ONLINE EMPIRICAL MODE DECOMPOSITION

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ABSTRACT

The success of Empirical Mode Decomposition (EMD) resides in its practical approach to dissect non-stationary data. EMD repetitively goes through the entire data span to iteratively extract Intrinsic Mode Functions (IMFs). This approach, however, is not suitable for data stream as the entire data set has to be reconsidered every time a new point is added. To overcome this, we propose Online EMD, an algorithm that extracts IMFs on the fly. The two key elements of Online EMD are a sliding window to compute local IMFs, and a stitching procedure to gradually append local IMFs to the final result. Using synthetic data we show that the decomposition quality of Online EMD is similar to classical EMD. We also present results obtained with a real data set to expose the practical advantages of Online EMD when dealing with data stream or large data set.

Index Terms— Empirical Mode Decomposition, online analysis, data stream

1. INTRODUCTION

Empirical Mode Decomposition (EMD) [1, 2] is an algorithm that dissects a non-stationary signal into a collection of additive oscillatory components. The core of EMD is the so called sifting procedure that extracts locally the higher frequency component from a signal. By iteratively sifting the data remaining after each extraction, EMD uncovers a finite set of non-stationary and oscillatory components with decreasing frequencies. These components are called Intrinsic Mode Functions (IMF) and satisfy the two following requirements: the number of zero crossings and extrema differ by at most one, and the two envelopes defined by the local maxima and local minima are symmetric with respect to zero.

Thanks to its practical approach, EMD has been successfully applied to a wide range of datasets [2], including medical [3], earthquake [4], and power consumption data [5, 6]. Nevertheless, the applications of EMD to large datasets (e.g. medical data with high sampling rate or data stream from sensor network) are particularly difficult due to an inherent drawback of the current algorithm. Namely, as each sifting step considers the entire data span, EMD (1) is not able to analyze data in real time (i.e. while it is collected), (2) requires increasing computational resources to store and analyze a growing data, and (3) converges in a number of sifting steps that increases for long data, hence causing over-sifting issues.

These drawbacks have been firstly addressed by processing the signal in a blockwise fashion [7, 8, 9, 10]. However, merging the IMFs of two sequential blocks is prone to discontinuities due to the border effect of EMD. Faltermeier et al. have proposed the weighted sliding EMD (wSEMD) that applies EMD on overlapping blocks and prevent discontinuities by merging the results with a smoothing function [11, 12]. To avoid blocks with a discordant number of IMFs, wSEMD restrains a constant number of sifting steps and IMFs for all analyzed blocks. Following a different approach, Chang et al. [13] have proposed a real-time EMD processor based on an online spline interpolation that suffers the same limitations. These two constraints (i.e. fix number of sifting and IMFs), however, fundamentally interfere with the adaptive and intuitive approach of EMD. Thus, this approach weakens one of the prime benefits of EMD that is its ability to empirically discover intrinsic components of an unexplored signal.

In this article, we leverage the sliding approach of wSEMD in a new algorithm called Online EMD. This new algorithm shares the same advantages as wSEMD (i.e. low computation and low memory requirements for analyzing data stream) while preserving the essence of EMD. Indeed, Online EMD gradually discovers and extracts fastest oscillations with no a priori knowledge, such as the number of underlying components in the dataset or the sifting steps required to extract them. In facts, Online EMD is designed to analyze data using any sifting stopping criterion proposed in the past literature.

The following section reminds the classical EMD algorithm and details the proposed Online EMD. Then, Section 3 presents Online EMD results using synthetic and real data, and, Section 4 concludes this article.

2. ALGORITHM

2.1. Classical EMD

The **classical EMD** is formally defined as follows:

- Input signal $X(t)$; initialize $X_1 = X$ and $k = 1$.

- *Sifting*: for k, compute $c_k(t)$ by iterating on ρ_m with $\rho_1 = X_k$:

  1. Identify all local maxima and minima of $\rho_m(t)$.

  2. Compute an upper (resp. lower) envelope by an interpolation of the local maxima (resp. minima).

  3. Compute the local trend $Q_m(t)$ as the average of the upper and lower envelopes.

  4. Extract the local oscillations and update $\rho_m = \rho_m(t) - Q_m(t)$.

  5. *Stopping criterion:* If ρ_m is not an IMF (satisfying the two required conditions), iterate Sifting from step 1 for ρ_{m+1}.
     If $\rho_m(t)$ is an IMF, set $c_k(t) = \rho_m(t)$, and extract the residual $X_{k+1}(t) = X_k(t) - c_k(t)$.

- Iterate: increase k to $k+1$ and apply *Sifting* on X_k.

- Stop the iterations on k when residual $X_{k+1}(t)$ has no more oscillations, at index $K+1$ and set the final residual to be $r_K(t) = X_{k+1}(t)$.

The stopping criterion is critical to determine the number of required sifting steps to output an IMF, hence it directly affects the EMD results. This original criterion was controlling the difference between two consecutive sifting results using a Cauchy-type convergence [1]. Later Huang et al. have proposed a criterion that stops the sifting process when the number of zero crossing and extrema stays constant for S successive iterations [4]. Rilling et al. proposed a criterion ensuring the two envelopes of an IMF to be globally symmetric while allowing local disparities [7]. Because these two criteria are more closely related to the definition of IMF, they yield better results than the original one. We hereafter refer to them as the Huang stopping criterion and the Rilling stopping criterion.

2.2. Online EMD

The proposed Online EMD monitors the data through a sliding window encompassing l local extrema. In each new window (shifted by one extremum), the fastest oscillation is extracted using classical EMD. Then, a procedure stitches the modes of this window to the previously extracted modes that overlap with the current window (Fig. 1). It weights the overlapping modes from different windows according to their position in time, and averages them. For the stitching procedure, we use a window function $\tilde{\phi}(s)$ on $[-\tau, \tau]$ (and 0 outside), e.g., $\tilde{\phi}(s) = \frac{1}{\sqrt{2\pi}}\exp(-\frac{s^2}{2}) - \frac{1}{\sqrt{2\pi}}\exp(-\frac{\tau^2}{2})$, with $\tau = 3$, that inhibits discontinuities from boundary errors. By the stitching procedure, the algorithm gradually uncovers the first IMF and the residual data. To discover other IMFs, one repeats the analysis using the residual as input signal.

The **Online EMD algorithm** to extract the fastest IMF from an input signal $X(t)$ is formally presented as follows:
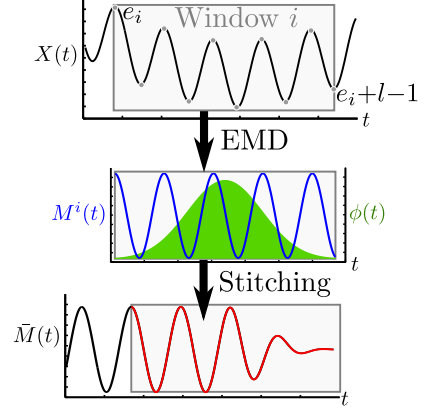

Fig. 1. Overview of Online EMD sliding window and stitching procedure with a window encompassing $l = 10$ extrema. The blue signal is the fastest oscillation, M^i extracted using the classical EMD, the window function ϕ is plotted in green and the weighted IMF, $\hat{M}^i$, stitched to the previous uncovered IMFs is red. Note that here $l' = l$.

0. Initialize $i = 1$, $\Phi^0(t) = 0$, $e_1 = 0$ the starting time of the signal and $\bar{M} = 0$.

1. Identify the window starting at e_1 containing l consecutive local extrema ($\{e_1, ...e_l\}$) of the signal $X(t)$.

2. Using classical EMD, extract the first IMF (i.e. fastest oscillation) $M^i(t)$ of the data in the window

3. Let $e'_1, \ldots, e'_l$ be the positions of the l' extrema in M^i. Set $s_k = -\tau + 2(k-1)\tau/(l'-1)$ for $k \in \{1, \ldots, l'\}$. We define warped weights $\phi_k(t)$ for $k \in \{1, \ldots, l'-1\}$ and $t \in [e'_k, \cdots, e'_{k+1}]$ as:

$$\phi_k(t) = \tilde{\phi}\left(s_k + (s_{k+1} - s_k)\frac{t - e'_k}{e'_{k+1} - e'_k}\right) \quad (1)$$

(and 0 outside). The weighted IMF $\hat{M}^i$ is defined as:

$$\hat{M}^i(t) = (\phi_1(t)M_1^i(t), \ldots, \phi_{l'-1}(t)M_{l'-1}^i(t))$$

where $M_k^i(t)$ is the mode between two extrema:

$$M_k^i(t) = M^i(t), \quad e'_k \le t < e'_{k+1}. \quad (2)$$

The total of weights is kept in memory:

$$\Phi^i(t) = \Phi^{i-1}(t) + \sum_{k=1}^{l'-1} \phi_k(t). \quad (3)$$

4. Stitch $\hat{M}^i$ on the weighted IMFs already extracted:

$$\bar{M} = \bar{M} + \hat{M}^i \quad (4)$$

and normalize the part of the data that will go out of the sliding window at the next iteration:

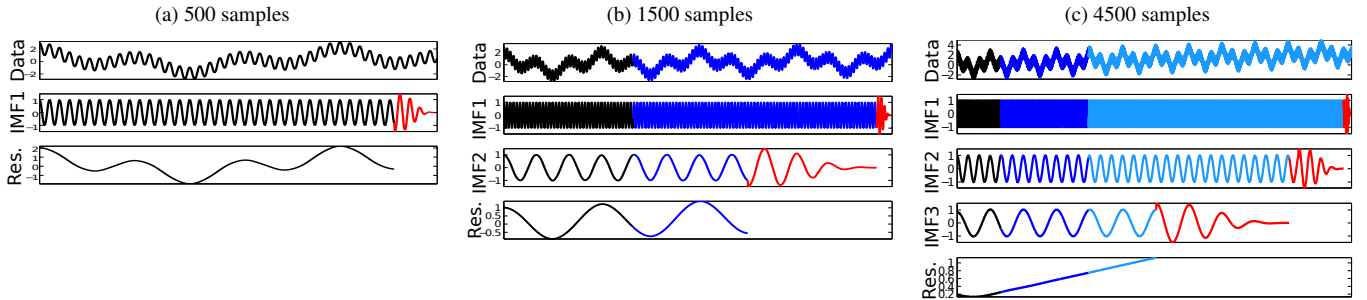$$\bar{M}(t) = \bar{M}(t)/\Phi^i(t) \quad \text{for all } t \in [e_i, e_{i+1}]. \quad (5)$$

(a) 500 samples   (b) 1500 samples   (c) 4500 samples

Fig. 2. Decomposition of Online EMD after analyzing 500, 1500, and 4500 samples. In red are the parts of the IMFs that are still incomplete. These results are obtained with a window size of 10 extrema ($l = 10$) and Rilling stopping criterion.

5. This newly finalized part of the IMF $\bar{M}(t)$, for $t \in [e_i, e_{i+1}]$ is subtracted from the data,

$$R^i = X^i(t) - \bar{M}(t) \quad \text{for all } t \in [e_i, e_{i+1}]. \quad (6)$$

The resulting data R^i is pushed to another instance of Online EMD in order to identify subsequent IMFs.

6. Increase i to $i + 1$ and go back to step 1.

Remarks: 1) Note that the head of the stitched IMF, $\bar{M}(t)$, $e_{i+1} \leq t \leq e_{i+l-1}$, needs subsequent data to be completed, thus, the IMFs uncovered by Online EMD feature a lag $e_{i+l-1} - e_i < \Delta t < e_{i+l} - e_i$. As the value of Δt depends on the distances between extrema, IMFs with lower frequencies exhibit longer lags. 2) For the stitching procedure of steps 3 and 4, the number of extrema l' of the IMF is possibly different from the number of extrema l that defines the sliding window; it occurs in (rare) situation where small fast oscillations are added to large slow oscillations. It can happen that some extrema of the fast oscillations do not lead to extrema in the combined signal – yet they can be recovered by EMD that will create new extrema in the extracted IMF. This is why this distinction is done between l and l'.

3. EXPERIMENTAL RESULTS

This section summarizes the results obtained with our implementation of Online EMD [14] and distinct datasets.

3.1. Decomposition of Synthetic Data

A non-stationary signal composed of three sinusoids and one monotonic function allows us to evaluate the decomposition quality of Online EMD. Figure 2 shows the synthetic signal and its on-going decomposition using the window length $l = 10$. After the analysis of 500 samples (Fig. 2a) the sinusoid with the highest frequency is identified as the first IMF whereas the other components of the signal remain in the residual. Nevertheless, analyzing the following samples reveals more than $l = 10$ extrema in the residual thus Online
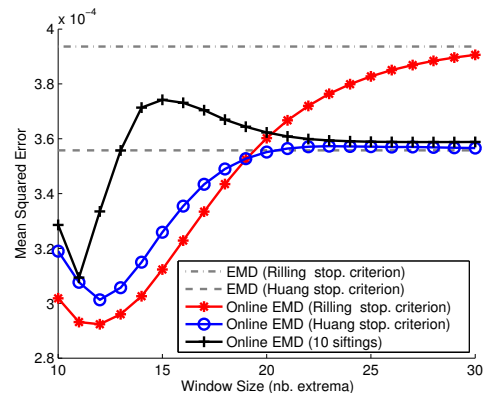

Fig. 3. Mean squared error for the 3 IMFs and the residual found by the proposed Online EMD (with three different stopping criteria) and the classical EMD using the Rilling stopping criterion, and the Huang stopping criterion.

EMD starts retrieving the second sinusoid with the highest frequency (IMF2 in Fig.2b), similarly, the third sinusoid is later uncovered (Fig. 2c). The red parts in Figure 2 highlight the section of the IMFs that are being stitched (i.e. not yet completed) and reveal the lag Δt of each IMF. For each IMF we observe a constant lag Δt which is determined by the frequency of the IMF. Consequently, IMF3 has a longer lag than the IMF1 one because its frequency is lower.

The decomposition quality of Online EMD is further evaluated by computing the mean squared error between the original components and the uncovered IMFs. One potential source of error for Online EMD is the stitching procedure that merges local IMFs all together. Intuitively, the error is function of the number of overlapping local IMFs which is determined by the window size parameter l. We measure the error of the three IMFs and the residual for diverse window sizes. To exclude the error caused by the border effects we compute the mean squared error of 5000 samples taken at the center of the signal. Figure 3 summarizes the error of the decomposition of Online EMD using a window length
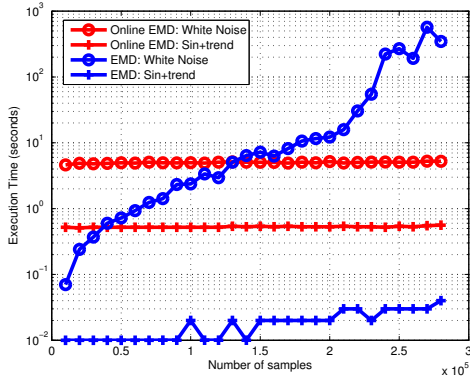
Fig. 4. Execution time of Online EMD ($l = 20$) and classical EMD (both using Rilling stopping criterion) with a white noise signal and a sinusoid with a trend.

l ranging $[10, 30]$ and three different stopping criteria: the Rilling stopping criterion, the Huang stopping criterion and a fixed 10 sifting passes. As a reference the mean squared error for the classical EMD is also shown. Surprisingly Online EMD with narrow windows (10 to 15 extrema) is performing slightly better than the classical EMD. Wider windows tend to produce similar results to the classical EMD. Overall the best results are obtained with a window size of 12 extrema although the improvement over classical EMD is subtle. Since IMF lag Δt is increasing with l, a small window size (e.g. $l < 20$) is also advantageous for low latency applications.

3.2. Execution Time

The main benefit of Online EMD is the possibility to analyze data streams. We demonstrate this advantage by analyzing two signals, a sinusoid with a monotonic function, and, a white noise signal, both including 280k samples. Figure 4 depicts the execution time of the classical EMD and Online EMD both using the Rilling stopping criterion[1]. These signals are analyzed in a streaming fashion, namely, each signal is split in batches of 10k samples that are sequentially analyzed. For each new batch, the classical EMD needs to reprocess all previous batches with the new one, hence, the execution time of the classical EMD grows with the number of batches. The execution growth rate depends on the number of uncovered IMFs. In the case of the sinusoidal signal the last batch analysis is four times longer than the one of the first batch, whereas, for the white noise the execution time of the last batch is four orders of magnitude higher than the one for the first batch (Fig. 4). The execution time of Online EMD also depends on the number of uncovered IMFs, however, the computational cost for each new batch is much more stable. The computational overhead of the sliding window

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[1] Note that the maximum number of sifting in *emdc.c* must be increased to analyze such long signals.
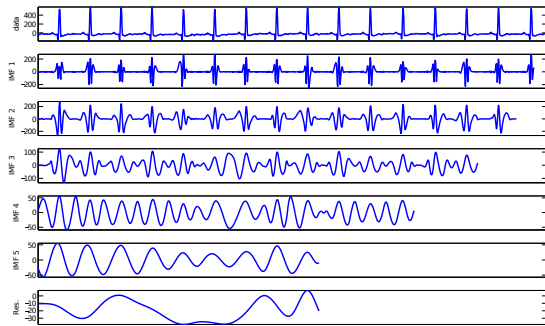
and stitching procedure makes Online EMD slower to analyze the sinusoidal signal and white noise with less than 130k samples. However, Online EMD benefits from an almost constant execution time for each batch, that is really advantageous for the analysis of streaming data with an increasing number of oscillatory components.

3.3. Decomposition of Real Data

We present results obtained with an electrocardiogram (ECG) signal from the MIT-BIH Normal Sinus Rhythm [15]. Torres et al. [3] evaluated their variant of Ensemble EMD (EEMD) with this ECG signal and they emphasized the challenging mode mixing problems faced with this kind of spiky signals.

Although the stitching process of Online EMD resembles to the IMF ensemble average of EEMD, Online EMD is not as robust as EEMD to mode mixing. This drawback is illustrated by the Online EMD decomposition of the ECG signal in Figure 5. Mode mixing issues are especially visible for the IMF3 and IMF4. Nevertheless, our experiments revealed that Online EMD is less sensitive to mode mixing than the classical EMD. For instance the IMF5 of the Online EMD decomposition (see Fig. 5) features the fundamental frequency of the original signal as reported in [3], whereas, this component is hardly identifiable using the classical EMD.

4. CONCLUSIONS

This article presents Online EMD, a new algorithm to decompose non-stationary data stream. Online EMD takes advantage of a sliding window and stitching procedure to discover IMFs in a single pass, which is particularly useful for online and large dataset analysis. Our evaluation with synthetic and real data shows that the decomposition quality is similar to the EMD one, and, emphasizes the lower computational cost of Online EMD to analyze data stream and large data sets.

Fig. 5. Decomposition of the ECG signal by Online EMD with $l = 10$ and the Huang stopping criterion ($S = 4$).

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