Chapter 1

Sliding Empirical Mode Decomposition - Brain Status Data Analysis and Modeling


Abstract  Biomedical signals are in general non-linear and non-stationary. Empirical Mode Decomposition in conjunction with Hilbert-Huang Transform provides a fully adaptive and data-driven technique to extract Intrinsic Mode Functions (IMFs). The latter represent a complete set of locally orthogonal basis functions to represent non-linear and non-stationary time series. Large scale biomedical time series necessitate an online analysis which is presented in this contribution. It shortly reviews the technique of EMD and related algorithms, discusses the newly proposed SEMD algorithm and presents some applications to biomedical time series recorded during neuromonitoring.

1.1 Introduction

1.1.1 Empirical Mode Decomposition

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 oscillatory components. The EMD represents a fully data-driven, unsupervised signal decomposition technique and does not need any a priori defined basis system. The empirical nature

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EMD offers the advantage over other empirical signal decomposition techniques like \textit{exploratory matrix factorization} (EMF) of not being constrained by conditions which often only apply approximately in case of biomedical signals. Especially with the latter one often has only a rough idea about the underlying modes and frequently their number is unknown. Furthermore, large scale biomedical time series recorded over days necessitate an on-line analysis while EMD can analyze data only globally so far. This contribution will review the technique of empirical mode decomposition and its recent extension, called \textit{Ensemble Empirical Mode Decomposition} (EEMD). The latter represents a noise assisted EMD which alleviates certain problems which inevitably accompany any EMD application. This contribution also proposes a new on-line EMD variant, called \textit{weighted Sliding EMD} (wSEMD), and discusses its application to biomedical time series recorded during neuromonitoring of brain injured patients in intensive care units.

\subsection*{1.1.2 Neuromonitoring}

The continuous and simultaneous monitoring of different physiological brain status parameters like Intra-Cranial Pressure (ICP), brain Tissue Partial Oxygen pressure (TiPO2) and the cerebral Blood Flow Velocity (BFV) in distinct cerebral vessels, is an increasingly employed technique during \textit{neuromonitoring} in neurosurgical intensive care units \cite{2}, \cite{3}. Such complex monitoring practice is used for early detection of neurological worsening of patients suffering from a brain injury. A major therapeutic goal is maintaining a sufficient supply of cerebral matter with blood and oxygen to avoid ischemic insults. But the human brain exhibits several control mechanisms, like the cerebral autoregulation or the cerebrospinal fluid circuit, which guarantee sustained cerebral perfusion. A severe brain trauma may suspend such control systems temporarily, partially or even globally, hence alter the response of cerebral perfusion to a neurosurgical treatment. Failure of the autoregulation often turns out to be fatal.

Knowledge of cerebral regulatory mechanisms in advance of any frightening event is thus mandatory to adapt patient management to an acute change in the physiological status of the patient. But the interpretation of recorded brain status data is difficult. Cerebral mechanisms lead to complex interdependencies between individual compartments depending on their actual functionality. Recently several mathematical methods have been developed based on correlation analysis simplifying the interpretation of brain status data \cite{4}. However, up till now there is no widely accepted comprehensive mathematical model of the cerebral physiology that reliably interprets the interrelation of the different data under different states of cerebral regulatory mechanisms, although some serious attempts have been undertaken \cite{5}, \cite{6}, \cite{7}, \cite{8}. Based on the characteristics of the data, a method for their analysis should be used which can reliably separate different oscillatory components belonging to different physiological mechanisms and simultaneously identify noise components.
1.1.3 Dynamic cerebral autoregulation

The assessment of the dynamic cerebral autoregulation (DCA) provides a major challenge in neuromonitoring in intensive care units. DCA can be described as the ability of the cerebral microvasculature to modulate cerebral perfusion in response to fast blood pressure fluctuations or an altered oxygen demand. Transcranial doppler ultrasound (TCD) measurements of the cerebral blood flow velocity (BFV) enables monitoring DCA during externally induced blood pressure variations (Vasalva maneuver). Usually the interdependencies of ABP and BFV are analyzed by means of coherence and transfer function analysis which are based on linear methods. But nonlinear interactions between non-stationary signals cannot be quantified based on theories of stationary and linearly superimposed signals. They cannot reliably assess nonlinear interactions in physiological systems.

A possible solution to this dilemma is discussed in [9]. A new technique called multi-modal pressure flow (MMPF) method is proposed, which utilizes the Hilbert-Huang transform to quantify interactions between non-stationary cerebral blood flow velocity (BFV) and blood pressure (BP) in specific frequency ranges as for example the respiratory component of the blood pressure (0.1-0.4 Hz). Using EEMD of both signals, BP and BFV are decomposed into their IMFs. Afterwards the IMFs containing the respiratory signal are identified in both signals by analysis of their instantaneous frequency. Subsequently the phase shift of the instantaneous phases is used to quantify the offset of both signals. Using this technique, the authors showed that the fast dynamic cerebral autoregulation can be characterized by specific phase delays between the decomposed blood pressure and blood flow velocity oscillations. They demonstrated that the phase shifts are significantly reduced in hypertensive, diabetics and stroke subjects with impaired cerebral autoregulation. Additionally, the new technique can reliably assess cerebral autoregulation using both induced blood pressure/blood flow velocity oscillations during clinical tests and spontaneous blood pressure/blood flow velocity fluctuations during resting conditions.

1.1.4 Modeling of cerebral circulation and oxygen supply

Recently [7] we presented a mathematical seven compartment model of cerebral circulation and oxygen supply including an autoregulation mechanism and a pressure dependent production and absorption of cerebrospinal fluid (CSF). The model is designed to interpret the slow temporal dynamics of neurophysiological parameters, recorded at a neurosurgical intensive care unit (ICU), and their interrelationships. In particular, we focused on the arterial blood pressure (ABP), the intracranial pressure (ICP), the partial oxygen pressure in brain tissue (TiPO2) and the relative oxygen saturation of hemoglobin in mixed arterial/venous cerebral blood (SatHbO2). To minimize the number of model parameters, we focused on a simple model which resembles the work of Ursino and Lodi [5], [10], which only incorporates the basic processes of cerebral circulation and oxygenation. The circulatory part of the model
is built up of seven compartments including arteries, capillaries, veins, brain tissue, cerebrospinal fluid, the sagittal sinus and an artificial compartment for the simulation of brain swelling. Currently we combine an oxygen diffusion model based on the theory of the Krogh cylinder with our hydrodynamic model. The combination of the hydrodynamic model with an oxygen diffusion model enables us to simulate the behavior of the partial oxygen pressure in brain tissue (TiPO2), a parameter which can be monitored continuously at an ICU. Using this hybrid model approach, we can reproduce the experimentally well known autoregulation curve [11] which describes a constant cortical blood flow over a wide range of ABP if the autoregulation mechanism is intact. In case of an impaired autoregulation, a linear relationship between pressure and flow emerges. Furthermore, similar interdependencies could be shown for ABP and TiPO2. Although the simulations show a clear nonlinear behavior in case of an impaired autoregulation, in the physiologically meaningful range of the arterial blood pressure a nearly linear correlation exists. Using the built-in artificial compartment for the simulation of brain swelling, we can show that the model reproduces exactly the behavior of experimentally determined pressure-volume curves [12], [13]. Such measurements are used to determine the cerebral compliance which describes alterations in ICP due to volume changes. A disturbed compliance may lead to an exponentially rising ICP for little variations in cerebral volume which in turn has a drastic impact on cerebral perfusion. Also recently [14], [8], we showed that different combinations of impaired or well functioning autoregulation and compliance lead to significantly different correlations of the above mentioned cerebral status parameters. From a medical point of view this can be used to determine which cerebral regulatory mechanisms are disturbed if we can identify simulated correlations with correlations appearing in time series data recorded from
impaired subjects. Despite some promising results the rather large signal-to-noise ratio (SNR) provides a major challenge for the identifications of these correlations. Additionally, the recorded data are composed of different dynamical modes which need to be separated reliably and un-distortedly. A favorable aspect lies in the time scale separation of the various superimposed and intermingled modes, though. The non-stationary part of the ABP signal needs special attention, as it serves as input for the model. Hence, EMD can be applied to separate the non-stationary components of ABP, ICP and TiPO2 from the recorded signals. As an example, Fig. 1.1 shows the extracted non-stationary part of an ABP signal which can be used as input to corresponding model calculations. The latter show promising preliminary results regarding the functionality of the proposed physiological regulatory mechanisms. These modeling efforts will thus be combined in future work with an EMD analysis to extract physiologically meaningful modes which can be directly compared to corresponding model predictions. Both aspects, signal processing and modeling are needed to extract the full biomedical information buried in brain status data recorded during neuromonitoring.

### 1.2 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 extremes, 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 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.
1.2.1 The Standard EMD Algorithm

The sifting process can be summarized in the following algorithm. Decompose a time series \( x(t) \) into IMFs \( x_n(t) \) and a residuum \( r(t) \) such that the signal can be represented as

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

Note that a residuum is a monotonous, i.e. non-oscillatory signal which does not fulfill the conditions for an IMF. Sifting then means the following steps:

- **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 as given above, 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 \( x_n(t) := h_k(t) \) and \( r_n(t) := r_{n-1}(t) - x_n(t) \)
- **Step 3:** 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 sifting process separates the non-stationary time series data into locally non-overlapping intrinsic mode functions (IMFs) which are **locally orthogonal**. Global orthogonality is not guaranteed as neighboring IMFs might have identical frequencies at different time points (typically in < 1% of the cases).

Fig. 1.2 provides a simple example of an EMD decomposition of a toy signal composed of a superposition of a chirp signal (\( |a(t)| = 1 \) [a.u.], \( 25 \text{[Hz]} \leq \omega/(2\pi) \leq 100 \text{[Hz]} \)), a sinusoid (\( |a(t)| = 1, \omega/(2\pi) = 10 \text{[Hz]} \)) and a straight line given by \( x(t) = 0.5 \cdot t \). Fig. 1.2 also presents the related first four IMFs with highest energy extracted by the algorithm. Note that the number of IMFs extracted depends on the stopping criterion employed. In the given example seven IMFs were extracted, the last IMF representing the monotonous trend.
Fig. 1.2  Top: The toy signal consisting of a superposition of a chirp, a sinusoid and a monotonous trend as detailed in the text. Bottom Left: The three IMFs corresponding to the toy signal components as obtained with plain EMD. Bottom Right: Hilbert - Huang spectrum of the first two IMFs of the toy signal.

1.2.2 The Hilbert - Huang Transform

After having extracted all IMFs, they can be analyzed further by applying the Hilbert Transform (HT) or processing them in any other suitable way [15], [16]. The combination of EMD decomposition of a signal into its IMFs plus residue and a subsequent Hilbert spectral analysis to extract instantaneous frequencies and phases is called Hilbert Huang Transform (HHT) [17], [18]. The Hilbert transform calculates the conjugate pair of $x_n(t)$ via

$$H\{x_n(t)\} = \frac{1}{\pi} P \left\{ \int_{-\infty}^{\infty} \frac{x_n(\tau)}{(t-\tau)} d\tau \right\} \quad (1.2)$$
where P indicates the Cauchy principal value. This way an analytical signal $z_n(t)$ can be defined via

$$z_n(t) = x_n(t) + iH\{x_n(t)\} = a_n(t) \exp(i\theta_n(t))$$

(1.3)

with amplitude $a_n(t)$ and instantaneous phase $\theta_n(t)$ given by

$$a_n(t) = \sqrt{x_n^2(t) + H\{x_n(t)\}^2}$$

(1.4)

$$\theta_n(t) = \arctan\left(\frac{H\{x_n(t)\}}{x_n(t)}\right)$$

(1.5)

Each IMF can now be expressed as

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

(1.6)

The signal can then be expressed as

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

(1.7)

An IMF expansion thus provides a generalized Fourier expansion. Note that because

$$\theta_n(t) = \arg(z_n(t)) = \int_{-\infty}^{t} \omega_n(\tau) d\tau = \int_{0}^{t} \omega_n(\tau) d\tau + \theta_n(0)$$

(1.8)

an instantaneous frequency $\nu_n(t)$ can be obtained as

$$\nu_n(t) = \frac{\omega_n(t)}{2\pi} = \frac{1}{2\pi} \frac{d}{dt} \theta_n(t)$$

(1.9)

Fig. 1.2 also shows the Hilbert - Huang spectrum of the toy signal considered.

### 1.2.3 Ensemble Empirical Mode Decomposition

Plain EMD faces problems resulting from boundary effects which lead to mode splitting and over-sifting. To fight these disturbances, a noise assisted variant, called Ensemble Empirical Mode Decomposition (EEMD) has been proposed by [19], [20] which assists and considerably improves the sifting process. 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. 1.3. Two signals \( x_1(t) = 0.1 \cdot \sin(20t) \), \( x_2(t) = \sin(t) \) are superimposed whereby signal \( x_1(t) \) is present only during 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 (see Fig. 1.3), using an ensemble of 15 different noisy signals, copes quite well with this complicated signal.

**Fig. 1.3** a) The first two IMFs obtained with an EMD analysis. Mode mixing is clearly visible due to the partial absence of mode \( x_1(t) \). b) IMFs obtained with an EEMD analysis. The component signals underlying the original signal are extracted almost perfectly.

### 1.3 Sliding Empirical Mode Decomposition

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 data, which often are recorded over very long time spans. Biomedical data, for example acquired during neuromonitoring accumulate to huge amounts of data when monitoring patients in intensive care units (ICU) is extended over days with an appropriate (up to 1000 Hz) sampling rate. Analyzing such large data sets is hardly possible because of
the computational load involved when using conventional EMD. Even more important, however, is the fact that data analysis has to wait until monitoring is finished. But an immediate on-line analysis of such time series data is of utmost importance in ICUs. As no proper EMD algorithm was available yet to achieve this goal, we recently proposed a robust and easy to implement version of EMD, called Sliding Empirical Mode Decomposition or SEMD [21]. This algorithm decomposes time series of arbitrary length into a residuum and a particular number of IMFs. In the subsequent paragraphs we will discuss the operating mode of SEMD and some characteristics of its IMFs and the residuum. We will focus on the impact of well known boundary problems of EMD on the reconstruction quality of SEMD. We will use toy data to analyze the reconstruction quality of the residuum an the IMFs for different parameter settings. We also present a new extension of SEMD, called weighted SEMD which accounts for unwanted boundary effects and tries to suppress them efficiently. An application of wSEMD to brain status data is presented also.

Note that SEMD combines ideas from localEMD as well as onlineEMD [22].

• Local EMD [22] 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

\[
h_k(t) = h_{k-1}(t) - w_{k-1}(t)m_{k-1}(t)
\]

(1.10)

This procedure essentially improves the sifting process and tries to avoid over-sifting.

• On-line EMD: Recently, a blockwise processing, called on-line EMD, has been proposed [22]. The method is still in its infancy and yields unsatisfactory results so far. It still needs to be developed to a robust and efficient on-line technique as the one proposed in this contribution.

### 1.3.1 The principle of SEMD

In a first step, the recorded time series \( x(t_n), n = 1, \ldots, N \) encompassing \( N \) samples, is split into \( M \) segments \( s_m, m = 1, \ldots, M \), each encompassing \( \delta_m = t_{n+\delta_m} - t_n \) samples, which can be analyzed with EMD. Simply adding up the IMFs extracted from the different segments would induce boundary artifacts, however. This is illustrated in a simple example in Fig. [1.4]

Thus segmenting a time series into non-overlapping windows for further analysis leads to strong boundary artifacts. The latter can be avoided when the segments, respectively windows \( s_m, n = 1 \ldots M \), each of length \( \delta_m \) overlap by \( \delta_m - \tau \) samples implying a step size \( \tau \). If, additionally, the window size \( \delta_m \) is a multiple of the step size \( \tau \), i.e. if
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Fig. 1.4 Left: Toy signal (top trace) and underlying signal components: \( \sin(7t) \) (second trace), \( \sin(4t) \) (third trace) and the trend \( 0.1 \cdot t - 1 \) (bottom trace). Right: EMD decomposition of the toy signal from Fig. 1.3. The time series has been segmented into 4 segments and decomposed with EMD. After joining the resulting IMFs together, boundary effects become clearly visible at \( t = 5, 10 \) and \( t = 15 \).

\[ q_m = \frac{\delta_m}{\tau} \in \mathbb{N} \quad \forall m = 1, \ldots, M \tag{1.11} \]

holds, neighboring windows can be joined without having discontinuities or gaps at the boundaries. With this choice, every sample is represented \( q_m \) times in overlapping windows corresponding to consecutive shifts of the time series by \( \tau \) samples. Thus for each sample \( x(t_n), n = 1, \ldots, N \) of the original time series, estimates are calculated within the different overlapping windows \( \delta_m \), at least after the first \( q_m \) iterations have been done. In a perfect world, all \( q_m \) estimates for a distinct sample \( x(t_n) \) would be identical, but due to boundary artifacts of the EMD algorithm, they usually differ. Similar to EEMD, we take the mean value of all estimates of a distinct sample \( x(t_n) \) as the resulting value of SEMD for this sample. If the conditions \( \delta_m \in \mathbb{N} \) and \( N \tau \in \mathbb{N} \) hold with \( N \) the number of samples, the number \( M \) of overlapping windows \( s_m \) of lengths \( \delta_m \), that have to be calculated for the decomposition is given by:

\[ M = \left( \frac{N - \delta_m}{\tau} \right) + 1 \tag{1.12} \]

A schematic illustration of the principle mode of operation of the SEMD algorithm is shown in Fig. 1.5 below. The time series in every segment \( s_m \) is decomposed by EMD into \( J - 1 \) IMFs \( x_{m,j}(t) \) and a local residuum \( r_m(t) \equiv x_{m,J}(t) \) according to

\[ x_m(t) = \sum_{j=1}^{(J-1)} x_{m,j}(t) + r_m(t) \tag{1.13} \]

whereby the number of sifting steps is kept equal in all segments. Resulting IMFs are collected in a matrix with corresponding samples \( x(t_n) \) forming the columns of the matrix with \( q = \frac{\delta}{\tau} \) entries. Columns corresponding to the beginning or end of the time series are deficient, hence are omitted from further processing. This assures
that all columns contain the same amount of information for estimating average IMF amplitudes at every time point $t_n$ in each segment $s_m$. This finally yields for $n > \delta_m$ average IMFs according to ($q$ - size of the ensemble)

$$\langle x_j(t_n) \rangle = \frac{1}{q} \sum_{m=1}^{m+q-1} x_{m,j}(t_n)$$  \hspace{1cm} (1.14)

$$\langle r(t_n) \rangle = \frac{1}{q} \sum_{m=1}^{m+q-1} r_m(t_n)$$  \hspace{1cm} (1.15)

$$m = \lfloor \frac{t_n - \delta}{\tau} \rfloor + 2$$  \hspace{1cm} (1.16)

Note that by the formulas 1.14, 1.15 and 1.16 the completeness of the decomposition process is warranted as for every sample $x(t_n)$ the mean value of $q$ decompositions of conventional EMD, which in turn are complete, forms the result of the SEMD decomposition.

Problems arise if different numbers of IMFs results in different overlapping segments, or if the same intrinsic frequency appears in different IMFs in different overlapping segments. To avoid such complications, the number of sifting steps and IMFs is kept constant for all decompositions. Except for the stopping criterion, any EMD algorithm can be applied but EEMD has proven to yield best results mostly.

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**Fig. 1.5** Schema of the SEMD algorithm. The time series segments in the shifted windows are decomposed with EMD. IMFs and the residuum are determined finally by mode amplitudes which are averaged over corresponding samples in all windows. $\delta_m$ describes the window size and $\tau$ the step size.
1.3.2 Properties of SEMD

Contrary to global EMD, the local residua estimated with SEMD for every segment may turn into low frequency oscillations when joined together into an average global residuum. By choosing the segment size properly it may be controlled which local oscillations should appear as distinct IMFs and which should be absorbed as apparent local trends into the respective local residua. These apparent local trends, which combine to low frequency oscillations in the final average global residuum, may be down-sampled and subsequently analyzed with SEMD as well. This process can be repeated until finally a truly monotonous trend remains. Hence, this cascaded application of SEMD acts as a low frequency filter for long-term oscillations and trends as can be found, for example, in biomedical time series.

Similar to EEMD, also with SEMD an averaging over differently decomposed data sets is achieved. While, due to added noise, with EEMD a given sample is associated with different amplitudes, with SEMD the same amplitude is associated with different samples in different shifted segments. This latter behavior alleviates effects related with a non-unique data decomposition via EMD. Furthermore, artifacts resulting from end effects loose their impact via averaging. Finally, segmentation with proper window size and step size does not result in boundary artifacts after combination of the local IMFs. SEMD is furthermore similar to local EMD in that the stopping criterion needs to be valid only locally, i.e. within the window considered. This substantially reduces over-sifting and also reduces the number of necessary sifting steps until the stopping criterion is met locally. Finally note that while local IMFs fulfill all defining conditions, this is not necessarily true for the resulting average IMFs though the related deviations should always be small.

1.3.3 Application of SEMD to toy data

The following simulations use well-chosen toy examples for investigating the impact of the window size on the estimated residuum as well as on the reconstruction quality. The analysis was performed with toy data to be able to assess the results quantitatively. Note that the number of IMFs to be extracted is fixed to \( \lceil j \rceil = \log_2(\delta_m) \) where \( \delta_m \) designates the size of the \( m \)-th segment. This assures an identical number of extracted IMFs in every segment which is necessary for the construction of appropriate IMFs. Furthermore, the frequencies of the underlying component signals have been chosen sufficiently different to avoid problems with frequency resolution.

The toy signal \( s(t) = \sum_i s^{(i)}(t) \) (see Fig. 1.6) consists of

- a sawtooth wave
  \[
  s^{(1)}(t) = (1.5708)^{-1} \arcsin (\sin(699 \cdot t))
  \]
• a sinusoid
\[ s^{(2)}(t) = \sin(327 \cdot t) \]

• a cosine function with a time-dependent frequency
\[ s^{(3)}(t) = \cos \left( 2 \cdot (t + 20)^2 \right) \]

• a monotonous trend, which renders the superposition of the signals non-stationary
\[ s^{(4)}(t) = 0.1 \cdot t - 1 \]

The oscillatory components are chosen carefully regarding their frequency so that mode mixing does not occur. For the time series \( N = 40,000 \) data points were used with \( \Delta t = t_{n+1} - t_n = 0.0005 \). Note that the oscillating signal components have a period much smaller than the window sizes studied. Hence, these component signals should be reconstructed within the IMFs. The decomposition has been effected using a segment with \( \delta = 2500 \) samples each and varying step size \( \tau \) and ensemble size \( q \), respectively.

**Fig. 1.6** A detail of the toy signal (top trace) consisting of a sawtooth wave, a sinusoid, a cosine function with time-dependent frequency and a monotonic function (lower traces).

### 1.3.3.1 Variable step size

The decomposition has been performed for all step sizes \( \tau = 2, \ldots, 1250 \) separately and the condition \( q = \frac{\delta}{\tau} \in \mathbb{N} \) has been assured in each case. For the three oscillatory components and the residuum, the quality of the decomposition can be judged by estimating the Minkowski distance \( (MD_p) \) of order \( p \) between the original sig-
nal components $s^{(i)}(t)$ and their corresponding IMFs $x_j(t)$ or the residuum $r(t)$, respectively.

$$MD_p = \left( \sum_{n=1}^{N} \left| s_i(t_n) - x_i(t_n) \right|^p \right)^{\frac{1}{p}} \quad (1.17)$$

Using $p = 1$ results in what is called Manhattan distance or $L_1$-norm which is related to an average reconstruction error $\langle RQE \rangle = N^{(-1)} \cdot MD_1$, while $p = 2$ provides an Euclidean distance or $L_2$-norm, which is related to a mean squared error (MSE) via $MSE = N^{(-1)} (MD_2)^2$. The latter will be used throughout in the following to measure reconstruction quality $RQ$. Fig. 1.7 shows the MSE of components 1-3 and the monotonous trend as function of the ensemble size $q$.

![Fig. 1.7](image)

**Fig. 1.7** Top: Mean square error (MSE) of components 1-3 and the monotonous trend estimated with SEMD for the toy signal given above as function of ensemble size $q$. The window size was $\delta_m = 2500$. Bottom: Mean square error of component 1-3 and the monotonic trend estimated with SEMD for the toy signal given above as function of the window size $\delta_m$. The ensemble size was kept constant at $q = 50$.

With increasing ensemble size $q$ or decreasing step size $\tau$, the reconstruction quality improves. Starting with an ensemble size of about $q = 50$ estimates, the MSE stays roughly constant. Therefore the results show that for practical applications an ensemble size of about $q = 50$ is a good trade-off between reconstruction quality and computational load.
1.3.3.2 Variable window size

In the following we studied the influence of the window size on the reconstruction quality. The decomposition was applied for different segment sizes and a constant ensemble size \( q = 50 \). Fig. 1.7 shows the resulting reconstruction quality of component 1-3 and the monotonic trend as a function of the segment size.

Especially for \( \delta = 500 \) and \( \delta = 1000 \) the MSE is higher than for larger segment sizes, but with a value of \( MSE \leq 0.0015 \) the reconstruction still can be considered very satisfactory. With increasing window size, the reconstruction error decreases, which also holds true for all other tested numbers of estimates. Supposing that the artifacts caused by the boundary conditions have an almost constant penetration depth, for larger windows the percentage of corrupted estimates decreases. This effect may lead to a better reconstruction in case of a larger window size. Only the reconstruction error of the residuum increases for larger window sizes. The MSE of the monotous trend obtained by SEMD fluctuates strongly, because the last component of the decomposition with SEMD is not necessarily a line after averaging over all suggestions for the data points. As the errors resulting from reconstructing the other components add up and reside in the residuum at the end, it is possible that the residuum is the most irregular component after the decomposition. In our example, the reconstruction of the residuum fluctuates with a larger ‘amplitude’ around the original monotonous function for larger window sizes, thus the error increases with window size (see fig. 1.8). The ‘true’ monotonous trend can be obtained by smoothing the data.

![Fig. 1.8](image-url) The figure shows a detail of the original monotonic component of toy example two compared to the residuum of the decomposition via SEMD with window sizes \( m = 5000 \) and \( m = 500 \).

1.3.3.3 Segment size and periodic components of the residuum

The residuum of SEMD may contain periodic components if the periodicity is much larger than the window size used. Components with a periodicity much smaller than the window size are recognized as IMFs. To evaluate the behavior of SEMD in the intermediate range, a toy signal \( x(t) = x_0 \cdot \sin(2 \pi \cdot t) + \epsilon(t) (\Delta t = 0.0005) \) con-
sisting of a sinusoid with a period of \( T = 2000 \) data points and i.i.d. noise \( \epsilon(t) \) with an amplitude \( \epsilon_0 = 0.1x_0 \) corresponding to 10\% of the maximal amplitude \( x_0 \) of the sinusoid is decomposed with SEMD. Different segment sizes \( \delta = 200, \ldots, 5000 \) were used, whereas the ensemble size \( q = 50 \) was kept constant and the central 26,000 data points (of 40,000 originally) were considered for the analysis. Eventually the MSE of the residuum compared to the sine function was computed, as can be seen in fig. 1.9.

![Fig. 1.9](image)

\textbf{Fig. 1.9} The figure shows the mean squared error of the residuum compared to the sinusoid depending on the window size.

For a larger window size, the MSE increases because the amplitude of the sine function decreases as it is split up into the residuum and an IMF. The sinusoid resides entirely in the residuum for a window size of about \( \delta = 1000 \) respectively \( \delta = 0.5 \cdot T \) or smaller. The component is found completely in an IMF for ca. \( \delta = 3500 \) respectively \( \delta = 1.75 \cdot T \) or larger. Depending on which oscillatory components of the original signal are supposed to appear in IMFs, an appropriate window size should be chosen.

\subsection{1.3.4 Performance evaluation of SEMD}

In order to be able assessing the performance of SEMD, its results were compared to existing versions of EMD. Again the toy example consisting of a sawtooth wave, a sinusoid, a cosine function with a time-dependent frequency and a monotonic trend (see fig. 1.6) was used for demonstration purposes. The described time series was then decomposed with SEMD, whereas different window sizes (\( \delta = 500, 1000, 1500, 2000, 2500, 3000, 4000 \) and 5000) and step sizes were used, so that the ensemble of suggestions \( q = 50 \) for each resulting date point remained constant. Figure 1.10 compares the dependence of the mean squared reconstruction error (MSE) of components 1 – 4 of the toy example on window size for decompositions invoking SEMD and EMD, respectively.

For \( \delta = 500 \) and \( \delta = 1000 \) the reconstruction error is generally slightly higher and therefore the use of such small window sizes is not recommended. The MSE of IMF 1, 2 and 3 is smaller for the decomposition with SEMD and, concerning
Fig. 1.10 The figure shows the reconstruction error of components 1 – 4 of toy example two after the decomposition with SEMD and EMD.

the residuum, mostly smaller for the decomposition with EMD. As has been said already, the reconstruction quality of the monotonous trend obtained by SEMD is worse than obtained by EMD for larger window sizes.

Flandrin et al., in a short note, already suggested, in a short note only, an online EMD [23]. Furthermore, because of the averaging operation, SEMD bears some resemblance to Ensemble EMD. Thus also these two methods have been evaluated and their respective MSEs are included for comparison as well.

Figure 1.11 shows the sum of the reconstruction errors of all four components of the toy example decomposed with EMD, SEMD, EMD online and Ensemble EMD for 50 iterations. That number was chosen for EEMD, as the ensemble of suggestions for one component decomposed with SEMD has been \( q = 50 \) as well in our tests.

As the reconstruction with EEMD exhibited strong mode mixing, a large reconstruction error resulted, and any comparison deemed inappropriate. Therefore fig. 1.11 also shows the reconstruction quality of the other three methods separately with higher resolution.

SEMD outperforms EMD and online EMD by far as is evident from its reconstruction error which is much smaller. Better results than with online EMD are still obtained with plain EMD. With an ensemble size of only \( q = 50 \), SEMD performs the most accurate decomposition of all tested methods and represents a high quality data analysis. Additionally, it is a true online method and constitutes a better and more sophisticated tool than the online EMD method proposed by [23].
Fig. 1.11 Top: Reconstruction error of the four components obtained with SEMD, EMD, EEMD and online EMD summed up. Bottom: Reconstruction error of the four components obtained with SEMD, EMD and online EMD summed up.

1.4 Weighted Sliding EMD

Using EMD, and especially SEMD, it is important to estimate the error range caused by boundary effects. In order to be able to evaluate how large a part of the data set at the beginning and at the end is affected by boundary effects, this impact was studied. A number of data points residing near the beginning or end of a window are used by SEMD for the calculation of the resulting IMFs or the residuum, respectively. Thus the ensemble contains data points which are probably defective. In order to diminish reconstruction errors due to such boundary effects, we developed the weighted Sliding Empirical Mode Decomposition (wSEMD).
1.4.1 Error range of EMD

In the following, the error range of EMD is studied depending on the frequency of the underlying components and the window size. In order to be able to quantify the reconstruction error, toy data examples were used. The results obtained with the toy example shown in fig. 1.6 are depicted in this section.

After the decomposition of a segment of the time series with EMD, the evolution of the error was calculated in the chosen window by subtracting the original component and the corresponding IMF, and recording the absolute value of the result. This time series was smoothed by averaging, which can be seen in fig. 1.12, where the crosses mark the error range. As a limiting value for the error spread, 2.5 times the average error of the middle part of the error time series was defined. In this case, the middle part of the time series means the time series without the first and last 200 data points, respectively.

As the reconstruction error for the monotonous trend is lowest where the two lines intersect, and an error spread cannot be defined in that case, only components 1 - 3 were used for the analysis. The window sizes $\delta = 500, 1000, 1500, 2000, 2500, 3000, 4000$ and $5000$ were considered. For every IMF and all window sizes a sample of $N = 1000$ different fragments of the data were tested regarding their error range. In the following diagram (fig. 1.13), average error ranges and their standard deviations at the beginning of the time intervals are shown as function of window size. They are only marginally different to the error ranges at the rear ends, which therefore are not shown.

For IMF 1 and 2 (not depicted) of the example, the error ranges remain constant, whereas for IMF 3 they are smaller for smaller window sizes, which is apparent in figure 1.13. That behavior can be caused by the evaluation method, since the reconstruction error is generally larger for smaller window sizes. Hence the limit value...
for the error range is higher. Further it can be noted, that the lower the frequency, the wider the error spreads from the boundaries towards the center of the segment.

Figure [1.14] shows the error range at the beginning and end of the window for all studied IMFs respectively frequencies with a fixed window size $\delta = 2500$.

Again the frequency dependence of the error is apparent. Presumably the reason for this effect is that for higher frequencies fewer extrema and accordingly knots for the spline interpolation are available, i.e. the signal reconstruction is less accurate.

In figure [1.14] the error spread is shown as average number of periods of the corresponding frequency component which is affected for window sizes $\delta = 2000$, 2500 and 3000. As the frequency of component 3 changes with time its average period was considered as reference.

It is demonstrated that the error range is weaker than linearly dependent on the frequency and the number of periods affected by the error spread is not constant. The average number of periods affected by the error spread is only marginally dependent on the window size. The frequency of the third component changes over time. As a reference period of the original component, the average period of the time series
was used, because the whole time series or all periods, respectively, were used for the calculation of the error spread.

Considering all results it can be concluded that the use of too small window sizes is not recommended for SEMD. Window sizes should amount to at least about $\delta = 1500$ data points. For smaller window sizes, the error range does affect a too large part of the windows. Generally the error spread hardly depends on the frequency of the underlying component.

1.4.2 The principle of weighted SEMD

In order to suppress the influence of boundary effects on the resulting time series, weight functions are used in the following. After the decomposition with EMD, the IMFs and the residuum, estimated within every window, is multiplied by a weighting function. Calculating the average of the estimates $q$ data points and $q$ coefficients, respectively, are used, and, at the end, every data point is normalized by the reciprocal of the sum of all used weights. Therefore the amplitude of every IMF is preserved.

Considering our results concerning the error spread in the data windows, we used the following weighting functions

- a parabola $f(x) = x(1-x)$ with $x = \frac{1}{\delta}, \frac{2}{\delta}, \ldots, \frac{\delta}{\delta}$, where $\delta$ denotes the window size
- a Gaussian distribution generated by the MATLAB command `gausswin(\delta)`, which generates a vector $w(n) = e^{-\frac{1}{2}(\alpha 2\pi n)^2}$ of rank $\delta$ where $-\frac{N}{2} \leq n \leq \frac{N}{2}$, $\alpha = 2.5$ and $N = \delta - 1$
- several step functions, which alternate between 0 near the boundaries and 1 in the central part of the time series

1.4.3 Performance evaluation of weighted SEMD

Again we used toy data to evaluate the performance of weighted SEMD. The results depicted were obtained with the example shown in [1.6].

In the following, IMF 1 generated by either EMD or weighted SEMD is illustrated. The algorithm wSEMD applied a step function with variable step length indicated by the parameter $w$ (see fig. 1.15).

The parameter $w$ indicates that $w$ data points at both ends of each window were multiplied by 0 and the rest of the data points by 1. The parameter $w$ was increased from $w = 25$ to $w = 225$. Because of the similarity of all diagrams which illustrate the reconstruction errors of the different IMFs, only the reconstruction error of IMF 1 is shown. The MSE is slightly increased for $\delta = 500$ and $\delta = 1000$, but also for $\delta = 2000$ in both diagrams. However, one has to take into account that the scale of
Fig. 1.15 Top: The mean squared error of IMF 1 obtained by SEMD weighted with different step functions respectively different parameters \( w \) and EMD. Bottom: The reconstruction error of the sum of all IMFs and the residuum generated with SEMD weighted with several functions (a step function with \( w = 150 \), a parabola and a Gaussian distribution), un-weighted SEMD and EMD compared to the original signal.

the MSE shows a quite small margin. Therefore, also its dependence on the window size is only marginal. The reconstruction error of IMFs 1-3 generated with weighted SEMD with the described weight function is generally smaller than with EMD and only slightly dependent on \( w \).

The MSE of IMF 1 and the residuum is also shown depending on different weight functions, and compared to SEMD and EMD as can be seen in fig. 1.18.

For the step function, the parameter \( w = 150 \) was used, because it yielded good results while still using a sufficient amount of estimates for the algorithm. The MSE functions for IMF 1, 2 and 3 (not depicted) generated by SEMD with different weight functions are all very similar. The evolution of the error resembles the one of SEMD, but the error itself is smaller. The reconstruction with EMD yields the
Fig. 1.16 Top: The reconstruction error of IMF 1, which was generated by EMD, SEMD and SEMD with different weight functions (namely a step function with \( w = 150 \), a parabola and a Gaussian distribution). Bottom: The reconstruction error of the residuum of toy example two, which was generated by EMD, SEMD and SEMD with different weight functions (namely a step function with \( w = 150 \), a parabola and a Gaussian distribution).

largest error for most window sizes. In order to obtain a good result in terms of reconstruction error, any of the tested weight functions can be used.

Applying a weighting function does not guarantee an improvement of the reconstruction of the residuum, though. This is because the error is minimal, when two lines intersect. However the intersection does not necessarily occur in the middle of the window. Furthermore, the residuum gained with (weighted) SEMD is not necessarily a monotonous function after averaging. Therefore the reconstruction of the trend is mostly best with EMD. For the IMFs, the use of weighted SEMD can be recommended strongly as the best results are achieved that way. Anyway, a true online analysis of a given time series can only be achieved with SEMD and the less satisfactory reconstruction of the residuum has to be accepted as a little grain of salt in the otherwise very satisfactory and robust performance of the SEMD algorithm.
1.4.4 Completeness

After applying weighted SEMD, we studied the completeness of the decomposition into IMFs and the residuum as obtained with weighted SEMD compared to the original signal. Again the MSE of the sum of all IMFs and the residuum of applying SEMD weighted by a step function with $w = 150$, a parabolic weight function and a Gaussian weight function, un-weighted SEMD and a plain EMD algorithm is analyzed (see fig. 1.15).

Only the decomposition with SEMD where a step function was used for weighting shows a complex behavior of the error function with larger errors which, however, in absolute value are still vanishingly small. The completeness of the other decompositions with weighted SEMD and SEMD is in accord with EMD. Contrary to SEMD, the reconstruction error of SEMD weighted with the parabola and the Gaussian distribution does not increase but stays constant. However, the reconstruction error of SEMD is smaller, hence the reconstruction is more complete, for small window sizes. Generally, EMD reaches a higher completeness than all other tested methods. The averaging, which is done using (weighted) SEMD, is possibly the reason for the slightly decreased completeness of the decompositions. But quantitatively the numerical value of the error is vanishingly small, hence the decomposition still can be considered complete in every respect.

1.4.5 Examination of the IMF criteria

Further it has to be verified if the components which were obtained by a decomposition with SEMD, weighted SEMD or Ensemble EMD truly represent IMFs in the sense that they obey the conditions to be fulfilled by an IMF by definition. First the mean value of an IMF has to be zero everywhere, second the number of local extremes and zero crossings can differ by one, at most. Once more toy data was used in order to examine if the two conditions are met.

Evaluating the results one has to keep in mind, that the number of sifting steps is kept constant in the algorithm so that SEMD, weighted SEMD and also Ensemble EMD work properly (see 1.13). This method was first introduced in [24], which means that also for plain EMD the stopping criterion respectively the IMF criteria are not necessarily fulfilled.

1.4.5.1 Mean value

Figure 1.17 shows the absolute mean value of IMFs 1 and 3 depending on the ensemble size of the decomposition.

In most cases SEMD and especially weighted SEMD produces an IMF that meets the first criterion even better than EMD as soon as an ensemble size of ca. 50 is utilized. The average value fluctuates only slightly beginning at $E = 50$ which
indicates again that a decomposition with that parameter value is a good trade-off between computational load and reconstruction quality. The right subfigure 1.17 shows one of the examples in which EMD reaches the best result. However, the average value of the (weighted) SEMD decomposition is still quite small and barely higher than the EMD result.

1.4.5.2 Number of extrema and zero crossings

The difference between the number of extrema and zero crossings depending on the ensemble size is depicted in fig. 1.18 for IMF 1 and 3 of the toy example.

Whereas the EMD decomposition generally fulfills the second criterion for all IMFs of the toy data examples, Ensemble EMD fluctuates strongly in some cases even for large ensemble sizes (not depicted). These large values of the difference originate from the potential ruggedness of the signals after the calculation of the average time series. SEMD and weighted SEMD, however, show only for small ensemble sizes a difference larger than 1 between the extrema and zero crossings. Especially weighted SEMD meets the IMF requirement already for very small ensemble sizes \( E \), therefore it is to be preferred. In summary, the IMF constraints are very well satisfied by the extracted components, hence the results of the (weighted) SEMD decompositions really can be considered true IMFs.
1.5 Analysis of Brain Status Data

After a thorough evaluation of all properties of the newly proposed algorithms, the following section discusses applications of SEMD and wSEMD to brain status data and compares them with respective results from EEMD.

1.5.1 EEMD applied to Brain status data

Non-stationary time series are difficult to deal with using classical analysis methods. However, EMD decomposes any time series into stationary IMFs and a non-stationary residuum. EEMD is a noise-assisted method to improve sifting [19]. In practice, EEMD works by repeatedly adding white noise to the data set in each iteration and decomposing the noisy data into IMFs. Finally, an ensemble average of the respective IMFs is calculated yielding the final result. In practice, EEMD helps to avoid over-sifting and mode-mixing.

1.5.1.1 EEMD decomposition of brain signals

Brain status data, especially ABP and ICP, have been recorded synchronously from a patient. Fig. [1.19] shows the signal recorded for 14 h with a sampling rate of 1 Hz. It
illustrates the non-stationary component, while the high-frequency oscillatory components become visible from an expanded segment of 300 s duration.

Plain EMD or EEMD was applied to these signals to extract their IMFs and residues. Only the first and last IMF are shown in Fig. 1.20 and 1.21 together with the original signal and the residuum. For better comparison, IMFs obtained with either algorithm are presented in corresponding figures. Both algorithms use the following parameters if not stated otherwise:

- The envelops are estimated using cubic splines.
• Boundary artifacts are avoided by adding data points as proposed in [24].
• The number of sifting steps is fixed to $N_{sifting} = 10$.
• The number of signal components is chosen to $j = \lfloor \log_2(N) \rfloor$ with $N$ the number of data points sampled.
• EEMD used normally distributed noise and an IMFs were estimated as an ensemble average over 100 realizations.

![Fig. 1.20](image)

The first extracted IMF in every case reflects the breathing mode with an average period of $\langle T_B \rangle = 4$ [s] corresponding to an average frequency of $\langle \nu_B \rangle = 0.25$ [Hz]. The corresponding Hilbert-Huang transforms (see Fig. 1.22) exhibit fluctuations of their instantaneous frequencies around the average frequency $\langle \nu_B \rangle$ due to the low sampling rate employed. Average frequencies and signal periods for the 300[s] segment of both pressure time series are collected in Tab. 1.1. Generally, an EEMD decomposition results in smoother IMFs than plain EMD as can be seen from a comparison (see Tab. 1.2) of average frequencies $\langle \nu \rangle$ and related standard deviations $\sigma_\nu$, deduced by applying a Hilbert-Huang transform (HHT) to the data, for some IMFs extracted from both ABP and ICP time series. The example demonstrates that
physiologically meaningful signal components can be extracted as single IMFs with either EMD or EEMD. Note that because of the low sampling rate faster modes like, for example, the heart beat cannot be resolved.

Table 1.1  Average frequency ⟨ν⟩ and related average period ⟨τ⟩ for a Δt = 300 s long segment of both pressure time series recorded

<table>
<thead>
<tr>
<th></th>
<th>⟨ν⟩ [Hz]</th>
<th>⟨τ⟩ [s]</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABP</td>
<td>0.2620</td>
<td>3.8168</td>
</tr>
<tr>
<td>ICP</td>
<td>0.2664</td>
<td>3.7538</td>
</tr>
</tbody>
</table>
Fig. 1.22 The time-frequency spectrum resulting from a Hilbert-Transformation of the first IMF extracted with EEMD from the recorded ABP signal (top) and the recorded ICP signal (bottom).

Table 1.2 Average frequencies $\langle \nu \rangle$ and related standard deviations $\sigma_{\nu}$ of some IMFs extracted with plain EMD and EEMD

<table>
<thead>
<tr>
<th></th>
<th>$\langle \nu \rangle$ [Hz]</th>
<th>$\sigma_{\nu}$ [Hz]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>EMD</td>
<td>EEMD</td>
</tr>
<tr>
<td>ABP: IMF 1</td>
<td>0.2687</td>
<td>0.2620</td>
</tr>
<tr>
<td>ABP: IMF 3</td>
<td>0.0660</td>
<td>0.0715</td>
</tr>
<tr>
<td>ABP: IMF 10</td>
<td>0.0056</td>
<td>0.0464</td>
</tr>
<tr>
<td>ICP: IMF 1</td>
<td>0.2596</td>
<td>0.2664</td>
</tr>
<tr>
<td>ICP: IMF 3</td>
<td>0.1641</td>
<td>0.1634</td>
</tr>
<tr>
<td>ICP: IMF 8</td>
<td>0.0288</td>
<td>0.0204</td>
</tr>
<tr>
<td>ICP: IMF 10</td>
<td>0.0086</td>
<td>0.0066</td>
</tr>
</tbody>
</table>

1.5.1.2 EEMD detrending of brain signals

EEMD can be used to remove non-stationary contributions, called trends, from any given time series. When analyzing brain status data, the non-stationary contributions correspond to long-term trends of the patient’s brain status which are of interest during neuromonitoring. This detrending of the recorded time series can be achieved by subtracting from the recorded time series $x^{(c)}(t)$ the residuum $r(t)$ and, possibly, some slowly varying IMFs $x_j(t)$, $j = J, J - 1, \ldots, J - k$. The resulting signal

$$x_{\text{stat}}^{(c)}(t) := x^{(c)}(t) - r(t) = \sum_{j=1}^{(J-1-k)} x_j(t)$$  \hfill (1.18)$$

is then checked for stationarity, and the number of IMFs being summed up finally is adjusted accordingly. As an example, recorded ABP and ICP time series $x^{(c)}(t)$, $c = ABP, ICP$ are considered encompassing $N = 50000$ samples col-
lected with a sampling rate of $(\Delta t)^{-1} = 0.2$ Hz. The resulting sum of 14 IMFs is oscillating around zero but some slow trends with long periods which are present, suggest that not all non-stationary contributions have been removed. This can be checked by monitoring the constancy of the mean of the $\delta_S = \frac{S}{N} \in \mathbb{N}$ samples of $x^{(c)}(t)$ in $S$ non-overlapping time windows. These mean values are estimated as

$$\langle x^{(c)}_s \rangle(s) = \frac{1}{M} \sum_{m=1}^{M} x^{(c)}_m(t + m \cdot (s - 1)), \ s = \{1, 2, \ldots, S\}$$  (1.19)

Finally the $(J - k|k = \{1, 2, \ldots\})$ lowest frequency IMFs, from all $J$ IMFs extracted, are additionally subtracted from the recorded data $x^{(c)}(t)$, leaving only the high-frequency IMFs to form the de-trended, stationary time series:

$$x^{(c)}_{J-k}(t) = \sum_{j=1}^{J-k} x^{(c)}_j(t) = x^{(c)}(t) - \left[ r(t) + \sum_{j=J-k}^{J} x^{(c)}_j(t) \right]$$

Again the mean of the resulting signal, i.e. the sum of the stationary high-frequency IMFs, is estimated in the $S$ time windows and the whole procedure is repeated for varying the number $S$ of segments chosen. Note that IMFs 12 and 13 show very low amplitudes only, hence have been neglected from further consideration. Fig. 1.23 shows the standard deviations of the resulting series of mean values of the recorded ICP time series as function of the number $S$ of segments.

The diagrams corroborate an apparent time dependence of the mean values estimated within the time windows. Depending on the chosen segment length, low frequency stationary oscillations are transformed into seemingly non-stationary trends which determine the mean value of the time series in the considered segment. Only with very few segments, encompassing a large number of samples, a convergence of the resulting mean values towards weak stationarity can be observed. In summary, stationarity cannot be defined uniquely within the realm of SEMD, rather it strongly depends on the segment length chosen and the lowest frequency oscillations present in the recorded signals. This is obvious from IMF 7 and IMF 8 which contain oscillations with a period of $T_7 = 240$ s and $T_8 = 600$ s, respectively, which correspond to relevant physiological signals, namely the so-called Mayer waves [25].

### 1.5.2 SEMD applied to brain status data

In this section the potential of SEMD to analyze and decompose real brain status data will be explored. The time series concern arterial blood pressure (ABP), intracranial pressure (ICP) and partial oxygen pressure (TiPO2) recordings sampled continuously over many days with sampling rates of $(\Delta t)^{-1} = 0.2[Hz]$ and $(\Delta t)^{-1} = 1[Hz]$, respectively. First, the dependence of the decomposition onto segment size and step size will be investigated. Next it will be studied how low
frequency oscillations can be separated via SEMD into the residuum. The latter often correspond to non-stationary signal components which are hard to deal with using classical signal processing paradigms. This detrending, applying EMD, has been discussed in the literature already by [26] and [23]. However, if not only a monotonous residuum but also certain low frequency oscillations need to be separated out, a subsequent sophisticated analysis of the estimated IMFs is necessary as discussed above. To the contrary, SEMD provides a very simple and efficient way to achieve this goal by simply varying the segment size accordingly.

Fig. 1.23 Top: Standard deviation of mean values of $x_{ICP}^{1}(t)$ as function of $S$ after various subtracted "residual" IMFs. Bottom: Dependence of the standard deviations of the mean values on the number $S$ of subsegments for the original ABP time series and its difference to the residues estimated with SEMD.
1.5.2.1 Step size and window size

Analyzing biomedical signals, their component signals are usually not known with sufficient precision. Hence reconstruction quality needs to be assessed despite the fact that no proper reference signal is available as is the case with toy data examples discussed above. Following, apparent residues will be estimated with SEMD varying the step size $\tau$ but keeping the window size $\delta_m$ fixed. Next, these apparent residues corresponding to subsequent step sizes will be subtracted sample by sample. The squared differences summed and divided by the number of samples then yield the mean squared reconstruction error (MSRE), i.e.

$$MSRE = \frac{1}{N} \sum_{n=1}^{N} \left( r_\tau(t_n) - r_{\tau+1}(t_n) \right)^2$$

(1.20)

Here $N$ designates the number of samples, $r_\tau(t)$ represents the "apparent" residuum for step size $\tau$ and $r_{\tau+1}(t)$ the corresponding "apparent" residuum for the subsequent step size $\tau + 1$. The window size $\delta = 256, 512, 1024, 2048$ used is always a multiple of the step size considered. In the following examples (see Fig. 1.24), a window size $\delta = 2048$ and a step size $\tau = 8$ was used for illustrative purposes.

The MSRE for two corresponding residues $\tau, \tau + 1$ has been estimated for the ABP, ICP and TiPO2 time series using segment sizes $\delta = 256, 512, 1024$ and $\delta = 2048$. Fig. 1.25 illustrates the MSRE for segment size $\delta = 1024$. Similar graphs result for all other segment sizes and are omitted here.

Under all conditions investigated, the MSRE as function of the step size quickly converges for small step sizes towards values close to zero. Hence, the estimated residues are very similar under such conditions. Clearly, the size $q$ of the ensemble is the key quantity determining the MSRE. An ensemble size $16 \leq q \leq 64$ provides a good trade-off between reconstruction error (MSRE) and computational load.

1.5.2.2 SEMD detrending of brain status data

The algorithm SEMD can also be used to remove non-stationary components from the recorded signals. Which underlying components contribute to the residuum, hence should be separated, can be controlled simply and efficiently by the segment size. The following study applies very small step sizes merely to achieve optimal results. In on-line applications such small step sizes are usually impractical. The investigations use ABP and ICP time series with $N = 50000$ samples, a variable segment size and step sizes $\tau = 2$. After decomposing the signal with SEMD, the residuum is subtracted from the original time series. Fig. 1.26 presents results of such a detrending of an ABP time series using SEMD with a segment size $\delta = 2048$ and a step size $\tau = 2$. The related Fig. 1.25 presents the mean and standard deviation of the difference between the residuum and the original ABP time series for different step sizes and a segment size $\delta = 2048$. Both parameters fluctuate only
slightly at small step sizes, indicating that a high reconstruction quality could be achieved robustly.

To test for stationarity, mean values of the original time series and the difference of the original time series and the estimated residuum are followed over time by estimating them in subsequent subsegments $s$ of variable segment size $\delta_s = 256$, 512, 1024 and 2048. Fig. 1.23 exhibits the dependence of the standard deviations of the fluctuations around their mean values on the number of subsegments $S$. 

Fig. 1.24 Arterial blood pressure (ABP) (top), intracranial pressure (ICP) (middle) and Partial oxygen pressure (TiPO2) (bottom) time series and corresponding residua estimated with SEMD, $\delta = 2048$, $\tau = 8$. 
Fig. 1.25 Top: Mean square distance $MSD$ of two neighboring residues $i, j$ of the ABP, ICP and TiPO2 time series estimated with $SEMD$ using a segment size $\delta = 1024$. Bottom: Mean (left) and standard deviation (right) of the ABP time series after detrending as function of the step size and a segment size $\delta = 2048$.

Fig. 1.26 Sum of all IMFs estimated from the ABP time series using $SEMD$ with $\delta = 2048$ and $\tau = 2$.

The results prove a substantial reduction of the non-stationary components in the difference signal. But weak stationarity is only reached if the number $S$ of sub-segments stays small in accord with results obtained earlier already. However, the amount of non-stationary signal parts removed with $SEMD$ is much larger than when the residues are estimated with $EMD$ and then subtracted from the original time series. Again a proper choice of the segment size is critical not to remove informative oscillations from the recordings.
1.5.2.3 SEMD versus EEMD detrending

The following study compares the residues estimated with SEMD with the residues plus the sum of low frequency IMFs estimated with EEMD. First, the mean square difference (MSD) between the residues estimated with either SEMD or EEMD is calculated according to

\[
MSD_1 = \frac{1}{N} \sum_{t=1}^{N} (r_s(t) - r_e(t))^2
\]  

(1.21)

Here \(N\) denotes the total number of samples, \(r_s(t)\) represents the "apparent" residuum estimated with SEMD and \(r_e(t)\) the corresponding "apparent" residuum estimated with EEMD. Next, the "apparent" residuum \(r_s(t)\) and the lowest frequency IMF are added and the sum is subtracted from the "apparent" residuum \(r_s(t)\). Next, the "apparent" residuum \(r_s(t)\) and the two lowest frequency IMFs are added and the sum is subtracted from the "apparent" residuum \(r_s(t)\). This process is iterated until the resulting MSD is negligible.

\[
MSD_{k+2} = \frac{1}{N} \sum_{t=1}^{N} \left( r_s(t) - \left( r_e(t) + \sum_{k=0}^{K} x_{14-K}(t) \right) \right)^2
\]  

(1.22)

The result of this iteration \(K = \{0, 1, \ldots, 13\}\) is summarized in Fig. 1.27 in case of the ABP time series using segment sizes \(\delta = 512, 1024, 2048\) and a step size \(\tau = 2\).

![Fig. 1.27 Mean square difference MSD_{k+2} of the decomposition of an ABP time series with either SEMD or EMD for segment sizes \(\delta = 512, 1024, 2048\) and a step size \(\tau = 2\) used within SEMD. Note that to the residuum estimated with EMD a variable amount of IMFs is added successively.](image-url)

It becomes obvious that the "apparent" residuum estimated with SEMD using a segment size \(\delta = 2048\) and the "apparent" residuum plus IMFs 10 to 14, all estimated from applying EEMD, are very similar. Much the same holds true in the
following constellations: segment size $\delta = 1024$ and $r_e(t) + \text{IMF}_8 + \ldots + \text{IMF}_{14}$ and segment size $\delta = 512$ and $r_e(t) + \text{IMF}_8 + \ldots + \text{IMF}_{14}$. Fig. 1.28 illustrates the result for the latter constellation.

![Graph showing residuum $r_e(t)$ estimated with SEMD and EMD.]

The results corroborate that SEMD yields a decomposition well in accord with standard EMD. However, SEMD offers the additional advantage of being a true on-line algorithm which, furthermore, is based on an ensemble of estimates. It thus provides an equally robust estimate of underlying intrinsic mode functions as EEMD. It is also as flexible as standard EMD in detrending applications, and allows to extract the stationary part of originally non-stationary biomedical time series data. Hence, for practical applications SEMD is to be preferred.

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References

8. M. Böhm, in Workshop Report VI (Graduate College 638 "Nonlinearity and Nonequilibrium in Condensed Matter", 2006)
18. N.E. Hunag, N. Attoh-Okine, Hilbert Huang Transform in Engineering (Taylor and Francis, 2005)