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Prediction Of Long Term Living Donor Kidney Graft Outcome: Comparison Between Different Machine Learning Methods

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ABSTRACT

Predicting the outcome of a graft transplant with high level of accuracy is a challenging task In medical fields and Data Mining has a great role to answer the challenge. The goal of this study is to compare the performances and features of data mining technique namely Decision Tree , Rule Based Classifiers with Compare to Logistic Regression as a standard statistical data mining method to predict the outcome of kidney transplants over a 5-year horizon. The dataset was compiled from the Urology and Nephrology Center (UNC), Mansoura, Egypt. classifiers were developed using the Weka machine learning software workbench by applying Rule Based Classifiers (RIPPER, DTNB),Decision Tree Classifiers (BF,J48) and Logistic Regression. Further from Experimental Results, it has been found that Decision Tree and Rule Based classifiers are providing improved Accuracy and interpretable models compared to other Classifier.

Indexing terms/Keywords

Data Mining; Machine learning; Kidney Transplanation; Classification; WEKA;Rule Based;Decision Tree.

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1.INTRODUCTION

In March 1976, the first renal transplantation in Egypt was carried out at the Department of Urology,University of Mansoura. A mother donated one of her kidneys to her daughter who was suffering from end-stage renal disease secondary to chronic pyelonephritis. Armed only with azathioprine and corticosteroids, the operative procedure and the functional outcomewere very successful.Atypical example of beginner's luck. Following a very slow start, the number of procedures increased gradually until it has currently reached a rate exceeding 80 cases every year[1].

The importance of having a possibility to predict the outcome after renal transplantation is helpful for decision makers to help better manage the overall renal transplantation process starting with who should get the renal and allow the choice of the best possible kidney donor and the optimum immunosuppressive therapy for a given patient and this will not only extend the longevity and quality of life for the recipient patient but also reduce medical expenses and increase the access to donor kidneys by reducing the need for multiple kidney transplants in the one patient[2,3].

Several prediction methods have been focused upon the use of standard statistical models to predict the outcome of renal transplantation [3,4,5,6] .machine learning algorithm applications are widely used in medical fields and in in nephrology namely, "espicialy" kidney transplantation, with good results [7,15] comparable" outcome" to traditional statistical tools[16,17,18,19,20,21].

In this paper we compare the performances and features of data mining technique namely Decision Tree , Rule Based Classifiers and with Compare to Logistic Regression as a standard statistical data mining method to predict the outcome of kidney transplants over a 5-year horizon using the patient profile information prior to the transplantation. with the challenge being to select the right kidney from the available kidney donors for a particular patient, in order to maximize the chances for the successful transplantation. The rest of the paper is organized as follows. The concept of Rule Based Classifiers,Decision Tree Classifiers , and logistic regression discussed in Section 2; and in Section 3- Methodology for our proposed work has been detailed; Section 4 outlines the Results and discussion and Section 5 illustrates Conclusions and future work.

2.RELATED RESEARCH

In medical fields There are Several studies have been focused on kidney Transplanation [table1].These studies have applied different Machine Learning Methods to the given problem and have achieved higher prediction accuracies rangingfrom 62% or highe.

Table 1. Several studies have been focused on kidney Transplanation

Source	Sample/Study Description	Purpose	Results
Jiakai Li,et al.[22]	using the University of Toledo Medical Center (UTMC) patient data as reported to United Network Organ Sharing (UNOS) and had 1228 patient records for the period covering 1987 through 2009.	To Predict renal transplantation graft status and graft survival period using Bayes net classifiers , Two separate classifiers were induced from the data set, one to predict the status of the graft as either failed or living, and a second classifier to predict the graft survival period.	prediction accuracy of 97.8% and true positive values of 0.967 and 0.988 for the living and failed classes, respectively. The second classifier to predict the graft survival period yielded a prediction accuracy of 68.2% and a true positive rate of 0.85 for the class representing those instances with kidneys failing during the first year, results indicated that it is feasible to develop a successful Bayesian belief network classifier for prediction of graft status, but not the graft survival period, using the information in UNOS database.
Akl A, et al. [23]	1900 patient data obtained from Urology and Nephrology Center (unc), Mansoura, Egypt, From March 1976 and June 2007.	To predict5-year graft survival of livingdonor kidney transplantation . comparing two potential methods—an artificial neural network (ANN) and a scoring nomogram calibrated from Cox regression coefficients	The ANNs sensitivity was 88.43 %, specificity was 73.26 %, and its predictions was 16% significantly more accurate than the Cox regression-based nomogram area under ROC curve was 88%. The Cox regression-based nomogram sensitivity was 61.84% with 74.9% specificity and area under ROC curve was 72%. the

			predictive accuracy of the ANNs prognostic model was superior to that of the nomogram in predicting 5-year graft survival.
J.-H. Ahn et al. [24]	using the publicly-available data from the United Network for Organ Sharing UNOS with 35,366 obtained from records for kidney-transplants performed between 1987 and 1991.	applied the Bayesian belief network to a large UNOS dataset to develop a predictor for renal graft survival period. The model was developed using a supervised, machine-learning approach, called the Advanced Pattern Recognition and Identification (APRI) system. The APRI system builds the Bayesian network The model was used to predict one-year graft survival rates. They illustrated the model's prediction for two hypothetical kidney-transplant patients. Patient A who is younger, never had a prior transplant, had fewer HLA mismatches, and a lower peak panel reactive antibody level was compared to those of patient B.	Because of these favorable health characteristics, patient A had a much higher average predicted graft survival rate (91.2%) than patient B (78.4%). Finally, they claimed the performance in predicting 1-year graft survival rates showed promise for providing valid information to better allocate such scarce resources as transplant organs..
D. Lofaro et al [7]	sample of 80 consecutive renal transplants performed between January 1996 and February 2003 including 52 male and 28 female Caucasians of Overall average age (41.6 ± 12.6) years (range=18±63 years) at time of transplantation. Patient follow-up was 60 months (mean = 55.20 ± 12.74).	Researchers have shown two classification trees to predict chronic allograft nephropathy (CAN),(no CAN) through an evaluation of routine blood and urine tests. Classification trees based on the C 4.8 algorithm were used to predict CAN development starting from patient features at transplantation and biochemical test at 6-month follow-up.	The first tree model (CAN) in the validation set showed a sensitivity of 62.5%, a false-positive rate of 7.2%, and an area under ROC curve of 0.847 (95% confidence interval [CI] 0.749–0.945) and reports the second tree model (no CAN) that showed a sensitivity of 81.3%, a false-positive rate of 25%, and an area under ROC curve of 0.824 (95% CI 0.713–0.934) in the validation set. Identification models have predicted the onset of multifactorial, complex pathology, like CAN. The use of classification trees represent a valid alternative to traditional statistical models, especially for the evaluation of interactions of risk factors.
Fariba ,et al[25]	they conducted an experiment on graft outcomes prediction using a kidney transplant datasetbut Not determined.	predict the outcome of kidney transplants over a 2-year horizon.compared a widely used ANN approach known as Multi-layer Perceptron (MLP) networks with logistic regression,	it has been found that ANN coupled with bagging is an effective data mining method for predicting kidney graft outcomes. and confirmedthat different techniques can potentially be integrated to obtain a better prediction. and proved that a limitation of the ANN approach is that the way predictions are produced is not obvious

Lasserre Jet al.[26]	data comprise 707 transplantations performed at Charité-Universitätsmedizin Berlin (Campus Virchow-Klinikum) between 1998 and 2008.	to predict the estimated glomerular filtration rate (eGFR) of the recipient 1 year after transplantation from donore-recipient data using f linear regression (LR) and support vector machines with a Gaussian kernel (G-SVMs) ,neural networks (NNs) and random forests (RFs)	he authors obtained a Pearson correlation coefficient between predicted and real eGFR (COR) of 0.48. The best model for the dataset was a Gaussian support vector machine with recursive feature elimination on the more inclusive dataset.

3. MATERIAL AND METHODS

3.1 Proposed Methodology

The proposed methodology and overall framework of the study for every machine learning techniques (see Figure 1).

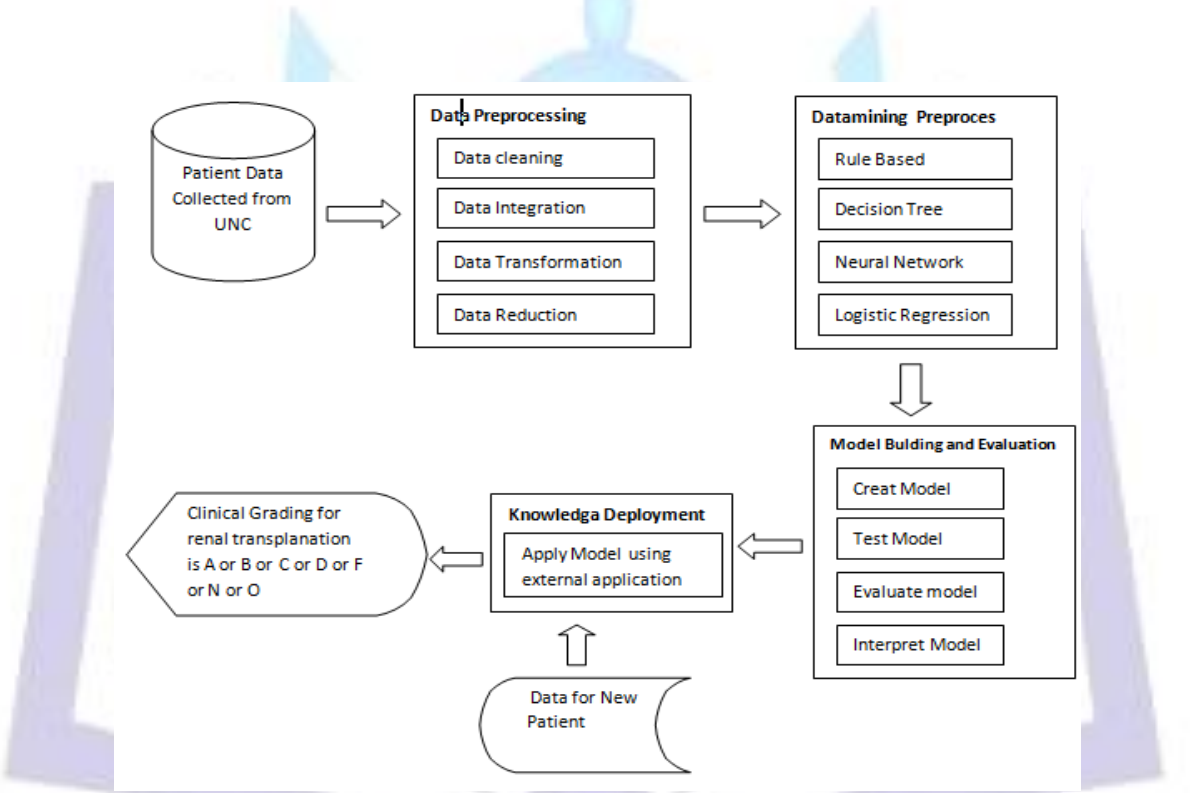


Fig1: Proposed methodology and overall framework of the study.

3.2 Data Mining Process

The following steps of data mining were carried out in order to effectively apply data mining [27,28].

3.2.1 Data set selection

Data were selected on the basis of the recommendations of the expert doctor.Between March 1976 and June 2007, 1900 consecutive living-donor renal transplants were performed in the Urology and Nephrology Center, Mansoura, Egypt. For recipients, our exclusion criteria included sensitization with a positive lymphocytetotoxic crossmatch, recent malignancy, addiction, psychiatric disorders, type I diabetes mellitus, and significant extra renal organ failure (pulmonary, hepatic, and cardiac). Absolute contraindications to donation included active infections, diabetes, any renal function impairment, arterial hypertension, and positive serology for hepatitis B virus or hepatitis C virus. There were 1564 related donors and 336 unrelated donors, including 118 spouses.Graft loss was defined as graft failure or patient's loss. The study applies to transplants that have complete records and have survived beyond 3months posttransplantation [23] .Table 2 Displays examples of some Attributes or variabled used in ourexperiment. Common fields were used in expriment according to Doctor's recommendations , The time-to-failure for the transplanted kidney is variable of interest for observation or

prediction for this study, so the diff erence between date of transplanation and date of last follow up for the patient was added to track the periods of the survival time after the renal transplantation under a field named “graft survival period”.

Table 2. List of some variables in UNC data

Attribute name	Description	Set of allowable Values
sex.reci	Sex of recipient	1 male,2 female
or.kid.d	Original kidney disease	1 messangio,2 membranous,3 F.S.G.S. ,4 messangioproliferati , 5 Crescentic ,6 chronic pyelonephrit ,7 nephrosclerosis ,8 end satage ,9 congenital ,10 obstructive uropathy ,11 hereditary ,12 amyloidosis ,13 others specify ,14 polycystic kidney ,15 hypoplasia ,88 inapplicable
consang	Consanguinity (donor)	1 parents,2 sibling,3 off springs,4 other relatives,5 unrelated,6 emotionaly related
rec.b.g	Recepient Blood group	1 A,2 B,3 AB,4 O
r_igmr	Recepient CMV IgM result	1.00 Negative,2.00 Positive,8.00 inapplicable
blood.gp	blood group (Recipient : Donor)	1 same,2 different
number.o	Number of blood transfusion	-1 missing,1 one to three,2 four to five,3 more than five,8 inapplicable
hypr_pre	Pre transplantation Hypertension	0 No,1 Yes
clin_gra	Clinical Grading Scheme at last follow up	A excellent graft function ,s.cr , B good graft function,cr1.5-3 , C medicore graft function,cr3-5 , D Poor function , Scr> 5 mg no dialysis, F Graft Failure , I Immunolgical rejection , N Nonimmunological failure,died with func. Graft , O Recurence of original desease , T Technical failure

3.2.2 Data cleaning and preprocessing

Data pre-processing is the important step in data mining because In "real world" database, will be The incomplete, inconsistent and noisy data. Therefore preprocessing is a very important stage [29]. In this experimrnt Noisy and inconsistent records were removed , redundancies variables were removed to prevent errors in the dataset , discretization by transform some variables from nominal value to numeric values and others from numeric value to numeric , Normalization of the numerical values into the interval , for missing values the data were used as it is besause the used algorithm support missing values[30].

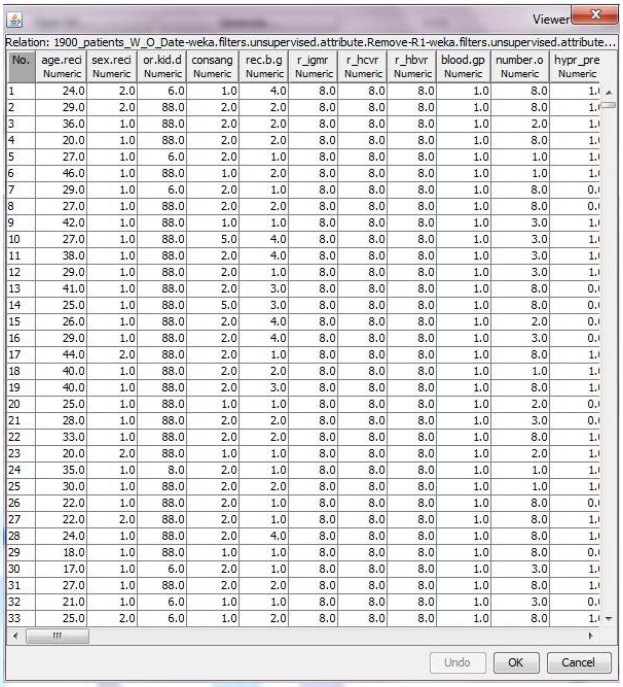
3.2.3 Data formatting:

Experiment done using WEKA (version 3.6.10) which is a suite of software learning machine written in Java and was developed at the University of Waikato (New Zealand). It is free software available under the GNU General Public License. In Weka System two data file formats are used, CSV(Comma SeparatedValue) or an ARFF(attribute relation file format)file is an ASCII text file that describes a list of instances sharing a set of attributes. so data were converted to a standard format CSV and Arff[31] . these are snapshot for training set used in our experiment in ARFF format (see Figure 2and 3).

```
@attribute age.reci  numeric
@attribute sex.reci  numeric
@attribute or.kid.d  numeric
@attribute consang  numeric
@attribute clin_gra  {F,N,I,B,A,C,D,T,O}

@data
24,2,6,1,4,8,8,8,1,8,1,0,1,42,2,4,0,3,2,1,50,1,1,1,
2,1,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?
,?,?,?,?,?,?,?,?,?,?,?,?,2.2,F,?
29,2,88,2,2,8,8,8,1,8,1,1,1,30,2,2,1,8,8,1,50,2,1,1
,2,1,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,?,
?,?,?,?,?,?,?,?,?,?,?,?,?,?,F,?
36,1,88,2,2,8,8,8,1,2,1,0,1,29,1,2,0,8,8,1,70,2,1,1
,2,0,1,1,0,0,0,0,0,0,0,0,0,1,1,0,0,0,0,0,0,0,1.2,1,
0,0,0,0,0,0,1.4,1,0,0,0,0,0,0,0,?,N,?
```

Fig 2: data in ARRFF formate



Relation: 1900_patients_W_O_Date-weka.filters.unsupervised.attribute.Remove-R1-weka.filters.unsupervised.attribute...

No.	age.reci Numeric	sex.reci Numeric	or.kid.d Numeric	consang Numeric	rec.b.g Numeric	r_igmr Numeric	r_hcvr Numeric	r_hbvr Numeric	blood.gp Numeric	number.o Numeric	hypr_pre Numeric
1	24.0	2.0	6.0	1.0	4.0	8.0	8.0	8.0	1.0	8.0	1.(
2	29.0	2.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	8.0	1.(
3	36.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	2.0	1.(
4	20.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	8.0	1.(
5	27.0	1.0	6.0	2.0	1.0	8.0	8.0	8.0	1.0	1.0	1.(
6	46.0	1.0	88.0	1.0	2.0	8.0	8.0	8.0	1.0	1.0	1.(
7	29.0	1.0	6.0	2.0	1.0	8.0	8.0	8.0	1.0	8.0	0.(
8	27.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	8.0	0.(
9	42.0	1.0	88.0	1.0	1.0	8.0	8.0	8.0	1.0	3.0	1.(
10	27.0	1.0	88.0	5.0	4.0	8.0	8.0	8.0	1.0	3.0	1.(
11	38.0	1.0	88.0	2.0	4.0	8.0	8.0	8.0	1.0	3.0	1.(
12	29.0	1.0	88.0	2.0	1.0	8.0	8.0	8.0	1.0	3.0	1.(
13	41.0	1.0	88.0	2.0	3.0	8.0	8.0	8.0	1.0	8.0	0.(
14	25.0	1.0	88.0	5.0	3.0	8.0	8.0	8.0	1.0	8.0	0.(
15	26.0	1.0	88.0	2.0	4.0	8.0	8.0	8.0	1.0	2.0	0.(
16	29.0	1.0	88.0	2.0	4.0	8.0	8.0	8.0	1.0	3.0	0.(
17	44.0	2.0	88.0	2.0	1.0	8.0	8.0	8.0	1.0	8.0	1.(
18	40.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	1.0	1.(
19	40.0	1.0	88.0	2.0	3.0	8.0	8.0	8.0	1.0	8.0	1.(
20	25.0	1.0	88.0	1.0	1.0	8.0	8.0	8.0	1.0	2.0	0.(
21	28.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	3.0	0.(
22	33.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	8.0	1.(
23	20.0	2.0	88.0	1.0	1.0	8.0	8.0	8.0	1.0	2.0	1.(
24	35.0	1.0	8.0	2.0	1.0	8.0	8.0	8.0	1.0	1.0	1.(
25	30.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	1.0	1.(
26	22.0	1.0	88.0	2.0	1.0	8.0	8.0	8.0	1.0	8.0	0.(
27	22.0	2.0	88.0	2.0	1.0	8.0	8.0	8.0	1.0	8.0	1.(
28	24.0	1.0	88.0	2.0	4.0	8.0	8.0	8.0	1.0	8.0	1.(
29	18.0	1.0	88.0	1.0	1.0	8.0	8.0	8.0	1.0	8.0	0.(
30	17.0	1.0	6.0	2.0	1.0	8.0	8.0	8.0	1.0	3.0	1.(
31	27.0	1.0	88.0	2.0	2.0	8.0	8.0	8.0	1.0	8.0	1.(
32	21.0	1.0	6.0	1.0	1.0	8.0	8.0	8.0	1.0	3.0	0.(
33	25.0	2.0	6.0	1.0	2.0	8.0	8.0	8.0	1.0	8.0	1.(

Undo OK Cancel

Fig 3: data set

3.2.4 Choosing the Function (Method) of Data Mining:

Classification is known assigning an unknown object to a predefined class after examining its characteristics . in machine learning Classification is considered as supervised learning. In classification learning, classified examples are presented with the learning scheme so , it is expected to learn a way of classifying unseen examples. [32] in our expriment classification method were applied using different datamining algorithms As Decision Tree Classifier (BF, J48) , Rule Based Classifiers (RIPPER, DTNB) , and Logistic Regression(LR) using WEKA (version 3.6.10) .

3.2.5 Choosing the Data Mining Algorithm

3.2.5.1 Classification Trees

Classification Trees, i.e. Decision tree is a classification technique commonly used in data mining [33]. Decision tree are work to organize the knowledge extracted from data in a recursive hierarchical structure consists of branches and nodes . an attribute are represented by Each internal node and is associated to a test relevant for data classification. Leaf nodes of the tree matched to classes. each of the possible results of the applied tests are represented by Branches . A new example can be classified following the nodes and branches until reached to a leaf node[34].Decision Trees Are used to create a model that predicts the value of a target variable based on several input variable. In our expriment WEKA was used to build the tree model and perform the classification analysis. we developed three decision tree to build three models.

The J48 algorithm: is WEKA's implementation of the C4.5 decision tree learner. The algorithm uses a greedy technique to induce decision trees for 20 classification and uses reduced-error pruning [35].
Training data wirth:weka.classifiers.trees.J48 class.
Best First Tree (BFTree): for for building a best-first decision tree classifier[36].
Training data wirth : weka.classifiers.trees.BFTree class.

3.2.5.2 Rule Based Classifiers

A Rule Based Classifier is considered as a classification technique that use logic propositional formulas in disjunctive or conjunctive normal form ("if then rules") for classifying the given records, this classification technique is also called ruled based [19]. Rule Based Classifiers Produce Descriptive Models ,and easy to interpret ,Especially in medical field through providing the medical doctor with a compact view of the analyzed data .We Applied the below as an examples of Rule Based Classifiers.

Repeated Incremental Pruning to Produce Error Reduction (RIPPER) : It produces a set of rules, one at a time, through two steps: growth and pruning Advantages [37].

Training data wirth :weka. weka.classifiers.rules.Jrip class

Decision Table with Naïve Bayes'(DTNB) : Used for building and using a decision table/naive bayes hybrid classifier. At each point in the search, the algorithm evaluates the merit of dividing the attributes into two disjoint subsets: one for the decision table, the other for naive Bayes. A forward selection search is used, where at each step, selected attributes are modeled by naive Bayes and the remainder by the decision table, and all attributes are modelled by the decision table initially. At each step, the algorithm also considers dropping an attribute entirely from the model[38].

Training data wirth : weka.classifiers.rules.DTNB class

3.2.5.3 Logistic Regression

Logistic Regression (LR) classifiers are considered as statistical models where a logistic curve is fitted to the dataset , modelling the probability of occurrence of a class. also LR classifiers are known as: logit model , maximum entropy and logistic model classifiers. building a logit variable, containing the natural log of the odds of the class occurring or not is The first step in LR . Then apply the max imum likelihood estimation algorithm inorder to estimate the probabilities. in Statistics ,LR models are largely used and have achieved success in several real-world problems[39].

3.2.6 Data Mining (Pattern Extraction)

when applying the Predifined algorithms we obtained different models algorithm that can be used to classify, predict, or rule out new clinical cases. 30 rules were obtained from JRIP algorithm (see Figure 4) , and apart of J48 Tree (see Figure 5 and 6) .

```
JRIP rules:
===========

(clin.gr1 = T) => clin_gra=T (5.0/0.0)
(ser_crea >= 5) and (liv_dial <= 0) and (Graft_surv_per_in_month >= 87) => clin_gra=D (8.0/1.0)
(ser_crea >= 3.1) and (prim.imm >= 5) and (ser_cr5y >= 1.2) => clin_gra=C (42.0/13.0)
(ser_crea >= 3.1) and (prim.imm >= 8) => clin_gra=C (10.0/3.0)
(ser_crea >= 3.4) and (ser_crea <= 4) and (age.reci <= 19) => clin_gra=C (4.0/0.0)
(prim.imm <= 4) and (liv_dial <= 0) and (Graft_surv_per_in_month <= 147) and (prim.imm <= 3) =>
clin_gra=N (68.0/2.0)
(clin.gr1 = N) => clin_gra=N (21.0/1.0)
(age.reci >= 35) and (age.donr <= 31) and (ser_crea >= 3.2) => clin_gra=N (6.0/0.0)
(p.urin.r <= 1) and (liv_dial <= 0) and (Graft_surv_per_in_month <= 200) and (prim.imm <= 4) =>
clin_gra=N (18.0/1.0)
(age.reci >= 35) and (clin.gr5 = N) => clin_gra=N (7.0/0.0)
(age.reci >= 32) and (clin.gr4 = N) => clin_gra=N (5.0/0.0)
(age.reci >= 33) and (clin.gr2 = N) => clin_gra=N (4.0/0.0)
(liv_dial <= 0) and (prim.imm <= 5) and (secn.imm <= 0) and (tot.dos1 >= 4.1) and
(Graft_surv_per_in_month <= 109) and (ser_cr2y >= 1.2) => clin_gra=N (15.0/2.0)
(liv_dial >= 1) and (secn.imm <= 0) and (num.g.bp >= 2) => clin_gra=I (106.0/27.0)
(liv_dial >= 1) and (prim.imm <= 4) and (num.g.bp >= 3) and (consang <= 2) and (don.b.g >= 2) =>
clin_gra=I (31.0/2.0)
(liv_dial >= 1) and (prim.imm <= 4) and (Graft_surv_per_in_month <= 109) and (ser_cr1y >= 1.1)
=> clin_gra=I (77.0/26.0)
(liv_dial >= 1) and (secn.imm <= 0) and (Graft_surv_per_in_month >= 99) and (or.kid.d >= 13) =>
clin_gra=I (14.0/1.0)
(liv_dial >= 1) and (clin.gr4 = I) => clin_gra=I (10.0/1.0)
(liv_dial >= 1) and (age.donr >= 54) and (or.kid.d <= 8) => clin_gra=I (15.0/5.0)
(liv_dial >= 1) and (ser_cr3y <= 1.3) and (ser_cr5y >= 1.5) and (don.b.g >= 2) => clin_gra=I
(12.0/3.0)
(liv_dial >= 1) and (clin.gr2 = I) => clin_gra=I (7.0/0.0)
(liv_dial >= 1) and (clin.gr5 = I) => clin_gra=I (5.0/1.0)
(liv_dial >= 1) and (clin.gr1 = I) => clin_gra=I (18.0/1.0)
(liv_dial >= 1) and (clin.gr3 = I) => clin_gra=I (5.0/0.0)
(liv_dial >= 1) => clin_gra=F (271.0/52.0)
(ser_crea >= 1.5) and (clin.gr4 = B) => clin_gra=B (197.0/16.0)
(ser_crea >= 1.5) and (Graft_surv_per_in_month <= 179) => clin_gra=B (291.0/51.0)
(ser_crea >= 1.6) and (Graft_surv_per_in_month >= 196) and (ser_cr5y >= 1.1) => clin_gra=B
(28.0/3.0)
(ser_crea >= 1.6) and (age.reci <= 31) and (num.arej >= 1) => clin_gra=B (7.0/1.0)
 => clin_gra=A (593.0/69.0)

Number of Rules : 30
```

Fig 4 : 30 rules obtained from JRIP algorithm

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```
liv_dial <= 0
|   ser_crea <= 1.4
|   |   cond.dis <= 1: N (10.38)
|   |   cond.dis > 1
|   |   |   p.urin.r <= 1: N (23.19/11.0)
|   |   |   p.urin.r > 1
|   |   |   |   tot.dos1 <= 5.6
|   |   |   |   |   clin.gr5 = A
|   |   |   |   |   |   tert.imm <= 0
|   |   |   |   |   |   |   clin.gr2 = A
|   |   |   |   |   |   |   |   prim.imm <= 5
|   |   |   |   |   |   |   |   |   num.arej <= 0
|   |   |   |   |   |   |   |   |   |   ser_crea <= 1.2
|   |   |   |   |   |   |   |   |   |   |   secn.imm <= 0
|   |   |   |   |   |   |   |   |   |   |   |   dr <= 2
|   |   |   |   |   |   |   |   |   |   |   |   |   num.rena <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   rec.b.g <= 1: A (9.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   rec.b.g > 1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   age.reci <= 42: A (11.9/1.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   age.reci > 42: N (3.96/0.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   num.rena > 1: A (2.9)
|   |   |   |   |   |   |   |   |   |   |   |   dr > 2: A (10.51)
|   |   |   |   |   |   |   |   |   |   |   secn.imm > 0: A (18.53)
|   |   |   |   |   |   |   |   |   |   ser_crea > 1.2: A (34.65/3.0)
|   |   |   |   |   |   |   |   |   num.arej > 0
|   |   |   |   |   |   |   |   |   |   ser_crea <= 1.3: A (5.18/0.22)
|   |   |   |   |   |   |   |   |   |   ser_crea > 1.3
|   |   |   |   |   |   |   |   |   |   |   num.g.bp <= 1: N (3.08/0.9)
|   |   |   |   |   |   |   |   |   |   |   num.g.bp > 1: A (2.0)
|   |   |   |   |   |   |   |   prim.imm > 5: A (159.07/0.96)
|   |   |   |   |   |   |   clin.gr2 = B: A (13.53/3.82)
|   |   |   |   |   |   |   clin.gr2 = N: N (1.22/0.26)
|   |   |   |   |   |   |   clin.gr2 = I: A (0.0)
|   |   |   |   |   |   |   clin.gr2 = C: A (0.0)
|   |   |   |   |   |   |   clin.gr2 = D: A (0.0)
|   |   |   |   |   |   |   clin.gr2 = F: A (0.0)
|   |   |   |   |   |   |   clin.gr2 = .: A (1.22)
```

Fig 5: part of tree obtained from J48 algorithm

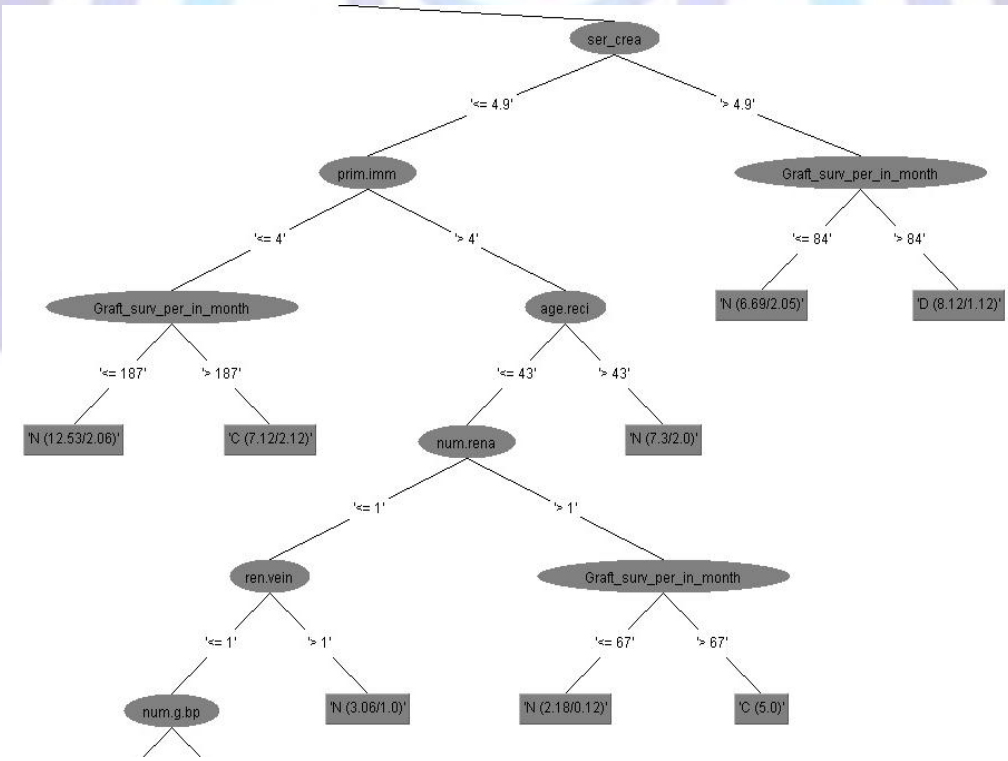

Fig 6: Fig 5: part of tree obtained from J48 algorithm

3.2.7 Evaluation and Interpretation

3.2.7.1 Validation

a 10 fold cross validation is used ,the training data is divided into 10 differentparts of equal size. Then one tenth of the instances present in the training set are usedfor testing and the remaining nine tenth for the training.Once the first round of validation is completed, another subset of equal size is used fortesting, and the remaining 90% of the instances used for training as before.The process is iterated 10 times to ensure the all instances become part of the trainingand test set.At the end, the recorded measures are averaged. The number of false positive, false negative, true positive and true negative classifications is simply accumulated across the 10 runs.

4. EXPERIMENTAL RESULT AND DISCUSSION.

To measure and investigate the performance on the selected classification method and algorithms namely Classification Desision Trees (BFTree , J48) ,Rule Based Classifiers (JRIP,DTNB) and logistic regression as a standard statistical data mining method .we use the same experiment procedure as suggested by WEKA. In WEKA, all data is considered as instances and features in the data are known as attributes. The simulation results are partitioned into several sub items for easier analysis and evaluation. On the first part, The Classification Accuracy of the different classifiers ,correctly and incorrectly classified instances will be partitioned in numeric and percentage value and subsequently Kappa statistic, mean absolute error and root mean squared error will be in numeric value only. also the relative absolute error and root relative squared error in percentage for references and evaluation will be shown .The results of the simulation are shown in Tables 3 below. Table 3 mainly summarizes the result based on accuracy and time taken for each simulation and shows the result based on error during the simulation. graphical representations of the simulation result are shown below (see Figures 7,8,9) .

Table 3. The summarized results of the simulation

Methods **Stratified cross-validation**	**BF_Tree**	**j48_TREE**	**Jrip_RULES**	**DTNB_RULES**	**Logistic Regression**
Correctly Classified Instances	1416 (74.53%)	1444 (76%)	1461 (76.89%)	1424 (74.95%)	1447 (76.16%)
Incorrectly Classified Instances	484 (25.47%)	456 (24%)	439 (23.11%)	476 (25.05%)	453 (23.84%)
Kappa statistic	0.6742	0.6939	0.7059	0.6785	0.6965
Mean absolute error	0.0739	0.0708	0.0703	0.078	0.0669
Root mean squared error	0.2055	0.2016	0.1994	0.2015	0.2007
Relative absolute error	42.19%	40.41 %	40.13%	44.54%	38.17%
Root relative squared error	69.45%	68.12 %	67.41%	68.11%	67.82%
Total Number of Instances	1900	1900	1900	1900	1900
Time Taken In Seconds	161.72	6.3	50.32	3810.21	7449.47

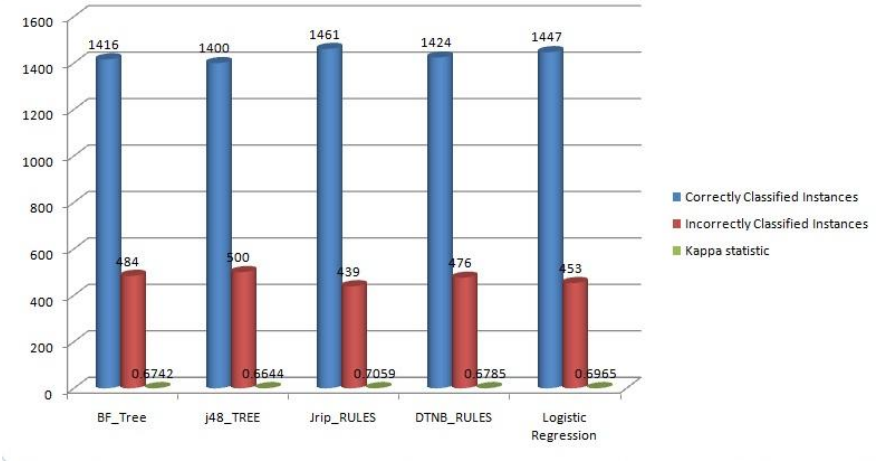

Fig 7: the simulation result for the used algorithms

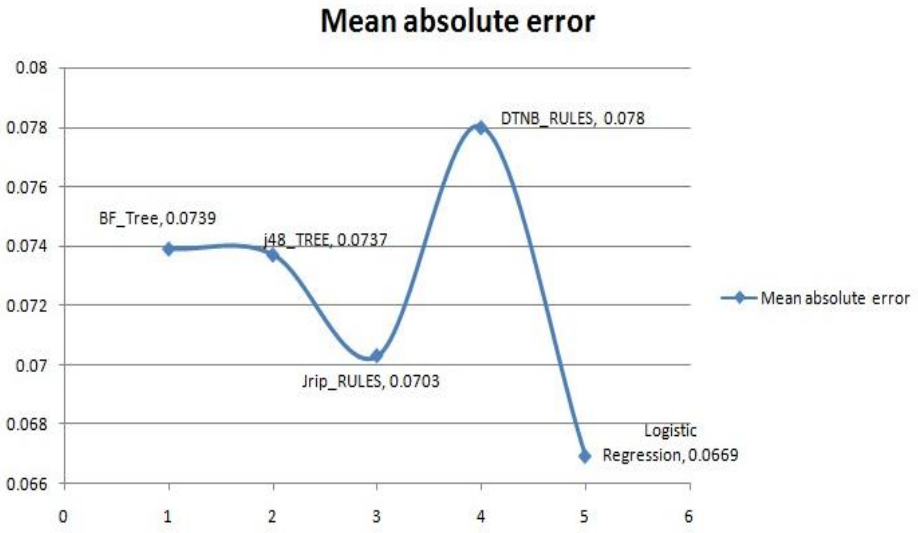

Fig 8: mean absolute error for the used algorithms

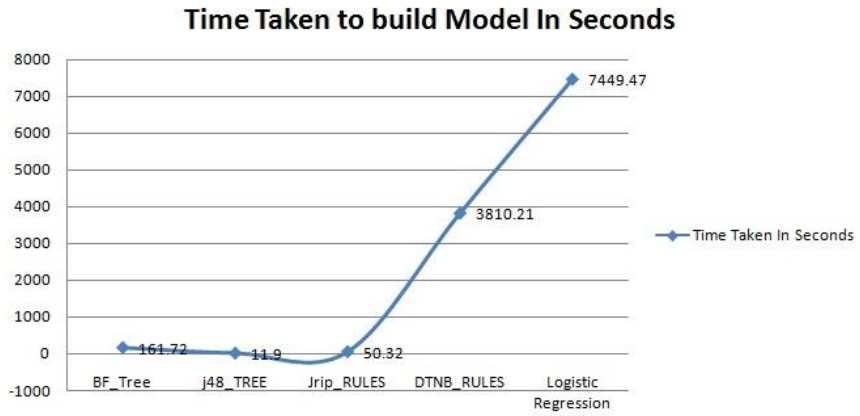

Fig 9: Time taken by the diffetent used algorithm to build model in seconds

The different classifiers were further analyzed to better understand and expose its performance characteristics through a number of measures .Set of performance measures included true positive rate(TP) , false positive rate(FP), precision, recall, F measure, and area under the receiver-operating characteristic (ROC) curve as presented in Table 4.

Table 4. Performance measures for Different Classifiers

Methods	TP Rate	FP Rate	Precision	Recall	F-Measure	ROC Area
BF_TREE	0.745	0.061	0.741	0.745	0.735	0.904
J48_TREE	0.737	0.061	0.729	0.737	0.732	0.9
JRIP_RULES	0.769	0.054	0.773	0.769	0.765	0.923
DTNB_RULES	0.749	0.063	0.748	0.749	0.736	0.935
Logistic Regression	0.762	0.058	0.763	0.762	0.761	0.937

According to the above Figures (7,8,9) and Table 3, we can clearly see that the highest accuracy is (76.89%) Belongs to RuleBased classifier (JRIP) and the lowest is (74.53%) Belongs to BFTree classifier (BF). An average of (1429) instances out of total (1900) instances is found to be correctly classified with highest score of (1461) instances compared to (1416) instances, which is the lowest score. The total time required to build the model is also a crucial parameter in comparing the classification algorithm. In this experiment,we can say that (j48) requires the shortest time which is around (6.3) seconds compared to the others , Logistic regression requires the longest model building time which is around (7449.47) seconds.The second on the list is (JRIP) with (50,32) seconds (see Figure 9). Kappa statistic is used to estimate the accuracy of any certain measuring cases, it is usual to make a distinction between the reliability of the collected data and their validity [40]. The average Kappa score from the selected algorithm is around (0.6-0.7) . the Kappa Statistic criteria is essential for accuracy of classification purposes [39].
we can see the differences of errors resultant from the training of selected classifiers (see figure 8) , This experiment presents usually used indicators which are mean of absolute errors and root mean squared errors. Also, the relative errors are used. It is found that the highest error is found (DTNB) with value (0.078) and and the lowest is logistic regression (0.67) where the rest of the algorithm ranging averagely around(0.07-0.73). in terms of medical fields, the algorithm with a lower error rate will be the better because it has more powerful classification capability and ability.
From Table 4, we can see the better performance is for (JRIP model) with ROC (0.923) and recall (77%).

5. CONCLUSION AND FUTURE WORK.

In this paper, we have discussed the need for data mining in the medical field especially in prediction of kidney transplant outcomes in unc mansoura,egypt. in this context we compared between classification desision trees (bftree , j48) ,rule based classifiers (jrip,dtnb) and logistic regression as a standard statistical data mining method to predict the outcome of kidney transplants over a 5-year horizon using the patient profile information prior to the transplantation. and found that classification trees and rule based classifiersare are more fast and easy to interpret compared to logistic regression and classification predictive accuracy of rule based classifiers(jrip) model was superior other models in predicting 5-year graft survival when run against kidney transplanation dataset obtained from urology and nephrology center, mansoura, egypt.further we have found rule set containing some interesting rules which were easy to interpret and familiar to represent them in spreadsheet were obtained from rule based classifiers and decision tree classifiers.the experimental results also reveal that rule based classifiers and decision tree classifiersare efficient approaches for extraction of patterns from kidney transplanation dataset.

in a future project, we shall implement the rule based classifiers model that was developed in this study in a form of web based application to make it available to estimate survival and prognosticate individual transplant recipients outcomes.

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