Dengue Recognition System for Srilanka

By using machine learning

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**Introduction**

In srilanka there are lot of viruses are spread. For an example dengue, malaria, HIV, etc. Among these viruses dengue is most threaten virus.

**Problem statement**

* Based on symptoms,machine learning existing applications or systems are fully created for health care professionals and doctors. At that moment there is no specific machine learning application or system is available for patient to detect the dengue by their own 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.

**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 cost, complexity, and takes lot of time to get the result etc. 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 created for assisting to doctors and healthcare professional to identify the patient dengue. 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. Based on 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, in balance dataset available.

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

The main reasons of this support vector machine model is used in dengue detection system are easily work with high dimensionality features, and memory efficient which means support vector machines don’t need all the data. It wants only near the decision boundary. And also support vector machines can be easily work with different data types by using the mathematical tricks called kernals(Nordin et al., The classification performance using support vector machine for endemic dengue cases 2020).

The reasons of decision tree algorithm used for dengue detection system are efficiency is very high. Which means by using this decision tree algorithm can be making the understandable decision. And also easy to apply this decision tree algorithm, and work with larger dataset (Jayasundara et al., Developing a decision support testing algorithm to detect severity level of Dengue 2017).

The reasons of random forest algorithm used for dengue detection system are efficiency is very high. Which means by using this random forest algorithm can be making the correct prediction. And also easy to apply this decision tree algorithm, and work with larger dataset (Katta et al., An efficient learning model selection for dengue detection 2022).

**Methodology**

**Data Collection**

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.

**Data Cleaning**

Checking the null values and duplicate values in created full dataset. Null values are going to be filled by using mean value of that particular column. And duplicated values are removed from that full dataset.

**Splitting the dataset**

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.

**Models**

For classifying this dengue, support vector machine, decision tree algorithm, random forest algorithms are the models going to be used.

Support vector machine model - The main reasons of this support vector machine model is going to be used in dengue detection system are easily work with high dimensionality features, and memory efficient which means support vector machines don’t need all the data. It wants only near the decision boundary. And also support vector machines can be easily work with different data types by using the mathematical tricks called kernals (Nordin et al., The classification performance using support vector machine for endemic dengue cases 2020).

Decision tree model - The main reasons of this decision tree model is going to be used in this dengue detection system are this model can be easily used, higher accuracy models can be created, and higher predictions can be produced (Huynh-Cam et al., Using decision trees and random forest algorithms to predict and determine factors contributing to first-year university students’ learning performance 2021).

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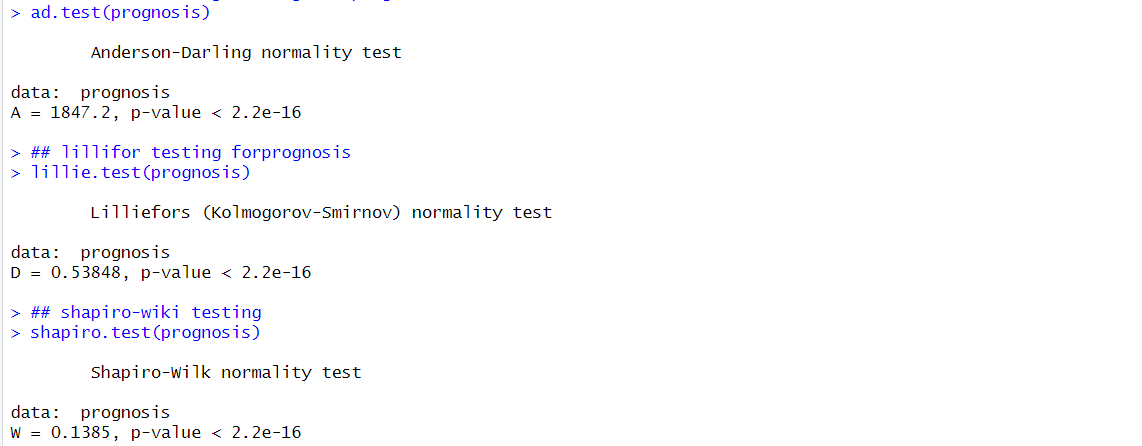
Random forest model -

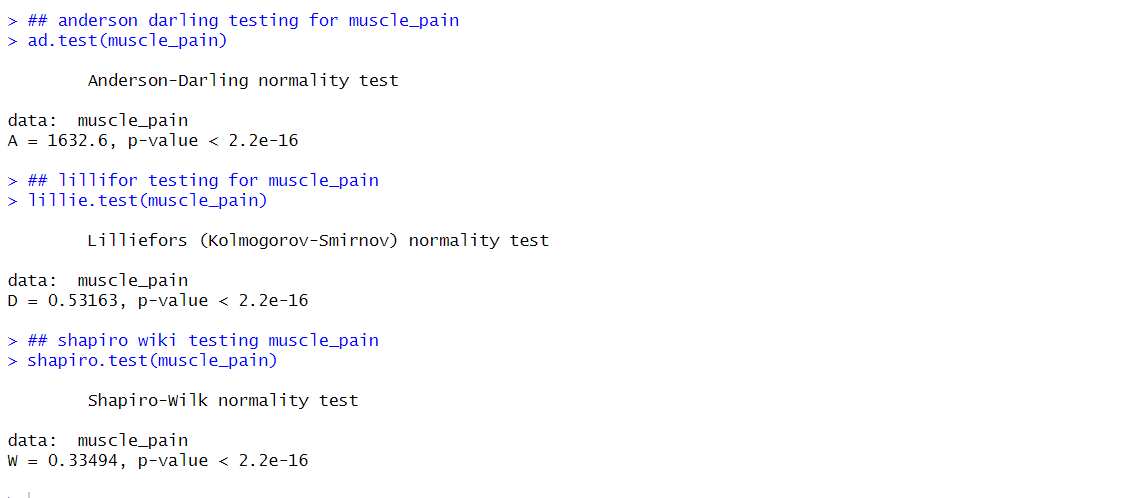
The main reasons of this random forest is used in this dengue detection system are increase the model accuracy, reduce the overfitting level, and handling the larger dataset (George & Ganesan, Advanced cuttlefish optimizer-random decision forest (ACORDF) based design of fractional order PID controller for higher-order time-delay system 2021).

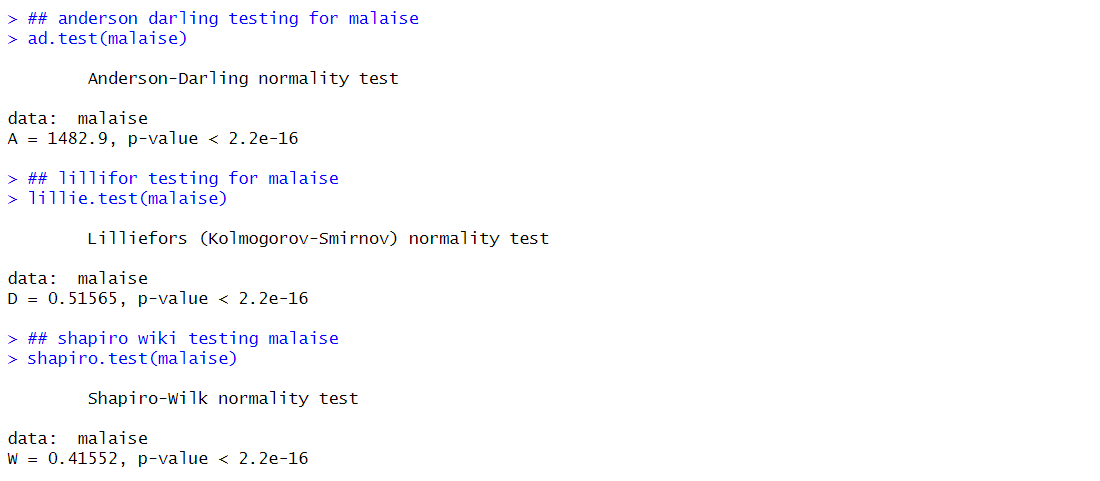
**Hypothitical Testing**

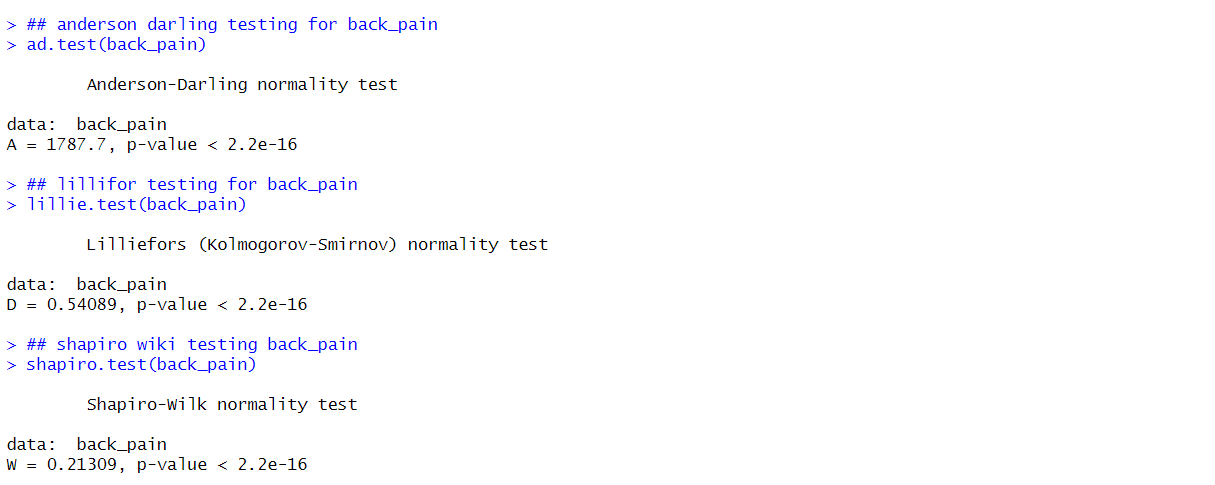
**Normality testing**

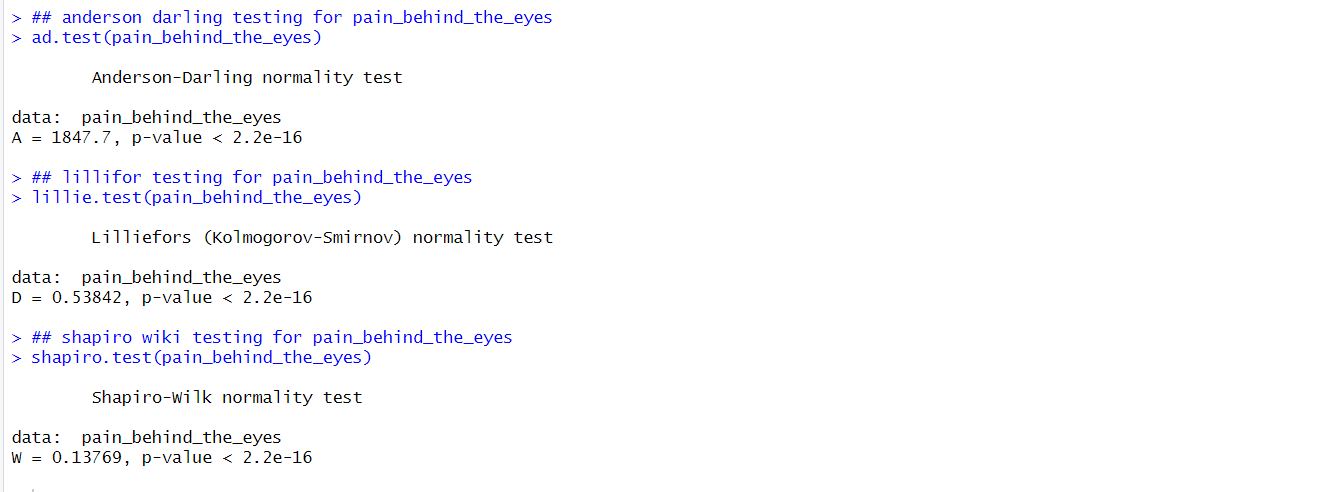
Normality testing means check whether data is normally distributed or not. Below images are examples for normality testing.

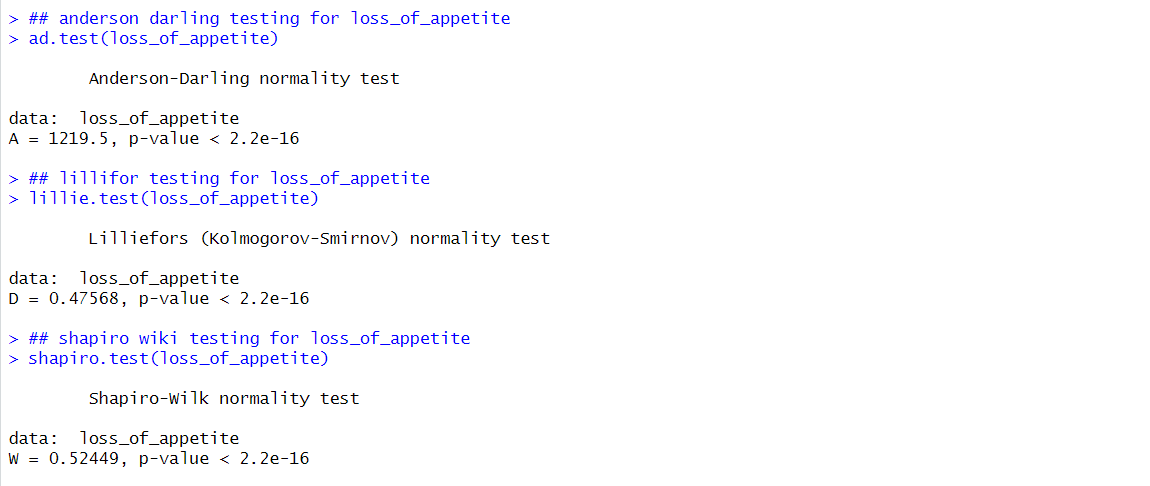


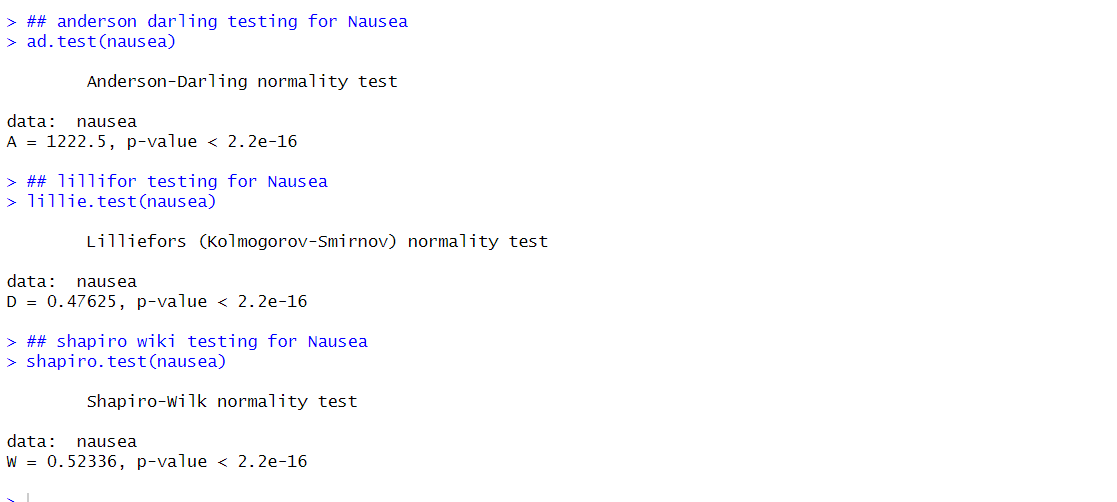


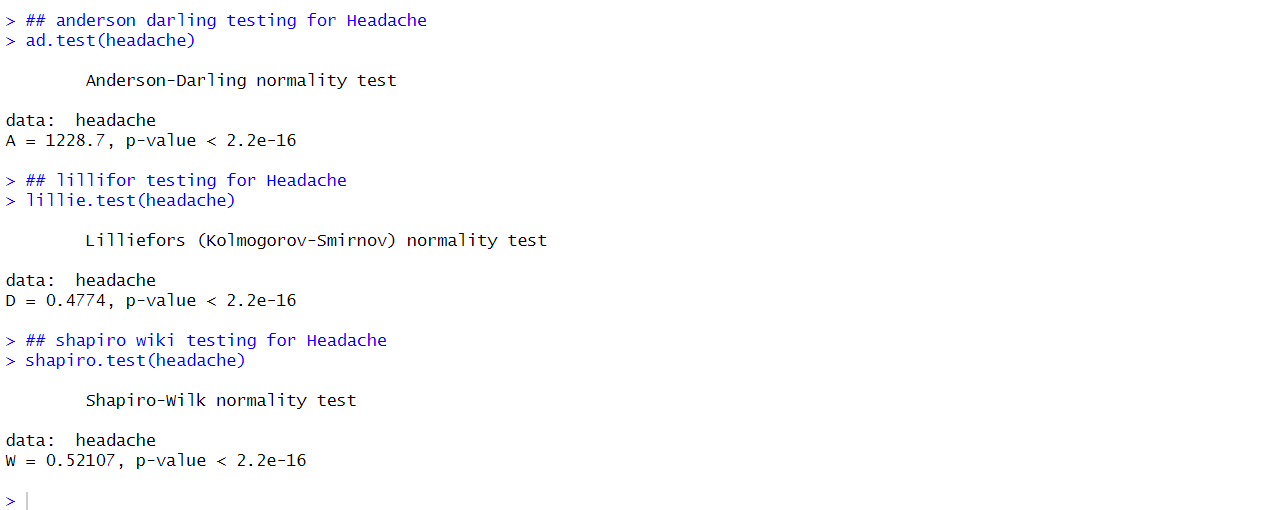


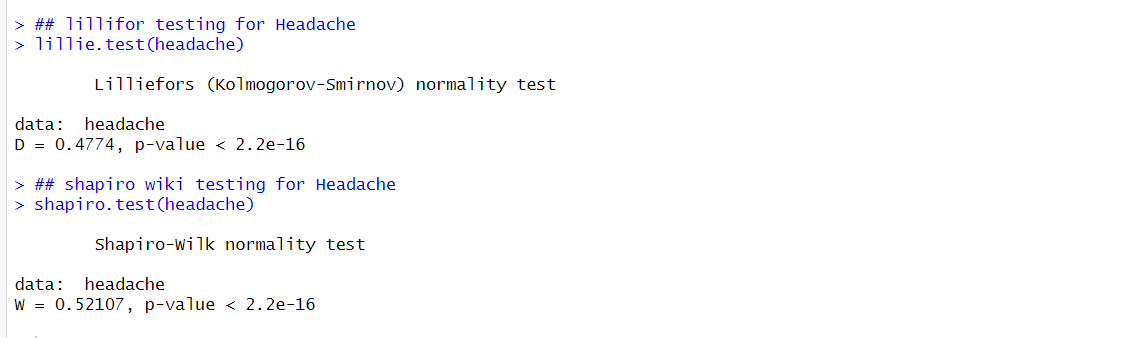


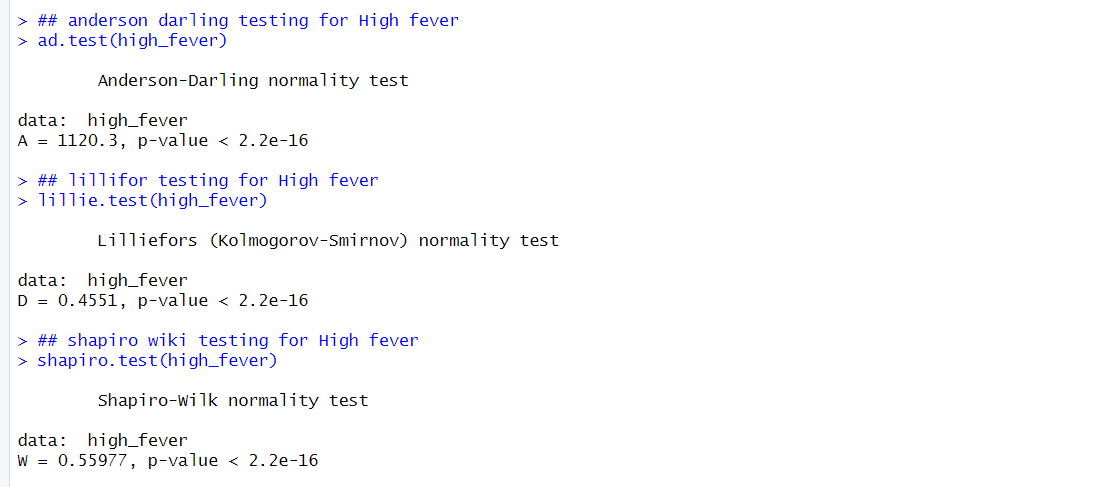


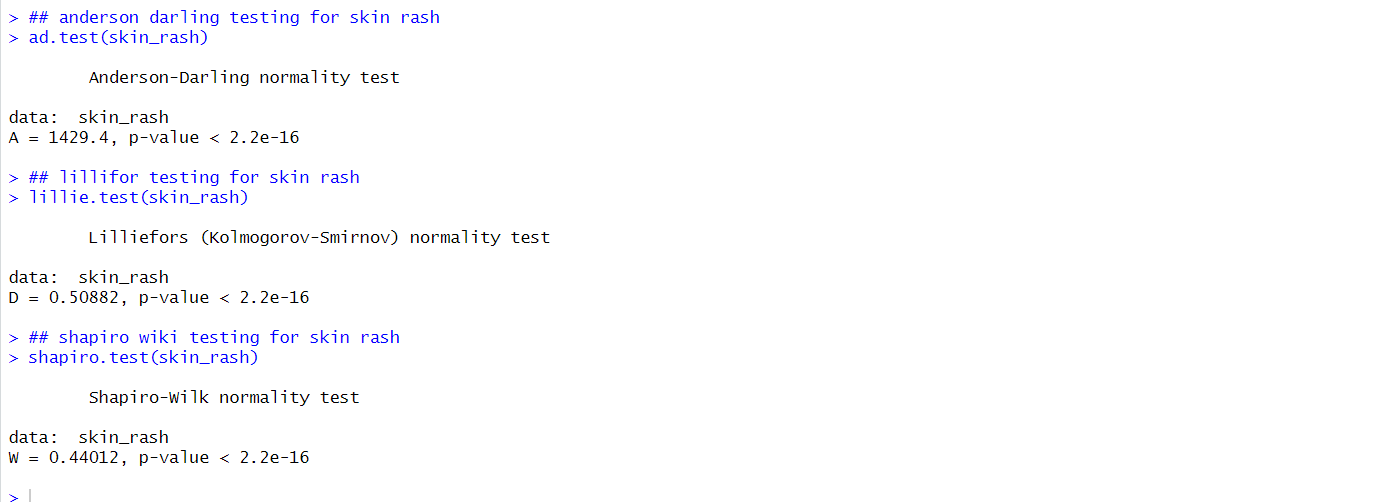


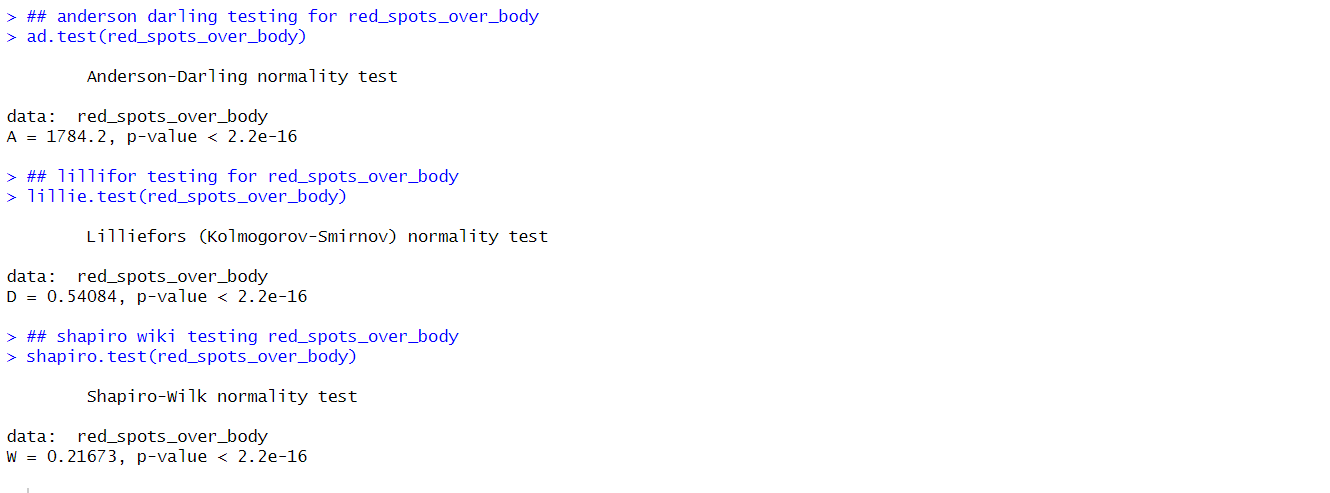












**Correlational analysis**

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 research. Below images are example for correlational analysis of dengue detection.

Sample field: muscle\_pain, prognosis

Significant level (α) = 0.05

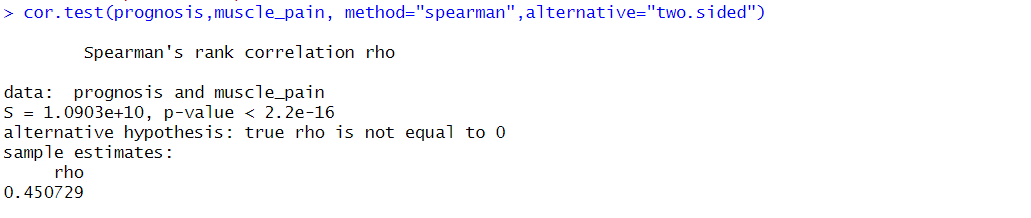
Confidence level = 95%

Let ῤ = the true population correlation coefficient between Temperature and Crop\_Yield

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

H0: There is no correlation (ῤ =0) between muscle\_pain and prognosis

H1: There is a correlation (ῤ ≠0) between muscle\_pain and prognosis



Conclusion of correlation test

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.

Sample field: malaise, prognosis

Significant level (α) = 0.05

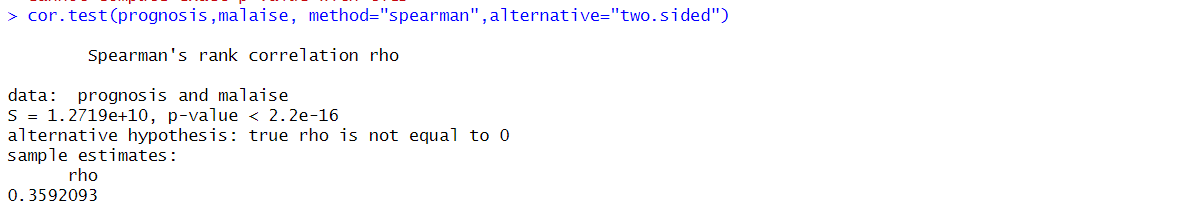
Confidence level = 95%

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

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

H0: There is no correlation (ῤ =0) between malaise and prognosis

H1: There is a correlation (ῤ ≠0) between malaise and prognosis



Conclusion of correlation test

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.

Sample field: back\_pain, prognosis

Significant level (α) = 0.05

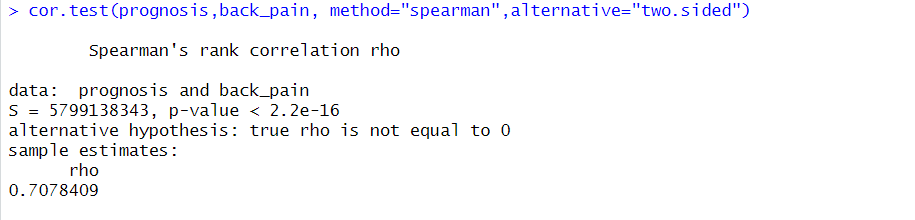
Confidence level = 95%

Let ῤ = the true population correlation coefficient between back\_pain and prognosis

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

H0: There is no correlation (ῤ =0) between back\_pain and prognosis

H1: There is a correlation (ῤ ≠0) between back\_pain and prognosis



Conclusion of correlation test

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

Significant level (α) = 0.05

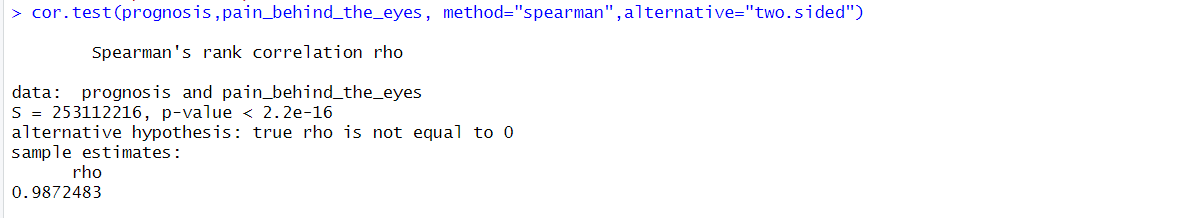
Confidence level = 95%

Let ῤ = 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?

H0: There is no correlation (ῤ =0) between pain\_behind\_eyes and prognosis

H1: There is a correlation (ῤ ≠0) between back\_behind\_eyes and prognosis



Conclusion of correlation test

A robust 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.

Sample field: loss\_of\_appetite, prognosis

Significant level (α) = 0.05

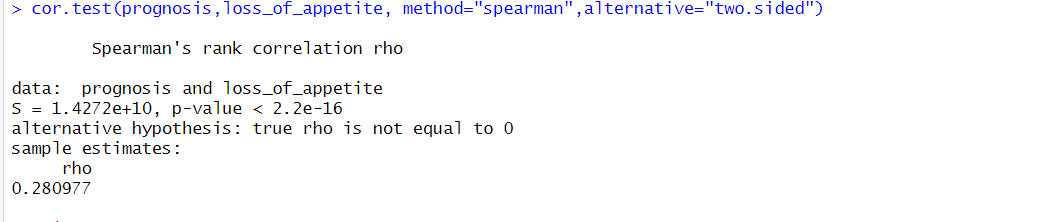
Confidence level = 95%

Let ῤ = 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?

H0: There is no correlation (ῤ =0) between loss\_of\_appetite and prognosis

H1: There is a correlation (ῤ ≠0) between loss\_of\_appetite and prognosis



Conclusion of correlation test

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.

Sample field: nausea, prognosis

Significant level (α) = 0.05

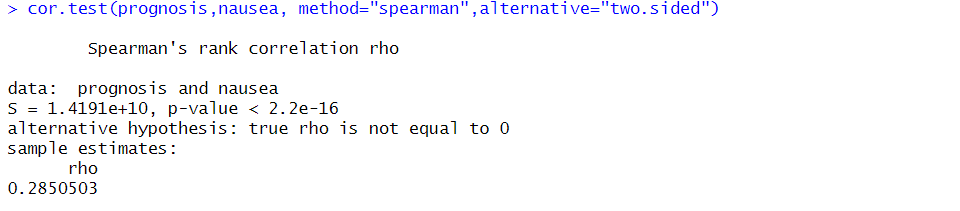
Confidence level = 95%

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

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

H0: There is no correlation (ῤ =0) between nausea and prognosis

H1: There is a correlation (ῤ ≠0) 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.

Sample field: headache, prognosis

Significant level (α) = 0.05

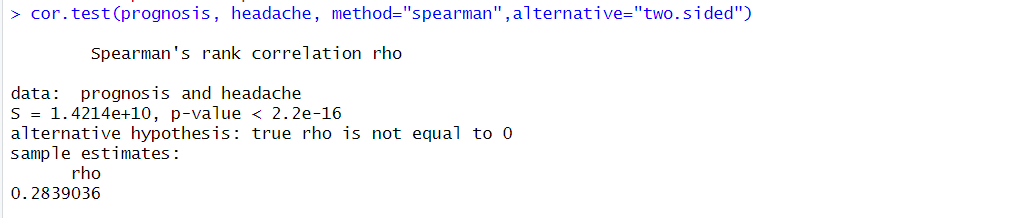
Confidence level = 95%

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

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

H0: There is no correlation (ῤ =0) between headache and prognosis

H1: There is a correlation (ῤ ≠0) between headache and prognosis



Conclusion of correlation test

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.

Sample field: high\_fever, prognosis

Significant level (α) = 0.05

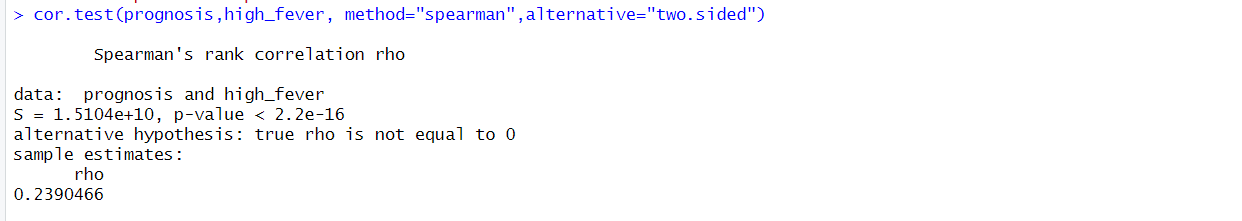
Confidence level = 95%

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

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

H0: There is no correlation (ῤ =0) between high\_fever and prognosis

H1: There is a correlation (ῤ ≠0) 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.

Sample field: skin\_rash, prognosis

Significant level (α) = 0.05

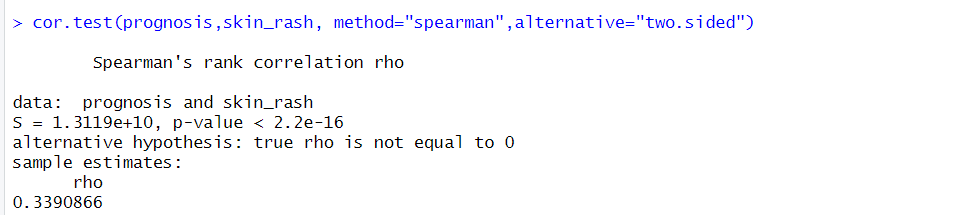
Confidence level = 95%

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?

H0: There is no correlation (ῤ =0) between skin\_rash and prognosis

H1: There is a correlation (ῤ ≠0) 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.

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

Significant level (α) = 0.05

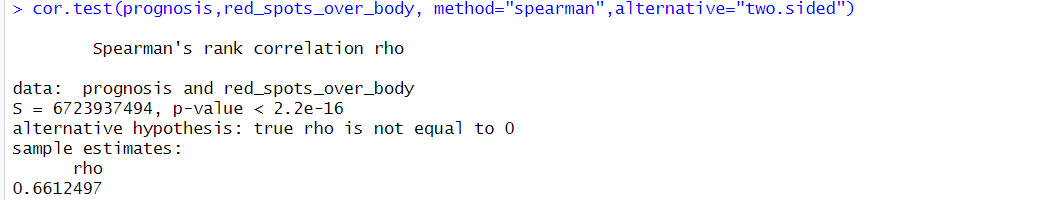
Confidence level = 95%

Let ῤ = 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?

H0: There is no correlation (ῤ =0) between red\_spots\_over\_body and prognosis

H1: There is a correlation (ῤ ≠0) between red\_spots\_over\_body and prognosis



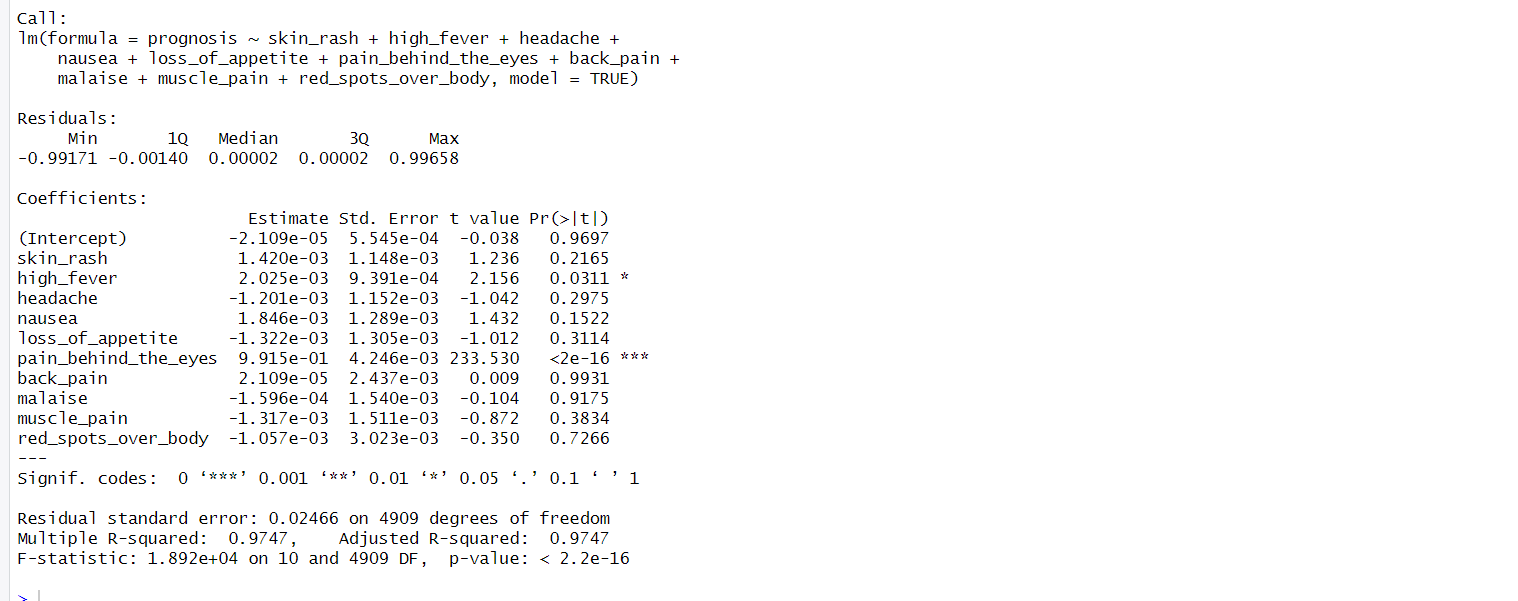
A moderate positive relationship (ρ = 0.66) exists between the presence of red spots on the body and the prognosis, with statistical significance at the 5% level, determined by Spearman rank correlation tests (p < 2.2e-16). These results indicate the need for additional exploration through regression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

**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 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.



According to the multiple linear model developed for predicting the prognosis based on symptoms such as skin rash, high fever, headache, nausea, loss of appetite, pain behind the eyes, 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 0.9915 and a large t-value of 233.530 (p < 0.001), indicating a strong positive association.

Other symptoms such as "high\_fever" also show a statistically significant impact on prognosis, with a coefficient estimate of 0.0025 (p = 0.0311), suggesting that an increase in high fever 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.

**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’s 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. 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**

**References**

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