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Appendix- A

Variable available in the data set collected from Apeksha Hospital Maharagama.

Rec.ID	Fluorouracil (5FU)
GenderAge	Imatinib 400mg
Diagnosis	Doxorubicin
Stage	docetaxel
patient state	Paclitaxel
treatment	Anastrozole
no of lab procedures	Asparaginase
DOSAGE	Dexakepyon
FREQUENCY	Dasatinib
Surgery	BMP
blood transfusion	radio Iodine
Conclusion	thyroxine
radio_theropy	immunization
Tamoxifen	Cyclophosphamide
cytarabine	
Cladribine	
Methotrexate	
Herceptin	
SF4	
Vincristine(VCR)	

Appendix- B

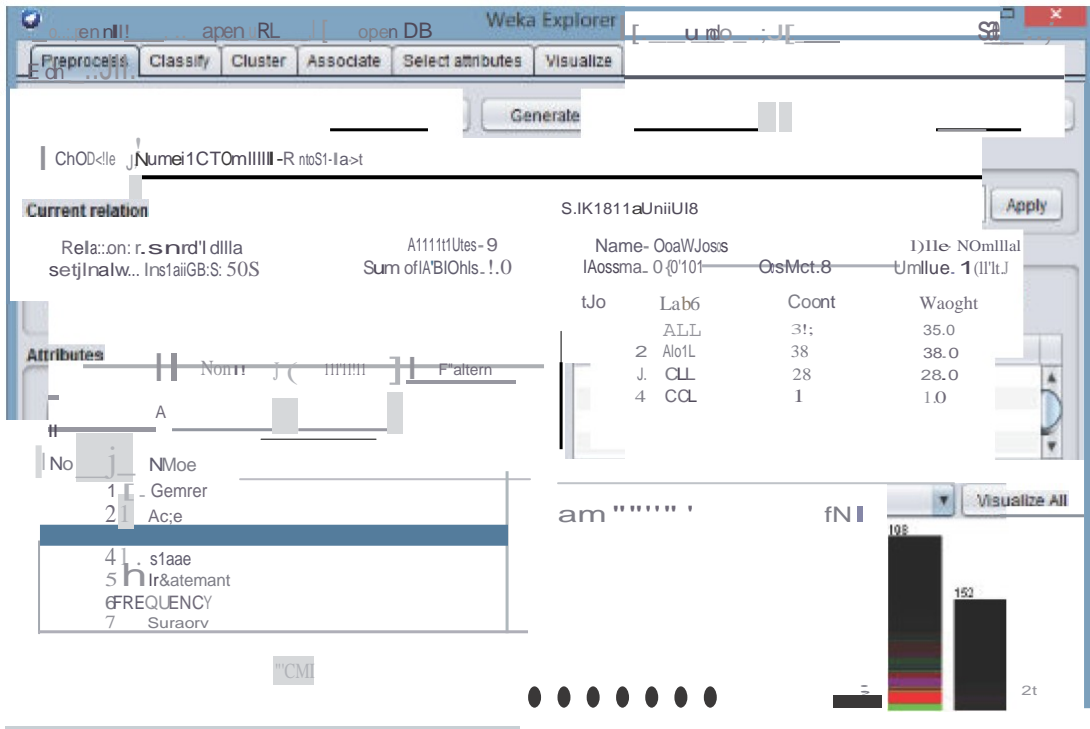


Figure 6.4.1 - Applying Numeric to Nominal filter before attribute selection.

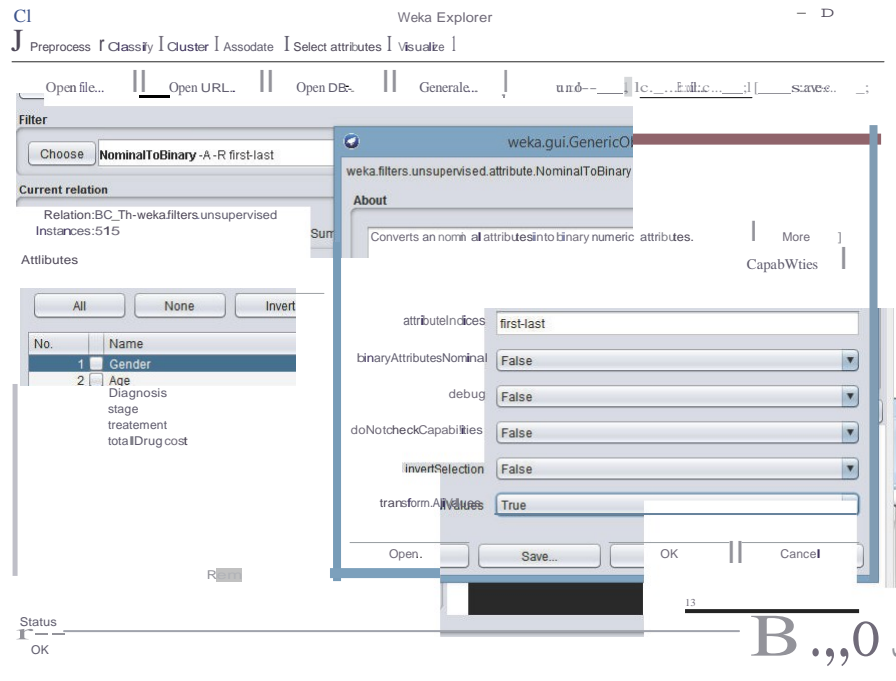


Figure 6.4.2 Apply NominalToBinary Filter

Weka Explorer

Preprocess Classify Cluster Associate Select attributes Visualize

Classifier

Choose LinearRegression-8 1 -R 1.0E-8 -num-decimal-places 4

Test options

Use training set

Supplied test set

Cross-validation Folds 10

@ Percentage split % 70

More options..

[(Num) totalDrug cost

Start Stop

Result list (right-click for options)

10:26:07 - functions.LinearRegression

10:28:28 - functions.LinearRegression

Classifier output

```

treatment=chemo
treatment=prevension drugs
treatment=Radio_iodine
treatment=Surgery
treatment=thyroxine
treatment=Radio_iodine+Surger
y
treatment=Chemo+Surgery
treatment=Surgery+radio_thero
py treatment=radiotheorapy
treatment=N/A
total Drug cost
Test mode: split 70.0\ train, remainder test

=== Classifier model {full training set} ===

Linear Regression Model

total Drug cost =

 29814.8949 * Gender=F +
-29835.8925 * Gender=M +
 1339.1647 * Age +
-128257.9989 * Diaqnosis=BC +
 1?A?i. 01 P. * OiAryno=Tyroirl -
-51723.2084 * stage=L2 +
 83899.8761 * stage=L1 +
 58763.1014 * stage=LO +
-95812.6997 * stage=L3 +
-207317.0552 * stage=L4 +
-109157.6335 * stage=LS +
 27072.8307 * treatment=chemo +
-326290.3963 * treatment=prevension drugs +
 352860.4075 * treatment=Radio_iodine +
-296217.5018 * treatment=Surgery +
-409628.5775 * treatment=thyroxine +
 502259.6805 * treatment=Radio_iodine+Surgery +
 133409.5185 * treatment=Chemo+Surgery +
 128006.2083 * treatment=Surgery+radio_therapy +
-236680.1912 * treatment=radiotheorapy +
-207350.2797 * treatment=N/A +
 301575.8523

Time taken to build model: 0.02 seconds

=== Evaluation on test split ===

```

Figure 6.3 -After applying Linear regression model

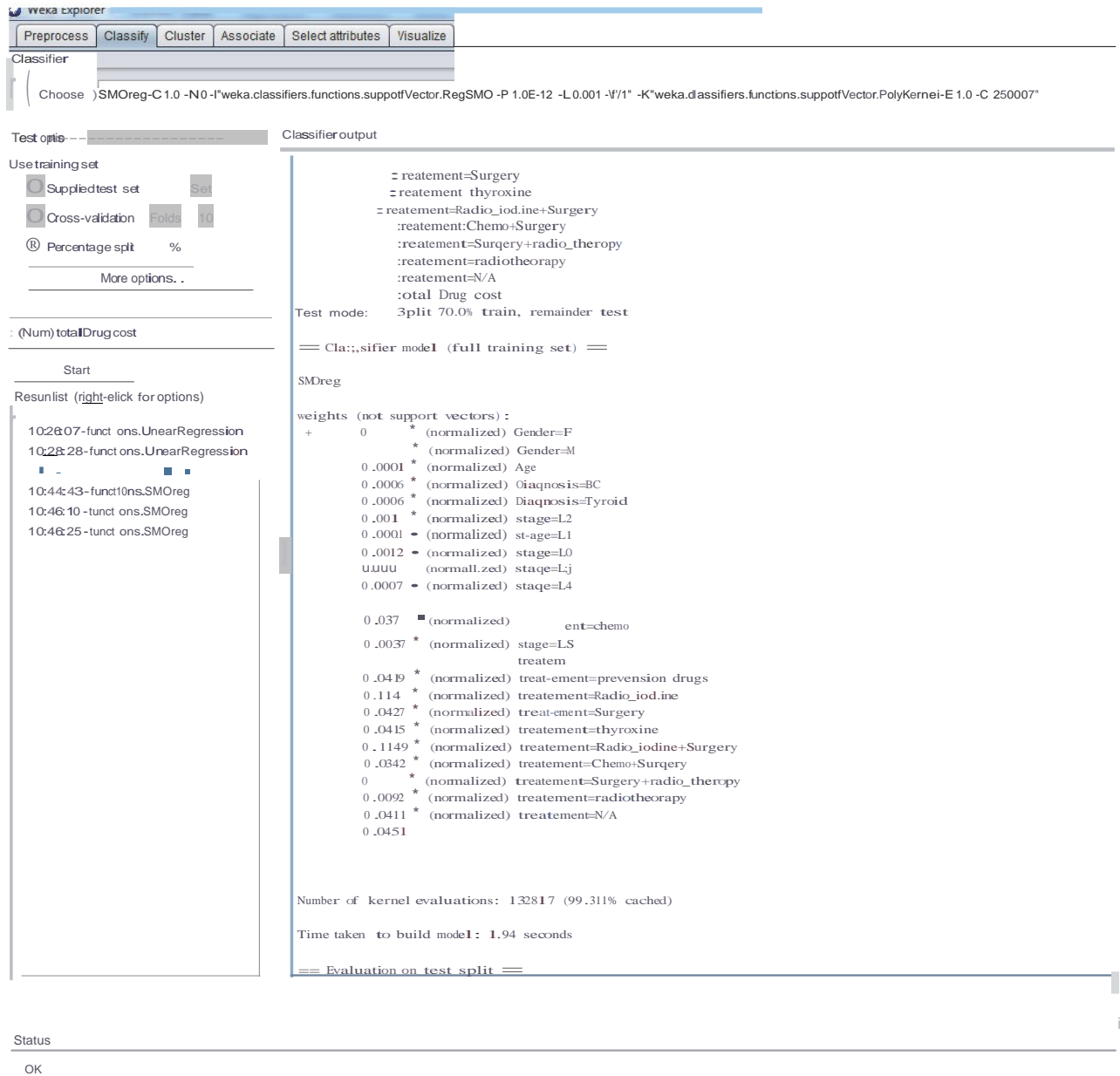


Figure 6.4 - After applying SMO regression model

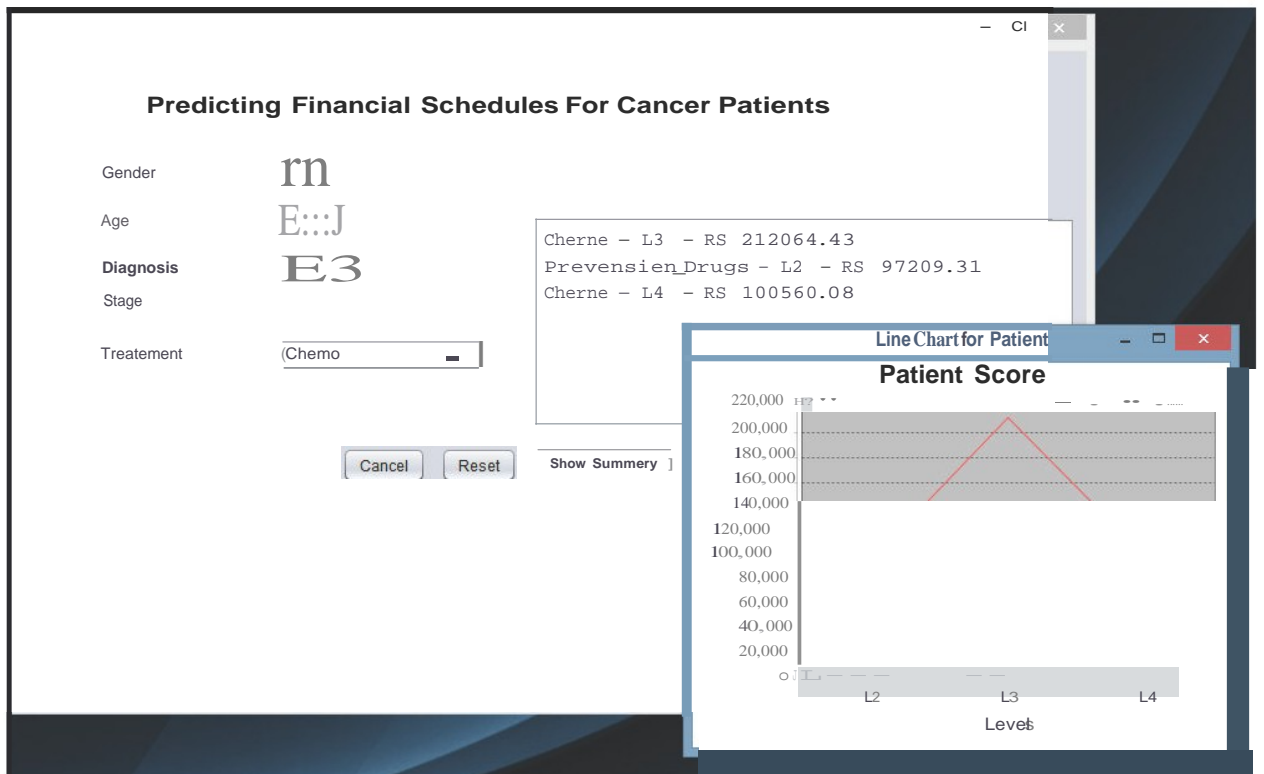


Figure 6.6-Graphical view of the application

weka 1: Xpoorer

Preprocess | Classify | Cluster | Associate | Select attributes | Visualize

Classifier: Choose LinearRegression -8 0-R t.OE-8 -num-decimal-places 4

Test options

Use training set

Supplied test set Set..

Cross-validation Folds 10

Percentage split %

Result list (right-click for options)

- 00:33:20 - functions.LinearRegress
- 00:35:37 - trees.REPTree
- 00:36:15 - functions.LinearRegress
- 00:38:53 - functions.LinearRegress
- 00:39:08 - functions.3MOreg
- 00:43:04 - functions.LinearRegress

Classifier output

```

-318697.2037 * traitement=prevention drugs +
423452.5928 * traitement=Radio_iodine +
-288488.8222 * traitement=Surgery +
-231744.4542 * traitement=thyroxine +
584076.2939 * traitement=Radio_iodine+Surgery +
407222.2256

Time taken to build model: 0.11 seconds

=== Evaluation on test split ===

Time taken to test model on training split: 0.03 seconds

=== Summary ===

Correlation coefficient           0.5725
Mean absolute error             333645.4507
Root mean squared error        553183.2528
Relative absolute error         64.9838 %
Root relative squared error     81.9472 %
Total Number of Instances      154

```

Status: OK

Figure 7.1- Evaluation results of the multiple linear regression model

Weka Explorer

[Preprocess | **Classify** | Cluster | Associate | Select attributes | Visualize]

Classifier

Choose SMOreg -C 1.0 -N 0 -l "weka.classifiers.functions.supportVector.RegSMOimproved-T 0.001 -V -P 1.0E-12 -L 0.001 -W 1" -K "weka.cll

Test options

Use training set
 Supplied test set Set..
 Cross-validation Folds 10
 Percentage split %

Classifier output

```

- 0.0411 * {normalized} treatment=N/A
+ 0.0451

Number of kernel evaluations: 132817 {99.311% cached}

Time taken to build model: 3.17 seconds

=== Evaluation on test split ===

Time taken to test model on training split: 0 seconds

=== Summary ===

Correlation coefficient          0.5889
Mean absolute error             223944.6529
Root mean squared error        581000.9477
Relative absolute error        43.6175 %
Root relative squared error    86.068 %
Total Number of Instances      154
  
```

More options...

(Num) totalDrug cost

Stop

Start

Result list (right-Click for options)

- 00:33:20 - functions.LinearRegress
- 00:35:37 - trees.REPTree
- 00:36:15 - functions.LinearRegress
- 00:38:53 - functions.LinearRegress
- 00:39:08 - functions.SMOreg
- 00:43:04 - functions.LinearRegress

Status

OK

Figure 7.2- Evaluation results of the SMO regression model

Appendix- C

Code for Building the Linear Regression Model

```
package com.cancer;

import weka.core.Instances;

import weka.core.converters.ConverterUtils.DataSource;

import weka.classifiers.functions.LinearRegression;

!import weka.classifiers.functions.SMOreg;

public class Regression{

    public static void main(String args[]) throws Exception{

        //load dataset

        DataSource source= new DataSource("E:/Msc/project_on_28-4/patient_data_reduce.arff");

        Instances dataset= source.getDataSet();

        //set class index to the last attribute

        dataset.setClassIndex(dataset.numAttributes()-1);

        //build model

        LinearRegression lr =new LinearRegression();

        lr.buildClassifier(dataset);

        //output model

        System.out.println(lr);

    }}
```

Code for Predicting the Cost For Future Medicine

```
package com.cancer; import

java.io.FileWriter; import

java.io.IOException;

import java.text.DecimalFormat;

import java.util.ArrayList;

import java.util.Arrays;

import java.util.Collections;

import java.util.List;

import weka.classifiers.functions.LinearRegression;

import weka.core.Instance;

import weka.core.Instances;

import weka.core.converters.ConverterUtils;

public class WekaService {

    private static String FILE_LOCATION = "E:I";

    private static String FILE_EXTENTION = ".arff";

    private static String MODEL_PATH = "E:/final presentation/Cancer/datamodelll-5/bc_th_model_test.model";

    SysCache cache = SysCache.getInstance();

    private static DecimalFormat df2 = new DecimalFormat("##");

    public List<String> writeToArffFormat(String gender, int age, String diagnosis,

        String stage, String treatment) throws IOException, Exception {

        String modStage = "";
```

```

String preTreatMent= treatment;

String aftTreatMent =treatment;

List<String> stageList =new ArrayList<String>();

stageList.add("LO");

stageList.add("L1");

stageList.add("L2");

stageList.add("L3");

stageList.add("L4");

stageList.add("L5");

stageList.add("L6");

cache.clearPredictedValues();

List<String> statusList =new ArrayList<String>();

statusList.add(generateWithContent(gender, age, diagnosis, stage, treatment,
FileType.CURRENT));

if (diagnosis.equals(Diagnosis.Tyroid.toString())) {

    switch (stage) {

        case "LO":

            aftTreatMent = Treatment.THYROXINE.toString();

            break;

        case "L1":

            preTreatMent= Treatment.THYROXINE.toString();

            aftTreatMent = Treatment.THYROXINE.toString();

            break;
    }
}

```

```

case "L2":

    if (treatment.equals(Treatment.RADIO_IODINE.toString())) {

        preTreatMent= Treatment.RADIO_IODINE.toString();

        aftTreatMent = Treatment.RADIO_IODINE.toString();

    } else if (treatment.equals(Treatment.CHEMO_SURGERY.toString())

        || treatment.equals(Treatment.SURGERY.toString())) {

        preTreatMent= Treatment.PREVENSSION_DRUGS.toString();

        aftTreatMent = Treatment.CHEMO.toString();

    } else if (treatment.equals(Treatment.RADION_THEROPY.toString())) {

        preTreatMent= Treatment.PREVENSSION_DRUGS.toString();

        aftTreatMent = Treatment.SURGERY.toString();

    } else if

(treatment.equals(Treatment.SURGERY_RADIO_THEROPY.toString())) {

        preTreatMent= Treatment.PREVENSSION_DRUGS.toString();

        aftTreatMent = Treatment.RADION_THEROPY.toString();

    }

    break;

case "L3":

    preTreatMent= Treatment.PREVENSSION_DRUGS.toString();

    aftTreatMent = Treatment.CHEMO.toString();

    break;

case "L4":

    preTreatMent= Treatment.PREVENSSION_DRUGS.toString();

```



```

    aftTreatMent = Treatment.CHEMO.toString();

    break;

case "L5":

    preTreatMent= Treatment.PREVENTION_DRUGS.toString();

    aftTreatMent = Treatment.CHEMO.toString();

    break;

}

} else if (diagnosis.equals(Diagnosis.BC.toString())) {

switch (stage) {

case "LO":

    aftTreatMent = Treatment.PREVENTION_DRUGS.toString();

    break;

case "L1":

    preTreatMent= Treatment.PREVENTION_DRUGS.toString();

    aftTreatMent = Treatment.CHEMO.toString();

    break;

case "L2":

    if (treatment.equals(Treatment.CHEMO.toString())) {

        preTreatMent= Treatment.PREVENTION_DRUGS.toString();

        aftTreatMent = Treatment.SURGERY.toString();

    } else if (treatment.equals(Treatment.CHEMO_SURGERY.toString()))

        || treatment.equals(Treatment.SURGERY.toString()) {

        preTreatMent= Treatment.PREVENTION_DRUGS.toString();

```

```

        aftTreatMent = Treatment.CHEMO.toString();

    } else if (treatment.equals(Treatment.RADION_THEROPY.toString())) {

        preTreatMent= Treatment.PREVENTION_DRUGS.toString();

        aftTreatMent = Treatment.SURGERY.toString();

    } else if
(treatment.equals(Treatment.SURGERY_RADIO_THEROPY.toString())) {

        preTreatMent= Treatment.PREVENTION_DRUGS.toString();

        aftTreatMent = Treatment.RADION_THEROPY.toString();

    }

    break;

case "L3":

    preTreatMent= Treatment.PREVENTION_DRUGS.toString();

    aftTreatMent = Treatment.CHEMO.toString();

    break;

case "L4":

    preTreatMent= Treatment.PREVENTION_DRUGS.toString();

    aftTreatMent = Treatment.CHEMO.toString();

    break;

case "L5":

    preTreatMent= Treatment.PREVENTION_DRUGS.toString();

    aftTreatMent = Treatment.CHEMO.toString();

    break;

}

```

```

    }

    //previous

    modStage = getPrevious(stage, stageList); System.out.println("Pre-" +
    modStage); statusList.add(generateWithContent(gender, age, diagnosis,
    modStage,
preTreatMent, FileType.PREVIOUS));

    //after

    modStage = getNext(stage, stageList);

    System.out.println("After-" + modStage);

    statusList.add(generateWithContent(gender, age, diagnosis, modStage,
aftTreatMent, FileType.AFTER));

    statusList.removeAll(Collections.singleton(null));

    return statusList;
}

public String generateWithContent(String gender, int age, String diagnosis,
    String stage, String treatment, FileType fileType) throws IOException,
Exception {

    String fileLocation = FILE_LOCATION;

    String predictValue =null;

    if (fileType == FileType.PREVIOUS) {

        fileLocation += "predict_file_previous";

    } else if (fileType == FileType.CURRENT) {

```

```

        fileLocation += "predict_file";

    } else if (fileType == FileType.AFTER) {

        fileLocation += "predict_file_after";

    }

fileLocation += FILE_EXTENTION;

FileWriter writer= new FileWriter(fileLocation);

List<CancerEntry> cancerEntrys = Arrays.asList(

        new CancerEntry(gender, age, diagnosis, stage, treatment, "?")

);

//if stage is empty that means previous of after stages are not available

if (stage != "") {

    //for header

    ArffUtils.writeHeaders(writer);

    for (CancerEntry d : cancerEntrys) {

        List<String> list= new ArrayList<>();

        list.add(d.getGender());

        list.add(String.valueOf(d.getAge()));

        list.add(d.getDiagnosis());

        list.add(d.getStage());

        list.add(d.getTreatment());

        list.add(d.getCost());
    }
}

```

```

        AtffUtils.writeLine(writer, list);
    }
} else {
    AtffUtils.writeLine(writer, Arrays.asList(" "));
}

writer.flush();

writer.close();

//Only stage is available we need to check the predicts values
// stage is empty then file is empty
if (stage != "") {
    //Predict Values for given Identifier
    predictValue = predictIdentifier(fileLocation, fileType, stage, treatment);
}
return predictValue;
}

public String predictIdentifier(String filePath, FileType fileType, String stage,
String treatment) throws Exception {
    //load model
    LinearRegression lr2 = (LinearRegression)
weka.core.SerializationHelper.read(MODEL_PATH);

String predictValue =null;

```

```

//load new dataset

ConverterUtils.DataSource source1 =new ConverterUtils.DataSource(filePath);

Instances testDataset = source1.getDataSet();

//set class index to the last attribute

testDataset.setClassIndex(testDataset.numAttributes() - 1);

//loop through the new dataset and make predictions

    for (inti = 0; i < testDataset.numInstances(); i++) {

        //get class double value for current instance

        double actualValue = testDataset.instance(i).classValue();

        //get Instance object of current instance

        Instance newinst = testDataset.instance(i);

        //call classifyInstance, which returns a double value for the class

        double predLR = lr2.classifyInstance(newinst);

        predLR = Math.abs(Double.parseDouble(df2.format(predLR)));

        System.out.println(actualValue + ", " + predLR);

        //predictValue = fileType.toString() + II- II+ actualValue +II , II+ predLR;

        predictValue =treatment+ || - || + stage+ || - RS || + Double.toString(predLR);

        cache.setPredictedValue(stage, predLR);

    }

return predictValue;

}

```

```
public String getNext(String uid, list<String> stageList) {  
  
    int idx = stageList.indexOf(uid);  
  
    if (idx < 0 || idx + 1 == stageList.size()) {  
  
        return "";  
  
    }  
  
    return stageList.get(idx + 1);  
  
}  
  
public String getPrevious(String uid, list<String> stageList) {  
  
    int idx = stageList.indexOf(uid);  
  
    if (idx <= 0) {  
  
        return "";  
  
    }  
  
    return stageList.get(idx - 1);  
  
}  
  
}
```