

Evolutionary Support Vector Machines for Time Series Forecasting

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Abstract. Time Series Forecasting (TSF) uses past patterns of an event in order to predict its future values and is a key tool to support decision making. In the last decades, Computational Intelligence (CI) techniques, such as Artificial Neural Networks (ANN) and more recently Support Vector Machines (SVM), have been proposed for TSF. The accuracy of the best CI model is affected by both the selection of input time lags and the model's hyperparameters. In this work, we propose a novel Evolutionary SVM (ESVM) approach for TSF based on the Estimation Distribution Algorithm to search for the best number of inputs and SVM hyperparameters. Several experiments were held, using a set of six time series from distinct real-world domains. Overall, the proposed ESVM is competitive when compared with an Evolutionary ANN (EANN) and the popular ARIMA methodology, while consuming less computational effort when compared with EANN.

Keywords: Evolutionary Computation, Support Vector Machines, Time Series, Forecasting.

1 Introduction

Forecasting the future using past data is an important tool to reduce uncertainty and support both individual and organization decision making. In particular, multi-step ahead predictions (e.g., issued several months in advance) are useful to aid tactical decisions, such as planning production resources or evaluating alternative economic strategies [2]. The field of Time Series Forecasting (TSF) deals with the prediction of a given phenomenon (e.g., umbrella sales) based on the past patterns of the same event. TSF has become increasingly used in distinct areas such as Agriculture, Finance, Production or Sales [14].

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Several Operational Research TSF methods have been proposed, such as Holt-Winters (in the sixties) or the ARIMA methodology [14] (in the seventies). More recently, several Computational Intelligence (CI) methods have been applied to TSF, such as Artificial Neural Networks (ANN) [12,6], and Support Vector Machines (SVM) [15,9,3]. CI models such as ANNs and SVMs are natural solutions for TSF, since they are more flexible (i.e., no *a priori* restriction is imposed) when compared with classical TSF models, presenting nonlinear learning capabilities. When compared with ANN, SVM presents theoretical advantages, such as the absence of local minima in the learning phase.

When applying these CI methods to TSF, variable and model selection are critical issues. A sliding time window is often used to create a set of training examples from the series. A small time window will provide insufficient information, while using a large number of time lags will increase the probability of having irrelevant inputs. Thus, variable selection is useful to discard irrelevant time lags, leading to simpler models that are easier to interpret and that usually give better performances [4,9,6]. On the other hand, CI models such as ANN and SVM have hyperparameters that need to be adjusted (e.g., number of ANN hidden nodes or kernel parameter) [8]. Complex models may overfit the data, losing the capability to generalize, while a model that is too simple will present limited learning capabilities.

Several hybrid systems, which combine two or more CI techniques, have also been proposed for TSF, such as Evolutionary ANN (EANN) [4]. Most EANNs use the standard Genetic Algorithm (GA). More recently, the Estimation Distribution Algorithm (EDA) was proposed [13]. Such algorithm uses exploitation and exploration properties to find a good solution. In [16], EDA was used as the search engine of an EANN, outperforming a GA based EANN. Following this result, in this paper we propose a novel Evolutionary SVM (ESVM) approach based on the EDA engine, in order to automatically select the best SVM multi-step ahead forecasting model. Moreover, we also compare ESVM with the EANN proposed in [16] and the popular ARIMA methodology.

The paper is organized as follows. First, Section 2 describes the ESVM approach. Next, Section 3 presents the experimental setup and the obtained results. Finally, the paper is concluded in Section 4.

2 Evolutionary Support Vector Machine

2.1 Time Series Forecasting

The problem of TSF using CI models, such as ANN [16] or SVM [3], is considered as obtaining the relationship from the value at period y_t and the values from previous elements of the time series, using several time lags $\{t-1, t-2, \dots, t-I\}$, to obtain a function as it is shown in [16]:

$$\hat{y}_t = f(y_{t-1}, y_{t-2}, \dots, y_{t-I}) \quad (1)$$

where \hat{y}_t denotes the estimated forecast as given by the function f (e.g., SVM), and I the number of input values.

In order to obtain a single model to forecast time series values, an initial step has to be done with the original values of the time series, i.e., normalizing the data. The original values (y_t) are normalized into the range $[0, 1]$ (leading to the N_t values). Once the model outputs the resulting values, the inverse process is carried out, rescaling them back to the original scale. Only one output was chosen and multi-step ahead forecasts are built by iteratively using 1-ahead predictions as inputs [4]. Therefore, the time series is transformed into a patterns set depending on the I inputs of a particular model, each pattern consisting of:

- I inputs values: with the I -th normalized previous values $N_{t-1}, N_{t-2}, \dots, N_{t-I}$.
- one output value: N_t (the desired target).

This patterns set will be used to train and validate each model generated during the evolutionary execution. Thus, the patterns set is split into two subsets, training (with the first 70% elements of the series) and validation (with the remaining ones), under a timely ordered holdout scheme.

2.2 Evolutionary Support Vector Machine Design

The problem of designing SVM for TSF can be seen as a search problem into the space of all possible solutions. While several Evolutionary Computation methods could be used for this search, we adopt the EDA algorithm, since it has outperformed the standard GA in our previous work [16]. When designing a ESVM, there are three crucial issues: i) setting the solution's space, i.e., what information of the SVM is previously set and what is included into the chromosome; ii) how each solution is codified into a chromosome, i.e., encoding schema; and iii) what are we optimizing, i.e., defining the fitness function.

When designing a SVM, there are three crucial issues it should be taken into account: the type of SVM to use, the selection of the kernel function and tuning the parameters associated with the two previous selections. Since TSF is a particular regression case, for the SVM type and kernel, we selected the popular ε -insensitive loss function (known as ε -SVR) and Gaussian kernel combination, as implemented in the LIBSVM tool [1]. In SVM regression [17], the input $\mathbf{y} = (y_{t-k_I}, \dots, y_{t-k_2}, y_{t-k_1})$, for a SVM with I inputs, is transformed into a high m -dimensional feature space, by using a nonlinear mapping (ϕ) that does not need to be explicitly known but that depends of a kernel function. Then, the SVM algorithm finds the best linear separating hyperplane, tolerating a small error (ε) when fitting the data, in the feature space:

$$\hat{y}_t = w_0 + \sum_{j=1}^m w_j \phi_j(\mathbf{y}) \tag{2}$$

This model requires setting three parameters: γ – the Gaussian kernel parameter, $\exp(-\gamma \|x - x'\|^2)$, $\gamma > 0$; C – a trade-off between fitting the errors and the flatness of the mapping; and ε – the width of the ε -insensitive tube.

In this paper, an evolving hybrid system that uses EDA and SVM, is adopted. Following the suggestion of the LIBSVM authors [1], SVM parameters are

searched in terms an exponentially growing scale. We also take into account the number of input values of the time series (I) used to train the SVM. Therefore, we adopt a direct encoding scheme, using a numeric representation with 8 genes, according to the chromosome $g_1g_2g_3g_4g_5g_6g_7g_8$, such that:

$$\begin{aligned} I &= \text{round}(\alpha \cdot n \cdot \frac{10g_1+g_2+1}{100}), \quad g_1 \in \{0, 1, \dots, 9\} \wedge g_2 \in \{0, 1, \dots, 9\} \\ \gamma &= 2^{(g_3+\frac{g_4}{10})-5}, \quad g_3 \in \{-9, -8, \dots, 9\} \wedge g_4 \in \{-9, -8, \dots, 9\} \\ C &= 2^{(g_5+\frac{g_6}{10})+5}, \quad g_5 \in \{-9, -8, \dots, 9\} \wedge g_6 \in \{-9, -8, \dots, 9\} \\ \varepsilon &= 2^{(g_7+\frac{g_8}{10})-8}, \quad g_7 \in \{-9, -8, \dots, 9\} \wedge g_8 \in \{-9, -8, \dots, 9\} \end{aligned} \quad (3)$$

where g_i denotes the i -th gene of the chromosome. The input search range includes only integer numbers, due to the use of round function, and depends on n , the length of the time series (#in-samples or training data), scaled by a constant α factor. Based on our previous research using EANN for TSF [16], we set $\alpha = 0.45$. Thus, the ranges for the search space are: I , depends on the series length (e.g., $I \in \{3, 7, 10, 13, 17, \dots, 331\}$ for Quebec); $\gamma \in 2^{[-14.9, 4.9]}$; $C \in 2^{[-4.9, 14.9]}$; and $\varepsilon \in 2^{[-17.9, 1.9]}$.

The evolutionary process consists of the following steps:

1. First, a randomly generated population (composed of to 50 individuals), i.e., a set of randomly generated chromosomes, is obtained.
2. The phenotypes (SVM model) and fitness value of each individual of the actual generation is obtained. This includes the steps:
 - (a) The phenotype of an individual of the actual generation is first obtained (using LIBSVM [1]).
 - (b) Then, for each model, training and validation subsets are obtained from time series data depending on the number of inputs nodes, as it was explained in Section 2.1.
 - (c) The model is fitted using the Sequential Minimal Optimization algorithm, as implemented in LIBSVM. The fitness for each individual is given by the Mean Squared Error (MSE) validation error, during the learning process. The aim is to reduce extreme errors (e.g., outliers) that can highly affect multi-step ahead forecasts. Moreover, preliminary experiments (with time series not present in Table 1), have shown that this choice leads to better forecasts when compared with absolute errors.
3. Once the fitness values for whole population have been already obtained, UMDA-EDA (with no dependencies between variables) [16] operators (selection, estimation of the empirical probability distribution and sampling solutions) are applied in order to generate the population of the next generation, i.e., a new set of chromosomes.
4. Steps 2 and 3 are iteratively executed until a maximum number of generations is reached.

The parameters of the EDA (e.g., population size of 50) were set to the same values used by the EANN proposed in [16]. Since the EDA works as a second order optimization procedure, the tuning of its internal parameters is not a critical issue (e.g., using a population of 48 does not does not substantially change the results). Also, this EDA has a fast convergence (shown in Fig. 1).

3 Experiments and Results

3.1 Time Series

We selected a total of six time series, with different characteristics and from distinct domains (Table 1). Five series were selected from the well-known Hyndman’s time series data library repository [10]. These are named Passengers, Temperature, Dow-Jones, Quebec and Abraham12. We also adopt the Mackey-Glass series, which is a common nonlinear benchmark. It should be noted that these six times series were also adopted by the *NN3* and *NN5* forecasting competitions [5]. Except for Mackey-Glass, all datasets are from real-world domains and such data can be affected by external issues (e.g., strikes), which make them interesting datasets and more difficult to predict.

Table 1. Time series data

Series	Description	#in-samples	#out-of-samples (H)
Passengers	monthly int. airline passengers	125	19
Temperature	monthly air temp. at Nottingham	206	19
Dow-Jones	monthly index closings (1968-81)	129	19
Abraham12	gasoline demand at Ontario	168	24
Quebec	daily number of births at Quebec	735	56
Mackey-Glass	chaotic series	735	56

3.2 Evaluation

The Symmetric Mean Absolute Percentage Error (SMAPE) is given by [11]:

$$SMAPE = \frac{1}{H} \sum_{t=T+1}^{T+H} \frac{|e_t|}{(|y_t| + |\hat{y}_t|)/2} \times 100\% \quad (4)$$

where $e_t = y_t - \hat{y}_t$, T is the current time period and H is the forecasting horizon, the number of multi-step ahead forecasts. SMAPE is a popular forecasting metric that has the advantage of being scale independent when compared with MSE, thus can be more easily used to compare methods across different series, ranging from 0% to 200%. SMAPE was also the error metric used in *NN3*, *NN5* and *NINGC1* forecasting competitions [5].

3.3 Results

For the comparison, we have chosen the EANN presented in [16], which is similar to ESVM except that it uses a multilayer perceptron trained with the RPROP algorithm, as implemented using the SNNS tool [18]. EANN optimizes the number of inputs ($I \in \{1, \dots, 100\}$) and hidden nodes (from 0 to 99) and the RPROP parameters ($\Delta_0 \in \{1, 0.01, 0.001, \dots, 10^{-9}\}$ and $\Delta_{max} \in \{0, 1, \dots, 99\}$). Both the

Table 2. Forecasting errors (%SMAPE, best values in **bold**) and best SVM models

Time Series	ARIMA	EANN	ESVM	$I \gamma$	C	ϵ
Passengers	4.50	3.39	5.35	14 $2^{-4.1}$	$2^{12.7}$	$2^{-8.6}$
Temperature	3.42	3.51	4.42	79 $2^{-1.9}$	$2^{-0.5}$	$2^{-8.8}$
Dow-Jones	4.78	6.28	6.35	19 $2^{-13.3}$	$2^{10.5}$	$2^{-5.3}$
Abraham12	6.20	4.71	4.86	28 $2^{-13.1}$	$2^{14.9}$	$2^{-15.0}$
Quebec	10.36	10.83	9.31	301 $2^{-13.6}$	$2^{12.7}$	$2^{-16.3}$
Mackey-glass	26.20	7.06	1.32	10 $2^{2.0}$	$2^{1.70}$	$2^{-16.0}$
Average	9.24	5.96	5.27			
Median	5.49	5.49	5.11			

ESVM and EANN experiments were conducted using code written in the C language by the authors. As the stopping criterion, we used a maximum of 100 generations for ESVM and EANN. For a baseline comparison, we have also chosen the ARIMA methodology, as computed by the ForecastPro© tool [7]. The rationale is to use a popular benchmark that can easily be compared and that does not require expert model selection capabilities from the user. The obtained results are shown in Table 2 (SMAPE errors and best SVM models).

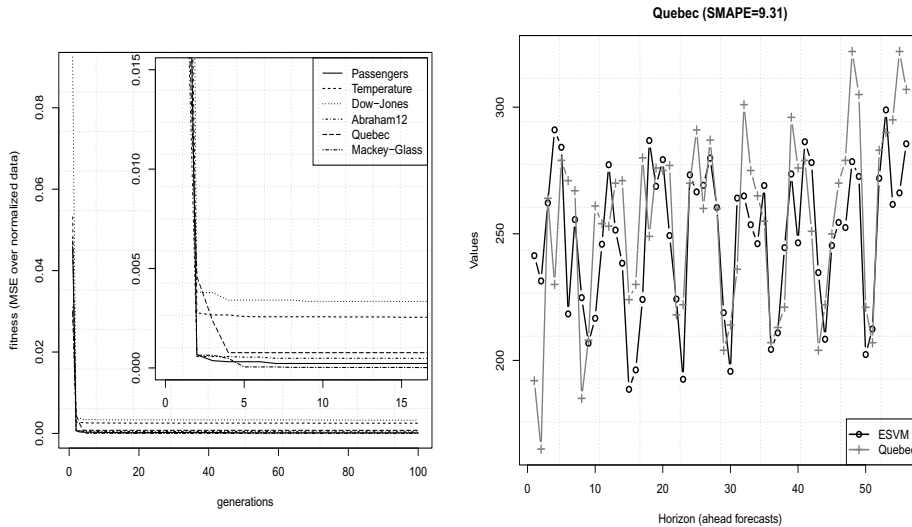


Fig. 1. Evolution of the ESVM best fitness value for all series (left, includes a zoom of the bottom left area) and example of the ESVM forecasts for Quebec (right)

An analysis to tables shows that the proposed ESVM provides interesting forecasts when compared with EANN and ARIMA. Each forecasting approach is the best option for two series. Yet, ESVM provides the lowest average and median (over all series, last two rows) results. The left of Fig. 1 plots the evolution of

Table 3. Comparison of computational effort required by ESVM and EANN

Time Series	EANN time (min)	ESVM time (min)	R_t
Passengers	165	5	96.7%
Temperature	315	6	98.1%
Dow-Jones	161	3	98.2%
Abraham12	420	6	98.6%
Quebec	6603	95	98.5%
Mackey-glass	5649	105	98.1%

the best fitness values for ESVM (left), showing a fast convergence of the EDA algorithm for all series. For demonstration purposes, the right of Fig. 1 plots the ESVM forecasts for Quebec, showing a good fit.

The experimentation was carried out with an exclusive access to a server (Intel Xeon 2.27 GHz processor using Linux). Table 3 shows the computational time (in minutes) required by each evolutionary method and series. The last column shows in percentage, the reduction of computational effort obtained by ESVM when compared with EANN, where $R_t = 1 - (t_{\text{ESVM}}/t_{\text{EANN}})$ and t_M is the time required for model M . As shown by the table, ESVM consumes much less computational effort in all the time series tested. It can be observed a reduction rate of at least 96% in all cases.

4 Conclusions

This paper proposes a novel Evolutionary Support Vector Machine (ESVM) method for multi-step ahead TSF, which automatically searches best number of inputs and SVM hyperparameters. The proposed ESVM was compared against two approaches, an Evolutionary Artificial Neural Network (EANN) and the popular ARIMA methodology. The experiments held using six time series from distinct domains, revealed the proposed ESVM as the best forecasting method. Moreover, when compared with EANN, ESVM requires much less computational effort, with a reduction rate (in terms of time elapsed) greater than 96%. Thus, ESVM is a good tool to quickly obtain accurate forecasts and this is a useful characteristic for several TSF domains, such as critical or control systems. In the future, we intend to address other SVM kernels (e.g., Polynomial) and extend the experimentation to include time series from more domains (e.g., Medical data).

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