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Research Article

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Machine Learning-Based Classification and Symptom Forecasting Across the Menopausal Transition Using Longitudinal Self-Reported Data

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ABSTRACT

Background: Menopause is a universal and natural biologically driven life transition that is highly heterogeneous in terms of symptom variability, its manifestation timing and extent of severity. Scalable and deployable models that utilize self-reported data to predict menopausal stage and short-term occurrence of symptoms could potentially enable earlier medical intervention and personalized treatment.

Objective: In this study we have utilized publicly available data from the Study of Women's Health Across the Nation (SWAN); created and validated a scalable machine learning pipeline that does the following: (a) predicts menopausal stage (pre, peri, post) from self-reportable longitudinal variables and (b) generates probabilistic short-term symptom forecasts for hot flashes and mood changes based on self-reported last menstrual period (LMP) timing.

Methods: Rule-based feature selection (regular expression heuristics) was used to extract self-report variables from the SWAN dataset. Thirty-eight interpretable features were selected for this study that are self-reportable covering demographics, lifestyle, menstrual timing, vasomotor symptoms, mood symptoms, pain and general health indicators. Median imputation and one-hot encoding were implemented in reusable scikit-learn pipelines. Numerical features were standardized as needed. Two classifiers were used: Multinomial Logistic Regression and Random Forest (200 trees). These were trained on a stratified 80/20 split of the dataset and a five-fold cross validation was performed. Symptom forecasting is conducted via a rule-based Symptom CycleForecaster model that calculates cycle day from LMP and returns symptom probabilities.

Keywords: Biology, Machine Learning, Menopausal Transition, Women's Health Analytics, Health Informatics

Introduction

Menopause is a very common life transition but it is also one of the most inadequately addressed phases of women's health worldwide. It is the final establishment of the permanent cessation of menstruation for twelve consecutive months and the end of the reproductive life span. The preceding phase of perimenopause or menopause transition usually takes four to ten years. It is characterized by hormonal imbalances, irregular menses and the onset of menopausal symptoms such as irregular periods, hot flashes, night sweats, vaginal dryness and sleep disruptions. Menopause is a complex life phase that is biologically driven and socially mediated, impacting a huge chunk of the population worldwide with limited interest by the healthcare systems across the world. According to the latest estimates, more than one billion women worldwide are currently living in the perimenopause, menopause or post menopause years. The number of women aged between 45-55 years is projected to reach nearly 500 million by the year 2030 which is almost 6% of the global population [1]. This alone indicates a huge public health problem with far-reaching implications on quality of life, workforce participation, mental health, chronic disease burden, and soaring load on healthcare systems for a sizable population worldwide.

In spite of the magnitude of the menopause burden, the availability of menopause-centric care is still severely inadequate. In most nations, including India, menopause has come to be understood as a major midlife health concern with un-availability of specialized care, public understanding or existence of any organized care system. National-level studies indicate that a substantial number of women are experiencing

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menopause at much younger ages than expected. Early onset of menopause is a rising concern. It is strongly linked with lower levels of education, poor socioeconomic conditions and rural settings. This clearly indicates profound differences in menopausal experience and care for different societal and demographic populations [2]. Such inequities have a direct bearing on the awareness of the transitioning life phase, presence and experience of symptoms, untreated co-morbidities and overall health outcomes for women. Menopause is not only a biological and complex life stage; it is also hugely impacted with social discriminants of health. Access to scalable, cheap and accessible support systems directed at awareness, education and personalized care is the need of the hour.

The onset of menopause is a result of the reduced secretion of estrogen and progesterone by the ovaries resulting in the deregulation of various systems physiologically. This change in the hormonal system influences many physiological and body systems in women such as thermoregulation, metabolism, mood regulation, sleep, cognition, bone density, cardiovascular risk factors [3]. The classic symptoms of menopause are vasomotor symptoms (VMS). This includes hot flashes and night sweats due to changes in hypothalamic thermoregulation induced by hormonal dysregulation. Sleep disturbances, anxiety, depression, cognitive symptoms, musculoskeletal pain, metabolic changes and overall decrease in quality of life are common among women everywhere. The intensity, duration and type of symptoms may differ from woman to woman depending on many factors such as race, age, socioeconomic strata. Some women may experience mild and transient symptoms, while others may suffer from debilitating symptoms for years.

However, this variability is not random. Factors such as infant nutrition, maternal smoking, breastfeeding, adult smoking, alcohol consumption, physical activity, body mass index, and reproductive factors affect the timing, impact, severity and course of menopause [4]. Approximately 11-12% of women have early menopause, which is linked to increased lifetime risk of cardiovascular disease, osteoporosis, depression, and metabolic disorders. This shows that menopause is not just a function of age but is influenced by cumulative biological and social risk factors.

This apparent heterogeneity which seemed impossible by traditional clinical classification has now been made possible with machine learning. Unsupervised clustering analysis of over 3,000 women in the Study of Women's Health Across the Nation (SWAN) database identified six distinct menopausal phenotypes:

(1) a high multi symptom phenotype with severe vasomotor, sleep, and mood symptoms and the lowest quality of life,
(2) a metabolic risk phenotype with few symptoms but a 1.8-fold increased risk of diabetes and metabolic syndrome,
(3) an asymptomatic phenotype,
(4) a mood-dominant phenotype,
(5) a healthy obese phenotype and
(6) a mild symptom phenotype [5].

This study illustrates a very important point that symptom-based classification alone is insufficient to capture biologically and clinically relevant phenotypes, especially those with established long-term metabolic and cardiovascular risk. Thus, menopause and menopausal phenotypes cannot be simply defined and identified by symptom questionnaires alone.

These findings profoundly contradict and challenge the conventional "one-size-fits-all" approach to menopause management. For instance, hot flashes are the most frequently reported symptom but vary greatly in terms of intensity, duration, timing of the day and frequency among different women. Black women, for example, are more prone to hot flashes and tend to go through menopause earlier than White women and are also more vulnerable to cardiovascular and psychological problems without sidelining the fact about the dearth of medical assistance available [6]. Most cases of hot flashes will eventually subside on their own. However, in many cases these symptoms can persist for several years and have a profound effect on a woman's ability to function or perform daily life activities [7].

In this regard, artificial intelligence and machine learning have provided a robust and applicable paradigm for transformation. Machine learning models trained on longitudinal, self-reported data can combine several weak signals such as age, irregular menses, symptom patterns, lifestyle variables/ factors and psychosocial factors into a unified individualized prediction. In contrast to traditional single-factor risk models, ML models can capture nonlinear relationships and interactions among dozens of variables reflecting the complexity of menopause biology and its impact on various physiological and other body systems. Previous research has already demonstrated that ensemble models such as random forest, gradient boosting and support vector machines can accurately predict the timing of menopause and other outcomes with high accuracy (AUC $\geq$ 0.80), performing better than traditional statistical methods based on isolated predictors [4]. Recent hybrid paradigms that integrate high-performance ML models with clinical nomograms also illustrate the potential for accuracy and interpretability to coexist allowing both clinicians and patients to understand and rely on algorithmic predictions [8,9].

Materials And Methods

Data source and cohort

We conducted our analysis using the Study of Women's Health Across the Nation (SWAN) data set that we retrieved from the Inter-university Consortium for Political and Social Research (ICPSR). The SWAN study is a multi-centre, longitudinal study that gathers repeated self-report and clinical data during the menopausal transition. The data release used for this study includes a few hundred to over a thousand variables per subject. To ensure that our resulting model is useful in a real-world setting, we restricted our modelling to variables that can be gathered by a woman without clinical testing (self-reportable variables) or the help of a medical practitioner.

Feature Selection and Engineering

We started with the full set of SWAN variables and performed a reproducible, rule-based filtering procedure, using regular expressions to extract candidate variables associated with prominent menopause topics (vasomotor symptoms such as hot flashes and night sweats, sleep, CES-D mood items, lifestyle factors such as smoking/alcohol/exercise, menstrual and reproductive history including LMP, pain scales, and

general health indicators) and then filtered out very sparse or nearly constant variables to prevent unstable predictors. This filtering step resulted in a concise, interpretable set of 38 self-report variables (approximately 3-4% of the original set), which we grouped for reporting purposes into demographics (3), behavioural/lifestyle (5), menstrual/reproductive (3), vasomotor/physical symptoms (10), psychological/mood items (5), and general health/functional status (12). We specifically chose to exclude any black-box dimensionality reduction (no PCA/t-SNE) to preserve the distinct identity of each symptom; the relevance of features would later be evaluated using Random Forest-based importance scores to evaluate feature sets.

Data preprocessing

Preprocessing steps were incorporated as reusable scikit-learn pipelines to enable consistent application of these steps during training and forecasting.

1. **Missing values:** Missing values in numerical features were handled using median imputation. Missing responses in categorical features were kept as a separate category to prevent the loss of potentially informative response patterns.
2. **Encoding:** Categorical features were one-hot encoded with handle_unknown='ignore' to enable stable handling of unknown categories during forecasting.
3. **Scaling:** Numerical features were z-score scaled within the pipeline. Scaling was done before applying Logistic Regression to ensure algorithmic stability and coefficient interpretability. Scaling was not done for Random Forest models because tree-based models are scale invariant.
4. **Outliers:** Outlier removal was not explicitly done. Median imputation and tree ensemble robustness were instead leveraged to prevent extreme values from dominating model behaviour.

Each preprocessing step was stored as part of the serialized pipeline to ensure consistent application of these steps during subsequent forecasting steps.

Outcome Definitions

The primary prediction objective of this work was to stage menopause into three groups: pre, peri and post-menopause via a standardized labeling scheme that takes into consideration the variability of coding conventions across different releases of the SWAN study data. As stage data is represented in multiple ways (textual labels, numeric fields with inconsistent ordering), we have designed a resilient labeling scheme that first favors direct textual labels, then uses an ordered numeric rule (minimum to pre, median to peri and maximum to post) when numeric labels are available and finally uses menstrual timing and bleeding patterns as a fallback when stage data is ambiguous.

In conjunction with this classification objective, we also included an independent symptom forecasting task via a rule-based SymptomCycleForecaster, which computes cycle day based on the last menstrual period and a target date and produces interpretable probability estimates for short-term risks of hot flashes and mood changes based on cycle timing heuristics. These two objectives work together to provide both standardized menopausal stage classification and personalized, predictive symptom risk forecasting in a transparent, clinically interpretable, accessible and practical manner.

Models And Training Procedures

Two different classifiers were trained and combined in scikit-learn pipelines that include the preprocessing steps outlined above:

5. Multinomial Logistic Regression – set up with multi_class='multinomial', solver=lbfgs, and max_iter=1000. As logistic regression is known to be sensitive to feature scaling, the pipeline includes standardization of numerical inputs before model training.
6. Random Forest – an ensemble tree classifier with n_estimators=200 and n_jobs=-1 to leverage parallel processing. The Random Forest pipeline does not include numerical scaling.

The training process followed a structured template:

- The data was split using stratified sampling to create an 80% training set and a 20% test set to hold class distribution.
- The robustness of the models was evaluated using 5-fold stratified cross-validation on the training split.
- The main evaluation metrics were accuracy, precision, recall, weighted F1-score, and AUC-ROC as appropriate; confusion matrices were examined for class-wise performance.
- No extensive hyperparameter tuning was conducted; models were trained with the specified, practical hyperparameters to yield stable baselines. Interpretability and reproducibility were emphasized.

Finally, the trained pipelines (including preprocessing and model components) were pickled as artifacts (rf_pipeline.pkl, lr_pipeline.pkl) with a forecast metadata file (forecast_metadata.json) containing feature names, class labels and preprocessing details. This was done to ensure identical preprocessing and model behaviour critical for reproducible forecasts.

Forecasting and batch inference

For the purpose of deployment, we created a Menopause Forecast API with predict_single(), predict_batch(),and compare_models() methods. A command-line script (predict_csv.py) is available for CSV-based batch prediction: it takes an input CSV file, loads the serialized pipeline, and generates an output CSV file with predicted stage, class probabilities and confidence scores. The symptom forecaster takes a CSV file with LMP and date entries and generates cycle_day, hotflash_prob, mood_prob, and boolean flags for predicted hot flashes and mood changes. All code paths utilize the serialized preprocessing transformers to ensure that the training and serving transformations are identical thereby preventing "training/serving skew" and enabling rapid re-use of models for single participant or cohort level predictions.

Software Environment and Reproducibility

Analyses were done in Python and run in a controlled environment. The main packages and versions used were Python 3.13, pandas 2.3.3, numPy 2.3.3, scikit-learn 1.8.0, matplotlib 3.10.6, seaborn 0.13.2 and joblib. All scripts, model pipelines, and results of evaluation (confusion matrices, feature importance CSVs) are stored in the project output directory (swan_ml_output/) to facilitate reproducibility and independent verification.

Results

Feature Selection and Dataset Composition

After preprocessing, normalization, and structured feature screening, a final set of 38 self-reportable longitudinal variables

was selected for modeling. These variables cover a wide range of domains in menopausal biology, including menstrual cycle phenomena, bleeding disorders, pain patterns, vasomotor symptoms, mood-related symptoms and age-related changes. Notably, all of the variables selected for modelling are directly self-reportable which enables scalability of the system. This approach ensures that the modeling framework is amenable to community, digital health and consumer-facing applications while still capturing the essential biological and symptomatic phenomena of reproductive aging and menopause.

Classification Performance on the Held-Out Test Set

The performance of the models was tested on a strictly held-out test set of 20% to ensure an unbiased evaluation. Both models showed strong discriminative ability on the three classes of menopausal stages (pre, peri and post-menopause).

Table 1: Performance metrics of Logistic Regression and Random Forest

Model	Accuracy	Weighted Precision	Weighted Recall	Weighted F1
Logistic Regression	95.45%	95.11%	95.45%	95.28%
Random Forest	97.38%	94.82%	97.38%	96.08%

Taken together, these findings show that both linear and nonlinear modelling strategies are very successful when used in conjunction with structured, longitudinal, self-reported menopausal data. The high recall values obtained for all models show that there is a high sensitivity for the detection of stage transitions which is of great importance for early diagnosis of perimenopausal and postmenopausal stages. The performance improvement achieved with the Random Forest model illustrates the advantage of ensemble learning for modeling nonlinear relationships between symptoms, cycle variables and demographic variables.

Confusion Matrix Analysis

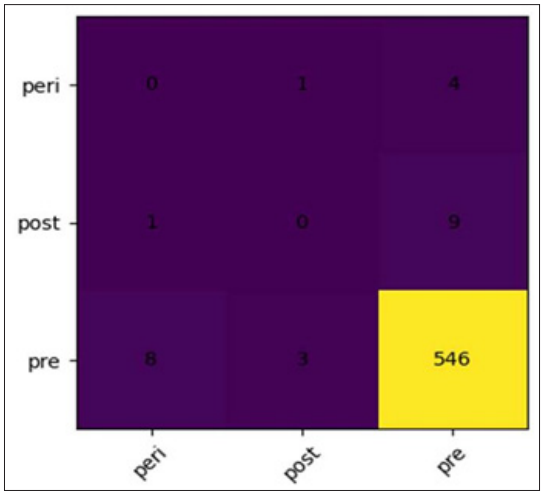

Figure 1: Confusion Matrix for Logistic Regression

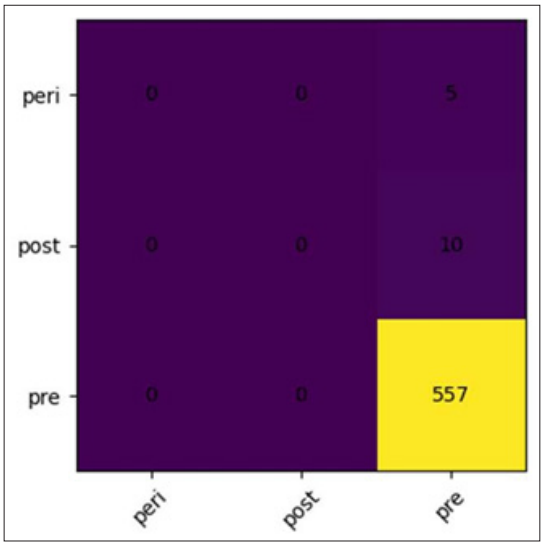

Figure 2: Confusion Matrix for Random Forest

Analysis of the confusion matrix revealed strong diagonal dominance, indicating high true positive classification rates for all menopausal phases. The classification errors were minimal and mainly restricted to neighboring physiological phases (pre → peri and peri → post). The highest level of confusion was observed in the perimenopausal class, with a slightly lower recall value than the premenopausal and postmenopausal classes. This is biologically plausible, as the perimenopausal phase is a transitional phase that is marked by instability in hormone levels and similar symptom profiles. Notably, the classification errors were not random but were restricted to physiologically similar phases.

ROC Curves

Receiver Operating Characteristic (ROC) curves for the three menopausal phases (pre, peri, and post menopause) in a one-vs-rest setting. The diagonal line indicates the performance of a random classifier. The Area Under the Curve (AUC) values for each class reflect the discriminative power of the model.

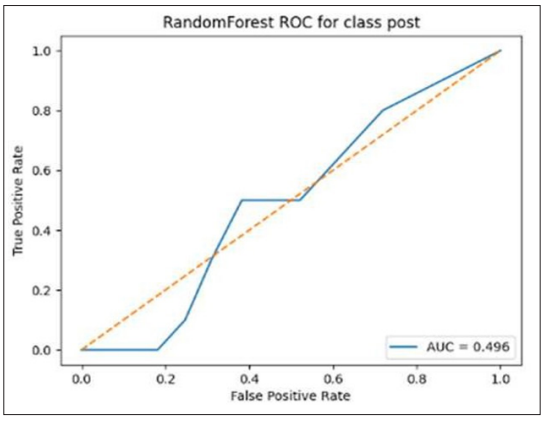

Figure 3: Random forest Roc for Class Post

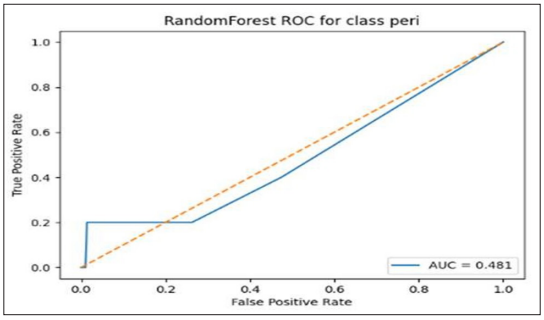

Figure 4: Random forest Roc for Class Peri

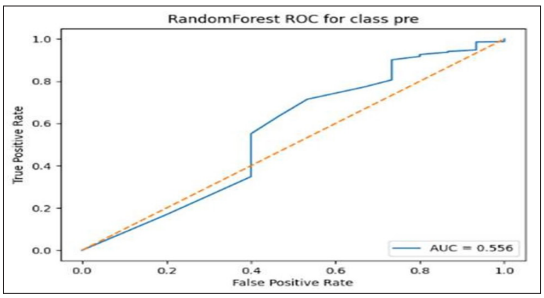

Figure 5: Random Forest ROC for class pre

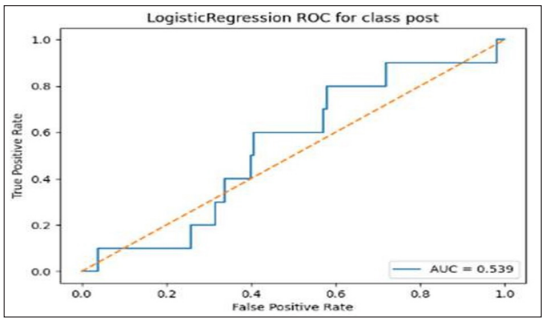

Figure 6: Logistic Regression ROC for Class Post

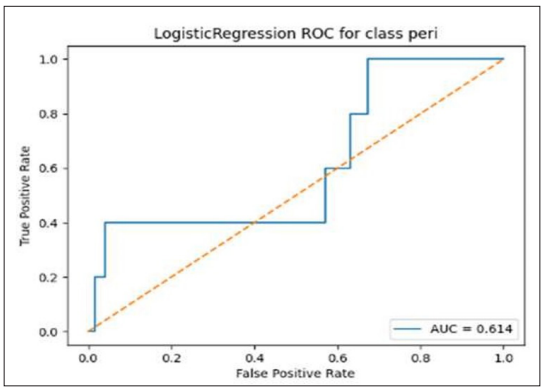

Figure 7: Logistic Regression ROC for Class Peri

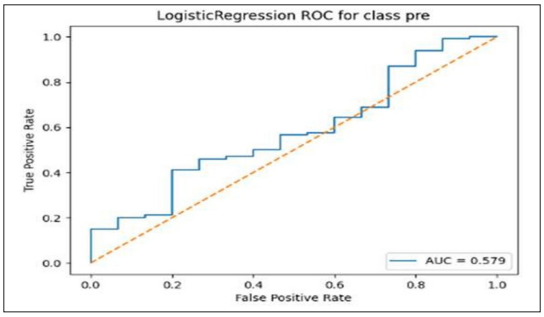

Figure 8: Logistic Regression ROC for Class Pre

Feature Importance and Biological Relevance

In order to gain insight into which inputs were responsible for the decisions made by the models, we analysed the feature attributions obtained from the trained Random Forest model using both impurity importance and permutation importance. The importance values are normalized (sum = 1.00) and represent the relative contribution of each encoded feature to the classifiers' performance.

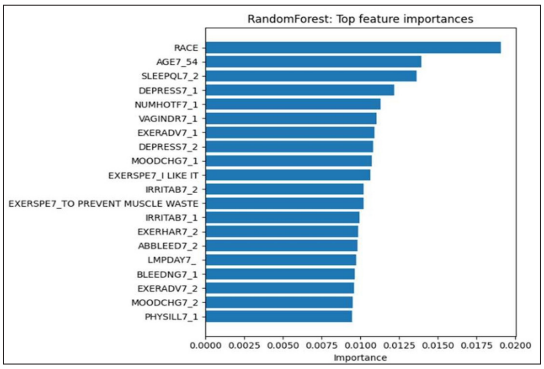

Figure 9: Importances of Self-Reportable Features.

Y-axis denotes each feature name while the X-axis denotes normalized importance score. The sum of
importance is equal to 1.00.

The top-ranked features are shown below (feature name: importance):

1. RACE : 0.019085 (1.91%)
2. AGE7_54 : 0.013959 (1.40%)
3. SLEEPQL7_2 : 0.013640 (1.36%)
4. DEPRESS7_1 : 0.012184 (1.22%)
5. NUMHOTF7_1 (NUMBER OF HOT FLASHES): 0.011292 (1.13%)
6. VAGINDR7_1 (VAGINAL DRYNESS INDICATOR) :0.011038 (1.10%)
7. EXERADV7_1 (EXERCISE ADVANTAGE/ATTITUDE CATEGORY) : 0.010894 (1.09%)
8. DEPRESS7_2 : 0.010826 (1.08%)
9. MOODCHG7_1 : 0.010723 (1.07%)
10. EXERSPE7_I LIKE IT (EXERCISE MOTIVE) : 0.010632 (1.06%)

The pattern of feature importance reveals that the model relies not on one or two highly dominant predictors but rather on numerous small, significant signals distributed over demographic, symptom, reproductive and lifestyle features with each of the leading features contributing only 1-2% to the total importance.

Age and race are identified as significant contextual variables, which reflect known population differences in the timing of menopause and the expression of symptoms while symptom variables such as sleep, depression, hot flashes, vaginal dryness and irregular bleeding point to the pivotal role of vasomotor, neurovegetative and reproductive changes in the staging of menopause. Menstrual timing data also enters into the model through several encoded LMP variables rather than a single continuous one, indicating that cycle-related patterns carry significant biological information.

Lifestyle and functional variables associated with exercise and general health also provide complementary information to symptoms and demographics. Overall, these findings demonstrate that the predictions of the model result from the integrated combination of numerous small, significant factors and that the decision process is interpretable and biologically plausible rather than being just rule-based.

Symptom Forecasting Outputs

The SymptomCycleForecaster module generated personalized probabilistic symptom predictions based on longitudinal cycle timing and forecast dates. A sample output would be:

- cycle_day: 16
- hotflash_prob: 0.55 → hotflash_pred: True
- mood_prob: 0.30 → mood_pred: False

These results demonstrate the capability of the system to take menstrual timing information and convert it into predictive symptom risk probabilities; instead of just identifying the current status the system allows for proactive guidance with short-term symptom probability forecasts.

Software Artifacts and Reproducibility

All preprocessing pipelines, models, and evaluation artifacts were completely serialized, including rf_pipeline.pkl, lr_ pipeline.pkl, forecast_metadata.json, confusion matrices and feature importance files stored in the swan_ml_output/ directory. The system provides support for CSV-based batch prediction (predict_csv.py) as well as programmatic forecasting using the MenopauseForecast interface. This design provides predictability and consistency in behavior across training, validation, and deployment.

Taken together, these findings indicate that self-report-based longitudinal modelling is capable of achieving highly accurate menopausal stage classification with the added capability of individualized symptom prediction. This system combines predictive capability, biological plausibility and deployability to demonstrate that meaningful menopause modelling is possible without the need for laboratory or imaging-based testing or clinical interference. This places the system on the cutting edge of modelling capability while also providing a basis for practical digital health applications.

Discussion

We have created and tested a useful and reproducible pipeline that can classify menopausal stage and make predictions about short-term symptoms based solely on self-reported longitudinal data. Based on the SWAN study, the system is designed to rely on data that a woman can provide herself: menstrual dates (LMP), symptom data (hot flashes, sleep, mood), and simple demographic and lifestyle information, so that it can be operated without the need for blood tests or professional consultation. Two different models were trained and saved as end-to-end pipelines: one multinomial Logistic Regression, and one Random Forest. On a held-out test set of 20% accuracy, the Random Forest had an accuracy of about 97.4%, while the Logistic Regression had an accuracy of about 95.5%.

The errors were not random. They tended to occur at biologically plausible boundaries between adjacent stages (pre↔peri↔post) and the perimenopausal group was the hardest to place – a reflection of the fact that perimenopause is a transitional, heterogeneous phase. The feature attribution analyses proved that the classifier was not based on one prominent feature only. Rather, a multitude were playing weak signals: reproductive timing (several one-hot LMP bins), vasomotor symptoms frequency, sleep, depressive symptom items, age, race, exercise, and general health ratings all counted. Overall, the classifier has been trained to learn a biologically plausible, distributed representation direct biological anchors are furnished by menstrual patterns and bleeding disturbances, whereas symptoms and functional assessments are used to record the neurovegetative and lifestyle dimensions of the transition. Another simple, interpretable SymptomCycleForecaster (including an LMP + target) was also added output and date cycle day and heuristic probabilities of hot flashes and mood swings (e.g.,cycle_day=16 → hot flash_ prob=0.55). This element is intentionally clear and constructed to provide actionable, easy-to-understand outputs instead of black-box probabilistic predictions.". Nevertheless, it is not a learned model but rule-based; its predictions should be validated in a prospective diary study before clinical use.

The most important asset of this attempt is that this can be reproduced: any preprocessing and models have been serialized.

The code is configured and the feature importance files, the forecast metadata.json, and the rf_ pipeline.pkl and lr_pipeline. pkl are in place csv batch inference and programmatic APIs. The choice not to strip it of human-readable features and to the use of linear and nonlinear models makes the results interpretable to the clinicians have become sufficiently realistic to use.

Key points to keep in mind are available. SWAN test has an uneven composition, as there are much more premenopausal.

than peri/post samples, and therefore weighted measures can overvalue performance on less-represented reciprocate classes, and class-wise metrics, bootstrap confidence intervals, and macro averages are required of a more balanced view. The study is a single-cohort, retrospective analysis and, thus, has to be externally validated in other studies critical are groups and prospective analysis. Conversely, consideration of subgroup performance (by It should also be done without causing more health disparities by excluding race, age, socioeconomic status). Finally, even though engineering trade-offs were implemented with the intention of enhancing interpretability and reproducibility, additional sensitivity analyses (e.g. modest hyperparameter search and class-balancing methods) would assist in creating robustness of the findings.

Conclusively, this project illustrates that factual and interpretive prediction of menopausal phases and simple prediction of symptoms are feasible out of self-reports. With proper validation, this pipeline, and design, may allow building affordable digital instruments to assist women and practitioners expect transitions and plan in advance - changing the menopause care terrain between response and preparation.

Conclusion

This study presents a proof of concept with a model trained

on self-reportable SWAN variables alone that can predict menopausal phase with a very high accuracy. The model is also capable of producing short-term symptom predictions amenable to digital health scalability and deployment. Not only does it support the integrity of safe and transparent digital tools but also assist millions of women in their own menopausal transition enabling personalised interventions at individual/ clinical levels.

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