Empirical Mode Decomposition - An Introduction

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Abstract—Due to external stimuli, biomedical signals are in general non-linear and non-stationary. Empirical Mode Decomposition in conjunction with a Hilbert spectral transform, together called Hilbert-Huang Transform, is ideally suited to extract essential components which are characteristic of the underlying biological or physiological processes. The method is fully adaptive and generates the basis to represent the data solely from these data and based on them. The basis functions, called Intrinsic Mode Functions (IMFs) represent a complete set of locally orthogonal basis functions whose amplitude and frequency may vary over time. The contribution reviews the technique of EMD and related algorithms and discusses illustrative applications.

I. INTRODUCTION

Recently an empirical nonlinear analysis tool for complex, non-stationary time series has been pioneered by N. E. Huang et al. [1]. It is commonly referred to as Empirical Mode Decomposition (EMD) and if combined with Hilbert spectral analysis it is called Hilbert-Huang Transform (HHT). It adaptively and locally decomposes any non-stationary time series in a sum of Intrinsic Mode Functions (IMF) which represent zero-mean amplitude and frequency modulated components. The EMD represents a fully data-driven, unsupervised signal decomposition and does not need any a priori defined basis system. EMD also satisfies the perfect reconstruction property, i.e. superimposing all extracted IMFs together with the residual trend reconstructs the original signal without information loss or distortion. The method is thus similar to the traditional Fourier or wavelet decompositions but the interpretation of IMFs is not similarly transparent [2]. It is still a challenging task to identify and/or combine extracted IMFs in a proper way so as to yield physically meaningful components. Also, if only partial reconstruction is intended, it is not based on any optimality criterion rather on a binary include or not include decision.

The empirical nature of EMD offers the advantage over other empirical signal decomposition techniques like empirical matrix factorization (EMF) of not being constrained by conditions which often only apply approximately. Especially with biomedical signals one often has only a rough idea about the underlying modes and mostly their number is unknown.

This contribution will review the technique of empirical mode decomposition and its recent extensions.

II. EMPIRICAL MODE DECOMPOSITION

The EMD method was developed from the assumption that any non-stationary and non-linear time series consists of different simple intrinsic modes of oscillation. The essence of the method is to empirically identify these intrinsic oscillatory modes by their characteristic time scales in the data, and then decompose the data accordingly. Through a process called sifting, most of the riding waves, i.e. oscillations with no zero crossing between extrema, can be eliminated. The EMD algorithm thus considers signal oscillations at a very local level and separates the data into locally non-overlapping time scale components. It breaks down a signal \( x(t) \) into its component IMFs obeying two properties:

1) An IMF has only one extremum between two subsequent zero crossings, i.e. the number of local minima and maxima differs at most by one.
2) An IMF has a mean value of zero.

Note that the second condition implies that an IMF is stationary which simplifies its analysis. But an IMF may have amplitude modulation and also changing frequency.

I) The EMD Algorithm: The sifting process can be summarized in the following algorithm. Decompose a data set \( x(t) \) into IMFs \( x_n(t) \) and a residuum \( r(t) \) such that the signal can be represented as

\[
x(t) = \sum_n x_n(t) + r(t)
\]  

Sifting then means the following steps (see Fig. [I]):

- **Step 0:** Initialize: \( n := 1 \), \( r_0(t) = x(t) \)
- **Step 1:** Extract the \( n \)-th IMF as follows:
  a) Set \( h_0(t) := r_{n-1}(t) \) and \( k := 1 \)
  b) Identify all local maxima and minima of \( h_{k-1}(t) \)
  c) Construct, by cubic splines interpolation, for \( h_{k-1}(t) \) the envelope \( U_{k-1}(t) \) defined by the maxima and the envelope \( L_{k-1}(t) \) defined by the minima
  d) Determine the mean \( m_{k-1}(t) = \frac{1}{2} (U_{k-1}(t) - L_{k-1}(t)) \) of both envelopes of \( h_{k-1}(t) \). This running mean is called the low frequency local trend. The corresponding high-frequency local detail is determined via a process called sifting.
  e) Form the \( k-th \) component \( h_k(t) := h_{k-1}(t) - m_{k-1}(t) \)

1) if \( h_k(t) \) is not in accord with all IMF criteria, increase \( k \rightarrow k + 1 \) and repeat the Sifting process starting at step \( b \).
2) if \( h_k(t) \) satisfies the IMF criteria then set 
\[ x_n(t) := h_k(t) \text{ and } r_n(t) := r_{n-1}(t) - x_n(t) \]

- Step 2: If \( r_n(t) \) represents a residuum, stop the sifting process; if not, increase \( n \rightarrow n + 1 \) and start at step 1 again.

The average period of each IMF can be calculated by dividing twice the sample size \( 2 \cdot N \) by the number of zero crossings. Note also that the number of IMFs extracted from a time series is roughly equal to \( \log_2 N \). Fig. 2 shows the result of an EMD analysis of a non-stationary signal consisting of a superposition of a sawtooth signal, a sinusoid and a linear trend. The sifting process separates the non-stationary time series data into the original, locally non-overlapping intrinsic mode functions (IMFs). However, EMD is not a sub-band filtering technique with predefined waveforms like wavelets. Rather selection of modes corresponds to an automatic and adaptive time-variant filtering.

Completeness of the decomposition process is automatically achieved by the algorithm as \( x(t) = \sum_{n=1}^{\infty} x_n + r \) represents an identity. Further, the EMD algorithm produces locally orthogonal IMFs. Global orthogonality is not guaranteed as neighboring IMFs might have identical frequencies at different time points (typically in < 1% of the cases).

A. Hilbert - Huang Transform

After having extracted all IMFs, they can be analyzed further by applying the Hilbert transform or processing them in any other suitable way [3], [4]. The Hilbert transform calculates the conjugate pair of \( x_i(t) \) via

\[
H\{x_i(t)\} = \frac{1}{\pi} \text{P} \left\{ \int_{-\infty}^{\infty} \frac{x_i(\tau)}{t - \tau} d\tau \right\}
\]

(2)

where \( \text{P} \) indicates the Cauchy principal value. This way an analytical signal \( z_i(t) \) can be defined via

\[
z_i(t) = x_i(t) + iH\{x_i(t)\} = a_i(t) \exp(i\theta_i(t))
\]

(3)

with amplitude \( a_i(t) \) and instantaneous phase \( \theta_i(t) \) given by

\[
a_i(t) = \sqrt{x_i^2(t) + H\{x_i(t)\}^2}
\]

(4)

\[
\theta_i(t) = \arctan \left( \frac{H\{x_i(t)\}}{x_i(t)} \right)
\]

(5)

1) Duffing oscillator: To illustrate the Hilbert transform, consider a Duffing oscillator as a simple example. The latter is characterized by the following equation of motion (neglecting dissipative terms for simplicity)

\[
\frac{d^2 x(t)}{dt^2} + (1 + c x^2(t)) x(t) = \gamma \cos(\omega t)
\]

(6)

Consider \( k(t) = (1 + c x^2(t)) \) a time-dependent spring constant. The frequency of the system then changes instantaneously which is the characteristic feature of a non-linear oscillator. Its instantaneous frequency can now be computed via a Hilbert Transform (see eqn. 5) according to

\[
\omega(t) = -\frac{d\theta(t)}{dt} = \frac{d}{dt} \left( \arctan \left( \frac{H\{x(t)\}}{x(t)} \right) \right)
\]

(7)

Note that the Hilbert Transform can only produce physically meaningful results for single component functions. Hence any non-linear and non-stationary time series needs to be
decomposed into stationary IMFs via an EMD. The combination of EMD plus Hilbert transform is called a Hilbert-Huang Transform.

2) Hilbert-Huang Transform vs Fourier Transform: Each IMF can now be expressed as

\[ x_n(t) = \text{Re} \left[ a_n(t) \exp \left( i \int \omega_n(t) dt \right) \right] \]  

(8)

The signal can then be expressed as

\[ x(t) = \text{Re} \left\{ \sum_{n=1}^{N} a_n(t) \exp \left( i \int \omega_n(t) dt \right) \right\} + r(t) \]  

(9)

Compare this with a Fourier representation with constant \( a_n \) and fixed \( \omega_n \)

\[ x(t) = \sum_{n=1}^{\infty} a_n \exp(i\omega_nt) \]  

(10)

An IMF expansion thus provides a generalized Fourier expansion.

Remember that a Fourier Transformation decomposes any time series into simple harmonic components with globally constant amplitudes and frequencies. Hence it is only applicable to stationary and linear time series.

3) Stationarity and Linearity: A time series of a random variable \( X(t) \)

\[ X(t) = [X(t_0), X(t_1), ..., X(t_{N-1})] \]  

(11)

called strongly stationary if the joint probability

\[ P(X(t)) = P(X(t_N - t_{N-1}, ..., t_1 - t_0)) \]  

(12)

does not depend on time \( t \) itself but only on time differences \( \tau = t_{n+1} - t_n \ \forall \ n = 0, ..., N - 1 \). Correspondingly, a time series is called weakly or wide-sense stationary if every data point has a finite variance, i.e. \( E[(X(t))^2] < \infty \), the mean is constant everywhere, i.e. \( E(X(t)) = m \) and the covariance only depends on \( \tau \), i.e.

\[ \text{cov}(X(t_1), X(t_2)) = \text{cov}(X(t_1 + \tau), X(t_1)) \]  

(13)

\[ = \text{cov}(X(0), X(\tau)) \]  

(14)

Weak stationarity thus only asks for the first (mean) and second (variance) moment of the data distribution \( P(X(t)) \) to be constant at all times.

A linear system follows a linear superposition principle, i.e. the following relation \( f(t) + g(t) = 0 \) describes a linear system despite \( f(t), g(t) \) being non-linear functions of the variable \( t \). As a consequence, in a linear time series, every data point \( x(t+1) \) depends only linearly on \( x(t) \). Prominent examples of such linear systems are auto-regressive moving average (ARMA) models characterized by

\[ x(t) = \sum_{i=1}^{p} \alpha(i)x(t-i) + \sum_{i=1}^{q} \beta(i)\epsilon(t-i) + \epsilon(t) \]  

(15)

where \( \alpha \) and \( \beta \) are parameters of the model and \( \epsilon \) represents white noise error terms. The latter are assumed to be i.i.d. sampled from a normal distribution \( \epsilon(t) \sim N(0, \sigma^2) \). ARMA models can, after choosing \( p \) and \( q \), be fit by a least squares regression to minimize the error term. Most natural systems are non-linear and can only approximately be represented by a linear system (corresponding to a time-independent spring constant in eqn. [6]).

Real biomedical signals usually do not fulfill such conditions because of noise and/or transient signal components.

B. Some shortcomings

Being a heuristic, EMD suffers from some shortcomings [5] which are shortly discussed in the following.

1) Estimating envelops: A major point concerns the way envelopes \( (U(t), L(t)) \) are estimated. Spline interpolation is a most often used technique to create the envelopes. Splines represent functions which are piecewise composed from polynomials of order \( n \). At their knots, splines obey conditions like being continuous or being \( n - 1 \)-times continuously differentiable. The envelopes are needed to identify the local mean at every time point. To locate extrema precisely, over-sampling is generally advisable. Most often cubic splines are used to interpolate maxima and minima of the time series \( x(t) \). They generally give good results but are computationally costly. Alternative interpolation schemes have been proposed using rational or taut splines which allow, depending on an extra parameter, a smooth transition between a linear and a cubic spline [6]. The former are simple but they often induce too many IMFs or cause over-sifting. The latter term describes the further decomposition of a single component into sub-components or the combination of different components into mixed components. Also quadratic cost functions were proposed which had to be optimized to determine the envelopes but these approaches are very costly numerically and show moderate improvement only [7]. As a further alternative, data have been highpass filtered before maxima and minima of the time series have been identified. For interpolation Hermite polynomials have been suggested [8]. Recently there have been attempts also to estimate local means directly and give up of the idea of using envelopes [9]. [10]. First results are encouraging but the technique needs to be developed further.

2) Boundary conditions: Spline interpolation induces mismatch at the boundaries of the intervals, hence leads to large fluctuations at the end and the beginning of the data set. If the first and last data point are considered knots of the upper and lower envelope, un-physical results are created. Such defects propagate to signal components extracted later (see Fig. [3]). Several procedures like padding the ends with typical waves [1], mirroring the extrema closest to the end [5] or using the average of the two closest extrema for the maximum or minimum spline [11] or the SZero method [6] have been proposed. Periodic boundary conditions seem also useful as long as there are no abrupt changes in the time series or strong time-dependent changes of frequency and amplitude.
These issues are illustrated in Fig. 3 using the time series \( x(t) = \sin(7t) + \sin(4t) + 0.1 \cdot t \).

![Fig. 3](image)

**A) An EMD decomposition of the non-stationary time series**

\( x(t) = \sin(7t) + \sin(4t) + 0.1t - 1 \) with improper boundary conditions. Here the first and last data point of the time series have been treated as knots of \( x(t) \). **B) An EMD decomposition of the same non-stationary time series with proper boundary conditions.**

3) **Stopping the sifting process:** Plain EMD continues the sifting process on the full signal as long as there exist local segments with means not yet close to zero. Criteria for stopping the sifting process depend on the amplitude of the related IMF. This easily leads to over-sifting and tends to split meaningful IMFs into meaningless fragments. A common stopping criterion is based on the total variance

\[
\sigma^2 = \sum_{n=0}^{N} \frac{(h_{i,k-1}(t_n) - h_{i,k}(t_n))^2}{h_{i,k-1}(t_n)}
\]

The first IMF is obtained whenever \( \sigma^2 < \delta \) holds for some appropriately chosen threshold \( \delta \) and so on. The whole procedure stops when the residuum \( r_n(t) \) is either a constant, a monotonic slope or contains only one extremum. This Cauchy-like convergence criterion, however, does not explicitly take into account the two IMF conditions and can be satisfied without satisfying the latter \[12\]. Alternatively, an evaluation function has been introduced by \[5\]

\[
\sigma(t) = \frac{U(t) + L(t)}{U(t) - L(t)}
\]

which uses two thresholds \( \delta_1, \delta_2 \). The sifting process is then iterated until \( \sigma(t) < \delta_1 \) for a prescribed fraction \( (1 - \alpha) \) of the total duration and \( \sigma(t) < \delta_2 \) for the rest. However, this introduces three new parameters which the user has to fix and which might influence the resulting IMFs.

4) **Amplitude and frequency resolution:** The decomposition strongly depends on the choice of parameters of the algorithm, hence uniqueness of the decomposition cannot be guaranteed. Critical parameters are the **stopping criterion**, the **boundary condition** and the **interpolation method** (B-splines or natural cubic splines). An improper choice of parameters might result in over-sifting and mode-mixing. Obtaining good results in terms of amplitude and frequency resolution requires certain conditions to be met. The sampling rate must follow the **Nyquist theorem** and the digitalized signal should have the same number of extrema as its continuous counterpart. **Over-sampling** improves results considerably and avoids over-sifting. Furthermore, for good results, the **Hilbert Transform** needs at least 5 samples per period. Concerning amplitude resolution, oscillations with very small amplitude cannot be extracted as the extrema of such small amplitude oscillations cannot be detected. As a result, the related time series will not be decomposed correctly (see Fig. 4).

Concerning frequency resolution, EMD behaves like a **dyadic filter bank**. Filters overlap and the number of extrema is reduced by one half from one IMF to the next. For every signal frequency \( \omega_i \) exists a frequency band \( B(\omega_i) = [\alpha_i \omega_i, \omega_i] \), \( \alpha_p < 1 \), \( \rho = \alpha_i/\alpha_j \) such that every frequency \( \omega_j \in B(\omega_i) \) is indistinguishable from \( \omega_i \), hence cannot be resolved. If two frequencies are filtered by the same filter, they are represented by the same IMF. An example is shown in Fig. 5.

C. **Interpretation of IMFs and statistical significance**

Being a heuristic, plain EMD does not admit any performance evaluation on a theoretical basis but requires extensive simulations which hardly exist on prototype toy data sets. A thorough understanding of the physical process that generated data is required before any form of scientific explanation can be attributed to any particular IMF.

1) **Interpretability:** As EMD is a completely empirical method, any physical meaning of the extracted IMFs cannot be guaranteed. This is, of course, also true for all time series analysis methods, especially those with a fixed basis system. However, IMFs preserve their positive local frequency and also keep their non-linearity. As stated above, uniqueness of
The figure shows an EMD decomposition of the time series
\[ x(t) = x_1(t) + x_2(t) = \exp(-0.1t)\sin(20t) + \sin(8t). \] Part A)
shows the time series and its component signals and Part B)
shows an EMD decomposition with the resulting IMFs. Mode mixing is clearly visible as soon as the amplitude of signal component \( x_1(t) \) is too small and the one of signal \( x_2(t) \) dominates.

The decomposition cannot be guaranteed. Hence, depending on the set of parameters applied, IMFs may be extracted which vastly differ in their appearance and characteristics. Furthermore note that in case of a spline interpolation scheme to estimate the envelopes, all except the first IMF are sums of such splines. This, however, presupposes that every oscillatory component of the original signal can be represented as a sum of splines. EMD is also very sensitive to any abrupt changes in the signal like in case of missing signal components in certain time intervals. This can easily lead to mode mixing which hampers the interpretation of the extracted IMFs.

The most serious drawback of the method is certainly its lacking any theoretical basis which would allow to evaluate the performance of the algorithm in objective terms. Hence to do so one needs to employ carefully designed toy data to simulate the decomposition process into single modes and the impact of the various parameters and constraints onto the sifting process. Despite all this, EMD has since been applied successfully to solve many practical problems (see for example [13], [14], [15], [16], [17], [18]).

2) Evaluation criteria: The quality of a sifting process may be evaluated by the number of sifting steps necessary to extract an IMF. With only few steps over-sifting can be avoided generally. Furthermore with only few sifting steps physically more realistic and plausible IMFs result [6]. Also one should take care of extracting IMFs which are as orthogonal as possible to each other. If this can be achieved then the variance of the data may be expressed as the sum of the variances of the extracted IMFs plus the variance of...
the residuum \[19, 6, 11\]. In practice the latter sum is always a bit larger because of additional tails resulting from the spline interpolation. In \[12\] a confidence interval for each extracted IMF was proposed. The latter is achieved by extracting a whole set of IMFs from the same original signal by varying the stopping criterion or the way the envelopes have been constructed. All IMFs lying within certain limits of the orthogonality index are grouped together and their average IMF and variance is calculated. Finally the marginal spectra, i.e. the time integral of the Hilbert spectrum, of the extracted IMFs and the marginal spectrum of the average IMF is compared.

3) Statistical significance: In \[20\] an approach is proposed to evaluate the statistical significance of an extracted IMF. It is based on the observation that the IMFs of white noise are normally distributed and their Fourier spectra are almost identical. Hence the product of the energy density of the IMFs and comparing it to the envelops of the energy spread function of white noise, informative IMFs can be identified as the ones whose energy densities lie outside of the envelopes. The method thus offers a possibility to estimate how well noise has been separated from underlying signal components.

4) Reconstruction quality: An important practical issue in applying EMD to biomedical signals is the reconstruction quality of signals, for example after denoising. The EMD extracts intrinsic modes of a signal in a completely self-adaptive manner. This unsupervised extraction procedure, however, does not have any implication on reconstruction optimality. In some situations, when a specified optimality is desired for signal reconstruction, a more flexible scheme is required. In \[21\] a modified method for signal reconstruction after EMD is proposed that enhances the capability of the EMD to meet a specified optimality criterion. The proposed reconstruction algorithm gives the best estimate of a given signal in the minimum mean square error sense. Two different formulations are proposed. The first formulation utilizes a linear weighting for the intrinsic mode functions (IMF). The second algorithm adopts a bidirectional weighting which uses weighting for IMF modes and also exploits the correlations between samples in a specific window and carries out filtering of these samples. These two new EMD reconstruction methods enhance the capability of the traditional EMD reconstruction and are well suited for optimal signal recovery.

D. Recent extensions of EMD

Plain EMD is applied to the full length signal which in view of limited resources like computer memory also limits the length of the time series to be dealt with. This is an especially serious problem with biomedical time series which are often recorded over very long time spans. A number of extensions to plain EMD have been proposed in recent years which will be discussed shortly in the following.

1) Ensemble EMD: Ensemble EMD (EEMD) is a noise-assisted method to improve sifting \[22\]. It is based upon investigations of the statistical properties of white noise \[23, 20, 24\]. EEMD considers true IMFs as an ensemble average of extracted IMFs according to

\[ x_j(t) = \frac{1}{N} \sum_{i=1}^{N} x_{ji}(t) \]  

An ensemble of data sets \(x^{(i)}(t)\) is created by adding white noise \(e_i(t)\) (finite amplitude, zero mean, constant variance) to the original time series \(x(t)\). Through averaging, noise contributions will cancel out leaving only the true IMFs. Noise amplitudes can be chosen arbitrarily high but the number \(N\) of noise components should be large. The number of sifting steps and the number of IMFs has to be fixed in advance to render extracted IMFs truly comparable. However, mode mixing is reduced in EEMD and an improved separation of modes with similar frequencies results. Due to the added noise, the time series contains a lot more local extrema which renders the estimation of the envelops much more demanding computationally. Also more high frequency components result naturally. In summary, EEMD is computationally costly but worth to be tried. In practice EEMD works as follows:

- Add white noise to the data set
- Decompose the noisy data into IMFs
- Iterate these steps and at each iteration add white noise
- Calculate an ensemble average of the respective IMFs to yield the final result

An illustrative example of the performance of EEMD vs EMD is given in Fig. \[6\]. Two signals \(x_1(t) = 0.1 \cdot \sin(20t), x_2(t) = \sin(t)\) are superimposed whereby signal \(x_1(t)\) is interrupted for certain time spans to simulate a situation which often happens with biomedical signals. Clearly, standard EMD shows strong mode-mixing in this case while EEMD, using an ensemble of 15 different noisy signals, copes quite well with this complicated signal. It is clear that the first few extracted IMFs in case of EEMD contain high frequency noise signals which may easily be identified as such. It is also clear that standard EMD shows mode mixing as soon as the high frequency part of the original signal appears.

2) Local EMD: The nonlinear nature of plain EMD does not guarantee that the EMD of segmented signals adds up to the EMD of the total signal. Furthermore, to satisfy the stopping criterion of sifting, the mean of both envelops needs to be close to zero everywhere (see Fig. \[7\]). This requirement easily leads to over-sifting in certain signal regions and an insufficient decomposition in others. Local EMD \[5\] pursues the idea to iterate the sifting process only in regions where the mean is still finite to finally meet the stopping criterion everywhere. Localization can be implemented via a weighting function \(w(t)\) which is \(w(t) = 1\) in regions where sifting is still necessary and decays to zero at the boundaries. This can be easily integrated into the EMD algorithm via

\[ h_{j,n}(t) = h_{j,n-1}(t) - w_{j,n}(t) m_{j,n}(t) \]  

This procedure essentially improves the sifting process and
a) Original signal and component signals

b) An EMD decomposition

c) An EEMD decomposition

Fig. 6
A) SUPERPOSITION OF THE SIGNALS

\[ x(t) = x_1(t) + x_2(t) = 0.1 \sin(20t) + \sin(t) \]

AND THE COMPONENT SIGNALS. NOTE THAT SIGNAL \( x_1(t) \) IS ABSENT FOR A LARGE PART OF THE TOTAL TIME SPAN. B) THE FIRST TWO IMFS OBTAINED WITH AN EMD OF THE SAME SIGNAL. MODE MIXING IS CLEARLY VISIBLE DUE TO THE PARTIAL ABSENCE OF MODE \( x_1(t) \). C) IMFS OBTAINED WITH AN EEMD OF THE SAME SIGNAL, REFLECTING THE COMPONENT SIGNALS UNDERLYING THE ORIGINAL SIGNAL. THE LATTER ARE EXTRACTED ALMOST PERFECTLY.

3) On-line EMD: The application of EMD to biomedical time series is limited by the size of the working memory of the computer. Hence in practical applications only relatively short time series can be studied. However, many practical situations like continuous patient monitoring ask for an on-line processing of the recorded data. Recently, a blockwise processing, called on-line EMD, has been proposed [5]. This is possible as EMD is based on the construction of envelopes which need only a few extrema (less than 5 in case of cubic splines) to yield a reasonable estimate of the interpolating polynomial. Thus a time series could be worked up step by step applying EMD to segments of the total data set only. However, to avoid discontinuities, the number of sifting steps must be identical in all blocks and needs to be fixed a priori without knowledge of the total signal. The advantage of on-line EMD would be a much reduced computational load as the latter increases exponentially with the number of time points over which the data are sampled. In [5] it is proposed to fix the number of sifting steps on the outset and to enlarge the window on the forefront whenever new data appear and reduce the size of the window on the back whenever the stopping criterion is reached. This approach, however, has some drawbacks related to the discontinuities occurring at the boundaries. The former strongly depend on the latter, of course. Furthermore, the question, which information remains in the residuum also strongly depends on the size of the window so that the signal decomposition as a whole strongly depends on the window size. Imagine long wavelength changes which would appear as monotonous trends in windows with a length small compared to the wavelength but would be recognized as oscillations and extracted as an IMF with sufficiently large window sizes. In summary, on-line EMD presents a nice idea, however, results are not yet satisfactory so far (see Fig. 8). The method is still in its infancy and needs yet to be developed to a robust and efficient on-line technique.

III. Conclusion

The paper summarizes the current state of the art in empirical mode decomposition. It is obvious that the method is still in its infancy, nonetheless a respectable and quickly growing number of applications to analyze biomedical time series already exists. The method provides specific advantages due to its applicability to non-stationary and non-linear time series. Perhaps the most difficult problem yet to solve is the interpretability of the extracted IMFs in physical terms.
potential of this heuristic to analyze and interpret huge and long going recordings. Undoubtedly the future will show the EMD method yet exists to allow an online evaluation of such spans extending over days and even weeks. No appropriate Also biomedical time series often are recorded over long time series analysis. Proc. Roy. Soc. London A, 454, 903–995, 1998.

\[ x(t) = \sin(7t) \] and the functions \[ x_2(t) = \sin(4t), \] respectively. B) The original signal from Fig. 8 and IMFs extracted with the on-line EMD algorithms of EMD. The original signal components are split into different IMFs during sifting.

Also biomedical time series often are recorded over long time spans extending over days and even weeks. No appropriate EMD method yet exists to allow an online evaluation of such long going recordings. Undoubtedly the future will show the potential of this heuristic to analyze and interpret huge and complex time series data sets.

REFERENCES


