Diagnosing breast tumor using machine learning

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1. Overview

The main purpose of the program is to predict breast cancer based on features computed from a digitised image of a fine needle aspirate (FNA) of a breast mass. For the prediction the program uses the *k*-nearest neighbours algorithm (*k*-NN) and and data from the UCI Machine Learning Repository, specifically Breast Cancer Wisconsin (Diagnostic) Data Set.[1]

2. Dataset overview

2.1. Dataset description

Dataset consists of 569 instances of cell nuclei from various breast tumors. Every instance describes features of the cell nuclei which are computed from a digitised image of a fine needle aspirate (FNA) of a breast mass.

The dataset has 32 columns - id number, diagnosis (M for malignant, B for benign), radius (mean of distances from centre to points on the perimeter), texture (deviation of gray-scale values), perimeter (mean size of the core tumor), area, smoothness, compactness ($compactness = (mean\ of\ perimeter)^2/(area - 1)$), concavity (mean of severity of concave portions of the contour), concave points (mean of severity of concave portions of the contour), symmetry, fractal dimension (mean for "coastline approximation" - 1), standard error of the radius, standard error of the texture, standard error of the smoothness, standard error of the compactness, standard error of the concavity, standard error of the concave points.[2]

Application uses only first 12 columns. First two columns are used only for identifying the results of the cell analysis. Remaining 10 columns are used for training and validating.

2.2. Dataset example

853201	M	17.57	15.05	115	955.1	0.0984	0.1157	0.0988	0.0795	0.1739	0.06149
853401	M	18.63	25.11	124.8	1088	0.1064	0.1887	0.2319	0.1244	0.2183	0.06197
853612	M	11.84	18.7	77.93	440.6	0.1109	0.1516	0.1218	0.0518	0.2301	0.07799
854253	M	16.74	21.59	110.1	869.5	0.0961	0.1336	0.1348	0.0602	0.1896	0.05656
854002	M	19.27	26.47	127.9	1162	0.0940	0.1719	0.1657	0.0759	0.1853	0.06261

3. Learning process and making predictions

Application is using the *k*-nearest neighbours algorithm that stores all available cases and classifies new cases based on similarity (distance function).

Before the actual process of learning the program standardises the data since values in first four columns have much bigger influence on calculating the distance between instances than the values in remaining columns.

$$X_s = \frac{X - Min}{Max - Min}$$

Next, the whole dataset is split into two parts. The first part contains two thirds of the dataset and is used for learning and the second part is used for validation. The training data are than fit into a classifier that is an instance of Python class `KNeighborsClassifier` from `scikit-learn` library. Application then finds the best *k* value for the inserted data by scoring the precision of the classifier using the validation part of the dataset. The classifier uses Euclidean distance as the metric function.

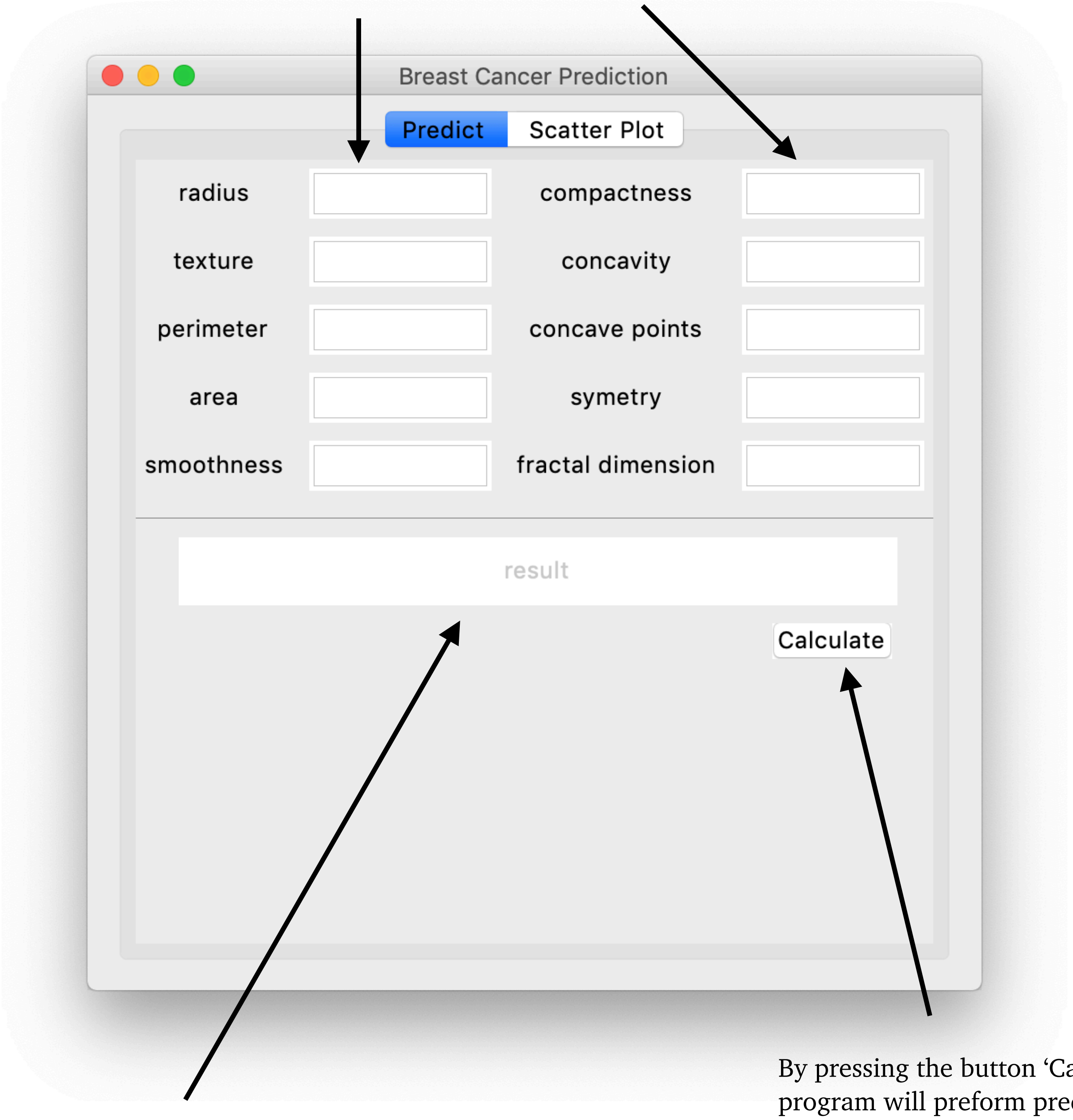
$$D = \sqrt{\sum_{i=1}^{n} (x_i - y_i)^2}$$

After picking the right *k* value the program is ready to make predictions based on values set by the user. The result is either that the breast tumor is malignant or benign. The program is able to predict that with precision around 95 % based on testing using the validation part of the original dataset, results may differ when the program is used for actual predictions.

The accuracy could be increased by using much larger dataset for learning and validating processes which would describe almost all possible situations, and taking measuring error into account. Another improvement in accuracy could be made by using different distance functions and comparing the results, or using a simple heuristic that would assign weights to the values based on the importance of that particular value in recognising the malignancy of the breast tumor.

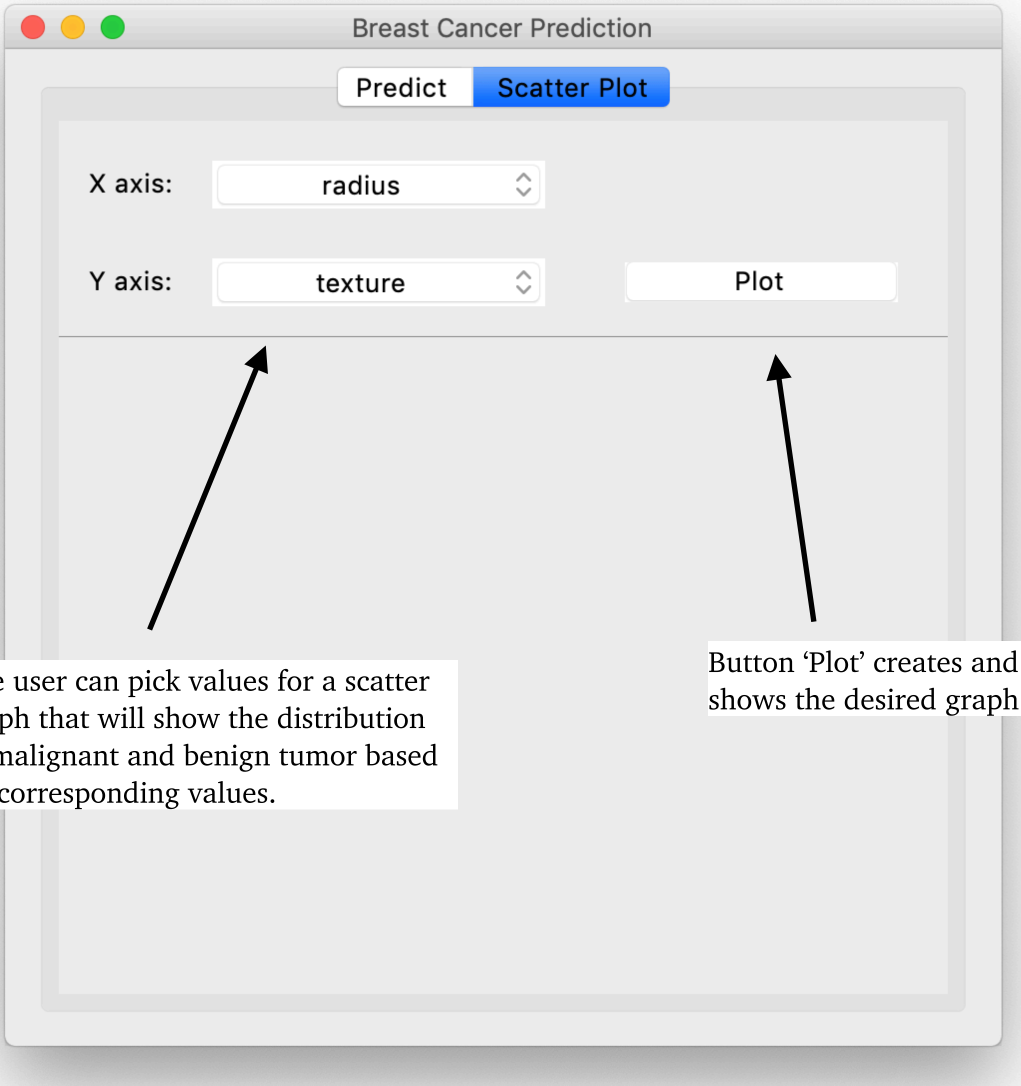
4. Sample run of the program

Entry fields for entering the values for which the user wants to make a prediction.



Text field for showing the result of the prediction. If not all of the entry fields are filled or do not contain numbers it is going to show an error message based on the value that is not right.

By pressing the button ‘Calculate’ the program will preform prediction based on the values in the entry fields.



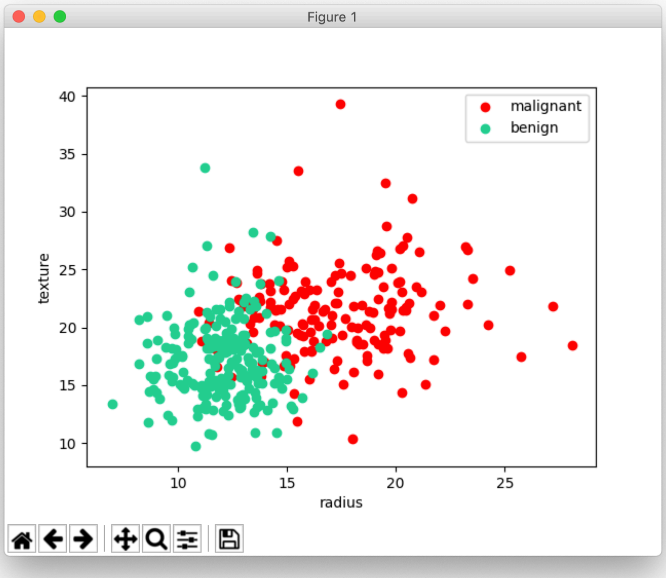
Breast Cancer Prediction

X axis: radius

Y axis: texture

The user can pick values for a scatter graph that will show the distribution of malignant and benign tumor based on corresponding values.

Button ‘Plot’ creates and shows the desired graph.



Example of plotted graph.

5. Sources

[1] https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Diagnostic)
[2] https://www.kaggle.com/uciml/breast-cancer-wisconsin-data