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# The complexity and variability mapping for prediction and explainability of the sleep apnea syndrome

Ireneusz Jabłoński, Rosario Morello, *Member IEEE*, Janusz Mroczka

***Abstract*—The paper introduces a research program formulated to uncover and describe a complex nature of the sleep apnea disorders. This study include the physiological sensing and the signal processing oriented towards the mapping of a dynamical profile of physiological system represented by its complexity and variability. To reconstruct a heatmap of the dynamical features significant for triggering sleep disorders we collected a set of procedures dedicated to qualitative and quantitative depiction of the intra- and inter-events, and then adapted them to the use with a polysomnography data. Research protocol was organized with reference to the patients and modified PNEUMA model, and the COMPASS Toolbox devoted to time series exploration. The outcome novelty consists in the complementary characterization of the sleep apnea dynamics, measured at various levels of the system, but also the original statements on the sensitivity of fractal and network oriented algorithms applied to physiological data has been formulated in the report in reference to the temporal patterns encoded in polysomnography data, e.g. a detection of the central sleep apnea with the use of nasal airflow has been documented. The complementary approach proposed in the paper is a prerequisite to understand the SAS phenotyping, predict that modes and the SAS states, and formulate an efficient procedures for personalized patient care.**

***Index Terms*— Biological system modeling, complexity theory, health informatics, sleep apnea, time series analysis**

## I. INTRODUCTION

METROLOGY as the interdisciplinary science cumulates knowledge across many theoretical and experimental disciplines. As a result, it offers the new strategies for object inspection, each concerning the concept of an efficient measurement scheme, i.e. minimal invasive, quick, reliable, cheap and easy accessible (e-access) protocol.

Physiological systems can be characterized in a context of complex dynamical processes that are continuously subjected to and updated by nonlinear feedforward and feedback inputs [1]. Information coded in system outputs usually exhibit wide varieties of behaviors due to dynamical interactions between system components, external noise perturbations, and physiological state changes. Complicated interactions occur at a variety of hierarchical levels and involve a number of interacting variables, many of which are unavailable for experimental measurement [1]. The challenge is to disentangle the individual channels of knowledge about the object when the record of experimental data additionally includes several types of variability at various levels, e.g.: random uncorrelated, random correlated, periodic, and nonlinear deterministic. So that, saying about complexity and variability one should take a transitivity between the system and data acquired into it into consideration.

Important support for complexity and variability analysis can be the tool of modeling, computer simulation and exploration of massive data, including the artificial intelligence (AI)/ machine learning (ML) approach. Describing the both sides of the measurement experiment: measured object and measurement path (with data processing procedures), it enables access to indirect source of data and reduces the observational scales through the virtual reality, among other things. But the problem in this domain very often can be too sophisticated abstract ideas and tools, limiting the access of clinicists to novel strategies of the system observation. Meanwhile, complexity and fluctuation analysis shows some potential to predict and diagnose pathological events through the subjects [2] giving also the chance to design of the procedures for their control [3], [4]. Joining these domains is one of the tasks for contemporary health informatics and personalized medicine.

The respiratory system is an example of the complex object, working in a multidimensional network of interconnections with other subsystems conditioning the process of respiration. It meets the paradigm of physiological rhythms, which suggests the application of some class of representations typical for nonlinear dynamics. The problems with supporting the stable periodicity, especially during sleep, are the subjects of vast research as they influence the quality of life and even can lead to death [5], [6]. In principle, the harmful sources of sleep apnea syndrome (SAS) comes from the central nervous system or obstructive changes in airways tract (mainly upper airways), but the mechanism of its triggering can be quite different and

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conditioned by various deterministic and/or stochastic internal or external processes [3], [7], [8]. Also mixed, central/obstructive scheme of apnea is possible. A typical strategy for attempts of description of sleep apnea scheme as a dynamical process very often uses selected (and even isolated) theoretical tool for mapping its complex and varying nature [6], [9]. Meanwhile, application of set of (modern) procedures with various levels and kinds of sensitivity could be more efficient in the circumstances of lack of versatile algorithm. This remark remains true also for other physiological objects.

The creation of library of numerical procedures devoted to the complexity and variability analysis of systems and data sets, universal in the context of possible applications to physiological systems, has been started. It fills the gap existing in the field of programming tools for the complex object and gives the clinicists and medical researchers the practical opportunity to view the systems in the new systematics and to test prospective hypothesis. The paper summarizes the issue by a survey of modern and popular methods applied in the COMPASS toolbox and indicates the possible path for its exploitation in the area of characterization of sleep apnea pathology.

## II. Overview of the Compass Toolbox

### A. Aims and Scopes

The COMPASS toolbox designed for complexity and fluctuation analysis is a set of known procedures adapted to work with experimental data in the form of time series. It assumes coherent structure, but also is open for easy extension with the next generation of algorithmic structures and functionalities. The library is organized around some key concepts working in the domain of complex dynamical systems: initial preprocessing of data, nonlinear dynamics, complexity and fluctuation analysis, inter-events characterization, synchronization, complex network reconstruction and quantification. Some program codes were adapted to the task of efficient monitoring of dynamical processes, e.g. by introducing the mechanism of moving window. The whole is enhanced by simple interactive demos for training the user. For realization of the task of respiratory complexity and variability analysis, the toolbox was supplied with a modified PNEUMA model [10]. All components comprised in indicated thematic segments of the library can be used interchangeably, depending on the demands of realized project.

### B. Related Works

The recent literature has presented a growing number of efforts focused on a qualitative and a quantitative depiction of the complexity and the variability in physical, technical and medical systems. They include both statistical and AI/ML-based approaches. The fundamental problem in this range concerns the lack of universal method suitable for the complex system characterization. There is no unique and a concise methodology available proper for extraction of the complex structure and functions from an experimental dataset [11, 12]. This is also reflected in the available IT tools dedicated to description of the complex systems and datasets, i.e. there are plenty of papers dedicated for the respiratory system complexity measurements which apply much or less original procedures and data collections, many of them exploring the problem at the various angles of its perception and with the tools of different sensitivity to extract and depicts the complex conditions of interplaying features and/or processes [13-16]. Even the recent advancement in AI/ML has shown the significant limitations in explainability of inference obtained with these algorithms, which has triggered the research polarized towards a causality depiction and the interpretability in the artificial intelligence, e.g. an explainable artificial intelligence (XAI) [17, 18]. Much of this work uses physical objects as the subjects for the study, and understanding the complex interrelations between the elements distinguished in these systems shed a light to the effectiveness of the procedure for data and object explorations. Here, the complex networks approach, a branch of the machine learning domain motivated by the mathematical theory of graphs, brings to some original statements, which in feedback contribute to the fundamental findings in the system-oriented research (e.g. [19-21]), the algorithms (e.g. graph neural networks [22]), and also the applications (e.g. [23, 24]). This regime of the complex system depiction tends to a reliable reconstruction of the structure of interplaying quantities and to depict reliably a complex character of the interactions governing the systems, which can be observed at various levels of the physical systems as the emergence of their unique features and behaviors [20, 21]. That network-oriented depiction can be used independently, providing the qualitative and/or quantitative insights into the complex nature of the systems, but the complex networks output(s) can be also used for further processing, both in regression and classification tasks, e,g, with the use of the (deep) learning schemes (Fig. 1). In physiological applications, a preliminary demonstration for duality between times series data and network-like modeling has been shown by Campanharo *et. al.* for the case of cardio applications [25]. To date, there is lack of a thorough studies in the network representation of the sleep apnea syndrome, and especially when a multimodal and multilevel data recorded in humans and surrounding environment are used. Only two representative works has been published which unveil the potential for differentiation between the sleep apnea phenotyping and severity prediction [26, 27]. Still there is no regular contributions to the interpretation-oriented research in this range. In fact, there are plenty of challenges in a range of the complex networks fundamentals, e.g. how the network can be reconstructed reliably from the experimental data, but also many of these problems – especially for non-specialists – arise between a non-trivial formalism of the complex network mathematics and its computer applications.

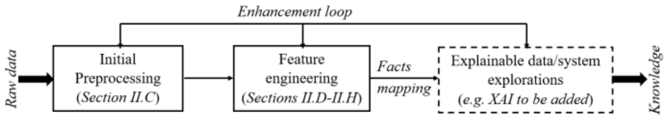

Fig. 1. A scheme of data processing for designed COMPASS Toolbox.

The paper joins the above-mentioned methodological stream, providing a preliminary demonstration of the possible path of studies for depiction of the sleep apnea complexity, using a multimodal data recorded during polysomnography and the set of procedures sensitive to uncover a diversity of patterns contained in the experimental data. These patterns can be studied further, e.g. using the intelligent-based procedures configured for regression and/or classification tasks, and most and foremost to understand and interpret the mechanisms governing the sleep apnea phenotyping.

### *C. Initial Processing of the Data*

Working with long sets of data can be ineffective and requires allocation of important memory resources in a computational unit. Additionally, very often it is a need of transformation of the whole string of data or its parts. To facilitate the task of initial preprocessing of data to complexity and fluctuation analysis, a dedicated application with a graphical interface was designed. Its main tasks are:

- loading the data from ASCII file containing the one-column data format or multi-column record of polisomnography (application identifies the channel for a built-in data format and a given device),
- viewing the analyzed time series (in a whole range or zoomed),
- windowing the data for further processing (the number of first sample and the whole number of samples in the window can be chosen optionally),
- enabling access to numerous procedures of initial data preprocessing (e.g. filtering, extracting the special features of time series, etc.),
- writing the transformed data to the file(-es), also in the mode of multi-window division of data (windows can overlaps each other with the defined number of samples).

In a case of biomedical signals, the character of periodicity very often is a subject of observation. For example, in respiratory measurements the trend of respiratory rate variability (RRV) or inter-breath interval (IBI) is formed, where the length of respiratory cycles or time interval between two significant tidal excursions is extracted from an original time series, e.g. airflow or abdominal movement [13]. The question is not trivial for signals with changing and individual dynamics, variations in amplitude and level of (external and internal) noise. The case can be a polisomnography record during sleep with the symptoms of apnea. The COMPASS toolbox implements some dedicated algorithms designed and tested for reliable solution of such tasks [14]. Their operation is simple and boils down to the introduction of the input arguments to the functions.

### *D. Nonlinear Dynamics Assessment*

Apart from the typical actions of time series data loading and its graphical presentation, the interface dedicated to nonlinear dynamics analysis of systems and data sets makes available the functionalities for reconstruction of 2-D and 3-D phase portraits. It offers also access to the algorithms devoted to estimation of measures typical for chaotic systems, i.e. Lyapunov exponent, capacity dimension and correlation dimension [14]. Moreover, it is possible to characterize the statistics of events, which is coded in recorded time series. In this case, the algorithm is based on power law rule described in [19].

The exploitation of the options of windowing of data sets, similarly to the initial preprocessing block of procedures, enables calculation of the values for the measures defined in nonlinear dynamics class in a mode of moving window. It gives the opportunity to follow the fluctuation of these indexes in a chosen horizon of time.

### *E. Procedures for Complexity and Fluctuation Analysis*

The group of procedures adapted to the complexity and fluctuation analysis of systems and data sets was provided with some algorithms: a multiscale fluctuation analysis – detrended fluctuation analysis (DFA), accessible also in a version of multifractal DFA, the Hurst rescaled range analysis, the procedure of description of event statistics (it uses the power law described for probability density function or power spectrum of the signal), estimation of Fano and Allan factor, a measure of Shannon entropy (*ShanEn*), sample entropy (*SampEn*) and approximate entropy (*AppEn*) – possible also in a mode of moving window (appropriate bibliography can be found, e.g. in [14]). Additionally, the set of tools associated with recurrence plots strategy (RP) [28], including cross recurrence plots (CRP) and joint recurrence plots (JRP), was programmed. Qualitative and quantitative description of complexity and variability of systems is possible in this class of projection. The first one according to the graphical representation in a multidimensional space, which expresses repeated states of behavior in phase space of the system, second by numerous quantitative indexes defined for recurrent plots (see e.g. [28]). Very promising direction for physiological research can be the exploitation of the family of RP tools in notation of the complex network [23]. It also expresses the planned strategy for characterization of the sleep apnea events.

### *F. Inter-Events Characterization Tools*

Existence of power law scaling has been observed in numerous physical, economical, social, etc. systems. It was stated that existence of this rule is strictly connected with a complex nature of the object [19]. First step in such procedure is distinguishing some clear and characteristic occurrences on the time axis of history of system evolution when the system is in a state, which can be called as an event. The essence of the power law is the observation that probability density of time distances between such events can be described with the power formula [13], [19]. For oscillating physiological systems, e.g. expressed in polysomnographic recordings of respiratory flow or abdominal movements during sleep, this measure is able to differentiate irregularities, their origin and statistical properties [13]. Other functions described in this paper are proper for the use during operation in this section of the COMPASS Toolbox, i.e. the procedure of IBIs extraction, algorithm devoted to the calculation of frequency distribution or plotting the log-log dependence of power spectrum density for input time series.

### *G. Algorithms for Measurement of Synchronization*

The other keywords suggestive here for complex systems

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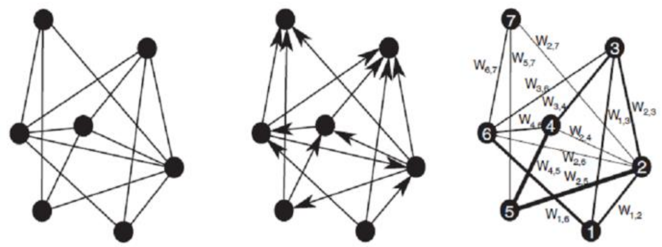

Fig. 2. Undirected (A) unweighted and directed (B) and weighted and undirected (C) graphs.

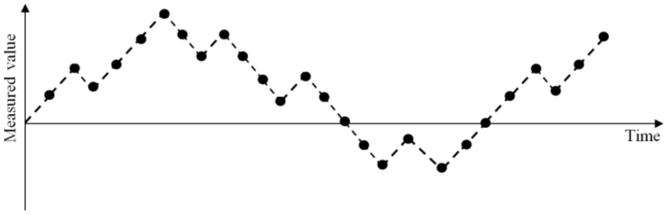

Fig. 3. Time series perceived as a network of (consecutive) states.

analysis can be synchronization. From a system theory point of view, this conception describes the adjustment of rhythms of oscillating objects due to their weak interaction [16]. Using the appropriate function, started in Matlab editor, or designed graphical interface, it is possible to represent the data in 2-D or 3-D phase space, obtain a Poincare map, make spectral analysis of the data, to assess the level of correlation between the subsystems and the value of mutual information and delayed mutual information [29], estimate Lyapunov exponent from the data and also explore the interrelations between subsystems by calculation the qualitative-quantitative markers typical for recurrence plots (RP, CRP and JRP are accessible here together with appropriate RQA). Additionally, the procedures which support the evaluation of coupling between subsystems were inserted in this part of the COMPASS library. They are, e.g. the visualization of time series loaded from file (in original or zoomed scale), working with synthetic data simulated in models for the equation of oscillators given by user, removing the constant trends from signals, filtering or zero-padding operation during spectral analysis.

### *H. Complex Network Reconstruction and Quantification*

The amount of available data and improvement in computer efficiency has raised a new field of algorithmic research with the fundamental assumptions in mathematical theory of graph [20, 21]. The complex network theory operates on network structures $g = (N, E)$ which consist of nodes or vertices $N = \{n_1, n_2, \ldots, n_N\}$ and links or edges between them $E = \{e_1, e_2, \ldots, e_M\}$. Complex network can be undirected or directed, unweighted or weighted (Fig. 2), uni- or multilayered, etc. [20, 21, 30, 31]. Mathematically, complex network can be represented by adjacency matrix $\mathbf{A}_{ij}$ [20, 21, 30] and this representation makes operation with real reconstructions of complex networks much more easy, due to their sparsity [21]. Modern science and engineering adapted complex network theory as an efficient tool for complex system characterization. In fact, there are numerous examples of complex network occurrences in real world. To analyze system in the mode of complex network theory it is sufficient to identify edges as a kind of system properties or states and links as interrelations between them. But especially interesting and advantageous for measurement is to operate directly on measured samples of data, e.g. on time series datasets. Here, one can also find some analogies to the complex network since time series can be perceived as structure of states (dots in Fig. 3) evolving in time. In result, the transformation of time series into complex network is defined and used for depiction of complex system behavior and properties [32-36]. From the metrology point of view, the measurement can be realized as qualitative and/or quantitative in the complex network regime.

COMPASS Toolbox implements time series–complex network transformation according to the rules defined in [25]. It means that complex network structure can be reconstructed for input time series, e.g. signal acquired during biomedical measurements in patient suffering from sleep apnea syndrome. Applied approach is simple in use, i.e. it is sufficient for user to set the number of quantiles ($Q$) as the input parameter for time series processing [25]. What is more, several quantitative coefficients can be calculated, e.g. the average shortest path length ($L$), the average node degree ($\langle k \rangle$), clustering coefficient ($C$) [20, 21, 30].

## III. SLEEP APNEA SCHEME – DESCRIPTION AND PREDICTION

Physiological time series show alterations to complexity and fluctuation properties with disease. Mackey and Glass [37] coined the term “dynamical disease” to describe diseases in which the temporal pattern of physiological variables differs from normal, reflecting some possible change to the mechanisms controlling these variables [38]. There are some individualized symptoms that sleep process can be depicted in the paradigm of complex systems. For example, inter-breath intervals from sleeping adults analyzed using DFA were more random during both deep and light non-REM sleep when compared to wakefulness and REM sleep [15]. However, IBIs in infants analyzed using Fano factor showed no differences between sleep stages [16], a disparity which may arise out of differences in control between the age groups, but which also highlights the need to account for the use of different techniques. Also, in obstructive sleep apnea, it was found that fractal analyses of heart rate variability were more sensitive than spectral analysis in detecting severity of disease [6]. Already there are the examples of methods devoted to complexity analysis being used to predict future risk or outcomes in disease [2], [39]. SAS is still poorly represented in this sense, while this may have direct implications on interventions, see e.g. results from [40] on continuous positive airways pressure (CPAP). These facts substantiate the multithread studies of sleep apnea scheme, with the use of spontaneous and provocative strategies and for various accessible measures, like in the COMPASS Toolbox.

Multi-scale and multi-compartment modeling studies can considerable support hypothesizing about respiratory properties during sleep. They enhance physiological interpretations of the results and provide specific information on the calibration of the theoretical tools used during investigations. The PNEUMA model [10] supplemented with more precise description of respiratory mechanics (like in [41]) is exploited for differentiation between various scenarios of breathlessness. Patients with stated symptoms of respiratory diseases during sleep and their general mathematical equivalent is used at the one side of experiment, and the COMPASS Toolbox at the other (which is connected with processing of experimental data). Comprehensive studies are aimed at broad aspects of apnea, which should provide a map of this transitive disorder and possible scenarios of its treatment. Only exemplary and preliminary results are given in the short form of the letter, prepared for chosen signals and measures. Detailed aspects of used methodologies and obtained results will be the subjects of forthcoming papers.

## IV. RESULTS

The multi-scale analysis of processes observed in patients during sleep are possible with the COMPASS Toolbox, with reference both to single physiological signal and measures operating on interdependencies between two sets of data. Exemplary results of mapping of SAS properties, showed in Fig. 4–Fig. 9, exhibit preliminarily the potential of the COMPASS library to differentiate qualitatively and quantitatively between normal and pathological cases. The patterns of textures generated in RPs, and the trends and levels of complexity and variability measures defined for data sets [23], [28], when considered them directly [13], [14] and in the networking context [23], can be the proof of this statement. Obtained results promote also the prospective idea of prediction and control of future states of the respiratory system during sleep.

Applied in the COMPASS Toolbox the algorithms proper for complex network approach provide for user hardly unexploited (in clinical practice) domain of the complex system measurement. In implemented version, the procedure offers qualitative and quantitative description for networks reconstructed with time series data. Results from Fig. 8 and Tab. 1 show that complex network theory enables differentiation between two dynamical systems – here exemplary theoretical objects have been used and defined by Lorenz and Rössler [42]. The complex network reconstructed for the Lorentz system exhibit two clear modules (Fig. 10a), whereas the complex network identified for the Rössler system is elongated due to periodic character of time series (Fig. 10b). Some differences in patterns of nodes degrees are visible in both system: in the Lorentz network equivalent nodes with relatively high degree are deployed quite uniformly throughout the network, and information in the Rössler network need to be transmitted through the several nodes of highest degree, which are located in the middle of the network (Fig. 10b). In result, the Lorentz system as a network is more efficient ($E$ = 10.22) than the Rössler one ($E$ = 2.43). Quantitative factors prove also that first network is more clustered ($C$ = 0.101) than the second one ($C$ = 0.025) – see Tab. 1.

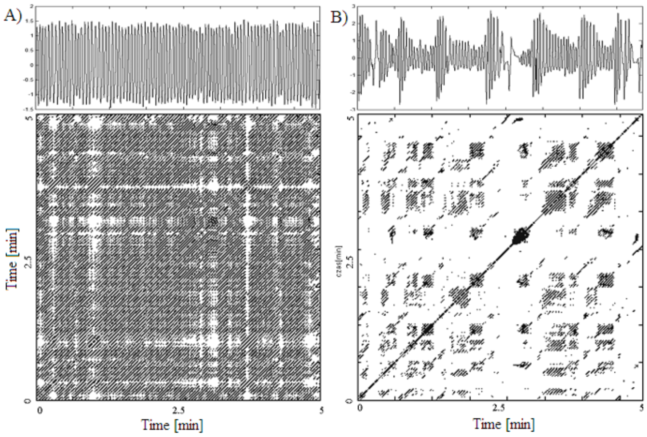

Fig. 4. Time series of nasal airflow $NF(t)$ and its recurrence plots in case of lack of apnea events (A) and with stated the central apnea episodes (B).

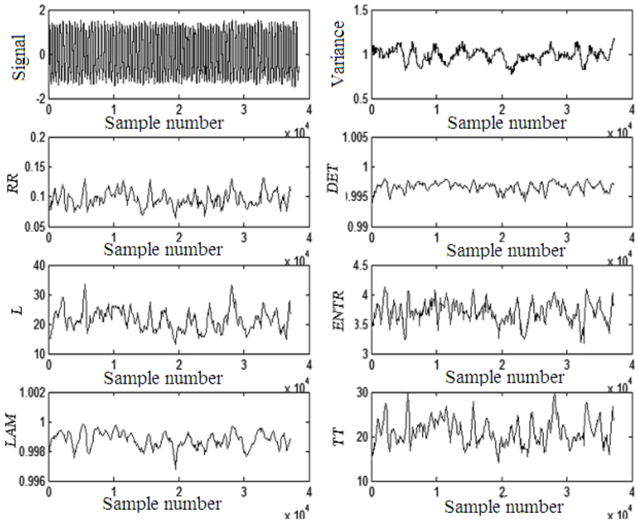

Fig. 5. Recurrence quantification analysis for nasal airflow measured in healthy subject; the length of time window $w_L$ = 1000, moving step $w_s$ = 100 (samples).

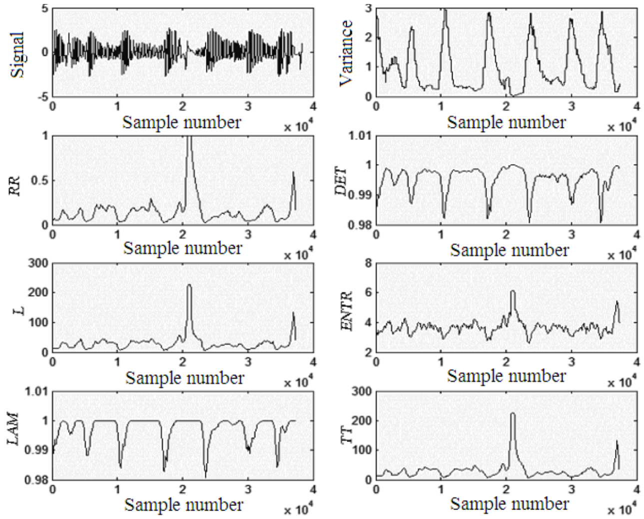

Fig. 6. Recurrence quantification analysis for nasal airflow measured (moving window) in patient with central apnea; $w_L$ = 1000, and $w_s$ = 100.

Studies with real data and COMPASS Toolbox bring to further original observations. ECG recordings stored in PhysioNet [43, 44] for healthy subjects (Subject 1 and Subject

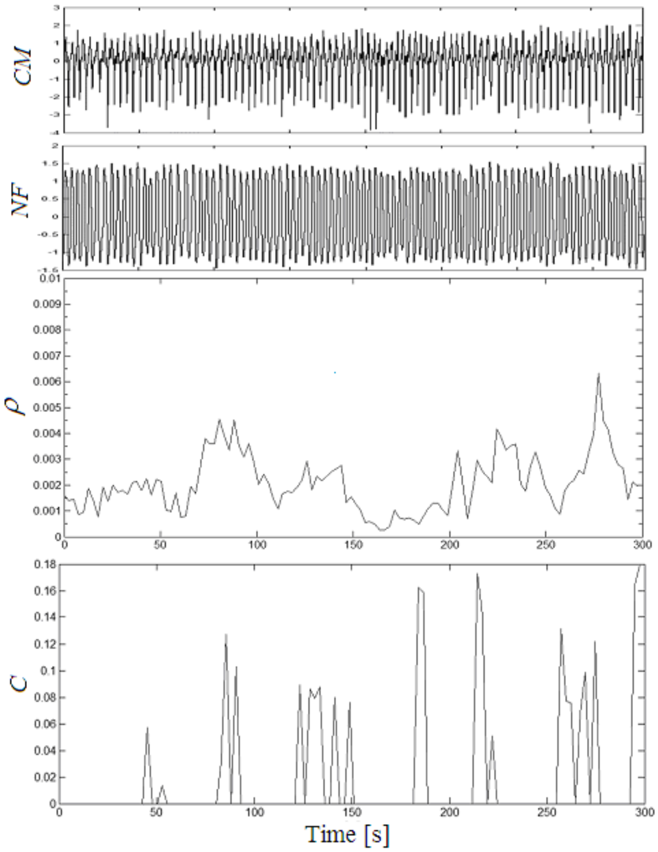

Fig. 7. Link density $\rho$ and clustering coefficient of nodes ($C$) [23] in the recurrence network of a time series of chest wall movement ($CM$) and nasal airflow ($NF$) acquired in healthy subject; $w_L = 3000$, and $w_s = 300$ (in samples).

2) and patients with sleep apnea syndrome (Subject 3 and Subject 4) were used for complex network reconstruction (Tab. 2). For time series of 6000 samples length and number of quantiles $Q = 77$ directed networks were calculated (Fig. 11 and Fig. 12) together with their parametric characteristics (Tab. 3).

The results prove that complex network theory has potential to differentiate between complex biological systems. Both

TABLE I
PARAMETRIC CHARACTERISTICS MEASURED FOR COMPLEX NETWORK RECONSTRUCTED FROM TIME SERIES DATA GENERATED IN LORENTZ AND RÖSSLER SYSTEMS

| | Sample no. | Quantiles ($Q$) | $L$ | $E$ | $C$ | $\langle k \rangle$ |
|---|---|---|---|---|---|---|
| Lorentz system | 1000 | 32 | 0.13 | 10.2 | 0.10 | 31.25 |
| Rössler system | 1000 | 32 | 1.18 | 2.43 | 0.02 | 31.25 |

TABLE II
CHARACTERISTICS FOR HEALTHY SUBJECTS AND PATIENTS SUFFERING FROM SLEEP APNEA SYNDROME; AI – APNEA INDEX (NUMBER OF APNEA EVENTS PER HOUR), HI – HYPOPNEA INDEX (NUMBER OF HYPOPNEA BREATHS COUNTED PER HOUR), AHI – TOTAL APNEA/HYPOPNEA INDEX (SUM OF AI AND AHI)

| Subject no. | Age [yrs] | Sex | Height [cm] | Weight [kg] | *AI* | *HI* | *AHI* |
|---|---|---|---|---|---|---|---|
| 1 | 28 | F | 169 | 57 | 0 | 0 | 0 |
| 2 | 27 | M | 184 | 72 | 0 | 0 | 0 |
| 3 | 29 | F | 183 | 100 | 86.8 | 6.7 | 93.5 |
| 4 | 39 | M | 180 | 120 | 61.2 | 18.3 | 79.5 |

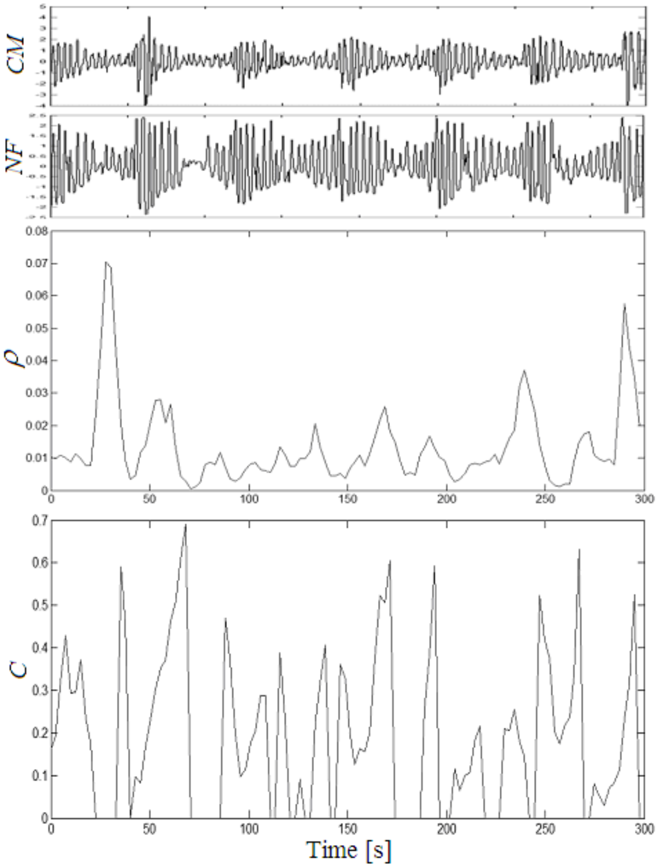

Fig. 8. Link density $\rho$ and clustering coefficient of nodes ($C$) [23] in the recurrence network of $CM$ and $NF$ time series acquired in patient with mixed (central/obstructive) apnea events; $w_L = 3000$, and $w_s = 300$ (in samples).

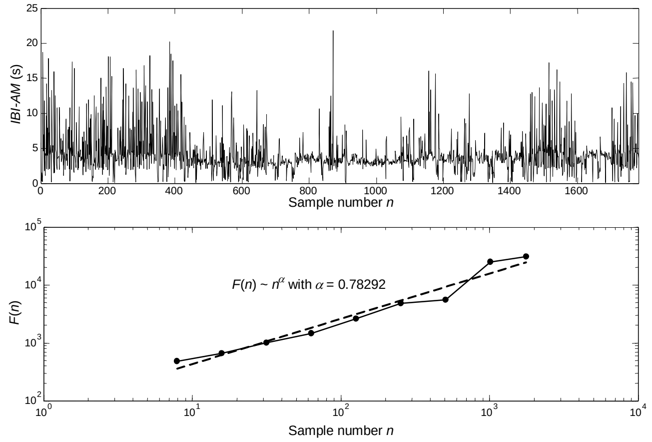

Fig. 9. Time series of $IBI\_AM$ (case: obstructive apnea patient) formulated from 2 hrs recording of abdominal wall movements $AM(t)$ and $\alpha$ parameter calculated with DFA algorithm implemented in the COMPASS Toolbox.

TABLE III
PARAMETRIC CHARACTERISTICS MEASURED IN COMPLEX NETWORKS RECONSTRUCTED FROM ECG DATA ACQUIRED IN HEALTHY SUBJECTS (SUBJECT 1 AND SUBJECT 2) AND PATIENTS WITH SLEEP APNEA SYNDROME (SUBJECT 3 AND SUBJECT 4)

| Subject no. | No. of samples | Quantiles ($Q$) | $L$ | $E$ | $C$ | $\langle k \rangle$ |
|---|---|---|---|---|---|---|
| 1 | 6000 | 77 | 0.44 | 12.1 | 0.33 | 77.9 |
| 2 | 6000 | 77 | 0.44 | 12.9 | 0.42 | 77.9 |
| 3 | 6000 | 77 | 0.21 | 18.5 | 0.36 | 80.8 |
| 4 | 6000 | 77 | 0.22 | 27.7 | 0.21 | 82.9 |

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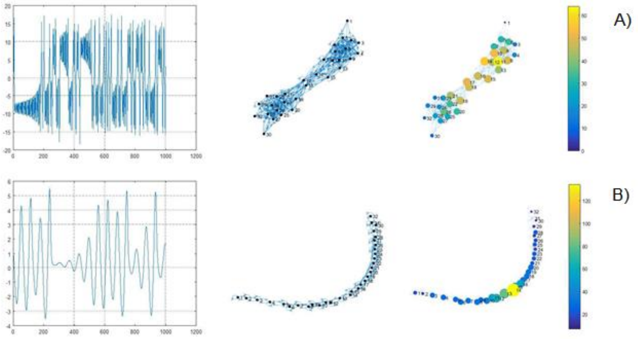

Fig. 10. Directed complex networks (also with inserted the clustering marks) reconstructed from time series data generated in Lorentz (A) and Rössler system (B).

qualitative (topologies of reconstructed networks) and quantitative information can be exploited to uncover hidden patterns in time series data recorded in healthy subjects and patients with SAS. The highest *AHI* (more advanced sleep respiratory disorders) the network architecture is more focused and the average shortest path length is smaller. The average node degree ($\langle k \rangle$) in healthy subjects is lower than in diseased ones and the same network interconnections are more homogeneously organized, which results in improved network efficiency ($E$), respectively (Tab. 3).

## V. SUMMARY

Although the experimental data processing is a well based domain of science and engineering, access to modern and universal algorithms adjusted to observed object is not so obvious. First of all, original research need to test the newest achievements in data science, which uses actualizations in mathematics and computer sciences. What is more, generalization of processing techniques is relatively slow process and typically modern methods are dedicated to selected applications [45-47]. This implicates some difficulties for potential users who are not directly associated with designing of procedures for data/object exploration, e.g. clinicists and medical researchers. Accessibility is not the only problem here, since results of observations are conditioned by multiple functional factors associated to algorithm performance [43, 48]. Validation of analysis algorithms (their software implementation) is not the routine practice, and in local use typically avoids peer review scheme, using private dataset for self-evaluations and unclear measures of performance.

To date, a major obstacle to the dynamic analysis of physiological signals has been the unavailability of open source computational tools necessary to promote multidisciplinary and collaborative efforts to find “hidden information” in such complex recordings. Also procedures included in the “PhysioToolkit” (Research Resource for Complex Physiologic Signals [35]) form a library with limited access to modern algorithmic solutions dedicated to complexity and variability analysis of the systems and data. These arguments have promoted the idea of creation of the COMPASS Toolbox, which fills the gap in this area. The library, designed and described in the letter, assembles the functions around some conceptual issues, typical for complexity analysis (i.e. initial preprocessing of data, nonlinear dynamics, complexity and variability, inter-event characterization, synchronization), but its structure is open to future development. It is universal as regards application to the multidisciplinary objects and processes, provide the simple

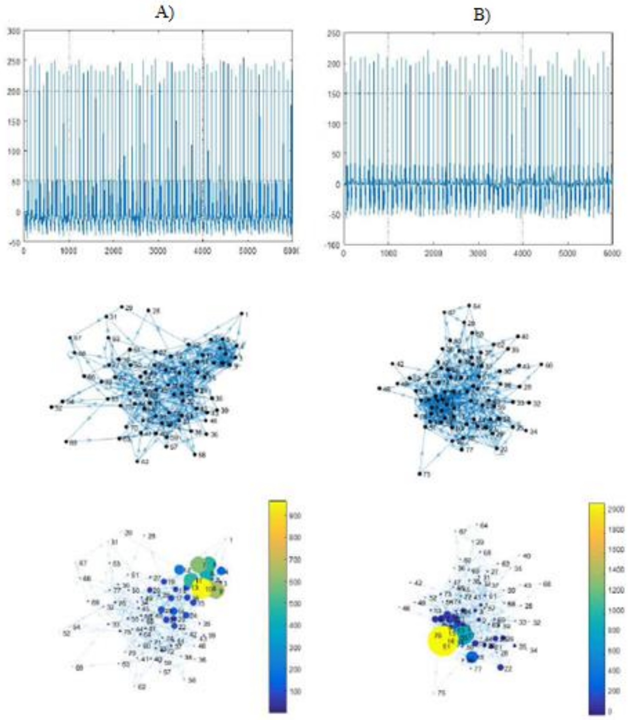

Fig. 11. Directed complex networks (also with inserted the clustering marks) reconstructed from time series data recorded in healthy subjects: a) Subject 1 and b) Subject 2.

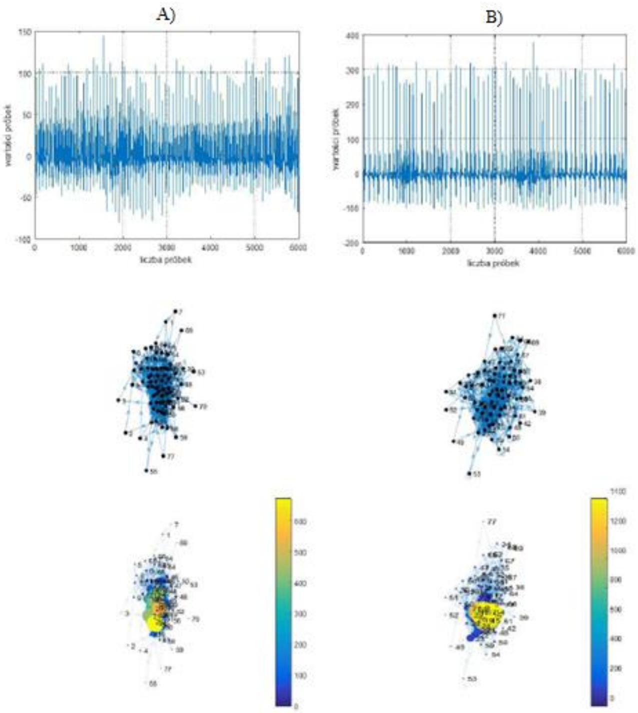

Fig. 12. Directed complex networks (also with inserted the clustering marks) reconstructed from time series data recorded in patients with sleep apnea syndromes: a) Subject 3 and b) Subject 4.

examples for educational purposes (training of the staff), includes both well established, verified algorithms and the novel structures for experimental testing and original investigations leading to potential breakthroughs.

To realize the overriding research aim – creation of a map of dynamic disease of sleep apnea process, the general idea of programming tools was associated with the extended PNEUMA model. The research protocol supplemented with a database of physiological system (this task is under realization) is oriented towards proposing the tools and strategy for forecasting, diagnosis/interpretation and original treatment in a case of sleep disorders in children and adult patients, also in a mode of e-health.

The paper summarizes the work in the programming domain for health (health informatics) and gives the methodological hints and some preliminary and exemplary results for a chosen subject with stated the syndromes of sleep apnea (personalized medicine). First of all, the set of procedures enclosed in the authorial COMPASS Toolbox has enabled reconstruction of numerous patterns encoded in the polysomnographic signals. This has been possible since a bunch of algorithms available in the COMPASS library are able to look into the experimental dataset at various angles, and in consequences provide a diversification in sensitivity to various factors triggering singular behaviors classified by medical doctors as the sleep apnea. What is more, apart from clear and direct patterns contained in time series, these algorithms are suitable to identify the hidden and multilevel patterns in multimodal datasets, which have never been studied in common for the sleep apnea disorders. Inference obtained in this way can open the possibility of fusion-like studies oriented towards interpretative and prescriptive actions, accompanied with ability to sleep apnea phenotyping identification and understanding.

In a presented stage of the project, reported results should be perceived rather as a demonstrative and only a partial findings of qualitative and quantitative nature can be compared to the other works in sleep/respiratory research. For example, qualitative depiction from Fig. 4 and quantitative statements from Fig. 5 and Fig. 6 enable reliable differentiation between healthy and patients with the central sleep apnea using only nasal airflow. The population sample used in our study is too small to conclude about the statistical properties of that clustering and to compare obtained results to the other works reported in literature (e.g. [26, 49]). On the other hand, the nasal airflow typically has been used for detection of the obstructive sleep apnea, which is easier in description than the central one, better understanded so far, and available naturally at the level of mouth and/or nose. Thus, demonstrated results show an increased sensitivity of the recurrence plots and RQA on the patterns detection in nasal airflow data and associated to the central sleep apnea. In analogy, application of the moving window functionality to the complex network description (realized in the COMPASS Toolbox) has enabled uncovering different temporal patterns in fused nasal airflow and chest wall movement, recorded in healthy and subjects with mixed (central/obstructive) sleep apnea – see Fig. 7 and Fig 8, respectively. Following the amplitude and the ordering in the link density $\rho$ (differences of at least one order in signal amplitude has been observed here) and clustering coefficient $C$ (the ordering in data can be quantified, e.g. with the use of entropy measures included in the COMPASS Toolbox, i.e. the approximate, sample and Shannon entropy [14]). This intra and/or inter-event characterization can be further extended with the multiscale view like in Fig. 9 – here, formulated the IBIs time series have exhibited a unique pattern in physiological data of abdominal movement, quantified with the value of the exponent coefficient calculated in DFA algorithm. Finally, the sleep apnea can be viewed from the angle of the performance of the cardiological subsystem in a human body. Although there have been numerous studies realized in this range (e.g. [49, 50]), they have not used the complex networks theory to uncover patterns associated with sleep disorders. In reported studies, we demonstrated that the application of that algorithms can provide additional information of qualitive and quantitative nature – see Fig. 11, Fig. 12, Tab. II and Tab. III. In this way, using the procedures implemented so far in the COMPAS Toolbox, we are able to map the complexity and variability associated to the sleep apnea syndrome much more completely during one experiment than it is available in other works. What is more, obtained results pave the way to the complementary system-oriented research for the example of the sleep disorders, including the interpretative approach (e.g. with the XAI scenarios, like in the scheme from Fig. 1) significant for identification of the causal factors, driving the singularities in sleep states, the SAS phenotype classification, prediction and prescription, including the intra- and the inter-subsystems sensing/measurements.

Demonstrated methodologies and tolls are universal and suitable to supplement the measurement pipeline consisting of multisensory set-up devoted to medical monitoring and diagnostics, including wearable devices orchestrated in cloud-based telemedical system. What is more, graph-based learning tools like the complex networks direct possible data explorations, thus medical treatment, toward designing of the personalized medicine services. In the paper, this methodology presented for the problem of sleep apnea syndrome contributes to description of complex structural-functional interrelations, which still has not been fully understanded. Finally, obtained results prove that the complex nature of the respiratory system and SAS process can be reconstructed in fusion-like scenario of multisensing signal processing, and the graph neural networks can be used to depict and predict this complexity in the next steps of the research actions [48]. Regarding human wellness and patient monitoring during sleep, reported results requires further interpretations and translation to objective medical actions.

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