The breast cancer data includes 569 examples of cancer biopsies, each with 32 features. One feature is an identification number, another is the cancer diagnosis, and 30 are numeric-valued laboratory measurements. The diagnosis is coded as "M" to indicate malignant or "B" to indicate benign.

The other 30 numeric measurements comprise the mean, standard error, and worst (that is, largest) value for 10 different characteristics of the digitized cell nuclei.

These include:

* Radius
* Texture
* Perimeter
* Area
* Smoothness
* Compactness
* Concavity
* Concave points
* Symmetry
* Fractal dimension

Based on these names, all the features seem to relate to the shape and size of the cell nuclei. Unless you are an oncologist, you are unlikely to know how each relates to benign or malignant masses.

Our task is to make a predictive model using Machine Learning, which classifies whether Cancer is ‘Malignant’ or ‘Benign’.

Steps to follow:

1. Save the complete dataset inside a variable
2. Remove the first two columns and save the dataset in another variable
3. Standardize all the columns from second dataset having numerical values using ‘Z-Score Standardization’
4. Divide the second dataset into two portions:
   1. Save 1st 469 rows in one variable as training set
   2. Save remaining in another variable as test set
5. Extract 1st 469 rows of the second column of the first dataset save it in one variable
6. Extract remaining rows of the second column of the first dataset and save it in another variable.
7. Install Packages ‘Class’ and ‘gmodel’
8. Apply ‘knn’ algorithm using knn function to the above dataset. (Use Step 4a as Training Set, 4b as Test Set, 5 as Label)
9. Verify using CrossTable function whether the result is right or not. (Use output of knn function as one argument and label generated in step 6 as another.
10. Analyse the cross table result and present your understanding.