ORIGINAL PAPER

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Avoiding spurious submovement decompositions II: a scattershot algorithm

Abstract Evidence for the existence of discrete submovements underlying continuous human movement has motivated many attempts to "extract" them. Although they produce visually convincing results, all of the methodologies that have been employed are prone to produce spurious decompositions. In previous work, a branch-and-bound algorithm for submovement extraction, capable of global nonlinear minimization, and hence, capable of avoiding spurious decompositions, was presented [Rohrer and Hogan (Biol Cybern 39:190–199, 2003)]. Here, we present a scattershot-type global nonlinear minimization algorithm that requires approximately four orders of magnitude less time to compute. A sensitivity analysis reveals that the scattershot algorithm can reliably detect changes in submovement parameters over time, e.g., over the course of neuromotor recovery.

1 Introduction

During a kinematic analysis of stroke recovery, Krebs et al. (1999) observed a striking feature of the earliest movements made by recovering patients. These movements were

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"fragmented," and each of the fragments was highly stereotyped. The existence of these fragments, or *submovements* as they are called, has been supported by a wide range of studies over the past 100 years. The studies include observations of slow movements (Vallbo and Wessberg 1993), eye saccades (Collewijn et al. 1988), cyclical movements (Woodworth 1899; Crossman and Goodeve 1983; Doeringer 1999), ballistic movements (Morasso 1981), movements of developing infants (von Hofsten 1991), and movements requiring high accuracy (Milner 1992).

The goal of submovement extraction is to infer the submovement composition of a movement from kinematic data. In the tangential velocity domain, a submovement is represented as a unimodal, bell-shaped function. Determining the number, relative timing, and amplitude of submovements that most closely reproduce the original tangential velocity data is a global nonlinear optimization problem. In general, global nonlinear optimization problems are difficult to solve. Although several submovement extraction algorithms have been proposed previously (Morasso and Mussa-Ivaldi 1982; Flash and Henis 1991; Milner 1992; Berthier 1996; Lee et al. 1997; Burdet and Milner 1998), all of them are subject to finding local, rather than global, minima and to producing spurious decomposition results (Rohrer and Hogan 2003). Principal components analysis was evaluated for use in submovement extraction, as well, but was found to be inappropriate in that it extracted continuous time components that spanned the entire movement and that contained parts of several submovements. An algorithm guaranteed to find the global minimum in extraction was proposed in Rohrer and Hogan (2003). Due to the computational demands of that approach, we developed an alternative submovement extraction algorithm based on the notion of "scattershot" optimization, which is local optimization starting from a number of random initial conditions. The scattershot algorithm finds the globally optimal submovement composition probabilistically, i.e., the probability of finding the globally best fit can be made arbitrarily close to 1 by increasing the number of random starting points used in the optimization.

2 Method

2.1 Algorithm outline: multiple local minimizations from random initial conditions

Submovements were extracted from tangential velocity data using MATLAB's *fmincon* function initialized at ten randomly selected points in the solution space. The extracted submovement functions were support-bounded lognormal (LGNB) curves, a class of submovement shape proposed by Plamondon (1992) and found to fit point-to-point drawing movements better than 22 other candidate functions (Plamondon et al. 1993). An LGNB curve is defined as a function $B(t)$ such that:

$$B(t) = \frac{D(T_1 - T_0)}{\sigma\sqrt{2\pi}(t - T_0)(T_1 - t)}$$
$$\exp\left\{\left(\frac{-1}{2\sigma^2}\right)\left[\ln\left(\frac{t - T_0}{T_1 - t}\right) - \mu\right]^2\right\} \quad (1)$$

for $T_0 \leq t \leq T_1$, where D is the displacement resulting from the movement, T_0 is the movement start time, T_1 is the end time, μ controls the skewness (asymmetry), and σ determines the kurtosis ("fatness") of the curve. The five independent parameters that define LGNB submovements allow them to take on a wide range of submovement-like shapes. In this study, submovements were allowed to take on a duration between 167 and 1500 ms. Submovements were not fit one at a time, as in a "greedy" algorithm. Instead, all the parameters of all the submovements were optimized simultaneously. An increasing number of submovements were fit to each movement until the "fit error," $\mathcal{E}$, fell below a predetermined threshold, which in this case was 2%. The fit error is defined as follows:

$$\mathcal{E} = \frac{\int |F(t) - G(t)|\mathrm{d}t}{\int |G(t)|\mathrm{d}t}, \quad (2)$$

where $G(t)$ is the movement speed profile, and $F(t)$ is the extracted speed profile. Figure 1 shows an example of successfully extracted submovements.

The scattershot algorithm is probabilistic in nature, i.e., the results are globally optimal with some probability close but not equal to unity. As a result, the actual submovement characteristics extracted for a given submovement may not be optimal. In other words, the extracted submovements cannot be guaranteed to be the best fit for that movement in a global sense. However, we will show that the data in a study

Fig. 1 Typical movements (*bold lines*) and their extracted submovements (*fine lines*) from the first and last days of therapy for a stroke patient

involving 479 movements of two stroke patients allow strong statistical statements to be made. Even if the results of any given extraction may be uncertain, the trends observed reach statistical significance.

2.2 Algorithm validation data: movements of stroke patients

The movements of two subjects were used to test the algorithm's performance. One subject was an acute-stage inpatient who had suffered his first unilateral infarct less than 1 month before beginning the study. The other subject was a chronic-stage outpatient 30 months post-stroke. Full details of the study protocol can be found in Rohrer et al. (2002). In brief, the planar-reaching movements of these two subjects were measured in eight directions several times a week over the course of several weeks.

Five characteristics of the submovements are summarized in the result plots. Each submovement is characterized individually by its (1) duration and (2) peak speed. The relative and collective characteristics of the submovements are represented by (3) the number of submovements in the entire movement, (4) the interpeak interval (interval between peaks of consecutive submovements, see Fig. 2a), and (5) the overlap (interval between initiation of a submovement and termination of the previous one, see Fig. 2a).

2.3 Algorithm validation method: sensitivity analysis

The scattershot extraction algorithm is not guaranteed to produce an optimal result. In fact, given the high dimensionality of the solution space (as high as 50 in the data we observed), the probability that the algorithm found the optimal solution in more than a few cases is negligible. To test how closely the extracted submovements can be expected to represent the actual (hypothesized) underlying submovements, a sensitivity analysis was performed. This analysis also tests whether the submovement characteristics were influenced by changes in the decomposition conditions. The submovements were extracted while both the submovement shape and the bounds on submovement duration were varied.

The sensitivity analysis was performed on data derived from the movements of two actual patients, subjects 203 and 708, who were representative of qualitatively different levels of motor recovery. The data set was generated by taking the original patient data for a given movement, extracting its submovements with the scattershot algorithm, and then summing the extracted submovements to create new movement data. These new data were similar to the original data (within a modest error), but different in that the new data could be perfectly fit by a small, known set of submovements. The resulting data were biologically plausible and had a known submovement composition; hereafter these are referred to as "actual" submovements. Using these data, we addressed the question: if a set of movements is composed of submovements, the characteristics of which change over time, can
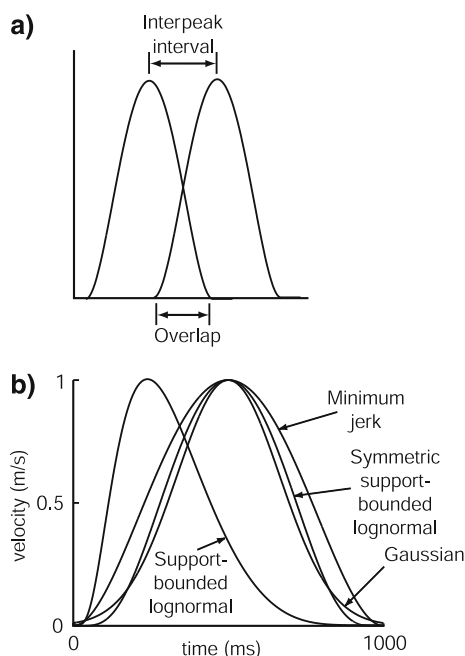
Fig. 2 a Definitions of interpeak interval and submovement overlap. Note that due to the nature of the overlap measure, overlap can be negative, indicating a period of no activity between submovements. **b** The four submovement shapes used in decompositions. In each case, the peak height is 1, the peak is centered at 500 ms, and the nominal duration is 1,000 ms. The symmetric LGNB curve has $\mu = 0$ and $\sigma = 0.7$. The asymmetric LGNB curve has $\mu = -0.9$ and $\sigma = 0.7$. Using six σ as the duration for the Gaussian curve allows it to closely overlay the others

those changes be reliably detected by the scattershot algorithm despite variations in the conditions of the extraction algorithm?

Submovements were extracted from the data set under five conditions:

(1) *LGNB submovements* Submovements were extracted under the same conditions as the original decomposition: support-bounded LGNB submovements with a maximum duration of 1.5 s and a fit error threshold of 2%. This decomposition was a check that the extraction algorithm was well behaved. One would expect the algorithm to produce results that are similar to the original, although not identical, as the algorithm had a 2% margin of error in which to differ.

In addition to LGNB submovements, several other submovement shapes were tested in decomposition. In each case, the fit error threshold was 2%, and the maximum duration was 1.5 s. These decompositions quantify the effect of submovement shape on the characteristics of the extracted submovements. See Fig. 2b for an illustration of each of the submovement shapes used.

(2) *Symmetric LGNB submovements* In this case, LGNB submovements were constrained to be symmetric and have a fixed kurtosis (see Fig. 2b).

(3) *Gaussian submovements* Gaussian submovements (see Fig. 2b) were among the first used in mathematical

descriptions of submovements (Crossman and Goodeve 1983). For analysis purposes, the duration was defined to be $\pm 3\sigma$, although the tails of the Gaussian curve were not truncated during extraction.

(4) *Minimum-jerk* Minimum-jerk functions (see Fig. 2b) are the most commonly used in submovement analyses. These functions have been shown to fit reaching movement speed profiles to within a few percent (Hogan 1984) and are inexpensive to compute.

(5) and (6) *LGNB submovements with varying durations (0.833 and 2.5 s)* The duration of the actual submovements that may compose a given submovement is unknown, yet the submovement extraction algorithm employed requires that an upper bound be placed on the duration of extracted submovements. Based on previous studies of arm movements that cite typical ballistic movement durations of less than 1 s, 1.5 s was chosen as a reasonable upper bound. However, the submovements generated during decomposition of the patient data showed that a significant fraction of submovements has the maximum permissible duration, 1.5 s. This suggests that an upper bound on submovement duration of 1.5 s may have been too low. Two sets of decompositions were performed with LGNB submovements, a fit error threshold of 2%, and maximum durations of 0.833 and 2.5 s. Decomposing the data using various submovement durations served to quantify the effect of selecting a maximum duration that was not well matched to the duration of the submovements underlying the data.

3 Results

3.1 Solution-finding performance

The decompositions performed in the sensitivity analysis produced submovement characteristic distributions that varied over time. The complete results are summarized in Fig. 3. Each of the submovement characteristics showed a wide range of variability, depending upon the conditions under which the characteristics were extracted (as great as a factor of 2 in the case of duration), and this dependence was structured. The effects of submovement shape and maximum duration of extracted submovements are considered separately.

3.2 Sensitivity of decompositions to submovement shape

In addition to extracting LGNB submovements, symmetric LGNB, Gaussian, and minimum-jerk submovements were extracted as well (columns 2–5 of the plots in Fig. 3). Of the four submovement shapes, only LGNB was capable of taking on asymmetric shapes. The similarity of the other three shapes (see Fig. 2b) led them to be very similar in all five submovement characteristics. LGNB's ability to take on a wider range of shapes than the other functions accounts for the slightly lower number of LGNB submovements extracted,
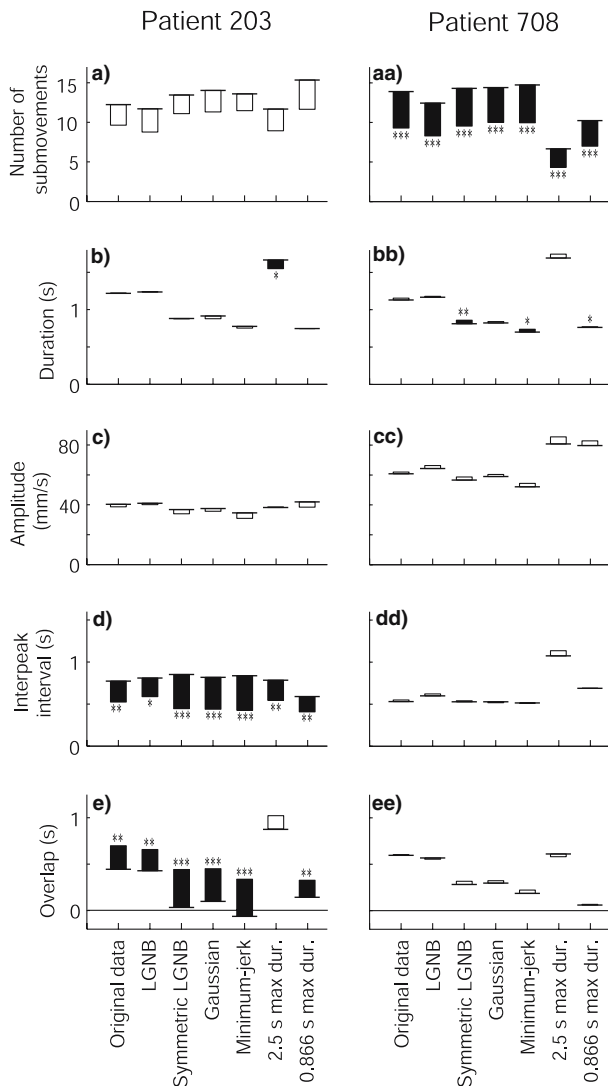
Patient 203 Patient 708

Fig. 3 Sensitivity analysis of submovement extraction to algorithm conditions: submovement shape and maximum duration. Data are based on the movements of patients 203 and 708. The initial value is represented by the horizontal bar. For statistically significant changes ($p < 0.05$), the box is *filled*; otherwise, it is left *hollow*. The level of significance is further indicated by *asterisks*: $*0.01 < p < 0.05$, $**0.001 < p < 0.01$, $***p < 0.001$

~ 12 versus ~ 14 (see Fig. 3, panels a and aa). Also, when the LGNB becomes markedly asymmetric, it develops long "tails," which account for its greater duration (panels b and bb) and overlap (panels e and ee).

3.3 Sensitivity of decompositions to duration constraints

The characteristics of the extracted submovements follow a clear pattern in both sets of test data (see columns 6 and 7 of the plots in Fig. 3). As expected, typical submovement duration is much longer in the 2.5 s case than in the 0.866 s case (see panels b and bb). Also, fewer submovements are extracted in the 2.5 s case (panels a and aa), presumably

because longer submovements can capture a greater portion of the data. Fewer submovements in a given movement imply a greater interpeak interval, which is also observed (panels d and dd). Overlap tends to be greater with longer submovements as well (panels e and ee). Amplitude appears not to be strongly affected, at least in the case of these data.

3.4 *Changes* in submovement characteristics consistent between decomposition conditions

The most notable result of the sensitivity analysis is that the *direction* of submovement changes over the course of therapy is robust to decomposition conditions. In every case where a submovement characteristic changed appreciably, say greater than 15% of the range, under at least one set of conditions, the sign of the change for that characteristic was consistent for every other set of conditions.

Furthermore, the *statistical significance* of the characteristic changes is robust to details of the extraction algorithm's parameters. Significant changes in a submovement characteristic under one set of test conditions was a strong indicator that other conditions would also yield significant changes (see panels aa, d, and e). Not only does the direction of change tend to be preserved across test conditions, but the statistical strength tends to be preserved as well.

Correlation coefficients were calculated for actual submovement characteristics with those of submovements extracted during the sensitivity analysis. The results are shown in Table 1. The most apparent pattern is that submovement characteristics associated with the peak of the submovement (amplitude, inter-peak interval, and indirectly the number of submovements) are consistently significant, while characteristics that are highly sensitive to the nature of the tails (duration and overlap) show less consistent correlation. This may be due to the fact that the extraction process is far more sensitive to the "hump" of the submovement speed profiles than to the tails, and hence can introduce large variability in the tails without degrading the quality of the extraction. Note that, despite weak correlation in the day-to-day values of overlap in Patient 203, the various extraction conditions maintained a remarkable consistency in reporting the overall trend (see Fig. 3e).

The sensitivity analysis indicates that, although the scattershot algorithm cannot promise that the submovements resulting from extraction necessarily represent those originally used to construct the movement, the algorithm can provide a probable range for the submovement characteristics. The key result of the analysis is that, despite uncertainties, the scattershot algorithm can reliably detect the direction and significance of changes in submovement characteristics.

3.5 Required computing power

While both the scattershot algorithm and the branch and bound algorithm avoid the pitfalls associated with getting trapped in local minima, they differ greatly in the amount

Table 1 Correlation (Pearson's *r*) of actual submovement characteristics with those extracted during the sensitivity analysis. Submovement characteristics were averaged over each therapy day. Bold numbers are significantly non-zero with a confidence interval of 95%.

Extraction condition	Number of submovements	Duration	Amplitude	Interpeak interval	Overlap
Patient 203					
LGNB	**0.89**	**0.51**	**0.92**	**0.95**	**0.94**
Symmetric LGNB	**0.89**	**0.65**	**0.97**	**0.89**	0.28
Gaussian	**0.94**	**0.54**	**0.98**	**0.88**	−0.23
Minimum Jerk	**0.89**	**0.61**	**0.97**	**0.88**	−0.01
2.5 s max. duration	**0.94**	0.32	**0.98**	**0.96**	**0.70**
0.866 s max. duration	**0.92**	−0.27	**0.98**	**0.92**	**0.79**
Patient 708					
LGNB	**0.91**	0.42	**0.95**	**0.81**	0.12
Symmetric LGNB	**0.91**	**0.67**	**0.94**	**0.82**	0.30
Gaussian	**0.91**	**0.70**	**0.95**	**0.86**	0.09
Minimum Jerk	**0.91**	**0.73**	**0.92**	**0.86**	0.16
2.5 s max. duration	**0.91**	**0.81**	**0.90**	**0.76**	0.27
0.866 s max. duration	**0.93**	0.30	**0.93**	**0.67**	**0.58**

of computation they demand. In a set of comparison tests on a Pentium IV 3.2 GHz processor, both algorithms fit a single minimum-jerk submovement in approximately 1.5 s. However, their performance differed dramatically when fitting more than one submovement (see Fig. 4). When fitting three submovements, the computation time was over four orders of magnitude lower in the scattershot algorithm, despite the fact that it makes ten separate attempts at the decomposition during each fit. Computation time grew polynomially in the scattershot algorithm and exponentially in the branch and bound algorithm, further increasing the time advantage of the scattershot algorithm with larger numbers of submovements.
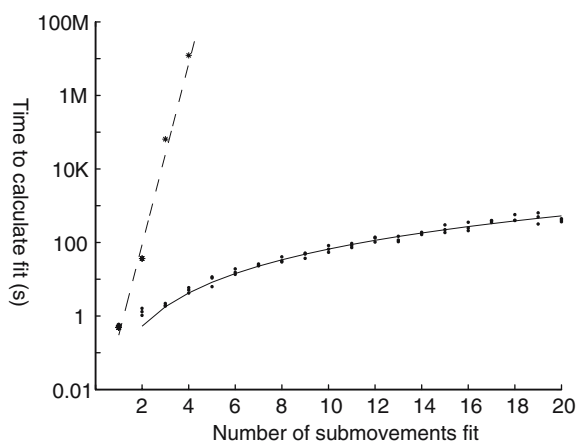

Fig. 4 Times required to extract minimum-jerk submovements using the scattershot algorithm (●) are described by a least-squares third-order polynomial fit (*solid line*). Times required to extract minimum-jerk submovements using the branch and bound algorithm (∗) are described by a least-squares exponential fit (*dotted line*). The highest point on the plot (over 10 Ms) was extrapolated; the fit calculation was halted after searching 9% of the solution space in 13 days.

4 Discussion

The scattershot algorithm described here can extract submovements whose characteristics are probabilistically related to actual submovements underlying kinematic data. The statistical analysis presented to demonstrate this utilizes data from only two patients, and hence this paper does not claim to reach any clinical conclusions. However, the 470 reaching movements analyzed, containing approximately 5,000 submovements, provides an ample data set from which to derive statistically significant results. The scattershot method, unlike previously proposed methods, seeks a globally optimal solution and is not susceptible to getting caught in local minima. As such, it has the potential to reliably find higher-quality and more biologically meaningful solutions.

The chief result presented here is that *changes* in the characteristics of extracted submovements are statistically reliable, and remain consistent across a wide range of extraction conditions. In particular, those characteristics associated with the peak of the submovement, rather than the tails, were shown to correlate well with the characteristics of the original submovements. This was shown to be true even with a small number (ten) of random initial conditions. The primary strength of the scattershot algorithm is that it does not rely on an operator's subjective judgment when performing submovements' extractions. It is fully automated in this sense, and it does not require the interaction of the researcher, except to establish the parameters of extraction.

Despite high-dimensional solution spaces (as high as 50), the proposed scattershot algorithm performed well using only ten sets of random initial conditions. In fact, during initial testing of the algorithm in decomposing constructed speed profiles, it was discovered that it typically finds the globally optimal solution two to four times out of ten. This may be due in part to the highly redundant nature of the submovement extraction solution space. Submovement order does not matter, so necessarily there exist multiple solutions that

are equivalent: $n!$, where n is the number of submovements being extracted. When attempting to extract ten submovements (from a 50 ($5n$)-dimensional solution space), this results in 3.63 million redundant "optimal" solutions, each of which is equally correct.

With this scattershot algorithm, it will be possible to meaningfully analyze the submovements composition of kinematic data produced during movement. Such an analysis has been performed on the movements of patients recovering from a stroke (Rohrer et al. 2004), and results indicate that submovement extractions provide a fine-resolution measure of motor recovery. The scattershot algorithm can be an effective tool for bringing to light subtleties of the human motor control system.

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