

Distinct RR Interval Correlations in Sleep Apnea and Heart Failure

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Abstract

We examine RR interval (RRI) correlations in subjects with obstructive sleep apnea (OSA) and congestive heart failure (CHF), aiming to identify nonlinear heart rate (HR) variability (HRV) features that distinguish these conditions. Healthy controls serve as a baseline. While HRV changes are known in both pathologies, direct comparisons remain limited, especially regarding new nonlinear measures.

Nighttime ECG recordings from Holter and polysomnography are analyzed for three groups: healthy (N=90), OSA (N=41), and CHF (N=42). We apply second-order scale-dependent detrended fluctuation analysis (sDFA) to extract scaling exponents $\alpha(s)$ and scale-to-scale changes. Classification is performed using random forest and compared to a combined classifier using conventional HRV metrics.

The sDFA method reveals significant group differences: CHF shows decreased α at short scales, while OSA exhibits elevated α at scales 20–30. Despite individual variability, group-level trends are clear. Classification using sDFA alone achieved a balanced accuracy of 72%, outperforming the combined conventional HRV metrics (RMSSD, LF/HF, and SD1/SD2) and mean RR at 69%. When both feature sets were combined, the balanced accuracy improved to 75%. These findings highlight sDFA's potential for enhancing the diagnostic sensitivity of HRV analysis.

1. Introduction

Obstructive sleep apnea (OSA) and congestive heart failure (CHF) are two prevalent and serious medical conditions that significantly impact cardiovascular health. OSA is characterized by repeated episodes of partial or complete obstruction of the upper airway during sleep, leading to intermittent hypoxia and fragmented sleep [1]. CHF, on the other hand, is a chronic condition in which the heart fails to pump enough blood, often due to myocardial infarction, hypertension, or cardiomyopathy [2].

Heart rate (HR) variability (HRV), the variation in time between consecutive heartbeats, is a key marker of autonomic function and cardiovascular health [3]. In OSA, the intermittent hypoxia and arousals from sleep lead to

increased sympathetic activity and reduced parasympathetic activity, resulting in changed HRV [4]. Specifically, measures such as the standard deviation of NN intervals (SDNN) and the root mean square of successive differences (RMSSD) are often reduced in OSA patients [5]. Similarly, CHF is associated with autonomic imbalance, characterized by heightened sympathetic activity and diminished parasympathetic tone, which also leads to decreased HRV parameters, particularly in measures like the low-frequency to high-frequency (LF/HF) ratio [6].

Here, we focus on an extension of detrended fluctuation analysis (DFA) [7], called scale-dependent DFA (sDFA) [8, 9]. By computing the mean fluctuations $F(s)$ around the local polynomial trends at multiple scales s , DFA is applied to assess the power-law scaling $F(s) \propto s^\alpha$ characterized by a scaling exponent α [10, 11]. Building on our previous work that investigated the impact of OSA on the DFA scaling exponent [12], we now extend this approach to study CHF. Specifically, we analyze night-time electrocardiogram (ECG) recordings to characterize both OSA and CHF, focusing on RR interval correlations across scales to reveal underlying pathophysiological patterns.

2. Data and preprocessing

We utilize five databases from Physionet [13]: Healthy controls from both MIT-BIH Normal Sinus Rhythm Database [14] and Normal Sinus Rhythm RR Interval Database [15], CHF patients from BIDMC Congestive Heart Failure Database [16] and Congestive Heart Failure RR Interval Database [17] and extra healthy controls and OSA patients from the Physionet Apnea-ECG database [18]. We focused on sleep periods because signal quality is typically higher and apnea events are more easily detectable during this time. For the healthy and CHF databases, we approximated sleep by identifying the continuous 7-hour segment with the lowest average HR. Although this approach does not perfectly correspond to actual sleep, it represents the closest approximation achievable with these datasets, even if it is not exactly consistent with the apnea database recordings.

Table 1 shows the sex and age distributions of the subjects in different datasets. Note that the OSA and CHF

Table 1. Basic characteristics of the study groups. N is shown for males (m) and females (f); other values are mean \pm standard deviation. *18 CHF subjects with unknown sex.

	Healthy	Apnea	CHF
N (m/f)	90 (46/44)	41(40/1)	42(19/5)*
age (years)	50 ± 17	51 ± 7	55 ± 12

populations are male driven, whereas the healthy control population is more balanced. Also despite the age ranges being somewhat similar there are big differences inside the healthy group between different databases. CHF patients include all the NYHA classes I-IV, however most of the patients are from classes III-IV. Similarly the OSA patients have relatively severe conditions with mean AHI index of (42 ± 22).

Based on previous studies, RR interval (RRI) data quality was assessed using the automatic filtering algorithm, which removes outlier RRIs from the time series. As the recordings in this study were obtained during continuous nighttime recordings outliers and low-quality samples could still occur due to various physiological or technical factors. To ensure data consistency, we applied median-based filtering and discarded outlier RRIs, following the procedure described in our earlier work [19]. Subjects with more than 10% of intervals removed were excluded, eliminating 4 OSA, 7 healthy, and 2 CHF cases.

3. Methods

Conventionally, DFA algorithm yields two scaling exponents, α_1 (scales 4-16) and α_2 (scales 16-64). Here, we utilize the sDFA, with which we can evaluate the spectrum of scaling exponents $\alpha(s)$ over a larger and continuous range of scales. Since the RRI time series can exhibit various phenomena outside of the conventional scale ranges captured by α_1 and α_2 it is important to be able to analyze the whole spectrum of scales to study the characteristics of different conditions, here OSA and CHF compared to healthy subjects. We utilize second-order polynomial fitting in all the calculations of detrended variances of sDFA. To achieve the $\alpha(s)$ distribution, we calculate the scaling exponents as a function of scale over the whole recordings [8, 9]. Additionally, we calculated the difference in α between subsequent scales as extra features describing the changes in the scaling exponent.

For comparison, we also compute other conventional HRV measures: mean RR interval duration (Mean RR) and the root mean square of successive differences (RMSSD) from the time domain, Poincaré plot indices SD1/SD2), and frequency domain high- (HF) and low-frequency power (LF) for the LF/HF ratio. For the frequency do-

main analysis, the time series are detrended using smoothness priors method (with the smoothing parameter $\lambda = 300$) [20] and transformed into frequency domain with Lomb-Scargle periodogram [21].

The classification task was performed using random forest algorithm. Model hyperparameters were optimized through an exhaustive grid search, with performance evaluated using a nested cross-validation strategy. The outer loop employed a 10-fold cross-validation to estimate generalization performance, while the inner loop conducted hyperparameter tuning within each training fold. This approach provides an unbiased assessment of model performance, reduces the risk of overfitting, and minimizes bias from randomly chosen test sets, which is a critical factor with such a small dataset.

4. Results and discussion

The sDFA scaling exponent, $\alpha(s)$, demonstrated significant group-wise differences across the examined populations (Fig. 1). In particular, patients with CHF exhibited markedly lower α values at the shortest scales, indicating reduced complexity in HR dynamics [19]. Conversely, individuals with OSA showed elevated α values at intermediate scales (20–30 RR intervals) [12], suggesting altered autonomic regulation compared to healthy controls. Despite substantial individual variability, the group-level trends were significant.

Importantly, this scale-dependent analysis highlights that the conventional division of α into short (4–16) and long (16–64) scales may not be optimal for distinguishing between all disease states. The continuous scale-wise approach employed here provides superior resolution, capturing nuanced differences in autonomic dynamics that are otherwise obscured by fixed-scale averaging. This methodological refinement enhances the diagnostic sensitivity of sDFA, particularly in differentiating between OSA and CHF.

Table 2 summarizes HRV metrics across healthy controls, apnea subjects, and CHF patients. Mean RR intervals decrease progressively from healthy to CHF, reflecting increased HRs in pathological groups. Although RMSSD appears similar between healthy and CHF subjects, this is misleading due to its inverse relationship with HR—suggesting reduced vagal activity in CHF when normalized.

Apnea subjects show elevated LF/HF ratios, consistent with increased sympathetic activity driven by disrupted breathing. The SD1/SD2 ratio remains relatively stable in apnea, indicating preserved variability structure, while CHF shows a marked increase, possibly reflecting altered autonomic dynamics. Notably, sDFA-2 values at scale 20 diverge significantly: apnea subjects exhibit higher long-range correlations, while CHF patients show reduced com-

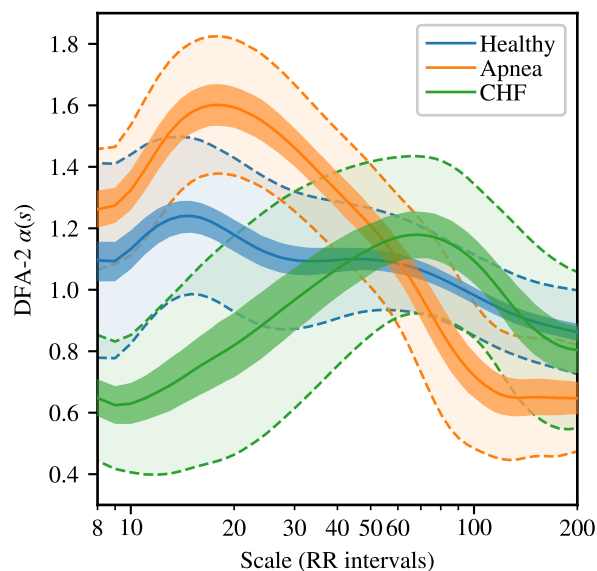


Figure 1. Scale-dependent detrended fluctuation analysis (DFA)-2 scaling exponent $\alpha(s)$ across RR interval scales for healthy, apnea, and CHF subjects. The continuous profile reveals distinct autonomic patterns across groups. Darker shaded regions represent 95% confidence intervals, while the lighter shaded areas show the standard deviation.

Table 2. HRV measures for healthy controls and apnea subjects as mean \pm standard deviation.

	Healthy	Apnea	CHF
Mean RR	951 \pm 103	868 \pm 90	754 \pm 124
RMSSD	46 \pm 27	33 \pm 17	45 \pm 29
LF/HF	235 \pm 163	441 \pm 198	290 \pm 141
SD1/SD2	0.25 \pm 0.12	0.19 \pm 0.05	0.44 \pm 0.24
sDFA-2 (scale=20)	1.18 \pm 0.25	1.59 \pm 0.22	0.82 \pm 0.36

plexity compared to healthy controls.

Classification performance based on conventional HRV measures is presented in Fig. 2(a), while results for the sDFA-based classifier are shown in Fig. 2(b). The combined classifier incorporating all features is illustrated in Fig. 2(c). For the sDFA classifier, the highest classification accuracy was observed in the healthy group (82% \pm 0.09), followed by the OSA and CHF groups with accuracies of 71% and 63% (\pm 21% and \pm 9%), respectively. The lowest misclassification rates were found in the healthy group, with only 14% and 4% of subjects incorrectly labeled as OSA or CHF, respectively. In contrast, 28% of OSA subjects were misclassified as healthy, and 31% of CHF subjects were incorrectly labeled as healthy.

Compared to the classifier based on a combination of conventional HRV features (Fig. 2(a)), the classifier using only sDFA achieved superior performance, with a bal-

anced accuracy of 72% versus 69%. However, the conventional HRV features yielded better classification for the CHF group, with an accuracy of 69% compared to 63%, likely due to differences in mean HR across groups.

The combined classifier with both feature sets (conventional HRV and sDFA) achieved a balanced accuracy of 75%, with the highest individual group accuracies for CHF (75%) and healthy subjects (93%). However, the classification performance for the OSA group decreased to 57%, compared to 71% with the sDFA classifier alone. The most influential features in the combined model were LF/HF ratio, sDFA at scale 8, and mean RR interval. Mean RR was particularly effective in identifying CHF cases, while sDFA and LF/HF were more discriminative for distinguishing OSA from healthy controls. Additional features capturing variations in the scaling exponent α also contributed meaningfully to the classification.

5. Conclusions

Overall, these findings underscore the potential of the scale-dependent DFA-2 method as a sensitive biomarker for differentiating autonomic regulation patterns among healthy individuals, OSA patients, and those with CHF, offering promising implications for early diagnostic applications. In particular, the method demonstrated improved discrimination in this multi-class classification task, particularly in capturing nuanced autonomic patterns. However, classification remains imperfect due to factors such as night-time definitions, and demographic variability. Future work should explore mixed pathologies (e.g., CHF with apnea), as such cases may confound classifiers and appear deceptively healthy.

Acknowledgements

We acknowledge KAUTE foundation (Grant No. 20240420) and The Finnish Foundation for Technology Promotion (Grant No. 10146). We are grateful to Matti Molkari for supplying us with the computer program used to calculate scale-dependent DFA.

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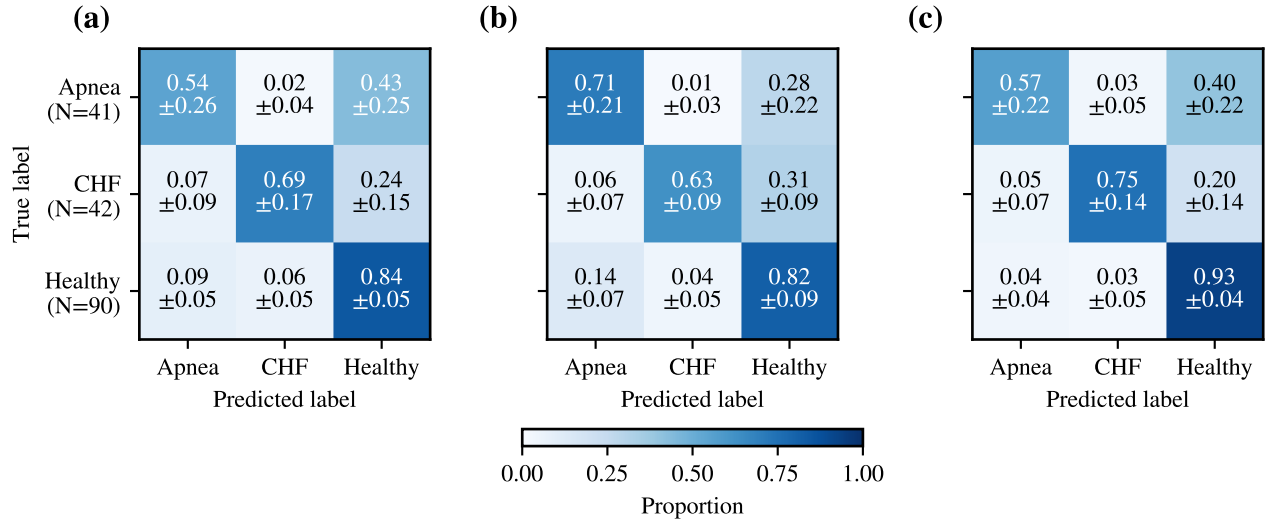


Figure 2. Confusion matrices with standard deviations from nested cross-validation for (a) combined conventional HRV parameters, (b) sDFA alone, and (c) both feature sets together.

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