Journal of Systemics, Cybernetics and Informatics (2025) 23(6), 20-26
https://doi.org/10.54808/JSCI.23.06.20

Assessing SVM and Logistic Regression Models for Live Birth Prediction in IVF: A Barbadian Case Study

Steven CUMBERBATCH
Department of Computer Science, Mathematics and Physics, The University of the West Indies
Cave Hill, St. Michael, Barbados
(steven.cumberbatch@mycavehill.uwi.edu)

Adrian ALS
Department of Computer Science, Mathematics and Physics, The University of the West Indies
Cave Hill, St. Michael, Barbados
(adrian.als@uwi.edu)

Peter CHAMI
Department of Computer Science, Mathematics and Physics, The University of the West Indies
Cave Hill, St. Michael, Barbados
(peter.chami@uwi.edu)

Juliet SKINNER
Barbados Fertility Center, Seaston House,
Hastings, Christ Church,

ABSTRACT

The success rates of in vitro fertilization (IVF) have significantly improved over recent decades due to advancements in both clinical practice and biomedical technologies. Clinicians rely on the analysis of large volumes of patient data to inform treatment decisions. Aggregated longitudinal data from multiple patients may reveal latent patterns that can further enhance IVF outcomes. In this study, three machine learning models — Linear Kernel SVM, RBF-Kernel SVM and Logistic Regression — were developed and implemented to predict live-births from IVF clinical and demographic data, and their performances were compared. Results show that the linear SVM achieved the highest global discrimination (ROC-AUC = 0.72) and the strongest cross-validated F1-score (0.56). Logistic regression followed closely in global discrimination (ROC-AUC = 0.69), but its cross-validation recall for the minority class was notably low (0.26). The RBF SVM demonstrated a higher recall for the minority class compared to the linear SVM (0.45 vs 0.36), yet its overall discriminative performance was weaker, as reflected by a lower ROC-AUC of 0.63. This research serves as an initial exploration of machine learning applications in IVF within developing countries in the Eastern Caribbean, such as Barbados. The findings may contribute to improved clinical decision-making, reduced treatment cycles, and lower healthcare costs in resource-constrained settings.

Keywords: In Vitro Fertilization (IVF), Machine Learning (ML), Live Birth Prediction, Support Vector Machine (SVM), Logistic Regression (LR), Caribbean.

1. INTRODUCTION

In vitro fertilization (IVF) is an example of an assistive reproductive technology where oocytes (female eggs) are retrieved from the ovaries and fertilized with sperm in a laboratory setting. The resulting embryo is then transferred to the woman's uterus to establish pregnancy. The initial IVF success in 1978 relied on overcoming the challenges associated with ovulation induction, timing of laparoscopy, ovarian stimulation, cycle monitoring, oocyte culture, sperm preparation and capacitation, insemination procedures and culturing for embryo cleavage [1-3]. Since these pioneering days, the increase in fertility success rates can be attributed to both clinical and technological improvements [4]. Fertility specialists supported by experienced teams of nurses, counsellors and scientists now have a much greater assortment of tools and methods at their disposal to improve outcomes. These means produce a plethora of multidimensional variable data that is rich in latent information. The experience of clinicians is invaluable when monitoring key fertility variables to determine the best opportunities to conduct activities such as, harvesting oocytes, selecting the best embryos and optimal transfer schedules for implantation. However, the sheer scope of data variables collected across multiple patients and cycles over many years makes spotting trends difficult. In such cases, leveraging machine learning (ML) can prove useful.

Machine learning is a sub-field of artificial intelligence (AI) that enables computer systems to learn from and make decisions based on data without having to be explicitly programmed. This branch of computational algorithms effectively emulates human intelligence and has been successfully employed in diverse fields ranging from pattern recognition and computer vision to data mining, image processing and biomedical applications [5, 6]. The strengths of ML algorithms extend beyond speed and automation, to "their ability to analyze diverse data types (e.g. demographic data, laboratory findings, imaging data, and doctors' free-text notes)" and incorporate them into accurate predictive outcomes [7]. They excel at uncovering correlations, clusters or anomalies that are not obvious to humans. However, in cases of high dimensionality, such as with IVF data, the feature space grows exponentially making data points sparse. This results in greater difficulty with pattern detection and an increased risk of overfitting due to memorization. Fortunately,

accuracy can remain high with model regularization or intelligent data reduction.

The pairing between the benefits of ML and the large dimensionality of IVF data makes provision for the optimal use of rich latent information therein. There is potential to lower IFV treatment costs, increase success rates and thereby reduce the stresses that may be associated with failed attempts. The literature is filled with examples where ML is employed in IVF research with promising results.

ML algorithms such as Support Vector Machines (SVM), Gradient Boosting (GB), Extreme Gradient Boosting (XGB) and Random Forest (RF) were examined by Abbas et al. in [8] to determine their ability to predict IVF clinical pregnancy outcomes when trained with a combination of Doppler and clinical parameters. Results showed that the best results were obtained when the GB was used in conjunction with RF for feature selection. The accuracy, sensitivity and specificity of the model were recorded as 0.823, 100% and 66%, respectively. ML algorithms have found application across the wider spectrum of IVF. Sujata et al investigated the use of ML techniques to improve the success rate of the IVF procedure [9]. Instead of relying on assessing embryo quality using visual morphological methods, a convolutional neural network (CNN) was trained on over 3000 images to assist with embryo selection to improve the implantation rate. The authors report a precision of >0.98 and an embryo selection success rate of more than 85%. Other researchers have also demonstrated the utility of machine learning in optimizing various stages of the IVF process. Khosravi et al. developed a deep learning–based system that evaluates time-lapse images to predict embryo viability with greater accuracy than traditional morphological assessments [10]. Liu et al. constructed machine learning–based live birth prediction models for first IVF cycles, achieving robust performance by integrating demographic, hormonal, and stimulation protocol data [11]. Goyal et al. applied multiple ML classifiers to forecast live-birth occurrence prior to embryo transfer, reporting significant gains over baseline logistic regression [12]. More recently, Borji et al. proposed an integrated optimization and transformer-based pipeline that combines feature selection with self-attention mechanisms, improving predictive AUC for live birth outcomes on held-out patient cohorts [13].

The relationship between anxiety and depression after failed IVF cycles is reported in the literature [14, 15]. These conditions are not aided by the financial pressures due to high treatment costs. As such, patient budgets may dictate that treatment be sought at smaller clinics that offer high valued services at competitive prices. Patients may then seek treatment at reputable clinics in developing countries such as Barbados. The incorporation of ML in these environments may provide low-cost solutions that improve IVF success outcomes leading to higher patient satisfaction, and greater competitive footing on the international market. The objective of this work therefore is to investigate the use of a ML algorithm on demographic and clinical IVF data as a predictor for live births.

2. METHODOLOGY

he research flow diagram shown in Figure 1 includes the raw dataset, feature extraction, pre-processing, the machine learning model, and performance evaluation. The raw clinical and demographic data, provided by the Barbados Fertility Centre comprised of 213 anonymized IVF cycle records. After preliminary data cleaning, which involved removing records with missing or invalid target outcomes, the final dataset used for modeling consisted of 190 cases. Guided by an experienced clinician seven clinical and demographic features were selected: Female Age at Cycle, AMH Levels (ng/ml), Antral Follicle Count (AFC), Number of MII Eggs after retrieval, BMI, Failed IVF Attempts, and Successful IVF Attempts. During the pre-processing stage any missing values in these features were imputed using the median strategy, and feature scaling was applied using ***StandardScaler*** to normalize the input values ensuring the selected features are on a comparable numeric footing. The cleaned dataset was then split into training and testing sets using an 80/20 stratified split, reserving 38 records for validation testing. Additionally, 10-fold stratified cross-validation was applied to the full dataset to assess generalization performance.

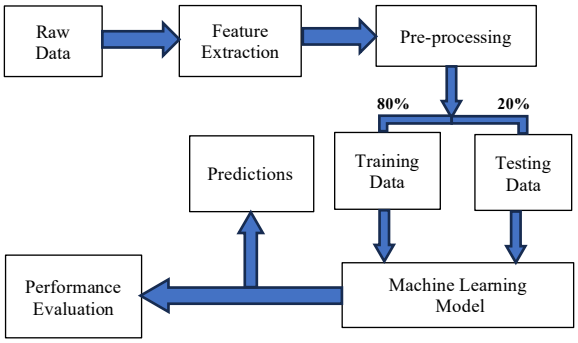

Figure 1 Machine Learning Model Block Diagram

Due to class imbalance in the target variable (live birth), the use of stratified sampling ensured that each fold preserved the same proportion of outcome classes. In this process, the dataset was divided into ten subsets, and the model was trained on nine while tested on the tenth, repeating the process ten times. This ensured that each record was used for both training and validation, while maintaining class distribution in each fold. Performance metrics were then averaged across all folds to provide a robust estimate of the model's predictive power. Specifically, performance was evaluated using accuracy, precision, recall, and F1-score metrics along with ROC-AUC and precision-recall curves. Probability estimates from the ***predict_proba()*** method were also used to provide a comparative outlook. Finally, linear model coefficients were extracted to identify key predictive features, and future iterations will explore model interpretability using ***SHAP (SHapley Additive exPlanations)*** values.

3. MACHINE LEARNING MODELS

The SVM Model

The Support Vector Machine (SVM) classification model has widespread application and has demonstrated effectiveness in numerous biomedical studies. Specifically, they underpin gene-expression–based cancer classification pipelines, enabling high-dimensional-omic discrimination with excellent accuracy [16, 17]. Khyathi et al. [18] demonstrated their applicability to large public-health datasets, highlighting SVM efficacy for disease diagnosis from routine clinical parameters. In medical imaging, an optimized SVM achieved state-of-the-art performance for CT-based lung-tumor detection and segmentation [19]. Guido et al. [20] provides a comprehensive review of recent SVM

advancements and medical deployments, underscoring the algorithm's versatility and strong generalization—qualities that make it a dependable choice for health-related predictive modeling tasks where interpretability remains paramount. Other strengths include [21]:

- Good performance in high-dimensional spaces.
- Works well with small datasets as they only require a small number of support vectors to define the decision boundary.
- Robust to noise in the data, as the decision boundary is determined by the support vectors, which are the closest data points to the boundary.
- Support regularization to avoid overfitting

The Linear-Kernel SVM (soft margin): This model aims to find the optimal hyperplane that maximally separates data points of different classes in linearly separable feature space. For a binary classification problem, given a training set (x_i, y_i), where $x_i \in \mathbb{R}^n$ and $x_i \in \{-1, +1\}$, the objective of the linear SVM is to solve the following optimization problem defined in Eq. (1).

$$\min_{\boldsymbol{w},b,\xi} \frac{1}{2}\|\boldsymbol{w}\|^2 + C\sum \xi_i$$
$$\text{subject } to\ y_i(\boldsymbol{w}^T\boldsymbol{x}_i + b) \geq 1 - \xi_i, \xi_i \geq 0, \forall i \quad (1)$$

Where:
- $\boldsymbol{w}$ is the weight vector perpendicular to the separating hyperplane,
- b is the bias term,
- ξ_i are slack variables that allow for soft-margin classification (permitting some misclassifications),
- $C > 0$ is the regularization parameter that controls the trade-off between maximizing the margin and minimizing classification error.

Eq (2) defines the decision function learned by the SVM [22].

$$f(x) = \text{sign}\,(\boldsymbol{w} \cdot \boldsymbol{x}_i + b) \quad (2)$$

RBF-Kernel SVM (soft margin): This model leverages the same core optimization framework as the linear SVM. However, it applies the kernel trick to allow the model to learn non-linear decision boundaries by implicitly mapping the input data to a higher dimension space. Similar to the SVM model, the non-linear SVM seeks to solve the following optimization problem defined in Eq. (3).

$$\min_{\boldsymbol{w},b,\xi} \frac{1}{2}\|\boldsymbol{w}\|^2 + C\sum \xi_i$$
$$\text{subject } to\ y_i(\boldsymbol{w}^T\phi(\boldsymbol{x}_i) + b) \geq 1 - \xi_i, \xi_i \geq 0, \forall i \quad (3)$$

Where $\phi(\boldsymbol{x}_i)$ is the function responsible for mapping of input features into the higher-dimensional space.

Eq. (3), which uses the kernel trick, defines the radial basis function (RBF) kernel employed in this work.

$$K(x, x') = \langle\phi(x), \phi(x')\rangle = e^{-\gamma\|x-x'\|^2} \quad (4)$$

Where $\gamma > 0$ is the gamma hyperparameter that controls the shape of the decision boundary and the flexibility of the model as it pertains to overfitting or underfitting of the data.

Only the data points that lie closest to the decision boundary — the support vectors — influence the final model. This makes SVM particularly well-suited to small, high-dimensional datasets like those encountered in medical and biomedical applications. When class imbalance or overlapping data exists, as is often the case in IVF datasets, SVM's margin-based formulation with soft constraints helps to maintain generalization.

Logistic Regression Model

The logistic regression model is a binary classification model that commonly features in IVF studies to predict various success outcomes such as fertility, clinical pregnancy and live-births [23-26]. Its strengths, particularly in biomedical and clinical contexts, include simplicity, interpretability and computational efficiency, even on large datasets, without the need for extensive hyperparameter tuning, as with SVMs. It models log-odds of the class label as a linear combination of the input features. The logistic (sigmoid) function, as defined in Eq. (5), ensures that the linear combination is mapped to the range (0,1).

$$P(y = 1 \mid x) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x_1 + \cdots + \beta_n x_n)}} \quad (5)$$

Here y, x and β, represent the target (outcome) variable, the input features and model coefficients (weights), respectively.

4. RESULTS

This section summarizes the performance of three class-balanced models—linear SVM, RBF SVM, and class-weighted logistic regression—trained with SMOTE oversampling and evaluated via 10-fold stratified cross-validation (CV) and an independent 20 % hold-out set.

Linear-Kernel SVM

Class weighting plus SMOTE raised minority-class sensitivity. The CV metrics and hold-out results for the Linear SVM are presented in Table 1 and Table 2, respectively.

Table 1 Ten-fold CV metrics – Linear SVM.

Metric	Mean ± SD
Accuracy	0.655 ± 0.078
Precision (live-birth)	0.471 ± 0.105
Recall (live-birth)	0.713 ± 0.138
F1-score (live-birth)	0.556 ± 0.075

Table 2 Hold-out classification – Linear SVM.

Class	Precision	Recall	F1-score	Support
No live-birth	0.76	0.85	0.80	26
Live birth	0.50	0.36	0.42	11
Overall accuracy			0.70	37

The associated ROC and precision-recall curves are shown in Figure 2 and Figure 3, respectively.

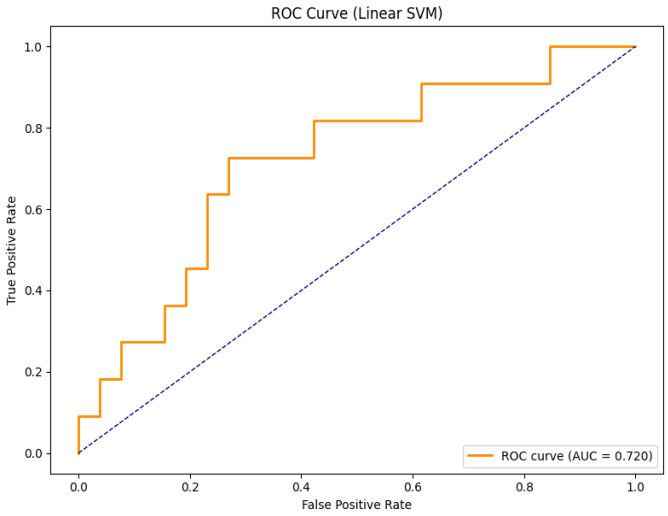

Figure 2 ROC curve (AUC = 0.72) for the linear SVM.

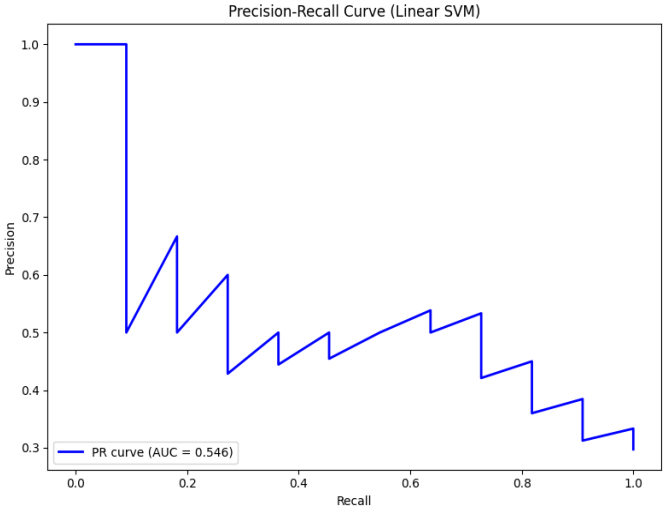

Figure 3 Precision–Recall curve (AUC = 0.55) for the linear SVM.

The model identifies 71 % of live-birth cases in CV and 36 % on the unseen test set, with precision 0.50—a balanced trade-off for this imbalanced dataset.

RBF-Kernel SVM

The results of the RBF SVM ($C = 10$, $\gamma = 0.1$) are summarized below. Table 3 and Table 4 list the CV metrics and hold-out results for the RBF SVM, respectively. Figure 4 shows the ROC curves for this model and Figure 5 shows associated precision-recall curves.

Table 3 Ten-fold CV metrics – RBF SVM.

Metric	Mean ± SD
Accuracy	0.583 ± 0.106
Precision (live-birth)	0.374 ± 0.137
Recall (live-birth)	0.480 ± 0.163
F1-score (live-birth)	0.410 ± 0.122

Table 4 Hold-out classification – RBF SVM.

Class	Precision	Recall	F1-score	Support
No live-birth	0.78	0.81	0.79	26
Live birth	0.50	0.45	0.48	11
Overall accuracy			0.70	37

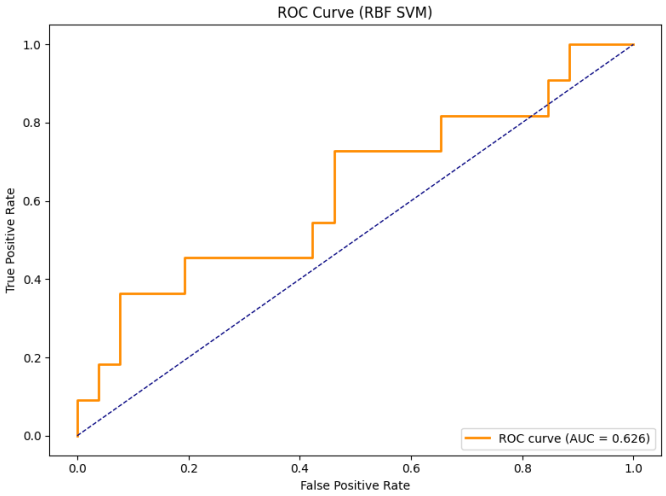

Figure 4 ROC curve (AUC = 0.63) – RBF SVM.

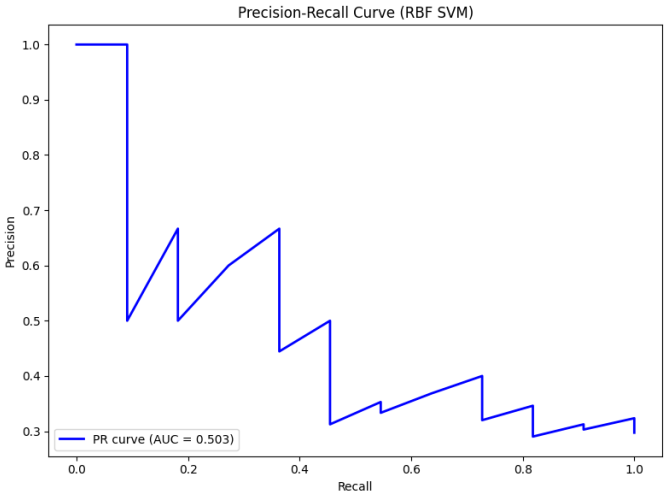

Figure 5 Precision–Recall curve (AUC = 0.50) – RBF SVM.

The RBF kernel yields slightly higher hold-out recall (0.45) than the linear model, but lower ROC-AUC (0.63), indicating limited benefit from added non-linearity.

Logistic Regression (Class-Weighted)

Results for the class-weighted logistic regression baseline follow are as follows. Table 5 and Table 6 list the CV metrics and hold-out results for the RBF SVM, respectively. Figure 6 shows the ROC curves for this model and Figure 7 shows associated precision-recall curves.

Table 5 Ten-fold CV metrics – Logistic Regression.

Metric	Mean ± SD
Accuracy	0.660 ± 0.091
Precision (live-birth)	0.464 ± 0.125
Recall (live-birth)	0.640 ± 0.192
F1-score (live-birth)	0.529 ± 0.122

Table 6 Hold-out classification – Logistic Regression.

Class	Precision	Recall	F1-score	Support
No live-birth	0.73	0.85	0.79	26
Live birth	0.43	0.27	0.33	11
Overall accuracy			0.68	37

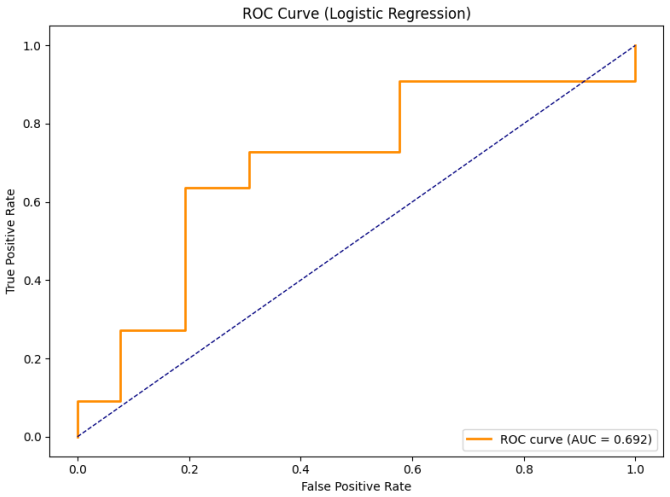

Figure 6 ROC curve (AUC = 0.69) – Logistic Regression.

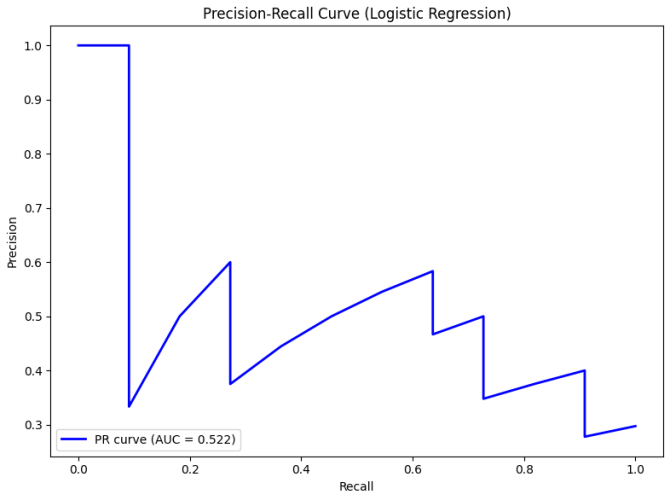

Figure 7 Precision–Recall curve (AUC = 0.52) – Logistic Regression.

Logistic regression delivers ROC-AUC 0.69—close to the linear SVM—yet lower minority-class recall on the hold-out set (0.27)

5. DISCUSSION

The linear SVM produced the highest global discrimination (ROC-AUC = 0.72) and the strongest cross-validated F1-score (0.56) for the live-birth class, confirming that a margin-based linear decision surface can capture most of the signal embedded in the seven demographic and clinical predictors. However, hold-out recall (0.36) indicates that more than half of positive cycles were incorrectly classified. Introducing a radial-basis-function kernel improved hold-out recall to 0.45, the best among the three models—while maintaining identical precision (0.50). However, the trade-off was a lower ROC-AUC (0.63) and a wider variance across folds, reflecting increased model flexibility and heightened overfit risk in a small dataset. Finally, the class-weighted logistic model offered interpretability and a respectable ROC-AUC (0.69) but retrieved only 27 % of live-birth cases on the test set, underscoring its limitation when minority-class sensitivity is critical.

The Clinical Perspective

In IVF practice the greater harm stems from false-negative predictions—dismissing an embryo or cycle that might have resulted in a live birth. Consequently, recall is the chief clinical metric, provided precision remains reasonable so as not to trigger unnecessary transfers or raise unrealistic expectations.

It is important to note that many IVF units already rely heavily on embryo-quality grading, particularly at the blastocyst (day-5) stage, as a primary determinant of which embryo to transfer. Future modelling work should therefore integrate morphological or morphokinetic scores alongside the demographic and clinical variables used here.

In routine clinical practice, a day-5 blastocyst has already cleared an implicit biological filter: only embryos capable of progressing beyond cleavage stage survive to blastocyst culture. Clinicians are often left with very few embryos, sometimes only one, so a model that predicts "low likelihood of live birth" cannot override the clinical imperative to transfer whatever is available. The real value of an ML predictor lies in two complementary areas: (i) patient counselling, by quantifying individualized odds so couples can prepare emotionally and financially for additional cycles; and (ii) embryo prioritization when several blastocysts exist, enabling transfer of the most promising embryo first and potentially shortening time-to-pregnancy while reducing cumulative cost.

Even marginal improvements in selection accuracy can spare patients the anxiety of unsuccessful transfers and the two-week wait, provided the model's false-negative rate is kept extremely low to avoid discarding potentially viable embryos. Thus, while negative predictions must be applied cautiously, especially in single-embryo scenarios, robust, well-calibrated ML tools can still deliver tangible clinical benefit by informing counselling, optimizing transfer sequence, and guiding resource allocation.

Limitations

Repeated cycles for the same woman were treated as independent observations. This could potentially introduce bias. The data set was taken from a single-center cohort and was constrained to 190 effective cycles. The small size of the dataset poses challenges

related to overfitting which could lead to poor generalization on unseen data. The models also exhibit high variance and are sensitive to small changes in the training data. Furthermore, external validity remains untested, therefore limiting wider application.

Additionally, the class imbalance between live-births and no live-births increased the difficulty in creating reliable validation and test splits without sacrificing training data. These limitations were addressed by comparing across simpler models (e.g. logistic and linear models) and applying regularization to avoid overfitting. Cross-validation was also undertaken for more stable performance estimates. Scaling this work will require validation on larger, multi-center cohorts. The present models were trained with minimal hyper-parameter tuning and no domain-specific feature engineering which is likely to yield further gains but was beyond the scope of this proof-of-concept.

Although our proof-of-concept, derived from Barbados Fertility Centre records, demonstrates feasibility, external datasets are needed to confirm generalizability across populations and treatment protocols. Longitudinal variables—such as embryo morphokinetic scores, stimulation regimens, and lifestyle factors—should be incorporated to build richer, more predictive models.

6. CONCLUSION & FUTURE WORK

Three machine learning models were developed and implemented to predict live-births from IVF clinical and demographic data, and their performances were compared. The linear SVM achieved the highest global discrimination (ROC-AUC = 0.72) and the strongest cross-validated F1-score (0.56). Although the RBG SVM achieved slightly higher cross-validated recall (0.45 vs 0.36), its lower ROC-AUC (0.63) suggests that the non-linear kernel did not improve classification performance. The Logistic Regression model showed similar global discrimination performance to the linear SVM (ROC-AUC = 0.69) was determined to be very similar to the liner SVM model, but its recall for the minority class was notably low at 0.26.

In the future the restricted feature set should be expanded to consider key embryo-quality metrics (morphology, morphokinetics) and hormonal trajectories should be incorporated to potentially improve performance. Additionally, tree-based ensemble models such as Random Forest and XGBoost which are naturally less sensitive to irrelevant features should be considered given that these models often excel on tabular healthcare data. Their built-in feature-selection mechanisms and robustness to mixed data types make them attractive alternatives or complements to margin-based methods. Systematic hyper-parameter tuning—via grid or Bayesian search—remains essential across all model families to balance complexity against overfitting.

Any improvements in ML-based decision-support tools can greatly benefit clinics in developing countries like Barbados by providing a low-cost way to improve IVF outcomes where advanced lab infrastructure or specialized expertise may be limited. Leveraging routinely collected demographic and clinical data, such systems can augment local clinicians' decision-making, standardize embryo selection, and optimize treatment protocols. Democratizing predictive analytics in this way holds promise for narrowing global disparities in reproductive healthcare and improving patient satisfaction and success rates in resource constrained environments.

7. REFERENCES

[1] J. D. Biggers, "IVF and embryo transfer: historical origin and development," *Reproductive BioMedicine Online,* vol. 25, pp. 118-127, 2012.

[2] M. H. Johnson, "A short history of in vitro fertilization (IVF)," *International Journal of Developmental Biology,* vol. 63, pp. 83-92, 2019.

[3] P. C. Steptoe and R. G. Edwards, "Birth after the reimplantation of a human embryo," *The Lancet,* vol. 312, p. 366, 1978.

[4] J. Wang and M. V. Sauer, "In vitro fertilization (IVF): a review of 3 decades of clinical innovation and technological advancement," *Therapeutics and clinical risk management,* vol. 2, pp. 355-364, 2006.

[5] I. El Naqa and M. J. Murphy, "What is machine learning?," in *Machine learning in radiation oncology: theory and applications*, ed: Springer, 2015, pp. 3-11.

[6] B. Mahesh, "Machine learning algorithms-a review," *International Journal of Science and Research (IJSR).[Internet],* vol. 9, pp. 381-386, 2020.

[7] K. Y. Ngiam and W. Khor, "Big data and machine learning algorithms for health-care delivery," *The Lancet Oncology,* vol. 20, pp. e262-e273, 2019.

[8] Z. Abbas, S. Ménigot, J. Charara, Z. Ibrahim, C. Fakih, and J.-M. Girault, "Predicting In-Vitro Fertilization Outcome from Ultrasound Measurements Using Machine Learning Techniques," in *2023 Seventh International Conference on Advances in Biomedical Engineering (ICABME)*, 2023, pp. 190-194.

[9] P. N. Sujata, S. Madiwalar, and V. Aparanji, "Machine learning techniques to improve the success rate in in-vitro fertilization (IVF) procedure," in *IOP Conference Series: Materials Science and Engineering*, 2020, p. 012039.

[10] P. Khosravi, E. Kazemi, Q. Zhan, J. E. Malmsten, M. Toschi, P. Zisimopoulos*, et al.*, "Deep learning enables robust assessment and selection of human blastocysts after in vitro fertilization," *NPJ digital medicine,* vol. 2, p. 21, 2019.

[11] X. Liu, Z. Chen, and Y. Ji, "Construction of the machine learning-based live birth prediction models for the first in vitro fertilization pregnant women," *BMC Pregnancy and Childbirth,* vol. 23, p. 476, 2023.

[12] A. Goyal, M. Kuchana, and K. P. R. Ayyagari, "Machine learning predicts live-birth occurrence before in-vitro fertilization treatment," *Scientific reports,* vol. 10, p. 20925, 2020.

[13] A. Borji, H. Haick, B. Pohn, A. Graf, J. Zakall, S. Islam*, et al.*, "An Integrated Optimization and Deep Learning Pipeline for Predicting Live Birth Success in IVF Using Feature Optimization and Transformer-Based Models," *arXiv preprint arXiv:2412.19696,* 2024.

[14] S. Maroufizadeh, E. Karimi, S. Vesali, and R. O. Samani, "Anxiety and depression after failure of assisted reproductive treatment among patients experiencing infertility," *International Journal of Gynecology & Obstetrics,* vol. 130, pp. 253-256, 2015.

[15] C. R. Newton, M. T. Hearn, and A. A. Yuzpe, "Psychological assessment and follow-up after in vitro

fertilization: assessing the impact of failure," *Fertility and sterility,* vol. 54, pp. 879-886, 1990.

[16] S. Huang, N. Cai, P. P. Pacheco, S. Narrandes, Y. Wang, and W. Xu, "Applications of support vector machine (SVM) learning in cancer genomics," *Cancer genomics & proteomics,* vol. 15, pp. 41-51, 2018.

[17] G. George and V. C. Raj, "Review on feature selection techniques and the impact of SVM for cancer classification using gene expression profile," *arXiv preprint arXiv:1109.1062,* 2011.

[18] G. Khyathi, K. Indumathi, A. Jumana Hasin, M. Lisa Flavin Jency, G. Krishnaprakash, and F. J. M. LISA, "Support Vector Machines: A Literature Review on Their Application in Analyzing Mass Data for Public Health," *Cureus,* vol. 17, 2025.

[19] M. O. Oyediran, O. S. Ojo, I. A. Raji, A. E. Adeniyi, and O. J. Aroba, "An optimized support vector machine for lung cancer classification system," *Frontiers in Oncology,* vol. 14, p. 1408199, 2024.

[20] R. Guido, S. Ferrisi, D. Lofaro, and D. Conforti, "An overview on the advancements of support vector machine models in healthcare applications: a review," *Information,* vol. 15, p. 235, 2024.

[21] n.d. (2023, 19). *Support vector machine in Machine Learning*. Available: https://www.geeksforgeeks.org/support-vector-machine-in-machine-learning/

[22] C. Cortes and V. Vapnik, "Support-vector networks," *Machine learning,* vol. 20, pp. 273-297, 1995.

[23] J. R. Trimarchi, J. Goodside, L. Passmore, T. Silberstein, L. Hamel, and L. Gonzalez, "Comparing data mining and logistic regression for predicting IVF outcome," Fertility and Sterility, vol. 80, p. 100, 2003.

[24] Q. Cai, F. Wan, R. Huang, and H. Zhang, "Factors predicting the cumulative outcome of IVF/ICSI treatment: a multivariable analysis of 2450 patients," Human reproduction, vol. 26, pp. 2532-2540, 2011.

[25] W. Shi, S. Zhang, W. Zhao, X. Xia, M. Wang, H. Wang, et al., "Factors related to clinical pregnancy after vitrified–warmed embryo transfer: a retrospective and multivariate logistic regression analysis of 2313 transfer cycles," Human Reproduction, vol. 28, pp. 1768-1775, 2013.

[26] A. Abdala, E. Kalafat, I. Elkhatib, A. Bayram, L. Melado, H. Fatemi, et al., "Predictive model for live birth outcomes in single euploid frozen embryo transfers: a comparative analysis of logistic regression and machine learning approaches," Journal of Assisted Reproduction and Genetics, pp. 1-10, 2025.