International Journal of Business, Human and Social Sciences
ISSN: 2517-9411
Vol:8, No:7, 2014

Forecasting US Dollar/Euro Exchange Rate with Genetic Fuzzy Predictor

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Abstract**—**Fuzzy systems have been successfully used for exchange rate forecasting. However, fuzzy system is very confusing and complex to be designed by an expert, as there is a large set of parameters (fuzzy knowledge base) that must be selected, it is not a simple task to select the appropriate fuzzy knowledge base for an exchange rate forecasting. The researchers often look the effect of fuzzy knowledge base on the performances of fuzzy system forecasting. This paper proposes a genetic fuzzy predictor to forecast the future value of daily US Dollar/Euro exchange rate time's series. A range of methodologies based on a set of fuzzy predictor's which allow the forecasting of the same time series, but with a different fuzzy partition. Each fuzzy predictor is built from two stages, where each stage is performed by a real genetic algorithm.

Keywords**—**Foreign exchange rate, time series forecasting, Fuzzy System, and Genetic Algorithm.

I. INTRODUCTION

FORECASTING exchange rates is an important financial problem that is receiving increasing attention especially because of its difficulty and practical applications. Exchange rates are affected by many highly correlated economic, political, and even psychological factors. This factor in interact in a very complex fashion [10].

Parametric models and intelligent approaches are the two main techniques used for financial time series forecasting. Parametric models such as autoregressive moving average ARMA, autoregressive conditional Heteroscedastic ARTCH, general autoregressive conditional Heteroscedastic GARTCH have been proposed and applied to financial forecasting [8]. While these models may be good for particular situation, they perform poorly for other situation. Intelligent approaches seen in the literature for the analysis of time series include fuzzy systems [9], hidden Markov models [11], and the support vector machines [4]. Some hybrid models are also seen in the literature: in [12], a combination of genetic and neural network has been proposed. In [6], support vector regression (SVR) and self organizing feature map (SOFM) technique have been hybridized to reduce the cost of training time and improve prediction accuracies. High –order fuzzy logical relationships and genetic simulated annealing techniques are combined in [7] for temperature prediction and the Taiwan futures exchange (TAIFEX) forecasting, where genetic-simulated annealing techniques have been used to adjust the length of each interval in the universe discourse to increase the forecasting accuracy.

Although fuzzy systems have been applied in several studies, a few of these have contributed to research in the financial time series. The fuzzy systems offer a powerful tool for knowledge representation as it has the ability to handle the amount of the information necessary to describe and model the decision support system [2]. On the other hand genetic algorithms propose a general purpose search mechanism adopted form natural paradigm that has proved robust and efficient in many applications [13].

This study contributes to the field of financial time series. The main of this study is to design an optimal fuzzy predictor that can extract fuzzy rule base and specify the membership function of inputs and output variables automatically starting from the values of time series. The fuzzy knowledge base extraction method is based on a genetic algorithm (GA) which doesn't require both the mathematical models of the time series and the human expert's help [3].

In this paper, a new two-stage design method of fuzzy predictors (FP's) is proposed in such a way that the first stage generates a fuzzy rule base, the second stage builds the membership functions so that they produce the prediction errors as so small as possible, for forecasting daily currency exchange rates of US Dollar (USD) against the EURO using their historical exchange rates from 02/01/2003 to 30/06/2011 was found on [14]. A total of 800 values of historical exchange rate data was collected and used as inputs for the first stage, and then last values of exchange rate data were used for the second stage. The results of this method are compared with [5] based on two evaluation indicators such as NMSE and MAE.

II. DESIGN OF THE FUZZY PREDICTOR BY REAL GA

The fuzzy predictor's set consists of 3 fuzzy predictors. They are made up mainly, as it is illustrated in Fig. 1, of 4 essential blocks: fuzzificator, fuzzy knowledge base, inference engine and defuzzificator. Each Fuzzy predictor is developed by the means of a real genetic algorithm including two stages: The first stage is used for producing a fuzzy rule base, which covers the maximum of training examples. The second stage serves to optimize the membership functions, by minimizing the prediction error. These two stages are independently repeated for all the fuzzy predictor's. The prediction error of the fuzzy predictor's set is calculated by the combination of the prediction errors of all the elements. This combination is ensured by the weighting method with a fixed weight. The

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representation of the parameters in GAs is generally into binary or real. In this work, we adopted the last (the representation or real Coding) to optimize the fuzzy knowledge base of fuzzy predictor's set PF_i. These fuzzy predictor's forecast the same time series but with different fuzzy partitions. Either P_{xi} is the number of partitions of x_i, P_{xi} thus takes a value among the set {5, 7, 9}.

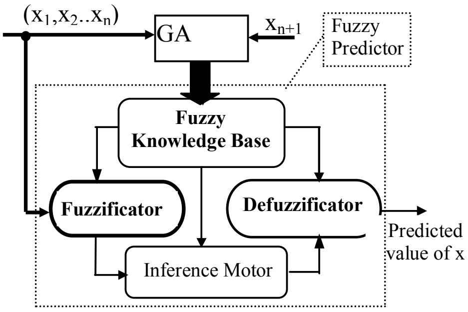


Fig. 1 Diagram of a fuzzy Predictor

A. First Stage: The Production of the Fuzzy Rule Base

We use for the optimization a number of $T = 800$ values of the daily US Dollar/Euro exchange rate time series grouped in a set of training examples $E = (e^1, e^2, ..., e^T)$. Each example $e^t (t = 1:T)$ consists of an ordered pair of n precedent values and the future value of the US Dollar/Euro exchange rate time series $(x_1, x_2, ...x_n; x_{n+1})$. Since it is important and necessary that the fuzzy rule base covers all training examples, then each example e^t is quantified by the compatibility degree [1].

$$C_{R_k}(e^t) = \Lambda_{i=1}^{n+1} M_{xi}^k(e^t) \qquad (1)$$

where Λ is an operation of the class T-norm, in our work it is an algebraic product operation.

$M_{x_i}(e^t)$: Represent the membership function of the variable x_i in the example e^t includes in the rule R_k. When an example e^t is included in several fuzzy rules, the example is treated in the rule in which C_{R_k} is maximal. The total compatibility degree of a rule R_k is given by:

$$C_{R_k}(E) = \sum_{\forall e^t} C_{R_k}^{\tau}(e^t) \qquad (2)$$

K represents the index rule $k = 1, 2, ..., R_B$. T represents the index example $t = 1, 2, ..., T$.

The rules that include any example are removed. In this stage we adapt the real GA to our application and we note it GA1.

1. Representation of the Chromosome:

We consider a specific representation of the partition model; the chromosome is constituted of P_{xi} membership functions $M(p)(p = 1 : P_{x_i})$. Every $M(p)$ is defined by the center and the width (C_p, W_p), therefore each chromosome is constituted of $2 \times P_{xi}$ genes.

2. Initial Population Generation:

The chromosome in the initial population is produced by the stochastic generation of (C, W) whose represents the center and the width of the membership function.

3. Fitness Function:

We have chosen like fitness function the total cover value of the rule base formed by the examples set E that is defined as the sum of cover values of all fuzzy rules.

$$F^{(1)}(E) = C_{R_B}(E) \qquad (3)$$

$$C_{R_B}(E) = \sum_{k=1}^{R_B} C_{R_k}(E) \qquad (4)$$

$$C_{R_B}(E) = \sum_{k=1}^{R_B} \sum_{\forall e^t} C_{R_k}^{\tau}(e^t) \qquad (5)$$

$F^{(1)}(E)$: The fitness function of the 1st stage

4. Genetics Operators:

A. Selection:

The selection is a procedure in which a chain is copy of proportion to the objective function. This function can be considered like a profit measure, utility or quality that we wish to maximize.

B. Crossover:

The fuzzy rule base can be treated like a grid G of dimension n+1, every cell $(x_1, x_2, ...x_n; x_{n+1})$ in the grid stocks the cover value $C_{R_k}(e^t)$ corresponding to the example $e^t = (x_1, x_2, ...x_n; x_{n+1})$ and to the rule R_k, when several training examples are included in the same cell, the cover value of these examples is added then associated to the cell. The total cover value $C_{R_B}(E)$ of the rule base is calculated as the sum of the cover values of all cells of the grid

$$C_{R_B}(E) = \sum_{x_1} .. \sum_{X_n} \sum_{x_{n+1}} grid(x_1, x_2 ... x_n; x_{n+1}) \qquad (6)$$

$$MC_{(xi, M(p))}(E) = \sum_{x_1} ... \sum_{x_{i-1}} \sum_{x_i} \sum_{x_{i+1}} ... \sum_{x_n} \sum_{x_{n+1}} grille(x_1, ... x_n, x_{n+1}) \qquad (7)$$

The marginal cover value $MC_{(xi,M(p))}(E)$ is the addition of all the cover values of the example having x_i belonged to the support of $M(p)$. After calculating all marginal cover values corresponding to all the membership functions $M(p)$, the weakest cover value $MC_{(xi,M(p))}(E)$ $p=(1:P_{xi})$ is the value that corresponds to the center and width (C,W) of the membership function that is going to be changed. Points of crossover between the two chromosomes P_1 and P_2 are chosen as follows: first, the set of marginal cover values $MC_{(xi,M(p))}(E)$ of P_1 noted by $EMC(p_1)$ and of P_2 noted by $EMC(p_2)$ are calculated independently, the linguistic terms corresponding to the weakest marginal cover in each parent (T_j for P_1 and T_1 for P_2) are selected to apply the operation of crossover. If the two linguistic terms are identical the operation makes between the representative genes of these two linguistic terms. In the contrary case, the crossover operation takes place in two different points.

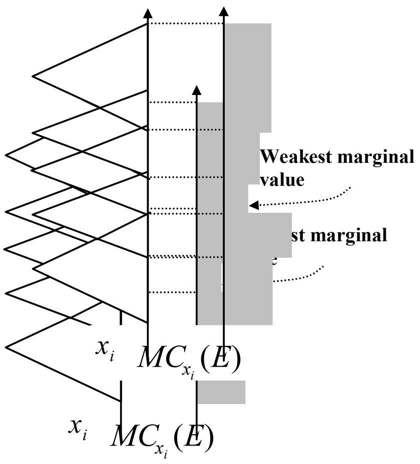


Fig. 2 An illustration of the marginal cover values

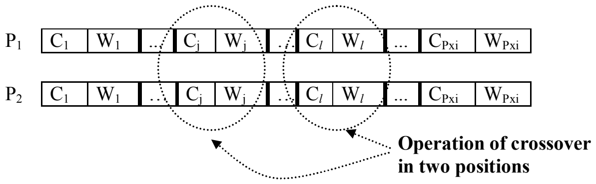


Fig. 3 Operation of crossover

The center and the width (C',W') of the new membership function associated with the linguistic term that result from the crossover operation is calculated from their equivalents (C_1,W_1) in the parent P_1 and (C_2,W_2) in the parent P_2 as follows:

$$C'^{(1)}=\frac{C_1.W_1+C_2.W_2}{W_1+W2}. \tag{8}$$

$$W'^{(1)}=random\ (\alpha,\beta) \tag{9}$$

$random\ (\alpha,\beta)$ is a value generated uncertainly in the interval $[\alpha,\beta]$ as $\alpha=\min(W_1,W_2)$ $\beta=\max(W_1,W_2)$.

C. Mutation:

The mutation is an operation that always applies on only one chromosome and in a point that is chosen uncertainly with a probability p_m. The center and the width (C,W) of the linguistic term selected uncertainly in the chromosome is changed to (C'',W'') as:

$$\begin{gathered}C''^{(1)}=C+random\left(-\Delta C^{(1)},\Delta C^{(1)}\right).\\ W''^{(1)}=C+random\left(-\Delta W^{(1)},\Delta W^{(1)}\right)\end{gathered} \tag{10}$$

where $\Delta C^{(1)}$, $\Delta W^{(1)}$ represent the maximal variation of the center and the width respectively.

B. Second Stage – Optimization of the Fuzzy Membership Function

The previous stage serves to produce the fuzzy rule base while maximizing the total cover value. The second stage consists to optimize the membership function of the inputs and output variables while minimizing prediction error. The representation of the chromosome is the same as the first stage. In the next section we explain in detail the genetic Algorithm used in this stage noted by *GA2*.

1. Chromosome Representation:

The representation of the chromosome is the same that the first stage.

2. Initial Population Generation:

The initial center and width of chromosome are generated by the addition of an uncertain number in the center and the width of chromosomes generated at the end of the first stage.

$$\begin{gathered}C^{(2)}=C^{(1)}+random\left(-\Delta C^{(2)},\Delta C^{(2)}\right).\\ W^{(2)}=W^{(1)}+random\left(-\Delta W^{(2)},\Delta W^{(2)}\right)\end{gathered} \tag{11}$$

3. Fitness Function:

The fitness function $F^{(2)}(E)$ used in this stage is the mean absolute error (MAE).

$$F^{(2)}(E)=MAE \tag{12}$$

4. Genetics Operators:

Genetic operators of this stage are the same to those of the first stage with the exception that in the crossover operation formulas used for calculating the new values of the center and width (C,W) are changed and are given by (13)

$$\begin{gathered}C'^{(2)}=\frac{C_1+C_2}{2}.\\ W'^{(2)}=\frac{W_1+W_2}{2}\end{gathered} \tag{13}$$

Another exception made for the operator of mutation where variations added ΔC and ΔW are smaller than those of the first stage.

III. GENETIC FUZZY PREDICTOR SET (GFPS)

In general the fuzzy predictor performance depends on several factors, among others there is the number of fuzzy partitions of inputs and output variables of the predictor. This factor is not taken in amounts in the conception of only one fuzzy predictor that we have just described. For not neglected this point, we propose a genetic fuzzy predictor set organized of several fuzzy predictors that makes the prediction of the same time series but using a different fuzzy partitions.

And as, we need only one output, we make the combination of the outputs of these fuzzy predictors, Fig. 4. The prediction error of the set and the coupling constant are calculated as follows

$$w_i = \frac{1}{\delta_i \times \sum_{j=1}^{3} \delta_j} \tag{14}$$

$$\delta_E = \frac{p}{\sum_{j=1}^{p} \frac{1}{\delta_j}} \tag{15}$$

The combination of (14) and (15) gives a relation between δ_E and w_i determined by:

$$w_i = \frac{\delta_E}{\delta_i p} \alpha \delta_i^{-1} \tag{16}$$

This equation implies that the FP that has weak prediction error has big coupling constant and vice versa [1]. The predicted value by the GFPS of US Dollar/Euro exchange rate time series:

$$\hat{x}_{n+1} = \sum_{i=1}^{p} w_i \hat{x}_{n+1}^{i} \tag{17}$$

where $\hat{x}_{n+1}^{i}$ represent the value of x predicts by the ith fuzzy predictor.

IV. EXPERIMENTAL RESULTS AND DISCUSSION

In the following, we describe the data collection, evaluation indicators to evaluate and compare the predictive power of the models and the simulation results.

A. Data Collection

The data used in this study is the daily US Dollar/Euro exchange rate time series: from 02/01/ 2003 to 30/06/2011 found on [14]. The Fig. 5 presents the 2000 points of the series. The first 800 values of data are used to produce the fuzzy rule base, and the last 1000 values are used to optimize the fuzzy membership function.

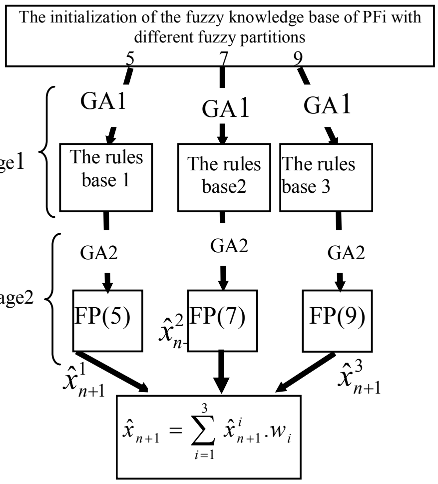


Fig. 4 Functional diagram of a (GFPS)

B. Evaluation Indicators

The forecasting performance of the above model is evaluated against a two evaluation indicators, namely, Normalized Mean Square Error (NMSE), Mean Absolute Error (MAE). These criteria are defined in Table I. y_i and a_i are the actual and predicted values, respectively. NMSE and MAE measure the deviation between actual and forecast value. Smaller values of these evaluation indicators signify higher accuracy in forecasting.

TABLE I
EVALUATION INDICATORS

Evaluation indicator	Equation
NMSE	$\sum_i (y_i - a_i)^2 \Big/ \sum_i (y_i - \bar{a}_i)^2$
MAE	$\frac{1}{N} \sum_i \lvert y_i - a_i \rvert$

TABLE II
THE CONTROL PARAMETERS OF THE GA

	First stage	Second stage
No of generation	100	100
Size of population	50	50
Size of chromosome	10-18	10-18
Probability of crossover	1	1
Probability of Mutation	0.08	0.08
The doorstep τ	0.001	/

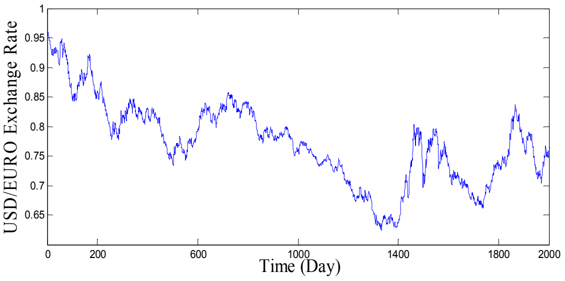


Fig. 5 Historical USD/EURO exchange Rate

C. Simulation Results

Of simulation result, we find that the prediction error decreases with the increase of the number of fuzzy partitions of inputs and output variables. To make comparison with the other works, we take 5, 7, 9 as number of fuzzy partitions of inputs and output variables. The description of procedure of simulation is as follows, first, a coarse fuzzy partition of all inputs and output variables select genetically by maximizing the cover value on the first 800 data pairs (6 inputs and 1 output). Secondly, the membership functions of the fuzzy rule base optimized in the first stage are optimized genetically by the minimization of the prediction error on the last 1000 pair's data. These two stages repeated for the different numbers of partitions (5, 7, 9) to develop the 3 fuzzy predictors that give different performances of prediction. Finally, the genetic fuzzy predictor set is developed by the combination of the 3 fuzzy predictors of which the prediction error is reduced genetically.

Table II presents the control parameters used to conceive the fuzzy predictors. In this table, the number of genes is 10 to 18 according to the fuzzy partitions of each variable and τ is the doorstep of the cover value that is used to exclude the fuzzy rules that have a cover value lower than τ.

Fig. 6 presents the membership functions of the inputs and output variables for different numbers of partitions (5,7,9). It is necessary to know that the shape of membership functions is very different for the different numbers of partition. This different shape of membership functions results different prediction error. The comparative diagrams showing the output forecast by the different fuzzy predictors and actual time series over 1000 days for USD/EURO exchange rate are shown in Figs. 7(a) ~10(a). Figs. 7(b) ~10(b) show the forecasting error of USD/EURO time series by the different FP.

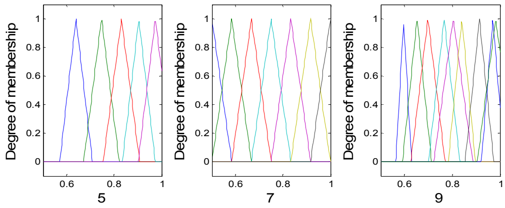
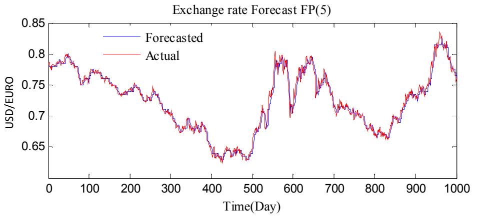
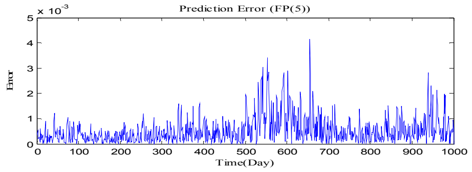


Fig. 6 The membership functions at the end of second stage

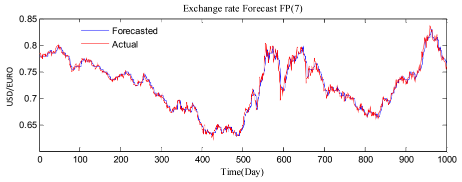


(a)

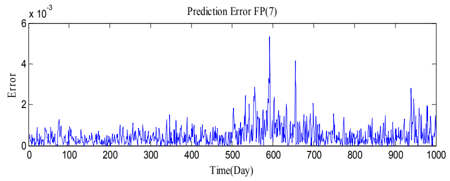


(b)

Fig. 7 (a) Actual and Forecasted exchange rate (b) Forecasting Error of the FP (5)

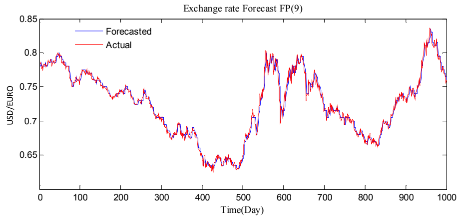


(a)

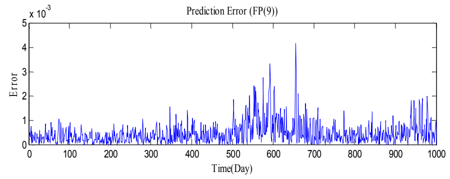


(b)

Fig. 8 (a) Actual and Forecasted exchange rate (b) Forecasting Error of the FP (7)

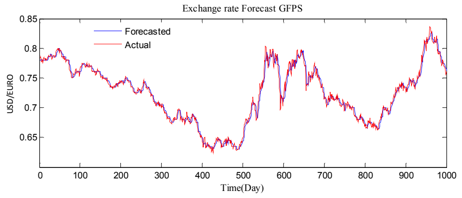


(a)

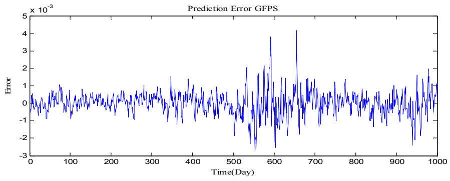


(b)

Fig. 9 (a) Actual and Forecasted exchange rate (b) Forecasting Error of the FP (9)



(a)



(b)

Fig. 10 (a) Actual and Forecasted exchange rate (b) Forecasting Error of the GFPS (9)

D. Comparison of Genetic fuzzy, Conditional Heteroscedastic Models

Table III shows the evaluation indicators achieved by each model over a forecasting period. The results show that genetic fuzzy Model consistently performs better than neural Network and Conditional heteroscedastic Models (GARCH, GARCH-M, EGARCH, TGARCH/GJR and IGARCH) in terms of the two Evaluation indicators for USD/ EURO exchange rate time series. This means that these models are capable of forecasting exchange rate more closely than neural network and Conditional heteroscedastic models. The reason of better performance of Genetic-Fuzzy Model is the improved genetic optimization which allows them to search efficiently the fuzzy rule base and fuzzy membership function. The results of the conditional heteroscedastic models and neural are taken from [5]. We can also observe in Table III that the fuzzy predictor FP associated with fuzzy partitions 9 give the weaker error than those given by the FP associated with the 7 partitions and 5 partitions and the prediction error of the set (GFPS) is weaker than those of the predictors separated.

TABLE III
COMPARATIVE ANALYSIS OF USD/ EURO SERIES

Model	NMSE	MAE.10^2
GARCH(1,1)	0.99998	0.34930
GARCH(1,1)-M	0.93987	0.34918
EGARCH(1,1)	0.89833	0.30927
TGARCH/GJR(1,1)	0.89986	0.31414
IGARCH(1,1)	0.92064	0.34999
Neural network	0.88442	0.38644
Fuzzy Genetic FP5	0.0241	0.053
Fuzzy Genetic FP7	0.0224	0.051
Fuzzy Genetic FP9	0.0173	0.045
GFPS	0.0101	0.039

V. CONCLUSIONS

In this study we investigate the optimization of the fuzzy rule base and the membership function of inputs and output of fuzzy predictors with different partitions using a real genetic algorithm. To evaluate the effectiveness of the proposed approach Daily USD/EURO exchange rates is predicted.

Our study shows that

1. The prediction error decreases with the increase of partition variable numbers;
2. The prediction error of the second stage is weaker than the error of the second stage;
3. The fuzzy predictor's set gives a weaker prediction error. A reason of the application of the proposed model in the second stage that the prediction error of GFPS of the first stage can't be reduced a lot by the combination of the fuzzy predictors (FP's) gotten in the results of the first stage. This because the goal of the first stage is of maximized the cover value.

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