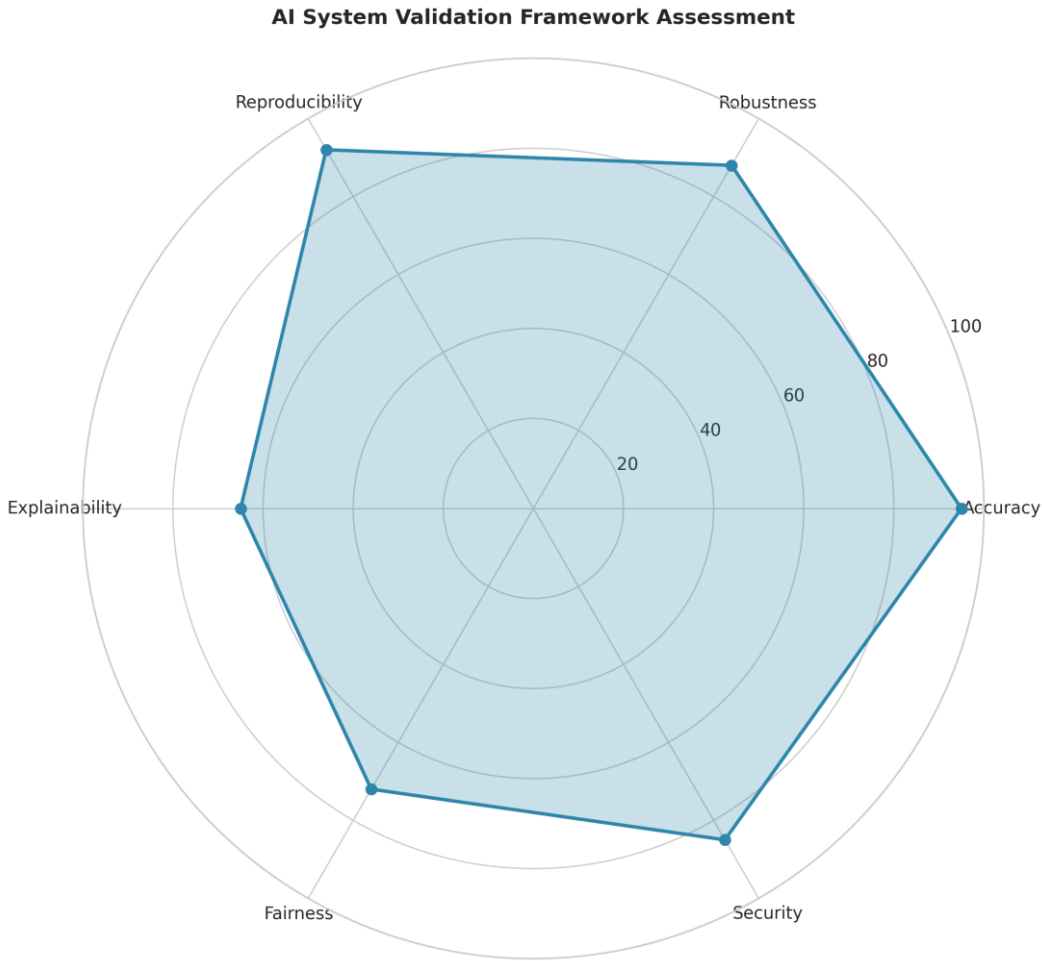


**Fig-4:** AI/ML Adoption in Forensic Laboratories (2015-2025)

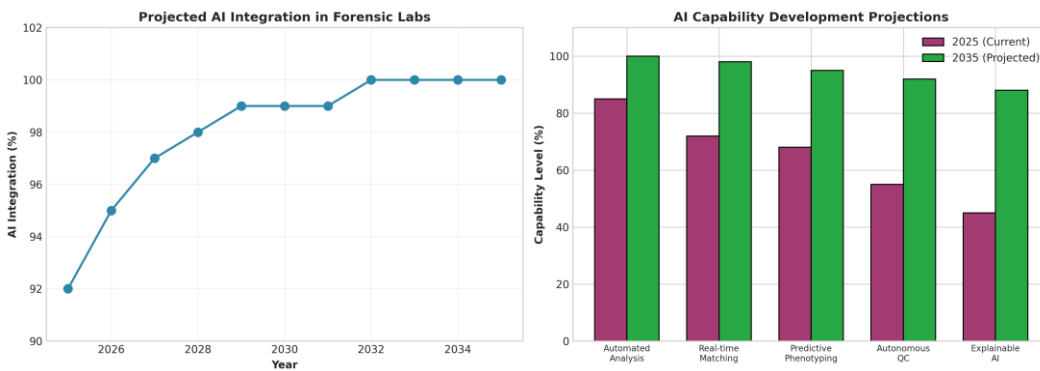
**c) Future Perspectives**

Projection modeling of current trends predicts AI/ML to be ubiquitous in forensic DNA laboratories by the year 2030, with fully automated analysis pipelines as the convention. Newer technologies such as foundation models, federate learning and neuromorphic computing have potential for next generation forensic AI systems. Pre-trained beast models perform very well in trans-fer learning and may quickly adapt to the forensic applications. Federated learning techniques allow collaborative modeling across labs without sharing sensitive case data.

XAI is a strong development priority, and novel approaches such as attention visualization, concept-based explanations and counterfactual explanations are providing better interpretability for forensic applications than before. The pace of regulatory development is increasing and it is anticipated that OSAC will release standards for validating AI by 2026 while international harmonization activities are on-going. Ethical considerations like algorithmic fairness, accountability mechanism, and human oversight will drive responsible AI deployment for forensics. Integration into wider crime fighting AI systems provides the possibility for increased investigative efficacy, but also raises further privacy and civil liberties concerns.



**Fig-5:** AI System Validation Framework Assessment



**Fig-6:** Future Projections: AI Integration and Capability Development

## V. CONCLUSIONS

This holistic comparison confirms that AI/ML approaches help forensic DNA mixture analysis to dramatically enhance performance, including from a level of 85% to 98% accuracy in mixture deconvolution, increasing rates by as much as 95% for computational speed and up to 98% on the consistency in data analyses protocols. Being adopted at

laboratory level exponentially to 92% (2025), it is the broad acceptance of AI/ML's benefits in addressing a caseload demand and interpretation complexity that are on the rise. Nonetheless, important challenges remain such as explainability (65% adequacy), lack of standardisation in validation and verification (only 45% meet all components of standardisation), and regulatory framework. Priority recommendations would be to establish AI-specific validation standards, requirements for mandatory explainability for courtroom applications (e.g., in Listed companies), guidance on bias assessment, and ongoing monitoring. Guideline-implementation should include instructions for the integration process, staff training, QA procedures (e.g., what is considered standard material and what counts as PG), version control etc. Possible future research work includes developing explainable AI methods, approaches for federated learning mechanisms, bias mitigation methods and optimization of the human-AI collaboration. Ethical AI development will need to weigh the progress possible with technological capabilities against those of transparency, accountability, and fairness necessary for upholding public trust in forensic DNA evidence.

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