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A hybrid decomposition method to infer the sub-movements composition of planar reaching movements

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1. Introduction

In the last decade's research on human arm motor control has been object of great investigation, leading to some themes of high interest, like planning, execution and learning [1]. Movement of primates is the result of information processing in a complex hierarchy of motor centres within the nervous system and there are several studies which support the idea that reaching and pointing movements are accomplished by the combination of primitive elements, namely discrete motion units called sub-movements. The empirical evidences of the existence of discrete sub-movements which compose continuous human movement, prompted the scientists to characterize them.

Like primitives in natural languages for generating complex grammatic paradigms, these discrete blocks can be combined by the central nervous system to produce more complex motor behaviours. A precise and quantitative definition of such discrete blocks represents the major goal of motor control investigations, so providing the possibility to investigate the human movement at a profounder level than has been previously conceivable. Moreover, the sub movements analysis can be performed on the movements of patients recovering from a stroke.

However, since the precise sub-movement shapes are not known (e.g., the time profile of any measured variable such as velocity), the detailed decomposition for extracting them from continuous movements has not been until now appropriately defined. Without the precise sub-movement shapes, the decomposition problem is indeterminate [2,3]. Consequently, any of an infinite set of candidate sub-movement shapes could be combined to compose a continuous movement.

The difficulty of the overall decomposition models, which try to deduce the correct structure of the sub-movement shapes, arises from the redundancy of the human motor system as well as the redundant nature of movement tasks.

For example, even a simple reaching movement toward a target in the free space, taking the hand from the initial to the final position, can admit several possible solutions and consequently several possible trajectory and velocity profiles.

In mathematical parlance, this is an "ill-posed" problem in the sense that many solutions are possible.

This redundancy results from of the 7° of freedom (DOF) of the kinematic structure of the human arm, so exceeding the minimum necessary number (6 DOF) to move the hand in the three-dimensional space [4–6].

Because of the previous statement, sub-movement decomposition is a non-linear optimization problem: simultaneously maximizing goodness of fit and minimizing the number of sub-movements used, given a sub-movement shape, e.g. minimum-jerk or Gaussian and a summing modality, e.g. scalar summation, or vector summation. As a non-linear optimization problem, the sub-movement decomposition may have multiple local minima and the optimality of the solution for these methods depends heavily on the quality of the initial guess; unless the initial guess is about the global minimum, they will not find the best solution.

Both local and global optimization methods [7–10] have been proposed in the last decades in the attempt to correctly infer the sub-movements shapes. The first were based on the examination of the derivatives of the trajectory to identify local peaks; however, even with visually convincing results, these methods were sensitive to getting caught in local minima, so leading to spurious decompositions. Even in a simulated "test" case, where continuous movements were composed by known a-priori sub-movements, these methods were not able to reliably recover the underlying blocks.

The Brunch and Bound method, a global optimization method, proposed by Rohrer [11–13] avoids spurious decompositions, is robust to the assumed sub-movement shape and can correctly extract the sub-movement even in the presence of substantial measurement noise. However, the high computational "costs" of the Branch and Bound induced Roher to develop an alternative sub-movement extraction algorithm based on the notion of "scattershot" optimization. The latter represents a local optimization method and it "offers" all the above-mentioned limitations related to such methods. The results are "globally excellent" with a probability very close but not equal to 1.

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Moreover, this method needs to define the number of components should be established in advance. In this paper, taking cue on the minimum jerk theory (bell-shaped velocity profile), a hybrid decomposition method to extract the sub-movements shapes is proposed, which ensures a robust initial guess for a correct decomposition. This method has been tested for the decomposition of one hundred simulated velocity profiles.

2. Methods

Despite the several possible solutions when humans are required to reach a target in free space, each one produces movements with certain invariant kinematic properties, showing the peculiarity to select one path from the many available. Several works [14–16] have shown that unimpaired planar reaching movements (RMs), regardless of whether single-joint or multi-joint movements and without any overriding requirement such as maximum speed or precision, are characterized by a straight path of the hand movement in the Cartesian space and by the bell-shaped velocity profile. This behaviour produces smooth and accurate movements, in according with the minimum jerk theory [14], with the smoothness which is referred as the major goal underlying movement control.

Here, to extract sub-movements composition, we take cue on the above mentioned minimum jerk theory stating that the shape of the velocity profile of the hand, in point to point human arm movements, is bell-shaped. Taking inspiration from the Gaussian Mixture Model, the velocity profiles are modelled as Gaussian pulses of various lengths [17], being known that the graph of a Gaussian function is a characteristic symmetric "bell curve" shape. In mathematical terms, each deterministic velocity profile is expressed with the following expression:

$$y(x) = \sum_{i=1}^{M} \frac{\alpha_i}{\sqrt{2\pi\sigma_i^2}} exp\left[-\frac{(x-\mu_i)^2}{2\sigma_i^2}\right]$$

where αi is the amplitude of the basic function, μi and σi are respectively the mean and standard deviation of the Gaussian base functions, M is the number of pulses. The estimation of the parameters of such deterministic model is reached by means of a probabilistic approach, typically used for the mixture parameters, by first computing an estimate of the parameter and then refining the estimate by maximizing a likelihood function (maximum-likelihood estimation method, MLE). Basically, MLE involves estimating the parameters by maximizing the likelihood function, l(X; Φ), this being simply the joint probability of the observations xj regarded as a function of the parameters:

$$l(X;\ \Phi) = \prod_{j=1}^{N} f\left(x_j; \Phi\right)$$

where N is the number of observation points and f(xj; Φ) is a mixture of M normal density functions. It is known that the algorithm for computing maximum likelihood estimates in the normal mixture case is the EM algorithm, which has several good computational properties, including a low storage requirement and a low work cost per iteration. The EM algorithm iteratively generates, starting from some initial approximation Φ(r), a sequence Φ(r+1) of estimates. However, it is widely acknowledged that EM suffers from some issues. Firstly, typical implementations of Expectation Maximization require the user to specify the number of model components. This is critical because users do not generally know the correct number of components. This problem is particularly "felt" in the decomposition problem of the reaching movements, where is not known in advance.

Secondly the EM, being a local maximum seeker, when the likelihood function is unbounded (for instance in the case of heteroscedastic model), may converge to some singularities and this causes the failure of the optimization procedure. So, EM is not guaranteed to converge to the global maximum of the likelihood function but may instead converge to a local maximum. Therefore, different initial parameter values can lead to different model parameters and different model quality.

Trying to overcome these limitations, a constrained-EM (CEM) algorithm [17] was proposed by Chen. At first, CEM algorithm uses the scale-space filtering (SSF) approach [18] to detect the number of components M0 which probably compose the mixture. The procedures of initial estimation are summarized as follows: i) apply a Gaussian filter of standard deviation σf to smooth the input signal by convolution; ii) record the pairs (upper and lower) of turning points which are determined from the zero-crossings of the second derivative in the scale-space image (SSI). The number of components (M0) is determined by the number of pairs of turning points. Once determined the number M0 of components, the initial set of the parameters σ0, μ0, α0 of the mixture was made.

Then, the CEM model iteratively refine the initial estimate and reaches, starting from the initial estimate (σ0, μ0, α0), to the final estimates of the σ, μ, α parameters and of the final number M of the components (merging or deleting the components if they are too small). To increase the robustness of the final estimates, the algorithm imposes several condition and constraints in the Maximization (M) step and at the end of the convergence test, to limit the search space and excluding spurious maxima.

The above described procedure has been applied by Chen [17] to decompose the EMG linear envelope signal but here is readapted to the decomposition of RM and improved with appropriate adjustments.

In fact, the results of the algorithm proposed by Chen strongly depend to the initial estimates of the number components M0. Different σf values leads to different number components M0 for the same velocity profile to be decomposed.

Moreover, the SSF may converge to a spurious maximum and thus multiple solutions could present. This is a critical issue in the extraction of sub-movements in a velocity profile, where no reliable a priori information is not available about the number of sub-movements in each velocity profile of a reaching movement.

In the original SSF approach, the decision of the correct σf value, was arbitrary set starting from several randomly candidate values and depends on the specific application. An unreliable value for the σf leads to set too many or too few components producing an over-fitting or underfitting, respectively. Moreover, the estimate of the parameters σ0, μ0, α0 is not accurate.

In this work, the initial estimate of the number M0 components and the initial set of the parameters σ0, μ0, α0 are obtained reinforcing the SSF with the Smoothing and Differentiation Savitzky-Golay Filter (SGF), polynomial order N = 3, frame length = 19.

At first, the velocity profile is filtered with the SGF to find the pairs of zero-crossings of the second derivative. The number of pairs of zero-crossings defines an initial estimate of number of components M0, which probably compose the velocity profile.

Subsequently, a modified SSF is considered. A Gaussian Filter of standard deviation σf (starting from a value of 0.01) is applied to the velocity profile. Then, the σf value is iteratively increased, until the current M number of founding components defined on the SSI is equal to that defined (i.e., M0) with the Savitzky-Golay Filter (Fig. 1). When this condition is verified (M == M0), the Gaussian Filter Scale is set, the turning points are identified and the initial set and the proper temporal position of the parameters σ0, μ0, α0 is made. Finally, the parameters are refined by the CEM and the final estimates σi, μi, αi are obtained.

3. Results

The above-described method has been tested in terms of number submovements extracted one hundred velocity profiles simulated as normal mixture densities (Gmidstribution – Statistic Toolbox –Matlab R2014a), each consisting of different Gaussian components (blue and green shapes) which characteristics which are known beforehand. The simulated profiles have been generated considering the typical profiles exhibited by humans when performing a reaching task [10,14,16]. Taking inspiration from the several stereotypical patterns which