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Original Research Article

Artificial intelligence-enhanced *in-vitro* fertilization outcome prediction for the Indian subpopulation: integrating pre-treatment parameters and Bayesian-optimized ensemble techniques

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ABSTRACT

Background: *In-vitro* fertilization (IVF) outcomes, particularly their socioeconomic impact, are a major concern for Indian couples. Predicting success using pre-treatment parameters can improve clinical decision-making. This study develops and validates Bayesian-optimized voting-ensemble (BoVe), a novel machine learning (ML) algorithm, to enhance predictive accuracy for live birth outcomes.
Methods: Clinical records from 2,908 IVF patients, encompassing 79 parameters-including maternal age, body mass index (BMI), Anti-Mullerian hormone (AMH) levels, number of IVF cycles, infertility type, and sperm parameters were analyzed following rigorous data preprocessing. The dataset was cleaned, transformed, and split 80:20 for training and validation. BoVe was evaluated against traditional ML models based on key performance metrics.
Results: BoVe identified AMH levels >3.5 ng/mL, BMI <23, and maternal age <35 as strong predictors of live birth in female patients. Male sperm parameters significantly influenced success rates. Compared to conventional ML models, BoVe achieved superior predictive performance with an ROC-AUC score of 0.93 and accuracy of 0.87, demonstrating robust effectiveness. Additionally, an AI-powered web application was developed for cloud-based fertility guidance, providing personalized recommendations based on patient parameters.
Conclusions: The BoVe model offers a highly accurate, population-specific approach to IVF prediction, surpassing previously published algorithms. Its integration into clinical workflows can enhance pre-treatment counseling, empower couples with data-driven reproductive insights, and improve success rates through personalized interventions.

Keywords: *In vitro* fertilization, Machine learning, Cloud application, Machine learning web application, Prediction modelling, Assisted reproductive technology

INTRODUCTION

In vitro fertilization (IVF) has changed the fertility landscape in India. It has been 45 years since the first IVF baby was born, giving people hope and forever changing the history of infertility medicine in India. With alarming infertility statistics and the increasing demand for IVF in the country, making IVF facilities more accessible and affordable becomes necessary. Using ML to predict IVF outcomes based on patient records has several advantages

since it can analyze vast amounts of complex data, identifying patterns and correlations that might be missed by traditional statistical methods.[1,2] This enables more accurate predictions of IVF success rates, helping clinicians tailor treatments to individual patients' needs.[3] Additionally, ML models can continuously learn and improve from new data, enhancing their predictive power over time.[4,5] By leveraging data-driven predictive methodologies, we can optimize IVF protocols, reduce costs, and improve patient outcomes, ultimately advancing reproductive medicine.[1,6]

Previous research focused on making models that can predict the likelihood of IVF success based on pre-treatment parameters.[7] Several pre-treatment tools based on big data have been made.[8-11] Other studies have also focused on live birth prediction after the patient had undergone their first successful IVF cycle and some studies include the significance of pre- and in-cycle characteristics in addition.[12,13] In most of these studies, various models have been developed and based on the performance of the individual models, the top performing model is reported. Most studies are usually based on the population of Europe or USA, and their performance and applicability in the countries and regions beyond these areas are largely unknown. Another major limitation of all these models is that they cannot be used for Indian sub-populations due to socio-cultural discrepancies and differences in the data distribution when compared to countries in Western countries.[14]

Moreover, national-level registry data on IVF is not available in low- and middle-income countries like India and models that are based on it are negligent or minimal.[15] It has been possible to make predictions for countries where national-level data is not available by using data from just one or a few clinics.[12,16-21] However, several studies that only looked at one center found center-specific models had notable discriminatory power.[12,16,17,21]

The study aims to develop an ML-based clinical prediction model for Indian subpopulations, addressing fertility trends and challenges in India. The primary objective of this study is to develop and evaluate a predictive algorithm to estimate the cumulative live birth probability for the first complete IVF cycle. Descriptive characteristics of patients who underwent an IVF cycle from January 2018 to October 2022 were collected from the centre for IVF, Sir Ganga Ram hospital. Pre-treatment features such as the number of IVF cycles (total count of times a patient underwent IVF procedure), type of infertility (information about the earlier pregnancies-primary infertility: no live births, no pregnancies and secondary infertility: no live births with past pregnancies or at least one previous live birth), duration of infertility (the period over which a couple attempted conception without success), AMH (Anti-Müllerian hormone level), Indication for IVF (the underlying cause of infertility), sperm type (describes the sperm type, whether normal or abnormal), BMI, maternal age (age during the current ongoing IVF cycle), total previous failures (No. of previous failed attempts at IVF) and β-hCG (hormone produced by the placenta after a successful implantation, indicating clinical pregnancy) were considered as the independent features to estimate the live birth rate. Additionally, an end-to-end web application was developed on a cloud-based platform to provide personalized assistance to users as shown (Figure 1).

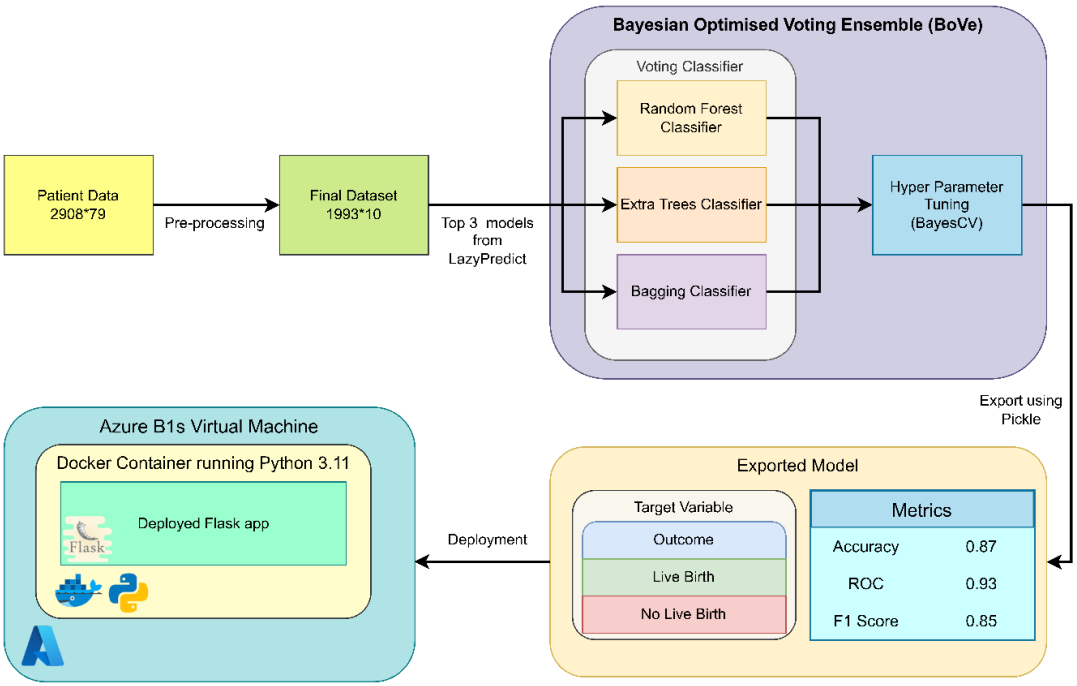

Figure 1: A representation of the overall architecture and workflow.

The objective of this study is to develop and evaluate a machine learning-based predictive model for estimating the cumulative live birth probability in the first complete IVF cycle among Indian subpopulations.

Additionally, we aim to enhance accessibility by integrating the model into a cloud-based web application for personalized user assistance.

METHODS

This is a retrospective cohort study that leverages machine learning techniques to predict the cumulative live birth probability for the first complete IVF cycle in Indian subpopulations. It utilizes patient data collected from a single medical center over a defined period to develop and evaluate the predictive model.

Data acquisition

Clinical data of patients who underwent IVF-ICSI procedures from 1st January 2018 to 31st October 2022 at Sir Ganga Ram hospital, Delhi, India, was used in this study. The original dataset had 2908 records and 79 features, including the target variable (Outcome-live birth/no live birth).

However, the interpretation of the patient's outcome in this dataset was unclear since each embryo transferred during the same cycle was considered as a separate entry. Hence, only cases where a full IVF cycle was carried out or a successful live delivery occurred were considered, which resulted in the elimination of 758 patient records from the original dataset.

Further, based on previous studies and domain expert's feedback, pre-treatment features such as number of IVF cycles, type of infertility, duration of infertility, AMH, Indication for IVF, sperm type, weight in kg, height in cm, maternal age, total previous failures and βhCG were selected for the analysis which resulted in a dataset of size 2150×12, including name and outcome (live birth/no live birth). The inclusion and exclusion criteria have been represented (Figure 2).

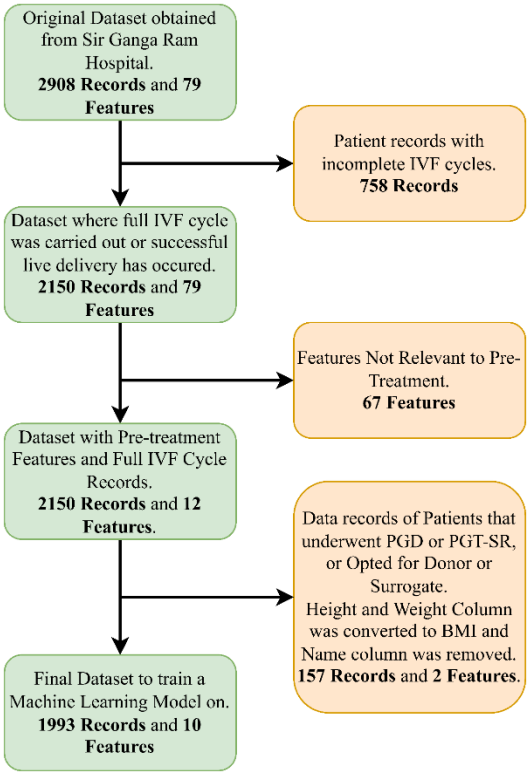

Figure 2: A diagram representing the inclusion and exclusion criteria for the final dataset.

Data pre-processing

Several preprocessing operations were carried out to ensure data quality such as label encoding and conversion of numerical data into standardized format. Additionally, BMI was derived by combining weight in kg and height in cm, resulting in producing a dataset with a size of 2150×11 that includes outcome. Remaining missing data points were imputed either with the most common category or K-nearest neighbor imputer, which considers the mean values of n nearest neighbors from training set. For imputation, 2 neighboring samples were used. Data records of patients where follow-up data unavailable/with preimplantation genetic diagnosis (PGD)/ preimplantation

genetic testing for chromosomal structural rearrangements (PGT-SR)/who opted for donor sperm or surrogacy were excluded from study since such samples could introduce noise and cause misclassification in prediction. Therefore, final dataset used for analysis and model building comprised 1993 records and 10 features, after removing name column as it does not contribute to ML training. Further, numerical features such as number of IVF cycles, duration of infertility, AMH (ng/ml), BMI, and maternal age discretized into intervals. Category wise representation of live birth and no live birth amongst the various features is represented (Figure 3).

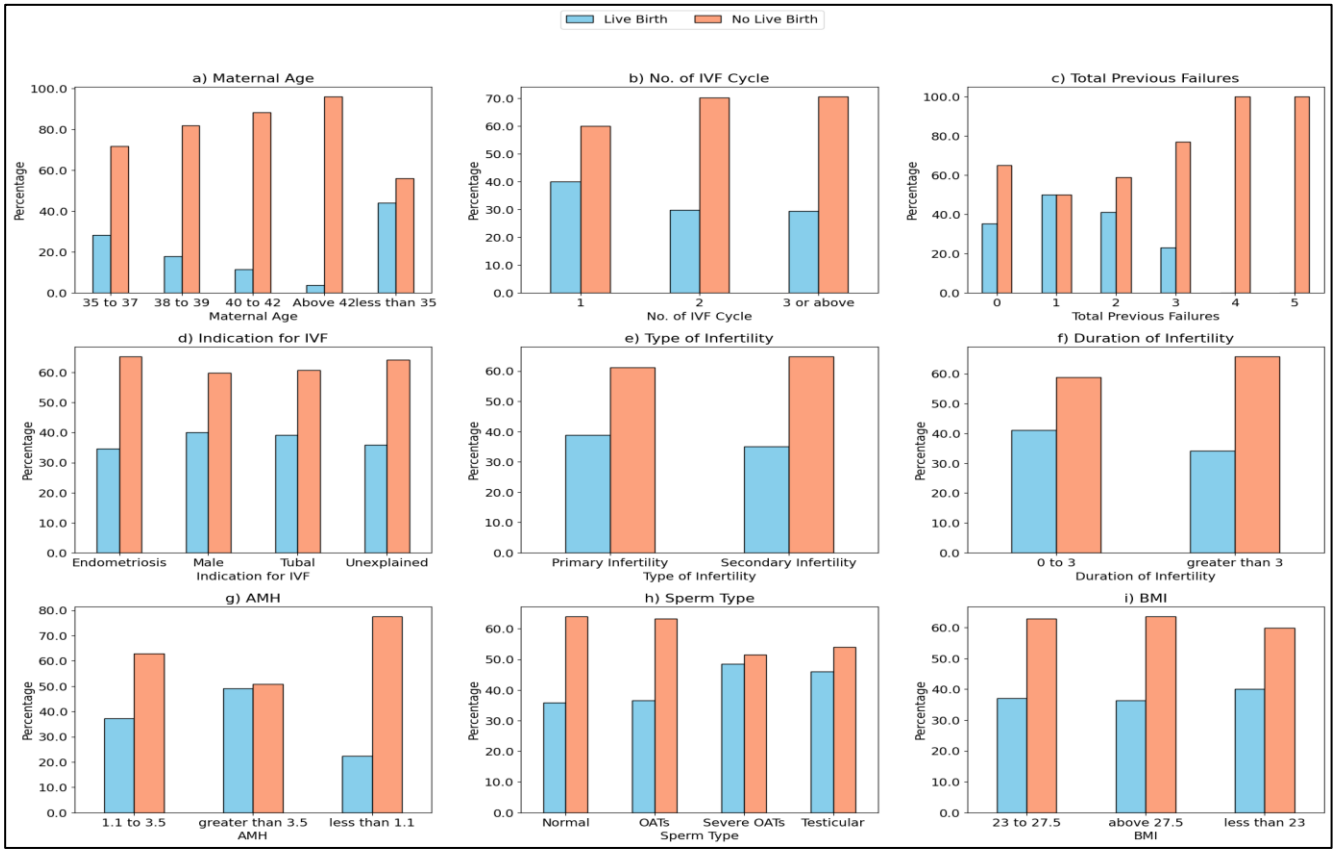

Figure 3: A category wise representation of live birth and no live birth amongst the various features.

Model training

Model optimization is an essential component of this study to best ML model performance. Additionally, fine-tuning of model parameters and hyperparameters was performed for increased precision and predictive capacity. All features were then chosen for the analysis, producing a dataset with a size of 1993×11, including Outcome. Following that, train-test splits-80:20 (Training: 1594 and testing: 399) were used to split the dataset. 80:20 split was considered because 70:30 and 60:40 split resulted in inferior metrics. A lazy classifier from the lazy predict package was applied to the dataset, which provides a streamlined interface for comparing multiple untuned machine-learning models, without having to run them.[22] These models are listed along with their metrics on the provided train-test datasets. The top seven models were selected for further testing. These models were extra trees classifier, random forest classifier, label propagation, label spreading, bagging classifier, LGBM classifier, and decision tree classifier.[23] Bayesian cross-validation (Bayesian CV) was used for hyperparameter tuning for each model.[24] The most promising hyperparameters were selected and applied for each model. The Accuracy, ROC AUC score, Precision, F1 score, and Balanced Accuracy for each model were calculated.

Bagging classifier reduces variance by averaging predictions from multiple classifiers trained on different data subsets. While its ensemble error is variance + bias + noise, this study uses it as a standalone model within a larger ensemble.

A random forest is a bagged ensemble of decision trees that also randomly selects features for each split, increasing diversity. Extra trees is a random forest variant that further improves variance by splitting training data and estimating leaf labels on separate partitions. The top three tuned models (RF, Extra trees and bagging) are combined using a soft voting classifier, which averages predicted probabilities.

This soft voting classifier is then optimized using a Bayesian cross validation technique using BayesSearchCV over a hyperparameter space (Table 1) including et__n_estimators, et__max_depth,

et__min_samples_split, et__min_samples_leaf, rf__n_estimators, rf__max_depth, rf__min_samples_split, rf__min_samples_leaf, and bc__n_estimators. This final model is called the BoVe.

Table 1: Hyperparameter space for BayesSearchCV.

Parameter name	Range	Description
et__n_estimators	(10, 1000)	Number of trees in the extra trees classifier
et__max_depth	(2, 10)	Maximum depth of each tree in the extra trees classifier
et__min_samples_split	(2, 10)	Minimum number of samples required to split an internal node in the extra trees classifier
et__min_samples_leaf	(1, 10)	Minimum number of samples required to be at a leaf node in the extra trees classifier
rf__n_estimators	(10, 1000)	Number of trees in the random forest classifier
rf__max_depth	(2, 10)	Maximum depth of each tree in the random forest classifier
rf__min_samples_split	(2, 10)	Minimum number of samples required to split an internal node in the random forest classifier
rf__min_samples_leaf	(1, 10)	Minimum number of samples required to be at a leaf node in the random forest classifier
bc__n_estimators	(10, 1000)	Represents the number of weak learners in the bagging classifier

Model deployment

A web interface was developed for the final algorithm using the flask microframework. This interface includes a homepage, a form for data input, and a results page where users can view the algorithm's predictions. The model is currently deployed on the Microsoft Azure platform, specifically on a B1s virtual machine, which is cost-effective and suitable for small applications.

To ensure smooth operation and easy management, the model is deployed in a Docker container, packaging the application and its dependencies for consistency across environments. The flask microframework handles web requests and serves the web interface. The application is accessible at the URL (artpre.sbdaresearch.in), allowing users to interact with the model through their web browsers.

RESULTS

Derivation cohort

Among a cohort of 2908 women, 1993 women who underwent IVF or ICSI were included in the analysis. The model consisted of 1594 women in the training set and 399 women in the testing set. A total of 1993 women from the Indian sub-population were used to build the final pre-treatment model. Out of the total cases, a higher value of AMH (greater than 3.5) resulted in a positive outcome for IVF, whereas with an AMH of less than 1.1, negative live birth rate was more than 75% of the cycle.

About BMI, it was observed that a BMI less than 23 had shown a 40% chance of live birth. In the case of age, 35 and less was the most likely to get a positive outcome, and as age increases the chances of a positive outcome decrease. It was also seen that in cases where the sperm type was severe oligospermia, asthenospermia and teratospermia (OATs), the chances of a positive outcome were better.

Model performance and validation

Evaluation metrics such as accuracy (the number of correctly predicted events made by the model across all predictions), precision (the instances predicted as positive were correct), sensitivity or recall (tells us what percentage of true positives was correctly identified), and F1-score (assigns weights to precision or recall based on their importance) are used to estimate the performance of the applied classifiers on the test dataset.

Table 2: Performance evaluation measures for 80:20 train-test split.

Model	Accuracy	ROC AUC	Precision	F1 score	Balanced accuracy	Recall score
Extra trees	0.86	0.92	0.77	0.83	0.87	0.89
Label propagation	0.68	0.65	0.56	0.57	0.65	0.57
Label spreading	0.68	0.65	0.56	0.57	0.65	0.57
RF	0.86	0.87	0.75	0.82	0.87	0.91
LGBM classifier	0.84	0.85	0.75	0.81	0.85	0.87
Decision tree	0.80	0.78	0.74	0.72	0.78	0.73
Bagging classifier	0.86	0.86	0.78	0.82	0.86	0.87
BoVe	0.87	0.93	0.75	0.85	0.89	0.85

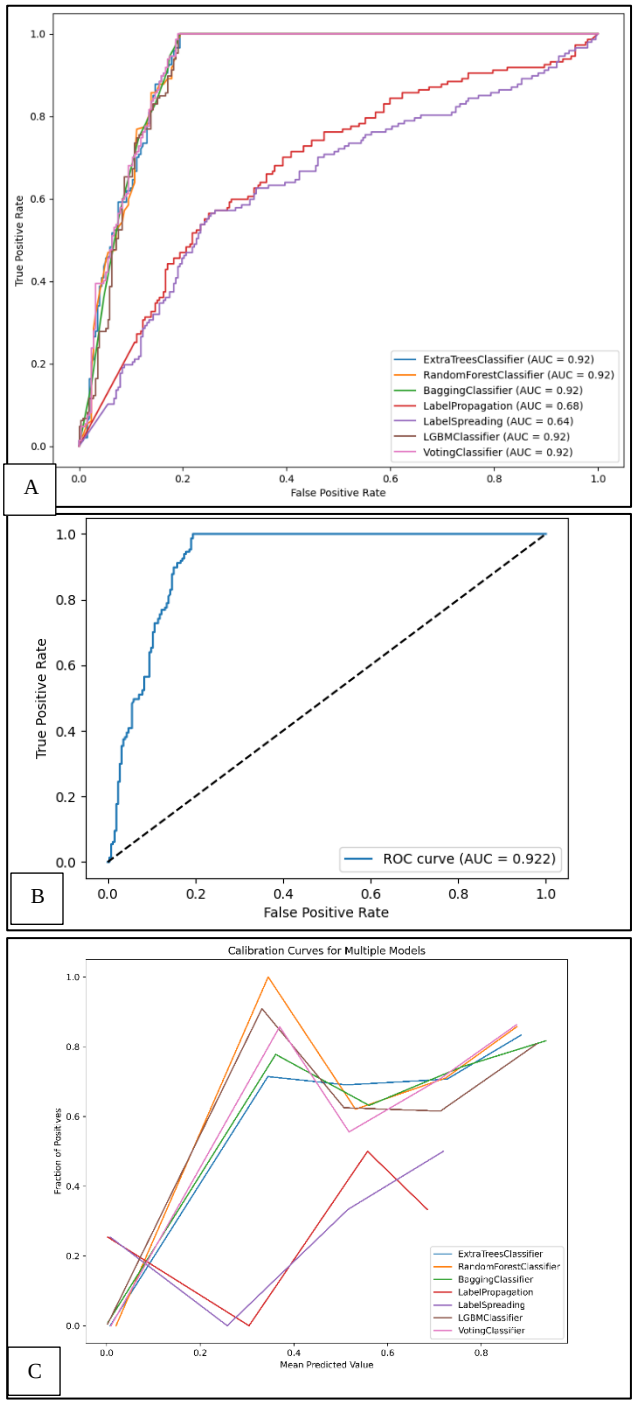

Figure 4 (A-C): AUC ROC curve for all models for 80:20 train-test split. AUC-ROC curve for BoVe for 80:20 train-test split. Calibration plot for all models for 80:20 train-test split.

The ROC-AUC score (Area under the ROC-receiver operating characteristic curve measures the model performance overall potential thresholds) and F1 score indicate that both precision and recall were given equal weights. Further, no notable improvement was seen once features were chosen (Table 2) (Figure 4).

For the 80:20 train-test split, extra trees, RF, bagging classifier, and BoVe had an accuracy of 86% or higher. Here, the ROC-AUC score greater than 0.92 was achieved by extra trees and BoVe.

DISCUSSION

Over the past decades, many IVF prediction models have been developed to evaluate individual outcomes of treatment but few of them were clinically practical due to their poor predictive ability and simple statistical methodology. We implemented all traditional algorithms and were able to engineer a niche ensemble algorithm, BoVe, which was able to give an AUC-ROC value of 0.93 to predict the live birth for the first complete IVF attempt. Our model outperformed the XGBoost model by Qiu et al which used 8 features and 7188 samples, in ROC AUC score (0.73) as well as accuracy (0.7); the values obtained for AUC and accuracy on our model was 0.93 and 0.87 respectively.[12] Results comparable to RF model by Goyal et al which used data from the UK and obtained an AUC score of 0.846 and an accuracy score of 0.7649.[25] We also compared BoVe to ART Models by Shen et al which also included treatment data.[26] First model, based on Adaboost, used data from patients with 2 embryo cycle treatments and had lower ROC-AUC and accuracy scores than BoVe i.e. 0.8129 and 0.7616. Similarly, 2 model, based on GBDT, used data from patients with 1 embryo cycle treatment and scored lower than BoVe in terms of ROC-AUC and accuracy which is 0.8066 and 0.8506 respectively. This comparison is summarized (Table 3).

In future iterations of our study, we aim to address several key limitations to enhance robustness and applicability of our ML-based clinical prediction model. Expanding our dataset beyond a single medical center will allow us to improve generalizability and ensure the model effectively represents diverse Indian subpopulations. Additionally, we plan to refine data collection methods to minimize biases associated with missing/inconsistent patient records. While our current model focuses on pre-treatment features, future enhancements will integrate embryo quality, lab techniques and clinician-related factors to create a more comprehensive predictive framework. Moreover, we will continuously refine our probabilistic estimates to capture complex, non-linear interactions that may influence IVF success. Finally, we are committed to validating and optimizing usability of our web application, ensuring accessibility and seamless adoption among both patients and healthcare providers. By addressing these challenges, we strive to further strengthen accuracy and reliability of our predictive algorithm.

Table 3: Table of comparison of model metrics of previously published papers.

Reference	Year	Model	Accuracy	ROC-AUC
ML predicts live-birth occurrence before IVF treatment (Goyal et al)	2020	Random forest	76.49%	84.60%
The application of artificial intelligence in predicting embryo transfer outcome of recurrent implantation failure (Shen et al) (Group A)	2022	AdaBoost	76.16%	81.29%
The application of artificial intelligence in predicting embryo transfer outcome of recurrent implantation failure (Shen et al) (Group B)	2022	GBDT	85.06%	80.66%
AI-enhanced IVF outcome prediction for the Indian subpopulation: integrating pre-treatment parameters and Bayesian-optimized ensemble techniques (Sengupta et al)	2025	BoVe	87.00%	93%
Personalized prediction of live birth prior to the first IVF treatment: a ML method (Qiu et al)	2019	XGBoost	70%±0.3%	73%

CONCLUSION

In the current study, we developed a pre-treatment model using Indian sub-population data. Our niche architecture, BoVe, tailored to Indian patient data descriptors, achieved an accuracy of 0.93, surpassing previous generalized models. AI in reproductive health can significantly impact and reduce the socio-economic burden on infertile couples undergoing IVF-ICSI treatment. To the best of our knowledge, this is the first predictive system based on the Indian population using pre-treatment parameters to estimate live birth rates. Additionally, we have incorporated a hybrid Bayesian architecture alongside commonly used ML algorithms, which proved to be the most efficient model. However, current limitation is that research was conducted using data from single healthcare center. Therefore, presently, we are cautious about model's reproducibility across India, given that there are hundreds of IVF centers with vastly different findings. To tackle this issue and enhance the model's generalization capability, we will need to take a more multicentric strategy. Additionally, due to dataset's limitations, we were unable to account for family genetic history and lifestyle variables such as smoking, alcohol, etc.

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