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M.N. SYED, P.G. GEORGIEV, and P.M. PARDALOS

ROBUST PHYSIOLOGICAL MAPPINGS: FROM NON-INVASIVE TO INVASIVE

Abstract. The goal of this paper is to highlight the challenges on the three methods of data analysis, namely: robust, component, and dynamical analysis with respect to the epilepsey. A forward and inverse mapping model for the human brain is presented. Research directions for obtaining robust inverse mapping, and conducting dynamical analysis of the epileptic brain are discussed.

Keywords: epilepsy, electroencephalography (EEG), robust measures, blind signal separation, independent component analysis, sparse component analysis, dynamical analysis.

INTRODUCTION

Robustness has been unanimously identified as one of the critical factors in developing successful analysis methods for experimental data. Typically, statistical inference methods are sensitive to the outliers, and they dictated the conventional theory of analyzing the data. In 1962, Tukey [1] in his awe inspiring paper kindled the importance of robust methods. He differentiated the term "Data Analysis" from "Statistical Analysis" by stating that the former can be considered as science, but the later is subjective upon the statistician's approach. Supporting Tukey's ideology, Huber [2] encouraged the usage of term data analysis, as the other term is often misinterpreted in an overly narrow sense (restricted to mathematics and probability). Thus, the seminal work of Tukey [1, 3] enlarged the scope of data analysis from mere statistical inference to something more.

During the shift from the traditional statistical analysis to the contemporary data analysis, one of the key analysis elements that remained valid is the usage of optimization based approaches in extracting knowledge from the data. Typically, the efficiency of an optimization based approach depends upon the type of objective function, feasible space, and the data quality. Traditionally, the data analysis methods were based on the impractical assumptions that provided mathematical advantage in proposing solution algorithms to the optimization problem. However, the traditional approaches neglected the criticality pertaining to the practicability and data quality. Existence of outliers (or noise) often taint the solution space, hence, practical data analysis calls for robust methods.

The importance of robust methods in data analysis has been early recognized, and can be traced back to the old famous dispute between Fisher and Eddington. Based on practical observations, Eddington [4] proposed the suitability of the absolute error as an appropriate measure. Fisher [5] countered the idea of Eddington by theoretically showing that under *ideal circumstances* (errors are normally distributed, and outliers free data) the mean square error is better than the absolute error. The dispute between Eddington and Fisher actually played a prominent role in shaping the theory of statistical analysis. After Fisher's illustration, many researchers incorporated mean square error as a default similarity measure in their analysis. Later, Tukey [1] reasoned that occurrence of the ideal circumstances for the practical scenarios is very rare. Noise as less as 0.2 %, which is ideal for many practical data, will favor the usage of the absolute error instead of the mean square error [6, 7]. Presently, the prevalence of sensitive measure in data analysis can be solely attributed to their mathematical

advantage in proposing the solution algorithms. Nevertheless, the practitioners, under the preamble of robust statistics, have been conducting research in the directions of robust methods, which have led to the insightful explicit studies [6–8].

Obviously relaxing all the distribution or statistical assumptions in a data analysis method is the most appropriate case for analyzing experimental data. However, the distribution assumptions cannot be discarded in most of the scenarios, mainly due to the loss of mathematical convenience in the analysis approach. Thus, most of the research in robust methods is based on incorporating ideas into the traditional methods that will result in insensitivity to the outliers and uncertainty. The major approaches of robust methods in data analysis can be divided into the following categories:

- Robust measure based approaches: In these approaches, a measure which is insensitive to outliers is used as an objective function [7, 8].
- Robust algorithm based approaches: In these approaches, subsamples from the given data sample is analyzed separately, and an average of all the subsample analysis results is considered as representative result [9–11].
- Robust optimization based approaches: In these approaches, an uncertainty based domain is considered around each data sample, and stochastic optimization based algorithms are used to conduct the analysis [12, 13].

In physiological data analysis, specifically in computational neuroscience, the invasive data recordings enhance the analysis and predictability than compared to non-invasive data recordings [14]. On the other hand, invasive data recordings are not easily available, and are recorded only in certain specific cases. The critical difference between the data, collected form invasive and non-invasive approaches, is the mixing of the sources, apart from the noise interference. For example, in the case of ElectroEncephaloGraphy (EEG) data recordings, the source signals generated at the active neurons are smeared through the surrounding brain matter by the volume conduction. Although the volume conduction is a passive resistive process in nature, signals at each scalp electrode is influenced by a local set of underlying active neurons [15]. In addition to that, the recordings collected on scalp not only involves mixture of the true source signals, but also involves the mixture of source signals and the influential artifacts. The typical artifacts may include ocular activity (eye movements, eye blinks), myographic activity (muscle, jaw tightening), cardiac cycle activity, electrical activity (50 Hz or 60 Hz noise). Moreover, the volume conduction from the active neurons to the electrodes involves no time delays, which is attributed to the effectively instantaneous mixing within the minuscular intra-cortical distances [16].

Challenges involved in extracting original source signals form EEG recordings of an epileptic brain is the theme of this paper. In addition to that, usage of synchronization based dynamical analysis methods on the source signals is highlighted. A forward mixing system, that mathematically describes the mixing process in human brain is presented in section 1. In section 2, series of assumptions that are used in the traditional and novel class of algorithms will be discussed. Section 3 presents the assumptions and limitations of the unmixing methods. Ultimately, the challenges in extracting the sources from an epileptic brain are presented in section 4. Finally, we conclude the paper by presenting few research directions.

1. THE FORWARD MIXING SYSTEM

The majority of the non-invasive vitals are instantaneous mixtures of their sources. The severity or triviality of the mixing problem, in physiological data analysis, depends upon the inter-source distances and artifact-source interference. Thus, a challenging task is to rightly identify the underlying function that maps non-invasive data to the invasive data. The task mathematically reshapes to finding

the solution of the inverse system, posed by the following forward system:

$$\mathbf{X} = \Phi(\mathbf{S}, \mathbf{M}) + \mathbf{N}, \tag{1}$$

where Φ is assumed to be continuous bijective (homeomorphism) unknown mapping, $\mathbf{X}$ is any representation of the observed non-invasive data, typically can be transformed into flat representation, i.e. $\mathbf{X} \in \mathbb{R}^{m \times P}$. Similarly, $\mathbf{S} \in \mathbb{R}^{s \times P}$ may denote the source signals inside the human body, $\mathbf{M} \in \mathbb{R}^{a \times P}$ may represent the mixed artifacts, and $\mathbf{N} \in \mathbb{R}^{m \times P}$ represents unmixed artifacts or external outliers. It is critical to highlight the difference between $\mathbf{M}$ and $\mathbf{N}$. Artifacts of type $\mathbf{N}$ can be filtered out using digital filters, whereas, artifacts of type $\mathbf{M}$ cannot be easily removed. P is always finite, representing the finite amount of data. Typically, P represents any acquisition variable, over which a sample of mixture (a column of $\mathbf{X}$ matrix) is collected. The most common types of acquisition variables are time and frequency. However, position, wave number, and other indices can be used depending on the nature of the physical process under investigation. Lastly, s and m may represent quantitative information of observed and actual data. Typically, m corresponds to the total number of observations, and s corresponds to the actual number of active sources.

Mixing in Epileptic Brain. For the epileptic brain, $\mathbf{X}$ can be seen as the EEG data recordings where each row is a channel and each column is a time point, $\mathbf{N}$ can be seen as those noise elements, that can be filtered using a bandpass filter. Let $\mathbf{X_f}$ be the filtered data represented as:

$$\mathbf{X_f} = \mathbf{X} - \mathbf{N}, \tag{2}$$

where $\mathbf{X_f} \in \mathbb{R}^{m \times P}$ represents a filtered form of given mixture data $\mathbf{X}$. Typically, exact information of $\mathbf{N}$ is unknown, and classical methods to solve Equation (2) involves designing a filter using frequency, amplitude, smoothness or geometry based information of $\mathbf{N}$ [17]. The preciseness and the solution quality of the inverse system are the two key factors that determines the validity and success of any physiological data analysis. Most of the experienced clinicians and surgeons merely observe $\mathbf{X_f}$, and are able to accurately identify pathological condition for certain cases. For example, asymmetrical slowing of EEG data (which is typically observed from $\mathbf{X_f}$) can indicate existence of pathological conditions [18]. Typically, existence and location of background asymmetry between left and right brain hemispheres is sufficient to identify focal slowing. Thus, mixing is not a critical issue when the focal slowing is dominant. Successful results for the focal slowing have been reported for these cases [19, 20]. Similarly, mixing does not play a critical issue when diffused slowing is diagnosed [21] (in the diffused slowing case, the total slowing of brain is considered).

Contrary to the above average source analysis scenario, epilepsy analysis does demand analysis of $\mathbf{S}$ rather than analyzing $\mathbf{X_f}$. For instance, consider the difficult problem of epilepsy prediction. Linear, nonlinear, dynamical methods have been rigorously applied to $\mathbf{X_f}$, and ambiguous results from different groups have been reported prior to formation of International Seizure Prediction Group (ISPG). After standardizations proposed by ISPG, a new hope arose in the field of epilepsy prediction. However, the results of the ISPG conferences were inconsistent and contradictory (see [22] and the references therein). But the worth noting summary from these conferences is that analysis from the invasive data techniques performed better than the scalp data techniques in early identification of the epilepsy [23]. This unequivocal result from decades of research directly points towards importance of analyzing $\mathbf{S}$ rather than analyzing $\mathbf{X_f}$.

2. UNMIXING APPROACHES

The representation of the inverse system for the system defined in Equation (1) is non-trivial. However, a traditional approach is to represent the inverse system as:

$$\mathbf{S_M} = \Phi^{-1}(\mathbf{X_f}), \tag{3}$$

where

$$\mathbf{S_M} = \begin{bmatrix} \mathbf{S} \\ \mathbf{M} \end{bmatrix}, \ \mathbf{S_M} \in \mathbb{R}^{(s+a)\times P}. \tag{4}$$

Similar to any typical notorious mathematical problem, the simple representation of inverse system illustrated in Equation (3) is veiling its complexity. Obviously, when the governing dynamics of a system in the analytical form is well known and invertible, solution to Equation (3) might be trivial. Unfortunately, such underlying knowledge of many physiological systems is intangible. Identifying Φ^{-1}, is principally impossible without additional assumptions on the sources. Thus, a specific function class from $\mathcal{F}$ is pre-selected for identifying Φ^{-1}. In fact, solutions for Equation (3) are available only when Φ^{-1} is taken as a linear mapping. Currently, there are no successful results reported for any other class of mappings. Assuming Φ^{-1} is linear, Equation (3) can be rewritten as:

$$\mathbf{S_M} = \mathbf{W}^{\mathrm{T}}\mathbf{X_f}, \tag{5}$$

where $\mathbf{W} \in \mathbb{R}^{m\times(s+a)}$. The system represented in Equation (5) is a variant representation of the linear matrix factorization. Since, the goal is not to find any factor matrices, but specific matrices $\mathbf{S_M}$ and $\mathbf{W}$, the problem forms a specific case of linear matrix factorization. A well known name of this problem is Blind Source Separation (BSS), where the term "Blind" is used for emphasizing unknowness of the factor matrices. The BSS problem suffers from uniqueness and identifiability:

- Uniqueness

Let $\Lambda, \Pi \in \mathbb{R}^{(s+a)\times(s+a)}$ be a diagonal matrix and permutation matrix respectively. Consider the following:

$$\mathbf{S_M} = \mathbf{W}^{\mathrm{T}}\mathbf{X_f},$$
$$(\Pi\,\Lambda)\mathbf{S_M} = (\Pi\,\Lambda)\mathbf{W}^{\mathrm{T}}\mathbf{X_f},$$
$$\mathbf{S}_\partial = \mathbf{W}_\partial^{\mathrm{T}}\mathbf{X_f}.$$

There can be infinite equivalent solutions of the form $\mathbf{S}_\partial$ and $\mathbf{W}_\partial$. The goal of a good BSS algorithm should be to find at least one of the equivalent solutions. Due to the inability of finding the unique solution, we not only loose the information regarding the order of sources and mixing artifacts, but also loose the information of energy contained in the sources. Generally, normalization of rows of $\mathbf{S}_\partial$ may be used to tackle scalability. Also, relative or normalized form of energy can be used in the further analysis. Theoretically any information pertaining to the order is impossible to recover. However, practically, problem specific knowledge will be helpful in identifying correct order for the further analysis.

- Identifiability

Let $\Theta \in \mathbb{R}^{(s+a)\times(s+a)}$ be any arbitrary matrix, consider the following:

$$\mathbf{S_M} = \mathbf{W}^{\mathrm{T}}\mathbf{X_f},$$
$$\Theta\,\mathbf{S_M} = \Theta\,\mathbf{W}^{\mathrm{T}}\mathbf{X_f},$$
$$\mathbf{S}_\gamma = \mathbf{W}_\gamma^{\mathrm{T}}\mathbf{X_f}.$$

The scenario depicted by the above equations is the critical identifiability issue. Clearly, the BSS problem without any further assumptions is intractable. The key idea of rightly identifying both the matrices (of course with unavoidable scaling and permutation ambiguity) is to impose structural restrictions on $\mathbf{S_M}$, while solving the BSS problem.

The BSS problem can be mathematically stated as: Let $\mathbf{X} \in \mathbb{R}^{m \times N}$ be generated by a linear mixing of sources $\mathbf{S} \in \mathbb{R}^{s \times N}$. Given **X**, the BSS problem is to find two matrices $\mathbf{A} \in \mathbb{R}^{m \times s}$ and **S**, such that the three matrices are related as **X** = **AS**. Matrix **A** is called as mixing matrix. In order to solve this problem up to certain level of uniqueness, following identifiability conditions are imposed on **A** and **S** matrices.

• Statistical Independence Assumptions:

One of the earliest approaches to solve the BSS problem was to assume statistical independence of the source signals. The widely known method that is dedicated to the above assumption is the Independent Component Analysis (ICA) method. The fundamental assumption in ICA is that the rows of matrix **S** are statistically independent and non-gaussian [24, 25].

• Sparse Assumptions:

Apart from ICA, the other type of algorithms, which provides sufficient identifiability conditions are based on the notion of sparsity in the **S** matrix. There are two major categories in the sparse assumptions:

— Nonnegative sources:

In this category, along with certain level of sparsity, the elements of **S** are assumed to be nonnegative. Ideas of this type of approach can be traced back to the Nonnegative Matrix Factorization (NMF) method. The basic assumption in NMF is that the sources (and dictionary) are assumed to be nonnegative [26]. However, in certain cases for the BSS problem the nonnegativity assumption on the elements of matrix **A** can be relaxed [27] without damaging the identifiability of **A** and **S**.

— Real sources:

In this category, no sign restrictions are assumed on the elements of **S**, i.e. $s_{i,j} \in \mathbb{R}$. The only assumption used to define the identifiability conditions is the sparsity of **S**. The methods using only sparsity assumptions are called as Sparse Component Analysis (SCA) [28].

At present, these are the only two (statistical and sparsity assumptions) available BSS approaches that can provide sufficient identifiability conditions (uniqueness upto permutation and scalability). In fact, the sparsity based methods (see [27, 29]) are relatively new in the area of BSS when compared to the traditional statistical independence methods (see [25]). For neurological data, recent studies have shown relevance of sparsity assumption when compared to statistical independence assumption [30].

3. ASSUMPTIONS AND LIMITATIONS

Makeig et al. [16] were pioneers in explaining the usage of BSS for EEG signals. They identified four critical properties that should be satisfied by source signals so as to successfully implement BSS approach. However, their focus was limited to ICA view of BSS. In the following we extend the properties in terms of general BSS, which is more broader area than ICA.

• The source signals should have **at least one** of the following properties:

— The source signals are statistically independent, and not more than one source signal follows Gaussian distribution.

— The source signals are non-negative, and partial spatial sparsity exists among the sources.

— The source signals are always spatially sparse.

• The mixing mechanism should have **all** of the following properties:

— Mixing is linear.

— Mixing is not illconditioned.

— The propagation delays occurs in the mixing medium are negligible.

• The number of source signals and observed signals are nearly (not necessarily exact) equal in number. Although, for ICA number of observed signals should be greater than or equal to the number of source signals.

Currently, in EEG analysis usage of ICA is prevalent. However, ICA in EEG is merely used for separating the mixing artifacts. The basic idea is to perform ICA on $\mathbf{X_f}$, and get as statistically independent as possible sources and artifacts. Let $\mathbf{S}_{\text{ICA}}$ denote the sources obtained after applying ICA. Since the mixing artifacts $\mathbf{M}$ are anatomically, fundamentally and functionally independent from the sources $\mathbf{S}$, the ICA solution $\mathbf{S}_{\text{ICA}}$ can be decomposed into $\mathbf{S}_{\blacksquare}$ and $\mathbf{M}$ blocks, i.e.

$$\mathbf{S}_{\text{ICA}} = \begin{bmatrix} \mathbf{S}_{\blacksquare} \\ \mathbf{M} \end{bmatrix}. \tag{6}$$

The enthusiasm among researchers to use ICA is mostly based on the notion of identifying and separating $\mathbf{M}$ form $\mathbf{S}_{\blacksquare}$. However, the relation between $\mathbf{S}_{\blacksquare}$ and $\mathbf{S}$ (the true sources) has been ignored in the research. Most of the time, authors were able to provide satisfactory arguments (based on their experimentation) that the overall information content in $\mathbf{S}_{\blacksquare}$ is sufficient for analysis than identifying the precise mapping between the rows of $\mathbf{S}_{\blacksquare}$ and $\mathbf{X}$ [31].

However, assumption of statistical independent sources $\mathbf{S}$, in human brain is hard to verify (due to the connectivity among the nodes). Thus, even after ignoring the ordering among rows, the remaining relation between $\mathbf{S}_{\blacksquare}$ and $\mathbf{S}$ is of critical importance. In fact, if statistical independent sources is invalid for epileptic brain, then $\mathbf{S}_{\blacksquare}$ is nothing but another mixture of rows of $\mathbf{S}$, where $\mathbf{S}_{\blacksquare}$ has as independent rows as possible. This can be seen as another way of representing $\mathbf{S}$, and such representation do have a practical advantage is physiological data analysis. Nevertheless, the curiosity to identify and extract $\mathbf{S}$ from the observed $\mathbf{X}$ should not be extinguished.

In the following section, we present the challenges that remains unanswered in EEG analysis, specifically in the diagnosis of epileptic seizures.

4. CHALLENGES

In this section, several challenges pertaining to the development of robust mappings in epileptic brain is systematical enlisted. We begin with the development of the tractable robust mapping formulation, proceed towards explaining the challenges that underlie in the development of such mappings.

Developing Tractable Robust Formulation for Seizure Analysis

The general Robust Physiological Mapping (RPM) for EEG data can be mathematically illustrated as:

$$\begin{aligned} &\text{find}: \\ &\qquad \Psi \\ &\text{such that}: \\ &\qquad \mathbf{S} = \Psi(\mathbf{X}) \end{aligned} \tag{7}$$

where Ψ is the robust inverse physiological mapping. $\mathbf{X}$ is the EEG data, where each row represents a channel. Similarly, $\mathbf{S}$ represents the source signals, where each row is a source. The abstract formulation needs precise definition of robustness and

mapping to obtain a tractable solution method. Since the superposition of signals is typical mixing phenomenon in the human brain, linear mapping assumption can be used without loss of generality. Furthermore, any known information pertaining to **M** and **N** is an additional advantage. Thus, a suitable modification of formulation (7), which is tangible for optimization will be:

$$\begin{aligned} &\text{minimize:} \\ &\qquad \mathcal{O}(\mathbf{S} - \mathbf{W}^{\mathrm{T}}\, \mathbf{X_f}) \\ &\text{such that:} \\ &\qquad \mathbf{S} \in \mathcal{S} \\ &\qquad \mathbf{W} \in \mathcal{W} \end{aligned} \tag{8}$$

where $\mathcal{S}$ is a set of structural assumptions placed on **S** based on the epileptic brain, and $\mathcal{W}$ is a set of assumptions that must be placed on **W** for successful unmixing. The function $\mathcal{O}$ is the robust function which is the key element for analyzing the experimental data.

Selecting Suitable Robust Measures $\mathcal{O}$

Robustness can be defined as insensitivity to the outliers in the context of data analysis. Traditional functions used in ICA like kutrosis, cross-cumilants are sensitive to outliers [25, 32]. Thus, a robust measure that ignores outliers while extracting sources is the key element of the EEG source analysis. However, adding a robust objective function $\mathcal{O}$ raises issue of finding optimal solutions, i.e. robustness, convexity and smoothness very rarely exists in a single real function. Thus, robustness comes with a trade off in either convexity or smoothness. Although in the literature, no specific criterion is available to choose from convexity or smoothness, but from optimization perspective, a robust smooth function with pseudodonvexity is auspicious. Thus, any function $\mathcal{O}$ that satisfies above criterion may be taken as the objective function. Under mild boundedness assumption, the correntropic loss function $\mathcal{F}_{\mathcal{C}}^{\sigma}$ has been identified recently as one of the robust smooth invex function [33]:

$$\mathcal{F}_{\mathcal{C}}^{\sigma}(\mathbf{v}) = \left[1 - \exp\left(\frac{-1}{2\sigma^2}\right)\right]^{-1}\left[1 - \sum_{i=1}^{n} \exp\left(\frac{-v_i^2}{2\sigma^2}\right)\right] \quad \forall \mathbf{v} \in \mathbb{R}^n \tag{9}$$

where $\sigma > 0$ is the kernel width parameter. Moreover, specific robust functions towards a similar direction of research (robust, pseudoconvex and smooth) can be designed based on the theoretical and experimental knowledge of the epileptic brain.

Developing Extendable Identifiability Conditions on A and S w.r.t Epileptic Brain

Another important challenge is to develop suitable identifiability conditions on **A** and **S** that imitate the brain mixing and brain sources respectively. Currently, independent source assumption prevail the literature of EEG analysis, due to the early development and widespread of ICA. Moreover, recent sparsity based conditions are still at the early stages, needs further exploration. Apart from independence and sparsity, other assumptions specific to epileptic brain can be exploited in developing sufficient identifiability conditions on **A** and **S**. In fact, for epileptic brain, the hypothesized synchronization phenomena among the source brain signals can be exploited in developing the conditions. For example:

- Rows of **S** can be assumed to be as synchronous as possible at the time of seizure. Methods using this information can be developed to extract **S** from **X**.
- Since epilepsy is a dynamical phenomenon, rank of the Henkel matrix between pair of signals can be used to identify total number of dynamically independent signals.

Understanding Temporal Changes in A and S

Typically, the impulsive synchronous neuronal activity in the cerebral cortex is considered as the main reason behind the occurrence of seizures. Furthermore, the synchronous activity may be kindled locally (in specific portions of cerebral hemispheres) or globally (in both cerebral hemispheres) in the brain. The seizures that are initiated from local activity and remained confined to the region are called as partial or focal seizures. Whereas, the seizures that are initiated from global activity involving almost the entire brain are termed as generalized seizures. However, if the mixing model of the brain (see Equation (1)) is relevant, then answering the following key point will open the doors of understanding dynamics of epilepsy.

- Is it the sources that are getting synchronized or is it the mixing that is getting singular?
- How does the rank of matrix **A** changes from pre-ictal to ictal periods?

Dynamical Inter-manifold Analysis of S

After resolving all the issues pertaining to the extraction of **S** form **X**, the next challenging task is to properly study the dynamics embedded in **S**. Typical methods like time delay embeddings [34] can be used to reconstruct manifolds. Furthermore, robust nonlinear embeddings [35] can be used to enhance the understanding of the core differences between pre-ictal and ictal periods of the epileptic brain. A manifold constructed from **S** can be used to calculate the traditional measures (correlation dimensions [36], Lyapunov exponents [37] and Kolmogorov entropy [38]) or the novel measures (see [39, 40]). Moreover, different multivariate synchronization measures can be used to identify the development of seizure [41]. Finally, for any traditional or novel dynamical analysis, surrogate test [42] should be conducted to validate the results.

See [43] for the current literature on dynamical methods in analyzing the EEG data. Currently, the multi channel analysis in dynamical methods is mere a concatenation of the single channel methods. Alternatively, dynamical analysis of every row of **S** can be conducted to create several manifolds. Then the critical issues in the dynamical analysis of EEG source data will be to:

- Develop a robust inter-manifold measures that can detect dynamically equivalent manifolds, and/or synchronous manifolds.
- Develop a multivariate method which results in the elimination of redundant information from **S**, during the manifold construction.
- Develop the corresponding efficient surrogate test for the proposed measures.

CONCLUSIONS

The noise factor in the success of dynamical analysis methods in the prediction of epilepsy can be extended via robust approaches. Furthermore, the advantage of invasive data over the scalp EEG data can be incorporated by developing a mapping between the two data sets. Since, typical EEG recording involve artifacts, robust mappings are the key approaches to tackle noise and invasive data factors. The reasons behind the patient specific (and for a given patient seizure specific) nature of dynamical measures can be studied by analyzing the source signals. Furthermore, the localization issue [44] among the sources can be eliminated by developing suitable methods that leaves markers in the sources, i.e. suitable experiments can be designed that indicates the linking of a particular source to a particular time span.

While applying the new sparsity based source separation methods, existence of sparsity in the actual EEG sources may appear dubious. However, similar to ICA techniques where independent noise is induced in the data via experimentation, sparsity can be induced by conducting experiments that results in the sparse activation of the neurons. Furthermore, transformations like discrete wavelet transform can be applied on **X** hoping the wavelet coefficients of sources **S** are sparse. Nevertheless, the

key issue is to identify structures in $\mathcal{S}$ and $\mathcal{W}$ which are both relevant and tractable to the practical physiological conditions in the epileptic brain. Thus, developing RPM that maps non-invasive data to invasive data will open the doors of the unidentified physiological phenomena, the epilepsy.

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