

QUANTIFYING EDA SYNCHRONY THROUGH JOINT SPARSE REPRESENTATION: A CASE-STUDY OF COUPLES' INTERACTIONS

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ABSTRACT

The co-variation degree between individuals in their physiological signals can reveal insights about the quality of their interaction as well as their personal characteristics. In an effort to capture the amount of synchrony between Electrodermal Activity (EDA) streams occurring in parallel during dyadic interactions, we propose Sparse EDA Synchrony Measure (SESM), an index derived from the joint sparse representation of EDA ensembles. Sparse decomposition is performed using Simultaneous Orthogonal Matching Pursuit (SOMP) from a knowledge-driven dictionary of tonic and phasic atoms, capturing the slow-varying trends and high-frequency signal fluctuations, respectively. At each iteration the atom having the maximum average correlation with the residuals is selected. We compute SESM as the negative natural logarithm of the joint reconstruction error and evaluate it with data from interactions of married and young dating couples participating in tasks of varying emotional intensity. Through statistical analysis and multiple linear regression experiments, our results indicate that SESM depicts significant differences across tasks in both datasets considered and can be associated to individuals' attachment-related characteristics.

Index Terms— Electrodermal activity, synchrony, sparse representation, simultaneous orthogonal matching pursuit

1. INTRODUCTION

Biomedical signal processing has traditionally focused on analyzing individual signal structures [1, 2], while little is explored about physiological co-evolution over time and across individuals. Evidence suggests that the coordination of bio-signals during human interactions can be linked to various social, psychological and developmental constructs [3, 4]. Finding ways to reliably capture such synchrony patterns can afford us new insights into the nature of interactions in the context of dysregulation and recovery [5].

The Sympathetic Nervous System (SNS) has been traditionally used to assess physiological changes associated with “fight-or-flight” responses that can elucidate dimensions of personality and temperament [6]. One of the widely used and unobtrusive techniques for assessing SNS responses involves the measurement of Electrodermal Activity (EDA), as a result of increased skin conductivity from sweat secretion [7, 8]. EDA has been related to a variety of psychological states and traits, such as anxiety and avoidance [6]. Co-evolution of EDA has been associated to couples' affective exchange [9], quality of social interactions [10, 11], as well as dyadic gaming experience [12] and regulatory behavior during therapy [13].

These support the relation of EDA synchrony to various social and communicative aspects and demonstrate the need for reliable ways to capture co-evolution of the corresponding signals.

EDA contains a tonic part representing the general signal trend, called skin conductance level (SCL), and a phasic part of skin conductance responses (SCR) consisting of rapid fluctuations superimposed onto the tonic signal [7, 8]. This distinctive signal structure motivates us the use of sparse models [14], compelling for analyzing EDA and other biomedical signals [15, 16], since they can reliably and efficiently recover the underlying low-dimensional signal information. Previous efforts in this direction have found that EDA-specific dictionaries along with sparse representation techniques can reliably reconstruct EDA and detect the corresponding SCRs [17].

Joint sparse representation has been used to model signals that are individually sparse with respect to a basis, but also correlated between them. It has been proposed for reconstructing signals from multiple sensors offering compression and reconstruction benefits [18, 19, 20, 21]. It has also been used for assessing similarity between streams of data because of its robustness to noise and scale invariance properties [22]. These benefits combined with the inherent low-dimensional EDA structure render joint sparse modeling a promising approach for capturing EDA synchrony.

We propose the Sparse EDA Synchrony Measure (SESM), an index that quantifies the similarity of EDA signals jointly modeled with sparse decomposition techniques, such as the Simultaneous Orthogonal Matching Pursuit (SOMP) [23], and EDA-specific dictionaries of tonic and phasic atoms [17]. SESM is expressed as a negative natural logarithm of the joint representation error so that similar signals achieve higher synchrony values and is evaluated with two datasets containing in-lab dyadic interactions between married and young couples, respectively. Statistical analysis indicates that SESM reflects differences across tasks of various intensity in both datasets. Regression experiments also suggest that it can be associated with measures of attachment collected from individuals' self-reports. These are consistent with previous findings on couples' physiological synchrony [9] and attachment style [24].

2. RELATION TO PRIOR WORK

Multivariate sparse models have been used in a variety of applications to represent joint signal streams with inherent low-dimensional information. Research in distributed communication and sensing has focused on recovering signal ensembles and characterizing the number of required sensors for reconstruction [18]. Multi-channel matching pursuit with data-dependent dictionaries has been proposed for electrocardiogram (ECG) [19] and electroencephalogram

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phy signals (EEG) [20] as well as for spatial audio coding [21]. Joint sparse models further found application to label propagation and action recognition [22]. Our work follows upon these by using SOMP [23] to identify common dictionary atoms of EDA streams.

Quantifying synchrony has been a core theme in various psychophysiological studies. Dynamical systems have been used to represent self- and co-regulation between individuals [11, 25]. Couples’ physiological linkage was further analyzed with bivariate time-series [9]. Most of these studies capture the association between average levels without considering the time-dependent signal variability. Our approach examines the joint evolution over time by selecting the dictionary atoms that best fit the ensemble of EDA signals.

3. DATA DESCRIPTION

3.1. Data Collection

3.1.1. Married Couples’ Interactions

The first set of our data was collected as a part of an ongoing study of communication and emotion in married couples at the University of Utah. We used EDA signals from 19 married couples (ages 21-47) recorded using the BIOPAC MP150 system at a sampling rate of 62.5Hz. Two gel electrodes were placed on the thenar and hypothenar parts of the palm at each participant’s non-dominant hand.

Couples were asked to sit quietly for 5 minutes in the same and then a separate room to develop a baseline for the physiology data, referred as “RestS” and “RestT”. A 5-minute events-of-the-day discussion (“Events”) followed, in which couples were asked to talk with one another however they would normally do when they reunite after the day. The relationship-history conversation (“History”) lasted 5 minutes and partners talked about the beginning of their relationships. Finally, during two 10-minute change discussions, they focused on areas of disagreement in their marriage. One conversation would be on a topic of concern for the husband (“ChangeH”) and one for the wife (“ChangeW”).

3.1.2. Young Dating Couples’ Interactions

The second database comes from an ongoing data collection of interactions between 8 young couples (ages 18-25 years) conducted at the University of Southern California. The same physiological equipment and recording settings were used as in the married couples data collection with similarly structured tasks.

Partners first watched a video of relaxing images for 15 minutes to establish physiological baseline (“Relaxation”). They were then instructed to engage in a 5-minute discussion in which they planned a date that they could have together (“Date”). During the 10-minute change (“Change”), partners had to talk to each other about things in their relationship that could be different. Finally, two loss conversations followed, in which they had to discuss for 10 minutes a significant loss in their life. One conversation was centered on male (“LossM”) and the other on female (“LossF”) loss.

3.2. Attachment Self-Reports

Participants completed a self-report in order to get a measure of the extent to which they relate to their romantic partners. For married couples, the “Adult Attachment Questionnaire” (AAQ) [26] was used, containing 17-items eventually combined into two orthogonal dimensions of *avoidance* and *ambivalence*. Avoidance reflects the tendency to withdraw from closeness and intimacy (scores 8-56), while ambivalence depicts conflicted thoughts and feelings about whether others can be counted on in relationships (scores 9-63).

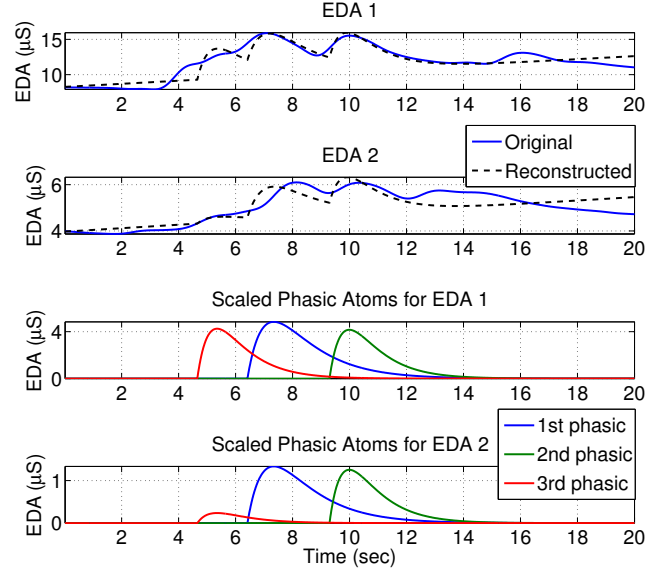


Fig. 1. Joint sparse decomposition of two EDA signals with simultaneous orthogonal matching pursuit (SOMP) and their commonly selected phasic atoms differently scaled per signal. Same legend applies to first/second and third/fourth plot and same time axis to all.

Young couples completed a similar survey, “Experiences in Close Relationships-Revised” (ECR-R) [27], designed to get self-reports of attachment-related *anxiety* and *avoidance*. Similar to AAQ, anxiety indicates how secure people are about their romantic partners, while avoidance captures how comfortable they are depending on others. Both are scored by averaging the relevant scores of a 18-item questionnaire with values ranging between 1 and 7.

3.3. Data Pre-Processing

Movement artifacts were manually removed from EDA using the visualization capabilities of BIOPAC’s *AcqKnowledge* software. High-frequency noise artifacts were further suppressed with a low-pass Blackman filter [28] of length corresponding to 1 second.

4. SPARSE EDA SYNCHRONY MEASURE

In the following, we will use $\mathbf{x} = [x(1) \dots x(L)]^T \in \mathbb{R}^L$ to denote a vector of length L and $x(t)$, $t = 1, \dots, L$, its corresponding value at the t^{th} sample in time. The p-order norm of signal \mathbf{x} is symbolized with $\|\mathbf{x}\|_p$ and the cardinality of a set Ω is written as $|\Omega|$.

4.1. EDA-Specific Dictionary

Since EDA presents a characteristic structure, it can be efficiently modeled through sparse decomposition by a small number of carefully designed parameterized dictionary atoms, each of length L , capturing its tonic and phasic parts [17].

Tonic atoms reflect the slow varying signal trends and can be represented with straight lines as $g_\beta(t) = \Delta_0 + \Delta \cdot t$, where $\Delta_0 \in \{-20, -10, 1\}$ and $\Delta \in \{-0.010, -0.009, \dots, -0.001, 0, 0.01, 0.02, \dots, 0.10\}$ are offset and slope.

Phasic atoms capture the abrupt increase and smooth decrease of SCRs. They can be expressed using a Bateman function, as proposed in [29], with equation $g_\gamma(t) = \left(e^{-a(st-t_0)} - e^{-b(st-t_0)} \right) \cdot u(t-t_0)$, where $a \in \{0.2, 0.4, \dots, 2\}$ and $b \in \{0.4, 0.8, \dots, 2\}$ control the steepness of recovery and onset ($a < b$). Scale $s \in \{0.06, 0.08, \dots, 0.14\}$ determines the compression and dilation of

atoms in time. Shift $t_0 \in \{0, 10, \dots, 10l\}$, $L = 10l$, allows different time positions of the atoms (at every 10 samples) to account for the various possible SCR locations. Equation $u(t) = 1, t \geq 0$ and $u(t) = 0, t < 0$ represents the unit step function centered at 0.

Dictionary parameters are empirically set to resemble observed SCRs and are experimentally shown to provide reliable representation [17]. Their combination results in a dictionary $\mathbf{D} = [\mathbf{g}_1 \dots \mathbf{g}_Q] \in \mathbb{R}^{L \times Q}$ of Q atoms; where $Q=7,813, 15,668$ and $23,438$ for analysis window of 10, 20 and 30 sec, respectively.

4.2. Sparse Representation of Co-occurring EDA Streams

Let $\mathbf{f}^{(m)} \in \mathbb{R}^L$, $m = 1, 2$, be two co-occurring EDA signals. According to joint sparse representation [18, 23], these can be represented as a linear combination of a small set of N common atoms from a dictionary $\mathbf{D} \in \mathbb{R}^{L \times Q}$ such that $\mathbf{f}^{(m)} \simeq \mathbf{D}\mathbf{c}^{(m)}$. The atom coefficients $\mathbf{c}^{(m)} \in \mathbb{R}^Q$, $\|\mathbf{c}^{(m)}\|_0 = N \ll Q$, of each stream are supported only on the same $\Omega \subset \{1, \dots, Q\}$ with $|\Omega| = N$. Sparse decomposition is performed with SOMP because of its simple implementation and theoretical guarantees of correctness [23]. SOMP is an iterative greedy algorithm selecting at each step $n = 1, \dots, N$ the dictionary atom with maximum average correlation such that:

$$\mathbf{g}_{\zeta_n} = \arg \max_{\mathbf{g} \in \mathcal{D}} \frac{1}{2} \sum_{m=1}^2 \langle R^n \mathbf{f}^{(m)}, \mathbf{g} \rangle, \quad n = 1, \dots, N \quad (1)$$

where $R^{n+1}\mathbf{f} = R^n\mathbf{f} - ((R^n\mathbf{f})^T \mathbf{g}_{\zeta_n}) \cdot \mathbf{g}_{\zeta_n}$ and $R^1\mathbf{f}^{(m)} \equiv \mathbf{f}^{(m)}$. This criterion is slightly modified compared to original SOMP, since atom selection is based on actual and not absolute correlation value. This preserves signal interpretability; negative correlations would cause reversed SCR atoms, disturbing the signal structure [17].

SOMP further follows a least-squares minimization to obtain the best approximation over all atoms that have been chosen at each step. If $\mathbf{D}_n = [\mathbf{g}_{\zeta_1}, \dots, \mathbf{g}_{\zeta_n}] \in \mathbb{R}^{L \times n}$ is the matrix of selected atoms at iteration n , the least-squares approximation of $\mathbf{f}^{(m)}$ for $m = 1, 2$ is:

$$\tilde{\mathbf{f}}_n^{(m)} = \mathbf{D}_n \left[(\mathbf{D}_n^T \mathbf{D}_n)^{-1} \mathbf{D}_n^T \mathbf{f}^{(m)} \right], \quad n = 1, \dots, N \quad (2)$$

Representation is assessed with the average relative root mean square (RMS) error between original and reconstructed signals:

$$RelErr = \frac{1}{2} \sum_{m=1}^2 \frac{\|\mathbf{f}^{(m)} - \tilde{\mathbf{f}}_N^{(m)}\|_2}{\|\mathbf{f}^{(m)}\|_2} \quad (3)$$

Taking into account the long duration of recordings, the original data are segmented and analyzed into K non-overlapping windows of predetermined length L , each yielding representation error:

$$RelErr_k = \frac{1}{2} \sum_{m=1}^2 \frac{\|\mathbf{f}_k^{(m)} - \tilde{\mathbf{f}}_{k,N}^{(m)}\|_2}{\|\mathbf{f}_k^{(m)}\|_2}, \quad k = 1, \dots, K \quad (4)$$

where $\mathbf{f}_k^{(m)}$, $\tilde{\mathbf{f}}_{k,N}^{(m)}$ are original and reconstructed signals at k window.

Intuitively we understand that when two signals are similar, the common dictionary atoms yield low representation error. In contrast, if they are less alike, the dictionary atoms jointly selected for both of them will not be able to reliably represent them, increasing the corresponding error. This allows us to define SESM, a synchrony index that captures the similarity between two EDA signals expressed as:

$$SESM = -\ln \left(\frac{1}{K} \sum_{k=1}^K RelErr_k \right) \quad (5)$$

More synchronized EDA streams will have higher SESM value, and vice-versa. As shown in Fig. 1, SCR fluctuations that are not common for the two EDA signals yield poor reconstruction (12-20sec), while those that co-occur result in commonly selected atoms that reliably reconstruct the corresponding parts of both streams (0-12sec).

Table 1. Repeated-measures ANOVA for overall significant differences of Sparse EDA Synchrony Measure (SESM) across tasks.

Database	F-score	P-value
Married couples	F(2.736,49.256)=7.799	p<0.01
Young dating couples	F(2.168,15.179)=5.272	p=0.017

4.3. Evaluation of SESM

Physiological synchrony cannot be directly observed challenging the evaluation of our model. We follow previous psychophysiological and engineering studies examining synchrony for different types of interactions [9, 10] and in relation to behavioral indices [11, 24]. SESM is computed between EDA signals of husband/wife and male/female for the two datasets.

4.3.1. Analysis of EDA Synchrony Across Tasks

The various degrees of task intensity in our data suggest the presence of distinct EDA synchrony patterns [9]. We perform a repeated measures analysis of variance (ANOVA) [30] to detect overall significant differences between mean SESM values (averaged for all couples) across tasks. We use the Greenhouse-Geisser correction [31], since our data violate the assumption of sphericity, meaning that the population correlation changes across pairs of tasks. We further perform paired t-tests to examine pairwise differences in SESM between tasks with Bonferroni correction to account for the inflation occurring from the multiple tests [32].

4.3.2. Prediction of Attachment Ratings from EDA Synchrony

Previous research indicates that couples' physiological synchrony can be related to the individuals' attachment characteristics [24]. Taking this into account, we use multiple linear regression (MLR) [33] to predict the attachment scores of each person based on the SESM values computed at the different tasks. MLR is performed within a nested leave-one-couple-out cross-validation [34]; outer cross-validation is used to assess the performance of the model, while inner to determine the model hyper-parameters, i.e. analysis window length and SOMP iterations. We report the correlation and the corresponding significance between predicted and ground-truth scores with two feature groups. The first is a 4-dimensional vector of SESM values from only the discussions, i.e. (Events, History, ChangeH, ChangeW) and (Date, Change, LossM, LossF) for married and young couples. The second includes SESM from all tasks resulting in 6 and 5 dimensions for the two datasets, respectively. Since one of the married couples did not provide attachment ratings, MLR results are obtained using 18 couples for the first dataset.

5. EXPERIMENTS

EDA signals were segmented using analysis windows of $W = 10, 20$ and 30 sec to capture various time-scales and represented with $N = 5, 10, 15$ and 20 SOMP iterations to account for multiple detail levels. For the sake of simplicity, statistical analysis (Section 5.1) is performed with 20 sec and 10 SOMP iterations, while similar results were obtained with the remaining parameter combinations. During the inner fold of the MLR nested cross-validation (Section 5.2), we perform a leave-one-couple-out cross-validation within the training set using a 3×4 grid of all combinations for parameters W and N . The one with the highest correlation during training is used to predict the attachment rating of the corresponding test data.

5.1. Analysis of EDA Synchrony Across Tasks

Repeated-measures ANOVA indicates a significant effect of the type of task on both databases (Table 1). For married couples, SESM

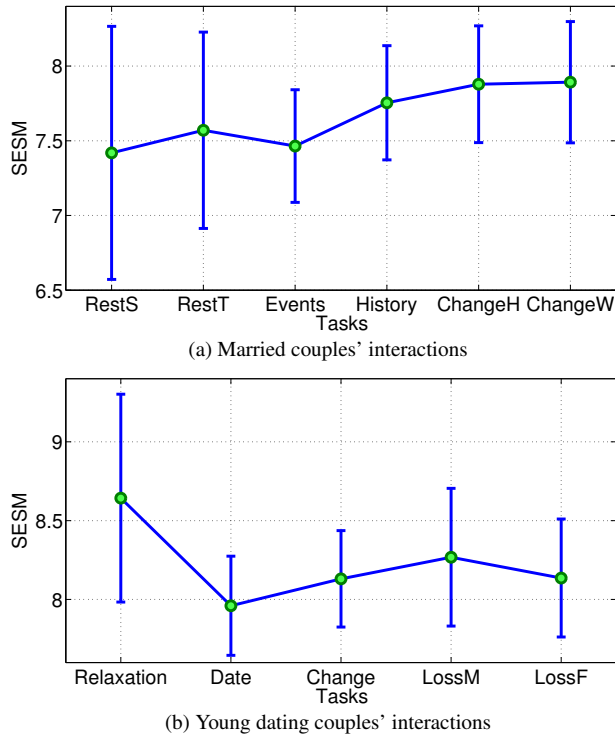


Fig. 2. Sparse EDA Synchrony Measure (SESM) across tasks. Error bars represent one standard deviation distance from the mean.

was significantly lower for the separate resting baseline compared to wife’s change discussion ($p=0.028$) and lower with approaching significance compared to relationship history ($p=0.112$) and husband’s change ($p=0.120$). Events of the day discussion showed significantly lower SESM than relationship history ($p=0.01$) and both change ($p<0.01$) discussions (Fig. 2a). For the small sample size of young couples (Fig. 2b), significant difference only occurred between relaxation and date planning ($p=0.059$).

5.2. Prediction of Attachment Ratings from EDA Synchrony

MLR results suggest that EDA synchrony quantified through SESM can be associated with attachment ratings (Table 2). Ambivalence scores of married couples tend to be accurately predicted for both wife and husband, while avoidance is moderately predicted without reaching statistical significance. Wife’s ambivalence is better predicted when we include the resting baselines in the features, indicating that these tasks might contain useful information about of individuals’ attachment patterns.

Male anxiety and avoidance in young couples tend to be related to SESM, especially during discussions. Female ratings show poorer prediction rates. This could be due to the small sample size resulting in models that might not capture the inherent variability. For most cases, including relaxation did not benefit prediction results.

6. DISCUSSION

Our results indicate that the proposed SESM is able to differentiate potential changes in synchrony patterns across tasks. The discussions occurring in the two datasets are of comparable intensity and can be studied in parallel. Events of the day and date planning conversations for married and young couples were in general more neutral. On the other hand, change discussions in both data, as well as relationship history and loss discussions from the first and second

Table 2. Pearson’s correlation between ground-truth and predicted attachment ratings using multiple linear regression with Sparse EDA Synchrony Measure (SESM) features.

Married couples’ interactions				
Tasks	Avoidance		Ambivalence	
	Husband	Wife	Husband	Wife
Discussions ^a	0.03(0.89)	0.39(0.11)	0.61(0.01)*	0.14(0.57)
Baselines ^b + Discussions ^a	0.32(0.19)	0.20(0.42)	0.62(0.01)*	0.57(0.01)*

^a (Events, History, ChangeH, ChangeW), ^b (RestS, RestT), * $p<0.05$

Young dating couples’ interactions				
Tasks	Avoidance		Anxiety	
	Male	Female	Male	Female
Discussions ^c	0.79(0.02)*	-0.10(0.82)	0.88(0)*	-0.65(0.08)
Relaxation + Discussions ^c	-0.35(0.40)	0.32(0.44)	0.69(0.06)†	-0.60(0.12)

^c (Date, Change, LossM, LossF), * $p<0.05$, † $p<0.1$

datasets, respectively, contain more intense emotions. SESM values differ between these neutral and more intense discussions suggesting higher synchrony patterns of the latter for both datasets (Section 5.1). These are consistent with previous findings [9] about higher physiological linkage during negative expression and exchange.

We further observed that SESM is associated with individuals’ attachment scores in both datasets (Section 5.2), as indicated in [24]. Ambivalence and anxiety seem to be reasonably predicted for husband and male partner, respectively. A weak association occurs between SESM and avoidance, the latter being harder to predict.

The two datasets involved quite different physiological baselines. Young couples watched together a video of images, while married couples performed two resting baselines. SESM depicted different patterns for the two, i.e. higher for young couples’ relaxation than their other discussions and lower for married couples’ resting baseline compared to their other tasks. The reason for this observation might be two-fold. SESM appears to be more reliable in capturing synchrony of simultaneous fluctuations of the phasic part, rather than co-variation of the smooth tonic signal. Potentially because of the relaxing images, young couples’ relaxation showed smooth decreasing trends with minimal fluctuations resulting in small reconstruction errors and high SESM values. We could overcome this by comparing the joint representation of EDA ensembles relatively to their univariate representations. The distinct nature of the two baselines could also affect differently the corresponding signals [35].

A limitation of our method might yield when co-occurring EDA signals have different levels. Despite the fact that tonic atoms detrend the signals, the EDA with higher amplitude might still preserve higher energy influencing more the atom selection process. Weighting the signal residuals might result in more balanced representations. Also the dictionaries in our setup contain predetermined atom parameters. Parametric dictionary learning techniques can create data-specific dictionaries that suppress noisy patterns and result in more reliable joint EDA models.

7. CONCLUSIONS

We proposed SESM, a synchrony index that captures the similarity between two EDA signals using joint sparse models with an appropriate knowledge-driven dictionary. Results on two datasets indicate that SESM shows distinct synchrony patterns across varying intensity tasks and is associated with couples’ attachment-related scores. Future work will focus on asymmetrical EDA models for identifying directional effects between people. We will also compare our approach to previously proposed dynamical systems and time-series analysis, and extend it to other biomedical signals, such as ECG.

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