

Spatial Filtering for Enhanced High-Density Surface Electromyographic Examination of Neuromuscular Changes and Its Application to Spinal Cord Injury

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Abstract

Background: Spatial filtering of multi-channel signals is considered to be an effective pre-processing approach for improving signal-to-noise ratio. The use of spatial filtering for preprocessing high-density (HD) surface electromyogram (sEMG) helps to extract critical spatial information, but its application to non-invasive examination of neuromuscular changes have not been well investigated.

Methods: Aimed at evaluating how spatial filtering can facilitate examination of muscle paralysis, three different spatial filtering methods are presented using principle component analysis (PCA) algorithm, non-negative matrix factorization (NMF) algorithm, and both combination, respectively. Their performance was evaluated in terms of diagnostic power, through HD-sEMG clustering index (CI) analysis of neuromuscular changes in paralyzed muscles following spinal cord injury (SCI).

Results: The experimental results showed that: 1) The CI analysis of conventional single-channel sEMG can reveal complex neuromuscular changes in paralyzed muscles following SCI, and its diagnostic power has been confirmed to be characterized by the variance of Z-scores; 2) the diagnostic power was highly dependent on the location of sEMG recording channel. Directly averaging the CI diagnostic indicators over channels just reached a medium level of the diagnostic power; 3) the use of either PCA-based or NMF-based filtering method yielded a greater diagnostic power, and their combination could even enhance the diagnostic power significantly.

42 **Conclusions:** This study not only presents an essential preprocessing approach for
43 improving diagnostic power of HD-sEMG, but also helps to develop a standard sEMG
44 preprocessing pipeline, thus promoting its widespread application.

45 **Keywords:** electromyography, noninvasive diagnosis, neuromuscular changes, spatial
46 filtering, spinal cord injury

47

1. Introduction

Spinal cord injury (SCI) is a leading cause of adult disability worldwide [1]. The disruption of communication between the brain and the spinal cord results in both loss of voluntary movement (i.e., paraplegia) and loss of sensation [1], [2]. However, the effect of a paraplegia on the survival and function of motor unit (MU) in pathological muscles remains unclear. Since the MU is regarded as the basic functional unit and the final pathway of the neuromuscular control system, it is of great importance to identify MU changes induced by specific mechanisms following the SCI [3], which can offer guidance for the design of effective SCI rehabilitation protocols.

In clinical routine, an invasive approach using concentric needle is applied to electrophysiological examination of MU properties [4], [5]. The insertion of the needle, however, has to deal with various issues including the invasive discomfort, a requirement of medical supervision and a risk of infection, limiting its wide applications including long-term monitoring and repetitive investigations [6]. In addition, the subjectivity during diagnostic evaluation based on the experience of the professional clinicians remains the most important factor when it comes to examine neuromuscular changes [7]. As a result, there is a huge demand for an objective, quantitative and noninvasive approach for convenient examination of neuromuscular diseases and injuries.

Surface EMG (sEMG) is a technique to record the electrical activity of muscle using electrodes placed over skin surface. Due to the benefits of non-invasive and low-cost properties, sEMG recording has been used in examining neuromuscular activities [8-

70 10]. However, traditional bipolar electrode configuration of recording sEMG may
71 suffer from difficulties such as noise contamination, cross-talks from a neighboring
72 muscular activities, attenuated motor unit action potential (MUAP) waveforms due to
73 the low-pass filtering effects of skin and subcutaneous body tissues, and the failure to
74 discern or characterize individual MUAP waveforms due to their severe superposition.
75 As a result, conventional sEMG has not been well accepted by clinicians towards
76 diagnostic applications. High-density (HD) electrode grid has been playing an
77 increasingly important role in the collection of sEMG signals. Although any individual
78 surface electrode within the grid works as the regular single-channel, the grid formation
79 warrants collection of important spatial information concerning muscle activation.
80 Therefore, the HD-sEMG measurement is able to better characterize the muscle's
81 structural and functional heterogeneity, which is regarded as the reflection of activities
82 from different sources such as subcomponent muscles [11-13], muscle-tendon units
83 [14-16], and even microscopic MUs [17-20]. Such spatial information is also helpful in
84 suppressing muscular cross-talks within channels so as to improve the signal-noise
85 ratio. All these prominent features of applying the HD-sEMG techniques can be
86 exploited and further promoted by the use of appropriate spatial filtering methods.

87 The spatial filtering technique can be employed to remove artifacts of HD-sEMG
88 data and to retain useful information given the muscular activation heterogeneity. Its
89 basic principle is to preserve the sources of interest and suppress unwanted components
90 from signals [21-26]. Various matrix factorization algorithms [15], [16], [27-35] relied
91 on different criteria concerning inherent structure of the input multivariate data. Among

92 them, both principle component analysis (PCA) [27-29] and nonnegative matrix
93 analysis (NMF) [14], [29], [33-35] algorithms have been commonly used due to their
94 signal component separation capability, with successful applications in the field of
95 decoding motor intentions including muscle strengths and patterns [27], [29], [38], [39].
96 The PCA is the most fundamental multivariate data analysis algorithm that can find a
97 new set of projection directions called principle components (PCs) that explain the
98 maximum variability of the original data. This projection allows specific manipulation
99 of individual data components, and it is used to remove artifacts (i.e., common mode
100 redundancy across multiple sEMG channels) and to retain useful information associated
101 with specific projected data components. In addition, the NMF algorithm uses a non-
102 negativity constraint that makes its outcomes physiologically meaningful [33]. Since
103 NMF is commonly used to extract muscle synergies driven by the central nervous
104 system to formulate muscle activities from multi-muscle sEMG recordings, it is more
105 reasonable to extract and locate composing sources (i.e., muscle-tendon units [14], [19]
106 or muscle belly regions [36], [37]) from heterogeneous muscle activation characterized
107 by the HD-sEMG [34], [35]. Therefore, it facilitates to determine the task-related region
108 within the coverage of the entire HD-sEMG array [14], [29]. In summary, relying on
109 different criteria, both the PCA and NMF algorithms are expected to emphasize
110 different signal components or to filter out different noises in the recorded HD-sEMG
111 signals. Considering their own strengths and relative weaknesses, it is worth an attempt
112 to use the combination of both algorithms due to their functional complementarity for
113 motivating a better preprocessing outcomes.

114 It is hypothesized that spatial filtering can help to enhance and mine useful
115 diagnostic-related information of HD-sEMG, thus improving diagnostic power of the
116 sEMG examination. The purpose of this study is to verify this hypothesis by the means
117 of testing it on the SCI data. Both the PCA and the NMF algorithms were selected for
118 performing the spatial filtering due to their artifact removal and task-related region
119 localization capabilities, respectively. Their combination was used as well by
120 considering their functional complementarity. Clustering index (CI) analysis [40] was
121 adopted as a representative and convenient approach for conducting the sEMG
122 examination in this study due to its capability of revealing complex neuromuscular
123 changes associated with the MU property alterations underlying paralyzed muscles.
124 The CI analysis was originally designed to process routine single-channel sEMG signal
125 for discriminating between neurogenic and myopathic diseases [40] and thereafter it
126 has achieved great success in non-invasive diagnosis of amyotrophic lateral sclerosis
127 [41], spinal and bulbar muscular atrophy [42] and stroke [43]. Our work not only
128 applies the sEMG CI examination to the SCI data to investigate neuromuscular changes,
129 but also proves the benefit of applying spatial filtering to HD-sEMG data for improving
130 CI diagnostic power. Meanwhile, it evolves a series of PCA-based and NMF-based
131 spatial filtering methods, which help to form a standard pipeline for HD-sEMG
132 preprocessing before its clinical applications including diagnosis of neuromuscular
133 changes.

2. Methods

2.1 Subjects

Nine subjects with incomplete cervical SCI (S1-S9, ASIA C or D) were recruited from the Clinical Neuroscience Research Registry at the Chicago Rehabilitation Institute (Chicago, IL). Demographic and clinical measures for the subjects with SCI are summarized in Table 1. In addition, thirteen neurologically intact subjects and (C1-C13) without any neuromuscular disorder or injury also participate into the experiments.

2.2 Experiments

The abductor pollicis brevis (APB) muscle was examined in this study. It is the largest and superficial muscle within the thenar muscle group on the palm with a distinct and simple function of thumb abduction. This distal muscle on the hand is representative for reflecting motor impairments [9], [10], [41], [43]. These features make it convenient to be examined following clinical routine. The data collection experiments were conducted on both sides of the subjects with SCI respectively, in a random order. The same experimental procedure was just applied to a randomly selected side of each control subject. On this basis, all the tested muscles can be categorized into three groups: the muscles on the left side of subjects with SCI (denoted as SCI-left group), the muscles on the right side of subjects with SCI (denoted as SCI-right group) and the control muscles from the neurologically intact subjects (denoted as control group). A flexible electrode array consisting of 64 electrodes in an 8×8 grid

156 formation was used to target at the examined APB muscles, as shown in Fig. 1. Each
157 electrode had a round recording probe in a diameter of 1.2 mm, and the center-by-center
158 distance was 4 mm between two consecutive electrodes. The surface EMG signals were
159 collected by a Refa128 EMG Recording System (TMS International BV, Enschede, The
160 Netherlands) in 64 recording channels as a result of mono-polar configuration. The
161 sampling rate was set at 2 kHz per channel. There is another round electrode
162 (Dermatode; American Imex, Irvine, CA) placed over olecranon of the tested arm as
163 the ground reference for the recording system.

164 The experiment was carried out in a quiet room in order to reduce the impact of the
165 environmental noises. During the experiment, subjects were seated in a comfortable
166 mobile chair. Their tested arm was bent approximately 90 degrees and was placed on a
167 height-adjustable desk. In the beginning of the experiment, the subject was encouraged
168 to perform three maximal voluntary contractions (MVCs). The maximum value of these
169 trials determined by monitoring the EMG amplitude was taken as a valid MVC. Then
170 the subject was asked to generate an isometric contraction by abducting the thumb with
171 increasingly graded force levels, roughly corresponding to 10%, 30%, 50%, 70%,
172 submaximal (90%) and maximal voluntary contraction (MVC) in terms of the MVC
173 percentage via the EMG amplitude. The subject was encouraged to remain at least 3
174 second as stable as possible for each contraction level. Sufficient rest was also allowed
175 to avoid muscle fatigue between two consecutive trials.

176 The raw HD-sEMG data collected from the APB muscles on both sides of subjects
177 with SCI and on a random side of control subjects were imported to the MATLAB

178 (Version R2016a, MathWorks, Natick, MA, USA) software for analysis. Fig. 2 shows
179 the entire framework for examining neuromuscular changes through spatial filtering
180 analysis and subsequent CI analysis of the HD-sEMG data, with more details described
181 as follows.

182

183 **2.3 Signal preprocessing**

184 A fourth-order Butterworth band-pass filter at 20-500Hz was applied to eliminate
185 potential low-frequency noises (e.g., motion artifacts) and high-frequency
186 interferences. Then, a set of second-order notch filters were used to remove the 50-Hz
187 power line interference and its harmonics. Subsequently, the spatial filtering methods
188 could be applied to the HD-sEMG data.

189 *1) Spatial Filtering using PCA*

190 In the PCA algorithm, the calculation of PCs is realized by diagonalization of the
191 covariance matrix of data. The relevance of the PCs can be ranked in terms of the
192 eigenvalues and reflect its contribution to the data in terms of variance for every PC.
193 Suppose that the original signal $M_0^{m \times t}$ is in a form of m rows and t columns, where m
194 represents the number of channels (64 in this study), and t is the sEMG signal sampling
195 points. The transpose matrix M of observation matrix $M_0^{m \times t}$ can be decomposed as
196 Eq. (1).

$$197 \quad M = UDV^T, \quad (1)$$

198 where $D = \text{diag}(\lambda_1, \dots, \lambda_m)$ is the $m \times m$ diagonal matrix with ordered eigenvalues,
199 the columns of the $t \times m$ orthogonal matrix U are the corresponding eigenvectors, and

200 the $m \times m$ orthogonal matrix V satisfies $UU^T = V^TV = 1$. Thus the eigenvalue λ and
201 the eigenvector U were calculated to decompose 64-channel sEMG signals into 64
202 PCs $[U_1, U_2, \dots, U_{64}]$ corresponding to their eigenvalues ($\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_{64} > 0$) in
203 a descending order. The eigenvectors describe the spatial distribution of the projected
204 EMG over the grid that evolves in time. It has been supposed that the high eigenvalues
205 of the first two components carry a substantial amount of redundant information (i.e.,
206 common mode) among multiple channels, and the components corresponding to the
207 smallest few eigenvalues contain noises unrelated to EMG signals [28], [29], [44].
208 Therefore, it is necessary to remove these components. The PCs with the largest two
209 eigenvalues and a number of smallest eigenvalues were intentionally selected and
210 discarded, and therefore the remaining PCs were used to reconstruct the filtered signal
211 M' . An sensitivity analysis was conducted to determine the number of components with
212 the smallest eigenvalues to be removed, according to the diagnostic performance.

213 2) Spatial Filtering using NMF

214 The NMF algorithm is formulated as a solution to a minimization problem with
215 nonnegative bound constraints [45]. In this study, the multi-channel normalized and
216 rectified sEMG matrix $X \in R^{m \times t}$ (m channels, t samples) was decomposed into two
217 non-negative matrices $W \in R^{m \times s}$ and $C \in R^{s \times t}$ (where $s < m$) by the NMF algorithm
218 according to Eq. (2).

$$219 \quad X^{m \times t} = W^{m \times s} C^{s \times t}. \quad (2)$$

220 The matrix W can be interpreted as a number s of activation patterns, while the matrix
221 C represents their corresponding time-varying activation coefficients. For processing

222 the HD-sEMG data recorded on an entire muscle, each column of W here represents a
 223 spatially correlated activation pattern over the m -channel electrode array, anatomically
 224 reflecting the localization of a specific signal source. Thus, each row of the matrix C
 225 here specifies how an activation pattern is modulated during the task performance. The
 226 variable s varies from 1 to m , representing the number of activation patterns. In practice,
 227 the average variability accounted for (VAF, ranges from 0 to 1) between the original
 228 matrix (X) and the reconstructed one (X^r) was calculated to determine the least number
 229 of activation patterns.

$$230 \quad \text{VAF} = 1 - \frac{\sum_{i,j}(X-X^r)_{ij}^2}{\sum_{i,j}X_{ij}^2}. \quad (3)$$

231 The value of VAF should be as large as possible while retaining original data
 232 information. Previous studies explained the success of reconstruction when the VAF
 233 reaches to 95% [29], [46]. Similarly, the number s was searched within a range between
 234 0-6 and determined in this study when the VAF value was beyond 95%.

235 For each activation pattern, its corresponding time-varying coefficients were
 236 summed up and defined as activation intensity, according to Eq. (4).

$$237 \quad \text{Intensity}(i) = \sum_{j=1}^t C_i(j), \quad (4)$$

238 where $C_i(j)$ represents the time-varying coefficients for the i -th activation pattern, and
 239 t indicates the length of samples indexed by j . Among s activation patterns, the one
 240 corresponding to the highest *Intensity* value was considered to be the major activation
 241 pattern. In the major activation pattern, a number of channels with top-ranked weighting
 242 factors were considered to form a major activation region, and the channels of the input
 243 sEMG in such major activation region were just selected for further processing.

244 It was very critical to determine the number of channels to be selected in the major
245 activation region. Similarly, a sensitivity analysis was conducted in this study by
246 varying the number from 14 to 18, and this number was appropriately set according to
247 the optimal diagnostic performance.

248

249 **2.4 Data segmentation and CI analysis**

250 The data (in a form of multiple channels regardless of whether they were spatially
251 filtered or not) presented several segments of sEMG activities according to the
252 experiment protocol. The onset and offset of each sEMG activity burst can be easily
253 determined. For CI analysis, a series of 1-s epochs (equivalent to 2000 sample points at
254 the sampling rate of 2000 Hz) need to be segmented from the EMG activity. Since
255 actual muscle force was not recorded in this study, the generally observed sEMG
256 amplitude intensities were used to roughly estimate the muscle force fluctuations. The
257 force was considered to be relatively stable when the sEMG intensity remained at a
258 consistent level. Otherwise, the corresponding epochs would be discarded especially at
259 the switch of two consecutive force levels. Thus, the number of epochs in a multi-
260 channel form ranged from 20 to 40 over all force levels for each of all subjects.

261 CI is a non-invasive quantitative method for analyzing uneven distribution and
262 cluster of the processed signal to different neurogenic and myopathic changes [43]. To
263 calculate CI, the signal in each epoch was divided into several non-overlapping
264 consecutive windows in length of 15 ms, which is regarded to approximately cover an
265 individual MUAP [40]. Suppose that there are K windows in total derived in an epoch

266 and A_i was the area of each window. The differential sequences between every
267 consecutive area value (DA_i), between every second window (DB_i) and between every
268 third window (DC_i) can be calculated. Then the CI of each epoch is defined as:

$$269 \quad CI = \{\sum_{i=1}^{K-1} DA_i^2 + \sum_{i=1}^{K-2} DB_i^2 + \sum_{i=1}^{K-3} DC_i^2\} / (6 \cdot \sum_{i=1}^K A_i). \quad (5)$$

270 The CI has a value between 0 and 1, and a relatively high value represents a highly
271 clustered signal, appearing with isolated large action potentials. If the EMG epoch
272 carries multiple channels (it is always the case in this study), the average CI value was
273 calculated from all chosen channels. While the values of CI depended on the contraction
274 level: the increase in contraction levels resulted in a lower value, the area of each epoch,
275 that is the area of all windows, was used to estimate the muscle contraction level [40].
276 It had been proven to be linearly related to CI values using double logarithmic scale
277 [47]. Hereafter, the average areas for all selected channels on each epoch were
278 calculated. For each analysis epoch on the same muscle, two values were obtained: a
279 mean log (area) and a mean log (CI), which were expressed as a point in the CI-area
280 plot. The points derived from the analysis epochs can be scattered to form a cloud over
281 the CI-area plane.

282 The quantification of the normal data reference in the CI-area plot is the prerequisite
283 to subsequent diagnosis. To establish the distribution of the normal cloud, a linear
284 regression analysis was performed on all analysis epochs ($1 \leq \text{area} \leq 100\mu\text{V} \cdot$
285 sec) from the healthy subjects was performed for both log(CI) and log(area). For each
286 epoch, the deviation of the log (CI) scale from the linear regression line was calculated.
287 Then these deviation values were averaged to obtain a mean residual (denoted as R_m),

288 which can be used to assess the presence of abnormality for each subject. The mean μ
289 and standard deviation (σ) of the Rm values on the two sides of all the subjects were
290 calculated and then a Z-score was computed as the final quantify indicator for the
291 evaluation.

$$292 \quad Z = \frac{Rm - \mu}{\sigma}. \quad (6)$$

293 A Z-score between ± 2.5 was defined as abnormal. A tested muscle with a Z-score
294 higher than +2.5 indicated neurogenic changes while a Z-score lower than -2.5 was
295 diagnosed as being myopathic changes.

296

297 **2.5 Performance evaluation and statistical analysis**

298 To evaluate the effect of spatial filtering in HD-sEMG-based diagnosis, the PCA-
299 based method, the NMF-based method and their combination termed the PCA-NMF-
300 based method were applied for spatial filtering of the HD-sEMG signals, with
301 comparison of the original HD-sEMG without any spatial filtering approach. These
302 three spatial filtering methods were shown together in Fig. 2, where the PCA-based
303 method and the NMF-based method can be used optionally and separately (each in a
304 dotted block representing an optional procedure). In the PCA-NMF-based method, both
305 the PCA-based method and the NMF-based method were implemented sequentially.
306 Regardless of whether the data were spatially filtered or not, the diagnostic analyses
307 relied on application of the CI method to HD-sEMG data recorded from three muscle
308 groups: SCI-left group, SCI-right group and control group.

309 Given a certain group of examined muscles, both the abnormal CI Z-core increase
310 and decrease can be simultaneously observed due to diversity of abnormality following
311 SCI. This was the case in this study (as reported in the following Results Section). For
312 a specific muscle with certain abnormal changes, the greater Z-score dispersion from
313 the normal range was yielded by the examination approach (including the signal pre-
314 processing method), the higher its diagnostic sensitivity became according to the CI
315 calculation. Given a group of tested muscles expected to have changes in various type
316 and degree, the variance of Z-scores over this group could be used to evaluate the
317 diagnostic sensitivity of the CI indicators, after different spatial filtering methods.
318 Suppose the Z-score variance was a_{SCI} and $a_{control}$ calculated over a group of tested
319 muscles from subjects with SCI and healthy controls, respectively. The value of
320 $a_{control}$ of each tested muscle is 1 due to the defined normalization of diagnostic
321 criteria in the CI method. The evaluation criterion abnormality discriminating index
322 (ADI) was defined as a quantitative indicator of evaluating diagnostic power of the
323 entire examination approach according to Eq. (7), which represents the sensitivity of
324 identifying various types of neuromuscular changes from abnormal signals.

$$325 \quad ADI = \frac{a_{SCI}}{a_{control}}. \quad (7)$$

326 The ADI values were calculated respectively under different conditions. In this study,
327 the condition was defined by the use of both the channel and the spatial filtering method
328 for data analysis. A special condition was designed as a representative approach without
329 any spatial filtering method for the comparison purpose, which simply averaged CI
330 values over all used channels when HD-sEMG data were used. The higher an ADI value

331 was yielded, the greater diagnostic sensitivity (to various alterations in the given subject
332 population) the corresponding method had.

333 In order to verify the generally sequential consistency of individual muscles'
334 diagnostic outcomes, a series of linear regression analyses were performed on the CI
335 Z-scores derived from both the SCI-left and SCI-right groups, between any two
336 different conditions. Two separate two-way repeated-measure ANOVAs were
337 performed on the Z-score, with the group (two levels: the control muscle group versus
338 each of two muscle group with SCI, respectively) considered as the between-subject
339 factor and the condition (four levels: the simply averaging approach and three spatial
340 filtering methods) considered as the within-subject factor, to simultaneously examine
341 their effect on the Z-score group means. Another two-way repeated-measure ANOVA
342 was performed, with both the side/group (two levels: the SCI-left group versus the SCI
343 right group) and the condition (four levels) considered as within-subject factors. The
344 level of statistical significance was set to $p < 0.05$ for all above analyses. All statistical
345 analyses were completed using SPSS software (ver. 22.0, SPSS Inc. Chicago, IL).
346

3. Results

347

348 Fig. 3 shows the resultant CI-area plot of the scattered data points from three muscle
349 groups in the double logarithmic scale, when the data were only from a deliberately
350 selected channel. For the normal cloud consisting of all data points from the control
351 muscle group, the CI showed a decreasing trend as the contraction level increased. This
352 was suitable for a linear regression analysis ($y = -0.0631x - 0.5470$). Along the
353 regression line, there is a banding region that can well characterize the distribution
354 region of the normal cloud.

355 Fig. 4 reports the CI Z-scores when using data from each of four different channels
356 (channel 28, channel 31, channel 37 and channel 64). It can be seen that although
357 different CI Z-scores and the corresponding diagnostic results obtained from different
358 channels, the order of the CI Z-scores was substantially the same. For example, for the
359 left muscle of S8, data from channel 31 gave a diagnosis of abnormal increase, but the
360 other three channels failed to report any abnormality. Using data from channel 37, the
361 left muscle of S8 had a CI value that approximated to the upper limit of the normal
362 boundary. It is surprisingly to find that the CI Z-score value of S8 was always the
363 highest on the SCI-left group. Similar observations can also be found in multiple cases
364 such as S2, S7 and S9 on the SCI-left group and S1 on the SCI-right group. Further, for
365 different channels, the data of the same group exhibited different degrees of dispersion.
366 More abnormal diagnostic conclusions could be found for the group with high
367 dispersion. It was confirmed that the ADI value was able to be used to judge the
368 diagnostic power. Therefore, using four different channels had an impact on the

369 diagnostic power, quantified by the ADI ranging from 2.3160 to 14.0252 for the SCI-
370 left muscle group and 2.5341 to 5.7445 for the SCI-right group.

371 The PCA-based method yielded varying ADI values when the number of components
372 to be removed corresponding to smallest eigenvalues was set from 0 to 6, respectively,
373 as shown in Table 2. It can be found that although the resultant ADI values of both SCI-
374 left and SCI-right groups were extremely closed, the highest ADI values were yielded
375 by removing the 4 components with the smallest eigenvalues. Therefore, for
376 implementing the PCA-based spatial filtering method, the number of PCs
377 corresponding to the smallest eigenvalues to be removed was determined to be 4 in the
378 following analysis throughout the study.

379 Fig. 5 shows the mean VAF values averaged over all muscles in three groups (SCI-
380 left, SCI-right, and control group) when the number s of activation patterns was set at
381 1, 2 and 3, respectively. Evidently, the mean VAF exceeded over 95% when the number
382 of patterns was increased from 1 to 2, and the addition of the 3rd activation pattern (the
383 number is three) did not help to increase the VAF much. Therefore, the variable s was
384 set to 2 in the NMF algorithm implementation.

385 Another sensitivity analysis was also performed to determine the number of selected
386 channels optimally for implementing the NMF-based spatial filtering method,
387 according to the diagnostic power. The ADI results were shown in Table 3 when the
388 number ranged from 14 to 18. It can be observed that the number set at 16 led to the
389 highest level of the ADI values for both muscle groups. Although the ADI was found
390 to vary slightly with the number of selected channels, the actual filtering effect was

391 insensitive to this number. Without loss of generality, this number was finally fixed to
392 16 (a quarter of the total channel number) in the following analyses when the NMF
393 algorithm was involved for any spatial filtering (including the PCA-NMF-based
394 method).

395 Fig. 6 reports the resultant Z-scores derived from multi-channel data for all three
396 examined muscle groups when different spatial filtering methods were used
397 respectively. The CI Z-scores from the same group of muscles almost had a consistent
398 order even comparing to that at any single channel in Fig. 4, regardless of whether the
399 data were filtered by any spatial filtering method or not. When different spatial filtering
400 methods were applied, however, the muscle with an abnormal decision had varied
401 dispersions from the normal boundary. Specifically, the Z-scores obtained by simply
402 averaging CI values over all used channels were shown in Fig. 6 a. Although some
403 muscles were reported to be abnormal, their Z-scores were extremely close to the
404 normal boundary, and the ADI value was reported to be 2.4936 for the SCI-left group
405 and 2.1671 for the SCI-right group. Both ADI values were found to remain at a median
406 level of the values derived from individual channels. After spatially filtering the HD-
407 sEMG data using three methods, more abnormal Z-scores are exhibited in Fig. 6 b-d,
408 and their dispersions from the normal boundary are relatively expanded as well. Thus,
409 it is not accidentally that the ADI values were improved to 3.1488 for the SCI-left
410 muscle group and 3.8785 for the SCI-right muscle group using the PCA-based method.
411 Both values were 8.0397 and 3.8033 using the NMF-based method. Apparently, the
412 PCA-NMF-based method presented the highest degree of Z-score dispersion, and

413 meanwhile it was able to reveal more abnormal muscles. For example, the use of the
414 PCA-NMF-based method successfully produced abnormally high Z-scores for the S3
415 and S5 on the SCI-right group, whereas the use of any other spatial filtering method or
416 any single channel failed to reveal any abnormality. Finally, the ADI values yielded by
417 the PCA-NMF-based method reached to 13.9157 for the SCI-left group and 11.7014
418 for the SCI-right group, which approximated into or even exceeded the maximal level
419 of the ADI values derived from individual channels.

420 The linear regression analyses reported strong correlations (R^2 from 0.80 to 0.93)
421 between the CI Z-scores made by any spatial filtering method and the simply averaging
422 approach (i.e., no spatial filtering method), and estimates of coefficients were all
423 statistically significant ($p < 0.001$). The ANOVAs revealed no significant main effect
424 of the group and no significant difference in group means of the CI Z-score between
425 any muscle group following SCI and the control muscle group, or no significant main
426 effect of the spatial filtering method ($p = 0.855$) on the CI Z-score. However, significant
427 difference was found between the SCI-left muscle group and the SCI-right muscle
428 groups ($p < 0.05$).

429 The final ADI values derived from original sEMG data at four individual channels
430 and spatially filtered HD-sEMG data via different spatial filtering methods were
431 summarized in Table 4. It showed that the ADI values of different channels might be
432 quite different. Comparing to the simply averaging HD-sEMG data without any spatial
433 filtering, the PCA and NMF spatial filtering methods had larger ADI values on both the
434 SCI-left and the SCI-right groups. Moreover, the PCA-NMF-based spatial filtering

435 method outperformed other methods by yielding almost the largest ADI values on both
436 groups of muscles following SCI.

437 **4. Discussion**

438 This study presents three spatial filtering methods for preprocessing HD-sEMG data
439 to enhance the power of assessing neuromuscular abnormalities following SCI. The
440 primary findings of the current study include: 1) the complex neuromuscular changes
441 following SCI were revealed by the CI analysis of conventional single-channel sEMG,
442 and the diagnostic power could be characterized by the variance of Z-scores derived
443 from a group of subjects (as shown in Fig. 4); 2) the diagnostic power was found to
444 vary across positions of individual channels for recording sEMG data (see Fig. 4 and
445 Table 4), and it only remained at a median level when all the CI values derived from
446 all recording channels were simply averaged (see Fig. 6); 3) The application of PCA-
447 based filtering method or NMF-based filtering method helped to improve the diagnostic
448 power significantly, and the method with their combination outperformed any single
449 method in terms of diagnostic power (as shown in Fig. 6 and Table 4); 4) A subject
450 with SCI might have pathological changes on both sides of muscles in different types
451 and at different degrees (see Fig. 6).

452

453 **4.1 MU alterations following SCI evaluated by CI method**

454 The CI method was traditionally used for single-channel sEMG analysis. Regardless
455 of any channel (within the array) used for analysis, it can be observed from Fig. 4 that

456 each examined muscles (in both SCI-left and SCI-right groups) tended to have a
457 consistent decision. Furthermore, all muscles from subjects with SCI exhibited three
458 different CI patterns including normal and abnormal increase and decrease of the CI
459 indicator.

460 Four muscles of the SCI subjects had an abnormal CI Z-score increase indicating
461 neurogenic changes. These changes can be attributed to loss of MUs and subsequent
462 reinnervation of denervated muscle fibers. The MU loss may take place after gray
463 matter is destroyed at and near the lesion epicenter and it can lead to a decrease in the
464 number of activable MUs and denervation of muscle fibers [3]. Complete denervation
465 due to motoneuron degeneration eliminates voluntary control of the affected muscle
466 fibers. Subsequently, the surviving MUs tend to undergo adaptive changes, such as
467 muscle fiber reinnervation for a functional supplement, thus contributing to an
468 abnormal enlargement of their structures [48]. These enlarged MUs lead to abnormal
469 MUAPs with large amplitude and multiple phases, overlying into scattered and isolated
470 EMG signals. In addition, after chronic (>1 year) SCI, MU properties of human hand
471 muscles shifted towards decreased firing rate and increased firing synchronization [49].
472 Simultaneously, other altered MU control properties including the compression of MU
473 recruitment threshold and the supplementary recruitment of enlarged MUs during
474 muscle contraction might also lead to an abnormal increase of CI [2], [50].

475 Eleven muscles had abnormally lower Z-scores indicating myopathic changes, which
476 could be related to muscle fiber disuse atrophy. Atrophied and angular muscle fibers
477 could lead to partial denervation, which can be indicated by intramuscular motor axon

478 sprouting, an important compensatory mechanism for recovery of muscle innervation
479 after death of some motoneurons [51]. A selective degeneration of the relatively larger
480 and superficial MUs may be another reason. Thus the induced flatter and denser surface
481 EMG signals would make decreased CI values [54].

482 The resultant Z-scores of remaining muscles were located within the normal range.
483 However, substantial muscle weakness was also found in these muscles. Their
484 paralyzes are likely to be attributed to a deficit of descending central drive as a result
485 of the severance of central nervous system axons and demyelination of central or
486 peripheral axons, while the affected muscles still function more or less normally [52].
487 Although the number of activable MUs drops, their recruitment and control property
488 remains similar to those of healthy controls. Thus, these muscles could only deliver a
489 fraction of the normal voluntary drive, leading to corresponding muscle weakness [42].
490 Another possible explanation for the distribution in the “normal range” might be a
491 combined or cancelled effect of both neurogenic and myopathic processes [53].
492 Moreover, the effect of injury on the lesion spinal cord segment and denervation of
493 muscle fibers might be contributors to muscular weakness [49]. Therefore, the
494 experimentally observed CI variations in paralytic muscles can be viewed as the overall
495 or collective effects of these different factors [47].

496 As a result, the experimentally observed CI abnormality consists of two patterns,
497 which lead to CI deviation in two different directions, respectively. Therefore, a pooled
498 analysis of a group of paralyzed muscles following SCI can allow their CI indicators to
499 spread from the centered normal range, indicating that there are complex

500 neuromuscular changes following SCI. This phenomenon explains why there was no
501 significant difference in group means of CI Z-scores in the ANOVAs, and therefore the
502 ADI was more appropriate to characterize the diagnostic power of the CI method in this
503 study.

504

505 **4.2 Examination with HD-sEMG recording**

506 Given the HD-sEMG recording, varied distributions of the CI Z-scores were
507 observed and thus different diagnostic decisions were made when data from different
508 channels were used (see Fig.4). Thus, it also directly led to different diagnostic power
509 quantified by the ADI value. This confirms our previous assumption that the important
510 diagnostic information is likely to be derived from some local regions of the electrode
511 array due to the heterogeneity of the targeted muscle. This finding also suggest a risk
512 of electrode placement when applying the routine single-channel sEMG recording,
513 while its clinical application has been increasingly investigated toward noninvasive
514 examination. Depending on the placement of the sEMG electrode (targeting at a local
515 region of the examined muscle), the CI diagnostic decision varied a lot, probably
516 leading to controversial results. This may dramatically impact the usability of the sEMG
517 examination. In addition, we also found that the channel with the highest diagnostic
518 power was not always located at the center of the array or over the position of main
519 muscle belly. Such a finding further indicates the importance of electrode placement
520 since the channel location yielding the most diagnostic power is usually uncertain solely
521 relying on anatomical knowledge.

522 Taking the averaged CI value over HD-sEMG channels is the most straightforward
523 method to extract the global information of muscle activity and eliminate the influence
524 of the electrode position. However, unsurprisingly, we found that the ADI diagnostic
525 power obtained in this way was only at the median level of those using individual
526 channels. This shows that simply averaging may smooth or cancel the useful diagnostic
527 information present in the local channels, which is detrimental to revealing specific
528 abnormalities in individual muscles. In this case, the resultant CI indicator reflected
529 poor understanding of underlying pathological muscle changes.

530

531 **4.3 The Advantages of Spatial Filtering**

532 After the determination of appropriate settings towards performance optimization
533 (see Fig. 5, Table 2 and Table 3), the improved performance yielded by the use of
534 either PCA-based or NMF-based spatial filtering method in terms of increased ADI
535 value can demonstrate the efficiency of applying the spatial filters. Furthermore, the
536 strong correlations revealed by the regression analyses between individual muscles' Z-
537 scores derived from any spatial filtering method and the simply averaging approach
538 indicate consistency of their diagnostic decisions (they are able to produce or tend to
539 produce the same type of abnormality for specific muscles). These findings suggest that
540 the use of spatial filters enhances the sensitivity of HD-sEMG CI indicator to various
541 neuromuscular changes.

542 The PCA-based filtering method was designed to deliberately remove PCs
543 representing homogeneously changing and common features, and detail PCs

544 representing high-frequency noise and cross-talk [29], [44]. Such processing helps to
545 enhance regional difference of the signal and is considered to be the main reason for
546 diagnostic power improvement by the PCA-based spatial filtering method. Unlike the
547 PCA-based method, the NMF-based method is equivalent to a channel-selection
548 method by extracting distinguishable muscle activation patterns based on muscle
549 heterogeneity [50]. The method is actually a dimensionality reduction processing that
550 locates and highlights the main areas within the HD-sEMG array contributing into
551 muscle activities.

552 According to their calculation principles, both algorithms were regarded to
553 emphasize different aspects of information conveyed in the raw HD-sEMG data. As a
554 result of their complementary effect, it is easy to explain that their combination can
555 further improve the diagnostic power in comparison to sole use of the PCA-based or
556 the NMF-based method.

557 The HD electrode array physically covers the examined muscles, providing a wealth
558 of spatial information in a large area. Direct averaging these channels is not satisfactory
559 for diagnostic improvement. By contrast, spatial filtering methods evidently improve
560 the performance of HD-sEMG examination, approximating to the maximal level of
561 diagnostic powers when individual channels are used. Thus, the use of spatial filtering
562 helps to highlight and refine useful diagnostic information associated with
563 heterogeneity of the muscle activation, and provides a necessary and convenient
564 approach to pre-process HD-sEMG data for further examination of neuromuscular
565 changes. In addition to enhancing diagnostic power, this can also minimize the potential

566 influence of electrode placement. The spatial filtering of HD-sEMG can facilitate
567 sEMG examination, indicating the ease of reflecting potential abnormality in certain
568 muscles by the means of a noninvasive approach.

569 It is worth noting that the presented spatial filtering methods involve an unsupervised
570 matrix factorization algorithm without any association with the diseased or the
571 diagnostic information (no label is required). The filtering approach was conducted
572 independently on the data recording trial or the examined muscle. Thus, it is
573 straightforward to apply the proposed method to data from any given muscle to be
574 examined, and the filtering outcome is supposed to rely on the structural nature of its
575 HD-sEMG data. All these features confirm a good generalization of the proposed
576 spatial filtering method. This is also a prerequisite to its involvement in a standard
577 pipeline for preprocessing the HD-sEMG signals towards various applications.

578 **4.4 Difference between two sides of the subject with SCI**

579 Since the CI analysis performed the examination of individual muscles, it is
580 straightforward to compare the neuromuscular changes in muscles on both side muscles
581 of a subject. It was observed that the two side muscles of some SCI subjects showed
582 different CI decisions. For example, the left muscles of S1, S3 and S5 were diagnosed
583 as being ‘myopathy’ while their contralateral muscles were diagnosed as being
584 ‘neurogenic’ changes. This may be attributed to the asynchrony of the left and right
585 muscles. When the physiological balance is broken following SCI, it always
586 overcorrects so that the left and right muscles may present different types of
587 neuromuscular changes at different degrees.

588

589 **4.5 Limitations of the current work and future expectations**

590 This paper just focuses on the application of spatial filtering and presents only three
591 types of common spatial filtering methods. The use of the CI method has also limited
592 performance in examining specific MU property alterations. More advanced methods
593 including sophisticated spatial filtering methods and more sufficient diagnostic
594 indicators can be developed for improved performance. In addition, the sample size
595 used in this study is relatively small. It is sufficient only for technically confirming the
596 benefit of using the spatial filtering methods in HD-sEMG diagnosis. Although the CI
597 method would be applicable for examining muscles with diverse impairments at any
598 degrees, the sEMG diagnostic approach requires more or less voluntary contraction
599 ability of the examined muscle to emit sufficient sEMG activities. This is the main
600 reason for recruiting subjects with incomplete SCI preserving certain hand functions in
601 this study. The small sample size limits clinical significance of the current study. In
602 order to establish diagnostic criteria and reveal neural or muscular pathology, a big
603 sample size from a large population of subjects with different impairments is demanded.
604 These will remain our future work.

605

5. Conclusion

606 This paper examined the feasibility of performing spatial filtering methods using the
607 PCA algorithm, the NMF algorithm and their combination, for enhancing HD-sEMG
608 examination of neuromuscular changes. The experimental results demonstrated that

609 spatial filtering of HD-sEMG can help to improve diagnostic power of CI method with
610 respect to that with no spatial filtering, and that the combined PCA-NMF-based spatial
611 filtering method yielded the highest diagnostic power in identifying complex
612 neuromuscular diseases following SCI. The proposed method facilitates HD-sEMG
613 examination of neuromuscular changes and it helps to develop a standard pipeline for
614 pre-processing the HD-sEMG data towards practical and meaningful applications.

615

616 **Abbreviations**

617 HD: high-density; sEMG: surface electromyogram; MUAP: motor unit action potential;
618 PCA: principle component analysis; NMF: non-negative matrix factorization; CI:
619 clustering index; SCI: spinal cord injury; MU: motor unit; APB: abductor pollicis brevis;
620 MVC: maximal voluntary contraction; PC: principal component (PC); ADI:
621 abnormality discriminating index.

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627 **Availability of data and materials**

628 The datasets of the experiments in the current study are available from the first author
629 on request.

630 **Author's contributions**

631 XZ, XL, XT and XuC designed this study. All authors conceived the experiments. XZ
632 and PZ conducted the experiments. XZ, XL, XT, XuC and XiC performed data analyses
633 and interpretations. XZ and XL drafted the manuscript. XuC and PZ substantially
634 revised the manuscript. All authors read and approved the final version of the
635 manuscript.

636 **Ethics approval**

637 The study was approved by the Institutional Review Board of the Northwestern
638 University (Chicago, IL). All subjects signed informed and written consent before any
639 procedure of the experiments.

640 **Consent for publication**

641 The authors consent this article for publication of Journal of NeuroEngineering and
642 Rehabilitation

643 **Competing interests**

644 The authors declare that they have no competing interests.

645

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820 Engineering. 2020; 28: 1836–45.

821

822 Table 1. Physical characteristic of subjects with spinal cord injury

ID #	Gender	Age (years)	Level of Injury	ASIA Class	Years Since Injury
S1	F	37	C7	C	4
S2	M	57	C7	D	17
S3	M	32	C6	C	11
S4	F	42	C4	D	7
S5	M	62	C4	D	8
S6	M	44	C5	C	11
S7	M	54	C4	D	12
S8	M	38	C7	C	12
S9	F	50	C8	D	7

823

824

825 Table 2. The ADI values derived from removing different numbers of the components
826 with the smallest eigenvalues, using the PCA-based filtering method. The number of 4
827 leads to the maximal ADI values for both data groups (in bold).

The number	ADI (SCI-Left)	ADI (SCI-Right)
0	3.1439	3.8592
1	3.1457	3.8628
2	3.1446	3.8654
3	3.1459	3.8681
4	3.1488	3.8785
5	3.1349	3.8663
6	3.1327	3.8632

828

829 Table 3. The ADI values for both SCI muscle groups when the number of the selected
830 channels ranged from 14 to 18 using the NMF-based spatial filtering method.

The number	ADI (SCI-Left)	ADI (SCI-Right)
14	7.7595	3.5425
15	7.8055	3.5491
16	8.0397	3.8033
17	7.9549	3.6820
18	7.8013	3.8356

831

832 Table 4. The ADI values derived from different methods

Condition	Left	Right
CH28	6.2292	3.4041
CH31	14.0252	5.7445
CH37	7.7690	2.5341
CH64	2.3160	2.7312
Simply Averaging	2.4936	2.1671
PCA-based	3.1488	3.8785
NMF-based	8.0397	3.8033
PCA-NMF-based	13.9157	11.7014

833

834 **Figure Captions**

835 **Fig 1** The flexible electrode array of 64 monopolar electrodes arranged in an 8×8 grid
836 formation.

837 **Fig 2** Block diagram of the framework for examining neuromuscular changes using
838 the CI method and the spatial filtering analyses.

839 **Fig 3** The CI-area plot of a deliberately channel presented in double logarithmic scale
840 for the three groups: SCI-left group, SCI-right group and control group. The normal
841 range (dotted line) is presented within ± 2.5 of the standard error of the linear regression.
842 The red dots and black circles represent the epochs of SCI-left group and SCI-right
843 group were found to be outside the banding region.

844 **Fig 4** Z-scores derived from four selected channels: (a) channel 28, (b) channel 31, (c)
845 channel 37 and (d) channel 64. The Z-scores from SCI-left group, SCI-right group
846 and control group are shown separately. The normal range (solid line) is presented
847 within ± 2.5

848 **Fig 5** Mean VAF values averaged over all subjects in three groups (SCI-left, SCI-
849 right, and Control group) when the number of activation patterns was set at 1, 2 and 3,
850 respectively.

851 **Fig 6** Z-scores derived from four methods: (a) simply averaging, (b) PCA-based spatial
852 filtering, (c) NMF-based spatial filtering, and (d) PCA-NMF-based spatial filtering.
853 The Z-scores from SCI-left group, SCI-right group and control group are shown
854 separately. The normal range (solid line) is presented within ± 2.5 .

Figures

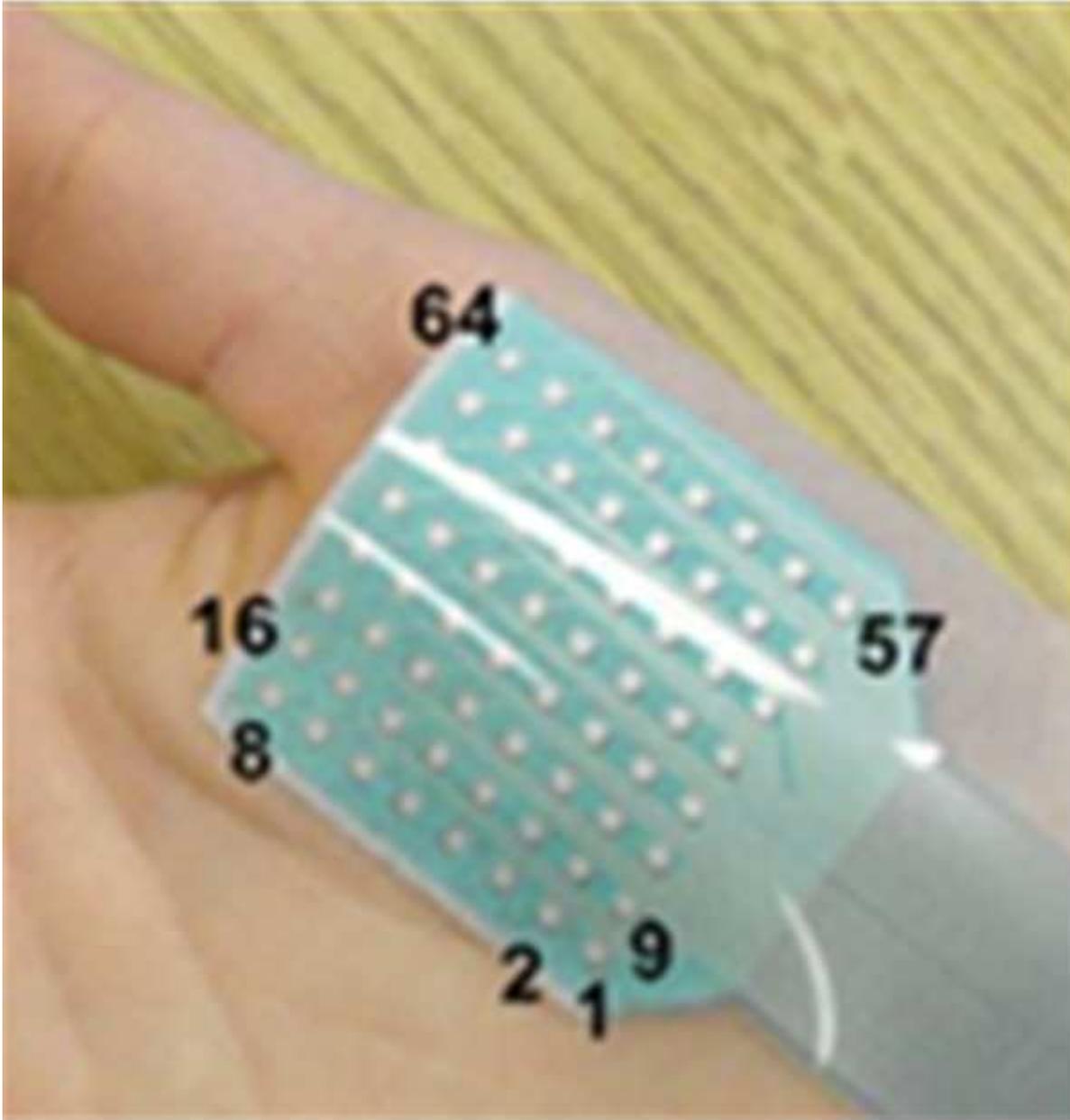


Figure 1

The flexible electrode array of 64 monopolar electrodes arranged in an 8x8 grid formation.

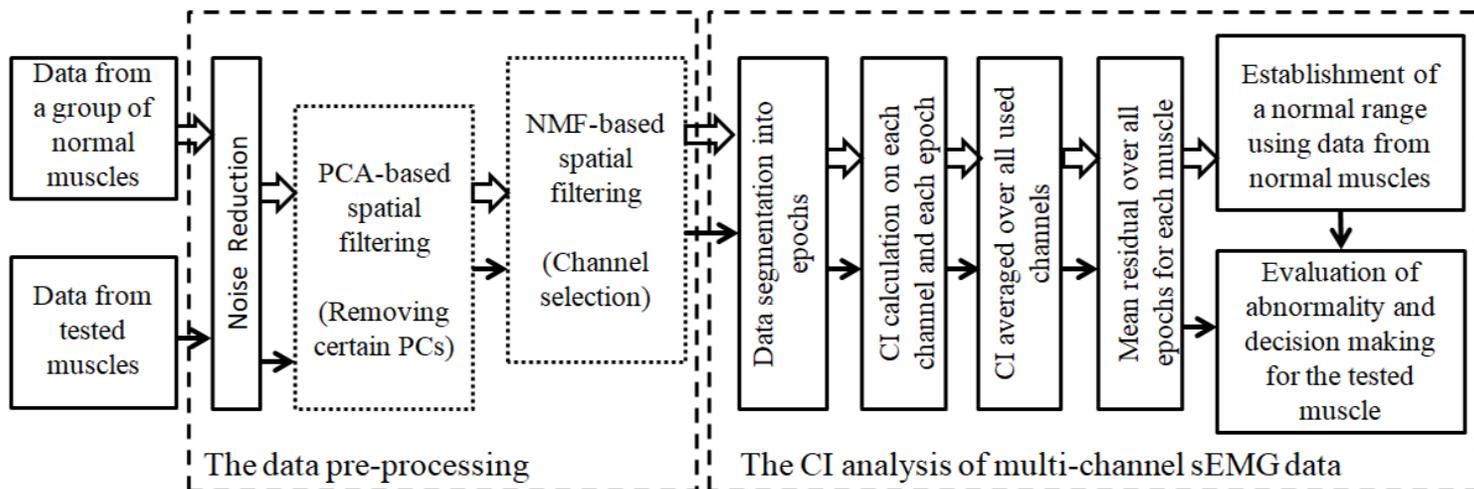


Figure 2

Block diagram of the framework for examining neuromuscular changes using the CI method and the spatial filtering analyses.

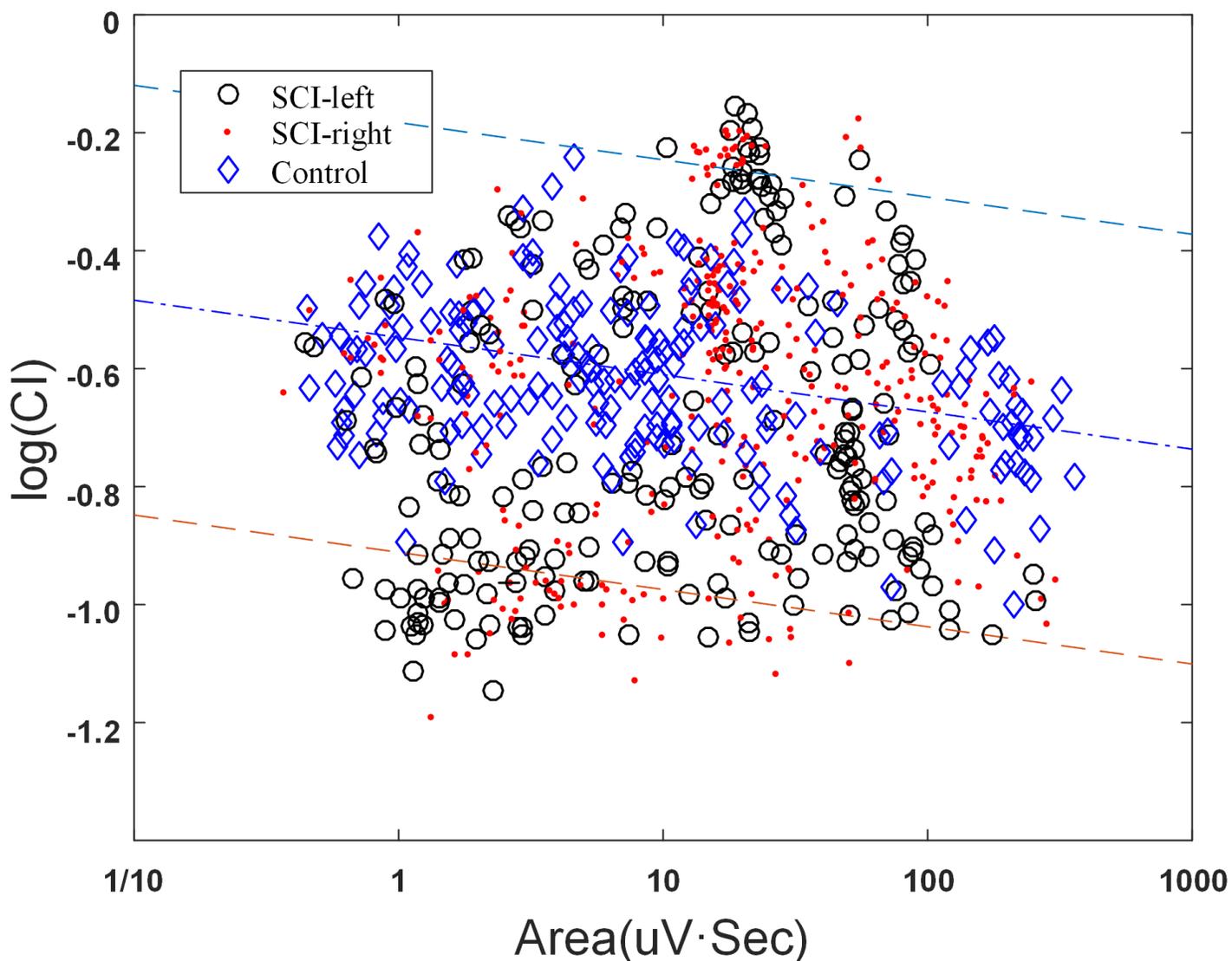


Figure 3

The CI-area plot of a deliberately channel presented in double logarithmic scale for the three groups: SCI-left group, SCI-right group and control group. The normal range (dotted line) is presented within ± 2.5 of the standard error of the linear regression. The red dots and black circles represent the epochs of SCI-left group and SCI-right group were found to be outside the banding region.

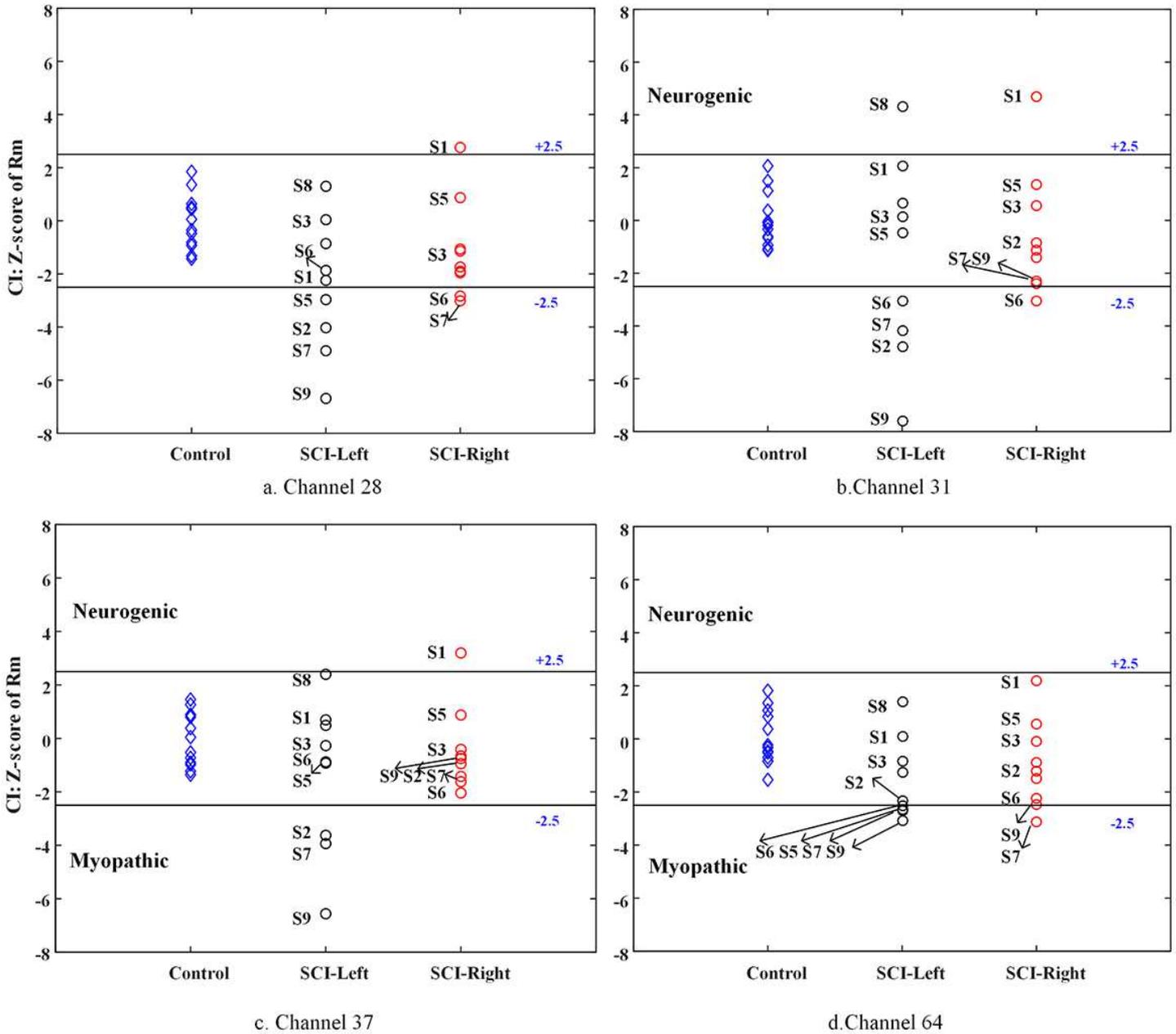


Figure 4

Z-scores derived from four selected channels: (a) channel 28, (b) channel 31, (c) channel 37 and (d) channel 64. The Z-scores from SCI-left group, SCI-right group and control group are shown separately. The normal range (solid line) is presented within ± 2.5

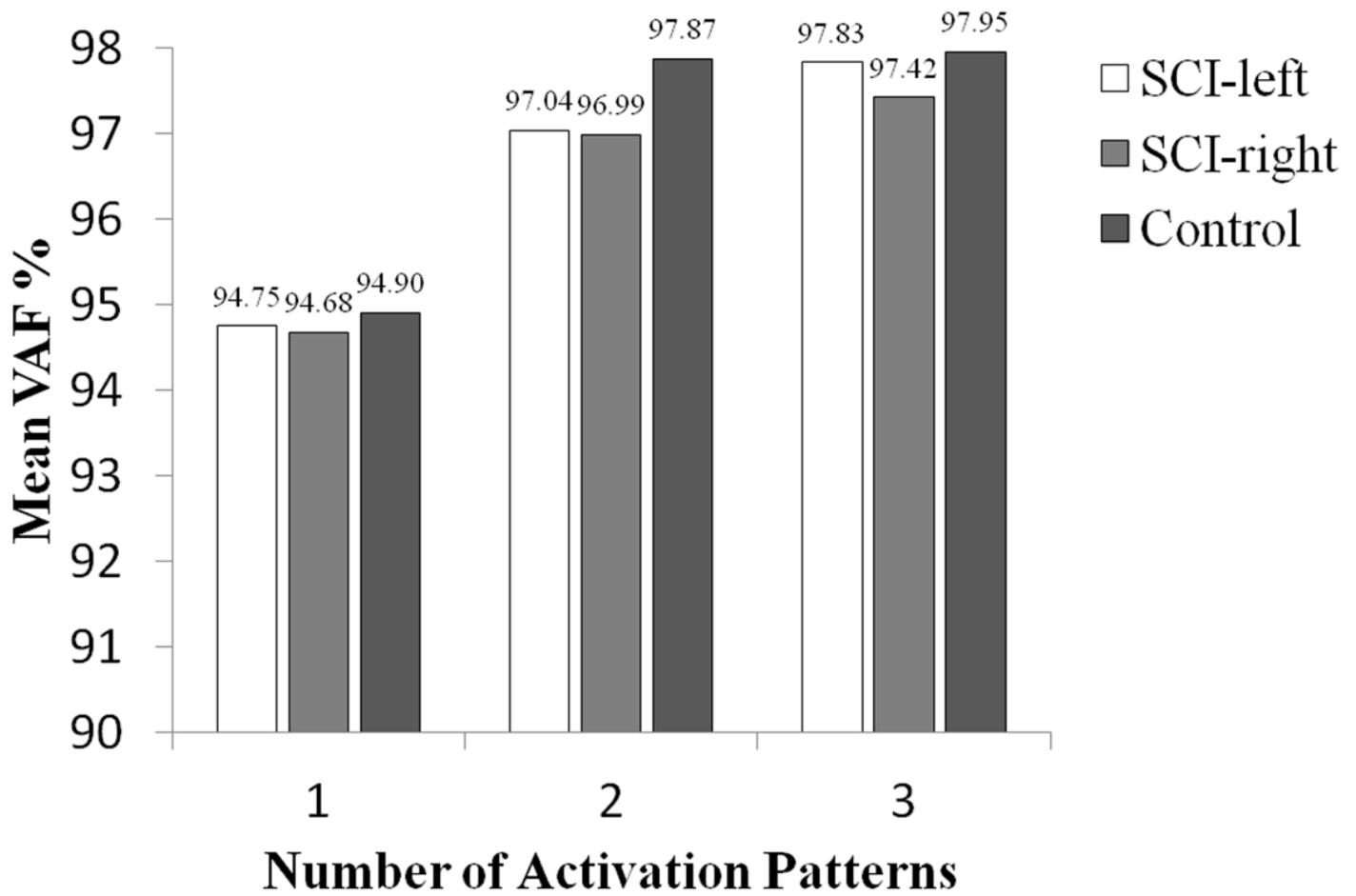


Figure 5

Mean VAF values averaged over all subjects in three groups (SCI-left, SCI-right, and Control group) when the number of activation patterns was set at 1, 2 and 3, respectively.

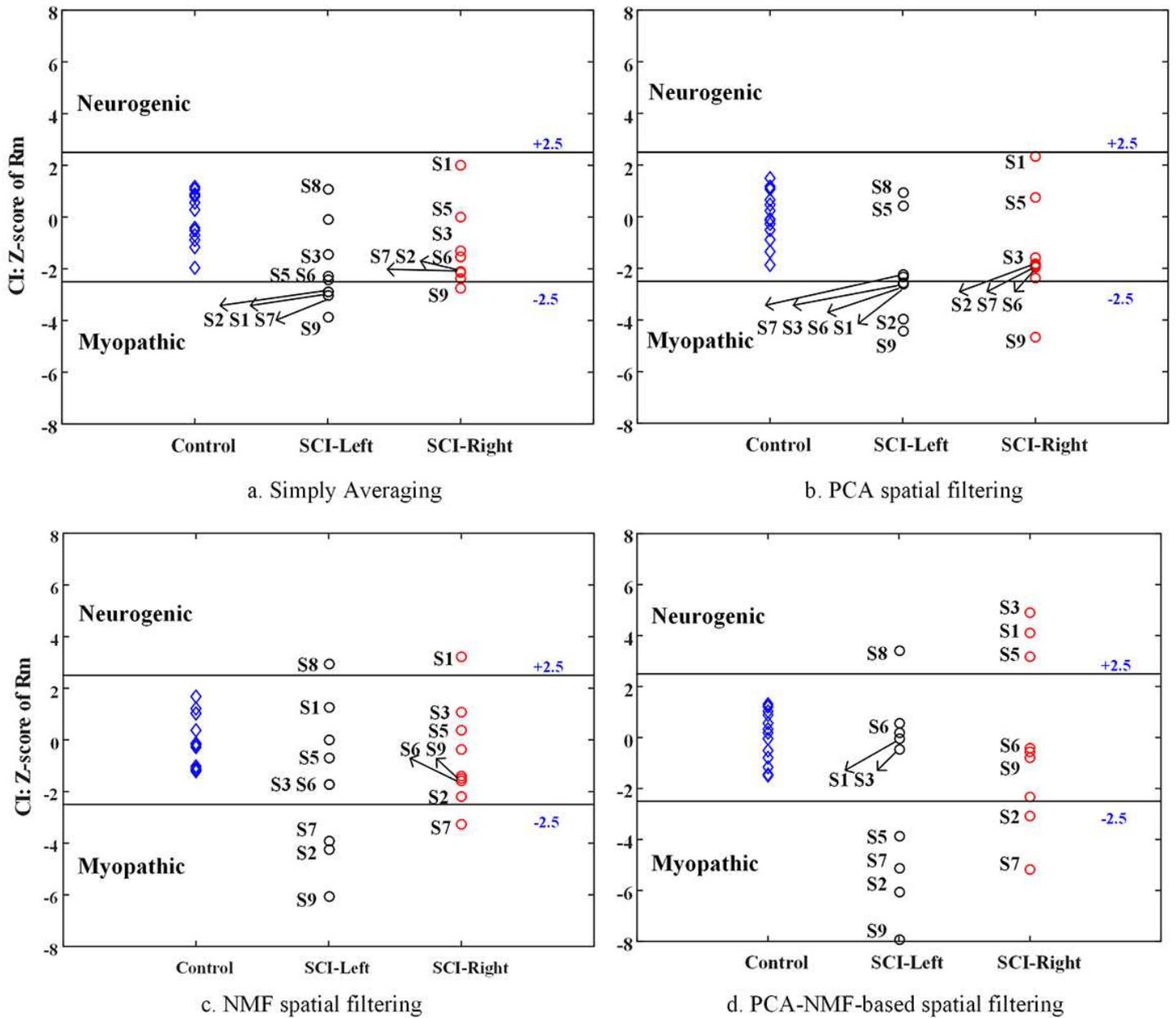


Figure 6

Z-scores derived from four methods: (a) simply averaging, (b) PCA-based spatial filtering, (c) NMF-based spatial filtering, and (d) PCA-NMF-based spatial filtering. The Z-scores from SCI-left group, SCI-right group and control group are shown separately. The normal range (solid line) is presented within ± 2.5 .