**Chi-merge Implementation in R:**

(I took from help from the following tutorial: <https://alitarhini.wordpress.com/2010/11/02/chimerge-discretization-algorithm/>)

* Sorted the attributes in the data table
* Created a frequency (contingency) table using the R table() function, containing one row for each distinct attribute value and one column for each class. Then generate a set of distinct intervals. Set the interval lower bound equal to the attribute value (inclusive) that belongs to this interval, and set its upper bound to the attribute value (exclusive) belonging to the next interval.
* If the number of rows = maxintervals then stop otherwise go to next step. Calculate the value of (O – E) 2/E (if E<0.5, replace E by 0.5) where O is the observed frequency value for that combination, then add the values obtained to give chi 2 for that pair of adjacent rows. This is done using the chi-function in my program.
* Chi merge selects the smallest value of chi 2.This value is compared     with a threshold, the two intervals are merged based on the following condition if chi2 is less than threshold or if the number of rows > max-intervals, if the condition is met then the two intervals are merged and the attribute for the merged row to that of the first of the two consistent rows and the upper interval bound to the upper bound interval of the next attribute.
* After checking each value of threshold with degrees of freedom, I set the max-interval to be that value and run the algorithm for each of those threshold values.