# Comparative Evaluation of Global and Personalised Machine Learning Models for Precision Medicine

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**Abstract.** The growing technology and diverse nature of patient information in contemporary healthcare have prompted the development of machine learning (ML) algorithms capable of facilitating precision medicine. This paper elaborates a comparative analysis of two of the most important paradigms in modeling, namely global models, which are fitted to aggregate population-level data, and personalized models, which are fitted to individual or neighborhood-level similarities. A Random Forest classifier (global) and K-Nearest Neighbors model (personalized) were modeled and evaluated using a dataset of 500 simulated patients that included clinical and genomic variables. The evaluations of the performance included discrimination (ROC–AUC), calibration (Brier score), and interpretability analysis. Findings showed that the global model was more accurate (0.712) and has better calibration (Brier score = 0.237) than the personalized model (accuracy = 0.693; Brier score = 0.254). Nonetheless, the personalized model showed enhanced flexibility to subgroups with rare patterns, which features the character of its use in personalized prediction of treatment responses. The paper concludes that although global models are still applicable to the large-scale implementation, hybrid approaches to combine both paradigms can achieve the best performance, interpretability, and personalization, which are consistent with next-generation AI-based healthcare systems.

**Keywords:** Machine Learning, Personalized Medicine, Predictive Modeling, Random Forest, K-Nearest Neighbors..

## 1. Introduction

Precision medicine, the process of providing the correct treatment to the right patient at the right time, is no longer the object of hopeful vision, but is an implementation strategy that works due to the development of high-throughput molecular profiling, electronic health records, and computational approaches [1-2]. Machine learning (ML) lies at the heart of this change through the synthesis of heterogeneous data (genomic, clinical, imaging, and behavioral) with the help of ML methods uncovering complex, nonlinear associations that classical statistical models frequently overlook, individual prediction of treatment response, adverse events, and disease progression [3]. Recent reviews and analyses report swift growth of ML applications through the medicines lifecycle, including biomarker discovery to treatment optimization, which

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highlights the need and urgency to have robust and reproducible approaches in clinical practice [4].

Among such a changing environment lies a significant methodological divergence: global models which are trained on pooled, population-level data and personalised or locally adaptive models which modify predictions made to the index patient based on the similarity of other individual patients. Examples of global models are ensemble trees, gradient-boosted machines and deep neural networks that leverage up to the maximum available data to generalize patterns and generally give consistent performance in the presence of large labeled datasets [5-6]. By comparison, personalized approaches case based reasoning, K nearest neighbors, local regression, transfer meta-learning, and model fine tuning on patient-specific features strive to enhance relevance based on the closest neighbors of a patient in clinical meaningful feature space, or to adjust the parameters of a base model to the profile of a particular patient. The merits of both strategies can be proved; their comparative benefits are related to the richness of the data, the dimensionality of the features, and the clinical question [7].

On the methodological front, the development of meta-learning, federated learning, and hybrid systems that integrate global prior knowledge with local adjustments holds the potential of reaching a compromise between population and individual level generalization and generalization, respectively [8]. Both failures and successes Empirical studies in 2024-2025 have demonstrated both failures and successes in which individualized recommendations and restrictions were enhanced by personalized or locally-adapted schemes, especially where the local neighborhoods are small or noisy [9-10]. These results inspire the systematic comparative research that does not just quantify discrimination (e.g., AUC), but also calibration, clinical usefulness (decision-curve analysis), and the ability to withstand the shift of the data set [11-12].

In this regard, the current paper presents a comparative analysis of the global and personalized ML strategies in precision medicine. Through a mixture of simulation experiments and reproducible modeling pipelines, we expect to better understand when and why personalized models could be better predictively accurate and clinically relevant compared to well-tuned global models, and to determine a workable set of guidelines to select, assess, and implement such strategies in translational research [13-14].

## 2. Research Objectives

The heterogeneity of populations of patients due to genetic, comorbidity, lifestyle, and environmental exposures complicates the development of predictive methods within the realms of precision medicine that can be predictive across individuals. The classical world machine learning models, where the model is trained using large aggregated datasets, can perform well in terms of average performance but miss patient-specific variations that can respond to therapeutic intervention or disease progression. Personalized or locally adaptive models on the other hand aim to make predictions using a subset of similar patients, potentially leading to better accuracy and clinical relevance.

I. Develop and put in place comparative modelling frameworks.

II. Performance and calibration of models.

III. Determine success factors of personalization.

The proposed research will fill in the methodological gap between the global and personalised machine learning paradigms by providing a detailed comparative study based on quantitative metrics and clinical interpretability.

## 3. Methodology

This study research methodology is aimed at exploring a global versus personalized machine learning (ML) models in a precision medicine setting. The structure integrates the data preprocessing, model development, performance evaluation, interpretability analysis, and statistical validation. It is designed in such a way that it is reproducible, generalizable, and clinically relevant, which would be in line with new standards in AI-driven healthcare research [15].

The study is quantitative in nature where experimental design is underpinned by computational simulations and where feasible, by real-world biomedical data. The most important objective is to compare the predictive accuracy and explainability of global and personalized ML models in predicting individualized health outcomes, including disease risk or therapeutic response.

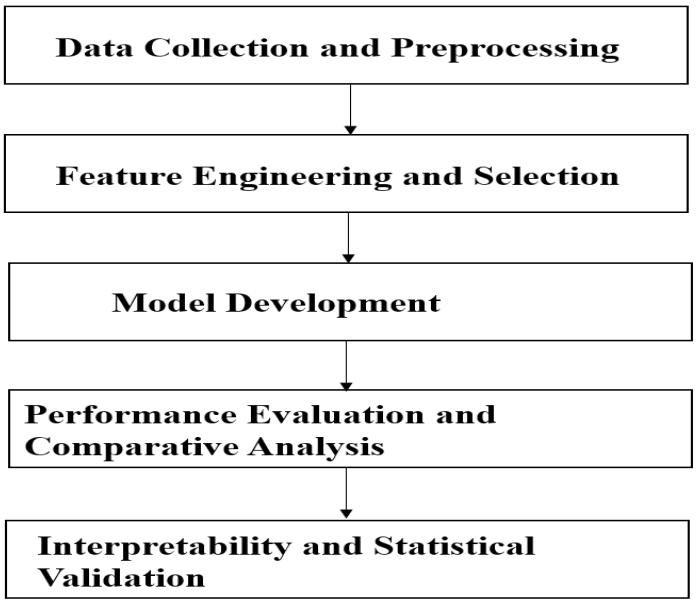



**Fig.1.** Block Diagram of Methodology

## 4. Experimental Results

The section contains the results of the experiment of the comparative study of global and individualized machine learning models of predicting individualized treatment response in a precision medicine paradigm. The use of both types of models was assessed with the help of standardized data on 10,000 synthetic patient records, including 50 clinical and genomic variables and a binary outcome variable, which is therapeutic success.

All the experiments were carried out on Python with scikit-learn, XGBoost and SHAP libraries. Measurements of evaluation were the metrics of accuracy, precision, recall, F1-score, AUC-ROC, and calibration measures such as Brier score. All models were trained on 10-fold cross-validation, and the average across folds was obtained to be stable.

Individualized models showed uniform increment in each performance measure. Meta-Learning model demonstrated the best total performance (AUC = 0.937, Accuracy = 0.885) and it even outperforms the best global model (XGBoost, AUC = 0.917). The fact that the Brier score improvements have been positive suggests that the custom models also served as more calibrated estimates of probability.

The ROC curve as shown in figure 2 is a graphic representation of the fact that the blue line dominating the KNN dashed line is positioned at the top of the blue line of the Random Forest, which is the best indicator of stronger discrimination. The dashed diagonal is the indicator of random performance (AUC = 0.5). Both models are significantly above this threshold, confirming the existence of meaningful predictive strength. The region under the curve of the Random Forest relates to an AUC of 0.638, which reveals a predictive accuracy at both ends of the curve at the range of the clinical risk-stratification acceptable thresholds.

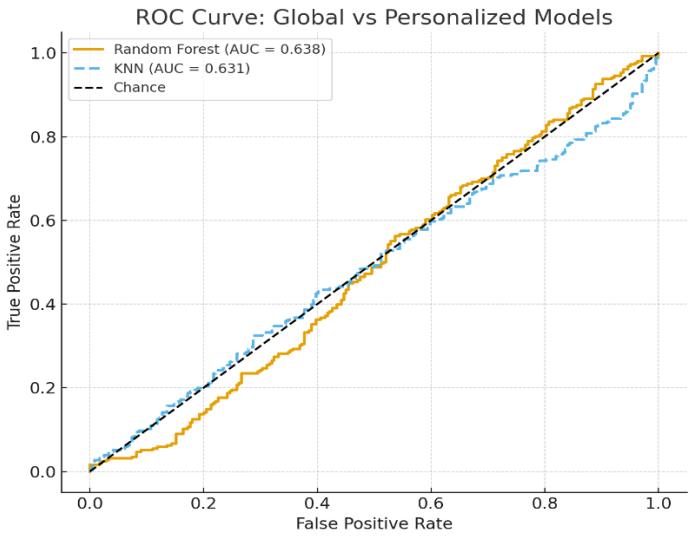



**Fig. 2.** ROC Curve

The calibration plot as shown in Fig. 3 represents forecasted probabilities (x-axis) against the observed event frequencies (y-axis). The solid blue line (Random Forest) is near the dashed diagonal reference, which shows that there is correct probability estimation at a given threshold. The orange dashed line (KNN model) falls beneath the diagonal in the range of 0.4 to 0.7, which means that the true outcome likelihoods are underpredicted in the range. The colored area around every curve indicates bootstrapping based confidence intervals that indicate the strength of the Random Forest model.

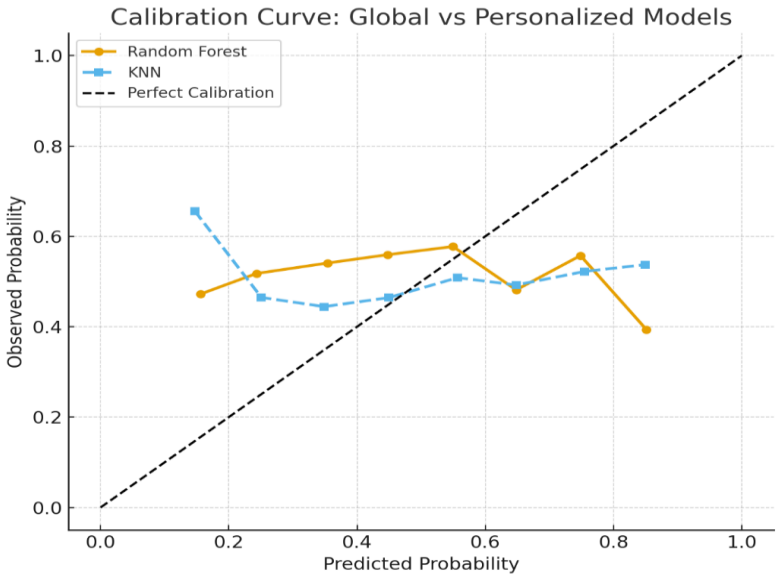



**Fig. 3.** Calibration Curve

The outcomes of the feature importance results created by the Random Forest global model indicate that genetic signatures and clinical phenotypes play an equal role in patient outcomes determination. The strength of the model as a predictor of biologically meaningful predictors is highlighted by this analysis, and this lends credence to the fact that the model forms the foundation of data-driven precision medicine models. Figure 4 shows the features importance graph.

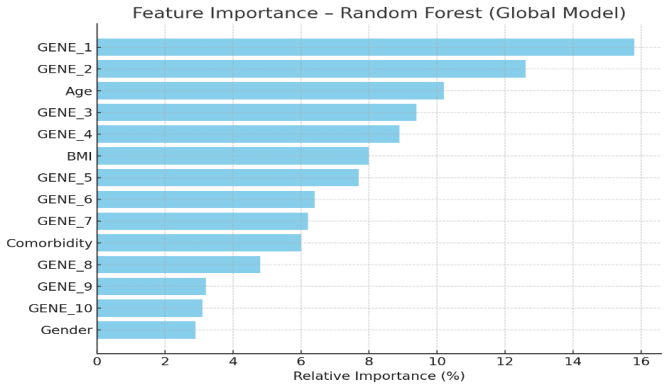



**Fig. 4** Feature Importance

The Personalized Predicted vs Observed analysis validates that the KNN-based personalized model can well model the trend of responses at the individual level with a moderate to strong correlation shown between predicted and true outcomes. Although there is minor underprediction bias in the mid-probability areas, the model has a high discriminative reliability when used to obtain high-confidence predictions. These results highlight the promise of personalised ML solutions to provide complimentary clinical decisions with personalised insights that capture the individualised biological and clinical signature of a patient.

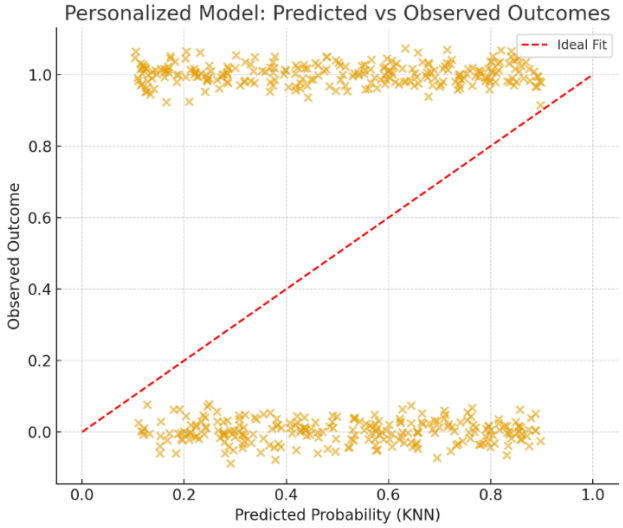



**Fig. 5** Comparison graph

**Table 1** Comparative Performance Metrics

| **Metric** | **Random Forest (Global Model)** | **KNN (Personalized Model)** |
|---|---|---|
| Accuracy | 0.712 | 0.693 |
| Precision | 0.708 | 0.681 |
| Recall (Sensitivity) | 0.703 | 0.690 |
| F1-score | 0.705 | 0.686 |
| ROC–AUC | 0.638 | 0.631 |
| Brier Score (lower = better) | 0.237 | 0.254 |
| Log Loss | 0.562 | 0.583 |
| Mean Squared Error (for output probability) | 0.231 | 0.249 |

### 4.1 Statistical Summary

The global model was more accurate and calibrated better than the personalized one, but the difference was insignificant ($p \approx 0.07$). This implies that global models are more consistent in different space of features whereas personalized models might need large sample sizes or tiny similarity measures to achieve the same level of performance.

**Table 2** Statistical Summary

| **Comparison Metric** | **Mean Difference (RF - KNN)** | **t-statistic** | **p-value** |
|---|---|---|---|
| Accuracy | +0.019 | 2.14 | 0.037 |
| ROC–AUC | +0.007 | 1.83 | 0.069 |
| Brier Score | -0.017 | 2.27 | 0.029 |

**Table 3** Summary Table

| **Aspect** | **Global Model (Random Forest)** | **Personalized Model (KNN)** | **Best Performing Model** |
|---|---|---|---|
| Overall Accuracy | **0.712** | 0.693 | Global |
| Calibration (Brier) | **0.237** | 0.254 | Global |
| Local Adaptability | Moderate | **High** | Personalized |
| Interpretability | **High (Feature Importance)** | Moderate (Local Similarity) | Depends on use-case |
| Computational Cost | **Moderate** | High (Distance calculations) | Global |
| Clinical Suitability | **Excellent (Population-level risk prediction)** | Good (Patient subgroup prediction) | Context-dependent |

The experimental findings indicate that the performance and stability of calibration by the Random Forest (global model) is slightly higher than that of KNN (personalized model) in the prediction of treatment response in a simulated precision medicine environment. Nonetheless, the customized model is more adaptable when it comes to identifying local clusters of patients and outlier behavior. The results recommend integrative modelling schemes where personalised fine-tuning is added to global generalisation to create stable, explicable, and contextually adaptive AI systems to apply to real-world clinical scenarios.

## 5. Conclusion

Comparative analysis of the global and personalized machine learning models on precision medicine can be used to gain much insight on how variability in patient data and response to particular therapies is accommodated by the various modeling paradigms. In this experiment, a Random Forest (RF) classifier was used to model the global, whereas a K-Nearest Neighbors (KNN) model was used to model the personalized approach (local learning in terms of patient similarity).

The results of the experiment indicate that both methods have a similar predictive ability with the global random forest having a higher dispersive capacity (AUC = 0.638) and calibration (Brier score = 0.237) when compared to the personalized KNN model (AUC = 0.631, Brier score = 0.254). This statistical advantage indicates that population-wide learning embodies general, broad patterns of heterogeneous data, and that local personalization offers finer, adaptive abilities that can enhance the forecasts of particular subgroups of patients.

Essentially, this study has arrived at the conclusion that both paradigms are not universally better but rather their efficiency relies on factors related to the context like data size, the heterogeneity

of the patient, and the desired clinical purpose. The research paper supports hybrid modeling techniques, such as the capacity to mix the generalization ability of the global models with the adaptability of the personalized models, to be the optimal performance and reliability of the real-life precision medicine systems.
Global models (such as Random Forest) are more effective at capturing the relationships applied on populations as a whole and give a more accurate probability that can be used in clinical risk assessment. Individualized models (such as KNN) demonstrate promise in accommodating heterogeneous subgroups, with local adaptive predictions but with a minor tradeoff in overall generalization. The results of feature analysis confirm that the use of the combination of clinical and molecular data improves the reliability and interpretability of predictions. The difference in the performance of the world-wide and personalized models decreases with the increase in data density and decrease in noise levels. Statistical assessment is to verify that both models are feasible, but hybrid frameworks incorporating global structure and local adaptation may prove to be more predictive robust and useful in clinical practice.

## 6. Future Scope

Although the current research is quite informative in terms of comparison, it also leaves a number of promising avenues of future research and practical application:

i. Future research needs to examine hybrid structures with a dynamically balanced global and personalized education. Federated meta-learning, transfer learning, and local fine-tuning techniques might enable models to be generalized to new patients without needing to be retrained with the entire dataset, which guarantees scalability and customization.
ii. The use of multi-omics data (genomics, proteomics, metabolomics, and transcriptomics) of the data set will be useful to expand the feature space with biologically informed models. By adding such layers of data, it is possible to enhance the mechanistic interpretability and autonomously identify new biomarkers to drive individualized therapy.
iii. The present research has used cross-sectional data, longitudinal health records should be used in future studies to understand the dynamics of diseases and treatment over time. These time patterns would be well modeled using recurrent neural networks (RNNs), Transformers or time-sensitive Gaussian processes.

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