I have applied the same SVM using inbuilt function on a Cancer patient dataset to predict whether the cell of the patient is malignant or benign. I read the cell dataset. Then I perform basic data preprocessing. The BareNuc column has an object data type and so we convert it into integer values. Also we have to drop some rows that have null values. We create X and Y variables using the data and simultaneously convert the data frame into nparray. Then train test data split. Then we fit the data to inbuilt SVM function using radial basis function which computes the kernel value as e raise to the power minus of x-x’ normalised square over 2 \* variance. Where x, x’ are to feature vectors. On predicting the values we get y-hat. To check the accuracy we create a confusion matrix. As we can see 85 benign patients are predicted correctly and 47 malignant were labelled correctly whereas 5 benign cells were misclassified as malignant.