Dengue Recognition System for patients in Srilanka

By using machine learning

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**Introduction**

Dengue fever poses a persistent threat to public health in Sri Lanka, exacting a heavy toll on individuals and the healthcare system alike. With its tropical climate fostering the proliferation of the Aedes mosquito—the primary vector for dengue transmission—the country contends with recurrent outbreaks of the disease, precipitating widespread illness, economic strain, and societal disruption (Malavige et al., Changing Epidemiology of Dengue in Sri Lanka—challenges for the future 2021).

Conventional methods of diagnosing dengue hinge largely on clinical assessment, a process fraught with challenges due to the disease's variable and overlapping symptoms. This diagnostic complexity frequently results in delays in treatment initiation, heightening the risk of severe complications and mortality. Moreover, the sheer volume of dengue cases overwhelms healthcare facilities, exacerbating resource constraints and impeding effective disease management (Raafat et al., A review of Dengue diagnostics and implications for surveillance and Control 2019).

Recognizing the imperative for more efficient and precise diagnostic tools, there has been a burgeoning interest in harnessing machine learning technologies for dengue detection. Machine learning, a facet of artificial intelligence, holds promise in scrutinizing extensive and diverse datasets to unveil hidden patterns and insights. By leveraging this computational prowess, machine learning algorithms can facilitate early detection of dengue, stratification of risk, and allocation of resources, thereby ameliorating clinical outcomes and optimizing resource utilization (Saturi, Development of prediction and forecasting model for dengue disease using machine learning algorithms 2020).

This project endeavors to craft a bespoke machine learning-driven dengue detection system tailored explicitly to the sri lankan milieu. Through the integration of disparate datasets encompassing clinical, epidemiological, and environmental variables, our objective is to fashion predictive models adept at accurately discerning dengue cases .

**Problem statement**

* Based on symptoms, machine learning existing applications or systems are fully created for health care professionals, doctors, and other professionals. At that moment there is no specific machine learning application or system is available for patient to detect the dengue by their own smart device.
* Lot of urban areas don’t have laboratory facilities for earlier detecting of dengue. Based on that urban area people need to go long distance for meet the doctor or health care professional to check the dengue or not. So at that time Dengue fever can be highly increase for them.

**Main Objectives**

Objective 1: Review Existing Machine Learning Applications for Dengue Detection

Examine and analyze current machine learning systems used for detecting dengue fever. Assess the existing systems and limitations of current methods.

Objective 2: Explore Patient Needs and Challenges in Dengue Diagnosis

Investigate the requirements and difficulties patients face regarding dengue diagnosis, particularly in urban settings where laboratory access is limited. Explore the obstacles patients encounter in obtaining prompt and accurate dengue diagnosis and their potential impact on public health.

Objective 3: Develop a User-Friendly Dengue Detection System

Create a new machine learning-based dengue detection system tailored to patients' needs and suitable for use on their personal smart devices. Prioritize ease of use, accessibility, and convenience to ensure the system is suitable for a diverse range of patients.

Objective 4: Optimize Machine Learning Algorithms for Dengue Prediction

Evaluate and compare various machine learning algorithms, such as binary logistic regression, decision trees, and random forests, for their effectiveness in predicting dengue fever. Investigate methods for improving model performance, such as tuning hyperparameters, selecting relevant features, and employing ensemble techniques.

Objective 5: Validate the Performance of the Dengue Detection System

Thoroughly test and validate the developed dengue detection system using symptoms data . Assess the system's accuracy, sensitivity, specificity, and predictive capabilities against established benchmarks and reference standards.

Objective 6: Offer Recommendations for System Enhancement and Future Development

Identify areas where the dengue detection system can be improved based on symptoms.

**Literature Review**

**Introduction**

In now a days dengue is a common health issue in the world. Because dengue is spread though the word faster. Especially in srilanka. For an example in srilanka in may 2023 61,361 total dengue patients are reported(Sri Lanka: Dengue Outbreak - May 2023). Earlier days lot of laboratory testing methods were doing for detecting the dengue. For example Reverse transcriptase-polymerase chain reaction (RT-PCR), viral isolation and identification, nuclear acid sequence-based amplification (NASBA), IgM and IgG seroconversion, PCR testing are used. But these tests have several disadvantages. for example accuracy of results, cost, complexity, and takes lot of time to get the result etc (Wong et al., Diagnosis of severe dengue: Challenges, needs and opportunities 2020). Based on these disadvantages different systems, and machine learning techniques already created for dengue detection. But now a days most of these created machine learning systems or applications, and normal application, and systems are created for assisting to doctors and healthcare professional to identify the patient has dengue or not. Which means there is no specifically created the any particular machine learning system or application for patient to dengue identify. In this literature review mainly focused on what are the already existing application, systems by using machine learning techniques and their problems. And also consider the other normal application, or systems. And their problems.

**Problems**

**Dengue prediction and diagnosis using machine learning techniques**

According to this “A dengue disease prediction and diagnosis model using sentiment analysis and machine learning algorithms” research paper, for the predicting the dengue KNN classifier, decision tree, random forest, Gaussian naive Bayes, and support vector classifier (SVC)(Gupta et al., DDPM: A dengue disease prediction and diagnosis model using sentiment analysis and machine learning algorithms 2023).

**The main limitations of this application**

Unbalance data set - when it comes to the dengue dataset. Where that contains positive cases of dengue may be rare compare to the negative cases.

Hyper parameter tuning problem - when using this models for increasing the model accuracy need to take lot of time to find out the best parameters.

Scalability - when using this KNN classifier, random, SVC are high expensive when we are dealing with larger amount of dataset (Jamwal & Bhatia, Prevalence of vector borne diseases in Jammu division, Jammu and Kashmir, India 2021).

**Classification of dengue application using machine learning techniques**

According to the “Classification of dengue using machine learning techniques” research paper, Simple Cart, C-4.5, Multi-layer perception algorithms used for classifying the dengue is infected or not (Sajana et al., Classification of dengue using Machine Learning Techniques 2018).

The main limitations of this models

* Overfitting - These simple cart, C-4.5, willing to overfitting, when trees becomes to the more deep, and complex. But this leads to generate the inaccurate predictions.
* Sensitive to small changes - these simple cart, C-4.5 algorithms highly respond to the training dataset. That leading to the different tree structure and potentially different predictive performance.
* Imbalance dataset - when it comes to the dengue dataset. Where that contains positive cases of dengue may be rare compare to the negative cases.
* Privacy and security problems - extracting the human sensitive information raise some privacy problems.
* Model accuracy - According to the “Dengue outbreaks prediction in bangaladesh perspective using distinct multi-layer perceptron NN and decision tree” research paper. Predicting accuracy of Multi-layer perceptron 68.5%. which means it not sufficient for using the predicting purpose (Khan et al., Dengue outbreaks prediction in Bangladesh perspective using distinct multilayer Perceptron NN and decision tree 2022).

**Presumptive diagnosis System for dengue fever by using machine learning**

Presumptive diagnosis system used the Decision Tree, Random Forest, Naive Bayes algorithms used for predicting the dengue fever. What ever this Random Forest , Naive Bayes, Decision Tree algorithms use for early detection of dengue in this system (Khan & Raza, Development and evaluation of a predictive diagnostic system for dengue fever using Machine Learning Techniques 2023).

The main Limitation of this system

* Less number of data points are available
* Accuracy of this models are very low
* Sensitivity - presumptive diagnosis system is lack with sensitivity for early stage of detecting (Khan & Raza, Development and evaluation of a predictive diagnostic system for dengue fever using Machine Learning Techniques 2023).

**Detection of dengue disease by using fused machine learning**

In this case use the PFDM model. In this PFDM model use two main ML-based procedures. For an example SVM and ANN. And this PFDM has two basic components. the training layer and the testing layer. In the training layer,

It has five steps (collecting, preprocessing, classification, efficiency, and machine-level combination). If the model fails to meet learning criteria, it is reassigned until satisfactory results are achieved. The outputs of ANN and SVM are then fused, and the trained model is stored in a cloud system. In the testing layer, data is obtained from a database, and preprocessed trained models are loaded from the cloud.

The fused model is used to predict whether a Dengue diagnosis is progressive or destructive, with the predicted outcome compared to the actual result to measure accuracy (Al Nasar et al., Detection of dengue disease empowered with fused machine learning 2022).

The main limitation

* One important factor in classification is class imbalance, and classification efficiency cannot be entirely determined by accuracy rates alone (Al Nasar et al., Detection of dengue disease empowered with fused machine learning 2022).
* Feature engineering - SVM(Support vector machine) is heavily depend on feature engineering to identify the relevant patterns (Hoyos et al., Dengue models based on machine learning techniques: A systematic literature review 2021).
* Complexity and overfitting - when dealing with the noisy and small datasets. Overfitting can generate unreliable predictions (Hoyos et al., Dengue models based on machine learning techniques: A systematic literature review 2021).
* Computational resources - when using ANN it required the computational resources including high performance GPU, and memory (Chakraborty et al., Forecasting dengue epidemics using a hybrid methodology 2019).

**Decision support system for dengue detection**

The use of decision support systems (DSS) is essential for the early diagnosis of dengue. A viable method for creating DSS for dengue care is case-based reasoning (CBR), which uses clinical guidelines and historical cases to forecast a patient's present state based on their vital signs and symptoms (binti Mohd Zainee & Chellappan, A preliminary dengue fever prediction model based on vital signs and blood profile 2020).

Limitation of decision support system

* Imbalance dataset - which means dengue infected positive cases significantly are lower than negative cases.
* Data is limited - dengue dataset size is small .
* Complexity of system - Dengue has several symptoms. That symptoms can be overlapped with similar similar illness (Lopez et al., An intelligent decision support system to prevent and control of Dengue 2018).

**Solution**

According to the above mentioned machine learning systems, applications and normal systems like decision support system there are significant limitations are available. Base on that machine learning system, applications limitations are complexity of model and system, low accuracy of models, overfitting, unbalance dataset etc. And also above mention systems are mainly created for doctor and healthcare professional. Then some urban area people need to go long distance for meet the doctor or laboratories for detecting the dengue is infected or not. According to that urban area people cannot be identify the dengue in earlier stage. These are the major problems existing in machine learning dengue systems and application. When it comes to the normal systems like decisions support system there is some issue like complexity of the system, data limitation, inbalance dataset available.

Based on above mentioned machine learning systems, applications and normal systems like decision support systems problems or limitations, dengue detection system is going to be implemented for patient by using decision tree, random forest, logistic regression algorithm while including the “grid\_search cv” for finding the best parameters, “ensemble technique” , proper dataset and other models parameter like random state.

**Methodology**

This research belongs to the both quantitative and qualitative aspects

**Technologies**

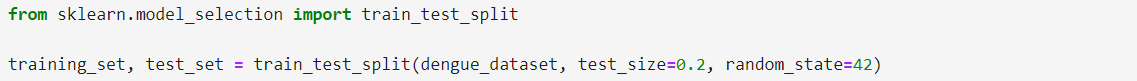
Qualitative description - For this dengue detection project by using machine learning used flask (python frame work) for back end, HTML, CSS, Bootstrap , and JavaScript for front end. And also testing for each software component of this application use the pytest( python framework).

**Data Collection**

Qualitative description - For the dengue detection system based on symptoms by using machine learning technique, data sets are received by websites and hospitals, and other medical institutions. Combine these datasets together and created the full dataset.

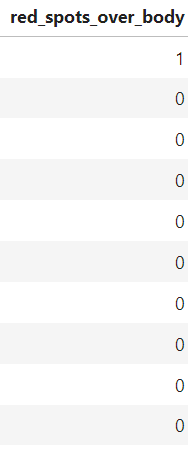
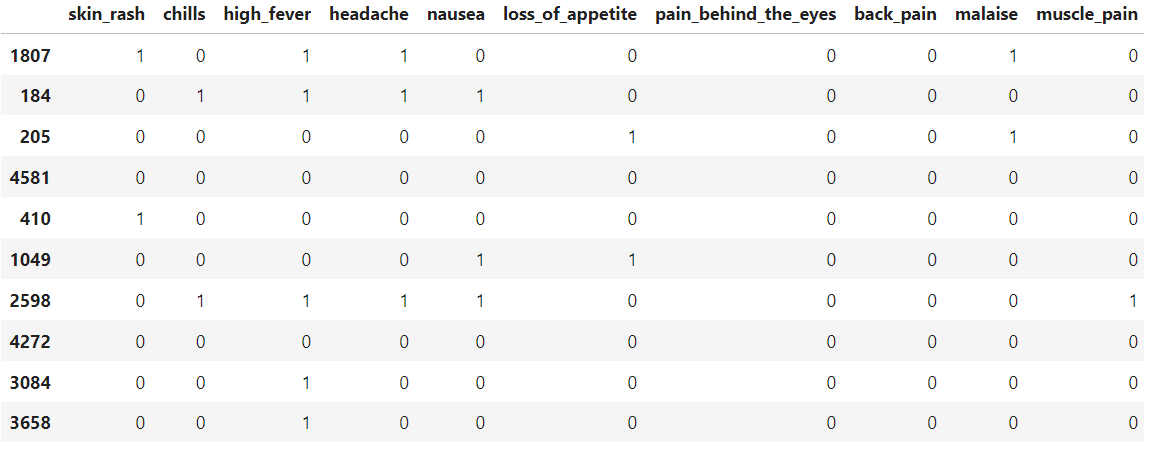
**Splitting the dataset**

Quantitative description - This dengue dataset is going to be divided into the two part by using “random splitting function” Training set and testing set. Training set size is 80%. Test set size is 20%. This training set is used for model training and testing is used for evaluate model performance.



**Data Cleaning**

Quantitative description - Checking the null values in created training and test dataset. According to this dengue prediction for srilanka by using machine learning, dengue dataset doesn’t have any particular null values. And also check the correlational coefficiency which means what are the important attributes for predicting the dengue. Based on that correlational coefficiency remove the unnecessary columns from the training and testing dataset. Below image represent dataset after removing the unnecessary columns.



**Model selection and explanation of machine learning models used**

For classifying this dengue, binary logistic regression, decision tree algorithm, random forest algorithms are the models going to be used.

Qualitative description  
Binary logistic regression - Binary logistic regression is chosen as a model for dengue prediction due to its simplicity and ease of interpretation. Unlike more complex models, logistic regression offers a clear understanding of the relationship between independent variables and the binary outcome of dengue presence. Its straightforward nature makes it particularly valuable in medical research, where comprehensibility is crucial. Logistic regression is also adept at handling large datasets efficiently, making it suitable for the extensive data often encountered in dengue prediction studies. Furthermore, it accommodates both continuous and categorical predictor variables, allowing for the incorporation of diverse data types commonly found in such studies. By estimating the probability of dengue presence based on various symptoms and risk factors, logistic regression serves as a valuable tool in the array of machine learning techniques for dengue prediction (Caicedo-Torres et al., Machine learning models for early dengue severity prediction 2020)).

Qualitative description

Decision tree model - The decision tree model is a key component of our dengue detection system for several compelling reasons. Firstly, decision trees are renowned for their simplicity and ease of use, making them accessible to a wide range of users, including healthcare professionals and public health officials. This simplicity

translates into ease of interpretation, allowing stakeholders to grasp the underlying decision-making process intuitively. Additionally, decision trees have demonstrated the potential to achieve high levels of accuracy in dengue prediction tasks. By efficiently partitioning the feature space into homogeneous regions, decision trees can capture complex relationships between environmental factors, demographic variables, and dengue incidence. This ability to model intricate interactions empowers our system to generate more accurate predictions, enabling proactive interventions and resource allocation. Moreover, decision trees excel in producing interpretable rules that align with domain knowledge, facilitating actionable insights for disease prevention and control strategies. Overall, the decision tree model represents a valuable asset in our quest to combat dengue fever effectively and mitigate its impact on public health. (Iqbal & Islam, Machine Learning for Dengue Outbreak Prediction: A performance evaluation of different prominent classifiers 2019)

Qualitative description

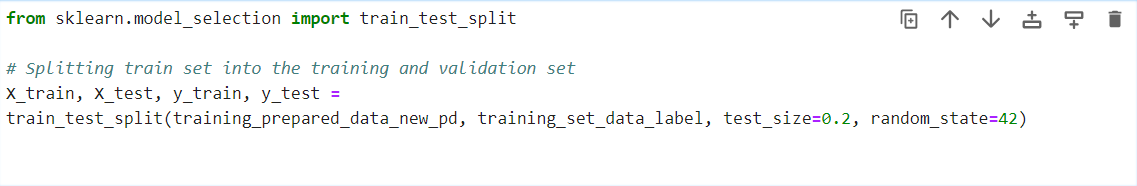
Random forest model -

Random forest is a cornerstone of our dengue detection system due to its multifaceted advantages. Firstly, random forest excels in enhancing model accuracy by leveraging the wisdom of crowds. By aggregating predictions from multiple decision trees trained on different subsets of the data, random forest mitigates the risk of overfitting and variance, resulting in robust and reliable predictions. This ensemble approach also enhances the model's generalization capability, enabling it to perform well on unseen data. Additionally, random forest is adept at handling large and complex datasets commonly encountered in dengue prediction tasks. Its inherent Parallelization and scalability make it well-suited for processing vast amounts of environmental, epidemiological, and clinical data, thereby facilitating comprehensive analysis and inference.

Furthermore, random forest offers built-in mechanisms for feature importance assessment, enabling us to identify the most informative variables driving dengue incidence prediction. This interpretability fosters a deeper understanding of the disease dynamics and informs targeted intervention strategies. Overall, the versatility, robustness, and scalability of random forest make it an indispensable tool in our efforts to combat dengue fever effectively and safeguard public health. (Sarwar & Al Mamun, Prediction of dengue using machine learning algorithms: Case study Dhaka 2022)

**Model training**

After spited the prepared data set into the training and testing dataset, This training set split into the training and validation test again . Below image is the example



**Techniques**

Qualitative description

In this methodology, utilize advanced techniques such hyperparameter tuning and grid search CV to optimize the performance of our models. These techniques involve identifying the most effective parameters for binary logistic regression, random forest, and decision tree algorithms, thereby fine-tuning the models for dengue prediction.

Binary Logistic regression model best parameters

logistic regression best parameers

Decision tree classifier model best parameters

Decision tree best parameters

Random forest classifier model best parameters

random_forest_best_parameters

By systematically exploring the above mentioned parameters, aim to enhance model accuracy and mitigate the risk of overfitting.

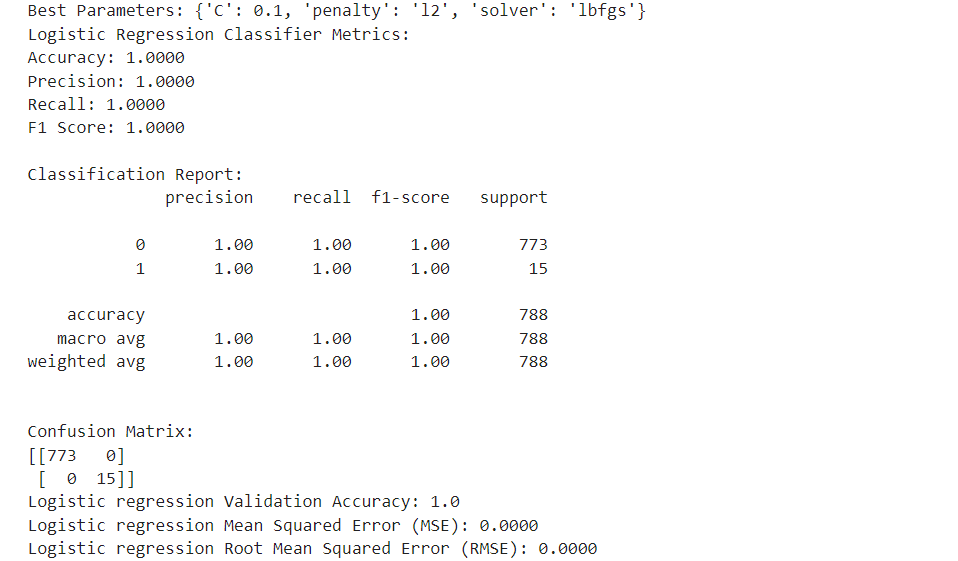
Additionally, we employ ensemble methods to further improve model robustness and generalization. Ensemble techniques involve combining predictions from multiple models, such as random forest, decision tree, and binary logistic regression that choose for dengue prediction.

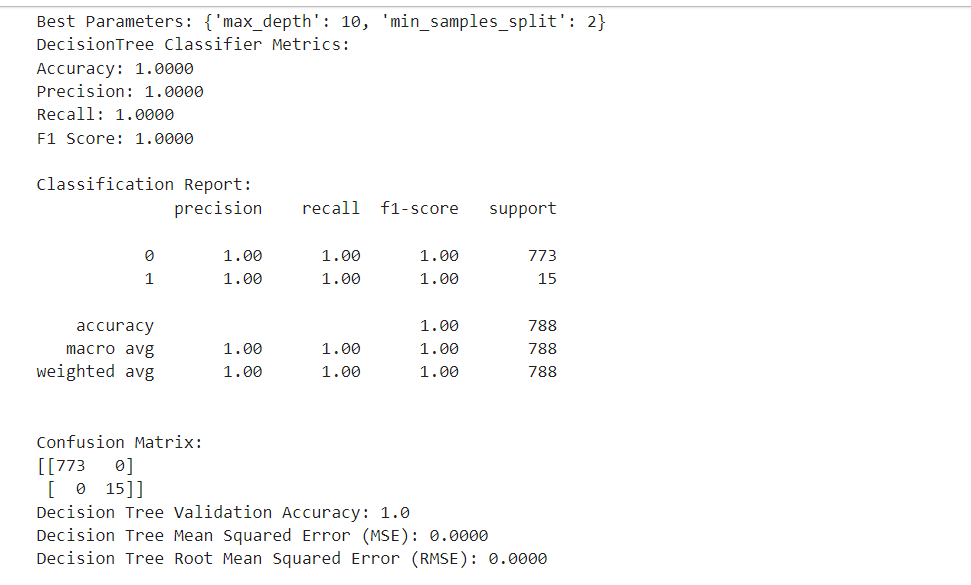
By leveraging the strengths of each individual model and mitigating their weaknesses, ensemble methods enable us to achieve superior predictive performance while reducing the likelihood of overfitting.

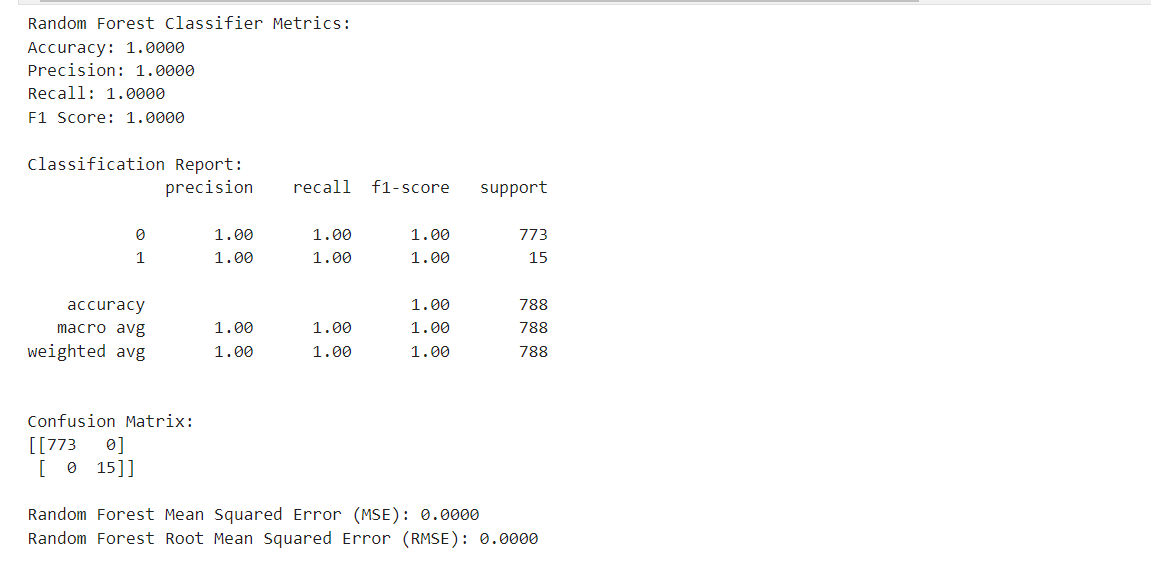
Overall, our approach integrates these advanced techniques within our methodology to optimize model performance, enhance accuracy, and ensure robust dengue prediction capabilities.

**Model results and final model evaluation**

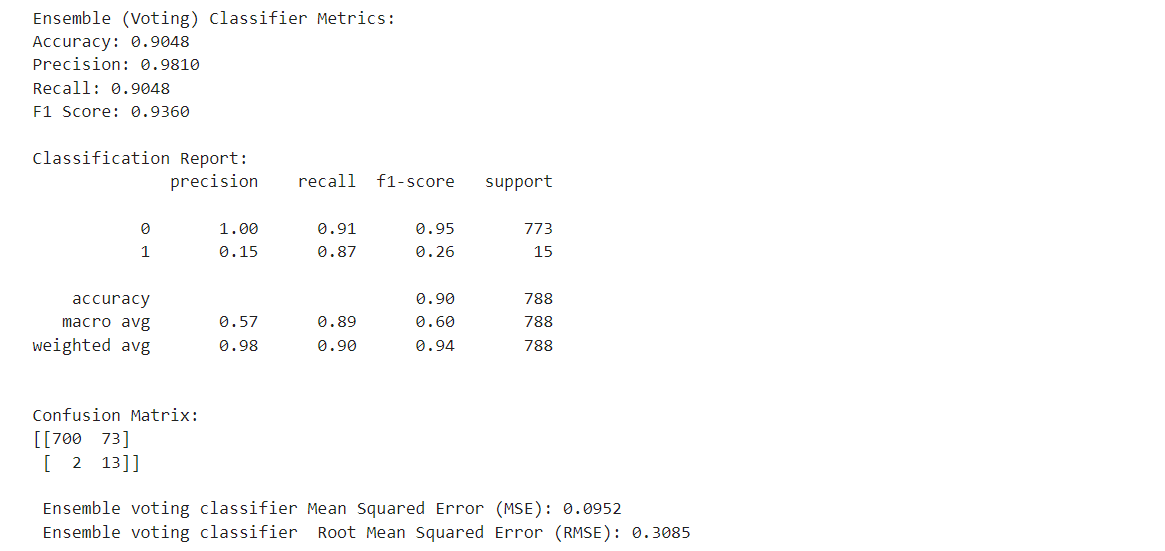
According to this dengue prediction project after doing the grid search cv for hyper parameter tuning, models metrices (accuracy, F1 score, precision, recall, F1 score) and model evaluations are shown below images.

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After doing the grid search cv and hyperparameter tuning model overfitting issue doesn’t fix. Because above random forest, decision tree, binary logistic regression accuracies are still 1.0(100%). So then, to avoid that overfitting issue use the ensemble technique. Below images is the example for using the ensemble technique and accuracy, precision, recall, F1 score after using the ensemble technique.

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When we consider the final model evaluation random forest, binary logistic regression, decision tree models accuracy is 1.0 (100%), and precision, recall, F1 score are 1.0 (100%). Mean squared error and root means squared error of this three models are 0.0000. which means overfitting. combine model by using ensemble technique metrices are accuracy is 0.9048 (90%), precision is 0.9810 (98%), recall is 0.9048 (90%), and F1 score is 0.9360 (94%). Mean squared error of this combine model is 0.952. And root means squared error of this combined model is 0.3085. So then final and best model is combined model by combining the binary logistic regression, decision tree classifier, random forest classifier.

**Model deployments**

After implementing ensemble techniques, the ensemble voting classifier emerged as the final model for dengue prediction. To make this model accessible for real-world use, we created a pickle file to store its parameters and import it into our application. With Flask framework, we seamlessly integrated this model into the bac kend, allowing it to interact with the front end interface. This integration ensures that our dengue detection system is user-friendly and readily available for deployment, empowering users to make informed decisions about dengue risk and management.

**Limitations of the methods have been identified in the methodology**

Limited Data Availability and Quality: One of the primary challenges in developing predictive models for dengue detection is the availability and quality of data. While data are collected from websites, hospitals, and medical institutions, there may be limitations in terms of completeness, accuracy, and representativenes. To overcome this limitation, efforts should be made to enhance data collection mechanisms, collaborate with relevant stakeholders to improve data sharing, and employ data augmentation techniques to expand the dataset size (Hoyos et al., Dengue models based on machine learning techniques: A systematic literature review 2021).

Imbalanced Dataset: Imbalance in the dataset, where the number of dengue-positive cases may be significantly lower than the dengue-negative cases, can impact the performance of the predictive models. This imbalance can lead to biased predictions and reduced sensitivity in detecting dengue cases. To address this issue, techniques such as oversampling of the minority class (dengue-positive cases) or using algorithms that are robust to class imbalance should be considered(Hoyos et al., Dengue models based on machine learning techniques: A systematic literature review 2021).

Model Interpretability: While complex machine learning models like random forest and may offer high predictive accuracy, they often lack interpretability, making it challenging to understand the underlying factors contributing to dengue prediction. To enhance interpretability, simpler models like logistic regression and decision trees are utilized in conjunction with more complex models. Additionally, techniques such as feature importance analysis and model visualization can aid in understanding the decision-making process of the models (Saturi, Development of prediction and forecasting model for dengue disease using machine learning algorithms 2020).

Generalization to Other Regions: The predictive models developed in this research may be tailored to the specific context of Sri Lanka, raising concerns about their generalizability to other regions with different environmental, demographic, and healthcare characteristics. To improve generalizability, future research should involve validation of the models across diverse geographical regions and populations, incorporating region-specific features and adjusting model parameters accordingly.

**Analysis and Discussion:**

In the analysis and discussion of dengue detection for Sri Lanka using machine learning models such as binary logistic regression, decision tree, and random forest, the interpretation of results provides valuable insights into the effectiveness and limitations of these models.

The models demonstrated promising performance in accurately predicting dengue presence based on symptom data. The binary logistic regression model, known for its simplicity and interpretability, offered a clear understanding of the relationship between symptoms and dengue presence. Decision tree models showed the potential for easy interpretation and high prediction accuracy, while random forest models enhanced accuracy by reducing overfitting and handling larger datasets effectively.

However, despite their effectiveness, the models also exhibited certain limitations. While binary logistic regression provides simplicity and interpretability, it may struggle with capturing complex relationships in the data. Decision tree models, although easy to understand, are prone to overfitting, especially with deeper trees. Random forest models, while robust, can be computationally expensive and challenging to interpret due to their ensemble nature.

The implications of these findings for dengue detection and public health are significant. Accurate prediction of dengue presence using machine learning models can facilitate early detection and intervention, helping public health authorities allocate resources more effectively and mitigate the spread of the disease. By leveraging these models, healthcare practitioners can prioritize high-risk areas for targeted interventions, such as mosquito control measures or public awareness campaigns.

Future research directions may include exploring the use of more advanced machine learning techniques, such as deep learning or ensemble methods, to improve prediction accuracy further. Additionally, integrating additional data sources, such as environmental or demographic factors, could enhance the models' predictive capabilities and support more comprehensive dengue surveillance efforts.

**Solution design and implementation**

In the design and implementation of machine learning models for dengue detection in Sri Lanka, careful attention must be given to ensure their seamless integration into existing surveillance systems and their potential impact on public health practices. Choosing appropriate models, such as binary logistic regression, decision trees, and random forests, requires considering their suitability for the specific needs and constraints of dengue surveillance. Each model presents its own advantages and challenges, necessitating thorough evaluation based on factors like interpretability, scalability, and computational requirements.

To integrate these models effectively into dengue surveillance systems, it is crucial to establish interoperability with current data collection, processing, and reporting mechanisms. This may entail developing standardized data interfaces, utilizing cloud-based solutions for scalability, and implementing real-time data integration pipelines to facilitate timely and accurate dengue risk assessments. Additionally, robust validation and evaluation frameworks are essential to continually monitor model performance and adapt to changing dengue dynamics and epidemiological trends.

Several challenges, including data quality issues, model interpretability concerns, and resource limitations, must be addressed for the real-world deployment of machine learning models in dengue detection. Strategies such as data preprocessing, feature engineering, and model explainability techniques can help overcome these challenges and enhance the reliability and trustworthiness of deployed models. Moreover, fostering collaboration among public health authorities, researchers, and local communities through stakeholder engagement and capacity building initiatives is crucial to maximize the impact of machine learning-based dengue surveillance efforts.

The potential impact of these models on public health practices in Sri Lanka is substantial, offering the opportunity to complement traditional surveillance methods with data-driven insights for more targeted and effective dengue control strategies. Leveraging the predictive capabilities of machine learning models enables public health authorities to identify high-risk areas, allocate resources efficiently, and implement proactive interventions to curb the spread of dengue fever, thus alleviating the burden on healthcare systems. Ultimately, successful integration and deployment of these models have the potential to revolutionize dengue surveillance and control efforts in Sri Lanka, leading to improved public health outcomes and greater resilience to dengue outbreaks.

**Research questions and Hypotheses**

For Normality testing, correlational analysis regression analysis,

* Sample dataset :DengueDataset
* Significant level (α) = 0.05 (5%)
* Confidence level = 0.95 (95%)
* H0 = Null Hypothesis
* H1 = Alternative Hypothesis

**Normality testing**

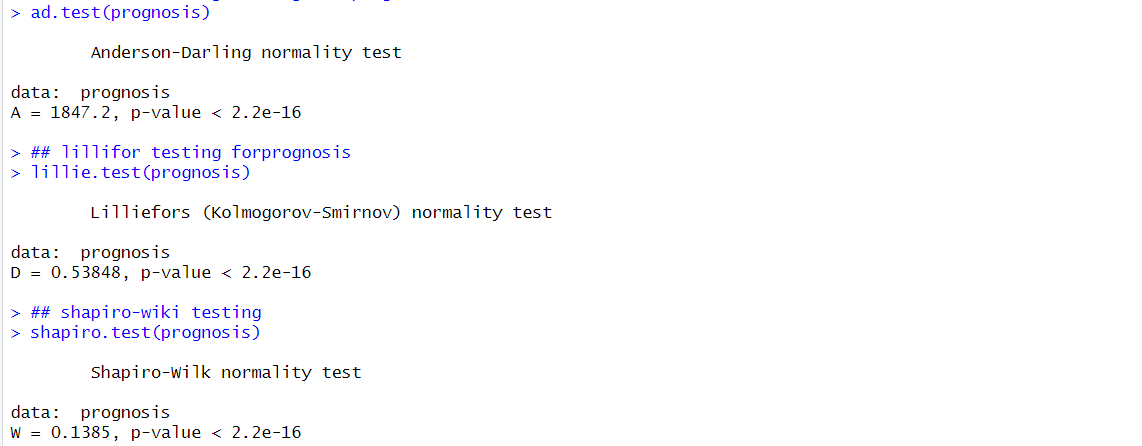
Normality testing means check whether data is normally distributed or not. Below images are examples for normality testing.

Variable = prognosis

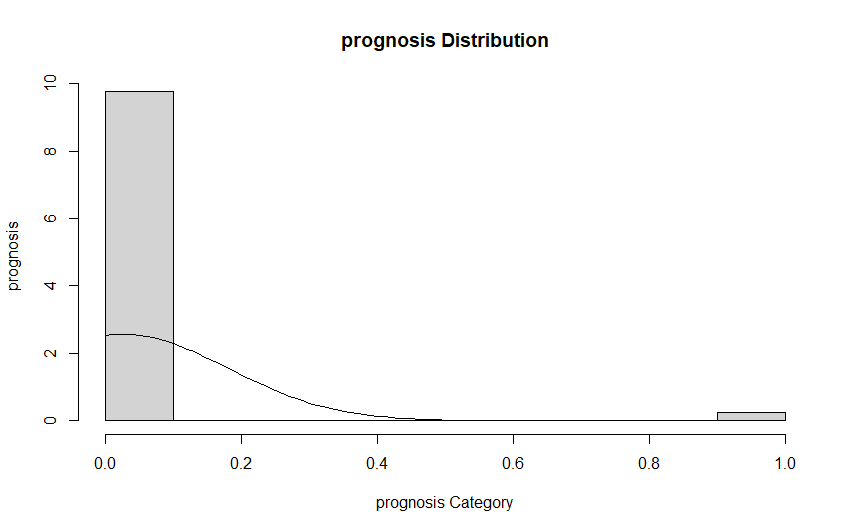
(\*) Whether or not prognosis is normally distributed?

the null hypothesis posits that the prognosis values follow a normal distribution.

Conversely, the alternative hypothesis suggests that the prognosis values do not conform to a normal distribution.



Based on the statistical analysis conducted, the obtained p-value of 2.2e-16 is significantly lower than the predetermined significance level (alpha) of 0.05. Consequently, we reject the null hypothesis and accept the alternative hypothesis. In simpler terms, this suggests that the prognosis does not follow a normal distribution.



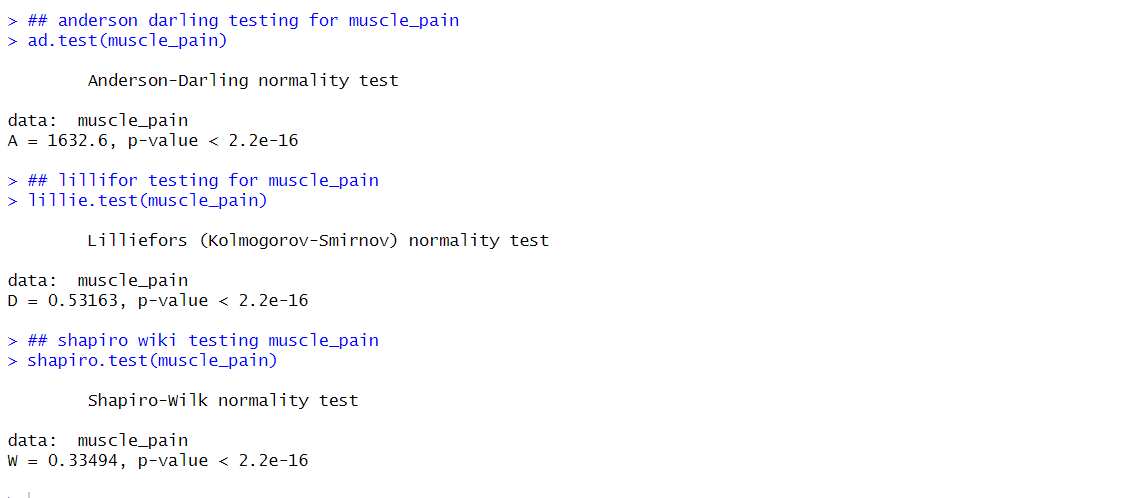
According to the above three test p value is 2.2e-16. which means p-value is less than the alpha value (0.05). conclusion of this test is reject the null hypotheses and accept the alternative hypothesis. Which means prognosis is not normally distributed.

Variable = muscle\_pain

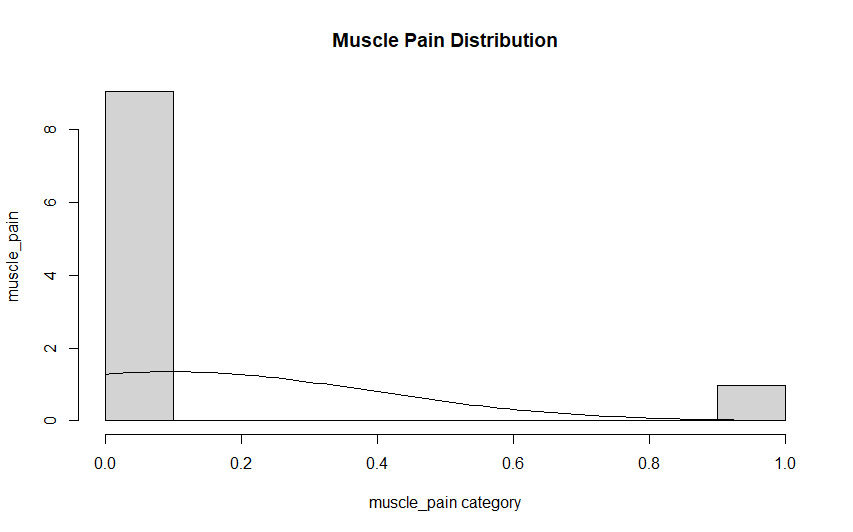
(\*) Whether or not muscle\_pain is normally distributed?

the null hypothesis states that the muscle\_pain values are normally distributed.

Conversely, the alternative hypothesis suggests that the muscle\_pain values are not normally distributed.



Above statistical tests yielded a p-value of 2.2e-16, indicating its significance compared to the chosen alpha level of 0.05. Consequently, we reject the null hypothesis and favor the alternative hypothesis. This indicates that the prognosis does not adhere to a normal distribution.

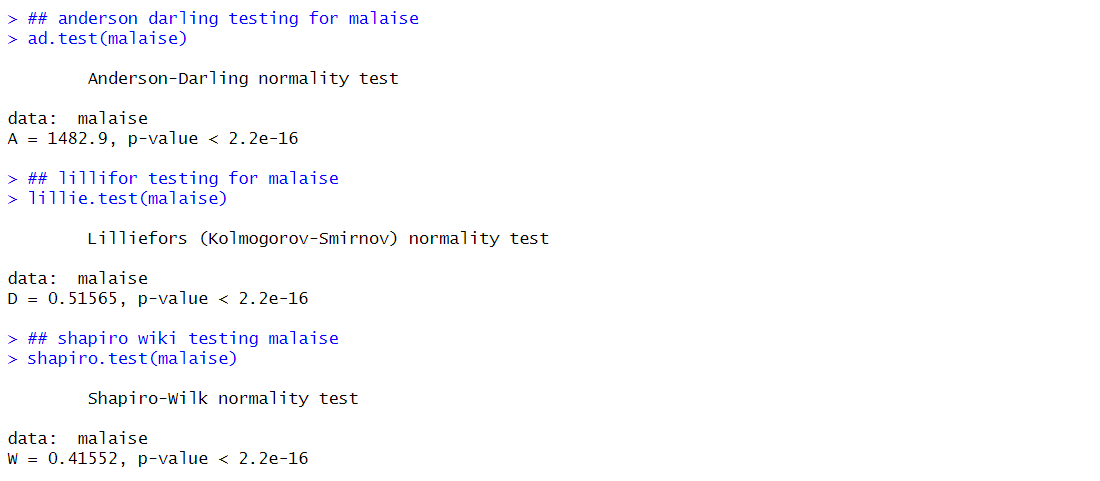


The graph's curve tilts towards the right, hinting that the malaise data may not conform to the usual distribution pattern, particularly when examining a 5% significance level.

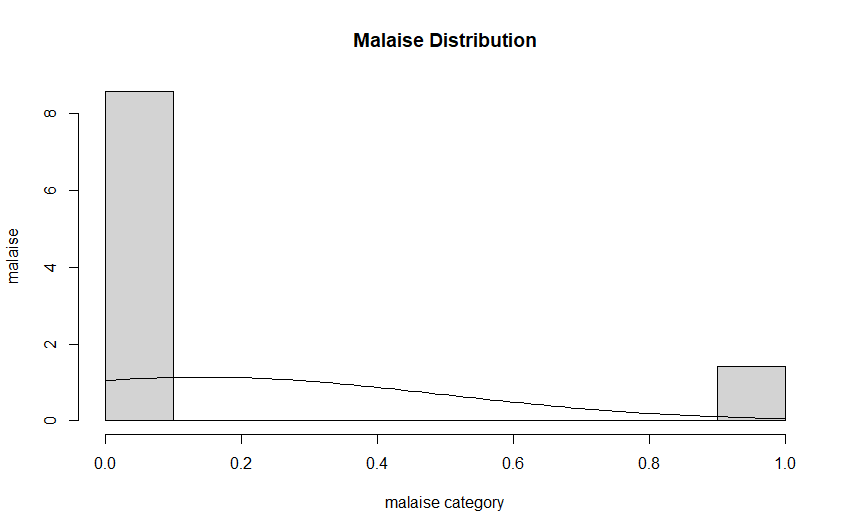
Variable = malaise

(\*) Whether or not malaise is normally distributed?

the null hypothesis proposes that the malaise values follow a normal distribution. Conversely, the alternative hypothesis suggests that the malaise values do not adhere to a normal distribution.



According to the above three test p value is 2.2e-16. which means p-value is less than the alpha value (0.05). conclusion of this test is reject the null hypotheses and accept the alternative hypothesis. Which means malaise is not normally distributed.

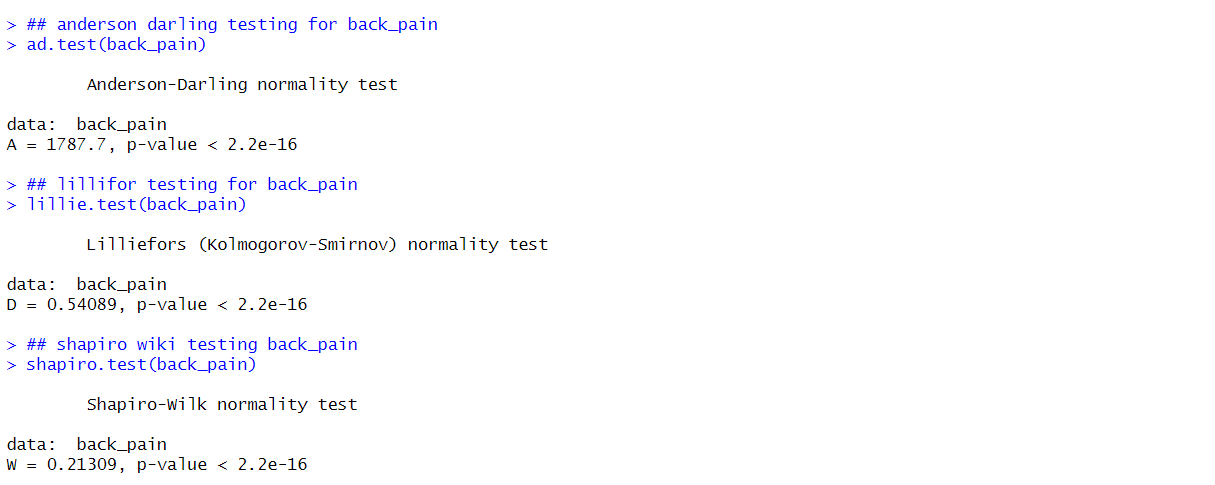
  
The curve on the graph slopes to the right, suggesting that the malaise data might not follow the typical distribution pattern, especially when considering a 5% significance level.

Variable = back\_pain

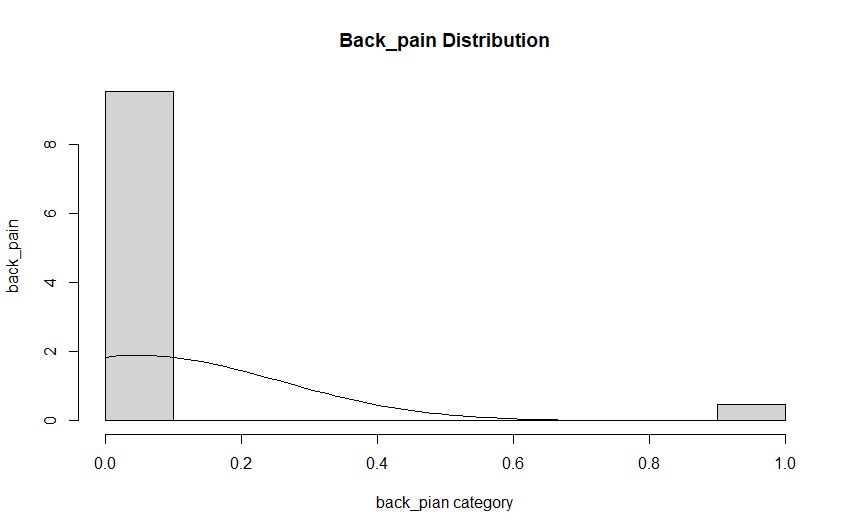
(\*) Whether or not back\_pain is normally distributed?

the null hypothesis assumes that the back\_pain values follow a normal distribution.

Conversely, the alternative hypothesis suggests that the back\_pain values do not conform to a normal distribution



With a p-value of 2.2e-16, significantly lower than the alpha level of 0.05, we reject the null hypothesis and accept the alternative hypothesis from the test results. This indicates that malaise is not distributed normally.

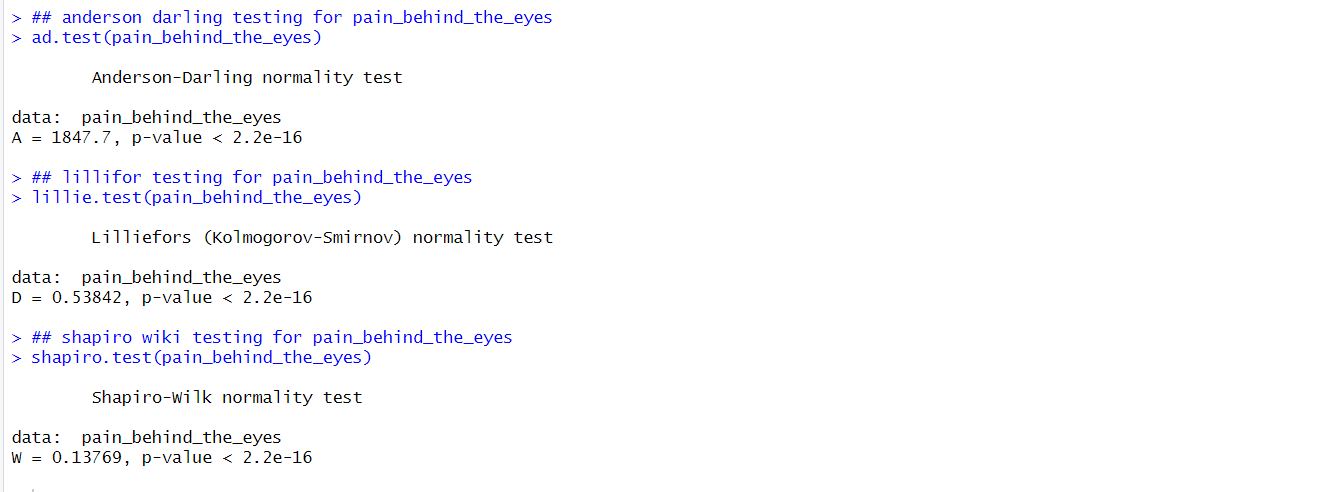


The curve on the graph slopes to the right, suggesting that the back\_pain data might not follow the typical distribution pattern, especially when considering a 5% significance level.

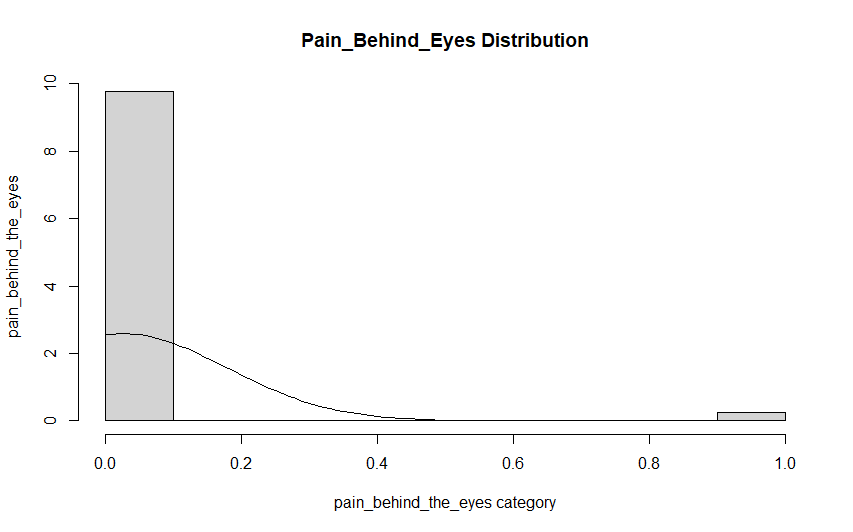
Variable = pain\_behind\_the\_eyes

(\*) Whether or not pain\_behind\_the\_eyes is normally distributed?

the null hypothesis asserts that the pain\_behind\_the\_eyes values are normally distributed. Conversely, the alternative hypothesis suggests that the pain\_behind\_the\_eyes values do not adhere to a normal distribution.



Based on the results of the three tests, the p-value obtained is 2.2e-16, indicating a significant deviation from the null hypothesis at the 0.05 alpha level. Consequently, we reject the null hypothesis and embrace the alternative hypothesis. In practical terms, this suggests that pain\_behind\_the\_eyes does not exhibit a normal distribution.

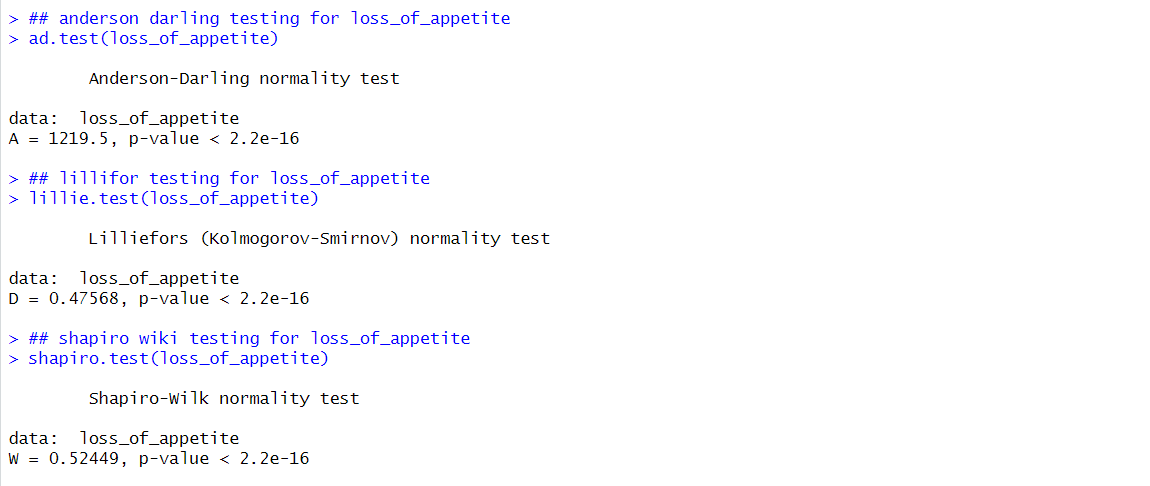


The graph's curve leans to the right, indicating that the pain\_behind\_the\_eyes data may not adhere to the normal distribution pattern, particularly at a 5% significance level.

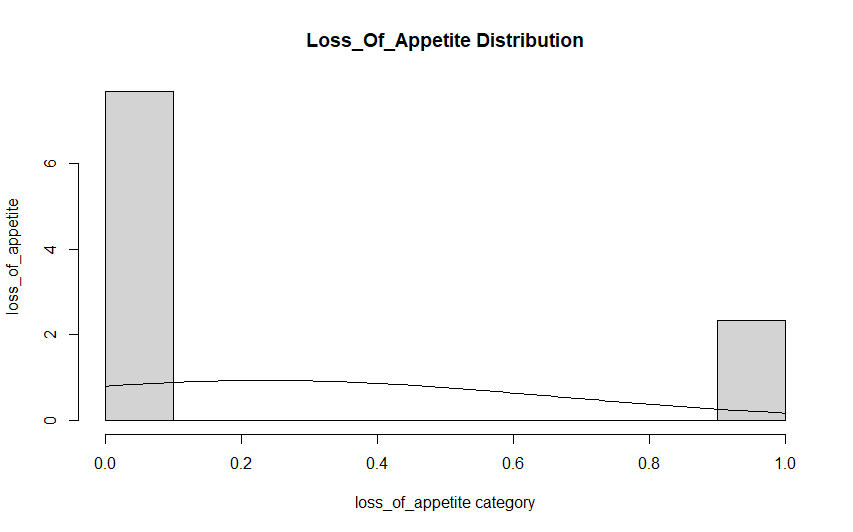
Variable = loss\_of\_appetite

(\*) Whether or not loss\_of\_appetite is normally distributed?

the null hypothesis states that the loss\_of\_appetite values follow a normal distribution. Conversely, the alternative hypothesis suggests that the loss\_of\_appetite values do not conform to a normal distribution.



Based on the statistical analysis conducted, the p-value obtained is 2.2e-16, which is significantly lower than the predetermined alpha value of 0.05. Consequently, we reject the null hypothesis and accept the alternative hypothesis. This implies that loss\_of\_appetite does not follow a normal distribution.

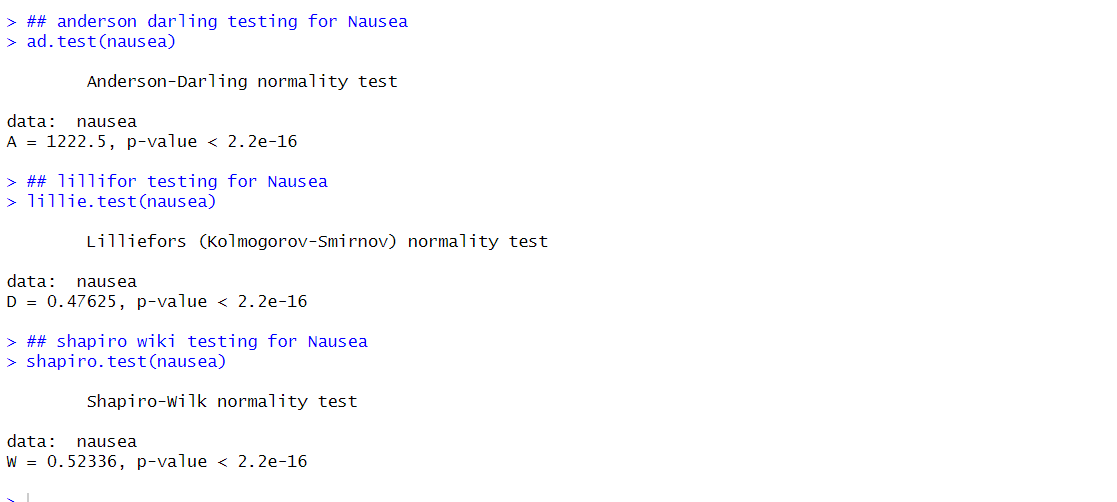


The curve in the graph tilts to the right, suggesting that the loss\_of\_appetite data might not follow the typical pattern of distribution, especially when we look at a 5% significance level.

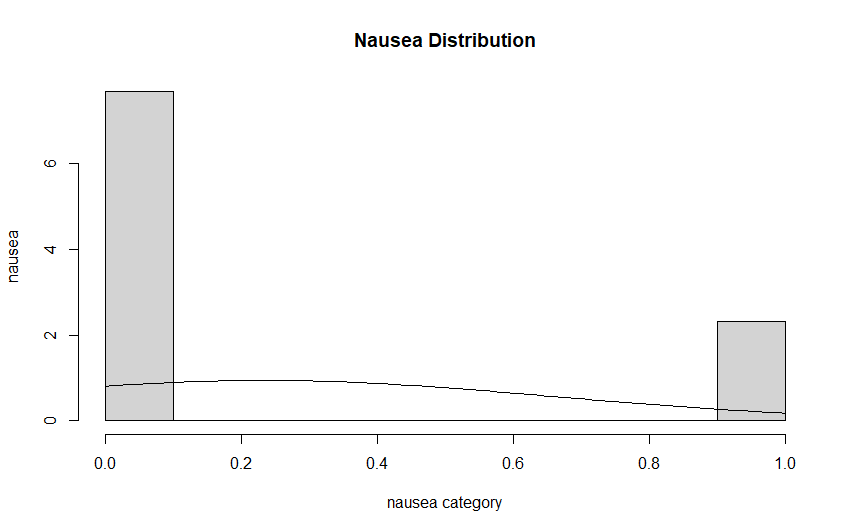
Variable = nausea

(\*) Whether or not nausea is normally distributed?

Null Hypothesis (H0): The distribution of nausea values follows a normal distribution. Alternative Hypothesis (H1): The distribution of nausea values does not follow a normal distribution.



The statistical analysis reveals a p value of 2.2e-16, indicating a significant deviation from the normal distribution for the variable "nausea." With this p-value being well below the conventional significance level of 0.05, According to this normality tests of nausea, reject the null hypothesis and accept the alternative hypothesis. Consequently, it is evident that "nausea" does not adhere to a normal distribution pattern.

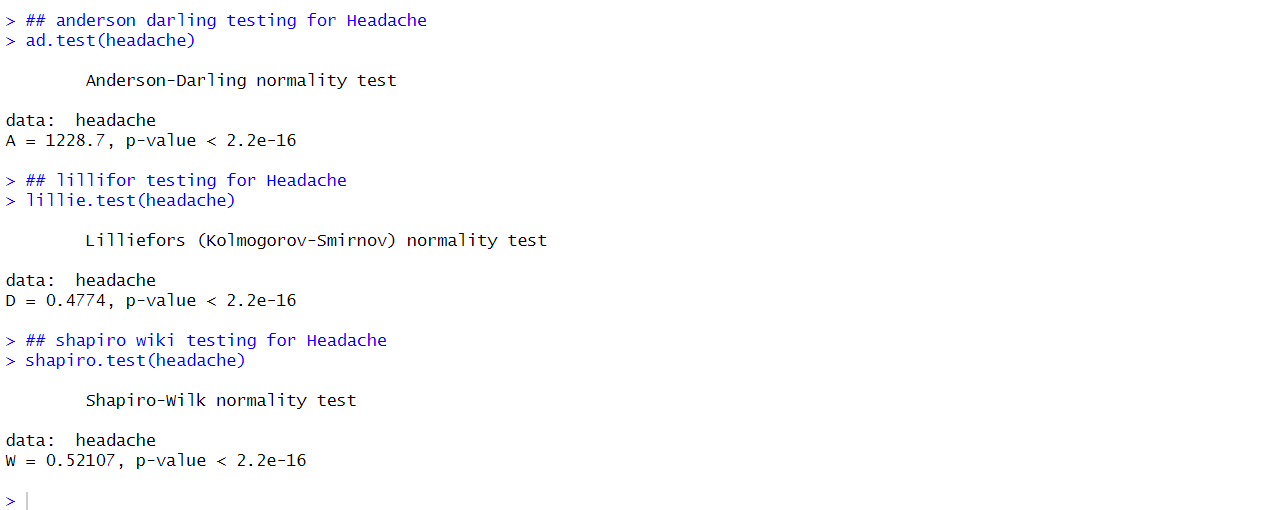


The bell curve displayed indicates a right-leaning shape. This implies that the nausea data may deviate from a normal distribution, especially when considering a 5% significance level.

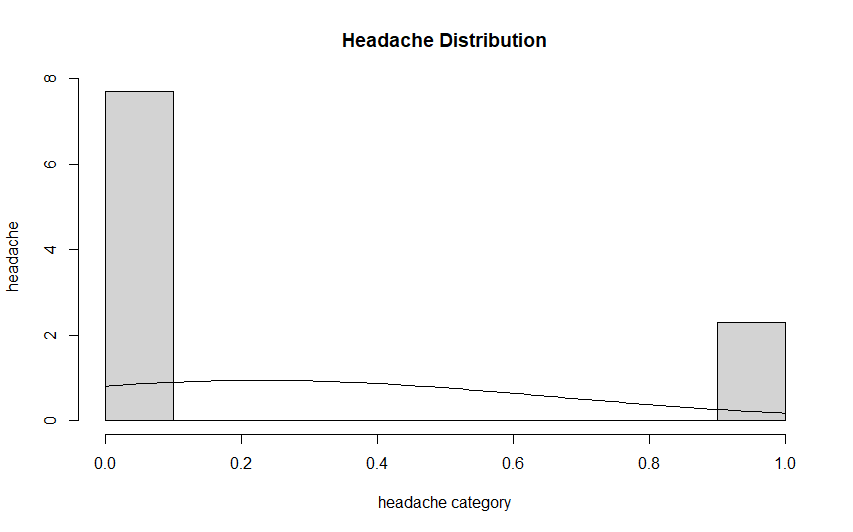
Variable = headache

(\*) Whether or not headache is normally distributed?

The null hypothesis (H0) assumes that the headache values are normally distributed, Alternative hypothesis (H1) suggests that the headache values deviate from a normal distribution.



The tests conducted yielded a p-value of 2.2e-16, indicating a significant deviation from the null hypothesis at the 0.05 alpha level. Consequently, we reject the null hypothesis and accept the alternative hypothesis, suggesting that headache does not exhibit a normal distribution.



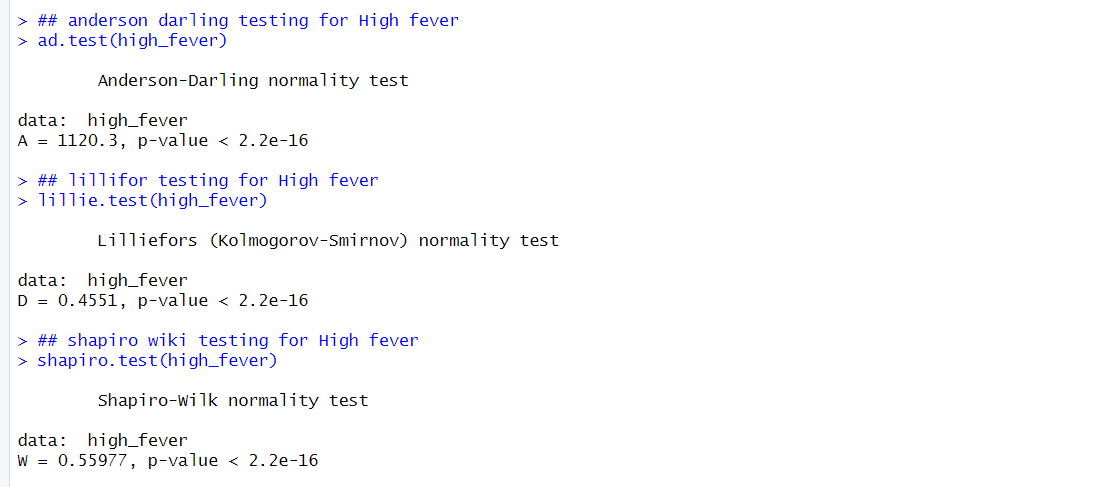
The bell curve displayed indicates a right-leaning shape. This implies that the headache data may deviate from a normal distribution, especially when considering a 5% significance level.

Variable = high\_fever

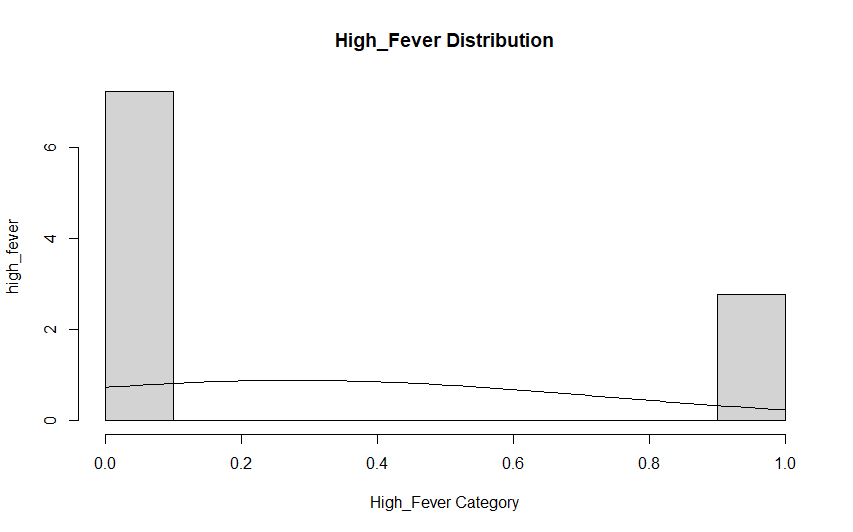
(\*) Whether or not high\_fever is normally distributed?

the null hypothesis posits that the distribution of high\_fever values conforms to a normal distribution. Conversely, the alternative hypothesis suggests that the distribution of high\_fever values deviates from a normal distribution.

窗体底端



Based on the statistical tests conducted, the obtained p value of 2.2e-16 is significantly lower than the predetermined alpha value of 0.05. This indicates that we reject the null hypothesis and accept the alternative hypothesis. Therefore, it can be concluded that the variable "high\_fever" is not normally distributed.



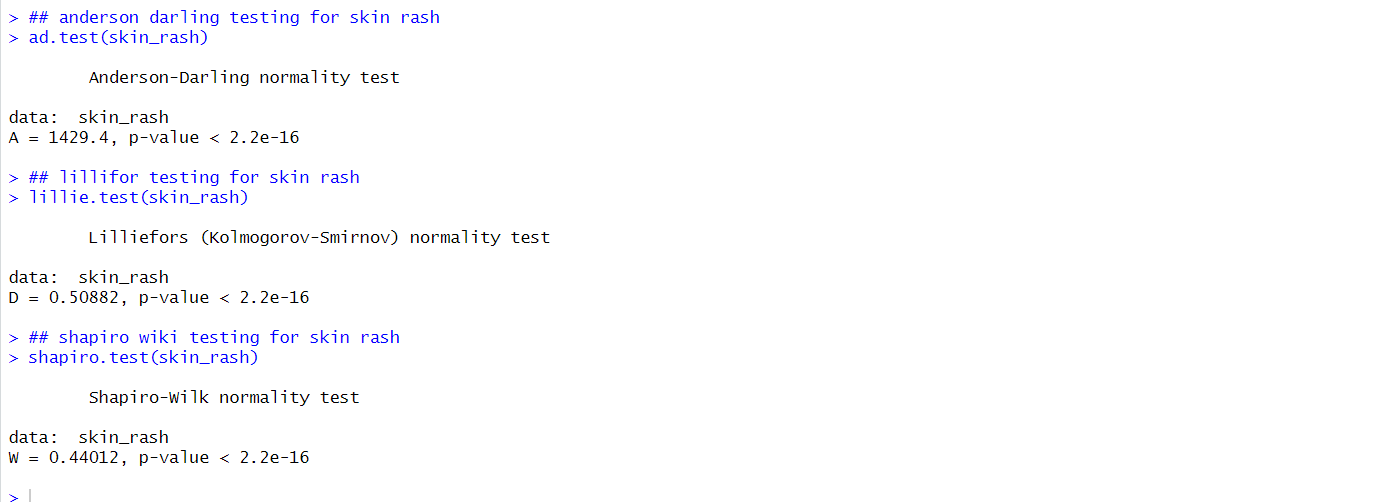
Based on the bell curve shown, which leans to the right, it suggests that the data for high fever might not follow a normal distribution at a 5% significance level.

Variable = skin\_rash

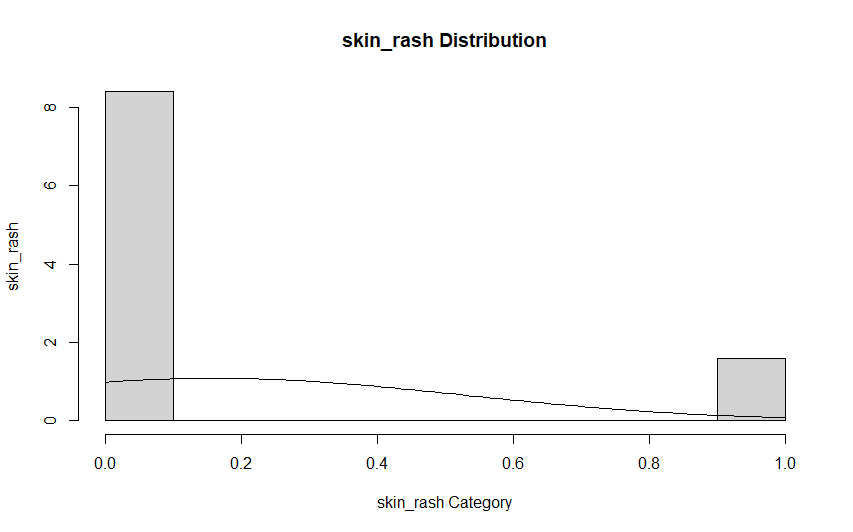
(\*) Whether or not skin\_rash is normally distributed?

Null Hypothesis The skin\_rash values follow a normal distribution.

Alternative Hypothesis The skin\_rash values do not adhere to a normal distribution.



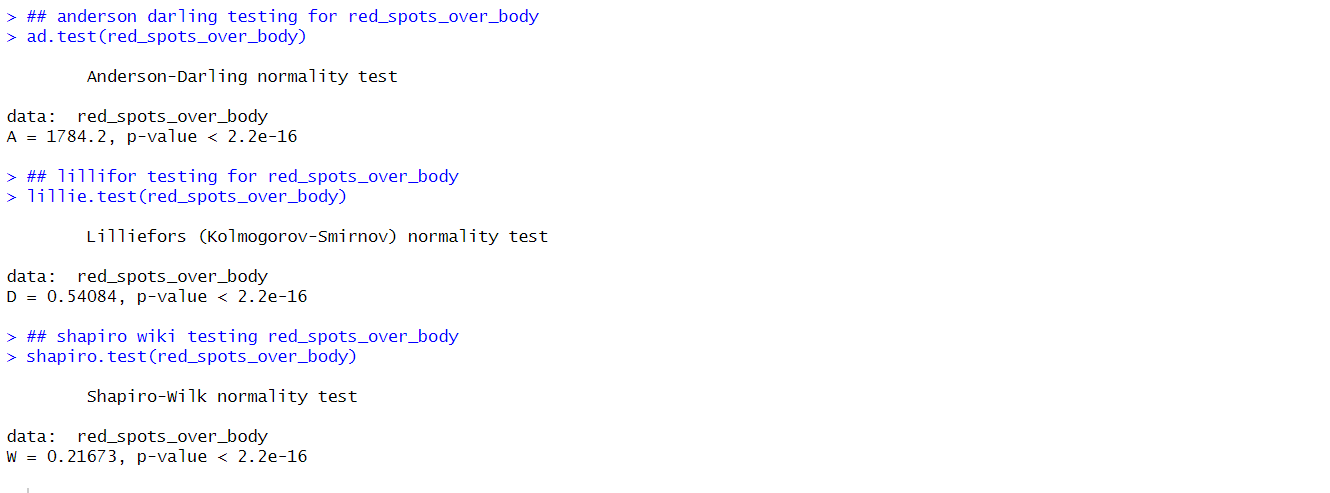
Based on the results of the three tests conducted, with a p value of 2.2e-16, which is significantly lower than the predetermined alpha value of 0.05, According to above tests reject the null hypothesis and accept the alternative hypothesis. Consequently, it can be inferred that the variable "skin\_rash" is not normally distributed.

  
The graph shows a curve that leans to the right. This suggests that the skin rash values might not follow the usual pattern of distribution, especially at a 5% significance level.

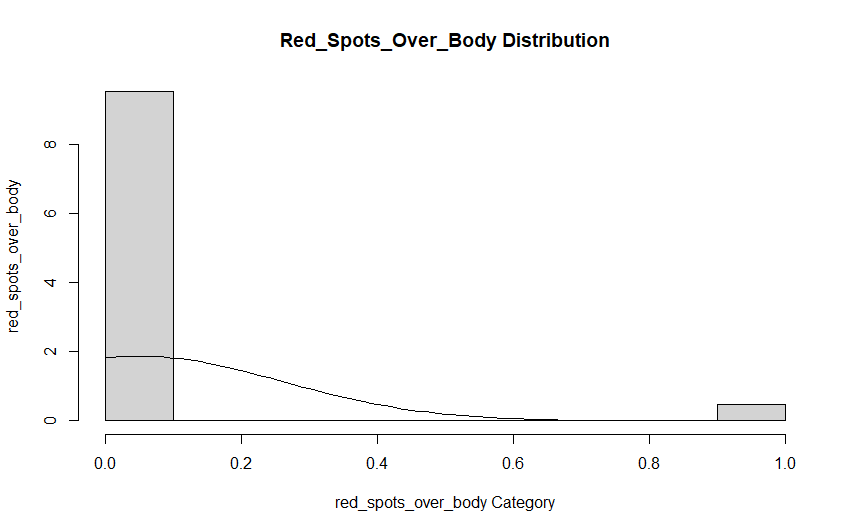
Variable = red\_spots\_over\_body

(\*) Whether or not red\_spots\_over\_body is normally distributed?

the null hypothesis suggests that the red\_spots\_over\_body values are normally distributed, while the alternative hypothesis proposes that they are not normally distributed.



The statistical analysis performed on the dataset produced a p-value of 2.2e-16, indicating a substantial deviation from the null hypothesis with respect to the 0.05 alpha level. Consequently, rejecting the null hypothesis and embracing the alternative hypothesis is warranted. In essence, this implies that the variable "red\_spots\_over\_body" does not conform to a normal distribution.



According to the above bell curve, curve titled to the right. As a result, at 5% significance, the red\_spots\_over\_body values might be regarded as not normally distributed.

**Correlational analysis**

In according to the above dengue dataset, based on the normality testing, data are not normally distributed. So then, to do the correlational analysis, spearman method suitable. Correlational analysis is means check the correlational coefficiency between the dependent(y) and independent(x) variables. Which means identify the what are the important attributes that directly affected to dengue prediction based on this project. Below images are example for correlational analysis of dengue detection.

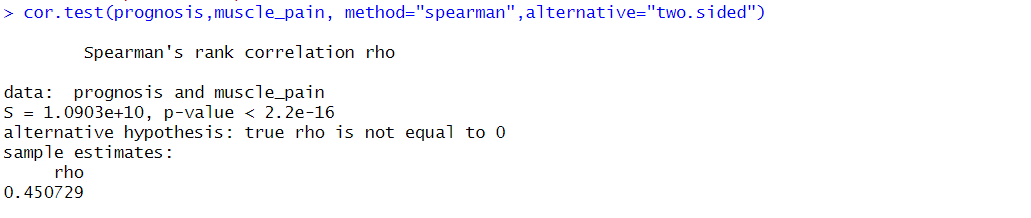
Sample fields = muscle\_pain, prognosis

Let's represent ῤ as the true population correlation coefficient between muscle\_pain and prognosis

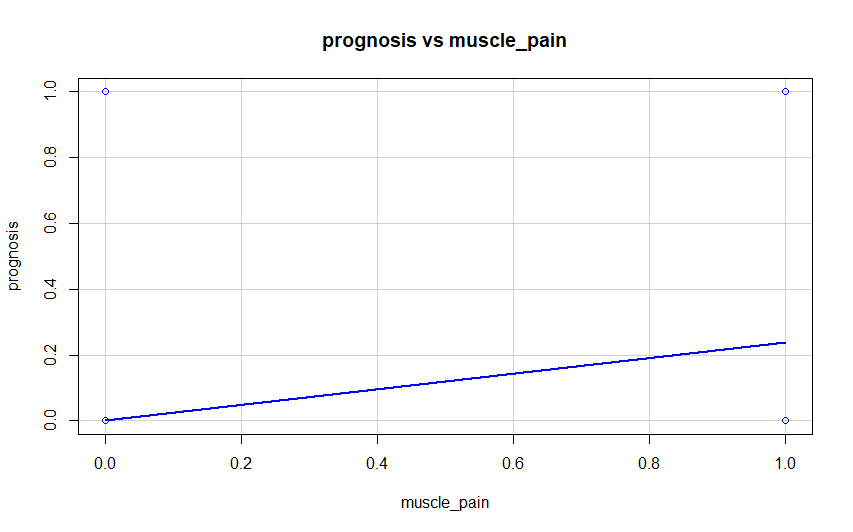
Whether or not there is a correlation found between muscle\_pain and prognosis?

the null hypothesis asserts that there is no correlation between muscle\_pain and prognosis.

Conversely, the alternative hypothesis suggests that there exists a correlation between muscle\_pain and prognosis.



At a significance level of 5%, there is statistically significant support for a moderate positive correlation (ῤ = 0.45) between muscle pain and prognosis, as determined by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. This suggests the necessity of conducting regression analysis to establish the regression model for further investigation.



Above scatter plot clearly shows that scatter plot values position according to a positive non constant trend. Based on that it is confirmed that there is a positive (direct) moderate relationship (ῤ = 0.45) available between prognosis and muscle\_pain at a 5% significance level.

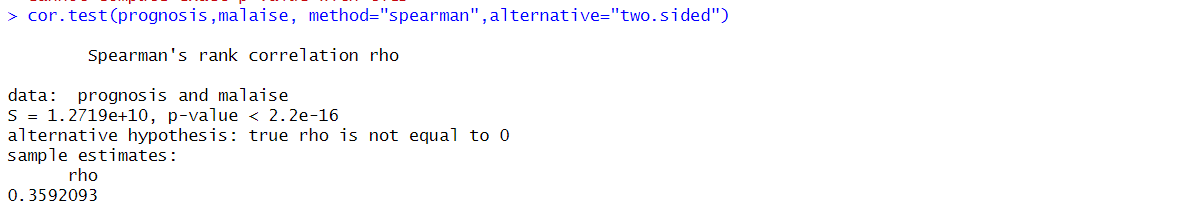
Sample field: malaise, prognosis

Let ῤ = the true population correlation coefficient between malaise and prognosis

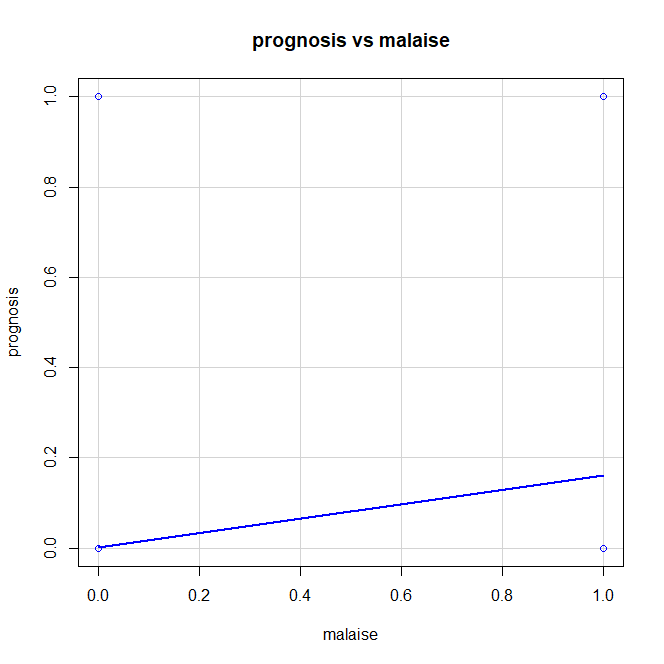
(\*) Whether or not there is a correlation found between malaise and prognosis?

the null hypothesis assumes that there is no correlation between malaise and prognosis.

Conversely, the alternative hypothesis suggests that there exists a correlation between malaise and prognosis.



At a 5% significance level, statistically significant support is found for a moderate positive correlation (ῤ = 0.36) between malaise and prognosis, as confirmed by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. Therefore, there's a need for regression analysis to establish the regression model for further investigation.



It is evident from (Figure 31) that the scatter plot values are positioned in accordance with a positive, non-constant trend. It is therefore proven that, at a 5% significance level, prognosis and malaise have a positive (direct) moderate association (ῤ = 0.36).

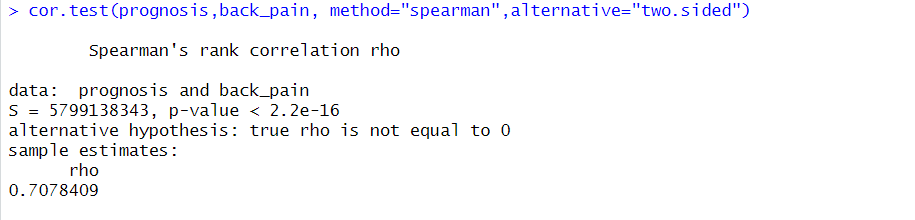
Sample field: back\_pain, prognosis

Let's denote ῤ as the true population correlation coefficient between back\_pain and prognosis.

Whether or not there is a correlation found between back\_pain and prognosis?

The null hypothesis states that there is no correlation between back\_pain and prognosis

Conversely, the alternative hypothesis posits that there is a correlation between back\_pain and prognosis.



A strong positive correlation (ῤ = 0.71) is found between back pain and prognosis, with statistical significance at a 5% level, as confirmed by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. This suggests the need for regression analysis to establish the regression model for further exploration.

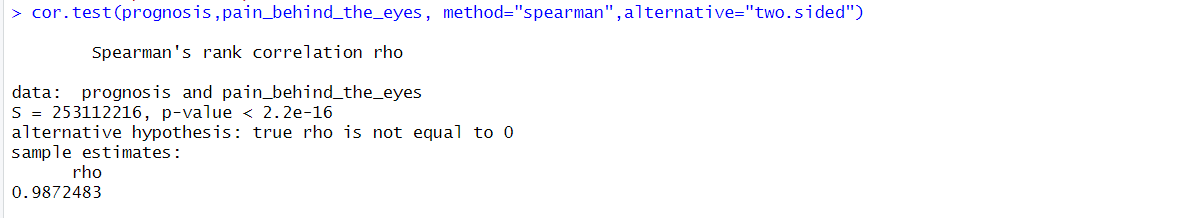
Sample field: pain\_behind\_eyes, prognosis

Let ῤ represent the true population correlation coefficient between pain\_behind\_eyes and prognosis.

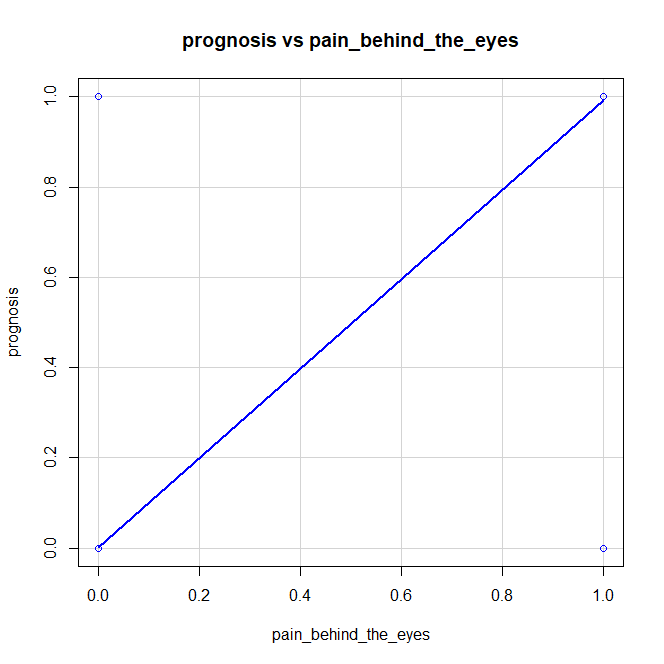
Whether or not there is a correlation found between pain\_behind\_eyes and prognosis?

The null hypothesis proposes that there is no correlation between pain\_behind\_eyes and prognosis.

Conversely, the alternative hypothesis suggests that there is a correlation between pain\_behind\_eyes and prognosis.



A strong positive correlation (ῤ = 0.99) exists between pain behind the eyes and prognosis, with statistical significance at a 5% level, as determined by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. These findings suggest the need for regression analysis to establish the regression model for further investigation.



The data depicted in Figure 31 unmistakably illustrate a scatter plot where values are arranged in alignment with a discernible positive trend. Consequently, statistical analysis confirms with a high level of confidence (at a 5% significance level) that there exists a robust positive correlation between prognosis and pain\_behind\_the\_eyes, denoted by a correlation coefficient (ῤ) of 0.99. This correlation suggests a strong, direct relationship between these variables, implying that as one variable increases, the other tends to increase as well

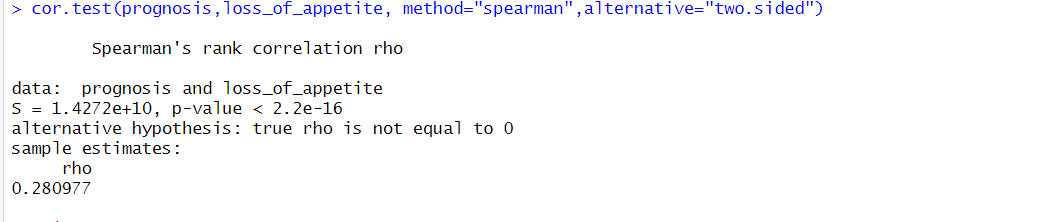
Sample field: loss\_of\_appetite, prognosis

Let ῤ represent the true population correlation coefficient between loss\_of\_appetite and prognosis

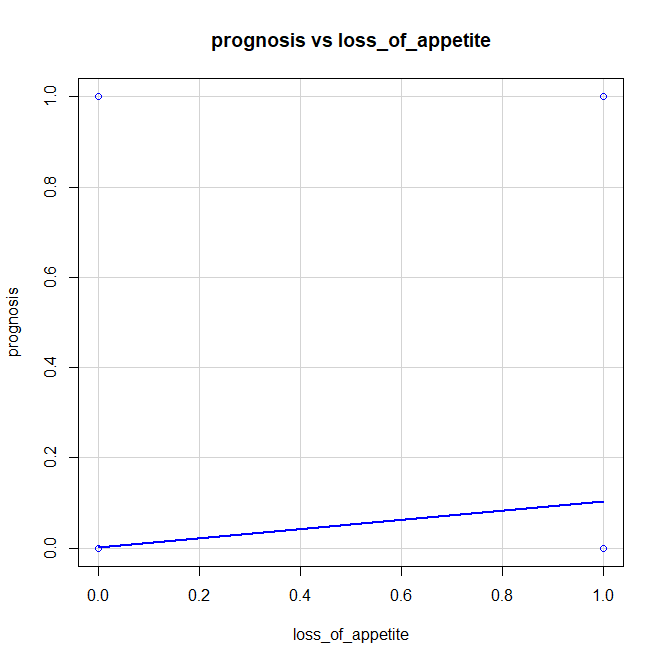
Whether or not there is a correlation found between loss\_of\_appetite and prognosis?

null hypothesis posits that there is no correlation between loss\_of\_appetite and prognosis

The alternative hypothesis asserts that there exists a correlation between loss\_of\_appetite and prognosis,



There is a statistically significant moderate positive correlation (ῤ = 0.28) between loss of appetite and prognosis, supported at a 5% significance level by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. Thus, further investigation via regression analysis is needed to establish the regression model.



The data depicted in Figure 31 unmistakably illustrate a scatter plot where values are arranged in alignment with a discernible positive trend. Consequently, statistical analysis confirms with a high level of confidence (at a 5% significance level) that there exists a moderate positive correlation between prognosis and loss\_of\_appetite, denoted by a correlation coefficient (ῤ) of 0.28. This correlation suggests a moderate, direct relationship between these variables, implying that as one variable increases, the other tends to increase as well

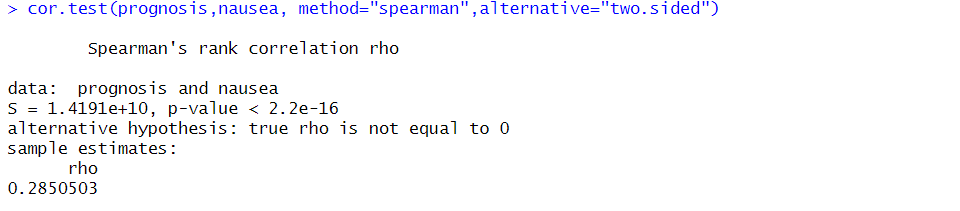
Sample field: nausea, prognosis

Let ῤ denote the true population correlation coefficient between nausea and prognosis.

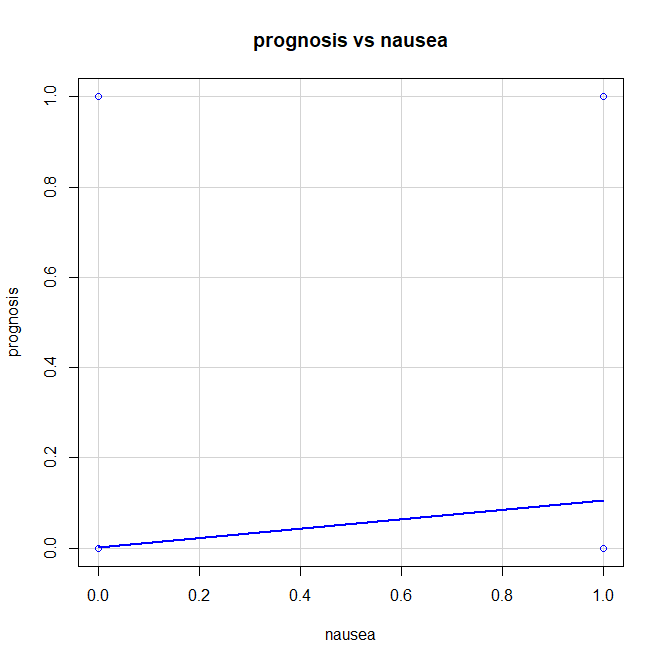
Whether or not there is a correlation found between nausea and prognosis?

The null hypothesis suggests that there is no correlation between nausea and prognosis.

The alternative hypothesis proposes that there exists a correlation between nausea and prognosis.



There is statistically significant support, at a 5% significance level, for a moderate positive correlation (ῤ = 0.29) between nausea and prognosis, as evidenced by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. Consequently, further investigation through regression analysis is required to determine the regression model.



It is evident from (Figure 31) that the scatter plot values are positioned in accordance with a positive, non-constant trend. It is therefore proven that, at a 5% significance level, prognosis and nausea have a positive (direct) moderate association (ῤ = 0.29).

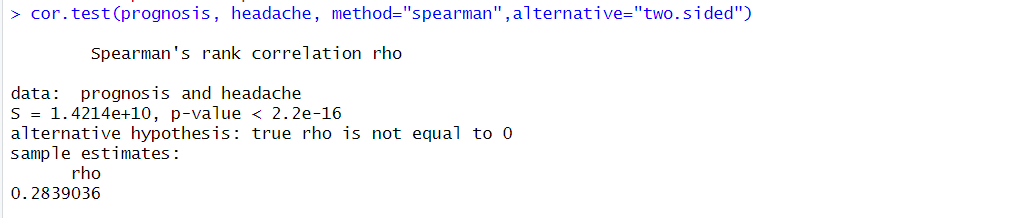
Sample field: headache, prognosis

Let's denote ῤ as the true population correlation coefficient between headache and prognosis.

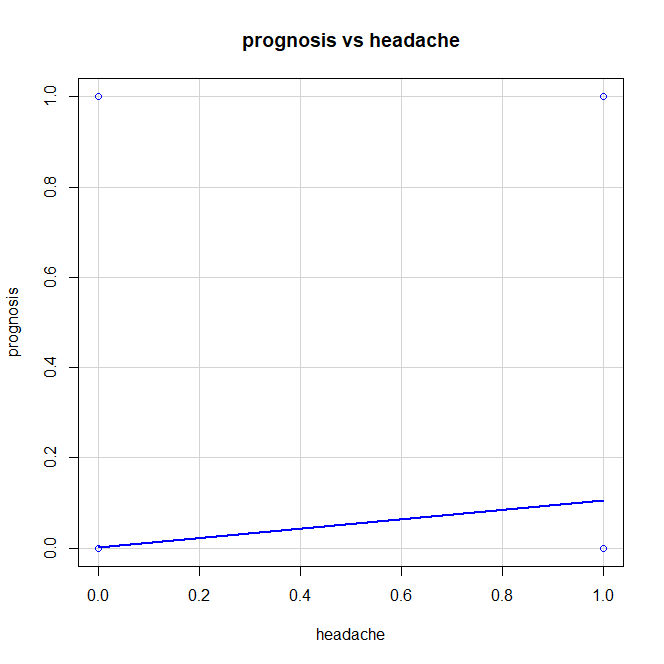
Whether or not there is a correlation found between headache and prognosis?

The null hypothesis states that there is no correlation between headache and prognosis.

The alternative hypothesis suggests that there is a correlation between headache and prognosis.



Statistically significant support at a 5% significance level is found for a moderate positive correlation (ῤ = 0.28) between experiencing headaches and prognosis, as determined by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. Consequently, there's a need for regression analysis to establish the regression model for further exploration.



It is evident from (Figure 31) that the scatter plot values are positioned in accordance with a positive, non-constant trend. It is therefore proven that, at a 5% significance level, prognosis and nausea have a positive (direct) moderate association (ῤ = 0.28).

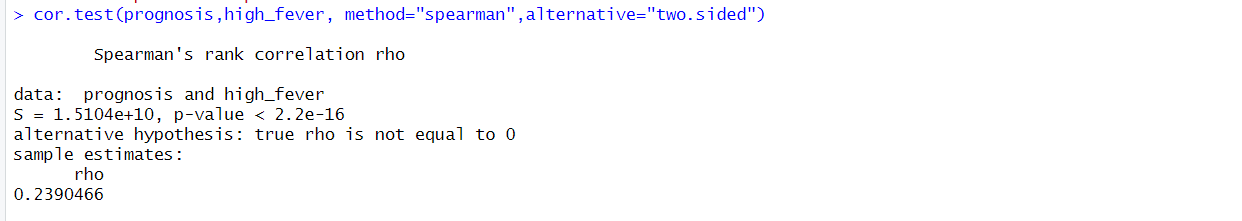
Sample field: high\_fever, prognosis

Let ῤ represent the true population correlation coefficient between high\_fever and prognosis.

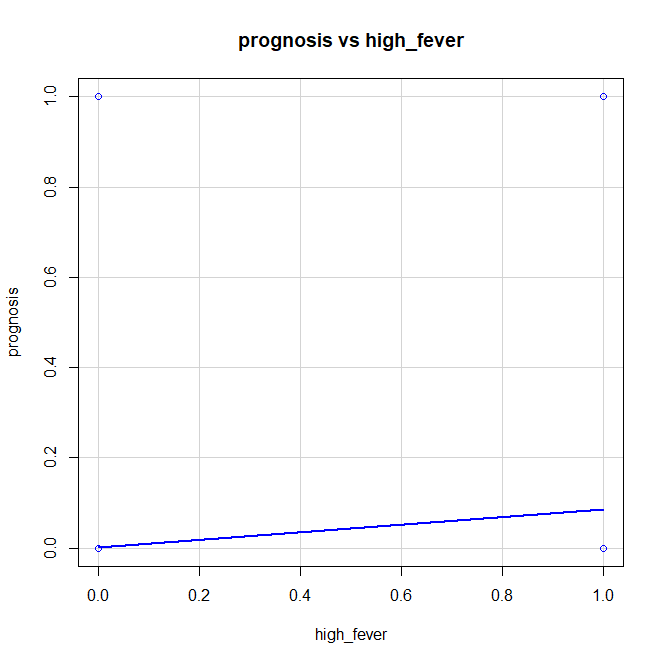
Whether or not there is a correlation found between high\_fever and prognosis?

Null hypothesis asserts that there is no correlation between high\_fever and prognosis.

The alternative hypothesis proposes that there exists a correlation between high\_fever and prognosis.



At a significance level of 5%, statistically significant support is found for a weak positive correlation (ῤ = 0.24) between high fever and prognosis, as indicated by Spearman rank correlation-tests (< 2.2e-16) analyzing sample correlations. Consequently, there is a requirement for regression analysis to establish the regression model for further investigation.



The scatter plot depicted in Figure 31 reveals a clear arrangement of values that conforms to a positive, non-constant trend. Based on statistical analysis conducted at a 5% significance level, it has been established that there exists a moderate positive association between prognosis and high\_fever, as indicated by a correlation coefficient (ῤ) of 0.24. This finding suggests a direct relationship between these variables, implying that as one variable increases, the other tends to increase as well, albeit moderately.

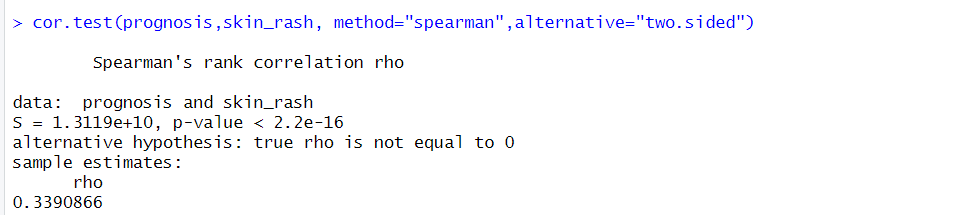
Sample field: skin\_rash, prognosis

Let ῤ = the true population correlation coefficient between skin\_rash and prognosis

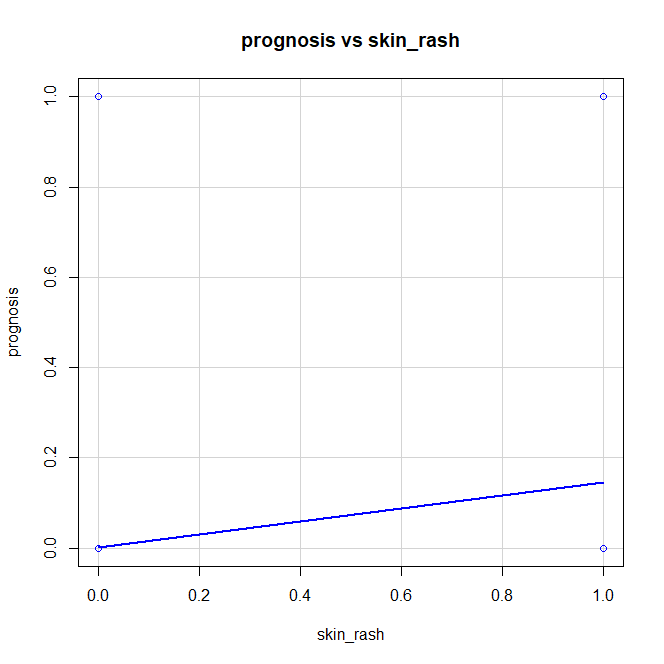
Whether or not there is a correlation found between skin\_rash and prognosis?

The null hypothesis suggests that there is no correlation between skin\_rash and prognosis.

Conversely, the alternative hypothesis proposes that there exists a correlation between skin\_rash and prognosis.



There is a moderate positive correlation (ῤ = 0.34) observed between the presence of a skin rash and prognosis, which is statistically significant at the 5% level according to Spearman rank correlation tests (< 2.2e-16). These findings suggest the need for regression analysis to develop a regression model for further examination.



The scatter plot depicted in Figure 31 reveals a clear arrangement of values that conforms to a positive, non-constant trend. Based on statistical analysis conducted at a 5% significance level, it has been established that there exists a moderate positive association between prognosis and high\_fever, as indicated by a correlation coefficient (ῤ) of 0.24. This finding suggests a direct relationship between these variables, implying that as one variable increases, the other tends to increase as well, albeit moderately.

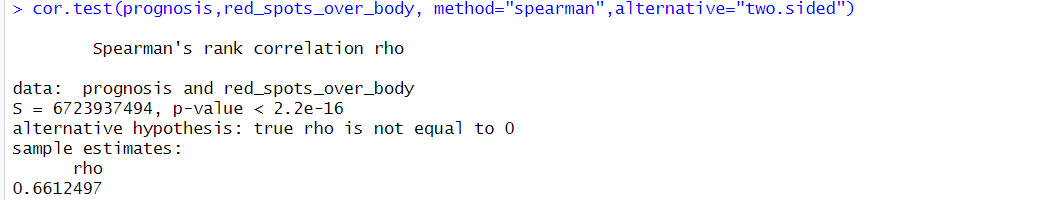
Sample field: red\_spots\_over\_body, prognosis

Let ῤ represent the true population correlation coefficient between red\_spots\_over\_body and prognosis.

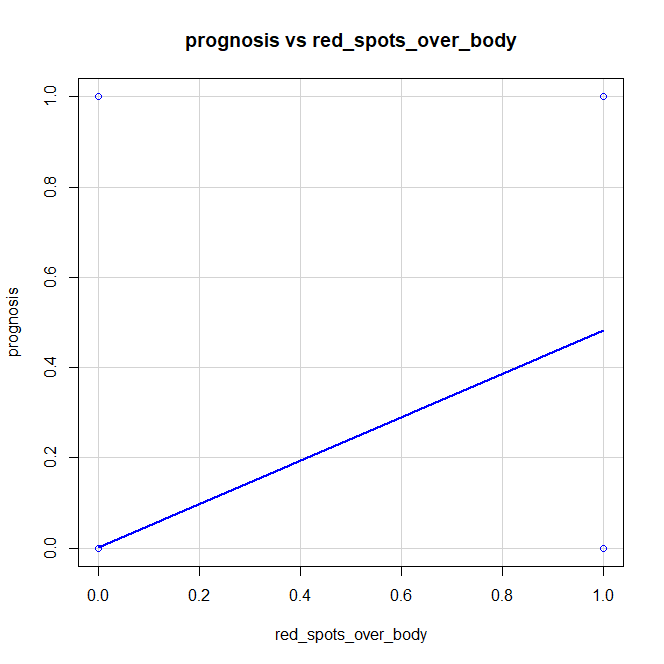
Whether or not there is a correlation found between red\_spots\_over\_body and prognosis?

The null hypothesis posits that there is no correlation between red\_spots\_over\_body and prognosis.

The alternative hypothesis suggests that there exists a correlation between red\_spots\_over\_body and prognosis.



A moderate positive relationship (ρ = 0.66) exists between the presence of red spots on the body and the prognosis, with statistical significance at the 5% level, determined by Spearman rank correlation tests (p < 2.2e-16). These results indicate the need for additional exploration through regression analysis to develop a predictive model for prognosis based on the occurrence of red spots on the body.



The scatter plot presented in Figure 31 visually demonstrates a discernible positive trend in the arrangement of values, indicating a relationship between prognosis and red\_spots\_over\_body. Through statistical analysis conducted at a 5% significance level, it has been conclusively established that there exists a moderate positive association between these variables, with a correlation coefficient (ῤ = 0.66). This correlation underscores a direct link between prognosis and red\_spots\_over\_body, suggesting that as one variable increases, the other tends to increase as well, though to a moderate extent.

**Regression analysis**

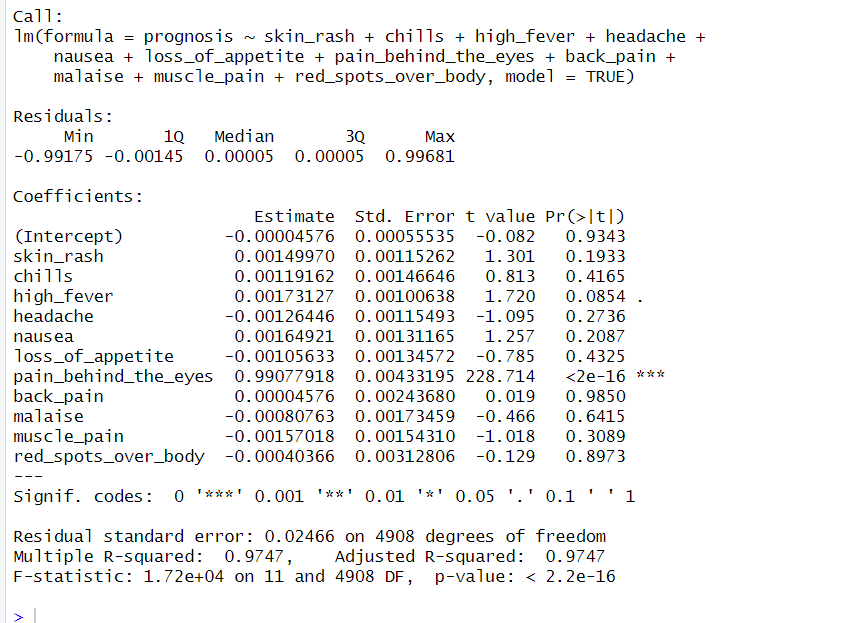
When it comes to the regression analysis there two type are there

1. Simple linear regression analysis
2. Multi linear regression analysis

When considering the simple linear and Multi linear model, Multi linear model give the best results. Because but when it comes real world scenario every problem are are associated with multiple factors. For an example this dengue prediction can be don based on multiple factors(symptoms) not only one symptom. Then fore regression analysis Multi linear model is suitable.

**Multi Linear Model**

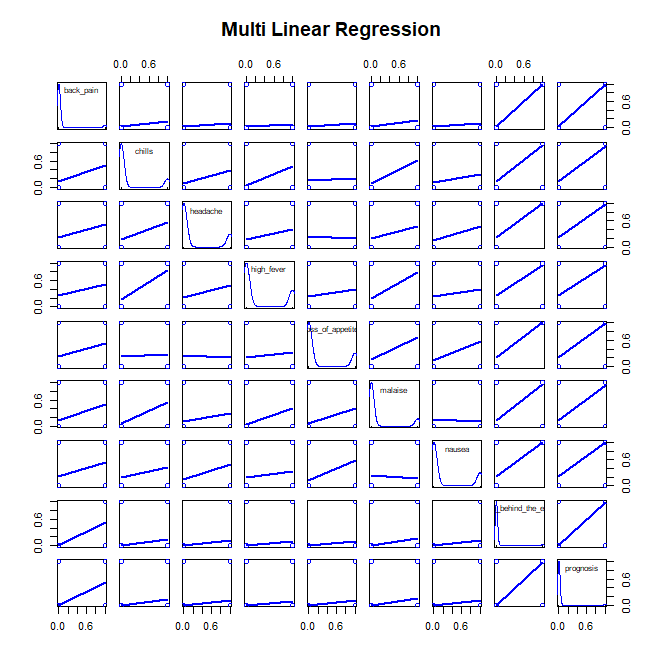
++++ +



Final multi-linear model

= -0.00004576 + (0.00149970)\*1+(0.00119162)\*0+ (0.00173127)\*0+(-0.00126446)\*0+(0.00162449)\*0+(-0.00105633)\*0+(0.99077918)\*0+ (0.00004576)\*0+ (-0.00080763)\*0+(-0.00177018\*0) +(-0.00040366)\*0

= 0.00145394

****

According to the multiple linear model developed for predicting prognosis based on symptoms such as skin rash, high fever, headache, nausea, loss of appetite, pain behind the eyes, chills, back pain, malaise, muscle pain, and red spots over the body:

The coefficients estimate the change in the predicted prognosis for a one-unit change in each predictor variable, while holding all other predictors constant. Notably, "pain\_behind\_the\_eyes" exhibits a highly significant effect on prognosis, with a coefficient estimate of 0.9908 and a large t-value of 228.714 (p < 2e-16), indicating a strong positive association. Other symptoms such as "high\_fever" and "chills" also show a statistically significant impact on prognosis, with coefficient estimates of 0.0017 (p = 0.0854) and 0.0012 (p = 0.4165) respectively, suggesting that an increase in high fever and chills is associated with an increase in prognosis.

However, some symptoms like "skin\_rash," "headache," "nausea," "loss\_of\_appetite," "back\_pain," "malaise," "muscle\_pain," and "red\_spots\_over\_body" do not appear to have a statistically significant effect on prognosis, as indicated by their higher p-values.

Overall, the model explains a large portion of the variability in prognosis, with an R-squared value of 0.9747. This suggests that approximately 97.47% of the variance in prognosis can be accounted for by the included symptoms. Additionally, the adjusted R-squared value remains the same at 0.9747, indicating that the model's explanatory power is not affected by the number of predictors.

The residuals, representing the differences between the observed and predicted values of prognosis, exhibit a small range from -0.99171 to 0.99658, with a residual standard error of 0.02466, indicating a good fit of the model to the data.

**Unit Testing**

Unit testing is a software testing method where individual units or components of a software application are tested in isolation to ensure they perform as expected. In Python, unit testing is commonly used to verify the correctness of functions, classes, or modules (Lukasczyk et al., An empirical study of Automated Unit Test Generation for Python 2023). This Unit testing has three main types

1. White box testing

In white-box testing, the tester has access to the internal structure, design, and implementation details of the software being tested. Test cases are designed based on an understanding of the code logic, paths, and data flows. The objective is to ensure that the code behaves as expected by testing its internal workings (Ehmer & Khan, A comparative study of white box, black box and grey box testing techniques 2019)

1. Black box testing

In black-box testing, the tester treats the software as a "black box" and does not have access to its internal structure or implementation details. Test cases are designed based on the software's specifications, requirements, and external behavior. The focus is on testing the functionality, inputs, and outputs of the software without considering its internal workings (Ehmer & Khan, A comparative study of white box, black box and grey box testing techniques 2019)

1. Grey box testing

Grey-box testing is a combination of white-box and black-box testing. The tester has partial access to the internal structure and design of the software while also testing its external behavior. This approach allows the tester to design test cases based on both the internal logic and the external requirements of the software. Grey-box testing can provide a balance between the thoroughness of white-box testing and the independence of black-box testing (Ehmer & Khan, A comparative study of white box, black box and grey box testing techniques 2019)

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**Benefits of Unit Testing:**

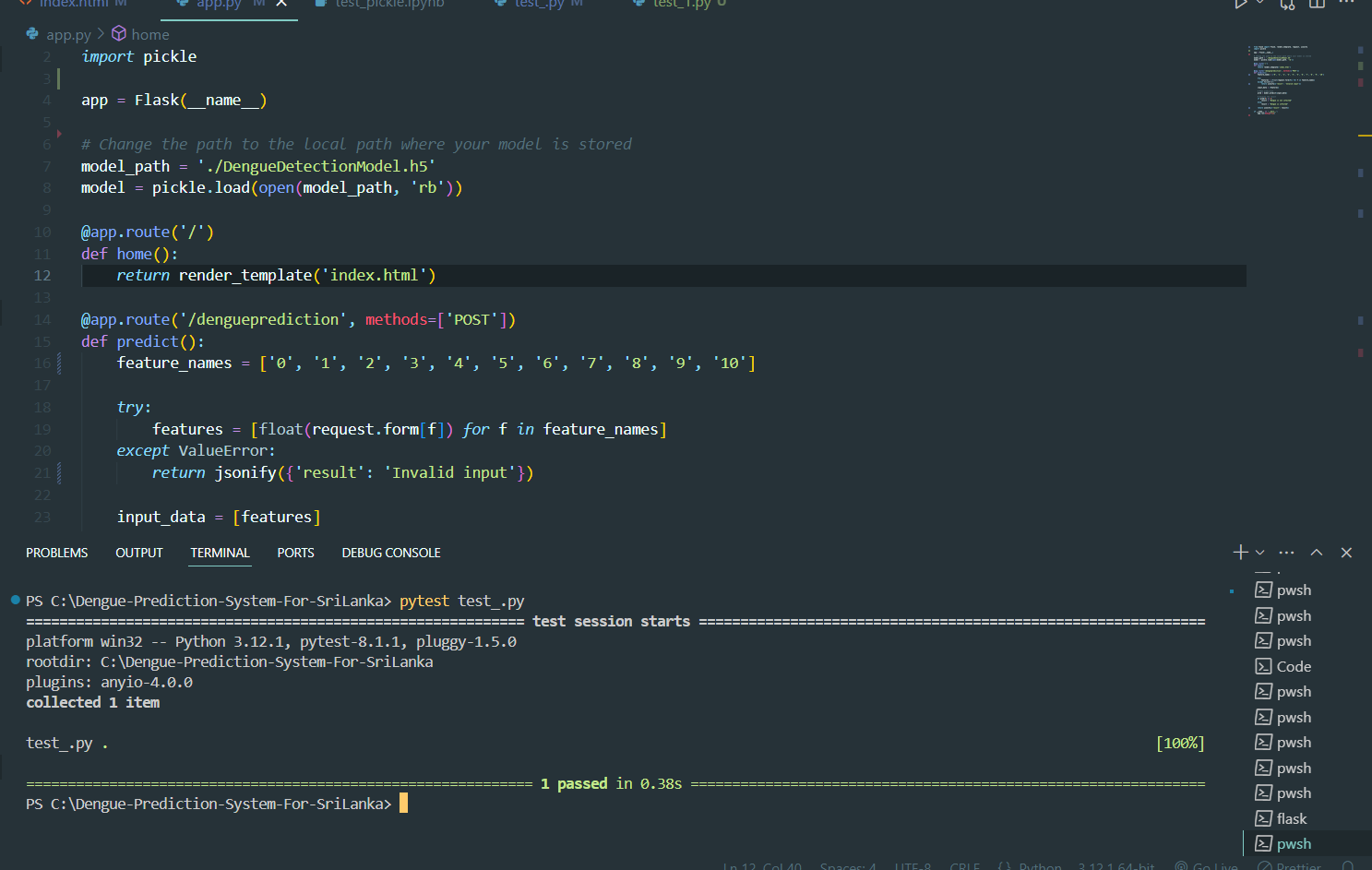
* Early Detection of Bugs: Unit tests allow you to catch bugs and issues in the early stages of development, making them easier and cheaper to fix(Mårtensson, Unit testing 2019).
* Regression Testing: Unit tests serve as a safety net, ensuring that changes made to the code base don't introduce new bugs or regressions(Mårtensson, Unit testing 2019).
* Improved Code Quality: Writing tests encourages writing modular, decoupled, and reusable code, which leads to better overall code quality(Mårtensson, Unit testing 2019).

In this unit testing there are several testings are available . One of the best testing is pytest that is python frame work. It is belong to the white box testing. Because White-box testing is like peeking inside a clock to check if all the gears are turning as they should. So then when using the pytest tester knows how the software works on the inside, checking if every part of the code functions correctly(A research paper on white box testing 2022).

**Key feature of pytest**

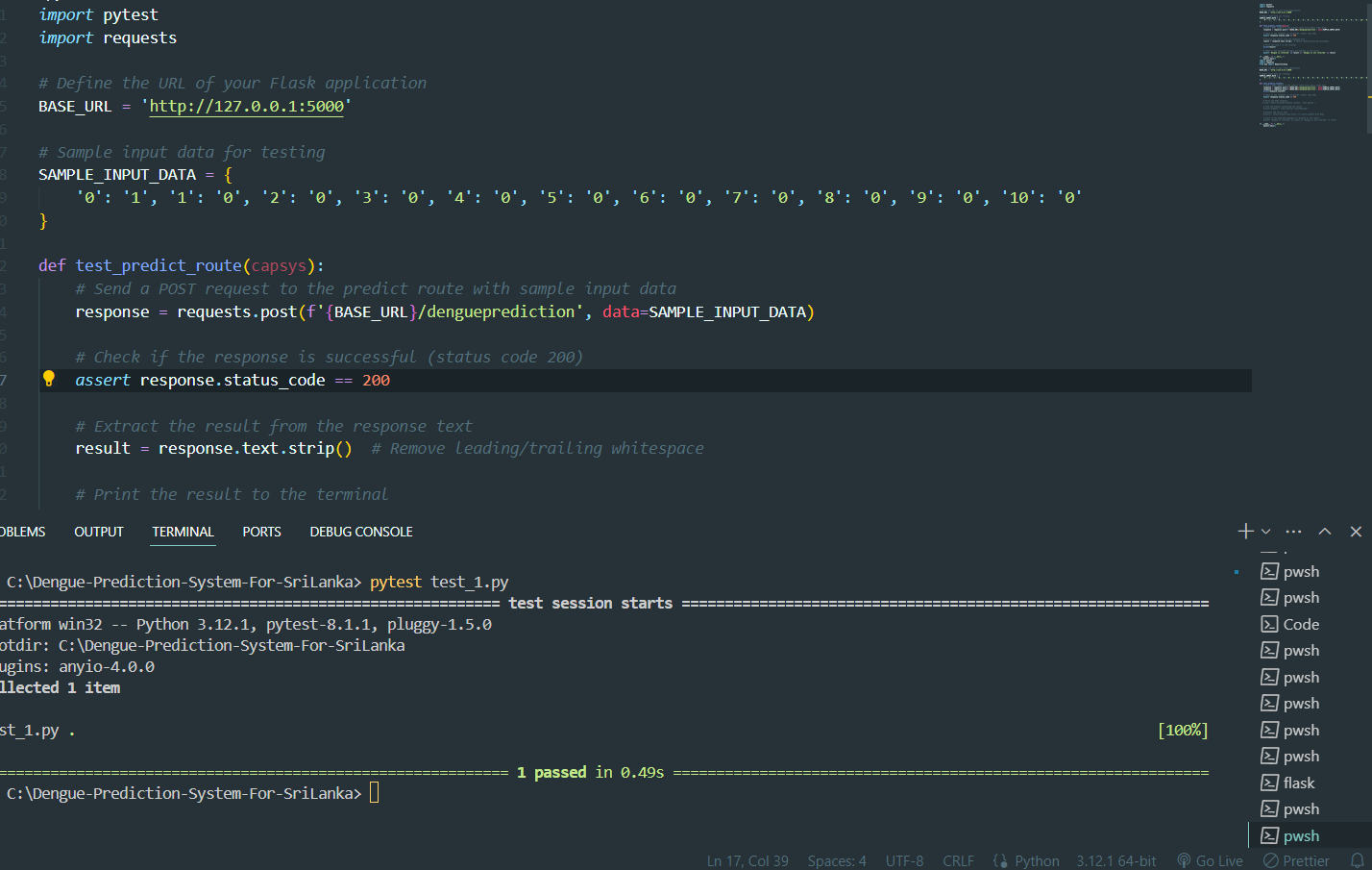
* Simple Syntax: pytest offers a simple and intuitive syntax for writing test functions, making it easy to get started with writing tests.
* Fixture Support: pytest provides a powerful fixture mechanism for setting up and tearing down resources needed by your tests.
* Parameter Testing: pytest allows you to easily parameterize your tests, enabling you to run the same test with multiple input values.
* Plugins: pytest is highly extensible through plugins, allowing you to customize and extend its functionality to suit your needs(Pajankar, Pytest 2021).

Test case 1 - Dengue is infected



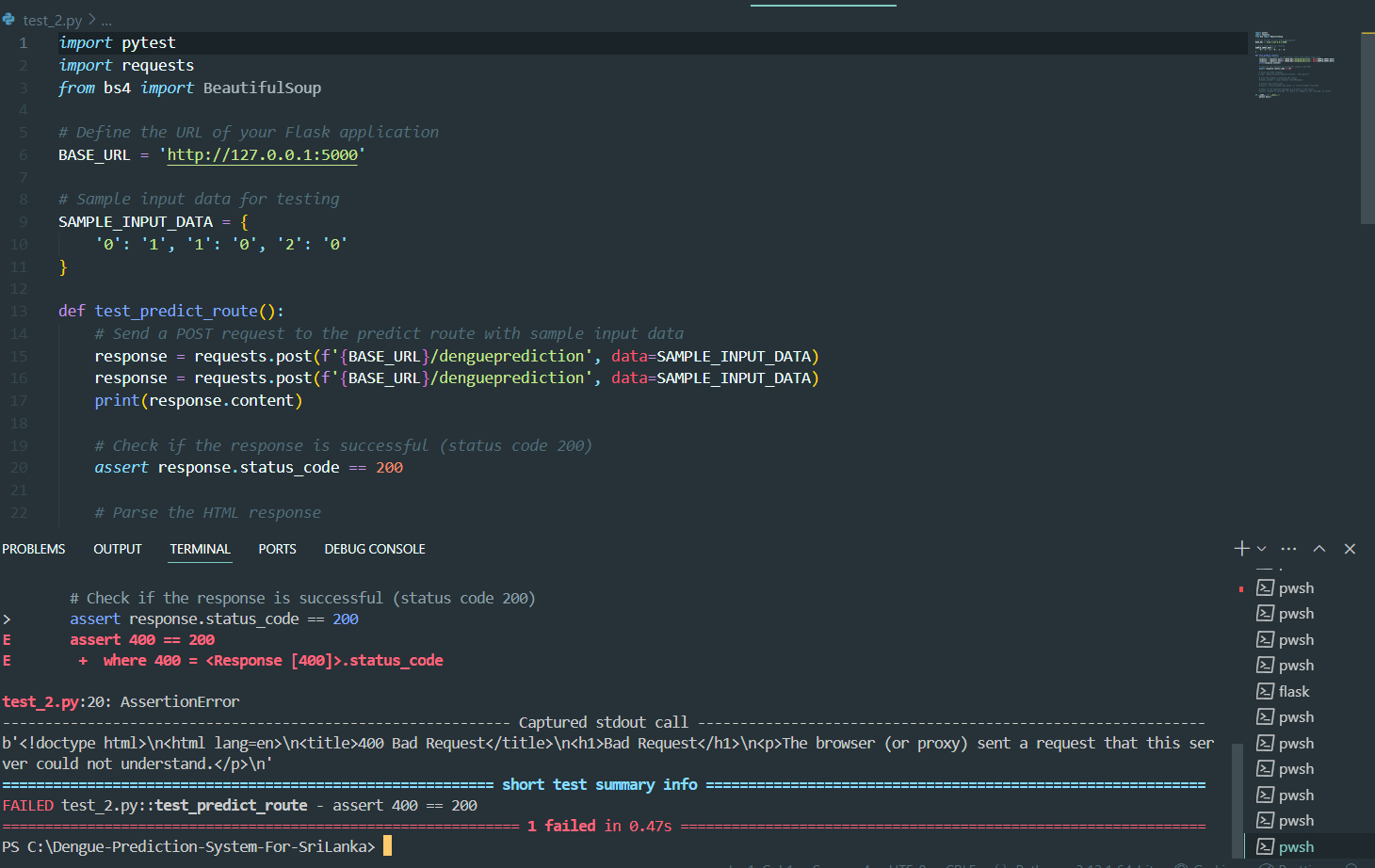
Test case 1 is passed

Test case 2 -Dengue is not infected

****

Test case 2 is passed

Test case 3 - dengue is not infected

****

Test case 3 is failed

According to the above mentioned test case 3, other test cases which have not completed input fields like test case 3, that test cases are fails. The reasons of the test cases are fail is assertion error throw.

**Future development and recommendation**

Currently, the dengue prediction system focuses on identifying whether an individual is infected with dengue fever at an early stage. However, future iterations of the system aim to expand its capabilities to categorize the specific serotype of the dengue virus, namely dengue virus serotype 1 (DENV-1), dengue virus serotype 2 (DENV-2), dengue virus serotype 3 (DENV-3), and dengue virus serotype 4 (DENV-4). This expansion is based on research findings reported in Nature news in 2022(Nature new, 2022). By incorporating these features into the system, it can provide more detailed and precise information about the specific type of dengue virus affecting an individual, enabling more targeted and effective treatment strategies.

**Conclusion**

In conclusion, this research explores the application of machine learning algorithms for dengue detection in Sri Lanka, a country where the disease poses a significant public health challenge. Through the utilization of various machine learning techniques such as classification algorithms, feature selection, and ensemble methods, aimed to develop accurate predictive models for early detection of dengue cases.

Based on the findings demonstrate that machine learning models, particularly those based on binary logistic regression, decision tree classifier, and ensemble method such as random forest exhibit promising performance in dengue prediction.

These models leverage diverse sets of features including symptoms to accurately classify individuals at risk of contracting dengue fever.

Furthermore, feature selection techniques such as doing the correlational coefficiency have been instrumental in identifying the most relevant predictors for dengue detection, thereby enhancing the efficiency and Interpretability of the models.

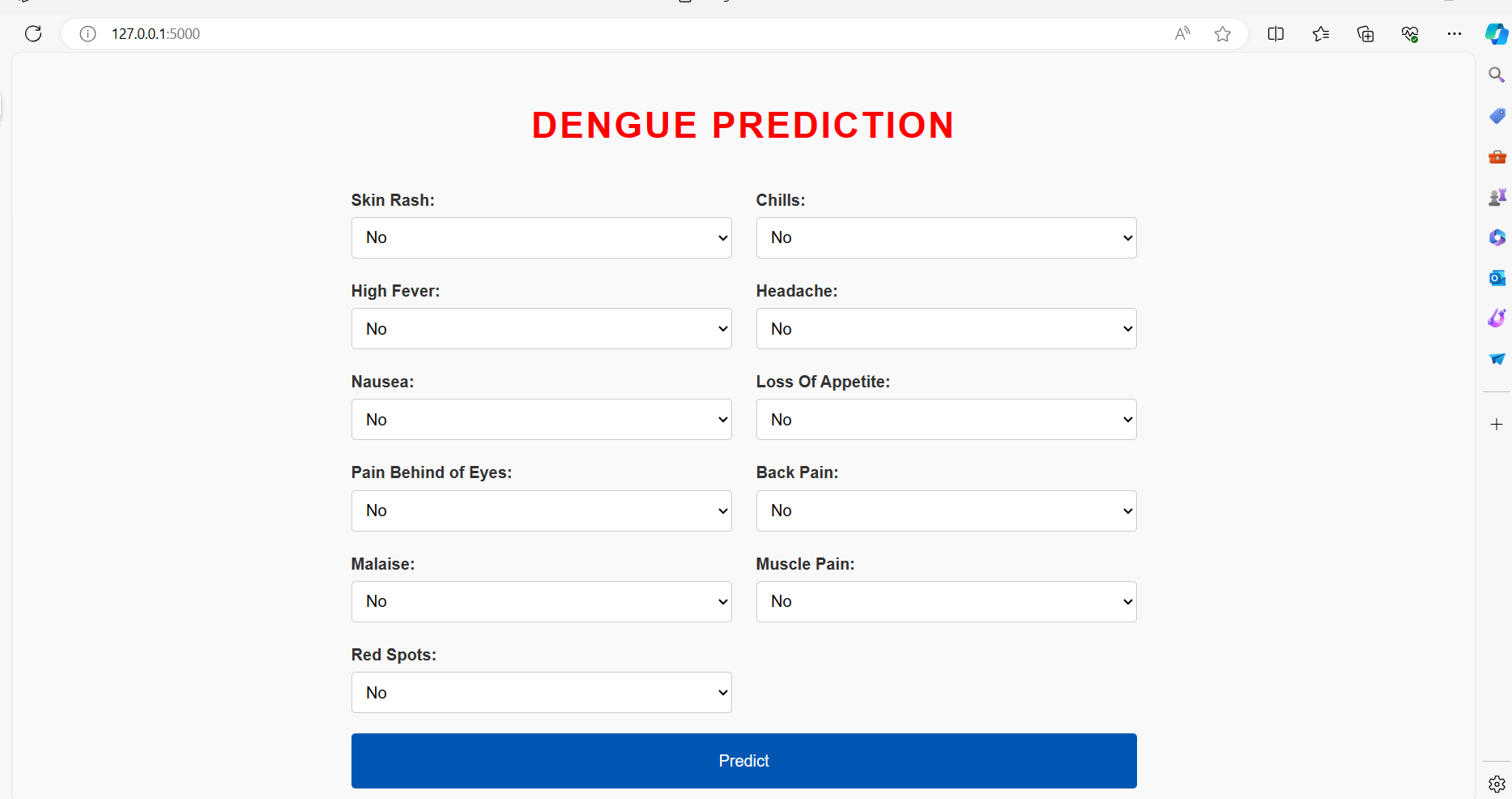
However, it is essential to acknowledge several limitations and challenges encountered during the course of this study. These include the availability and quality of data, the dynamic nature of environmental factors influencing dengue transmission, and the need for real-time data integration to enhance the predictive accuracy of the models.

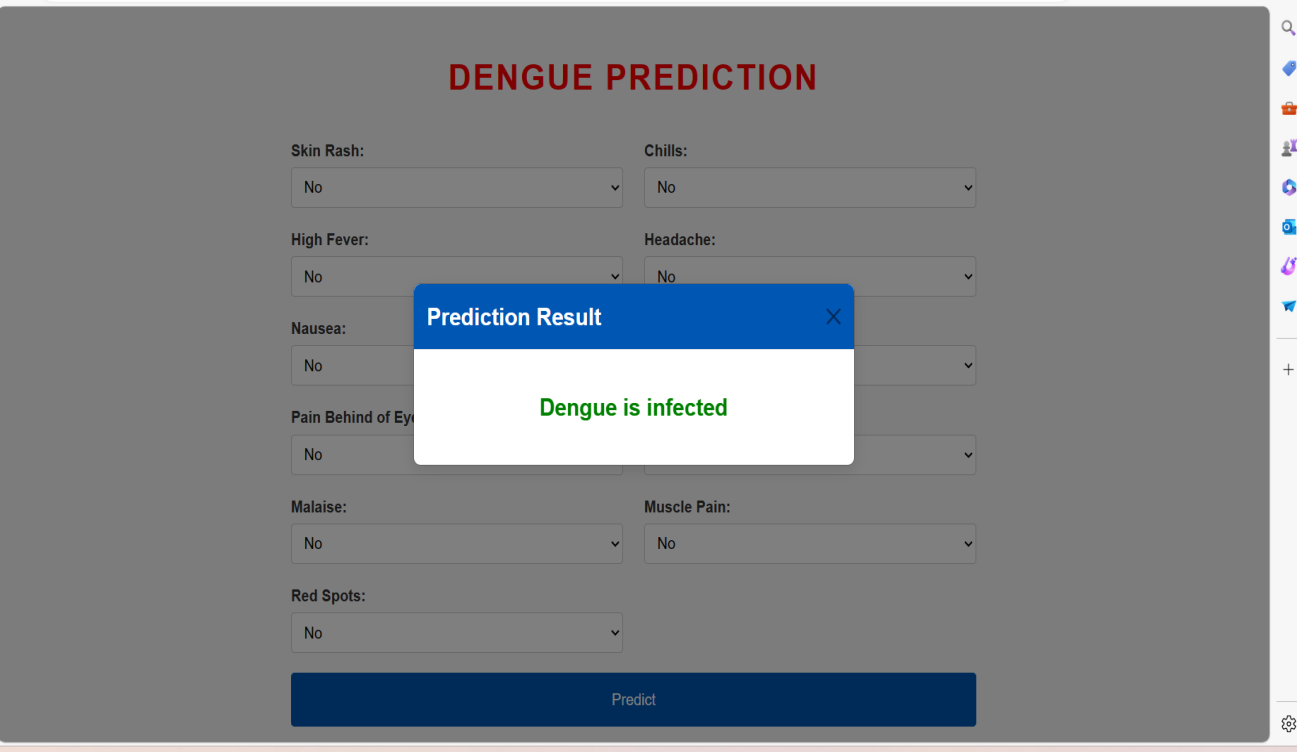
Despite these challenges, the results of this research hold significant implications for public health authorities and policymakers in Sri Lanka. By leveraging machine learning algorithms for dengue detection, it is possible to improve the early warning systems, allocate resources more efficiently, and implement targeted interventions to mitigate the burden of dengue fever in the country.

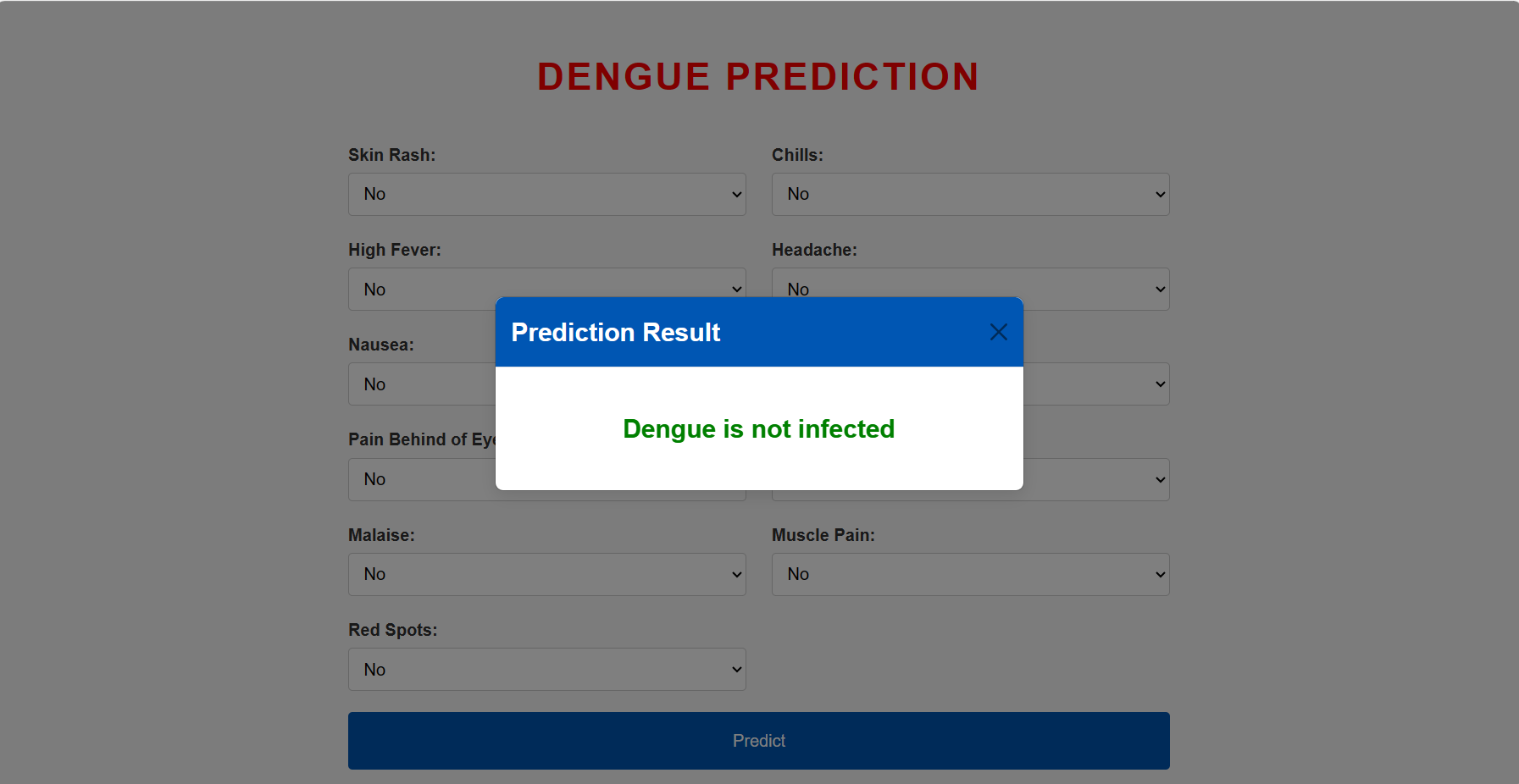
Moving forward, future research directions may involve the integration of additional data sources such as satellite imagery, climate forecasts, and social media data to enhance the predictive capabilities of the models. Additionally, the development of user-friendly and scalable predictive tools tailored to the needs of healthcare practitioners and decision-makers could facilitate the adoption of machine learning-based approaches in routine dengue surveillance and control efforts.

In conclusion, while there are challenges to be addressed, the application of machine learning in dengue detection offers tremendous potential to advance our understanding of disease dynamics and ultimately improve public health outcomes in Sri Lanka.

**Sample UI images**







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