Title: A Data-Driven Machine Learning Model for Effective Diabetes Diagnosis

LIME-Based Explainability Analysis of the XGBoost Classifier

To improve model interpretability, Local Interpretable Model-Agnostic Explanations (LIME) were applied to the XGBoost classifier to analyze feature contributions toward class-specific predictions. The LIME plots illustrate the local importance of clinical features, where positive contributions support the predicted class and negative contributions oppose it. Across all diabetes classes, blood glucose emerged as the dominant predictor, while age and cholesterol contributed moderately in selected classes. Features such as BMI, waist circumference, insulin, and pancreatic health showed comparatively lower influence.

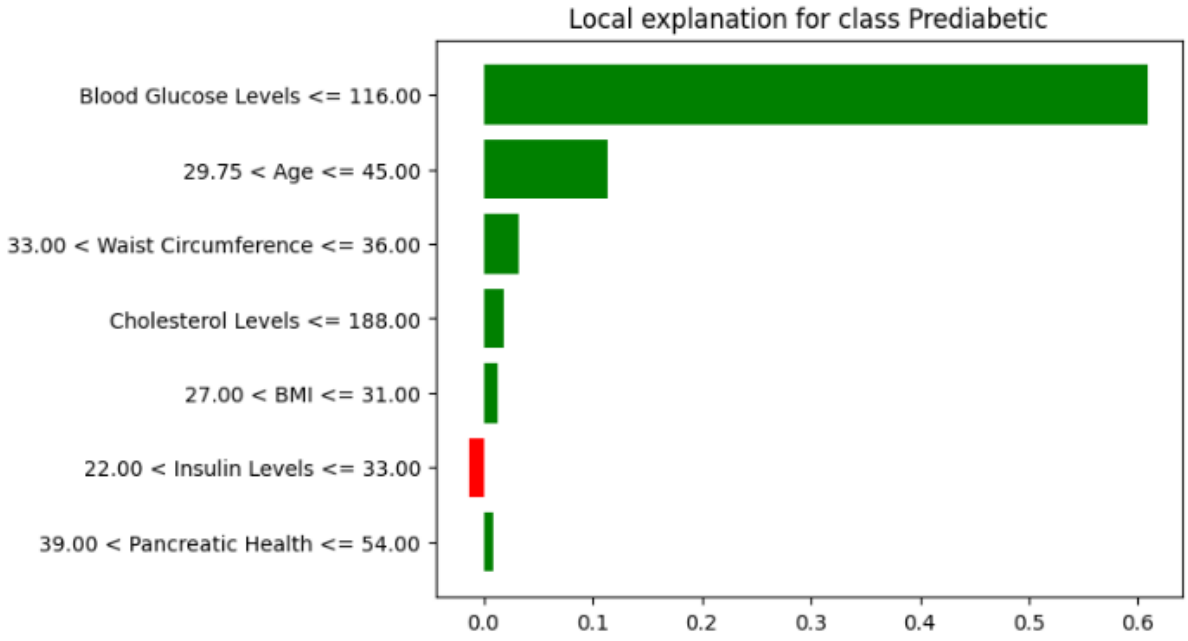

Figure S1. LIME explanation for Prediabetes classification using XGBoost.

The LIME plot for a representative prediabetic sample shows that blood glucose is the strongest positive contributor, followed by age. Other features, including BMI, waist circumference, cholesterol, insulin, and pancreatic health, contributed minimally, indicating that the model primarily relies on mild hyperglycemia for prediabetes identification.

The model primarily identified mild hyperglycemia as the key indicator of prediabetes, consistent with clinical diagnostic criteria. Age contributed meaningfully, whereas obesity-related markers were underutilized despite their known clinical relevance.

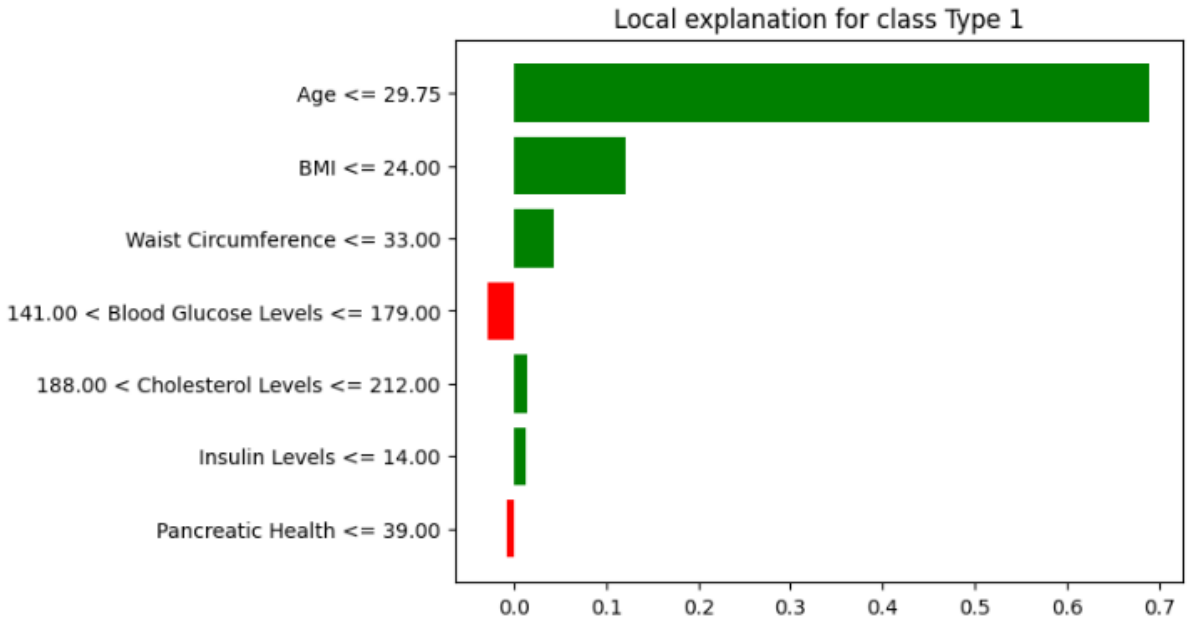

Figure S2. LIME explanation for Type 1 Diabetes classification using XGBoost.

The LIME plot for a representative Type 1 diabetes sample indicates that younger age is the dominant contributor, followed by lower BMI and smaller waist circumference. These findings are clinically consistent with the typical presentation of Type 1 diabetes in younger and relatively lean individuals.

This aligns well with clinical knowledge, as T1D commonly occurs in younger, lean individuals. The strong influence of age and body composition makes this class highly clinically consistent.

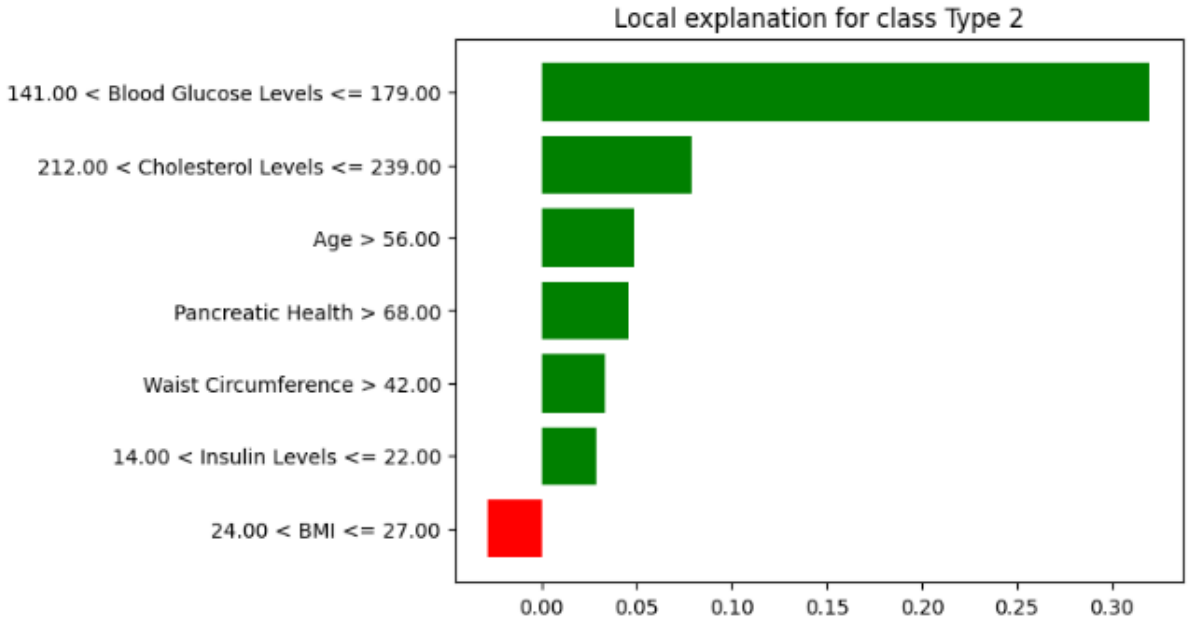

Figure S3. LIME explanation for Type 2 Diabetes classification using XGBoost.

The LIME plot for a representative Type 2 diabetes sample highlights elevated blood glucose as the primary contributor, with cholesterol and age providing secondary support. The limited contribution of BMI and waist circumference suggests reduced utilization of obesity-related markers in classification.

The model captured clinically relevant T2D patterns involving hyperglycemia and metabolic dysregulation. Cholesterol contribution suggests recognition of metabolic syndrome, though the weak BMI contribution indicates limited use of obesity-related biomarkers.

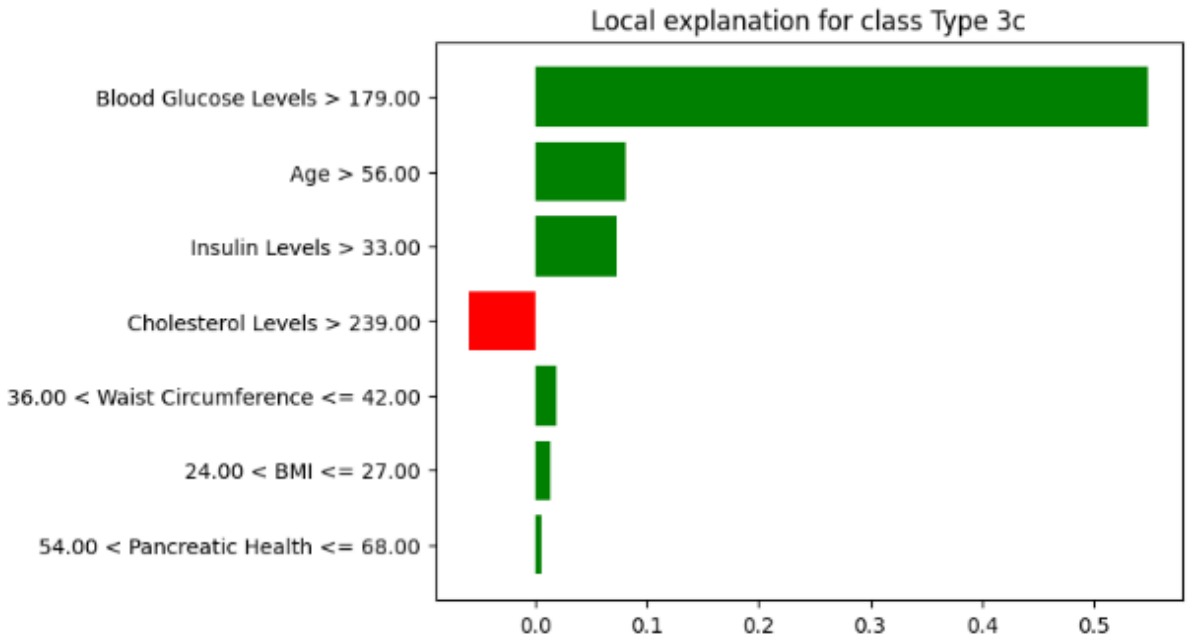

Figure S4. LIME explanation for Type 3c Diabetes classification using XGBoost.

The LIME plot for a representative Type 3c diabetes sample shows blood glucose as the dominant contributor, with moderate influence from age and insulin. Notably, pancreatic health exhibited negligible contribution, indicating limited discriminative value of this feature despite the pancreatic origin of Type 3c diabetes, highlighting a dataset-related limitation.

While glucose and insulin contributions were clinically plausible, the negligible importance of pancreatic health is a major limitation, since pancreatic dysfunction is central to Type 3c diabetes. This suggests limited clinical relevance of the pancreatic health feature.

Conclusion

Across all diabetes classes, LIME analysis indicated that the XGBoost classifier primarily learned glucose-driven decision patterns, consistent with clinical diabetes diagnosis. Age and cholesterol provided secondary contributions in specific classes, while the limited influence of obesity-related and pancreatic-specific biomarkers suggests reduced utilization of multidimensional clinical features, particularly in Type 3c diabetes classification.

Although pancreatic dysfunction is a defining characteristic of Type 3c diabetes, LIME analysis revealed minimal contribution of the pancreatic health feature in classification. This may be attributed to the limited clinical interpretability and unclear documentation of this feature in the dataset. Consequently, Type 3c predictions appear to rely predominantly on glucose-driven patterns rather than pancreas-specific biomarkers, highlighting a limitation of the current dataset and the need for clinically validated pancreatic markers in future studies.