### **Project Title:** Breast Cancer Risk Prediction System **Project Description:**

Breast cancer is one of the main causes of cancer death worldwide. Early diagnostics significantly increases the chances of correct treatment and survival, but this process is tedious and often leads to a disagreement between pathologists. Computer-aided diagnosis systems showed the potential for improving diagnostic accuracy. But early detection and prevention can significantly reduce the chances of death. It is important to detect breast cancer as early as possible.

This project builds a model in Watson Studio and deploys the model in IBM Watson Machine Learning.

#### **IBM Watson Services:**

- 1. IBM Services Used:
- 2. IBM Nodered
- 3. IBM Watson Studio
- 4. IBM Machine Learning
- **5**. IBM Cloud Object Storage

#### **Project Architecture:**

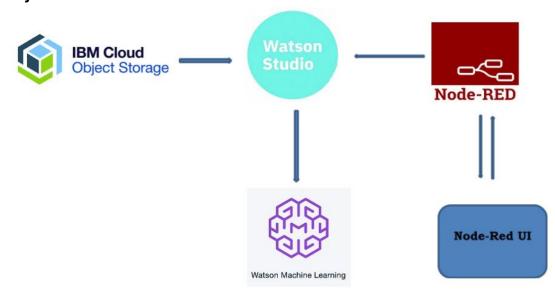


Figure 1 Project Architecture

#### **Project Objectives:**

- 1. To design a python notebook code for breast cancer prediction
- 2. To perform comparative analysis of various machine learning algorithms
- 3. Design a User Interface for prediction of Breast Cancer from various health

parameters

#### **Dataset Description:**

The Breast Cancer Prediction model is designed using Wisconsin cancer dataset. This dataset consists of 569 patient information. There are total 30 health attributes for each patient. Table 1 describes all the 30 attributes of the dataset.

Table 1 Wisconsin Cancer Dataset

| Attribute             | Numeric values | Description                              |  |  |  |
|-----------------------|----------------|--|--|--|--|
|                       | (Min,Max)      |  |  |  |  |
|                       | 6.98, 28.1     | Mean of distances centre point to points |  |  |  |
| radius_mean           |                | on perimeter                             |  |  |  |
|                       |                |  |  |  |  |
| Texture_mean          | 9.71,39.3      | Standard deviation of gray-scale pixel   |  |  |  |
|                       | ,              | values                                   |  |  |  |
| Perimeter_mean        | 43.8,189       | Mean size of tumor                       |  |  |  |
| Smoothness_mean       | 0.05,0.16      | Mean of local variations in radius       |  |  |  |
| Compactness_mean      | 0.02, 0.35     | Mean of compactness                      |  |  |  |
|                       |                | Mean value of severity of concave        |  |  |  |
| Concavity_mean        | 0,0.43         | proportions of contour                   |  |  |  |
|                       | 3,21.13        |  |  |  |  |
|                       |                | Mean of total number of concave          |  |  |  |
| Concave points_mean   | 0,0.2          | proportions in contour                   |  |  |  |
|                       |                |  |  |  |  |
| Symmetry_mean         | 0.11,0.3       |  |  |  |  |
| Factal_dimension_mean | 0.05,0.1       | Mean value of coastline approximation    |  |  |  |
|                       | 0.00,0.1       | -1                                       |  |  |  |
|                       |                | Standard error for the mean of the       |  |  |  |
| Radius_se             | 0.11,2.87      | distances from centre to points on the   |  |  |  |
|                       | ,              | perimeter                                |  |  |  |
|                       |                | Standard error of standard deviation of  |  |  |  |
| Texture_se            | 0.36,4.88      | gray-scale pixel values                  |  |  |  |
| . 5.7(4) 0_00         |                | gray scale pinel values                  |  |  |  |
|                       | 1              |  |  |  |  |

| Perimeter_se         | 0.76,22   | Standard error of size of tumor                                     |  |  |  |
|----------------------|-----------|---|--|--|--|
| Area_se              | 6.8,5.42  |   |  |  |  |
| Smoothness_se        | 0,0.03    | Standard error for local variation in radius length                 |  |  |  |
| Compactness_se       | 0,0.14    | Standard error for compactness                                      |  |  |  |
| Concavity_se         | 0,0.4     | Standard error for concavity proportions                            |  |  |  |
| Concave_points_se    | 0,0.05    | Standard error of no of concave points in contour                   |  |  |  |
| Symmetry_se          | 0.01,0.08 | Standard error of symmetry  |  |  |  |
| Fractal_dimension_se | 0,0.03    | Standard error for coastline approximation-1                        |  |  |  |
| Radius_worst         | 7.93,36   | Worst case mean of distances from centre to points on perimeter     |  |  |  |
| Texture_worst        | 12,49.5   | Worst case mean of standard deviatio of gray scale pixel values     |  |  |  |
| Perimeter_worst      | 50.4,251  | Worst case mean of perimeter  |  |  |  |
| Area_worst           | 85,4250   | Worst case area mean  |  |  |  |
| Smoothness_worst     | 0.07,0.22 | Worst case value of local variation in radius lengths               |  |  |  |
| Compactness_worst    | 0.03,1.06 | Worst or largest mean of compactness                                |  |  |  |
| Concavity_worst      | 0.1, 25   | Worst case mean of severity of concave proportions of countour      |  |  |  |
| Concave points_worst | 0,0.29    | Worst or largest mean for number of concave proportions of countour |  |  |  |
| Symmetry_worst       | 0.16,0.66 | Largest mean value of symmetry                                      |  |  |  |

| Fractal_dimenstion | 0.06,0.21 | Worst  | or               | largest | argest mean of coastline<br>on-1 | coastline |  |
|--------------------|-----------|--------|------------------|---------|----------------------------------|-----------|--|
| worst              | 0.00,0.21 | approx | ima <sup>-</sup> | tion-1  |                                  |           |  |

#### **Design of Classification Model**

The Breast Cancer Risk Prediction User Interface is designed with a purpose to help the doctor or physians in making a right prediction about breast cancer risk from the patient's health reports. Figure 2 shows the design methodology of the entire system. The design is divided in three sections.

- 1. Import dataset and train machine learning dataset using Python Notebook and Scikit Learn library
- 2. Deploy the trained model in IBM Cloud space
- 3. Interface model API with nodeRED flow and generate UI

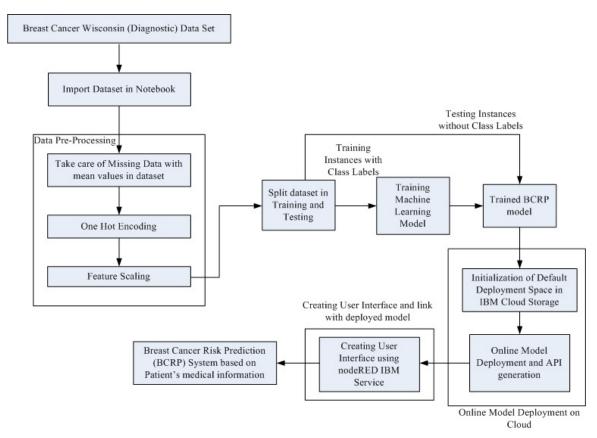


Figure 2 Project Design Methodology

#### **Comparative Analysis:**

In order to analyse the performance of various machine learning models various quantitative measures are used. These measures demonstrates the effectiveness of machine learning model for the prediction of diabetes mellitus based on patient's health parameters. The quality measures used for the comparative analysis are as follows:

- 1. Accuracy: Total number of correct classifications out of total test instances.
- 2. Precision: Correctness over the positive detections.
- **3.** Recall: Total positive detections out of total positive instances.
- **4.** ROC Curve: The plot between True Positive Rate (TPR) and False Positive Rate (FPR) while changing the threshold for positive classification.

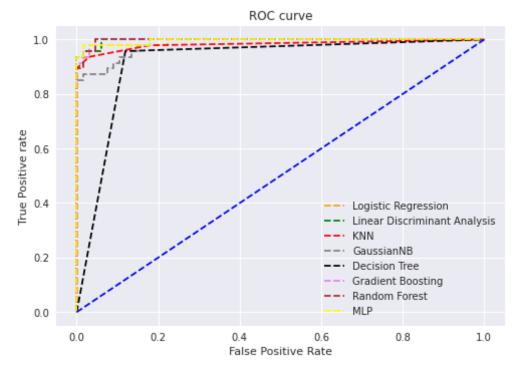


Figure 3 ROC for various Machine Learning Models

- **5.** Area Under Curve (AUC): It is obtained from the graph ploatted between Precision and Recall.
- **6.** F\_measure: It represents the weighted harmonic mean of the Precision and Recall.
- 7. Confusion Matrix: Table 2 shows the confusion matrix.
  - TP: True Positive i.e. Positive sample are classified as Positive
  - TN: True Negative i.e. Negative samples are classified as Negative
  - FP: False Positive i.e. Negative samples are classified as Positive
  - FN: False Negative i.e. Positive samples are classified as Negative

Table 2 Confusion Matrix

| Confusion Matrix |                       |          |                 |  |  |  |
|------------------|-----------------------|----------|-----------------|--|--|--|
| Total Number     | tal Number of Samples |          | Predicted Class |  |  |  |
| Total Nullibe    | or Sarriples          | Benign   | Malignant       |  |  |  |
|                  | Benign                | True     | False           |  |  |  |
|                  |                       | Negative | Positive        |  |  |  |
| True Class       |                       | (TN)     | (FP)            |  |  |  |
| True Class       | Malignant             | False    | True            |  |  |  |
|                  |                       | Negative | Positive        |  |  |  |
|                  |                       | (FN)     | (TP)            |  |  |  |

Table 3 Comparative Performance of Various Machine Learning Algorithms

| Performance parameter        | Logistic<br>Regressio<br>n | Linear<br>Discrimina<br>nt Analysis | KNN  | Gaussian<br>Naïve<br>Bayes | Decision<br>Tree | Gradient<br>Boosting | Random<br>Forest | Multilay<br>er<br>Perceptr<br>on(MLP) |
|------------------------------|----------------------------|-------------------------------------|------|----------------------------|------------------|----------------------|------------------|---------------------------------------|
| Accuracy                     | 96.5                       | 96.5                                | 95.6 | 90.4                       | 91.2             | 97.4                 | 95.6             | 97.4                                  |
| Precision                    | 95.7                       | 100                                 | 100  | 87.5                       | 84.9             | 95.8                 | 93.8             | 95.8                                  |
| Recall                       | 95.7                       | 91.5                                | 89.4 | 89.4                       | 95.7             | 97.9                 | 95.7             | 97.9                                  |
| F_Measure                    | 95.7                       | 95.6                                | 94.4 | 88.4                       | 90.0             | 96.8                 | 94.7             | 96.8                                  |
| Area Under<br>Curve<br>(AUC) | 99.333                     | 99.714                              | 4    | 98.412                     | 91.902           | 99.745               | 99.714           | 99.555                                |

#### **Design of User Interface**

Once the prediction model is designed using IBM Auto AI service, it is deployed using IBM Cloud storage and API is obtained. In order to make the UI another IBM service named nodeRED App is used. nodeRED contains various types of nodes which helps to design the flow and user interface. The flow of proposed model designed in nodeRED is shown in Figure 4.

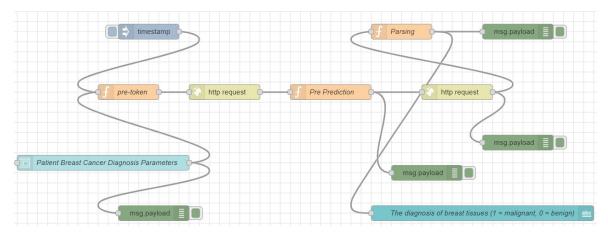


Figure 4 nodeRED flow for Breast Cancer Risk Prediction Model UI

#### **User Interface Output:**

Figure 5 shows the output of User Interface for Breast Cancer Risk Prediction system.

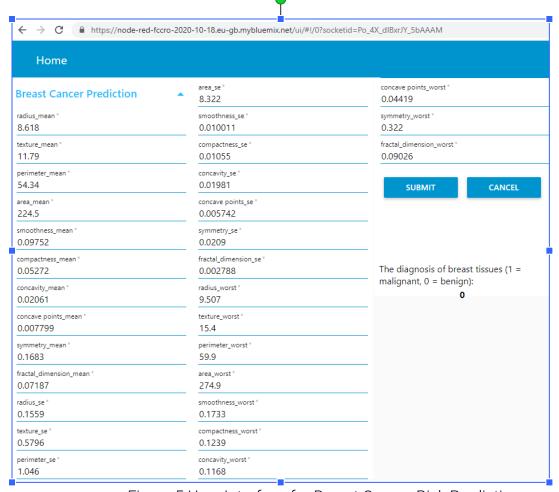


Figure 5 User Interface for Breast Cancer Risk Prediction

#### **Conclusion:**

After analyzing the quantitative results gradient boosting algorithm based machine learning classification model is deployed using IBM Cloud services. Gradient boosting algorithm provides the accuracy of 97.4%, recall of 97.9% and F\_measure of 96.8% along with AUC of 99.74%. The model is capable of correctly predicting the malignant and benign classes from the patient's health features.

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