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Multiobjective clonal selection algorithm for solving forecasting problems

N N Astakhova1,4, L A Demidova1,2, A V Kuzovnikov3 and R V Tishkin1

1 Ryazan State Radio Engineering University, Gagarin Str., 59/1, Ryazan, Russian Federation, 390005
2 Moscow Technological Institute, Leninskiy pr., 38A, Moscow, Russian Federation, 119334
3 JSC Academician M.F. Reshetnev Information Satellite Systems, Lenin Street, 52, Zheleznogorsk, Krasnoyarsk region, Russian Federation, 662972

E-mail: asnadya@yandex.ru

Abstract. The multiobjective modified clonal selection algorithm based on the use of the notion “Pareto dominance”, which can be applied for the development of the forecasting models on the base of the strictly binary trees has been offered. It is suggested to use the affinity indicator based on the average forecasting error rate, and the tendencies discrepancy indicator in the role of the objective functions of this algorithm. The multiobjective modified clonal selection algorithm can be applied for solving problems of individual and groups’ forecasting. The experimental results which confirm the efficiency of the offered algorithm in comparison with the basic modified clonal selection algorithm have been given.

1. Introduction
The problem of the right choice of the best forecasting model is the main problem of forecasting [1 – 3]. In particular, in the forecasting model on the base of the strict binary trees (SBT) and the basic modified clonal selection algorithm (MCSA) [1, 2] this model is presented in the form of antibodies. The MCSA allow generating the different variants of the forecasting models to find among them the best forecasting model according with the chosen quality indicator. The antibody is coded by a sequence of symbols randomly selected from the corresponding alphabets. Such sequence will be transformed to the analytical dependence which represents some function [1, 2]. This function will be applied to obtaining the predicted values of a time series (TS).

The best forecasting models must be determined at each step of the iterative process in the MCSA. Such models become parents for the next generation of models at the next step [1, 2, 4 – 7]. Obviously, the correct selection of antibodies is very important for the effective use of the MCSA.

The MCSA possesses a number of benefits in comparison with analogic optimization algorithms. It allows weakening the requirements to data representation and establishing the optimum settings. Also, the MCSA provides high speed and high efficiency of calculations. This algorithm applies the evolutionary principles to modification and selection of antibodies constructed on the base of the SBT. As a result, it is possible to find the best antibody and the best forecasting model corresponding to this
antibody. The MCSA is applicable for forecasting of TSs with a short length of an actual part which are characteristic for a large number of real processes and statistical indicators.

Nowadays, the one-factor forecasting models and multiple-factor forecasting models on the base of the SBT and the MCSA which use the values of elements of TSs and the values of their increments for creation of the training data sequence are developed by authors of this paper [1, 2]. Also, we have offered the forecasting method for the groups of TSs which uses the MCSA to create the general forecasting models for each cluster of TSs [4 – 6].

Usually, the average forecasting error rate, calculated for the training data sequence, is used as the main quality indicator of the forecasting model. Herewith, the average forecasting error rate should be minimized [1 – 7]. The MCSA steadily shows the low value of this quality indicator for data of various subject domains.

However, the use of the average forecasting error rate as the single quality indicator of the forecasting model is not always sufficient to determine the best forecasting model. Often it is required to consider the additional quality indicators of the forecasting model, such as the compliance to the seasonal tendencies of TS, the compliance to the trend of TS, lack of emissions, complexity of the forecasting model, etc. [2]. But it isn’t possible to choose the single quality indicator correctly. Therefore, the problem of the choice of the quality indicators is very actual. It is expedient to use the additional quality indicator which will allow estimating the general tendency of values’ change of the known elements of TS (for example, the tendencies discrepancy indicator) along with the average forecasting error rate [2].

Now, a number of multiobjective evolutionary algorithms (MOEAs) have been suggested. First of all, it is neccassary to say about the multiobjective genetic algorithms [8 – 17] and the multiobjective clonal selection algorithms [18 – 25]. These algorithms provide a solution of the account’s problem of the several objective functions (criteria, quality indicators) at the analysis of various applied problems.

Obviously, it is possible to increase the efficiency of the forecasting models on the base of the SBT, using the multiobjective MCSA (MMCSA) at the solution of the problem of the medium-term forecasting. The MMCSA has to borrow the best ideas of the MOEAs in the context of forecasting problems. It is suggested to use in this algorithm the affinity indicator based on the average forecasting error rate and the tendencies discrepancy indicator in the role of the objective functions.

The rest of this paper is structured as follows. Section 2 presents the main ideas of the MCSA. Then, Section 3 details the proposed approach for solving the problem of multiobjective optimization for the MCSA. Here the review of the multiobjective evolutionary optimization algorithms and the choice of the prototype for the realization of the MMCSA have been carried out. The experimental results comparing the original MCSA to the MMCSA follow in Section 4. Finally, conclusions are drawn in Section 5.

2. Forecasting models on the base of the strictly binary trees and the modified clonal selection algorithm

The main ideas of development of the forecasting models on the base of the SBT and the MCSA were investigated in [1]. The MCSA allows forming an analytical dependence on the base of the SBT, which describes the certain TS values and provides a minimum value of the average forecasting error rate (AFER):

\[
AFER = \frac{\sum_{j=k+1}^{n} |(f^j - d^j)/d^j|}{n-k} \times 100\%
\]

where \(d^j\) and \(f^j\) are respectively the actual (fact) and forecasted values for the \(j\)-th element of the TS; \(n\) is the number of TS elements; \(k\) is the model order.

The possible options for analytical dependences are presented in the form of antibodies \(Ab\) which recognize antigens \(Ag\) (certain TS values). An antibody \(Ab\) is selected as “the best one”. It provides
the minimum value of the affinity indicator \( Aff \) [1, 2]. Coding of an antibody \( Ab \) is carried out by recording signs in a line. The signs are selected from three alphabets [1, 2]:

- the alphabet of arithmetic operations (addition, subtraction, multiplication and division) – \( Operation = \{+,-,\cdot,=\} \);
- the functional alphabet, where letters ‘\( S \)’, ‘\( C \)’, ‘\( Q \)’, ‘\( L \)’, ‘\( E \)’ define mathematical functions “sine”, “cosine”, “square root”, “natural logarithm”, “exhibitor”, and the sign ‘\( _{} \)’ means the absence of any mathematical function, – \( Functional = \{S,C,Q,L,E,\_\} \);
- the alphabet of terminals, where letters ‘\( a \)’, ‘\( b \)’, ‘\( c \)’, ‘\( d \)’, ‘\( z \)’ define the arguments required analytical dependence and the sign ‘\( ? \)’ defines a constant, \( Terminal = \{a,b,c,d,z,?\} \).

The use of these three signs alphabets provides a correct conversion of randomly generated antibodies into the analytical dependence. The structure of such antibodies can be described with the help of the SBT [1, 2]. The use of the SBT allows building the complex analytical dependence and provides high accuracy of the forecasting TS [2].

The MCSA applied to the searching for “the best” antibody defining “the best” analytic dependence includes the preparatory part (realizes the formation of the initial antibody population) and iterative part (presupposes the ascending antibodies ordering of affinity \( Aff \) the selection and cloning the part of “the best” antibodies, that are characterized by the least affine value \( Aff \) the hypermutation of the antibodies clones; self-destruction of the antibodies clones “similar” to the other clones and antibodies of the current population; calculating the affinity of the antibodies clones and forming the new antibodies population; suppression of the population received; generation of the new antibodies and adding them to the current population until the ingoing size; the conditional test of the MCSA completion.

The forecasting model on the base of the SBT can be applied for for the individual and groups’ forecasting of time series [3 – 5]. In the second case this model is used as the general forecasting model for describing the clusters’ centroids. Herewith, the general forecasting model can be specified for some individual TS during the additional iterations of the MCSA.

3. The multiobjective modified clonal selection algorithm
In the context of working with the MSCA the average forecasting error rate \( AFER \) can be considered as the affinity indicator \( Aff \) [1, 2]. It can be used as the first quality indicator for the forecasting model.

The rate of discrepancy between the tendencies of two TSs (the tendencies discrepancy indicator \( Tendency \)) can be used as the second quality indicator for the forecasting model [2]. The tendencies discrepancy indicator \( Tendency \) can be calculated as:

\[
Tendency = \frac{h}{n-k-1},
\]

where \( h \) is the number of negative multiplications \((f^{(j)} - f^{(j)}) \cdot (d^{(j)} - d^{(j)})\); \( j = k + 2, n; \ d^{(j)} \) and \( f^{(j)} \) are respectively the actual (fact) and forecasted values for the \( j \)-th element of TS; \( n \) is the number of TS elements; \( k \) is the model order; \( n-k-1 \) is the total number of multiplications \((f^{(j)} - f^{(j)}) \cdot (d^{(j)} - d^{(j)})\).

This indicator allows adapting the forecasting models on the base of the SBT and the MCSA for the medium-term forecasting.

Both indicators (\( Aff \) and \( Tendency \)) determine the similarity of the predicted values of the TS with the real ones. However, these indicators use the different principles of assessment. The affinity indicator \( Aff \) is used in the implementation of the MCSA to define value of “adaptability” (quality) of the antibody \( Ab \) on the base of elements’ values of the TS. The tendencies discrepancy indicator
**Tendency** allows estimating the quality of the antibody \( Ab \) taking into account the coincidence with the trend of the TS. Herewith both indicators must be minimized. These indicators are based on the various principles of the quality assessment of the forecasting model. The affinity indicator \( Aff \) estimates the similarity and difference between the predicted and actual values of the known elements of the TS. The tendencies discrepancy indicator \( Tendency \) estimates the similarity and difference of the change’s directions between the predicted and actual values of the known elements of the TS. This indicator helps to analyze tendencies in the TS and the presence of seasonal fluctuations.

These indicators (\( Aff \) and \( Tendency \)) must be used simultaneously at the quality assessment of the forecasting models on the base of the SBT to solve the problem of the medium-term forecasting. Now the problem of the simultaneous accounting of the several quality indicators can be successfully solved using the multiobjective optimization algorithms, including, evolutionary algorithms.

In recent years, a number of multiobjective evolutionary algorithms (MOEA) have been suggested. The main reason for this is their ability to find the multiple Pareto-optimal solutions [8 – 25] in one single simulation run. These algorithms work with a population of solutions. Therefore the primary attention has to be paid to maintaining the diversity and spread of solutions. Such multiobjective evolutionary optimization algorithms provide a solution of the account’s problem of the several objective functions (criteria, quality indicators) at the analysis of various applied problems.

Nowadays the multiobjective genetic algorithms (MOGA) [8 – 17] are the most known algorithms of the multiobjective optimization. It is necessary to say about the multiobjective clonal selection algorithms (MOCSA) [17 – 24]. However these algorithms are less designed and, in the majority, borrow the principles of multiobjective optimization underlain in the genetic algorithms. The possibility of this loan can be explained with many similar mechanisms of the evolutionary process realization in the MOGA and MOCSA. At the beginning of the 1990s, a number of different multiobjective genetic algorithms were suggested. Such algorithms as Fonseca and Fleming’s FFGA (Fonseca and Fleming’s Genetic Algorithm) [10], Horn, Nafpliotis and Goldberg’s NPGA (Niched Pareto Genetic Algorithm) [11], Srinivas and Deb’s NSGA (Non-dominated Sorting Genetic Algorithm) [15, 16] are the most known among them.

The main common features of these multiobjective evolutionary optimization algorithms are the following: i) assigning fitness to the population members based on the nondominated sorting and ii) preserving the diversity among the solutions of the same nondominated front. These algorithms have been shown to find multiple nondominated solutions. The essential interest has been to introduce elitism to enhance the convergence properties of a MOEA. Among the existing elitist MOEAs, Zitzler and Thiele’s SPEA (Strength Pareto Evolutionary Algorithm) [12], Knowles and Corne’s PAES (Pareto Archived Evolution Strategy) [13], and Rudolph’s elitist GA [14] are well studied. They appeared at the end of 1990s.

The fast and elitist MOEA, called the NSGA-II, has been suggested in 2002 by Deb K., Agrawal S., Pratap A. and Meyarivan T. This algorithm uses a fast nondominated sorting procedure with \( O(MN^2) \) computational complexity (where \( M \) is the number of objectives and \( N \) is the population size), an elitist-preserving approach, and a parameterless niching operator [15, 16]. As result, the NSGA-II alleviates the following difficulties: i) the performance of the sharing function method in maintaining a spread of solutions and better convergence near the true Pareto-optimal front compared to the PAES and SPEA, which are the elitist MOEAs that pay special attention to creating a diverse Pareto-optimal front. Also, the NSGA-II uses new the modified definition of dominance in order to solve constrained multiobjective problems efficiently. In the NSGA-II the sharing function approach is replaced with a crowded-comparison approach (on the base of the notion of the “crowding distance”) that eliminates the following difficulties: i) the performance of the sharing function method in maintaining a spread of
solutions depends largely on the chosen value of the sharing parameter; the overall complexity of the sharing function approach is $O(N^2)$, since each solution must be compared with all other solutions in the population. The NSGA-II does not require any user-defined parameter for maintaining diversity among population members. The basic operations of the NSGA-II and their worst-case complexities are as follows: i) nondominated sorting is $O(M(2N)^2)$; ii) crowding-distance assignment is $O(M(2N)\log(2N))$; iii) sorting on the base of the ranks and the crowding distances is $O(2N \log(2N))$. The overall complexity of the NSGA-II is $O(MN^2)$, which is governed by the nondominated sorting part of the algorithm. It should be noted that the diversity preserving mechanism used in the NSGA-II is the best than in the PAES and the SPEA [15, 16].

Later, in 2012 the reference-point based multiobjective NSGA-II, called the NSGA-III, with $O(MN^2)$ computational complexity was been suggested [17]. The NSGA-III uses a predefined set of the reference points to ensure the diversity in the obtained solutions. The chosen reference points can either be predefined in a structured manner or supplied preferentially by the user. In the absence of any preference information, any predefined structured placement of the reference points can be adopted. The NSGA-III uses Das and Dennis’s [17] systematic approach, that places the points on a normalized hyperplane – a $(M - 1)$-dimensional unit simplex – which is equally inclined to all objective axes and has an intercept of one on each axis. If the $p$ divisions are considered along each objective, the total number $H$ of the reference points in the $M$-objective problem is given by the $\tilde{N}_{M+p-1}^p$. This algorithm emphasizes the population members which are in some sense associated with each of these reference points. Since the reference points are widely distributed on the entire normalized hyperplane, the obtained solutions are also likely to be widely distributed on or near the Pareto-optimal front. In the case of a user-supplied set of the preferred reference points, ideally the user can mark $H$ points on the normalized hyperplane or indicate any $H$ vectors for the purpose (a herewith these vectors must be $M$-dimensional). For the rest the NSGA-III is similar to NSGA-II at the realization. The NSGA-III works better on the different classes of multiobjective optimization problems, than others MOEAs, but demand to use a predefined set of the reference points.

At the beginning of the 2000s, the first multiobjective clonal selection algorithms were suggested. The most known MOCSAs are the following: MISA (Multiobjective Immune System Algorithm) [18], MOIA (Multiobjective Immune Algorithm) [19], MOCSA (Multiobjective Clonal Selection Algorithm) [20], IDCMA (Immune Dominance Clonal Multiobjective Algorithm) [21], ACSAMO (Adaptive Clonal Selection Algorithm for Multiobjective Optimization) [22], CNMOIA (Constrained Nonlinear Multiobjective Optimization Immune Algorithm) [23] and NNIA (Nondominated Neighbor Immune Algorithm) [24]. All these algorithms are based on the principles of the Pareto dominance. Such algorithms as MISA, IDCMA, ACSAMO and NNIA use elitism in their realization. A herewith, the NNIA is the modification of the IDCMA. The NNIA as the NSGA-II and NSGA-III uses the notion of the crowding distance as the measure of density of solutions in the neighborhood. It allows maintaining the diversity among the solutions in the population. The computational complexity of the MOCSAs depends on the number of objectives $M$, the population size $N$, the clone population size $N_c$ and so on. For example, The computational complexity of the IDCMA and the NNIA is $O((N_d + N_c)^2)$, where $N_d$ is the size of immune dominance antibody population, $N_c$ is the size of generic antibody population (the clone population size) [25].

The analysis of merits and demerits of the MOEAs shows that such the MOGAs as the NSGA-II and the NSGA-III are significantly better than others because they can successfully solve more difficult problems of the multiobjective optimization [15 – 17]. Besides, the MOGAs have more successful development and application in the solution of many real difficult problems. A herewith the MOCSAs borrows some ideas of the MOGAs (for example, the NNIA uses the notion of the crowding distance for the first time introduced in the NSGA-II).
In this regard the decision on expediency of the adaptation of the ideas put in the NSGA-II at the realization of the MMCSA which is applied for the selection of the forecasting models on the base of the SBT had been made. In this case, it is necessary to understand the forecasting model (and the antibody corresponding to it) as the decision, and the quality indicator of the forecasting model as the objective function at the realization of the MMCSA when developing the forecasting models on the base of the SBT. All forecasting models with use of the notion “Pareto dominance” can be divided to dominated and nondominated models.

Let \( Q_{sv} \) be a value of the \( v \)-th quality indicator for the \( s \)-th forecasting model; \( v = \overline{1,V} ; \; s = \overline{1,S} \); let \( V \) be a quantity of the quality indicators of the forecasting model; let \( S \) be a quantity of the forecasting models (for example, in the population, that is the population size).

The \( s \)-th forecasting model is dominated by the \( z \)-th forecasting model \((s = \overline{1,S} ; \; z = \overline{1,S})\), if the following conditions are satisfied: the \( s \)-th forecasting model is dominated by the \( z \)-th forecasting model \((s = \overline{1,S} ; \; z = \overline{1,S})\), if the following conditions are satisfied for all quality indicators:

\[
Q_{sv} \geq Q_{zv} \; (v = \overline{1,V}),
\]

and there is at least one the \( v^* \)-th \((1 \leq v^* \leq V)\) indicator for which the condition

\[
Q_{sv^*} > Q_{zv^*}
\]

is satisfied.

Here, all quality indicators must be minimized (the smaller the values of the quality indicators, the better the forecasting model).

The rank \( R_s \) must be calculated for every \( s \)-th forecasting model \((s = \overline{1,S})\). The rank \( R_s \) is equal to the quantity of the forecasting models in the population which dominate over the \( s \)-th forecasting model. The rank \( R_s \) of the \( s \)-th nondominated forecasting model is equal to zero \([15 – 16]\).

Let \( V = 2 \), \( Q_{sv1} = Aff_s \), \( Q_{sv2} = Tendency_s \), where \( Aff_s \) and \( Tendency_s \) are the values of the affinity indicator \((1)\) and the tendencies discrepancy indicator \((2)\) for the \( s \)-th forecasting model \((s = \overline{1,S})\) accordingly. Then the \( s \)-th forecasting model is dominated by the \( z \)-th forecasting model \((s = \overline{1,S} ; \; z = \overline{1,S})\), if the following conditions are satisfied:

\[
\begin{align*}
( Q_{sv1} \geq Q_{zv1} \text{ and } Q_{sv2} \geq Q_{zv2}) \lor ( Q_{sv1} > Q_{zv1} \text{ and } Q_{sv2} \geq Q_{zv2}), & \quad \text{that is} \\
( Aff_s \geq Aff_z \text{ and } Tendency_s \geq Tendency_z) \lor ( Aff_s > Aff_z \text{ and } Tendency_s \geq Tendency_z).
\end{align*}
\]

The crowding distances \( \tau_s \) \((s = \overline{1,S})\) can be calculated using the following algorithm \([15 – 17]\).

Step 1. To calculate ranks for all forecasting models in the population.

Step 2. For every group of the forecasting models:

- to sort the forecasting models according to each quality indicator value in ascending order of magnitude;
- to assign infinite distance to boundary values of the forecasting models in the group, i.e. \( \tau_1 = \infty \) and \( \tau_W = \infty \), where \( W \) is the quantity of the forecasting models in the \( w \)-th group \((w = \overline{1,W})\); \( W \) is the groups’ quantity; to assign \( \tau_s = 0 \) for \( s = 2,W - 1 \);
- to calculate the the crowding distance \( \tau_s \) as:

\[
\tau_s = \sum_{v=1}^{V} \frac{Q_{sv+1,v} - Q_{sv-1,v}}{Q_{vmax} - Q_{vmin}},
\]

where \( Q_{sv-1,v} \) and \( Q_{sv+1,v} \) are the values of the \( v \)-th quality indicator \((v = \overline{1,V})\) for the forecasting models with the numbers \((s-1)\) and \((s+1)\), which are the nearest “neighbors” for
the $s$-th model; $Q_v^{\min}$ and $Q_v^{\max}$ are the minimum and maximum values of the $v$-th quality indicator ($v = 1, V$) accordingly.

Figure 1 shows, how we can calculate the crowding distance on the base of two quality indicators. The points, marked with solid circles, correspond to the models with the minimum (zero) value of the rank (i.e. these points correspond to the Pareto front with the zero rank).

To calculate the crowding distance for the $s$-th forecasting model it is required to define values of both quality indicators for the $(s-1)$-th and the $(s+1)$-th models, which are the nearest “neighbors” for the $s$-th model and have the same rank. Also, it is necessary to define the best and worst values of each quality indicator (regardless of the decision rank). The crowding distances $\tau_s$ ($s = 1, S$) for the $s$-th forecasting model on the base of two quality indicators can be calculated as:

$$\tau_s = (Q_{s+1,2} - Q_{s+1,1})(Q_v^{\max} - Q_v^{\min}) + (Q_{s+1,2} - Q_{s+1,1})(Q_v^{\max} - Q_v^{\min})$$

At the realization of the MMCSA the $s$-th forecasting model will be better than the $z$-th forecasting model, if: $(R_s < R_z$) or $(R_s = R_z$ and $\tau_s > \tau_z$). If the $s$-th forecasting model is better, than the $z$-th forecasting model, the $s$-th forecasting model is the candidate for transfer into the new generation.

![Figure 1. The points using for calculation of the crowding distance.](image)

It should be noted that the forecasting models at the realization of the MMCSA will be exposed twice to the selection procedure providing the maintenance of a variety in the population: at first, when the suppression of antibodies has been carried out, and then, when the simultaneous analysis of values of ranks and values of the crowding distance has been executed.

The MMCSA can be described by the following sequence of steps.

Step 1. To generate initial population of antibodies. Each antibody is coded on the base of the SBT and represents some forecasting model.

Step 2. To perform the nondominated sorting to population of antibodies on the base of two quality indicators for the forecasting model (Aff and Tendency).

Step 3. To choose the parents-antibodies for the next generation of the clones-antibodies based on the values of the rank and crowding distance.

Step 4. To pass to step 5 if desirable values of the quality indicators are reached or the quantity of generations in the MMCSA is settled. Otherwise to pass to step 2.
Step 5. To accept the antibody with the minimum value of the affinity indicator (1) in the last population as the optimum decision. To use the forecasting model corresponding to this antibody for the forecasting.

As a result of application of the offered MMCSA the Pareto set of the nondominated forecasting models will be received. These models provide the best combinations of values of the used quality indicators for the forecasting models. The received forecasting models can be applied at the solution of a problem of the medium-term forecasting.

4. Experimental studies
To confirm the prospects of the MMCSA the experiments for 5 following TSs were conducted:

T1 (TS “The Brent crude oil price”; range of values: 15.12.2015 – 02.01.2016; unit of measure: ruble) = [46.04; 45.11; 44.46; 44.38; 44.30; 43.97; 44.70; 44.08; 45.92; 47.08; 47.32; 47.46; 48.05; 48.84; 50.25; 48.90; 49.50];

T2 (TS “Total number of the made energy resources”; range of values: 1992 – 2012 years; unit of measure: quadrillion Btus) = [47.99; 44.69; 42.30; 41.42; 39.35; 38.74; 39.07; 40.81; 41.70; 42.63; 44.16; 49.86; 51.05; 52.06; 52.52; 52.52; 50.01; 53.74; 54.63; 55.30];

T3 (TS “Number of Internet users per 100 people”; range of values: 1990 – 2014 years; unit of measure: percent) = [0.00000; 0.00067; 0.01345; 0.05382; 0.14815; 0.26975; 0.47296; 0.81274; 1.01899; 1.97723; 2.94437; 4.12827; 8.29886; 15.22667; 17.02328; 24.66000; 26.83000; 29.00000; 43.00000; 49.00000; 63.00000; 67.97000; 70.52000];

T4 (TS “Passenger traffic”; range of values: 1989 – 2012 years; unit of measure: millions passenger-kilometers) = [3669.202; 3635.441; 3305.227; 3145.413; 3087.016; 3251.615; 2714.314; 3268.434; 3743.247; 4249.406; 4648.123; 4489.569; 4651.419; 4726.832; 4986.468; 5054.200; 5482.314; 5655.296; 5129.103; 5987.268; 5933.041; 5973.308];

T5 (TS “Value added in agriculture”; range of values: 1992 – 2013 years; unit of measure: dollar) = [270112; 274000; 255000; 253200; 272475; 227102; 192117; 181200; 170300; 152900; 141042; 167100; 158000; 152900; 155573; 164272; 164262; 173699; 173411; 175800; 153500; 139028; 139842; 144612].

These TSs describe the macroeconomic indicators of the Russian Federation.

Values of the forward forecasting errors (for 1 – 5 steps forward) specify that the offered MMCSA is effective as for the solution of problems of the short-term forecasting (for 1 – 3 steps forward) as for the solution of problems of the medium-term forecasting (for 4 and 5 steps forward). It should be noted that use of the additional quality indicator of the forecasting model (the indicator \( Tendency \)) allowed carrying out the “search” of the forecasting model in the necessary (correct) direction. As a result, for all reviewed examples of time series for the small number of generations of the MCSA the smaller values of the affinity indicator \( Aff \) (training error (1)) and in most cases the smaller values of the forecasting errors for 1 – 5 steps forward were received (table 1). These errors were calculated on the base of 1000 program runs for 100 generations of population. The size of population is set by 20 antibodies. Results of the forecasting for TS “The Brent crude oil price” have been presented in figures 2 and 3. These results are received with use of the forecasting models on the base of one and two quality indicators respectively.

The presented graphic dependences show that the second model repeats the mathematical law of initial TS for the training set of data better than the first one. Moreover, this feature is kept also for the test set (when the forecasting for 5 steps forward is carried out). Herewith, the forecasting model on the base of two quality indicators (\( Aff \) and \( Tendency \)) demonstrates the best survival for the extended forecasting horizon than the forecasting model on the base of one quality indicator (\( Aff \)). Besides, this model is more effective for the short-term forecasting. The same results had been obtained for all other TSs.

Also, both variants of optimization have been applied for the development of the forecasting models intended for forecasting of the names' references' quantity of the E-Commerce systems in the requirements to vacancies posted on the websites of 2 famous recruiting network services –
HeadHunter.ru (Russia) and Indeed.com (USA). Each of the TSs contains the information on the number of vacancies which include a specific keyword (Magento, OpenCart, PrestoShop, Hybris, Demandware). This keyword defines the name of E-Commerce system for development of online stores. Herewith, 7 TSs have been considered: 4 TSs with information on vacancies in Russia and 3 TSs with information on vacancies in USA.

The chosen TSs have the different number of elements, the scale level of elements values, sampling points, amplitude and period. It allows considering the further conclusions universal.

Table 1. The forecasting errors.

| Error type          | Forecasting error with use of Aff (%) | Forecasting error with use of Aff (%) and Tendency |
|---------------------|--------------------------------------|---------------------------------------------------|
| TS #1 (“The Brent crude oil price”) |                                      |                                                   |
| Training error (1)  | 3.12                                 | 1.10                                              |
| Error for 1 step    | 1.43                                 | 0.22                                              |
| Error for 2 step    | 0.85                                 | 0.01                                              |
| Error for 3 step    | 0.67                                 | 0.38                                              |
| Error for 4 step    | 1.06                                 | 0.22                                              |
| Error for 5 step    | 0.45                                 | 0.57                                              |
| Average error       | 0.89                                 | 0.28                                              |
| TS #2 (“Total number of the made energy resources”) |                                      |                                                   |
| Training error (1)  | 5.23                                 | 2.89                                              |
| Error for 1 step    | 1.14                                 | 0.62                                              |
| Error for 2 step    | 0.87                                 | 0.20                                              |
| Error for 3 step    | 1.53                                 | 0.73                                              |
| Error for 4 step    | 0.29                                 | 0.29                                              |
| Error for 5 step    | 0.97                                 | 0.68                                              |
| Average error       | 0.96                                 | 0.50                                              |
| TS #3 (“Number of Internet users per 100 people”) |                                      |                                                   |
| Training error (1)  | 5.49                                 | 3.29                                              |
| Error for 1 step    | 1.48                                 | 0.57                                              |
| Error for 2 step    | 3.75                                 | 0.13                                              |
| Error for 3 step    | 7.41                                 | 0.65                                              |
| Error for 4 step    | 5.86                                 | 0.12                                              |
| Error for 5 step    | 9.14                                 | 0.42                                              |
| Average error       | 5.53                                 | 0.38                                              |
| TS #4 (“Passenger traffic”) |                                      |                                                   |
| Training error (1)  | 5.47                                 | 2.54                                              |
| Error for 1 step    | 1.58                                 | 1.75                                              |
| Error for 2 step    | 2.84                                 | 1.42                                              |
| Error for 3 step    | 3.54                                 | 1.98                                              |
| Error for 4 step    | 3.17                                 | 1.10                                              |
| Error for 5 step    | 3.69                                 | 1.38                                              |
| Average error       | 2.96                                 | 1.52                                              |
| TS #5 (“Value added in agriculture”) |                                      |                                                   |
| Training error (1)  | 3.98                                 | 2.75                                              |
| Error for 1 step    | 0.82                                 | 0.82                                              |
| Error for 2 step    | 1.37                                 | 0.54                                              |
| Error for 3 step    | 1.89                                 | 0.86                                              |
| Step       | Error | for 5 step | Average error |
|-----------|-------|------------|---------------|
|           | 2.29  | 1.09       | 2.27          |
|           | 3.97  | 0.22       | 0.71          |

**Figure 2.** Forecasting of the TS “The Brent crude oil price” (with one quality indicator (\(\text{Aff}\))).

**Figure 3.** Forecasting of the TS “The Brent crude oil price” (with two quality indicators (\(\text{Aff}\) and \(\text{Tendency}\))).

**Figure 4.** Forecasting of the TS “Magenta (USA)” (with one quality indicator (\(\text{Aff}\))).

**Figure 5.** Forecasting of the TS “Magenta (USA)” (with two quality indicators (\(\text{Aff}\) and \(\text{Tendency}\))).

Forecasting for each TS was executed with use of one (\(\text{Aff}\)) and two (\(\text{Aff}\) and \(\text{Tendency}\)) quality indicators of the forecasting model. The average errors values of the forecasting are presented in Table 1. Figure 4 shows the forecasting results for the TS “Magenta (USA)” on the base of the MCSA. Figure 5 shows the forecasting results for the TS “Magenta (USA)” on the base of the MMCSA. These results have been received under the same conditions that were in the experiment considered above. It is obvious that in this case the MMCSA has worked also better, than the MCSA. Herewith, the time expenditures have not increased practically (they are equal to 133.483 seconds and 136.984 seconds respectively).

The same results had been obtaited for all other TSs. It should be noted a problem which was revealed for this ts group of TSs. It is the problem of the choice of urgent length of the training data sequence. This problem undoubtedly requires the fastest solution.

The obtained forecasting results allow making the following conclusion: the use of the second quality indicator of the forecasting model provides a way to increase the life time of the forecasting model.
The efficiency of the forecasting model for performing of the short-term forecasts is saved, that, in general, confirms the success of the offered MMCSA based on the ideas of the “Pareto dominance”. Herewith, the computing complexity of the MMCSA is \( O(M(N + N_c)^2) \), where \( M \) is the number of the quality indicators \( (M=2) \), \( N \) is the population size, \( N_c \) is the clone population size.

5. Conclusions

Initially, the basic MCSA was developed for solving the short-term forecasting problems. However, the fulfilled researches showed the possibility of application of the MMCSA for solving the medium-term forecasting problems. Herewith, the computing complexity of the MMCSA increases slightly.

It has been proved during the experiments on forecasting of the macroeconomic indicators of the Russian Federation and others, that the application of the principles of the Pareto dominance is the effective solution of the account’s problem of the several quality indicators at the development of the forecasting models, which represent the analytical dependences on the base of the SBT.

Further, it is planned to use the offered MMCSA at the realization of the forecasting method for the groups of TSs, when it is necessary to create the general forecasting models for each cluster of TSs. The k-means algorithm, the FCM algorithm and some others will be involved in an experiment.

The application of the MMCSA will allow giving the more exact description of the TS centroids of clusters, and, as a result, to increase the forecasting accuracy. Herewith, any general forecasting model can be specified for some private TS in the cluster (if it is necessary) with the use of the same multiobjective optimization algorithm.

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