

Set-membership Affine Projection Algorithm with Selective Regressors

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Abstract. In this letter, the concept of set-membership filtering (SMF) is extended to the affine projection algorithm with selective regressors (SR-APA), a novel set-membership SR-APA (SM-SR-APA) is established. The proposed algorithm exhibits superior performance with significant reduction in overall computational complexity due to data-selective step size. The usefulness of the proposed algorithms was demonstrated through simulations.

Keywords: set-membership filtering; affine projection; data-selective; system identification

1. Introduction

In adaptive filtering, the affine projection algorithm (APA) is attractive due to its fast convergence [1]-[2]. However, its complexity is still too high for many applications. To improve the performance of the APA, the selective regressor APA (SR-APA) [3] have been recently proposed by selecting a subset of a fixed number of members from the input vectors at every adaption. Another approach to reduce computational complexity in adaptive filtering is set-membership filtering (SMF) [4]-[6], which feature reduced complexity due to data-selective updates. Based on the concept of SMF, Werner and Diniz proposed a simple SM-APA [5] with data-selective adaption. To further reduce the overall computational complexity the SM-APA with variable data-reuse factor (SM-APA vdr) [6] was presented by utilizing the information provided by the data-dependent step size. In this paper we extended the SMF concept to the SR-APA, and established a set-membership version SR-APA (SM-SR-APA). The proposed algorithm exhibits superior performance with significant reduction in the overall computational complexity compared with the original SR-APA.

2. Improved SM-APA

In SMF the weight vector \mathbf{w}_k is updated such that the magnitude of the output estimation error, $e_k = d_k - \mathbf{w}_{k-1}^T \mathbf{x}_k$, is less than or equal to a deterministic threshold γ for all possible input desired signal pairs. where x_k , d_k and e_k are the input, the desired and the output error signals, respectively. \mathbf{w}_k is the $L \times 1$ column vector of filter coefficients at time k . As a result of the bounded error constraint, there will exist a set of filters rather than a single estimate.

The SM-NLMS algorithm [4] uses only one constraint set in the adaptation whereas the SM-APA uses multiple constraint sets. The SM-APA performs weight adaption such that the updated weight vector belongs to the constraint sets at the P most recent iterations [5]. The weight update of SM-APA is performed as follows:

$$\mathbf{w}_{k+1} = \begin{cases} \mathbf{w}_k + X_k (X_k^T X_k)^{-1} (E_k - G_k) & |e_k| > \gamma \\ \mathbf{w}_{k+1} & \text{otherwise} \end{cases} \quad (1)$$

where $G_k = [g_k \ g_{k-1} \ \dots \ g_{k-P+1}]^T$ is the error-bound vector, $D_k = [d_k \ d_{k-1} \ \dots \ d_{k-P+1}]^T$ is the desired signal vector, $X_k = [x_k \ x_{k-1} \ \dots \ x_{k-P+1}]$ is the input signal matrix, and $\mathbf{x}_k = [x_k \ x_{k-1} \ \dots \ x_{k-L+1}]^T$ is the input-signal vector, $E_k = D_k - X_k^T \mathbf{w}_k$ is

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the $P \times 1$ error vector, i.e., $[e_k \ e_{k-1} \dots e_{k-P+1}]^T$, and e_k is the first element of E_k . The choice of G_k can vary for different problems. Werner and Diniz proposed a particularly simple SM-APA [5] by assigning $g_{k-i+1} = d_{k-i+1} - w_k^T x_{k-i+1}$ for $i \neq 1$ to a *posteriori* error and $g_k = e_k / |e_k|$. However, in the particular case of variable data reuses number, the simplified version is no longer guaranteed to provide $|e_{k-i+1}| \leq \gamma$ for $i \neq 1$, to overcome this problem, the authors in [6] provided an algorithm that choose the elements of error-bound vector G_k as follows

$$g_{k-i+1} = \begin{cases} \gamma \text{sign}(e_{k-i+1}), & \text{if } |e_{k-i+1}| > \gamma \\ e_{k-i+1}, & \text{otherwise} \end{cases} \quad (2)$$

for $i=1,2,\dots,P$. With the above choice G_k , the SM-APA recursions become

$$w_{k+1} = \begin{cases} w_k + X_k (X_k^T X_k)^{-1} \Lambda_k E_k & \text{if } |e_k| > \gamma \\ w_k & \text{otherwise} \end{cases} \quad (3)$$

Where $\Lambda_k = \text{diag}(\mu_k(1), \mu_k(2), \dots, \mu_k(P))$ is a diagonal matrix with

$$\mu_k(i) = \begin{cases} 1 - \gamma / |E_k(i)| & \text{if } |E_k(i)| > \gamma \\ 0 & \text{otherwise} \end{cases} \quad \text{for } i=1,2,\dots,P.$$

To distinguish from the SM-APA in [5], we name it SM-APA with Matrix Step-size (SM-APA-M). Specially, by setting $\mu_k = \mu_k(1) = \dots = \mu_k(P)$ we can get a simpler version of the above recursion as follows:

$$w_{k+1} = w_k + \mu_k X_k (X_k^T X_k)^{-1} E_k \quad (4)$$

Where

$$\mu_k = \begin{cases} 1 - \gamma / |E_k(1)| & \text{if } |E_k(1)| > \gamma \\ 0 & \text{otherwise} \end{cases}$$

We call it SM-APA with uniform step-size (SM-APA-U).

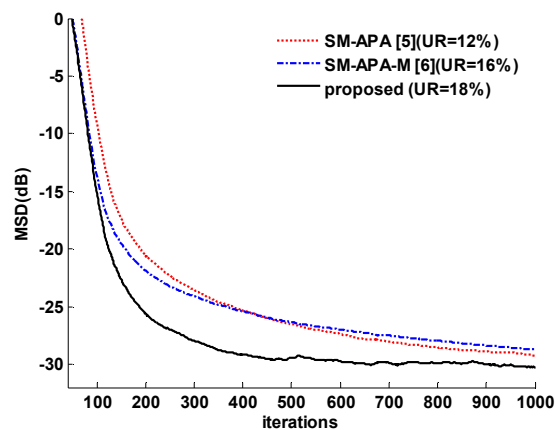


Fig.1 the proposed SM-APA compared with SM-APA [5] and SM-APA-M [6]

Fig.1 shows the convergence curves of three SM-APA algorithms with their update rate (UR) in the brackets. It is seen that the improved SM-APA-U has the fastest convergence as well as lowest steady-state misadjustment. The SM-APA-M in [6] has similar performance to the SM-APA in [5]. In the following context, we take the SM-APA-U as default benchmark in comparison with other algorithms, and we call it SM-APA simply on the premise of no confusion.

3. The Proposed SM-SR-APA

The SR-APA in [3] tends to reduce the computational complexity of the conventional APA by selecting K input regressors among P given input regressors ($K \leq P$). Let $T_K = \{t_1, t_2, \dots, t_K\}$ denote a K -subset (subset with K members) of the set $\{1, 2, \dots, P\}$, t_k denotes the indexes of the selected input regressors. Due to the high complexity associated with the subset selection, the authors in [3] circumvented it with an alternative simplified algorithm by focusing only on the diagonal components.

The simplified SR-ARA algorithm has faster convergence speed than the conventional APA. However, it still involves large computations in weight update and additional sort routine. To reduce computational complexity further, we incorporate the method of SM-APA with the SR-APA, and establish SM-SR-APA algorithm, which is formulated in Tab.1.

Tab.1 SM-SR-APA formulation

Initialization: $W_0 = \mathbf{0}, \gamma = \sqrt{5}\sigma_v$

Iterations:

$$E_k = D_k - X_k^T W_{k-1}$$

if $|E_k(1)| > \gamma$

% Select K max regressors and errors among P

$$T_k = \text{sort} (E_k^2(i) / \|X_k(:, i)\|); i \in \{1, 2, \dots, P\}$$

% Where T_k is K -subset among P regressors

$$X_{T_k} = X_k(:, T_k(1:K));$$

$$E_{T_k} = E_k(T_k(1:K));$$

$$W_k = W_{k-1} + (1 - \gamma / |E_k(1)|) X_{T_k} (X_{T_k}^T X_{T_k})^{-1} E_{T_k}$$

else $W_k = W_{k-1};$

end;

The introduction of Set-membership step-size involves one additional division and one additional comparison respectively. Experimental results show that the proposed SM-SR-APA can reduce over 70% calculations associated with weight update and additional sort routine due to sparse time update.

4. Simulation Results

We illustrate the performance of the proposed algorithms by carrying out computer simulations in a channel identification scenario. The unknown channel has 32 taps and is selected at random. We assume that both adaptive filter and the unknown channel have the same number of taps. The input signals are obtained by filtering a white, zero-mean, Gaussian random sequence through a second-order system $G(z) = (1 + 0.6z^{-1}) / (1 + 1.0z^{-1} + 0.21z^{-2})$. The measurement noise $v(n)$, with SNR=30dB was added to the noise

free desired signal. The mean square deviation (MSD), $E\|\mathbf{w}^o - \mathbf{w}_k\|^2$, is employed as performance evaluation by ensemble averaging over 100 independent trials. In simulation the parameters are set as follows:

$K=8, P=16, L=32, \gamma = \sqrt{5}\sigma_v$ for two SM-APAs, and $\mu=1$ for APA and SR-APA. The selection ratio (K/P) is set $r=0.5$ for SR-APA and SM-SR-APA.

Fig.1 shows the MSD learning curves of the proposed SM-APA compared with SM-APA in [5] and SM-APA-M in [6]. We can see that the proposed SM-APA has superior convergence and misadjustment performance at the expense of a slightly higher update rate.

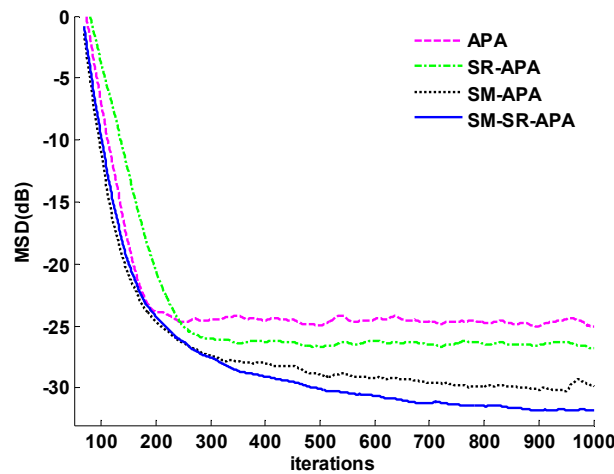


Fig.2 MSD learning curves in stationary signal and Gaussian noise

Fig.2 shows the MSD learning curves of APAs in Gaussian noise and stationary input signal. We can see the proposed SM-SR-APA has lowest steady-state misadjustment with comparable convergence rate with others. The two SMFs have similar update rate (UR): UR=12.1% for SM-SR-APA and UR=12.2% for SM-APA.

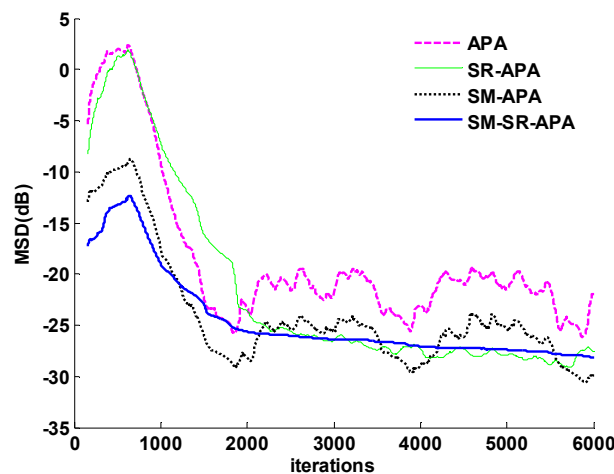


Fig.3 MSD learning curves of the proposed algorithms,

In Fig.3, we consider an echo cancellation with speech input signals sampled at 8 KHz and an echo path of model 5 in [7] with ERL=12dB. The MSD curves are obtained by ensemble averaging over 50 independent trails with the following parameters: SNR=20dB, K=8, P=16, L=96 and $\mu=1$. The update rates for two SMFs are: 13.1% for SM-SR-APA and 21.2% for SM-APA. As can be seen in Fig. 3, the proposed SM-SR-APA exhibits fast initial convergence and robust steady-state misadjustment in speech signals.

5. Conclusions

In this letter, we extend the SMF concept into the SR-APA, and a novel SM-SR-APA was proposed. The introduction of set-membership step-size reduced overall computation complexity significantly due to sparse time update. Simulation results show the SM-SR-APA exhibits superior to other algorithms in terms of lower computational complexity and misadjustment as well as comparable convergence rate.

6. References

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