A Proposed Ensemble Model with Feature Selection Technique for Classification of Chronic Kidney Disease

A. K. Shrivas, Sanat Kumar Sahu

***Abstract:** Healthcare diagnosis system is very important and critical task in medical science for doctors and medical students. Chronic kidney disease is a very serious and dangerous problem which is directly related to the human life. In this research work, we have used data mining and feature selection technique to develop the robust and computationally efficient model for classifying chronic and non chronic kidney disease. An ensemble model is constructing through combination of two more similar types of trained model which helps to improve the performance. Feature selection is frequently used in machine learning area to raise a model with a few numbers of features which increase the performance of classification accuracy. The proposed feature selection techniques principle of Genetic Search (GS) and Greedy Stepwise Search (GSW). This proposed technique called GS-NB utilizes a pursuit methodology which is embedded in the Genetic Algorithm to select the features based on natural selection, the procedure that drives biological evolution. Then proposed technique called GSW-NB utilizes a search strategy that is included in the Greedy Stepwise to search the relevant feature based on problem solving heuristic for settling the locally ideal decision at each stage. The performance of suggested technique were estimated on Chronic Kidney Disease (CKD) classification problems and compared with proposed feature selection method. The classification techniques namely the Single Rule Classification (SRC), Conditional Inference Tree (CIT) and their ensemble model (SRC, CIT) have used for classification of CKD. The proposed ensemble model have used stacking learning technique which combines multiple classifiers, hence we can improve the performance of classifiers. The classifier performance is measured with observed accuracy, sensitivity and specificity. The experimental results demonstrated that the ensemble model (SRC, CIT) with GS-NB and GSW-NB can recognized CKD better than existing model. The proposed model can be beneficial and useful in medical science for identifying and diagnosis of chronic kidney disease.*

***Keywords:** Chronic Kidney Disease, Conditional Inference Tree, Ensemble Model, Feature Selection Technique, Genetic Algorithm, Greedy-Stepwise, Single Rule Classification.*

I. INTRODUCTION

Chronic kidney disease (CKD) [1], [2] is a widespread public health issue, influencing around 10% of the people around the world. Yet, [3] there's very slight authentication on however CKD are frequently identify in fast and automated way. In medical science, CKD diagnosis of health conditions is a very challenging task. The medical history data contains various tests fundamental to analyze a specific disease and the analysis depends on the experience of the doctor; a less experience doctor can analyze an issue erroneously. In present scenario, classification of CKD data is very important and has gained attention of medical researchers in previous few years. The diagnosis of CKD done by the doctors, they are the key factors on which treatment of patient is done. They have used different kinds of machine learning techniques to classify CKD. Classification of disease is very important role for diagnosis of health condition. Classification [4] is technique in health care system to diagnose critical chronic diseases problem in more accurate and easy way; this classification may be helpful for the medical practitioners as well as for the medical students. Machine learning techniques are commonly used to plan and progress of health care system to make diagnosis the problem in more efficient way. In this study, we have used the decision tree classifiers like conditional inference tree and Single rule classifier (One R) and their ensemble model as proposed model. This model is used to classify the CKD data and compared the performance of each individual's model with proposed ensemble model. Feature selection play major role to eliminate the irreverent feature from original feature space and improve the performance of model. We have used to wrapper based feature selection techniques namely Genetic Search (Genetic Algorithm) and Greedy Stepwise Search [5]. A best classification model obtained through experimental work i.e. Ensemble model. The proposed ensemble model gives better performance and accuracy with reduced number of features.

II. RELATED WORK

Many authors have used to diagnose various human diseases using machine learning techniques. There [6] are two types of feature selection techniques like wrapper and filter methods were selected to decrease the feature of CKD dataset. The Support Vector Machine (SVM) classifier gives better accuracy rate as 98.5% using filtered subset evaluator with Best First Search engine for diagnosis of CKD. They [7] have used two classification techniques like Naive Bayes and artificial neural network with Rapid Miner tools. They have obtained the highest accuracy in case of Naive Bayes for classification of CKD. There [8] are three classifiers namely Naive Bayes, J48 and SMO have used for classify the CKD where J48 is the most excellent performing algorithm out of three algorithms used for identifying Chronic Kidney Disease.

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Authors [9] have suggested filter techniques for selecting relevant attribute form synthetic data set and studying the performance of the techniques with reduced feature subset. The classification techniques have increased the performance with a reduce number of attribute set while the performance decreased when the number of attributes increased. Authors [10] have used wrappers approach with Genetic Algorithm as random search with different learning algorithms are decision tree, C4.5, Bayes Networks, Naive Bayes and Radial Basis Function as subset evaluator. The reduced relevant features identified by different wrappers methods: GA+DT, GA+Naive Bayes, GA+ Bayesian and GA+RBF. All standard datasets has enhanced accuracy after using wrapper method of different classifiers namely C4.5, RBF, Naïve Bayes & Bayesian. Authors [11] have used to classify the Chronic Kidney Disease dataset the two classification techniques based on the classifications accuracy and execution time performance factors. The SVM given better performance compared to Naive Byaes classifier.

III. CLASSIFICATION TECHNIQUE

Classification [12] is data mining task to classify the samples into respective class. Classification process consist two steps: training and testing where training samples are use to trained the classifiers and testing data is used to test the trained classifiers. Classification is a supervised learning technique [8]. There is some classification techniques used in this research work.

A. One R or Single Rule Classification

One R[13],[14] [15] abbreviated for "One Rule," is a straight forward and correct classification algorithm that generates one rule for each predictor in data, and then select the rule with the least total error as a "single rule". The frequency table creates for each predictor in opposition to the target and generating a rule for a each predictor. One R is a classification technique to produce slightly less precise rules than the next-generation classification algorithms, while producing simple rules to be interpreted by humans.

B. Conditional Inference Tree

Learning the decision-making element utilize a decision tree to go from explanation to an factor to finale on the objective value. Tree methods in which the objective variable can guess a discrete set of values are called classification trees; in these tree structures the leaves represent class labels and the branches represent conjunctions of features that lead to those class labels. The classification tree analyzed the samples where the each sample is belonging to the respective class.

Similar [16] to traditional decision trees, conditional inference trees also divide recursively data by executing a univariate division on the dependent variable. In any case, what makes conditional inference trees to traditional decision trees is that conditional inference trees adjust importance test methodology to choose factors as opposed to choosing factors by augmenting data measures.. In this way, we will present how to fit a conditional inference tree to build a classification [17], [18].

C. Ensemble Model

The technique of ensemble model is to create a classification model combining the multiple models. It [19] is well-known that ensemble model can be used for improving classification performance. Stacking [20], [21], [22] method that consolidates numerous groupings whose outputs are utilized as contributions to a second level meta-classifier to learn the mapping between the ensemble output and the actual correct classes.

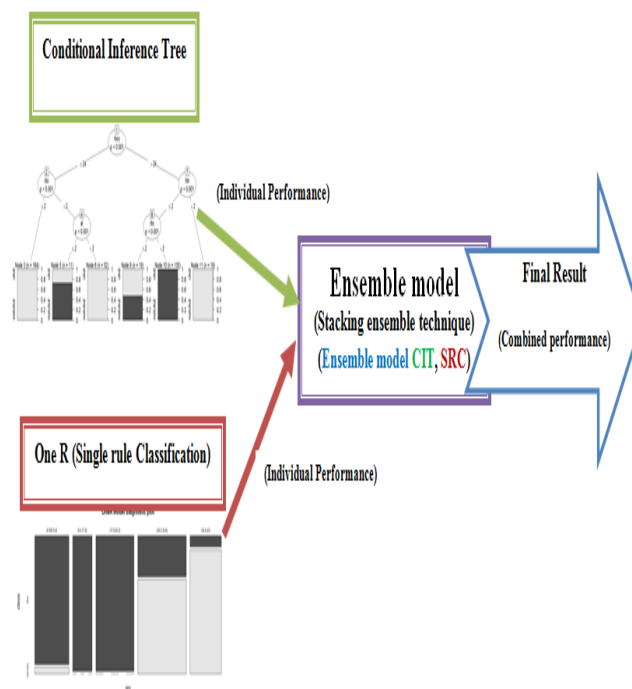The figure 1 shows the ensemble model.

Fig. 1.Proposed Ensemble model.

In this proposed model, we have combined the two individual classifiers through stacking ensemble techniques. The Single Rule Classification (SRC) has the base classifier model and Conditional Inference Tree (CIT) has second level meta-classifier. We have ensemble the SRC and CIT classifier using stacking ensemble technique.

IV. FEATURE SELECTION TECHNIQUE

Feature [23] selection technique is used to select the important features from data set and also improve the classification accuracy with reduce and relevant feature subset. To diagnose the CKD, wrapper approaches were select to decrease the features of CKD dataset [6]. In [24] wrapper approach, wrapper subset evaluator with greedy stepwise search engine and Genetic search engine were used.

Wrapper methods approach applies the method of classification itself to compute the significance of features subset; due to this reason, the selected features based on the model of the classifier used. Wrapper [25] methods usually result in better performance than filter methods due to the optimization of the selection process for the classification algorithm to be used.

The wrapper methods are also expensive for the high dimensional dataset in circumstances of computational complexity and time because each feature subsetset careful be evaluated through the classifier algorithm [26], [27]. Feature selection consists of two parts: Search Methods and Attribute Evaluation Methods.

- *Attribute Evaluation Methods:* Subset evaluators [13], [28] receive a subset of feature and return a numerical computation that lead the search. Like any other WEKA object, they are configured.
- *Search Methods:* Search methods [13], [28] pass through the feature space to find a suitable subset. Value [29] is calculated by the selected feature subset evaluator. The search method can be configured with WEKA object editor.

A. Greedy Stepwise

The Greedy Stepwise [30] is run the greedy forward or backward searching during the space of attributes subset. It [31] [32] will be stopped when the addition or deletion of any remaining attributes results in a decrease in evaluations. It [33] can rank the features by traversing the space from one side to the other and making the order that features are selected[34].

B. Genetic Algorithm

The feature selection, random selection techniques is used namely genetic algorithms (GA). It is a random search method. The genetic algorithm is capable of effective exploring the large search space, which is generally required in case of attribute selections. The GA is search algorithms motivated by the principal of natural selection. The major plan is to develop a population of each individual, where every individual is a candidate solution for a given problem [35], [36].

V. PROPOSED FRAMEWORK

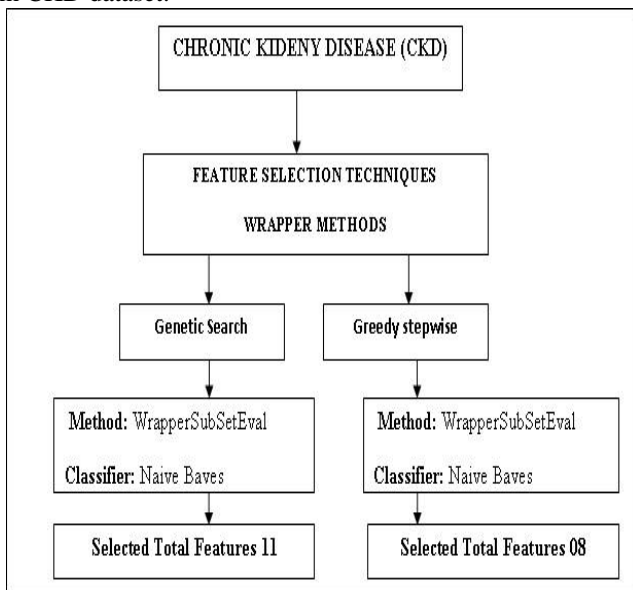Figure 2 shows that proposed feature selection technique in CKD dataset.

Fig. 2.Proposed feature selection techniques.

The figure 2 shows that the process of proposed feature selection techniques in CKD dataset. In this process, we have used two wrapper methods namely Genetic Search and Greedy stepwise. In Genetic search method, wrapper subset evaluator with naive bayes is used to select the relevant 11 features from CKD data set. Similarly, in case of greedy stepwise, wrapper subset evaluator with Naive bayes classifier is used to select the relevant 08 features from CKD data set.
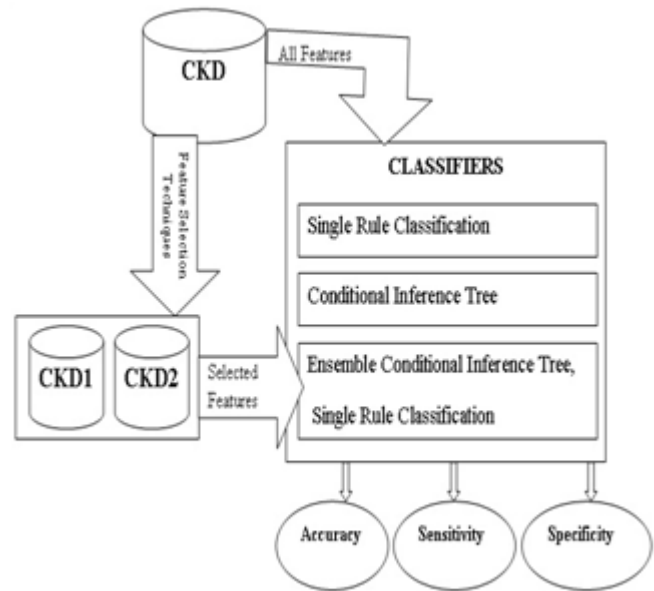
Figure 3 shows that proposed classification technique.

Fig. 3.Proposed classification models.

The Above figure 3 shows that the process of the classification techniques with feature selection in CKD data set. We have applied two FST as Genetic search and Greedy stepwise FST. We have generated two datasets as CKD1 and CKD2 data set in case of Genetic search and Greedy stepwise FST respectively. The CKD1 dataset contains 11 features and CKD2 data set contains 8 features. We have applied the both data set to SRC,CIT and its ensemble model.The proposed ensemble model gives better performance compared to individual classifiers in case of CKD1 and CKD2 data set.

VI. RESULT AND DISCUSSION

This [37] experiment have used CKD dataset from the UCI Machine Learning Repository named uploaded in 2015. This dataset has 25 features, 11 numeric and 14 nominal features, 400 instances including class labels (ckd, notckd) where 250 has labelled CKD and 150 has label non-CKD [37]. The dataset is applied to classification algorithms for the evaluation training and testing performance.

CKD dataset have used the feature selection task using WEKA [38] data mining tool and R[39] programming for classification task. The result analysis and discussion section is sub-divided in the three parts. The first part discussed the process of feature selection, the second part discussed the process of classification task and third part compared the proposed model with the existing models.

A. Process of Feature Selection

The WEKA software offers a variety of feature selection techniques (FSTs) for studying dataset and related factors for feature selection. In this experiment we have used two types of wrapper approach feature selections techniques namely Genetic Search and Greedy Stepwise.

These FSTs have used two parameters like Feature Evaluation Methods and Search Methods. The table I and table II show the parameters details in our proposed FSTs. Table I shows the list of Feature Evaluator with tuning parameters.

Table II shows completely different search algorithms with their tuning parameters.

Table- I: Feature Evaluation Methods and Parameter Tuning details

Evaluation Algorithm	Name	Parameters Tuning	Function
Attribute Subset Evaluator	Wrapper SubsetEval	classifier = "Naïve Bayes" fold=5 seed=1 threshold=0.01	Use a classification techniques with cross-validation data partition techniques

Table- II: Search Methods and Parameter Tuning details

Search Methods	Tuning Parameters	Function
Genetic Search (GS)	crossoverProb=0.6 , maxGenerations=20,mutationProb=0.033 , PopulationSize=20, reportFrequency =20,seed=1 startSet=NULL	Performs a search using the simple genetic algorithm described in Goldberg [40].
Greedy Stepwise Search (GSS)	conservativeForwardSelection = false, generateRanking = false numToSelect =-1 searchBackwards = false startSet = NULL threshold -- -1.797793134862E308	Performs a greedy forward search through the space of attribute subsets [30].

The feature selection techniques perform the combination of table I and table II parameters. Table III shown the selected features of CKD dataset with proposed FST.

Table- III: Description of feature selection techniques of CKD dataset

Proposed FST	Search Method	Classifier	Number of Selected Features	Selected features_ID
GSS-NB	Greedy Stepwise	Naive Bayes	08	F4, F12, F14, F15, F18, F19, F20, F22
GS-NB	Genetic Search	Naive Bayes	11	F1, F4, F6, F9, F12, F13, F18, F19, F20, F22, F23

B. Process of Classification Task without Feature Selection Technique

In this research work, we have applied 10-fold cross validation for division of data into training and testing. Classification techniques evaluations were carried out on the basis of performance measures such as classification accuracy, sensitivity, specificity.

The table IV shows the classification techniques and their performances measures without feature selection technique (WFST).

Table- IV: Classification techniques and their performance (in %) without feature selection technique

Name Of Algorithms	Accuracy	Sensitivity	Specificity
Single Rule Classification (SRC)	92.00	92.00	92.00
Conditional Inference Tree (CIT)	93.75	91.60	97.33
Ensemble model (SRC, CIT)	94.25	96.40	90.66

Table IV shows that the performance of classification techniques are Single Rule Classification, Conditional Inference Tree and their ensemble model. The proposed ensemble model gives better performance compare to the individual classifiers as shown in table IV.

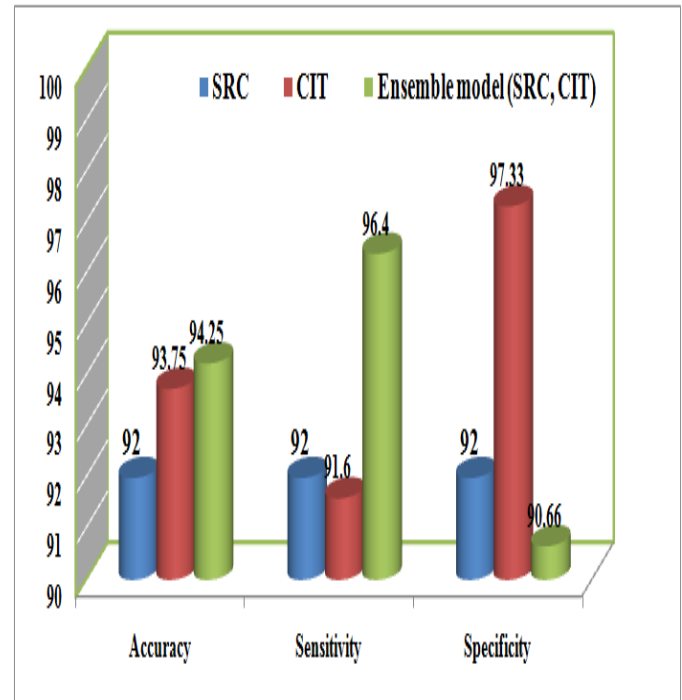The figure, graph, chart can be written as per given below schedule.

Fig. 4. Comparison of performance (%) of the classifiers.

Figure 4 shows that the proposed ensemble model gives higher accuracy as 02.25% compared to Single Rule Classification (SRC) and 00.50% compared to Conditional Inference Tree (CIT). We have achieved best classification accuracy with proposed ensemble model without FST.

B. Process of Classification Task With Feature Selection Techniques

The FST is implemented in the CKD dataset in which the irrelevant features are removed from original feature space.

The new formed CKD data set with reduced feature subset is applied in the ensemble model to achieve better classification accuracy.

The table 5 shows the classification techniques and their performances measures with feature selection technique (FST).Table- V: Ensemble model and their performance (in %) with feature selection technique.

Table-V: Proposed classification techniques and their performances (%) with FST.

Number of Features	Accuracy	Sensitivity	Specificity	Remark
24	94.25	96.40	90.66	WFST
08	94.75	94.80	94.66	GSW-NB
11	95.00	93.20	98.00	GS-NB

Table V shows the performance of proposed ensemble model in terms of accuracy, sensitivity and specificity with and without FST where the accuracy and specificity is increased when applied the FST.

In case of 8 features, the accuracy of ensemble model with FST gives higher accuracy 00.50% compared to ensemble model without FST. In case of 11 features, the accuracy of ensemble model with FST gives higher accuracy 00.75% compared to ensemble model without FST.

The result shows that proposed ensemble model gives better classification accuracy with FST compare to proposed ensemble model without FST.

Figure 5 & 6 shows the comparative graphs of proposed ensemble model (SRC, CIT) and their accuracy with related feature subset.
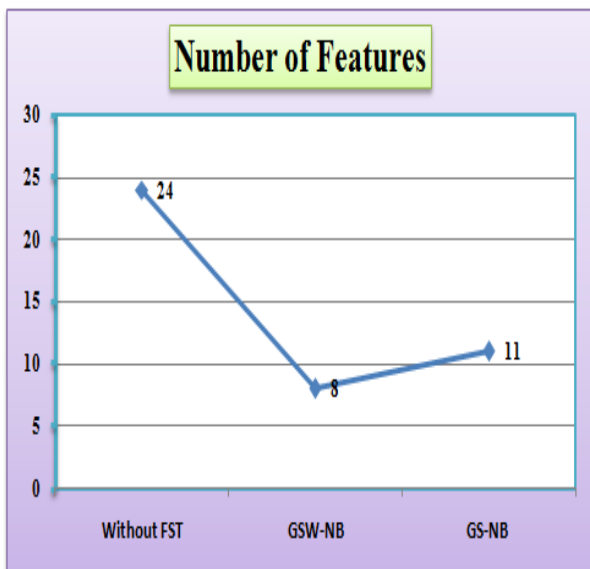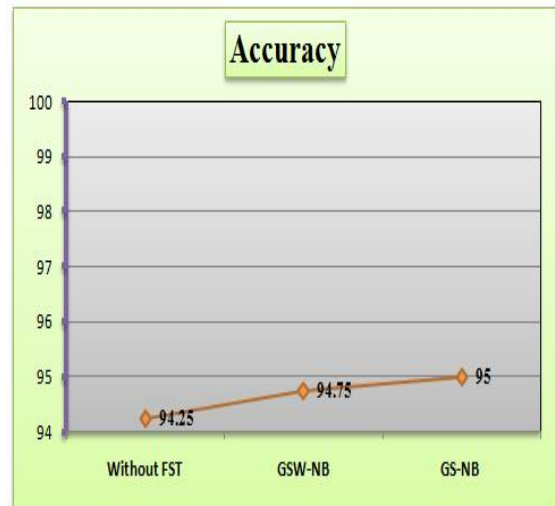

Fig. 5.Features used in CKD dataset.

Fig. 6.comparative graph of accuracy in proposed ensemble model (In %).

The Figure 5 & 6 shows that the comparative graph of the proposed ensemble model with respect to the accuracy and the number of features. The accuracy of the proposed ensemble model is enhanced after applying FST, So that proposed ensemble model is more robust and computationally efficient for diagnosis of CKD.

C. Comparison of Proposed Model with Existing Models

Table VI shows that the comparative analysis chart of proposed model and existing model in terms of accuracy. The outcome demonstrates that the proposed model significantly improves the CKD classification accuracy. The highest accuracy has obtained by proposed ensemble model with feature selection method as Genetic Search with selected 11-feature subset.

Table-VI: Accuracy of the proposed model compared with existing models.

Author	Diseases	Tools	Techniques	Accuracy
Our proposed model	CKD	R TOOLS and WEKA	Ensemble model (SRC	95%
Boukenze et. al[41]	CKD	WEKA	SVM	Achieved best accuracy with C4.5 (63%))
Padmanaban et.al[42]	CKD	Rapid Miner	DT	Achieved best accuracy with DT (91%)
Ramya et. al[43]	CKD	R TOOL	ANN	Achieved best accuracy with DT (85.3%)
Vijayarani et. al[11]	Kidney	MATLAB	ANN	Achieved best accuracy with ANN (87.70)

VII. CONCLUSION

Diagnosis of health condition is incredibly difficult and significant issue in the field of medical science. A classification and feature selection technique help quick and perfect identification and diagnosis of disease in simple and perfect way.

This research work focuses the classification of CKD using robust developed classification model. The performances of the classification model have improved once the numbers of features are decreased. We have compared the performance of ensemble model (SRC and CIT), Single Rule Classification and Conditional Inference Tree. The ensemble model (SRC and CIT) gives better accuracy compared to Single Rule Classification and Conditional Inference Tree. In case of FSTs like Genetic Search (GS-NB) and Greedy Stepwise (GSW-NB), an ensemble model of (SRC and CIT) gives better accuracy for classification for CKD. Finally we have concluded that an ensemble model of (SRC and CIT) gives the highest accuracy 95.00% with FST GS-NB with 11 features in CKD dataset. The suggested model in the similar works is better than a large portion of the previous models. Finally, we recommend that ensemble model with Genetic Search is a robust and computationally efficient model for CKD classification. Suitable other possible FST, optimization techniques and different kind of tools that can be applied to obtain better results in the proposed model.

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