

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:

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

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, $E_k = D_k - X_k^T W_k$ 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 *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).

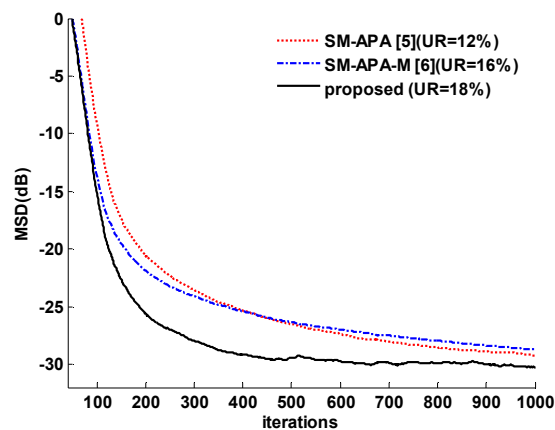


Fig.1 the proposed SM-APA compared with SM-APA [5] and SM-APA-M [6]