



# How to improve the muscle synergy analysis methodology?

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## Abstract

Muscle synergy analysis is increasingly used in domains such as neurosciences, robotics, rehabilitation or sport sciences to analyze and better understand motor coordination. The analysis uses dimensionality reduction techniques to identify regularities in spatial, temporal or spatio-temporal patterns of multiple muscle activation. Recent studies have pointed out variability in outcomes associated with the different methodological options available and there was a need to clarify several aspects of the analysis methodology. While synergy analysis appears to be a robust technique, it remains a statistical tool and is, therefore, sensitive to the amount and quality of input data (EMGs). In particular, attention should be paid to EMG amplitude normalization, baseline noise removal or EMG filtering which may diminish or increase the signal-to-noise ratio of the EMG signal and could have major effects on synergy estimates. In order to robustly identify synergies, experiments should be performed so that the groups of muscles that would potentially form a synergy are activated with a sufficient level of activity, ensuring that the synergy subspace is fully explored. The concurrent use of various synergy formulations-spatial, temporal and spatio-temporal synergies- should be encouraged. The number of synergies represents either the dimension of the spatial structure or the number of independent temporal patterns, and we observed that these two aspects are often mixed in the analysis. To select a number, criteria based on noise estimates, reliability of analysis results, or functional outcomes of the synergies provide interesting substitutes to criteria solely based on variance thresholds.

**Keywords** Matrix factorization · Model selection · EMG processing · Motor module · Primitives

## Abbreviations

EMG	Electromyography
ICA	Independent component analysis
iEMG	Integrated EMG
NNMF	Non-negative matrix factorization
PCA	Principal component analysis
pNMF	Projective non-negative matrix factorization

RMS	Root mean square
SNR	Signal to noise ratio
SSE	Sum of squared errors
SST	Total sum of square
SVD	Singular value decomposition
VAF	Variance accounted for

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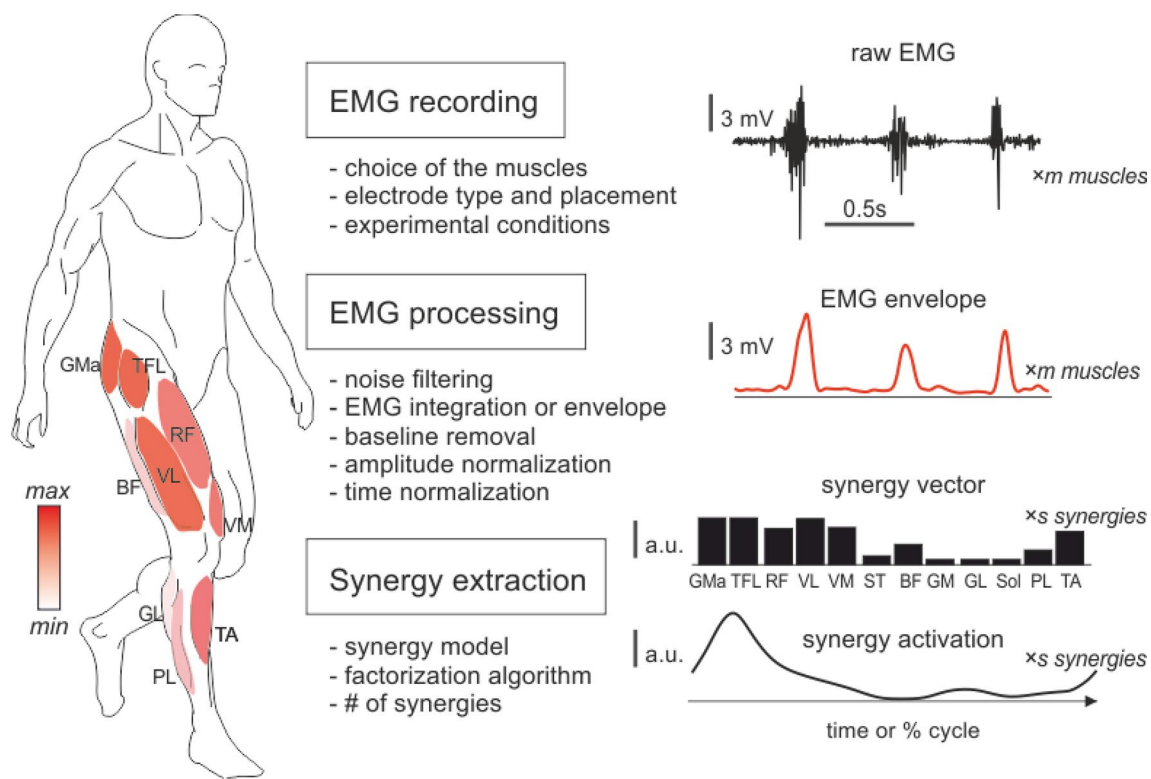
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## Introduction

Muscle synergy analysis is a tool used in various domains such as neurosciences, robotics, sport sciences or rehabilitation to gain insights about basic motor control science, motor coordination strategies or to quantify functional deficits in pathologies. The core of the method is to reduce the number of dimensions of the electromyographic (EMG) data, i.e., the number of muscles, to a limited set of meaningful variables, referred to as synergies. Synergy analysis and in particular muscle synergy analysis suffers from a critical lack of consensus throughout the many steps it requires (presented in Fig. 1). Several authors cautioned that their results are sensitive to methodological choices (Banks et al. 2017) and



**Fig. 1** Synergy analysis steps. Muscle synergy analysis consists of identifying the structure of muscle activations, either at the spatial level—represented by muscle synergy vectors—or at the temporal level—represented by muscle synergy activations. The analysis requires three main steps: EMG recording, EMG processing and synergy extraction. A lower limb synergy during walking is illustrated. Weightings of the different muscles in the synergy vector represent their relative contribution, and the synergy activation represents how the group of muscles is activated over time. The synergy vectors and

synergy activations are unitless. However, multiplying the synergy vector by the synergy activation allows to recover the level of activity of the different muscles associated with a given synergy in the unit of the EMG envelopes (illustrated in color on the left of the image). *Gma* gluteus maximus, *TFL* tensor fasciae latae, *RF* rectus femoris, *VL* vastus lateralis, *VM* vastus medialis, *ST* semi-tendinosus, *BF* biceps femoris, *GM* gastrocnemius medialis, *GL* gastrocnemius lateralis, *Sol* soleus, *PL* peroneus longus, *TA* tibialis anterior

experimental conditions (Steele et al. 2015b). Some issues, of which model selection is the most prominent example, remain unresolved. We reviewed different aspects of synergy analysis to provide a better understanding of the effects of choosing one methodological approach over another and to provide recommendations whenever possible.

A systematic review of the literature was first performed to analyze the methodologies in use (see Supplementary Material). Only the conclusions are presented below. In this review the synergy extraction techniques are presented first as they are essential to understanding how characteristics of EMG signals affect the synergy analysis results.

## Definition of the terms

A vast amount of literature demonstrated that motor actions and movements in both vertebrates and invertebrates can be decomposed into elemental coordinative structures often referred to as *synergies*, which etymologically means “work together”. Other terms which have been used include mode,

motor module, motor primitive, motor schemas, prototypes, or sub-movement (Latash 2020; Hogan and Sternad 2013; Mussa-Ivaldi and Solla 2004; Flash and Hochner 2005). These elemental structures have been evidenced at several levels of the motor hierarchy in the form of coordinated neural ensembles, joint angles, joint torque or muscle activations, for example (Gallego et al. 2017; Giszter 2015; Flash and Hochner 2005; Holdefer and Miller 2002). It is widely accepted that these basic elements represent building blocks of human movement patterns and that they could simplify the control of the numerous degrees of freedom of the body. These basic elements are also thought to be independent, meaning that they can be combined without interacting with each other—referred to as the principle of superposition (Flash and Hochner 2005; Bizzi and Cheung 2013).

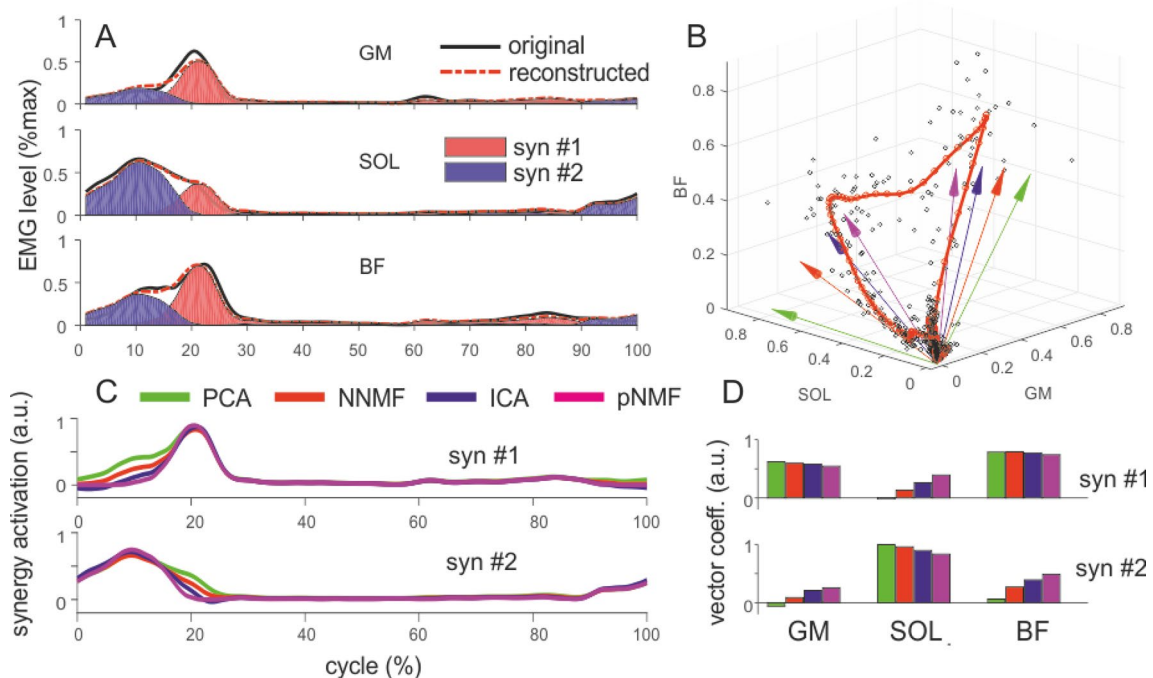
Synergies have been particularly studied in relation to structured muscle activation patterns. This strategy appears reasonable given the high number of muscles that need to be controlled in general and given the fact that spinal motoneurons are considered to be the final common pathway of both

spinal and supraspinal motor influences. A simple definition of a muscle synergy given by Lee (1984) is “a set of muscles which act together to produce a desired effect”. Drew and collaborators offered a definition free from the principle of superposition and defined a synergy as a group of muscles that are coextensive with respect to the onset and offset of the EMG activity (Drew et al. 2008; Krouchev et al. 2006). Bizzi et al. proposed that synergies are units of balanced muscle activations whose (linear) combinations give rise to complex muscle activity patterns (Bizzi and Cheung 2013; Tresch et al. 1999). This latter definition is consistent with observations made during both isometric or dynamic contractions showing that the activity of several muscles can be represented as the sum of activities of a small number of independent units which regroup multiple muscles, the synergies, and whose activity co-vary in magnitude (Davis and Vaughan 1993; Roh et al. 2012). Further studies provide evidence that the structure of these groups—i.e., relative activation level of the muscles within a synergy—is relatively conserved across different tasks and biomechanical conditions (Barosso et al. 2014; Hug et al. 2011; Torres-Oviedo

and Ting 2010), suggesting that the synergies could form a repertoire from which more complex muscle activity patterns can emerge. Other formulations were proposed to take into account the fact that muscle activations during movements also possess a temporal structure, i.e., that they are organized into precise temporal sequences (e.g., Wong and Krakauer 2019; Overduin et al. 2015). The different synergy formulations found in the literature all have in common that the complexity of muscle activity patterns can be reduced to small sets of synergies due to their underlying structures. Therefore, dimensionality reduction techniques such as principal component analysis appeared particularly powerful for synergy identification (e.g., Davis and Vaughan 1993).

Muscle synergies can be conceptualized as vectors in the multidimensional muscle activation space (Fig. 2). This representation is useful for understanding analysis results and some of the behaviors associated, e.g., the necessity to have enough variations in muscle activity to properly identify the synergies (“Data acquisition and experimental conditions”).

Formally, the EMG activity of  $m$  muscles at a given time  $t$  (noted  $\mathbf{e}(t)$ ) is obtained by the linear combination of  $s$



**Fig. 2** Representation in the muscle activation space. **a** Muscle activations (solid black line) and their reconstruction by the synergy model (dashed red line). The contributions of each synergy are colored in red and blue (projective non-negative matrix factorization method—pNMF). **b** 3D representation of muscle activations. The red line is the trajectory of the average muscle activations. A sample of 100 pts are plotted as black circles. Unit vectors in green, red, blue and magenta were obtained using principal component analysis (PCA+varimax rotation), non-negative matrix factorization (NNMF Lee and Seung algorithm), independent component analysis (ICA

Infomax), and pNMF, respectively. VAF was 97.3% for ICA, NNMF and PCA and 96.0% for pNMF. Data were from a rowing task (Turpin et al. 2011). **c, d** Synergy activations and synergy vector coefficients obtained from the different methods. The data cloud seems to evolve in some privileged directions (close to the ICA and pNMF vectors here) but all vectors define roughly the same subspace. The degree of overlapping of synergy activation coefficients varies with vector orientation, which depends on the algorithm. *GM* gastrocnemius medialis, *SOL* soleus, *BF* biceps femoris

synergy vectors noted  $\mathbf{w}_j$  (of dimension  $1 \times m$ ) and scaled in amplitude by a time- (or condition-) varying synergy activation coefficient, noted  $c_j(t)$  (Ting and Chvatal 2010):

$$\mathbf{e}(t) = \sum_{j=1}^s c_j(t) \mathbf{w}_j + \text{residual},$$

where  $s \leq m$  is the number of synergies,  $j$  the synergy index going from 1 to  $s$ . This equation is rewritten in matrix form as:

$$\mathbf{E} = \mathbf{W} \times \mathbf{C} + \text{residual}, \quad (1)$$

with  $\mathbf{E}$ ,  $\mathbf{W}$ ,  $\mathbf{C}$  and **residual**, matrices of dimensions,  $m \times T$ ,  $m \times s$ ,  $s \times T$  and  $m \times T$ , respectively.  $T$  being the number of time samples.

This representation allows to separate the spatial ( $\mathbf{W}$ ) and temporal ( $\mathbf{C}$ ) components of EMG data and to define their dimensionality—a notion that appeared very useful when studying pathological movement patterns (Steele et al. 2015a; Clark et al. 2010). The spatial structure of EMG patterns refers to the subspace in which most of the EMG data lie and is defined using the synergy vectors in  $\mathbf{W}$ . The weightings define the direction of the vectors and represent how much each muscle increases its activation when a synergy is activated. The dimensionality of the EMG data can be defined as the minimal number of vectors necessary to explain most of the data variance (variance accounted for or VAF > 80–95%). The temporal structure refers to how the activation coefficients are sequenced in time relative to each other.

## Synergy extraction

### The question of the algorithm

Given Eq. (1) the common method of synergy identification is matrix factorization applied to the EMG data matrix. The goal of matrix factorization as a dimensionality reduction technique is to form a reduced set of vectors in the muscle activation space whose linear combination can explain most of the data variance (Fig. 2b). In other words, the method regroups muscles that co-vary with each other to form synergies, which are the vectors delineating the subspace. However, these vectors can be oriented in an infinite number of ways. This means that the relative weighting of each muscle within a synergy can also vary in an infinite number of ways (Fig. 2b), questioning the physiological meaning of the extracted synergy vectors. Therefore, some constraints are used to generate a unique set of vectors, such as non-negativity, sparseness or mutual orthogonality of the vectors, or statistical independence of the time-varying activation. As a consequence, a large variety of algorithms was proposed to

satisfy one or several of these constraints (Choi et al. 2005; Singh et al. 2018).

The issue of algorithm selection for synergy extraction has been investigated in numerous papers, including the seminal paper of Tresch and collaborators (Tresch et al. 2006). They tested several algorithms such as factor analysis, principal component analysis (PCA), non-negative matrix factorization (NNMF) and independent component analysis (ICA), and showed that the diverse factorization techniques provide similar results in terms of synergy vectors and synergy activation. This suggests that extracted vectors are not artifacts of the algorithms, but reflect basic aspects of the organization of muscle activation patterns (Tresch et al. 2006). However, and as exemplified in Fig. 2, some differences can be found between the outcomes of the different algorithms. During relatively similar experiments, previous results concluded that muscle synergies were either robust (using NNMF) or variable (using PCA) across experimental conditions, such as in postural control (e.g., Krishnamoorthy et al. 2004; Torres-Oviedo and Ting 2010), or pedaling (Wakeling and Horn 2009; Hug et al. 2011). Based on real and simulated data, Tresch et al. (2006) recommended the use of ICA applied to the subspace defined by PCA. However, most previous studies preferred the use of NNMF algorithms (Rabbi et al. 2020). Minimization of the residuals coupled with non-negativity constraints appear to give NNMF interesting properties such as generalizability and interpretability (Lambert-Shirzad and Van der Loos 2017; Lee and Seung 1999). Generalizability refers to the ability of a set of synergies identified in a given condition to explain EMG variations in another condition. Interpretability is made easier, because the NNMF algorithm allows only additive combinations of the synergies, and the synergies found are often sparse, each representing/activating only a few number of muscles. For example, when comparing synergy vectors, previous studies found large similarities between different tasks or different conditions of the same task using NNMF (Hug et al. 2011; Scano et al. 2019). Further studies tested and compared NNMF to other techniques such as PCA, ICA or factor analysis and concluded that it is superior when fixed and positive synergy vectors are assumed (Lambert-Shirzad and Van der Loos 2017; Steele et al. 2015b; Ebied et al. 2018).

However, the other above-mentioned techniques should not be discarded as they provide insightful results regarding the structure of motor output at both spatial and temporal levels (Yang et al. 2019; Kargo and Nitz 2003). Most factorization techniques actually appear similar in terms of subspace representation, and they are all able to fit data to similar degrees of accuracy (Fig. 2). The major distinction between the different algorithms lies in the vector orientation rather than in the subspace that they define. Given that vector comparisons (correlations) and subspace comparisons



(cross-validations) might provide different results (Oliveira et al. 2014), the choice of algorithm may, therefore, have an effect at this level. In our opinion, a seldom recognized consequence of these direction changes is that they introduce variations in the degree of overlapping of synergy activations, which appear more or less correlated with each other for the same dataset (Fig. 2c). Therefore, the choice of algorithm may have an impact on the study of the temporal structure. In the example provided in Fig. 2, vectors from the ICA and projective non-negative matrix factorization (pNMF) algorithms provide the least amount of overlapping between activation coefficients. This is consistent with their objective-functions, i.e., ICA maximizes the independence of activation profiles and pNMF, their orthogonality (Bell and Sejnowski 1995; Yang and Oja 2010). Limiting overlapping between synergy activations would be consistent with the supposed sequential nature of the motor command, as observed at the cortical level for example (Drew et al. 2008), but further studies are needed to clarify this point.

Solutions to the factorizations are associated with ambiguities in the scaling of the two components,  $\mathbf{W}$  and  $\mathbf{C}$ , and in the order of vectors in each component (permutation ambiguity). Scaling ambiguity implies that the information about EMG amplitude is lost, making it difficult to compare the components in terms of magnitude and to interpret the activation levels of the synergies. To allow for comparisons, previous studies forced vectors to have unit  $l_2$ -norm, or each synergy vector was normalized with respect to the greatest weighting coefficient in that synergy (Muceli et al. 2014). Note that to preserve the equality in Eq. (1), if  $\mathbf{D}$  is the diagonal matrix used to normalize  $\mathbf{W}$ , i.e.,  $\mathbf{W} \times \mathbf{D}$ , then  $\mathbf{C}$  should be pre-multiplied by  $\mathbf{D}^{-1}$ . As for the permutation, this only becomes a problem when the synergies need to be compared with those extracted from other conditions or other subjects (Cappellini et al. 2016). The way the components should be compared between subjects and conditions deserves further studies.

A greater problem is that several  $\mathbf{W}$  and  $\mathbf{C}$  can satisfy  $\mathbf{E} = \mathbf{W} \times \mathbf{C}$  with similar residuals (Rickard and Cichocki 2008). Figure 2 illustrates this fact using different algorithms. However, solutions are generally not unique, even for a given algorithm, because of the presence of local minima, a common problem when one wants to optimize a function. To avoid local minima, previous studies ran the algorithm several times and then took the solution with the lowest cost. In the literature reviewed, the number of runs ranged between 10 and 100 (Cappellini et al. 2016; Cheung et al. 2012; Hug et al. 2011), although there is no consensus about the ideal number of runs, and a lack of evidence to indicate whether or not diverse local minima are associated with great differences in terms of solutions. It is worth noting that we also observed a global minimum attained with even a single run using PCA initialization (Turpin et al. 2020).

The existence of several minima is exacerbated when synergy activation coefficients are correlated with each other (Tresch et al. 2006; Soomro et al. 2018; Steele et al. 2015b). The phenomenon is illustrated in Fig. 3, where two groups of muscles (synergy #2 and synergy #3) are activated simultaneously without being coupled in amplitude.

This configuration can prove problematic as the “true” synergies become difficult to identify. A simulation study previously indicated that sparse initialization can improve the identification of correlated synergies (Soomro et al. 2018). Using PCA solutions, which were close to the input vectors in our example in Fig. 3, it was actually possible to recover the input synergy vectors. Initialization using SVD or PCA solutions also has the advantage of hastening the convergence of the algorithm (Zheng et al. 2007; Boutsidis and Gallopoulos 2008). The influence of this phenomenon on real EMG data is difficult to evaluate. During a pedaling task, Soomro et al. (2018) compared the results of a synergy analysis using either random or sparse initializations and found very little differences in the synergies extracted, suggesting an absence of correlated synergies in this task. However, such a conclusion might not be generalizable to other tasks.

## The different synergy models

In various tasks such as walking (Barroso et al. 2014), cycling (Hug et al. 2011) or postural responses (Torres-Oviedo and Ting 2010), previous studies found evidence that muscles within a synergy could be activated in a relatively fixed balance despite changing biomechanical contexts, meaning that synergy vectors possess very similar directions in the muscle activation space in these various contexts. The identification of synergies as fixed vectors corresponds to the model in Eq. (1) and is often referred to as the *synchronous* or *spatial synergy model*. This model assumes that the activations of synergies ( $\mathbf{C}$ ) can vary across time or conditions while the spatial structure,  $\mathbf{W}$ , remains fixed. In this case the  $\mathbf{E}$  matrix is organized as follow:

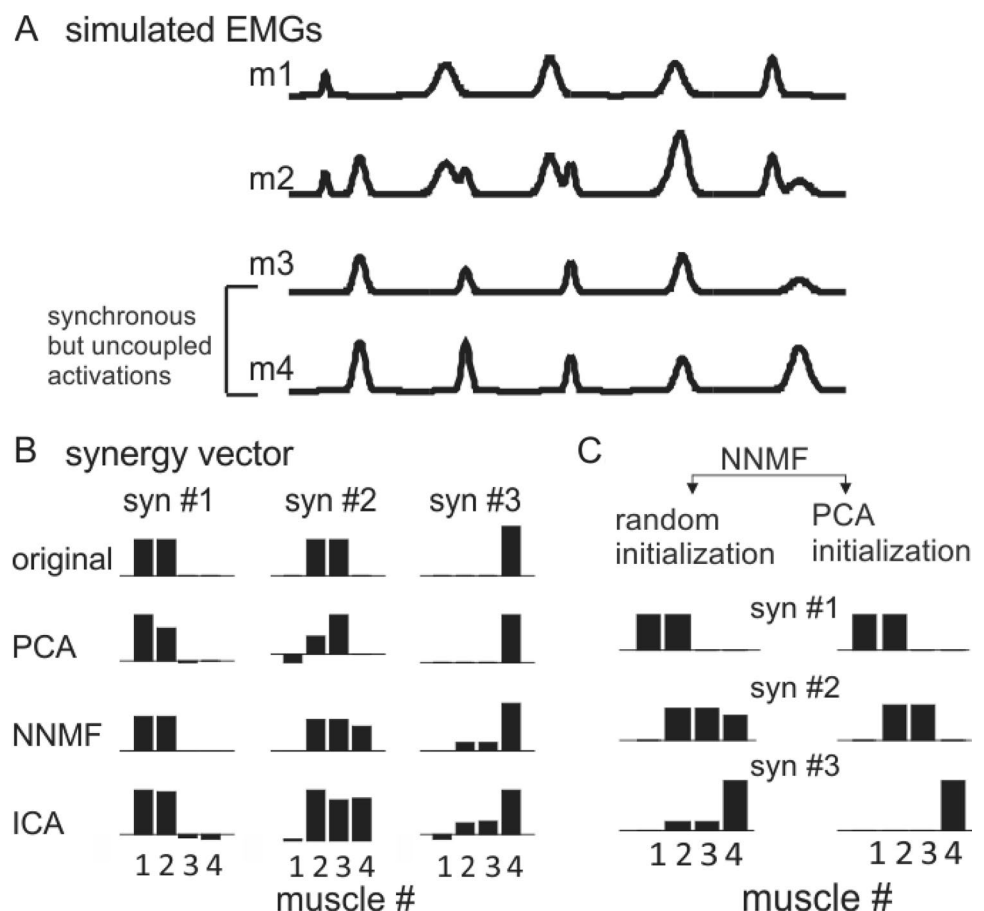
$$\mathbf{E} = [\mathbf{E}_1 | \mathbf{E}_2 | \dots | \mathbf{E}_n] \cong \mathbf{W} \times [\mathbf{C}_1 | \mathbf{C}_2 | \dots | \mathbf{C}_n],$$

with  $\mathbf{E}_k$  and  $\mathbf{C}_k$ , the  $\mathbf{E}$  (muscle  $\times$  time) and  $\mathbf{C}$  (synergy#  $\times$  time) matrices for condition  $k$  ( $k = 1 \dots n$ ), concatenated in line. Time is not necessarily normalized in this model, as the focus is put on identifying the muscle weighting coefficients ( $\mathbf{W}$ ). It is also possible to fix the activation coefficients while allowing  $\mathbf{W}$  to vary across time or conditions (the *temporal synergy model*), and in this case the  $\mathbf{E}_k$  should be concatenated in column (Delis et al. 2014):

$$\mathbf{E} = [\mathbf{E}_1; \mathbf{E}_2 \dots; \mathbf{E}_n] \cong [\mathbf{W}_1; \mathbf{W}_2; \dots; \mathbf{W}_n] \times \mathbf{C}.$$

An important point is that, contrary to the previous formulation, each column of  $\mathbf{E}_k$  should possess a certain

**Fig. 3** The case of synchronous but uncoupled muscle activations. **a** Here we used a simple simulation to obtain muscle-like waveforms (m1...m4) that show synchronous but uncoupled activations, i.e., in m3 and m4. Activation coefficients were modeled as Gaussians scaled differently in amplitude. Original synergy vectors used in the simulation are shown in **b**. The co-variation between m3 and m4 are captured by non-null coefficients in syn #2 and syn #3 for both NNMf and ICA methods, but not for PCA. **c** Initializing the NNMf algorithm using PCA results instead of random values in this case resulted in a better identification of the input synergy vectors. VAF explained by different algorithms and initializations was 100% (no noise added), demonstrating the presence of several solutions to the equation  $E = W \times C$



congruence over the different  $k$ , e.g., correspond to similar percentages of time, for example. It is assumed in this model that activations of the synergies are sequenced similarly across cycles or tasks and that the weightings of muscle synergies can vary. Such a model is widely used to analyze activity of the so-called central pattern generators, which are supposed to organize the rhythmic activity of both upper and lower limbs during locomotion (Ivanenko et al. 2005). Therefore, matrix factorization is able to specifically extract spatial or temporal structures of muscle activations depending on the organization of the matrices. Even so, mainly the first form— $W$  fixed—was used for analyzing both spatial and temporal structures of motor output (Ivanenko et al. 2005; Kargo and Giszter 2008).

During dynamic movements the temporal structure of muscle activation often takes the form of sequenced, Gaussian-like impulses called basic patterns, unit bursts or primitives (Lacquaniti et al. 2012; Giszter et al. 2007; Sartori et al. 2013). A priori, the numbers of synergy vectors and basic patterns are different. For example, during simple reaching movements of the arm, 4 or 5 muscle synergies are necessary to reconstruct the muscle activations in various directions (Cheung et al. 2009; Muceli et al. 2010; Roh et al. 2013) though each single movement is composed of only 2

or 3 basic patterns (the so-called tri-phasic pattern). Delis and colleagues proposed a space-by-time decomposition in which both components explicitly appear, i.e., each module  $C_i$ , and each synergy vector  $W_j$  can be independently combined to produce complex muscle activation patterns (Delis et al. 2014). This decomposition is performed by a tri-factorization algorithm which essentially use the Lee and Seung (2001) to first find (fixed)  $C$  and (fixed)  $W$  from the  $E_k$  concatenated in line or in column, respectively, and then find the association matrices  $A_k$  for each condition separately, such that

$$E_k \cong W \times A_k \times C.$$

The decomposition clearly separates temporal and spatial structures in a single analysis.

Another proposed formulation in which spatial and temporal structures are linked together is the *spatio-temporal* or *time-varying synergy* model (d'Avella and Tresch 2006; d'Avella et al. 2003, 2006; Chiovetto et al. 2016). In this formulation each synergy is viewed as a temporal sequence of multiple muscle activations, each of which can be shifted in time and scaled in amplitude, depending on the conditions. This model reflects the idea that

complex movements are generated by learning sequences of sub-movements, in which the overall organization might eventually constitute modules recruited as independent units (Shmuelof et al. 2012; Klein Breteler et al. 2007; Viviani and Laissard 1991). Although it is debatable whether the temporal sequence of motor actions can be encoded together with muscle synergy vectors (Wong and Krakauer 2019; Kargo and Giszter 2008), the analysis certainly provides valuable information about the spatio-temporal organization of the motor output (Berger et al. 2020). A simple way to extract spatio-temporal synergies is to use the formulation proposed in Klein Breteler et al. (2007):

$$\mathbf{E} = [\text{vec}(\mathbf{E}_1); \text{vec}(\mathbf{E}_2); \text{vec}(\mathbf{E}_k) \dots \text{vec}(\mathbf{E}_n)] \cong \mathbf{W} \times \mathbf{C}.$$

With  $\text{vec}(\mathbf{E}_k)$  indicating the vectorized matrix  $\mathbf{E}_k$ , where the lines of the matrix are placed end to end to form a single line vector. Similar to the temporal synergy model, columns of each  $\mathbf{E}_k$  should be congruent, e.g., time-normalized data. The  $\text{vec}(\mathbf{E}_k)$  from different trials or conditions are then concatenated in column.  $\mathbf{W}$  contains the spatio-temporal vectors (in line) and  $\mathbf{C}$  contains the coefficients modulating the activation amplitude of the synergies. Notice that the formulation proposed by d'Avella et al. (2003) is more refined, because the synergy onset times can also be modulated. Although the *time-varying synergy* model has been less frequently used than the synchronous synergy model, it is comparable in its ability to explain EMG data, and it also provides additional information about the relation between spatial and temporal components (Esmaeili and Maleki 2020; d'Avella et al. 2006).

While each of these models—spatial, temporal, and spatio-temporal—provide different information about the structure of motor output, a recent study has provided evidence that they can complement each other in synergy analysis (Berger et al. 2020). Such an approach, using different synergy formulations, should be encouraged in future studies.

## EMG signal acquisition and processing

Synergy analysis is based on the examination of the amplitude of EMG signals, using either averaged activity or different measures of its envelope (Ting and Macpherson 2005; Valero-Cuevas et al. 2009; Zandvoort et al. 2019). EMG amplitude reflects the output of spinal motoneurons but their relation is not simple (Milner-Brown and Stein 1975; Martinez-Valdes et al. 2018). Therefore, the technique used to obtain and process EMG signals is of fundamental importance.

## EMG envelope

Synergy analysis inherits every EMG drawback, such as amplitude cancellation or cross-talk (Farina et al. 2014). Basic recommendations for acquiring and processing this signal are generally well-followed and have been largely documented (De Luca et al. 2010)—see also the guidelines of Surface Electromyography for the Non-Invasive Assessment of Muscles—SENIAM—<http://www.seniam.org/>.

In the synergy literature, however, there appears to be no consensus of the best method used to validate EMG envelopes (Shuman et al. 2017). The most commonly accepted method to obtain the envelope is to low-pass filter the rectified EMG (using a zero-lag, Butterworth filter in most cases): the EMG envelope is obtained by smoothing the EMG signal after rectification, i.e., taking its absolute value or using Hilbert transformation (Zandvoort et al. 2019). Other filtering methods include those similar to moving average (iEMG, RMS, etc. Yang et al. 2019; Turpin et al. 2017) or intensity analysis using wavelet transform (Frere 2017). Although not thoroughly investigated, the differences between these various methods are likely to be small.

There is evidence that the degree of smoothing of EMG envelope affects spatial and temporal structures of synergies and the determination of the number of synergies (Shuman et al. 2017; Hug et al. 2012; d'Avella and Tresch 2006). Large variations in cut-off frequencies are found in the literature when using low-pass filters, ranging from 1 (Muceli et al. 2014) to 40 Hz (Kim et al. 2018a). Decreasing this cut-off frequency “widens” the EMG profiles, thereby increasing their degree of overlapping, which naturally affects synergy vectors (Shuman et al. 2017; Santuz et al. 2017; Kieliba et al. 2018). Zandvoort et al. (2019) performed a synergy analysis on the modulus of the Hilbert transform of the EMG signals to preserve their higher spectral contents (without low-pass filtering the data) and found similar synergy vectors compared to a more commonly-used filter (second order, low-pass Butterworth, cut-off = 9 Hz). Therefore, using very smooth EMG patterns doesn't seem to be justified when the spatial structure is investigated. Based on previous studies we suggest that a cut-off frequency of approximately 9–12 Hz may preserve subject-specific information while reducing the amount of noise (Hug et al. 2019; Shiavi et al. 1998).

In addition, other processing techniques such as demeaning the raw signal or removing the baseline (minimal value) from the envelope were sometimes used (Roh et al. 2013) to correct a possible bias in the amplifier and to remove baseline noise or constant tonic activity in the muscles (Law et al. 2011; d'Avella et al. 2006). Baseline correction is not commonly used in the synergy literature, but may improve the signal-to-noise ratio (SNR) of the EMG signal (Law et al. 2011), which is known to strongly influence synergy

analysis results (d'Avella and Tresch 2006; Steele et al. 2013). Therefore, it deserves further investigations.

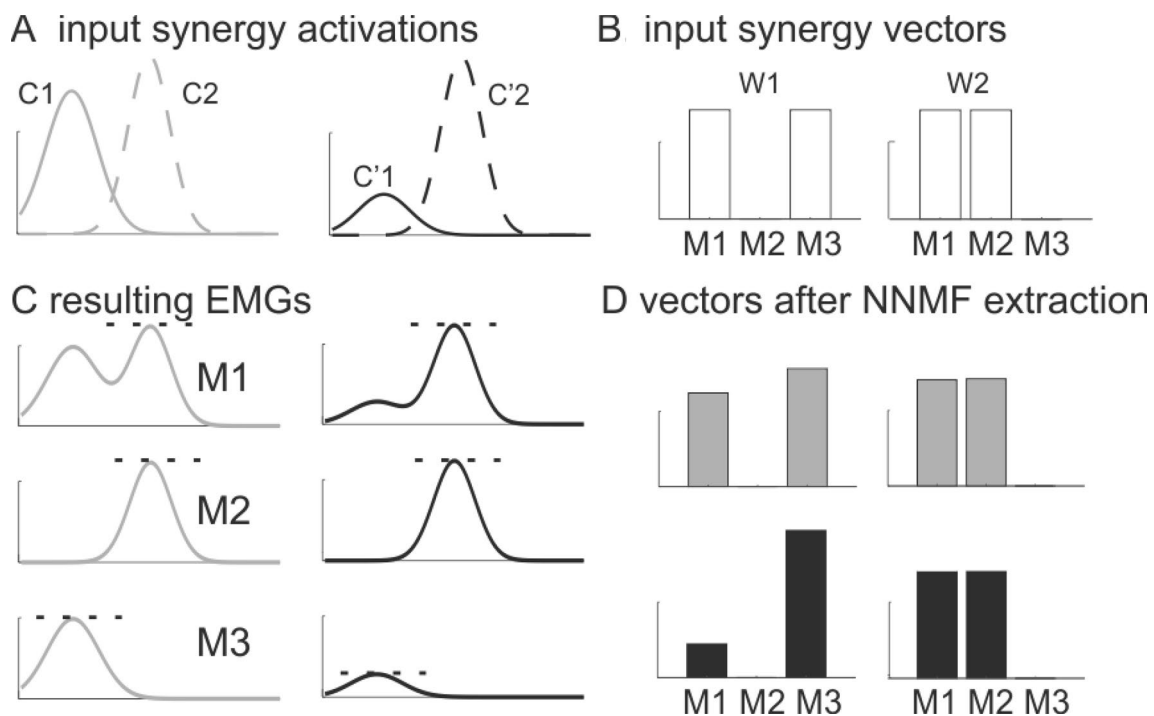
### Amplitude normalization

EMG envelope amplitudes are often normalized by a reference value before extracting the synergies. Normalization allows to redistribute the variance equally among the muscles and to regularize the amplitude of the different synergy vector coefficients, making them more interpretable. Although EMG envelopes are generally normalized by the maximum value, the mean value or the standard deviation computed over the entire dataset (Shuman et al. 2017; Banks et al. 2017; Turpin et al. 2017), muscle synergies were extracted without any normalization in a few studies (Muceli et al. 2014; Yang et al. 2019; Cappellini et al. 2016). As indicated by Muceli et al. (2014), normalizing by the maximum value amplifies noise as well as signal, which could have negative effects on synergy identification. It can be shown that synergy vectors and residuals are directly influenced by normalization. Normalizing EMGs corresponds to the pre-multiplication of the non-normalized version of Eq. (1)

by a diagonal matrix **D**, composed of the inverses of the normalization values:

$$\mathbf{E} = \mathbf{D} \times \mathbf{E}_{un-norm} \times \mathbf{D} = \mathbf{D} \times \mathbf{W}_{un-norm} \times \mathbf{C} + \mathbf{D} \times \mathbf{residual}_{un-norm},$$

with the subscript *un-norm* denoting the un-normalized versions of the matrices. Therefore, it is not surprising that normalization can affect the similarities between synergy vectors (Banks et al. 2017) and the determination of the number of synergies, as this determination is mainly based on the study of the residuals (Kieliba et al. 2018). It appears that the effect on VAF is significant (Kieliba et al. 2018), although, the effects on synergy vectors are not always clear. Generally speaking, and as demonstrated in Fig. 4, the absence of task-independent normalization is a strong limitation when comparing different subjects. In particular, this should be taken into account when comparing healthy and pathological subjects for whom the signal-to-noise ratio of the recorded EMG channels are often very different. Still, Cappellini et al. (2016) compared different subject populations using both normalized and non-normalized EMG and did not report divergent conclusions. Kieliba et al. (2018) normalized EMG envelopes by either the maximum over



**Fig. 4** Illustration of the normalization effects. We simulated the activity of 3 muscles (M1, M2 and M3) as the combination of two synergy activations (solid and dashed lines in **a**) and two synergy vectors (W1 and W2 in **b**) in two conditions (gray and black). No noise was added in these simulations. The difference between these two conditions is that the activation coefficient of the first synergy is higher in the gray condition (i.e.,  $C1 > C'1$ ). Here C1 and C'1 activate

W1, while C2 and C'2 activate W2. In **c**, the dashed horizontal lines indicate the maximum of each muscle. **d** The NMF algorithm was applied after normalization of the EMGs relative to their respective maxima. The presence of M1 in two different synergies make its amplitude relative to the other muscles depending on how the different synergies are activated during the task. Original synergy vectors could not be identified in either case



all data or by the maximum obtained during maximal voluntary contractions (MVC), and found no significant effects on synergy vectors. Normalization by the maximum value obtained during isometric MVCs was sometimes performed (Manickaraj et al. 2017; Kieliba et al. 2018; Israely et al. 2017), but it is difficult to obtain a true maximum for all muscles that are generally recorded ( $> 5$ ) during such a test and might be exhausting or even impossible for populations with pathologies, pain or unaccustomed to the task (Lindstroem et al. 2012). However, such normalization would enable suitable comparison between subjects and studies. Alternative methods have not been considered in the synergy literature (Sousa and Tavares 2012; Yang and Winter 1984; Besomi et al. 2020).

## Data acquisition and experimental conditions

Intra-muscular recordings were sometimes performed in humans in addition to surface EMGs (Valero-Cuevas et al. 2009; Heales et al. 2016; Ajiboye and Weir 2009; Saito et al. 2018; Ivanenko et al. 2004; Turpin et al. 2020). In these studies, deep muscles did not produce specific synergies. Although these muscle recordings did not likely have much impact on the number of synergies, they clearly provide a more refined analysis of the spatial structure (Heales et al. 2016).

Inter-electrode distance affects the selectivity of recordings, that is, the volume detection of muscle fiber activity, i.e., large inter-electrode distance allows to record a greater volume of muscle fibers (Fuglevand et al. 1992), but, at the same time, it is associated with greater probability of cross-talk (Farina et al. 2014; Campanini et al. 2007). Cross-talk might exaggerate positive correlations between adjacent muscle recordings, and therefore, it would affect the spatial structure rather than the temporal structure of synergies (Ivanenko et al. 2004). In the literature reviewed, inter-electrode distances were not always reported; in those studies that did report it, the distances appear variable, i.e., from 10 to 22 mm (Zandvoort et al. 2019; Muceli et al. 2014). However, the influence of cross-talk on synergy analysis results is difficult to estimate (Farina et al. 2014).

The number of recorded muscles varies widely across studies, ranging between 5 and 32 (van der Krogt et al. 2016; Van Crielinge et al. 2019). We found no recommendation about any “optimal” set of muscles to study for a given task. A common-sense rationale for choosing the set of muscles is that they should all participate in the task, but the recording of all muscles participating in one given task is feasible only in a few cases (Valero-Cuevas et al. 2009). There is evidence suggesting that some synergies might be composed of muscles spanning more than one joint (Drew et al. 2008;

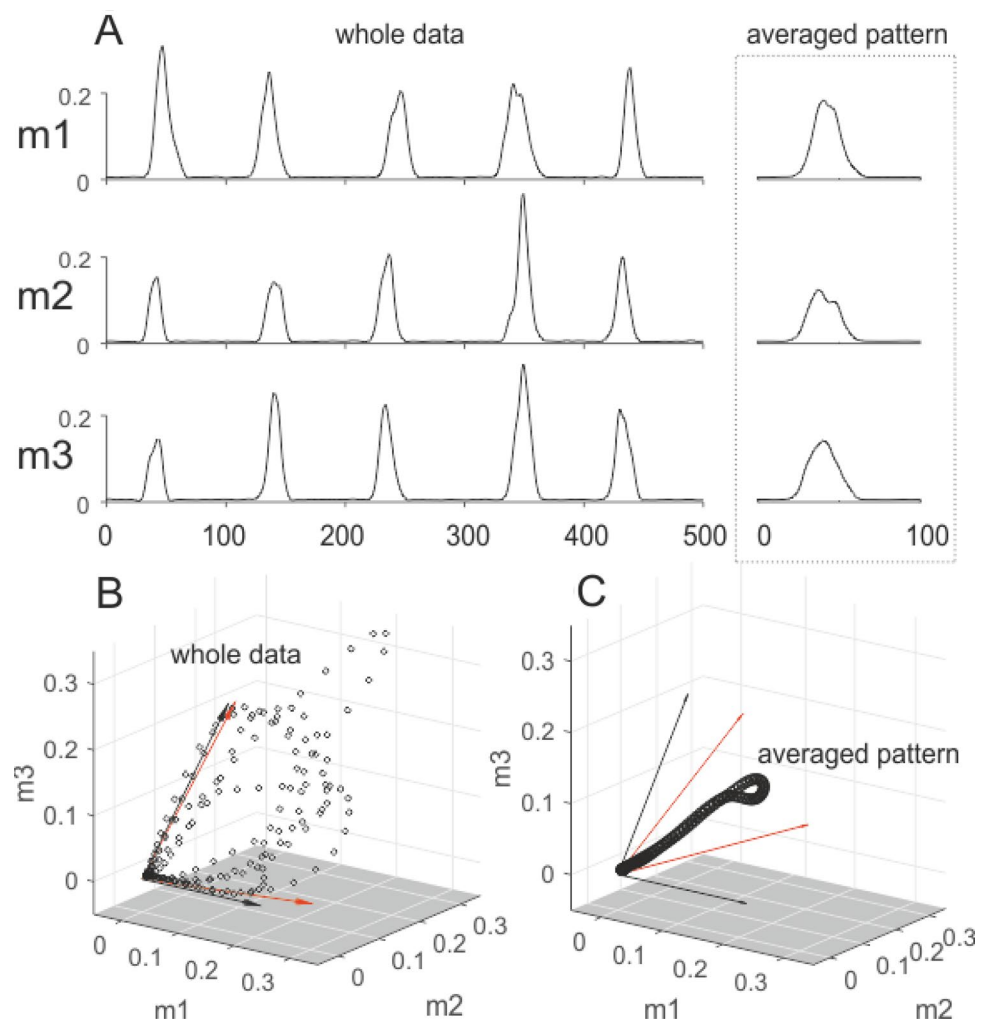
Levine et al. 2014), and that at a functional level, even upper and lower limb muscles can be coordinated in a synergistic fashion (Ivanenko et al. 2005). Still, it is difficult to identify a priori all muscles or muscle groups that would create independent components, and in our opinion exploratory studies are required before a new task can be fully investigated.

The specific set of muscles chosen and grouped together may affect the number of synergies and their structure. For example, Gizzi et al. (2011) and Chia-Bejarano et al. (2017) compared their results during walking using different sets of muscles (7 vs. 16 and 8 vs. 13, respectively) and found similar but not identical synergy vectors. The relative magnitude of the synergy vector coefficients differed slightly between results obtained from the two sets of muscles that were used, suggesting that the algorithm (NNMF in both) is sensitive to the variance of the different muscles included in the analysis. The results of Steele et al. (2013) on simulated data confirmed such a behavior for the NNMF algorithm, and these authors suggested to ensure that the selected set of muscles contains the muscle with the highest coefficient or with the highest isometric force to improve the similarity between synergy vectors.

This creates the problem of missing EMG channels which is frequent in clinical evaluations and certainly affects analysis outcomes. Previous studies used a weighted version of the NNMF algorithm to cope with missing muscle channels (Shuman et al. 2019) but this problem has not yet been addressed thoroughly.

The amount of data used to extract synergies also varies substantially across studies. For example, during walking, the number of cycles used to extract synergies can range between 1 and 40 (Oliveira et al. 2014; Hinnekens et al. 2020). Oliveira et al. (2014) compared synergies obtained with averaged EMG data or with concatenated EMG matrices and suggested a minimum of 20 cycles to obtain synergy vectors that would be generalizable. Other studies showed that the correct identification of synergy vectors actually requires the presence of substantial data variability in terms of activation amplitude (Oliveira et al. 2014; Steele et al. 2015b; Ranganathan and Krishnan 2012), notably during biomechanically constrained tasks (Burkholder and van Antwerp 2013; Steele et al. 2015b). The magnitude of EMG variation may have a direct influence on synergy analysis results, in particular on the orientation of synergy vectors and their ability to explain other datasets. In Fig. 5 we show how the absence of a proper exploration of the synergy subspace can adversely influence the synergy analysis outcomes. In the data in Fig. 3, for example, if averaged patterns were used instead of the entire data, the muscles that co-vary without being coupled in amplitude would have belonged to the same synergy and two synergies instead of three would have accounted for 100% of the variance. However, the temporal structure, composed of two sequential

**Fig. 5** Data range affects NNMF results. Non-negativity constraints coupled with the optimization of both  $\mathbf{W}$  and  $\mathbf{C}$  (in  $\mathbf{E} = \mathbf{W} \times \mathbf{C}$  + residuals) implies that the vectors are “outside”—at the edges—of the data cloud, i.e., they form a simplicial cone. This outside area may be large if the range of data variation is small, which may be the case when averaging the data. Therefore, this range may have an effect on NNMF results. The waveforms in **a** (m1, m2 and m3) were generated by activation coefficients ( $\mathbf{C}$ ) consisting in Gaussians with varied amplitudes and using the bases  $\mathbf{w}_1 = [0, 0.6, 0.8]^T$  and  $\mathbf{w}_2 = [1, 0, 0]^T$  (black vectors in **b** and **c**). The resulting  $\mathbf{E}$  matrix ( $\mathbf{E} = \mathbf{W} \times \mathbf{C}$ ) was corrupted with white noise (amplitude = 0.01) and then low-pass filtered (cut-off = 9 Hz). In **b** and **c**, the vectors in red were obtained using NNMF applied on  $\mathbf{E}$  (random initialization) and the average patterns of  $\mathbf{E}$ , respectively. Using cross-validation (Lee and Seung updates), the red vectors in **b** explained 99.8% of data variation in **c** (vs. 99.8% using the original vectors), while the red vectors in **c** explained only 97.3% of data variation in **b** (vs. 99.3%)



bursts, could still be identified by the algorithm. This indicates that averaging across cycles or repetitions can lead to mixed or merged synergies. Therefore, matrix factorization might be able to identify the temporal structure of EMG data from averaged data (MacLellan et al. 2014; Zelik et al. 2014; Ivanenko et al. 2005), but some information about the spatial structure may be lost.

Besides its variability, the actual level of muscle activation is of importance in the detection of synergies. Muscle synergies must be activated above noise level to be identified. For example, during standing cycling, a synergy linked to knee flexors is barely activated below ~250 W (Turpin et al. 2017) and cannot be robustly identified in any of the subjects at low exercise intensity. Similarly, in pathology, neural input to the muscles is often diminished (Klein et al. 2010), and this may influence the recruitment of synergies. In this respect, Kim et al. (2018b) suggested that children with cerebral palsy may have similar synergies compared to typically developing children during walking, but that these synergies appear to be recruited less frequently and with more variability across the walking strides. Although

previous studies have suggested to remove the small and inconsistent muscle activations to increase the consistency of the analysis (Ghislieri et al. 2020), these small activations may have significant functional effects and be clinically relevant (Kim et al. 2018b; Barradas et al. 2020). These problems are difficult to eliminate and should be taken into account when designing and performing experiments.

## The number of synergies

### The VAF vs. number-of-synergies curve

An important measure in synergy analysis is the VAF by the model, which is taken as a measure of goodness of fit. VAF (un-centered) is typically computed as:

$$\text{VAF} = 1 - \text{SSE}/\text{SST},$$

with SSE the sum of squared errors and SST the total sum of square (the sum of all elements in  $\mathbf{E}$ , after they have been

squared; *cf.* Equation (1). In some studies VAF (centered) was computed with the term SST replaced by the trace of the covariance matrix of **E** (d'Avella et al. 2006; Hinneken et al. 2020). Other measures of goodness of fit such as log-likelihood ratio or Pearson's  $R^2$  can be found in the synergy literature (Tresch et al. 2006; Togo and Imamizu 2017). These different VAF computations provide different values for a given decomposition (Togo and Imamizu 2017). Using different normalizations of EMGs, different numbers of muscles or different factorization algorithms, the values or the allure of the VAF curve may change drastically (Tresch et al. 2006; Kieliba et al. 2018; Castellini and van der Smagt 2013) (Fig. 5b). VAF is also strongly influenced by level of noise or unstructured EMG and by data filtering (Hug et al. 2012; d'Avella and Tresch 2006). Therefore, measures of goodness of fit and VAF appear difficult to compare between studies.

Both cross-validation and bootstrapping procedures have been used in previous studies to yield better estimates of true VAF values. Cross-validation is a procedure in which VAF is measured in parts of the dataset not used to extract synergies, thereby ensuring that the values truly estimate the amount of errors—as VAF is maximized by the optimization process (Hirashima and Oya 2016; d'Avella et al. 2003; Muceli et al. 2010). Bootstrapping allows estimating both mean and confidence intervals by computing VAF from different and randomly sampled parts of the dataset (Allen et al. 2017). However, the advantage of using these methods have not been confirmed.

## Selecting an appropriate number of synergies

A sticking point in synergy analysis is the determination of the number of synergies. This is a historic problem (Jackson 1993) and is significant since the number of synergies influences comparisons between subjects or conditions (Kim et al. 2018b).

Several methods used to defined the number of synergies rely on identifying a knee point—a sharp inflexion- and the straight line that should follow it on the VAF vs. number-of-synergies curve (Tresch et al. 2006). This straight line is generally taken as evidence that only unstructured data or noise are captured by the components that follow. The knee point can be determined by visual inspection in some cases (Catell's scree test in factor analysis) but can be impossible if the VAF curve is too smooth (Fig. 6).

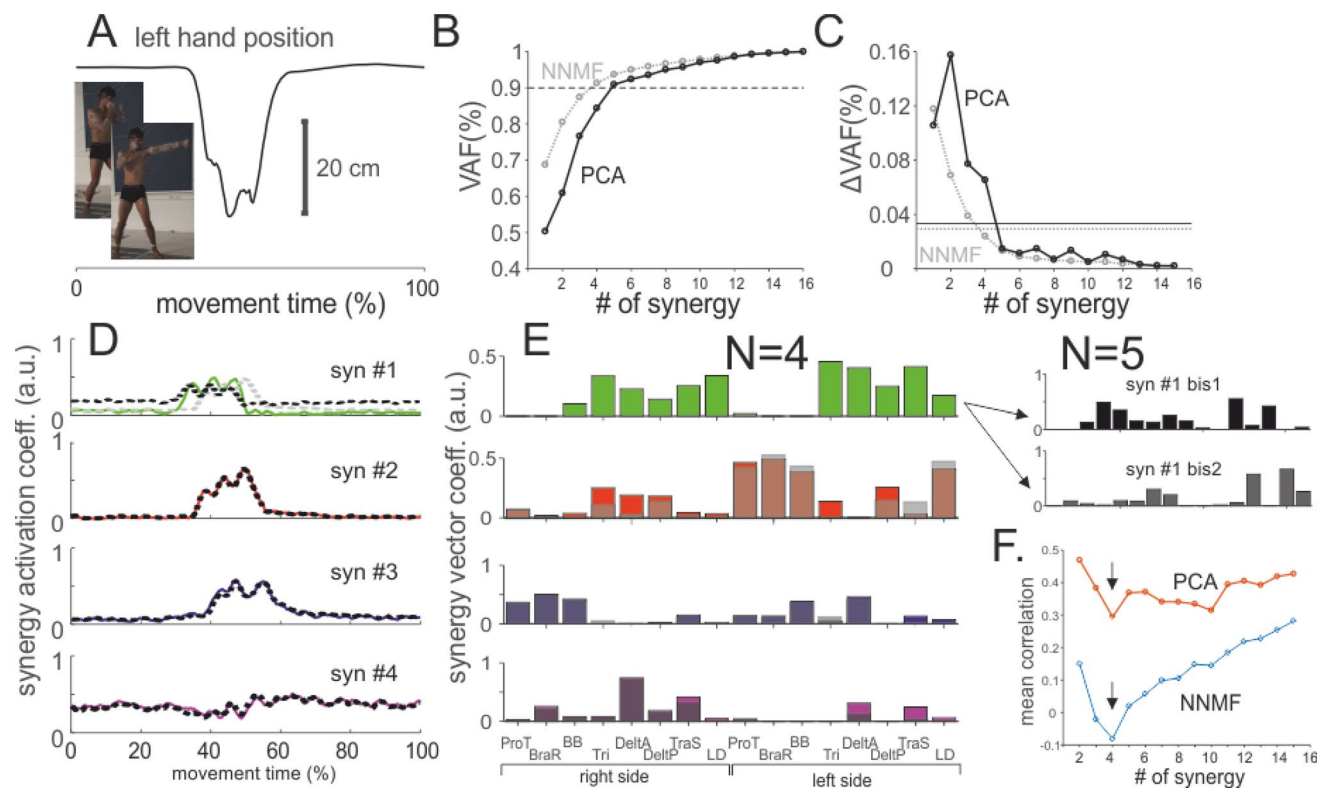
Fixed VAF thresholds are a commonly used criteria for defining the number of synergies, i.e.,  $\text{VAF} > 80\text{--}95\%$  associated with the constraint that VAF per muscle  $> 75\text{--}85\%$  or that further increase in VAF is less than 2–7% (Kaiser criterion in factor analysis) (Sawers et al. 2015; Chia Bejarano et al. 2017; Hug et al. 2011; Maclellan et al. 2014). These thresholds are often determined heuristically based

on the specificity of each dataset to ensure that most of the variance is accounted for when choosing the first  $N$  dimensions. The comparisons with VAF increase for unstructured data is also very common (Cheung et al. 2005; Takei et al. 2017) (Horn's parallel analysis in factor analysis—Fig. 6c). In particular, this method proved to be robust with regards to the degree of EMG smoothing (Hug et al. 2012). There are other methods relying on information criteria such as Akaike or Bayesian information criteria (Tresch et al. 2006; Chiovetto et al. 2014). However, all these methods showed only limited performances (Severini and De Marchis 2018; Tresch et al. 2006). Despite the great amount of work on this subject, defining the number of synergies without ambiguity continues to be difficult.

As a consequence, the criterion  $\text{VAF} > 0.9$  might appear to be conservative as it ensures a “sufficient” representation of the data. Still, this also is debated (Kim et al. 2016; Barradas et al. 2020). First, VAF is sensitive to several factors, including the level of noise (Shuman et al. 2017), which indicates that this criterion may give different results depending on the quality of the EMG signal or processing techniques. Second, the residuals—which account for 5–20% of total variation—are not merely noise (Valero-Cuevas et al. 2009; Barradas et al. 2020). They may actually represent small synergies (Kim et al. 2018b) or results from a certain degree of flexibility or non-linearity of the spatial structure that is not captured by the linear model (Barradas et al. 2020).

Alternatively, some authors suggested to determine the number of synergies based on either their ability to discriminate between different motor tasks or their functional outcomes (Delis et al. 2013, 2018). Kim et al. (2016) proposed a form of stability-based criterion consisting of an analysis of the synergies extracted from several cycles (during walking). Because of their observation that at a certain (optimal) number the synergy structure became stable across cycles, they recommended to select the number of synergies according to which inter-cycle similarity is the highest. These methods are promising for solving the model selection problem and should be further investigated.

Previous studies also extracted the same number of synergies for all subjects based on results at the population level (Turpin et al. 2017; Maclellan et al. 2014; Gizzi et al. 2011; Lunardini et al. 2017). Knee points were often more clearly visible when the VAF curves were averaged across subjects (Gizzi et al. 2011; Hug et al. 2011). Additionally, there is evidence suggesting that the distribution of the number of synergies at the population level—notably when using the criterion  $\text{VAF} > 90\%$ —resembles a normal distribution with a clear mode (Roh et al. 2013; Shuman et al. 2019). These observations may justify using the same number for all participants. However, possible inter-individual differences would be lost.



**Fig. 6** Behavior when increasing the number of synergies. **a** Antero-posterior position of the left hand. The task consisted of punching toward a target with the left hand and to come back to the initial position (unpublished data). A set of 16 muscles from the right and left sides of the body were recorded over 10 repetitions of the task (see method in Supplemental Data). **b** VAF as a function of the number of synergies in the model for NNMF (in gray) and PCA (in black). A defined knee point is visible for PCA at  $N=5$ . VAF reached 90% at  $N=4$  for NMF and  $N=5$  for PCA. **c** VAF-slopes ( $\Delta VAF$ ). The slopes were computed as  $VAF(N+1) - VAF(N)$ . The horizontal lines represent 75% of the slope for shuffled data (Cheung et al. 2005), which is an almost constant value.  $\Delta VAF$  was lower than the threshold at  $N=4$  for NMF and  $N=5$  for PCA. **d**, **e** Synergy activation (**d**) and

synergy vectors (**e**) at  $N=4$  (colored data) and  $N=5$  (gray and black data) extracted with NNMF. Because of their similarity, the synergy vectors at  $N=5$  and  $N=4$  were superimposed for syn #2, #3 and #4 (in shaded gray). Increasing the number of synergies from 4 to 5, synergy #1 was further dissociated into syn #1 bis1 and syn #1 bis2. **f** Minimum correlation criterion. Mean correlations between the column of **C** (temporal component of EMG data, cf. Eq. 1) were plotted as a function of the number of synergies extracted for PCA and NMF. Arrows indicate the minima, which suggest the presence of only 4 distinct temporal components. *ProT* pronator teres, *BraR* brachioradialis, *BB* biceps brachii, *Tri* triceps brachii, *DeltA* deltoid, anterior part, *DeltP* deltoid, posterior part, *TraS* trapezius, superior part, *LD* latissimus dorsi

While the reviewed literature can be divided into studies focusing on temporal modules (Zelik et al. 2014) and those focusing on synergy vectors (Cheung et al. 2012; Ting and Macpherson 2005), the synergy extraction algorithms and methods used for model selection were often the same. In the following paragraph we show how ambiguity in the determination of the number of synergies might also result from an indifferenciation between the numbers of independent temporal patterns and synergy vectors.

In the data provided in Fig. 6 we found that 4 synergies were necessary to achieve a  $VAF > 90\%$  using NNMF, whereas the VAF curve crossed this threshold at  $N=5$  while using PCA. Using the thresholds determined by the evolution of VAF for unstructured data (Fig. 6c), these numbers were confirmed for each algorithm. Extracting 5 synergies instead of 4 led to the split of synergy #1 (panel E). The

resulting synergies possessed very similar activation profiles (panel D). We measured the mean correlations between the columns of **C** and plotted them as a function of the number of synergies. A clear minimum appeared at  $N=4$ , suggesting that only 4 distinct synergy activations underlain these data. However, the well-defined knee point on the VAF curve for PCA (Fig. 6b) also suggested that the data were composed of 5 synergies. PCA was obtained by an Eigen-decomposition of the covariance matrix of EMG data and, as in Fig. 3, this algorithm may be more efficient than NNMF for capturing correlations in the EMG amplitudes. This suggests that synergy #1 could actually be constituted of (at least) two (correlated) synergies. The point of this example is that the number of “minimally-correlated” activation coefficients is in principle less than the number of synergy vectors, as several synergies might be activated simultaneously (Fig. 3).



The first number is rather linked to the temporal structure, and the second to the spatial structure of the motor output. Previous studies used a notion of *fundamental synergies*—defined as synergies activated with a single peak during gait stride (Santuz et al. 2017)—to define the number of synergies. This approach may provide a less ambiguous way to define the number of components but, as explained above, the number of chosen components may depend on which aspect—spatial or temporal—the study is focusing on.

## Other identification methods

In this review we focused on techniques that analyze the amplitude of surface EMGs to identify regularities in spatial, temporal or spatio-temporal patterns of multiple muscle activation, with the basic assumption that the activations of muscles within a synergy co-vary in amplitude. In this context, matrix factorization became a standard technique, but other techniques can also be used to identify muscle synergies. For example, Drew et al. (2008) used a cluster analysis applied on the onsets and offsets of muscle activations to identify the groups of muscles that are activated together. Their identification technique was consistent with the phasic and sequential activity observed in pyramidal tract neurones recorded in cats during locomotion. Interestingly, the composition of synergies was quite close to what could be extracted using matrix factorization (Krouchev et al. 2006). However, this technique does not provide information about amplitude modulation of muscle activations within a synergy. Cross-correlation, mutual information or coherence analysis can also be used to identify information shared in the activity of pairs of muscles to regroup them into functional synergies (Del Vecchio et al. 2019; Kerkman et al. 2018; Holdefer and Miller 2002). Boonstra et al. (2015) presented an interesting work in which after they identified what they called a functional muscle network by analyzing the coherence between different pairs of muscles, they found that even right and left side muscles can belong to the same functional group (Kerkman et al. 2018). Coherence and spectral analysis is becoming more and more popular to identify muscle synergies, and researchers have suggested that these methods may separate purely functional synergies—in which muscles would simply show some correlated activities—from synergies in which muscles would genuinely share common inputs (Frere 2017; Bruton and O'Dwyer 2018; Del Vecchio et al. 2019). Coherence analysis seeks to identify how synaptic inputs to the motor neuron pools are shared between different muscles (Laine and Valero-Cuevas 2017; De Marchis et al. 2015; Charissou et al. 2017). Identification of these common inputs appears difficult using conventional surface electrodes, notably during movements

(Farina et al. 2014), and although they can be regrouped a posteriori, the analysis in itself is limited to the study of pairs of muscles. However, advances in technology, notably the use of matrix of electrodes (Farina et al. 2016), may facilitate such analysis in the future and provide new insights about the formation of muscle synergies.

## Conclusions

The goal of this review was to clarify selected aspects of the muscle synergy analysis methodology that may create potential confusions. Note that some results of this review are presented as supplemental material. The key points of this review can be summarized as follows.

In terms of algorithm, most matrix factorization algorithms that were used in the literature provided insightful results about the motor output structure and the omnipresence of the non-negative matrix factorization technique in the literature (> 60% of publications—Rabbi et al. 2020) might not be fully justified. PCA for example is efficient in describing the subspace in which the data lie (see Supplemental Material), but vector orientation is not robust across datasets. NNMf provides generalizable and interpretable (sparse and positive) components. However, NNMf is sensitive to the number of muscles included in the analysis as well as to the data range, and it generally possesses multiple solutions. We suggest that other algorithms besides NNMf might be better suited to study the temporal structure (e.g., ICA). The different models of synergy structure (spatial, temporal and spatio-temporal) provide different information and are also complementary with each other. The concurrent use of these different formulations should be encouraged in future studies. In terms of data analysis and acquisition, we showed that amplitude normalization has a major influence on synergy analysis outcomes. Previous studies showed that (1) strong smoothing of EMG envelopes is detrimental to the study of spatial structure, (2) experimental conditions should induce sufficient variability in the EMG amplitudes to properly explore the synergy subspace and robustly identify the spatial structure and (3) identification of the number of synergies should not be based solely on VAF-thresholds. The number of synergy vectors and the number of basic patterns (also called unit bursts or temporal primitives) are often combined in the analysis but may deserve separate determinations and descriptions. We suggest that the separation of these aspects in the analysis might make it less ambiguous to select the appropriate number of synergies.

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**Author contributions** All authors contributed equally to this work.

## Compliance with ethical standards

**Conflict of interest** The authors declare that they have no conflict of interest.

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