**Orange Software Implementation for HAR using Emaptica E4 device**

Steps taken to download Orange :-

1. Download Orange software from website : <https://orange.biolab.si/download/>.
2. Install the application on the machine
3. Run the software

Steps taken to compare efficiency of different algorithms :-

The application GUI consists of 2 columns. 1 column consists of modules categorized as Data, Visualise, Model, Evaluate and Unsupervised, each with several functional modules. Column 2 is the workspace/execution area.

1. Drag a “FILE” module to Column 2.
2. Double click on a “FILE” to open an upload window. Browse for data file that was downloaded from GIthub repository. The table columns will bee displayed on the window. Select column “ACT” and change the type from “FEATURE” to “TARGET”.
3. Add “Preprocess” module to workspace. Double click on “Preprocess”, and choose Discretize Continuous Variables. Select equal frequency discretion = 5. Choose Normalize Features = Center by Mean, Scale by SD.
4. Draw a line to connect the “FILE” module to “Pre-processed” module.
5. Add machine learning modules Logistic Regression, SVM, Random Forest, KNN and Naïve Bayes.
6. To each module, add the parameters mentioned in the paper
7. Draw a line to connect “Preprocessor” module to these the machine learning modules
8. Add Test & Score module and Confusion matrix module
9. Draw a line to connect these modules to Test & Score module
10. Draw a line connecting Test & Score to Confusion Matrix
11. Double click Test & Score and Confusion Matrix to view results.