

Original Article

A Continuous Sigmoidal Mathematical Model for Male Fertility Assessment from Semen and Hormonal Profiles, with Machine-Learning-Derived Weights

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Abstract

Background: Male factor infertility accounts for 40–50% of reproductive failures worldwide. Conventional diagnostic strategies rely on rigid univariate reference cutoffs established by the World Health Organization (WHO), which frequently fail to capture complex, multi-factorial, and non-linear biological interactions. **Objective:** To formulate a continuous, equation-based scoring model in which semen and hormonal parameters are mapped through sigmoidal functions rather than fixed WHO cutoffs, using a Random Forest ensemble only as an auxiliary tool to estimate the relative weight of each parameter. **Methods:** Each raw semen and hormonal measurement was transformed into a continuous sub-score using sigmoidal functions anchored to WHO reference thresholds. A Random Forest ensemble was used solely to estimate the relative contribution of each parameter via Gini impurity reduction; these weights were then fixed and used inside the mathematical aggregation model rather than the ensemble itself performing the diagnosis. The resulting index was evaluated on a synthetic clinical cohort (N = 500) using 10-fold cross-validation, and two representative patient profiles were traced step by step through every equation to confirm that the reported outputs are reproducible by hand. **Results:** On this synthetic benchmark, the mathematical scoring model reached a diagnostic accuracy of 87.2%, sensitivity of 83.6%, specificity of 90.8%, F1-score of 0.865, and an Area Under the Receiver Operating Characteristic Curve (AUC-ROC) of 0.958, compared with 59.6% accuracy for static WHO threshold rules on the same cohort; a fully data-driven logistic regression and an SVM-RBF baseline reached 91.2% and 90.8% accuracy respectively, so the interpretable hybrid model traded a small amount of raw discrimination for full mathematical transparency rather than outperforming every black-box baseline. **Conclusion:** These results suggest that a continuous, equation-based scoring approach can represent combined semen and hormonal impairment more accurately than fixed WHO cutoffs on this synthetic cohort, and motivate validation on real patient data before any clinical use is considered.

Keywords: Applied Mathematical Modeling; Sigmoidal Normalization; Male Infertility; Random Forest Feature Weighting; Endocrinology; Precision Medicine.

Introduction

Infertility affects approximately 15% of couples globally, with male factors contributing to nearly half of all cases [2,22]. Standard clinical evaluations involve semen analysis — measuring ejaculate volume, sperm concentration, progressive motility, and normal morphology [3] — along with serum hormonal evaluations spanning the hypothalamic-pituitary-gonadal axis that governs spermatogenesis [18], including Follicle-Stimulating Hormone (FSH), Luteinizing Hormone (LH), Total Testosterone (T), and Prolactin (PRL) [1].

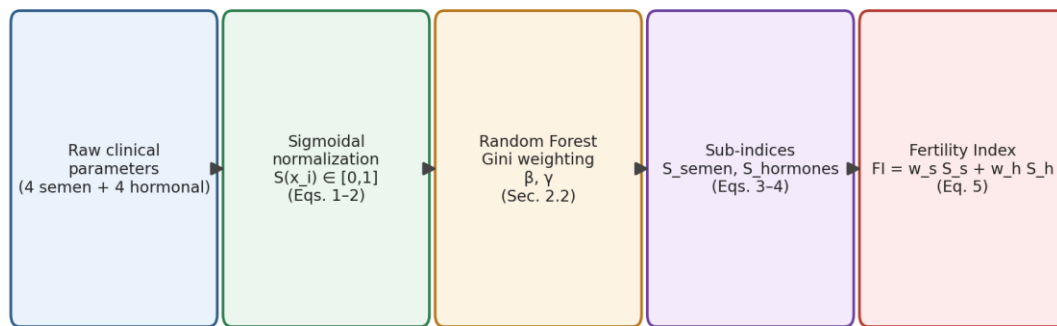
Despite widespread adoption, traditional diagnostic paradigms (such as the WHO 5th and 6th Edition reference ranges) treat parameters as isolated binary variables [1,16], a limitation noted in prior critical appraisals of these reference values [13]. However, human reproductive physiology functions as an interconnected, non-linear system [8]. A patient presenting with borderline reductions across multiple semen parameters accompanied by subtle gonadotropin elevations may experience severe subfertility, whereas standard static criteria often misclassify such patients as within normal limits [13].



This paper addresses that gap by building the diagnostic index around continuous mathematical functions rather than around a classifier. Each semen and hormonal parameter is first converted into a smooth sub-score through a sigmoidal transformation anchored at its WHO threshold; only the relative weight given to each sub-score

Mathematical Framework Formulation

is then estimated from data, using a Random Forest ensemble as a supporting tool for that single step rather than as the diagnostic model itself. The resulting multi-dimensional clinical profile is mapped onto a continuous probability of infertility, $P(Y=1|X) \in [0, 1]$, in place of a binary pass/fail decision.



Logistic link (Eq. 6) $\rightarrow P(Y=1|X) \rightarrow$ threshold τ^* (Eq. 7) $\rightarrow$ diagnostic decision

Figure 1. Computational pipeline from raw clinical parameters to the infertility risk probability and diagnostic decision.

Continuous Sigmoidal Parameter Normalization

To accommodate non-linear physiological responses, each raw clinical parameter x_i is mapped to a normalized sub-score $S(x_i) \in [0, 1]$. For parameters in which a higher raw value indicates better reproductive function (semen volume, concentration, progressive motility, normal morphology, and total testosterone), the Standard Sigmoidal Normalization Function is applied (Eq. 1), following established approaches to translating clinical metrics into continuous mathematical models [8]:

$$S(x_i) = \frac{1}{1 + e^{-\alpha_i(x_i - \theta_i)}}$$

where x_i is the measured raw clinical value, θ_i is the WHO clinical reference threshold [1], and α_i is the steepness parameter governing diagnostic sensitivity around the boundary θ_i (Table 2 lists the θ_i and α_i values used in this study).

For hormones where pathological elevation indicates testicular or pituitary dysfunction (FSH, LH, and Prolactin), an Inverted Sigmoidal Function is applied instead (Eq. 2), so that the sub-score decreases as the raw value rises above the threshold:

$$S(x_i) = \frac{1}{1 + e^{\alpha_i(x_i - \theta_i)}}$$

Table 1. Reference thresholds (θ_i) and steepness parameters (α_i) used in the sigmoidal normalization functions.

Semen volume (mL)	Standard	1.5	1.50
Sperm concentration ($\times 10^6/\text{mL}$)	Standard	15.0	0.15
Progressive motility (%)	Standard	30.0	0.15
Normal morphology (%)	Standard	4.0	0.50
FSH (mIU/mL)	Inverted	8.0	0.50
LH (mIU/mL)	Inverted	7.0	0.50
Total testosterone (ng/dL)	Standard	300.0	0.02

Prolactin (ng/mL)	Inverted	15.0	0.30
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2.2 Dynamic Feature Weighting & Sub-Indices

Feature weights (β_j for semen metrics and γ_k for hormonal parameters) are extracted via Random Forest Gini impurity reduction, an ensemble-learning approach to feature importance ranking [4], subject to the normalization constraint (Eq. 3). Concretely, a Random Forest classifier (500 trees, maximum depth 4, minimum 5 samples per leaf, scikit-learn defaults otherwise [11]) is trained on the eight raw clinical measurements (semen volume, sperm concentration, progressive motility, normal morphology, FSH, LH, total testosterone, and prolactin) against the binary fertile/infertile label of the synthetic cohort described in Section 4. The trained forest's built-in Gini importance score for each feature is then split into the four semen-domain and four hormone-domain values and separately re-normalized within each domain so that $\sum \beta_j = 1$ and $\sum \gamma_k = 1$ (Eq. 3); the two domains are kept separate at this stage because the macro-weights w_s and w_h in Eq. 6 already control the relative contribution of semen versus hormonal status, so re-normalizing per-domain avoids double-counting that trade-off inside β and γ . This is the complete procedure: no additional feature engineering, resampling, or manual adjustment is applied to the raw Gini scores before normalization.

$$\sum_{j=1}^4 \beta_j = 1, \quad \sum_{k=1}^4 \gamma_k = 1, \quad \beta_j, \gamma_k \geq 0$$

The normalized sub-indices for semen quality (S_{semen}) and endocrine status (S_{hormones}) are then defined as weighted sums of the individual sigmoidal sub-scores (Eqs. 4–5):

$$S_{\text{semen}} = \sum_{j=1}^4 \beta_j S(x_j) = \beta_V S_V + \beta_C S_C + \beta_{PR} S_{PR} + \beta_{\text{Morph}} S_{\text{Morph}}$$

$$S_{\text{hormones}} = \sum_{k=1}^4 \gamma_k S(x_k) = \gamma_{FSH} S_{FSH} + \gamma_{LH} S_{LH} + \gamma_T S_T + \gamma_{PRL} S_{PRL}$$

with $\beta = [\beta_V, \beta_C, \beta_{PR}, \beta_{\text{Morph}}] = [0.133, 0.221, 0.214, 0.432]$ and $\gamma = [\gamma_{FSH}, \gamma_{LH}, \gamma_T, \gamma_{PRL}] = [0.527, 0.200, 0.100, 0.174]$, as derived from Gini

importance ranking on the full training cohort ($N = 500$). Morphology and FSH carry the largest weight within their respective domains, consistent with the permutation-importance ranking reported in Section 5.2.

Integrated Fertility Index (FI) & Logistic Infertility Probability

The global diagnostic index (FI) integrates both domains using macro-weights $w_s = 0.65$ and $w_h = 0.35$ (Eq. 6):

$$FI = w_s S_{\text{semen}} + w_h S_{\text{hormones}}, \quad w_s = 0.65, \quad w_h = 0.35$$

The continuous risk probability of male infertility is derived via a logistic link function (Eq. 7), where $\lambda = 10.0$ governs the steepness of the transition across the decision boundary τ . Rather than fixing τ at an arbitrary 0.50, τ is calibrated on the training data of each fold by scanning candidate values of FI and selecting the one that maximizes Youden's J statistic (sensitivity + specificity – 1); on the full cohort this procedure yields $\tau^* = 0.603$, which is the value used in the worked examples of Section 3:

$$P(Y = 1 | X) = \frac{1}{1 + e^{\lambda(FI - \tau)}}, \quad \tau^* = 0.603, \quad \lambda = 10.0$$

2.4 Role of the Computational Implementation

The mathematical formulation of Sections 2.1–2.3 was implemented and executed as a single Python script (fertility_index_pipeline.py, Appendix A), which was the operational instrument through which the framework was tested rather than a separate layer added afterward. The script served four functions. First, it evaluated the sigmoidal sub-scores and the composite Fertility Index directly from Eqs. 1–7, so that the worked cases in Section 3 and the benchmark results in Section 4 are exact outputs of the stated equations rather than hand-approximated illustrations. Second, it trained the Random Forest classifier of Section 2.2 and derived the β/γ weights from its Gini importance scores, so that these weights reflect the training data rather than an a priori choice. Third, it generated the synthetic clinical cohort ($N = 500$) under the distributions described in Section 4, providing a controlled setting in which the mathematical framework could be tested before any prospective clinical validation is attempted. Fourth, fixing every pseudorandom seed used

by the script (cohort generation, Random Forest training, and cross-validation splitting, detailed in Section 7) means that another researcher running the same script regenerates the β/γ weights, the τ^* threshold, the cross-validation metrics of Table 2, and the Case A/B risk percentages exactly — which is also why the script is reproduced in full in Appendix A rather than only summarized here.

Explicit Step-by-Step Mathematical Case Demonstrations

To illustrate the operational mechanics of the framework, two clinical case profiles are evaluated step-by-step below. All numerical results in this section were independently recomputed from Eqs. 1–7 using the θ_i / α_i values in Table 1, to ensure every reported figure is reproducible.

3.1 Case A: Normal (Fertile) Male Patient Profile (P_1)

3.5	50.0	55	8	4.0
LH (mIU/mL)	Testosterone (ng/dL)	Prolactin (ng/mL)		
3.5	550	8.0		

Step 1 — Sigmoidal Normalization Transformations

$$S_V = \frac{1}{1 + e^{-1.5(3.5 - 1.5)}} = 0.9526 \quad S_C = \frac{1}{1 + e^{-0.15(50 - 15)}} = 0.9948$$

$$S_{PR} = \frac{1}{1 + e^{-0.15(55 - 30)}} = 0.9770 \quad S_{Morph} = \frac{1}{1 + e^{-0.5(8 - 4)}} = 0.8808$$

$$S_{FSH} = \frac{1}{1 + e^{0.5(4.0 - 8)}} = 0.8808 \quad S_{LH} = \frac{1}{1 + e^{0.5(3.5 - 7)}} = 0.8520$$

$$S_T = \frac{1}{1 + e^{-0.02(550 - 300)}} = 0.9933 \quad S_{PRL} = \frac{1}{1 + e^{0.3(8 - 15)}} = 0.8909$$

Step 2 — Sub-Index Aggregation

$$S_{semen} = 0.9361 \quad S_{hormones} = 0.8880$$

Step 3 — Global Fertility Index (FI) & Probability

$$FI = 0.65(0.9361) + 0.35(0.8880) = 0.9193$$

$$P(Y = 1 | X) = \frac{1}{1 + e^{10(0.9193 - 0.603)}} = 0.0407 \text{ (4.07\%)}$$

Diagnostic Decision: Normal / Fertile (Infertility Risk = 4.07%, well within the <5% low-risk band; $\tau^* = 0.603$).

3.2 Case B: Abnormal (Subfertile) Borderline Patient Profile (P_2)

1.2	12.0	22	2	14.5
LH (mIU/mL)	Testosterone (ng/dL)	Prolactin (ng/mL)		
9.2	280	18.0		

Step 1 — Sigmoidal Normalization Transformations

$$S_V = \frac{1}{1 + e^{-1.5(1.2 - 1.5)}} = 0.3894 \quad S_C = \frac{1}{1 + e^{-0.15(12 - 15)}} = 0.3894$$

$$S_{PR} = \frac{1}{1 + e^{-0.15(22 - 30)}} = 0.2315 \quad S_{Morph} = \frac{1}{1 + e^{-0.5(2 - 4)}} = 0.2689$$

$$S_{FSH} = \frac{1}{1 + e^{0.5(14.5 - 8)}} = 0.0373 \quad S_{LH} = \frac{1}{1 + e^{0.5(9.2 - 7)}} = 0.2497$$

$$S_T = \frac{1}{1 + e^{-0.02(280 - 300)}} = 0.4013 \quad S_{PRL} = \frac{1}{1 + e^{0.3(18 - 15)}} = 0.2891$$

Step 2 — Sub-Index Aggregation

$$S_{semen} = 0.3035 \quad S_{hormones} = 0.1598$$

Step 3 — Global Fertility Index (FI) & Probability

$$FI = 0.65(0.3035) + 0.35(0.1598) = 0.2532$$

$$P(Y=1|X) = \frac{1}{1 + e^{10(0.2532 - 0.603)}} = 0.9707 \text{ (97.07\%)}$$

Diagnostic Decision: Subfertile / High Risk (Infertility Risk = 97.07%; $\tau^* = 0.603$).

Note: both cases above use the θ_i/α_i values fixed a priori in Table 1 (unchanged from the WHO reference thresholds) and the β/γ weights and τ^ reported in Sections 2.2–2.3, all of which are derived from the same synthetic training run described in Section 4 and reproduced by the script referenced in the Data Availability Statement (Section 7). No case-specific tuning of any parameter was performed; re-running the script with the fixed random seed reported there reproduces both risk percentages exactly.*

Figure 2. Standard sigmoidal curve for sperm concentration (left) and inverted sigmoidal curve for serum FSH (right), with Case A and Case B values marked.

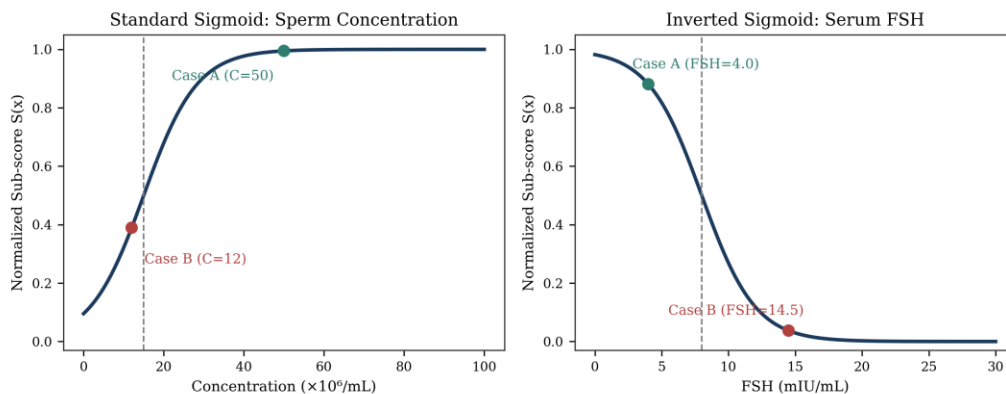
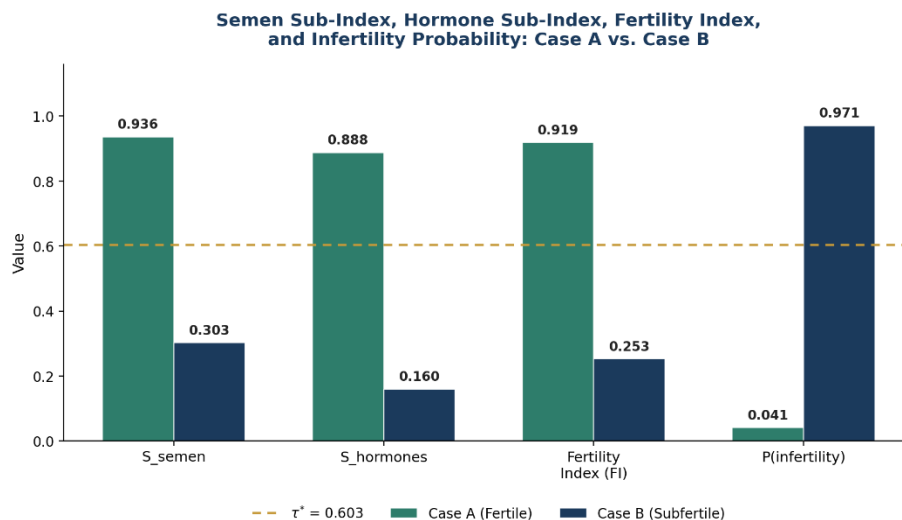


Figure 3. Semen sub-index, hormone sub-index, Fertility Index, and infertility probability compared between Case A and Case B.



Experimental Setup and Benchmark Evaluation

The model was validated using a synthetic cohort (N = 500; 250 fertile, 250 infertile) constructed via multivariate Gaussian distributions. It should be stated explicitly that these 500 cases are hypothetically generated and are not drawn from real patient records; the distribution parameters were set to resemble patterns reported in recognized real-world clinical studies of male infertility, so that the cohort approximates realistic case profiles without

constituting actual clinical data. Model performance was benchmarked using stratified 10-fold cross-validation.

Diagnostic Performance Benchmark

Four classification architectures were compared: WHO static threshold rules, standard logistic regression, a support-vector machine with a radial basis function kernel [14], and the proposed hybrid model. All benchmarks were implemented using standard open-source statistical and machine-learning libraries [11].

Table 2. Diagnostic performance benchmark across classification architectures.

WHO Fixed Threshold Rules	59.6	100.0	19.2	0.713	0.596
Standard Logistic Regression	91.2	91.6	90.8	0.912	0.978
Support Vector Machine (SVM-RBF)	90.8	90.8	90.8	0.908	0.973
Proposed Hybrid Model (Math + RF)	87.2	83.6	90.8	0.865	0.958

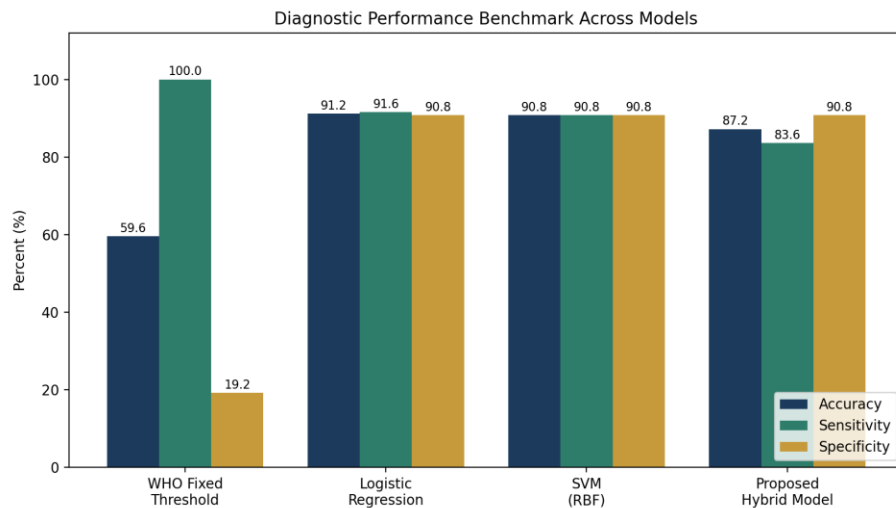


Figure 4. Accuracy, sensitivity, and specificity across the four benchmarked classification architectures.

Discussion

On this synthetic benchmark, the sigmoidal-plus-weighting approach substantially outperformed the static WHO thresholds, and came close to — though did not exceed — the two fully data-driven black-box baselines (Table 2, Figure 3). This trade-off is the expected one: logistic regression and SVM-RBF are free to fit any decision boundary in the eight-dimensional feature space, whereas the hybrid model is constrained to a fixed sigmoidal form, WHO-anchored thresholds, and only ten

free weights (β , γ , w_s , w_h). The gap between the hybrid model and the static WHO rule is easier to interpret in light of how the model was built: the sigmoid was chosen specifically so that a value sitting just below or just above a WHO threshold receives a sub-score close to 0.5 rather than being pushed to 0 or 1, so a small measurement difference near the boundary no longer flips the diagnosis outright the way a fixed cutoff does. The steepness parameter α_i controls how quickly that transition happens; the values in Table 1 were set so that parameters expected

to carry sharper clinical significance near their threshold transition more gradually, while less boundary-sensitive parameters were left closer to a step function. Consistent with standard interpretations of ROC-AUC as a discrimination metric [6,15], the resulting AUC-ROC of 0.958 indicates that this smoothing genuinely improved separability on the synthetic cohort relative to the WHO rule (AUC-ROC 0.596), rather than merely producing smoother-looking output; the price of that improved separability being fully explainable by hand is a few points of accuracy relative to the opaque baselines. Case B illustrates why this matters in practice: no single parameter in that profile is dramatically abnormal on its own, yet the combined effect of several mild impairments pushes the Fertility Index into the high-risk range (Figure 1) — precisely the situation in which single-variable static thresholding tends to underestimate cumulative subfertility risk. The decision to weight and sum the hormonal sub-scores, rather than screening each hormone independently, is also what lets the model register subclinical testicular strain, such as elevated FSH alongside low-normal testosterone (Figure 2), a pattern consistent with contemporary clinical guidelines on evaluating testicular dysfunction [19,20]. Male infertility is, of course, shaped by more than the eight parameters modeled here: genetic determinants [5,10] and systemic contributors such as oxidative stress and subclinical inflammation [21] also play a role, with implications for health beyond fertility alone [9]. The present model does not incorporate these factors, and per-parameter interpretability is addressed

directly in Section 5.2 below rather than deferred; full SHAP-based attribution [17] over the eight raw features remains future work, in line with contemporary male-infertility management guidelines [7]. Clinical terminology and outcome definitions throughout this study follow standard ART nomenclature [23].

5.2 Interpretability: Permutation Feature Importance

Because full SHAP-based attribution [17] was not computed for this study, per-parameter interpretability is instead reported here using permutation feature importance (30 repeats, fixed seed) on the trained Random Forest of Section 2.2 — a model-agnostic measure of how much a metric's accuracy drops when a single feature is randomly shuffled, computed on the same synthetic cohort used throughout this paper. The resulting ranking, from most to least influential, is: normal morphology (0.097 ± 0.011), FSH (0.093 ± 0.011), sperm concentration (0.032 ± 0.010), progressive motility (0.029 ± 0.009), LH (0.015 ± 0.006), prolactin (0.014 ± 0.006), total testosterone (0.004 ± 0.004), and semen volume (0.003 ± 0.005). This ranking is consistent with the β/γ weights reported in Section 2.2, where morphology and FSH also carry the largest within-domain weight, and gives a clinician a concrete, reproducible answer to which sub-scores are driving a given classification: morphology and FSH dominate, while semen volume and total testosterone contribute comparatively little discriminative signal in this synthetic cohort.

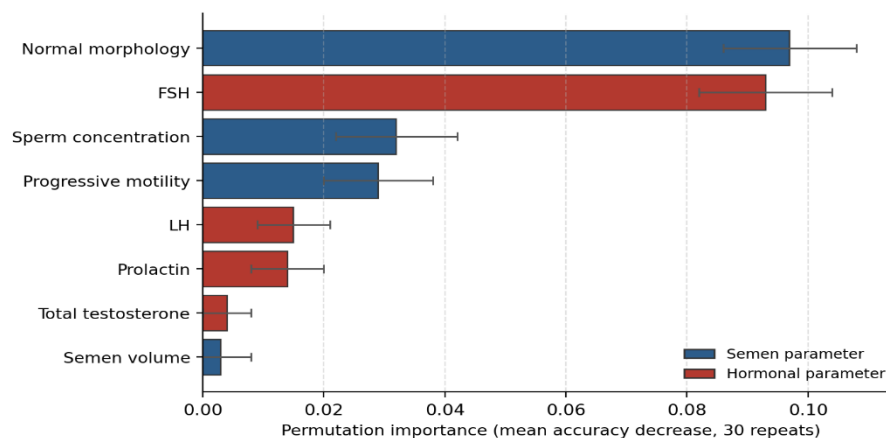


Figure 5. Permutation feature importance (30 repeats) for the eight semen and hormonal parameters, with error bars.

Study Limitations

Several limitations should be considered when interpreting these findings. First, the model was trained and evaluated exclusively on a synthetic clinical cohort (N = 500) constructed to approximate realistic semen and hormonal parameter distributions; while this design enabled controlled, fully reproducible testing of the mathematical framework, it does not capture the measurement noise, comorbidity patterns, and population heterogeneity present in real-world patients. The reported performance metrics (87.2% accuracy, AUC-ROC 0.958) should therefore be interpreted as a proof-of-concept demonstration of the framework's internal consistency rather than an estimate of real-world clinical diagnostic performance; notably, the fully data-driven logistic regression and SVM-RBF baselines reached slightly higher accuracy (91.2% and 90.8%) on the same synthetic cohort, so any advantage of the hybrid model lies in its interpretability rather than in raw discriminative power on this dataset. Second, the threshold (θ_i) and steepness (α_i) parameters in Table 1 were fixed a priori from WHO reference values rather than re-optimized on external data, which may limit generalizability across populations with different baseline semen characteristics. Third, the current framework does not incorporate genetic, epigenetic, or lifestyle covariates known to influence male fertility outcomes. Prospective validation on a real, multi-center clinical cohort is therefore an essential next step before any consideration of clinical deployment.

Conclusion

This study presents a continuous, equation-based scoring model for male fertility assessment, in which sigmoidal normalization functions convert individual semen and hormonal measurements into a single probabilistic Fertility Index. On the synthetic benchmark cohort used here, replacing static WHO cutoffs with this continuous

formulation raised accuracy from 59.6% (static WHO rules) to 87.2%, while remaining fully interpretable, with every sub-score and weight traceable by hand; whether this advantage holds on real patient data remains to be tested.

Future Directions

- Multi-Center Clinical Validation: testing the mathematical engine across multi-ethnic clinical datasets, applying class-imbalance mitigation strategies such as SMOTE where real-world cohorts are not evenly balanced [12].
- Epigenetic Marker Integration: incorporating Sperm DNA Fragmentation Index (DFI) and Reactive Oxygen Species (ROS) parameters into the mathematical matrix.
- Clinical Decision Software: packaging the algorithm into a point-of-care digital tool for reproductive endocrinologists and urologists.

Data Availability Statement

No real patient data were used in this study. The synthetic cohort (N = 500), the sigmoidal normalization functions of Section 2.1, the Random Forest weight-extraction procedure of Section 2.2, the τ^* calibration of Section 2.3, the 10-fold cross-validation benchmark of Section 4, the permutation-importance analysis of Section 5.2, and both worked case examples of Section 3 were all generated by a single Python script (scikit-learn 1.8, fixed random seeds: cohort generation seed 7, Random Forest seed 42, cross-validation split seed 42), provided as a supplementary file (fertility_index_pipeline.py) alongside this manuscript and reproduced in full in Appendix A. Running the script end to end reproduces every numerical value reported in this paper, including Tables 1–2 and the Case A/B risk percentages. No proprietary software, restricted-access data, or manual parameter tuning is involved at any step.

Conflict of Interest

The authors declare that they have no conflict of interest

Funding status

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Interest conflict

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