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International Journal of Industrial Ergonomics 25 (1999) 19–28

International Journal of
Industrial Ergonomics

www.elsevier.nl/locate/ergon

Automated job analysis using upper extremity biomechanical data and template matching

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Received 20 April 1998; received in revised form 1 August 1998; accepted 4 August 1998

Abstract

Spectral analysis of upper limb kinematic measurements has been previously demonstrated useful for quantifying physical stress in repetitive motion tasks. The method requires manually separating the data into segments corresponding to individual tasks or work elements, computing power spectra, and averaging. This study investigated using signal pattern recognition to help further automate the analysis by separating the data through identification of stereotypical patterns for cyclical tasks. Joint angles for five industrial jobs were continuously measured using electrogoniometers attached to the wrist, elbow and shoulder of the dominant limb. A multimedia computer system enabled the analyst to review the videotape and interactively indicate element breakpoints. The breakpoints were also automatically identified using a template matching (TM) algorithm. The algorithm identified the cycle terminal points within 0.997 s (S.D. = 2.762 s) of the human analyst's reference breakpoint. Analysis using TM breakpoint identification resulted in average differences in the spectra of 9.3° for RMS joint deviation, 14.1° for mean joint angle, and 0.445 Hz for repetition frequency. This study concludes that signal pattern recognition had potential applications in automated job analysis. The current implementation could be useful for indicating approximate breakpoints, and interactively fine-tuning the breakpoint selection as a means for reducing the time required to perform an analysis.

Relevance to industry

Job analysis involving large quantities of upper limb biomechanical data can be tedious and prohibitively time-consuming. Automated computerized methods can help make these analyses more practical for use in industry. The current algorithm and implementation can be used as an interactive assistive tool to help reduce the time to do an analysis, and may lead to better automated analysis methods.

1. Introduction

Radwin and Lin (1993) demonstrated the use of spectral analysis for quantifying repetitiveness, postural deviation, and sustained posture for repetitive manual tasks. The magnitude of the spectral components indicated postural deviation, and frequency corresponded to repetition rate. Yen (1997) showed that this method was applicable for a variety of repetitive industrial jobs. It was considered efficient because it could directly measure magnitude, repetition and duration for

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0169-8141/99/$ - see front matter
PII: S0169-8141(98)00073-0

large quantities of biomechanical data. The method, however, was not completely automatic since it required manually separating the time domain biomechanical data into segments corresponding to individual tasks or work elements before producing spectra (Radwin et al., 1994).

A multimedia computer-controlled video analysis system was has been developed (Radwin and Yen, 1993; Yen and Radwin, 1995) for interactively identifying movements and exertions associated with specific task elements from videotape records. The work element breakpoints are used for parsing the biomechanical data into specific tasks and elements for spectral analysis, and for computing the duration that specific exertions and motions are performed. Although the multimedia system facilitates the process (Yen, 1997), considerable human analyst time is needed to prepare the data for analysis. The current study investigates if a signal pattern recognition algorithm may be used to identify specific movement patterns for automatically determining cycle breakpoints.

Signal and pattern recognition techniques are commonly used for determining specific features of biomedical signals such as detection of the QRS complex in electrocardiograms (Furno and Tompkins, 1983; Ahlstrom and Tompkins, 1985; Pan and Tompkins, 1985; Silka et al., 1992; Chow et al., 1992; Reddy et al., 1992; Laguna et al., 1992). These methods include (1) linear digital filtering, (2) nonlinear transformations, (3) template matching, and (4) artificial neural networks. The accuracy and reliability of these methods for signal detection depends not only on the specific method, but also on the particular input signal.

A common pattern recognition technique is template matching (Silka et al., 1992). A template of a waveform with the desired pattern is first obtained, usually from a previously determined average waveform, and compared to against the test signal on a point-by-point basis using correlation. Although the method can be very accurate, the intensive calculations often prevent real-time implementation unless the computer is very fast.

This paper will demonstrates the feasibility of using a template matching technique to automatically identify the cycle breakpoints in repetitive manual tasks. The breakpoints identified by the template matching algorithm using biomechanical data were compared with those determined by a human analyst using observation for five industrial jobs. The effectiveness of the template matching technique in terms for accuracy and speed was determined.

2. Methods

2.1. Biomechanical data acquisition procedures

Upper extremity joint motion was measured using strain gage electrogoniometers (Penny and Giles) attached to the wrist, elbow and shoulder of the dominant limb of each operator. The goniometers were affixed across the joints using double-sided adhesive and surgical tape. The measurements included wrist flexion/extension, and ulnar/radial deviation, elbow flexion/extension, shoulder flexion/extension, and shoulder adduction/abduction. By individually calibrating each of the joints within the range of motion for each task, less than 5% error was obtained for the wrist and elbow joints, and 10% error was obtained for the shoulder.

A video-based data acquisition system recorded and synchronized the biomechanical data associated with work activities in relation to the video information (Radwin and Yen, 1993; Yen and Radwin, 1995). Analog signals from the electrogoniometers were sampled at 60 points/s, digitized to 8-bit resolution, encoded, and recorded directly on the audio track of VHS tape along with the video image. This system enabled the computer to extract the biomechanical data in synchronization with the video record. As the joint angle data was sampled, video cameras simultaneously recorded the operators from two camera viewpoints and the video was mixed into a split screen image.

A multimedia video analysis system (Radwin and Yen, 1993; Yen and Radwin, 1995) provided the platform on which the manual breakpoint identification was implemented. A computer-controlled VCR enabled the analyst to interactively review a tape of work activities at any desired speed or arbitrary sequence (real-time, slow motion, fast

Table 1
Description of the jobs studied

Job name	Job description	Tape duration (min)	Total breakpoints processed
(1) Product packaging	Pick up product off conveyor and stack in a box. The box was angled so the open end faces the worker. The worker was either seated or standing.	8.12	367
(2) Parts counting and sorting	Count six parts and slide into bins on conveyor for packaging.	8.49	201
(3) Large parts hanging	Pick up parts from a bin and hang on hooks located at two different heights traveling on a vertical conveyor system. The worker was standing facing the parts bin and conveyor.	12.55	346
(4) Small parts hanging	Pick up parts from a tray and hang on hooks located at three different heights traveling on a vertical conveyor system. The worker was seated facing the parts tray and conveyor.	14.47	260
(5) Press operation	Pick up part in one hand and transfer it to a tool in the other hand. Transfer the part to a press fixture. Activate press by depressing buttons with both hands.	42.38	364

motion, or frame-by-frame in either forward or reverse direction).

Each cycle is comprised of a set of repetitive joint movements for a single unit of work. Cycle breakpoints are visually discernible actions that indicate the start of a cycle. Breakpoints for each cycle were assigned to the set of distinctive motions observed in the video for the respective joint. A computer program maintained a table of video time codes corresponding to the cycle breakpoints.

Five industrial jobs were studied. All of the jobs were considered highly repetitive. The same analyst assigned all of the cycle breakpoints for all five jobs. These jobs are described in Table 1. Conventional time study mean cycle times and percent accuracy for a 95% confidence interval are shown in Table 2.

Table 2
Mean and standard deviation breakpoint interval and percent accuracy for jobs analyzed

Job	Mean breakpoint interval (± 1 S.D.) (s)	Accuracy[a] (%)
(1) Product packaging	1.33 (0.53)	4.3
(2) Parts counting and sorting	1.82 (0.88)	7.1
(3) Large parts hanging	2.15 (0.64)	4.7
(4) Small parts hanging	2.28 (0.47)	4.4
(5) Press operation	5.29 (1.02)	2.5

[a]95% confidence interval.

2.2. Template matching algorithm

Representative template waveforms (T) were selected based on visually discernible actions in a cycle. The template arrays (T_j) were extracted from the biomechanical data for each joint j corresponding to the joint motions for the entire cycle as defined by the breakpoints. The template set

$$T = \{T_1, T_2, T_3, \ldots, T_J\}$$

for each joint template T_j is defined as an array containing M data points.

$$T_j(m) = \{T_j(1), T_j(2), T_j(3), \ldots, T_j(M)\}.$$

The joint kinematic waveform W for joint j is an array of N points which contains the biomechanical data to be analyzed. The joint waveforms are processed in sets of M points (same as the template) at each incremental time t such that:

$$W_j(t) = \{W_j(t), W_j(t+1), W_j(t+2), \ldots, W_j(t+(M-1))\}.$$

A flow chart for the template matching algorithm is shown in Fig. 1. The algorithm starts by performing point-to-point correlation ($R_{TWj}(t)$) between the template (T) and the kinematics data (W) for each joint j. The correlation value ($R_{TWj}(t)$) is computed for each joint at each point in time for $1 \leqslant j \leqslant J$, where J is the number of joints.

The individual joint correlation values are multiplied by a constant weighting coefficient (w_j) for each joint and averaged to determine the mean correlation value ($\bar{R}_{TW}(t)$) for that point in time.

$$\bar{R}_{TW}(t) = \frac{1}{J}\sum_{j=1}^{J} W_j\, R_{TWj}(t).$$

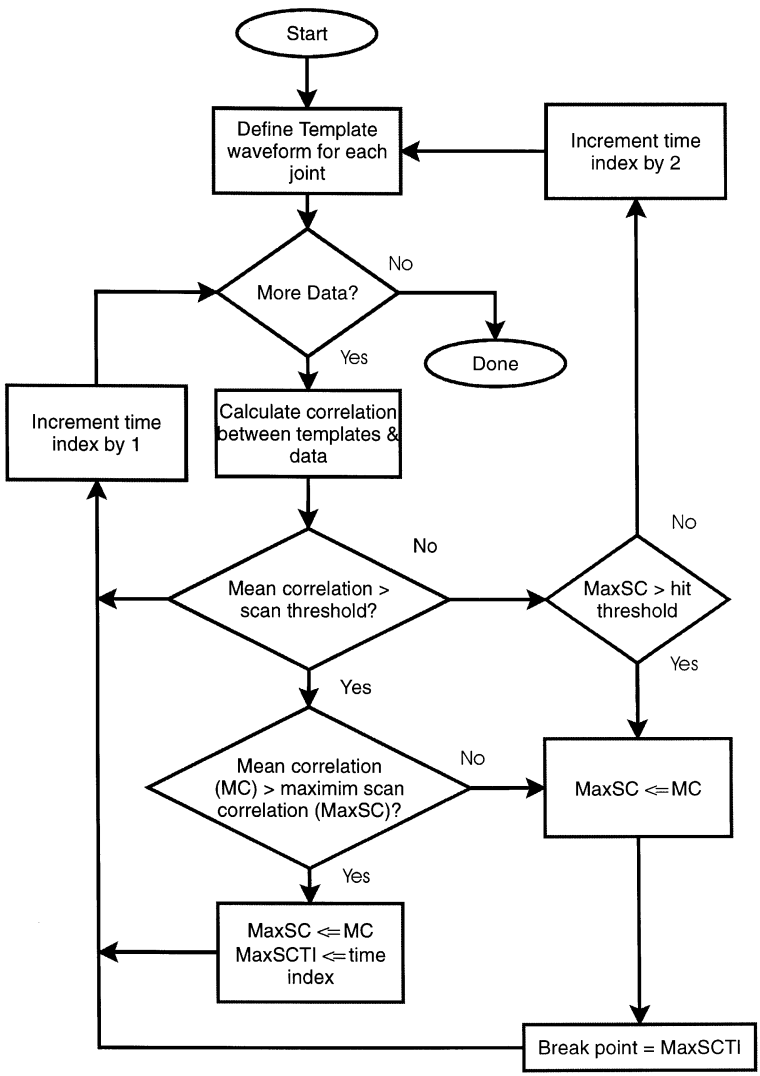

Fig. 1. Flow chart diagram of template matching algorithm.

The weighing coefficients are determined by the importance of the joint motion relative to the overall motion. The importance of each individual joint motion depends on the specific actions contained in the job and is arbitrary determined. The joint weighting coefficients for all jobs in the current study were set to a value of 1 for equal importance.

The kinematic data was processed in data segments, the scan array (S) which is defined by the scan threshold. A segment is defined by a consecutive sequence of mean correlation values greater than the scan threshold producing a scan array (S) containing K points (see Fig. 2). The scan array records the mean correlation values ($\bar{R}_{TW}(t)$) for the associated time index t such that

$$S(k) = \{S_1, S_2, S_3, \ldots, S_K\},$$

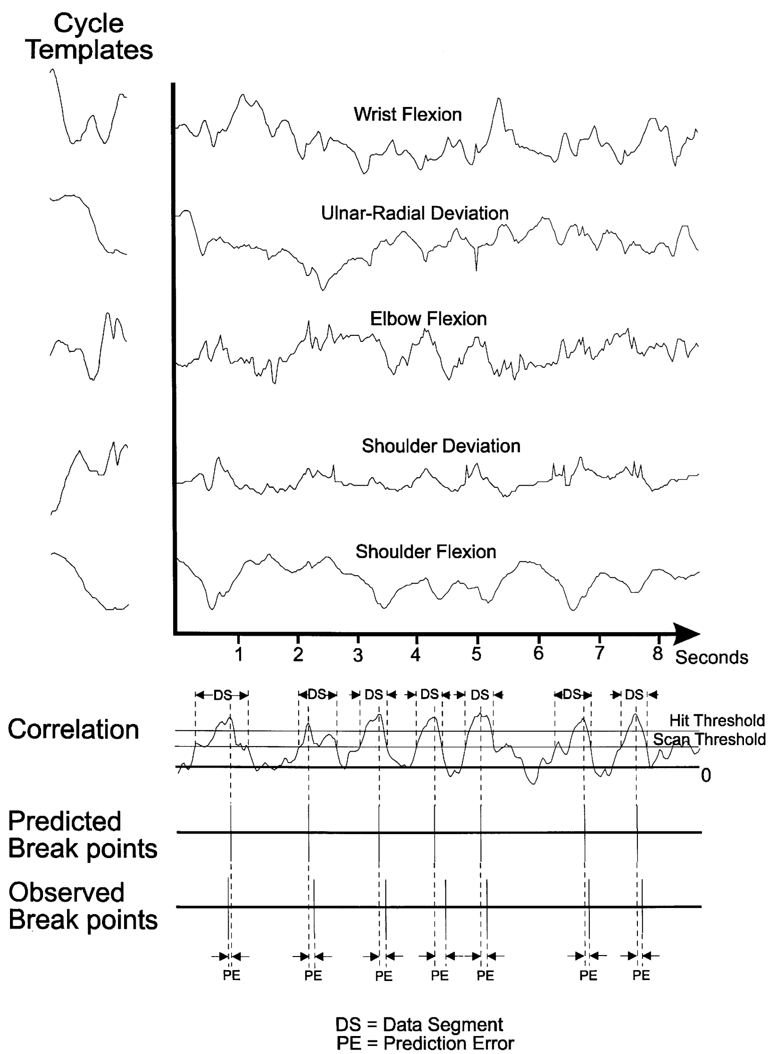

Fig. 2. Template matching algorithm with observed and predicted breakpoints. The templates are from the joint motions for the entire cycle. The templates are swept point by point to produce a mean correlation from the individual joint correlations. The maximum mean correlation that exceeds the hit threshold indicates the time for the predicted breakpoint. The prediction error is the difference between the predicted and observed breakpoint.

where

$$S_k \leftarrow \bar{R}_{TW}(t) \Leftrightarrow \begin{cases} S_k^1 \leftarrow \bar{R}_{TW}(t), \\ S_k^2 \leftarrow t, \end{cases}$$

if $\bar{R}_{TW}(t) > Scan\ Threshold$ then $S_k \leftarrow \bar{R}_{TW}(t)$.

If the maximum mean correlation in the scan array $S(k)$ exceeded the hit threshold, the predicted cycle breakpoint is the time t associated with it:

if $\mathrm{Max}(S_k^1) > Hit\ threshold$ then

$Predicted\ breakpoint = \text{time } t \leftarrow S_k^2$.

A scan threshold of 0.2 and a hit threshold of 0.3 were arbitrarily selected.

The prediction error (in seconds) was the mean difference between the predicted breakpoint and the observed breakpoints determined by the human analyst (see Fig. 2, bottom). The templates were then shifted one sample time unit ($t \leftarrow t + 1$) and then another set of correlations was computed, repeating the process until the templates were scanned across all the entire biomechanical data record.

2.3. Experimental procedures

The template matching algorithm was executed on a Pentium™ microcomputer with a 90 MHz CPU, 24 MB of RAM, using the Windows 95™ operating system and written in object Pascal using the Borland Delphi programming environment. The pattern recognition algorithm was applied to the individual wrist (W), elbow (E) and shoulder (S) joints biomechanical data and their combinations (WE, WS, ES, WES). The TM breakpoints were compared to the reference breakpoints determined by the human analyst.

3. Results

The mean difference between the cycle breakpoints determined by the TM algorithm and human analyst, and the standard error of the mean for different combinations of joint motions are shown in Table 3. Histograms of the mean differences are shown in Figs. 3–8. A small negative skew was observed in the distributions for the parts counting and sorting job, the small parts hanging job, and the press operation. Two-way analysis of variance using all jobs revealed statistically significant differences between the algorithm error for jobs ($F(4,10742) = 153.00$, $p < 0.05$) and joint combinations ($F(6,10742) = 8.22$, $p < 0.05$). Statistical significance was also observed for the job × joint interaction ($F(14,10742) = 9.20$, $p < 0.05$).

Table 3
Mean difference (s) and standard error between predicted and reference breakpoints for five jobs using different combinations of biomechanical data

	Joints (W: Wrist Joint, E: Elbow Joint, S: Shoulder Joint)						
Job	W	E	S	WE	WS	ES	WES
1	– 0.29	– 0.36	– 0.18	– 0.28	– 0.15	– 0.21	– 0.13
	(0.02)	(0.02)	(0.03)	(0.03)	(0.03)	(0.04)	(0.04)
2	– 2.55	– 2.29	– 2.33	– 1.78	– 2.26	– 1.66	– 1.70
	(0.20)	(0.19)	(0.18)	(0.19)	(0.22)	(0.18)	(0.21)
3	– 0.54	0.01	– 0.11	– 0.09	– 0.05	0.10	– 0.02
	(0.04)	(0.04)	(0.04)	(0.05)	(0.05)	(0.03)	(0.05)
4	– 2.68	–	–	–	–	–	–
	(0.14)						
5	– 2.08	– 4.19	–	0.97			
	(0.34)	(0.34)		(0.29)			
Mean	– 1.87	– 2.05	– 1.00	– 0.8	– 0.86	– 0.65	– 0.65
(S.D.)	(4.69)	(5.99)	(2.76)	(3.70)	(2.72)	(2.18)	(2.28)

Note: –, Not Available.

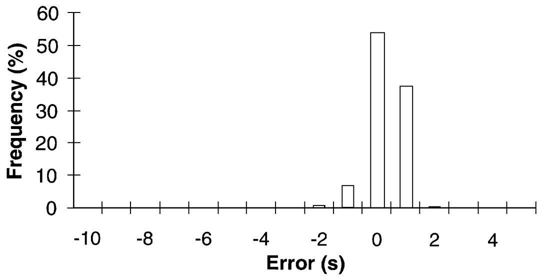

Fig. 3. Histogram of mean error (s) between predicted and reference breakpoints for the product packaging job.

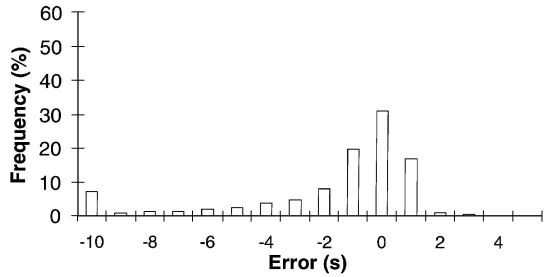

Fig. 6. Histogram of mean error (s) between predicted and reference breakpoints for the small parts hanging job.

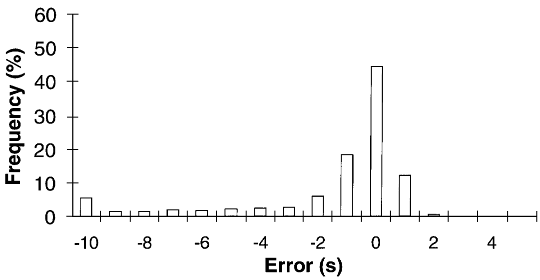

Fig. 4. Histogram of mean error (s) between predicted and reference breakpoints for the parts counting and sorting job.

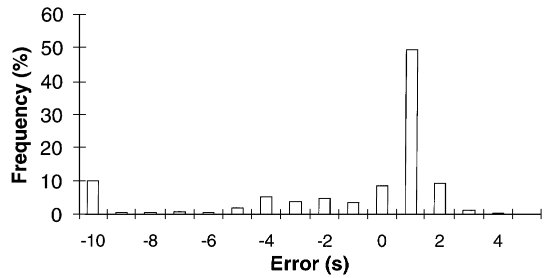

Fig. 7. Histogram of mean error (s) between predicted and reference breakpoints for the press operation.

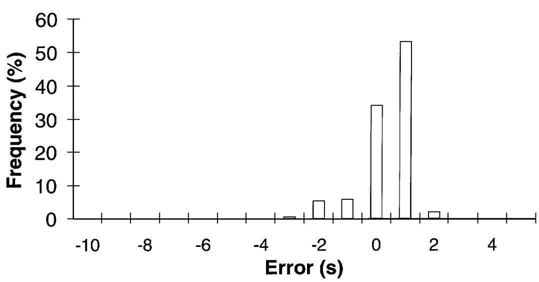

Fig. 5. Histogram of mean error (s) between predicted and reference breakpoints for the large parts hanging job.

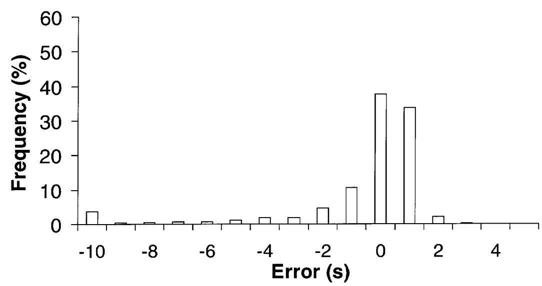

Fig. 8. Histogram of mean error (s) between predicted and reference breakpoints for all jobs.

When averaged across jobs, multiple joint combinations produced less error than single joints ($F(6,10760) = 33.44$, $p < 0.05$) but the individual shoulder joint produced error similar to multiple joints. The least error was observed when all available biomechanical data was used (wrist/elbow/shoulder). The error for individual wrist and elbow joints were significantly difference ($p < 0.05$) for the Tukey's pairwise comparison between all remaining joint combinations (shoulder, wrist/elbow, wrist/shoulder, elbow/shoulder, and wrist/elbow/shoulder).

The main purpose for executing the TM algorithm is to extract data for spectral analysis. The differences in RMS joint deviation, average joint angle, and repetition frequency obtained using spectral analysis for the human observer and the TM algorithm extracted data are shown in Table 4.

Table 4
Mean difference (and standard deviation) between spectral results for automated and reference breakpoints for five job average using different combinations of biomechanical data

	Joints (W: Wrist Joint, E: Elbow Joint, S: Shoulder Joint)						
	W	E	S	WE	WS	ES	WES
Joint deviation (deg.)	7.4 (4.30)	8.8 (5.17)	8.8 (5.52)	9.1 (5.40)	8.6 (5.60)	9.1 (5.89)	9.3 (5.88)
Joint angle (deg.)	7.8 (35.53)	10.7 (39.30)	14.0 (40.60)	10.3 (38.89)	13.9 (41.20)	14.1 (41.90)	14.1 (41.30)
Repetition frequency (Hz)	0.66 (0.20)	0.45 (0.11)	0.65 (0.17)	0.53 (0.20)	0.61 (0.13)	0.50 (0.17)	0.45 (0.10)

A two-way analysis of variance using all jobs revealed statistically significant differences between jobs for joint deviation ($F(4,117) = 5.67$; $p < 0.05$) and repetition frequency ($F(4,117) = 12.82$; $p < 0.05$). There were no statistically significant differences between the spectral results for joint deviation ($F(6,117) = 0.10$, $p \geqslant 0.05$) and average joint angle ($F(6,117) = 0.00$, $p \geqslant 0.05$). The spectral result differences based on the automated breakpoints produced on average up to 9.3° (S.D. = 5.88°) for joint deviation, and 14.1° (S.D. = 41.90°) for average joint angle.

Statistically significant differences for repetition frequency were also observed for joint motion combination ($F(6,117) = 7.61$, $p < 0.05$) and job × joint combination interaction ($F(14,117) = 4.39$, $p < 0.05$). The greatest difference on average for repetition frequency was 0.659 Hz (S.D. = 0.189 Hz). The least difference of 0.445 Hz (S.D. = 0.099 Hz) was observed for the WES joint motion combination.

4. Discussion

Given the small but significant error, the current TM algorithm implementation may be most useful for interactive semi-automated analysis. A multimedia computer program can control a video recording and assist a human analyst in the prediction of breakpoints. The analyst could visually verify the predicted breakpoint by accepting, rejecting or manually fine-tuning the breakpoint proposed by the computer program. As the analyst interacts with the program by fine-tuning the breakpoints, the algorithm can update the threshold values and joint weighting coefficients to improve future accuracy. This should help to greatly reduce analysis time.

The scan and hit threshold, and joint weighting coefficients values can affect the overall performance of the template matching algorithm. It is difficult to select appropriate parameters without previous analysis of the job and the joint motions. These parameters are different for different jobs. The selection of 0.2 for the scan threshold and 0.3 for the hit threshold produced good results across all the jobs. Individually selecting a scan and hit threshold for each job may improve the algorithm's performance.

Performance of the TM algorithm varied with each job. When the cycle joint motions were distinct and consistent, the TM algorithm's suggested breakpoints were closer to the actual analyst breakpoints producing lower mean time errors such as for some jobs. The large standard deviation for the mean errors revealed the difficulty for the algorithm to consistently pin-point the breakpoint in other jobs.

Mean error was reduced when the TM algorithm combined more joint motions. The wrist/elbow/shoulder or all available joints resulted in the least mean error across all jobs. This held for each individual job. Therefore efforts to reduce the number of joint measured will result in less accurate algorithm results.

Joint combinations had a significant effect on the repetition frequency measured using spectral analysis. The WES combination or all available joint motion combinations produced the least differences. The frequency data from spectral analysis was less influenced by the breakpoints than the postural deviation amplitude data.

The TM algorithm may not be capable of completely automatically identifying the cycle breakpoints in substitution for the human analyst. On average, the algorithm predicted reference breakpoints to within 0.997 s (2.762 s) when using the multiple joint combinations and the individual shoulder joint (see the means in Table 3). The prediction errors were normally distributed about zero. A slight negative skew was due to the way the errors were computed. Error was defined as the time difference between the closest reference breakpoint and the predicted breakpoint, minus the predicted breakpoint. In most cases the closest reference breakpoint was the previous breakpoint resulting in a negative error. If a breakpoint was missed by the algorithm, the error was computed from where the reference breakpoint should have occurred minus the time to the next reference breakpoint, since this was the greatest error possible. This was always a negative error. The magnitude of the negative distribution indicated the number of missed breakpoints.

On average, the algorithm took less then 10 s per cycle to make a breakpoint suggestion. The speed of the template matching algorithm should be greatly improved by software optimization as well as execution on a more power computer. Computational efficieny was not an objective of the current study. An analyst can usually visually identify a breakpoint within 10 s but the manual adjustment of a VCR can require additional time and effort. In its current form and implementation, the template matching algorithm may actually be slower and less accurate than a human analyst. This research however, is the first step and it has demonstrated that automated breakpoint determination is feasible.

Until a fully automated method is available, this interactive assistive approach has the potential to reduce the overall effort required by the analyst by transferring some of the mental and manual processing effort to the computer. The time and effort required to analyze upper extremity biomechanical data has made large-scale epidemiological studies impractical and prohibitively expensive in the past, and therefore methods to reduce the analysis time are very desirable.

The consistency of the human analyst's performance in identifying cycle breakpoints directly influences the overall accuracy of the analysis. Break point identification among human analysts can vary by as much as 0.164 s (Yen, 1997). This accounts for at least 20% of the mean time error produced by the algorithm. Considering the breakpoint assignment variability observed for an analyst, use of a computer to identify breakpoints based on biomechanical data features may actually be more consistent than an individual human analyst. The differences between analyst and algorithm breakpoints may be also due to differences in criteria for determining the breakpoint. The analyst used a visual or auditory event to guide the breakpoint assignment where the algorithm used joint posture. The visual or auditory events may not always be associated with the exact posture or motion.

All the jobs used to test the template matching algorithm were highly repetitive short cycle upper limb intensive jobs. Template matching worked best with jobs that were highly repetitive, regular, and had consistent motions. Lower extremity, back and whole body motions may also be applicable if it is sufficiently repetitive and regularity is present. Template matching performance on irregular cycle jobs may be poor. Template matching on repetitive long cycle jobs may not be as good as short cycle jobs due to the possible increase in movement variation. This should be studied further.

5. Conclusions

Signal pattern recognition was shown promising for automating job analysis of upper extremity biomechanical data. The TM algorithm identified cycle breakpoints within 0.997 s (S.D. = 2.762 s) of the human analyst's reference breakpoint. TM breakpoint identification resulted in average differences up to 9.3° for RMS joint deviation, 14.1° for average joint angle, and 0.445 Hz for repetition frequency in the spectra. The current algorithm implementation may not be practical as the sole means of identifying breakpoints but should be useful for indicating approximate breakpoints interactively fine-tuning the selection as a semi-automatic means for reducing the time required to perform an analysis.

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