

## **DETERMINING OPTIMAL TRIAL SIZE USING SEQUENTIAL ANALYSIS**

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## **DETERMINING OPTIMAL TRIAL SIZE USING SEQUENTIAL ANALYSIS**

**KEY WORDS:** Sequential analysis; Mean stability; Trial size; Overarm throw; Kinematic profile

## **Abstract**

When characterising typical human movement profiles, the optimal number of trials analysed for each participant should ensure a stable mean. Sequential analysis is one method able to establish the number of trials to stability by assessing a moving point mean against a set bandwidth. As the total trial number determining this bandwidth is selected arbitrarily, the effect of applying different total trial numbers on the results of sequential analysis was investigated. Twenty participants performed 30 trials of overarm throwing and sequential analyses were applied to three dimensional (3-D) kinematic data over 10, 20, and 30 trial numbers. We found a total of 20 to be the preferred trial number for sequential analyses. Erroneous results were produced consistently by 10 trial number groups, while moving point means were statistically unchanged after the 10<sup>th</sup> trial. Subsequently, sequential analyses were applied to 20 trials to establish trials to stability in discrete and time series elements of the 3-D kinematic data. The results suggest that a trial size between 13 and 17 provides stable means for overarm throwing kinematics.

## 1. Introduction

In human movement research, reported values of movement profiles should be as representative as possible. As Mullineaux and colleagues (2001) noted, values from the single best trial are often reported. However, when the typical performance is investigated, values obtained from a single trial may be considered inadequate. As a result, the number of trials from which a representative mean is calculated must be determined involving several considerations including power and reliability (Mullineaux, et al., 2001). It has been suggested that for sample sizes of 20, 10 and 5, trial sizes of 3, 5 and 10 respectively provide sufficient statistical power (Bates, Dufek, & Davis, 1992). Similarly, increases in trial size enhance reliability (Salo, Grimshaw, & Viitasalo, 1997). Yet, even after these factors have been addressed, an insufficient trial size may result in unstable means, compromising the reliable representation of the true performance. Perhaps due to this reason, justification of trial size is rarely reported in human movement literature.

One approach to resolve this issue is to implement sequential analysis which can determine the minimum number of samples required from an individual to provide an acceptable estimate of stability in the mean. The sequential analysis technique uses a moving point mean coupled with a criterion against which trials to stability is determined (Wald, 1947). This criterion is a bandwidth, established by the mean and standard deviation (SD) of total trials (commonly  $\text{mean} \pm 0.25 \text{ SD}$ ). Due to the arbitrary selection of the number of trials used to determine the criterion for sequential analysis, it is important to understand the effect of using different trial numbers when employing this technique. As such, the first aim of this study was to investigate the effect of using different trial numbers on the results of sequential analysis.

The sequential analysis technique has been used to determine trials to stability in a number of biomechanical measures including ground reaction forces during running (Bates, Osternig, Sawhill, & James, 1983), walking (Hamill & McNiven, 1990), landing (James, Herman, Dufek, & Bates, 2007), jumping (Racic, Pavic, & Brownjohn, 2009), cricket bowling (Stuelcken & Sinclair, 2009), joint power

and moment during vertical jumping (Rodano & Squadrone, 2002) and time to postural stability (Colby, Hintermeister, Torry, & Steadman, 1999). Most research has concentrated on discrete kinetic variables from lower limb movements, while kinematic variable stability has only been addressed in one study (Amiri-Khorasani, Osman, & Yusof, 2010). Use of sequential analysis for upper limb kinematics is under-reported and stability in complete time series kinematic data has not been quantified. Yet, the technique provides an easily applied method for determining trial size within these data. Hence, the second aim of this study was to employ sequential analysis to establish the number of trials to stability in discrete and time series kinematic data from an overarm throwing task.

## **2. Method**

### **2.1. Participants**

Ten male [20.7 (2.1) years; 175.9 (9.2) cm; 72.2 (10.2) kg] and ten female [22.2 (3.0) years; 165.7 (7.8) cm; 62.8 (10.2) kg] participants provided informed consent and had their data included in this study. Throwing experience ranged from novice to semi-experienced. All methods and procedures were approved by the Human Research Ethics Committee of the University.

### **2.2. Equipment**

Three dimensional (3-D) motion capture, sampling at 400 Hz, was performed using 10 Vicon cameras (6 MX and 4 T-Series), Vicon Nexus software and the unilateral Vicon Upper Limb Model plug-in (Oxford Metrics, Oxford, UK). Two dimensional (2-D) data of the ball trajectory in the sagittal plane were captured using a Basler A602fc camera (Basler AG, Germany), synchronised with the 3-D motion capture, sampling at 100Hz. Participant preparation, including marker placement (13 markers across trunk and throwing arm), was performed as outlined in the Vicon Upper Limb Model product guide (Taylor, Landeo, & Coogan, 2013; Vicon Motion Systems, 2007).

### **2.3. Laboratory Configuration**

An image of a round target consisting of 5 equally spaced concentric circles (radius increasing by 7 cm per circle to a maximum of 70 cm) was displayed via a beam projector (Dell Inc., Round Rock, Texas) on a cloth screen (5 m x 3 m) suspended from the ceiling. The vertical position of the projected target centre was located 2 m from the ground. An adjustable piano stool was placed square to the cloth screen at a distance of 7 m in line with the target centre.

### **2.4. Procedure**

Participants performed 30 overarm throws seated on the piano stool. They maintained 90° flexion at the hip, knee and ankle joints and began each throw with their frontal plane aligned parallel to the projection screen. Participants were instructed to throw a regulation tennis ball as accurately as possible toward the centre of the target using the hand of their choice. The chosen hand was used for all trials. Participants were asked to begin each throw with their hands placed on their knees. No other directions regarding throwing technique were provided though all participants performed the throw with one of two general techniques. These included a more developed technique where the humerus was held in the frontal plane, and ball velocity was produced primarily by both elbow extension and internal rotation of the shoulder, equivalent with stage 3 throwing development or higher (Gallahue, Ozmun, & Goodway, 2012). The second technique was “front on” where degrees of freedom were more constrained. The humerus was held in the sagittal plane, and elbow extension was the primary joint rotation contributing to ball velocity. This technique was equivalent to a stage 1 throwing development (Gallahue, et al., 2012). Most participants maintained their chosen technique throughout testing with little deviation/experimentation noted. Participants familiarised themselves with the task until they were ready to proceed (2–3 minutes). Time between throws was self-determined. Once the ball was returned, participants were notified when data collection had begun and were instructed that they were free to throw at any point following this

cue. Most participants performed three or four throws per minute during testing. All participant trials were included in analyses regardless of movement outcome and accuracy.

## **2.5. Data Analysis**

To represent 3-D displacement values in three axes (X, Y, and Z) across proximal, distal, bony and fleshy locations and where large and small movement was expected, four anatomical markers were chosen for analyses: T10 (10<sup>th</sup> thoracic vertebra), Upper Arm (over the muscle belly of triceps), Elbow (lateral epicondyle) and Finger (distal end of the 3<sup>rd</sup> metacarpal bone) of the throwing arm. Three joint angles - shoulder internal/external rotation and flexion/extension at the elbow and wrist - from the kinematic model (Vicon Motion Systems, 2007) were chosen for their role in producing ball velocity (van den Tillaar & Ettema, 2004). Discrete values of the final determinants of ball trajectory (ball release angle, height and velocity) were also included from 2-D data.

Following analyses of the frequency content and residuals of the power spectra (Winter, 2005) of the displacements of two distal markers (Finger and radial styloid process) of all participants, a cut off frequency of 12 Hz was employed in a low pass, 4<sup>th</sup> order, dual Butterworth filter on the kinematic time series data. The start of the movement was determined as the beginning of elbow flexion during wind up. The end of the movement was ball release. Filtered data were trimmed to these instants and time-normalised to 101 data points.

## **2.6. Sequential Analysis**

The sequential analysis technique was employed to determine the point of mean stability (i.e. trial size). This technique is illustrated in Figure 1 using mock data. The dashed grey line represents the N<sup>th</sup> trial mean taken from all (1 to N) trials and two solid grey lines labelled +0.25 SD and -0.25 SD represent a 'bandwidth' based on SD calculated from all trials. These elements form the criterion against which stability is assessed. For example, for a 20 trial condition the N<sup>th</sup> trial mean is the mean of all trials up to and including the 20<sup>th</sup>. The value of one SD about this mean is then multiplied by

+0.25 and -0.25 to create the upper and lower bounds of the bandwidth. Once the bandwidth is established, the technique requires the calculation of a moving point mean (solid black line), starting with the mean of the first two values and moving through the first three, first four etc., until reaching the N<sup>th</sup> trial. Stability is determined when the moving point mean rests within the SD bandwidth and stays within for all remaining trials as indicated by A in Figure 1. It is worth noting that while points B and C also rest within the bandwidth in this example, they do not represent the point of stability as there are excursions of the moving point mean outside of the SD bandwidth between B and A or C and A.

\*\*\*\*Figure 1 near here\*\*\*\*

The sequential analysis technique was employed on both discrete and time series kinematic data (Table 1). To perform sequential analysis on 3-D marker displacement and joint angle time series data, each of the 101 sample points were treated as a discrete point, providing trials to stability for each sample point along the entire time series. To determine the effect of using different trial numbers on sequential analysis score, three main conditions - first 10 (1<sup>st</sup> to 10<sup>th</sup> trial), first 20 (1<sup>st</sup> to 20<sup>th</sup> trial) and first 30 (1<sup>st</sup> to 30<sup>th</sup> trial) trials - were assessed with the criterion mean and 0.25 SD bandwidth calculated using all trials included in each condition. Similarly, mid 10 (11<sup>th</sup> to 20<sup>th</sup> trial), last 10 (21<sup>st</sup> to 30<sup>th</sup> trial) and mid 20 (6<sup>th</sup> to 25<sup>th</sup> trial) conditions were compared to establish if results were dependent on where in the sequence of throws a sample was extracted.

\*\*\*\*Table 1 near here\*\*\*\*



## 2.7. Comparing Trial Number Conditions

To qualitatively assess the behaviour of the sequential analysis elements, the moving point mean for all discrete variables from the 30 trial condition was plotted against the criterion bandwidth from that condition and viewed for each participant (see Figure 3). While this bandwidth was specific to the 30 trial condition, the moving point mean is the same for each condition, up to the total trial number of that condition (for first 10, 20 and 30 conditions only).

For further determination of the condition from which to report sequential analysis values, two scores were submitted to statistical analyses, the sequential analysis score (trials to stability) and a relative sequential analysis score. The relative sequential analysis score is novel to this investigation and is calculated by dividing the sequential analysis score by the total trial number of the condition from which it was taken. This relative score can highlight differences in the behaviour of the sequential analysis technique between conditions in respect to the percentage of maximum possible trials taken to achieve mean stability.

The sequential analysis score for all time series variables were compared using a 4 x 101 (first 10, first and mid 20 and first 30 conditions x 101 time series samples) two way repeated measures analysis of variance (ANOVA) and a 3 x 101 (first, mid and last 10 x 101 time series samples) two way repeated measures ANOVA with Fisher's least significant difference post hoc tests. The time series ANOVA outcomes were considered as the primary results from which a determination would be made as all discrete variables were contained within the time series. To confirm any patterns observed within time series, group mean sequential analysis scores for the discrete marker variables taken from individual participant time series data were also compared across trial number conditions (first, mid and last 10, first and mid 20 and 30 trials) using a 6 x 1 one way repeated measures ANOVA with Fisher's least significant difference post hoc test. Discrete marker variables were analysed in this manner as they provided 12 cases (4 markers x 3 axes) per condition (minimum, maximum and release), whereas joint angle and ball release variables only provided 3

cases per condition and thus were not included in the analyses. Relative sequential analysis scores were compared across conditions in the same manner as the sequential analysis score.

To determine if any statistical differences existed between the 10<sup>th</sup>, 20<sup>th</sup> and 30<sup>th</sup> trial means of time series and discrete marker values, these elements were also compared in a similar manner to sequential analysis score and relative sequential analysis score. This comparison consisted of a 3 x 101 two way repeated measures ANOVA for time series variables and a 3 x 1 one way repeated measures ANOVA for group mean discrete marker values.

For repeated measures ANOVA testing an alpha level of 0.05 was taken to indicate significance. Fisher's least significant difference post hoc test significance was assessed against the relevant Bonferroni adjusted p-value in each instance. Discrete variable testing was conducted using IBM SPSS Statistics, version 19 (SPSS Inc, Chicago, Illinois). Due to the need to analyse 101 data points per participant, time series analyses were conducted using Statistica 7 (StatSoft Inc, Tulsa, Oklahoma).

## **2.8 Reporting Sequential Analysis Results**

To guide trial size selection, discrete variable sequential analysis results were reported from the chosen condition - first 20 (see results and discussion for reasoning) - as group mean and 95% confidence interval (95% CI) values. A 101 x 1 one way repeated measures ANOVA was conducted on all time series sequential analysis results. Fisher's least significant difference post hoc test was used to determine whether differences existed across the 101 points. Where upon no differences were found, the point (out of the 101 time normalised points) displaying the greatest group mean sequential analysis result (95% CI) was extracted and reported to guide trial size selection for time series analyses.

### 3. Results

#### 3.1 Comparing Trial Number Conditions

The sequential analysis scores were significantly different across all time series variables,  $F(3, 57) \geq 48.51$ ,  $p < 0.01$ ,  $\eta^2 \geq 0.72$ . Pairwise comparisons displayed significant differences between all conditions of different sizes while same sized conditions formed homogenous groups. This result was mirrored within the discrete marker group mean variables  $F(1, 11) \geq 2367.84$ ,  $p < 0.05$ ,  $\eta^2 \geq 0.99$  (Figure 2).

\*\*\*\*Figure 2 near here\*\*\*\*

Figure 3 shows a sample plot of the sequential analysis (Finger marker in X axis) from one participant, illustrating the most frequent pattern observed amongst the discrete variables, across all participants, in the 30 trial condition (54%; 523 out of 960 plots viewed). It can be seen that the moving point mean (solid black line) undergoes a 'transition phase', most commonly occurring during the first 10 trials, moving up or down toward the criterion bandwidth (dashed grey line). While this was the most frequent pattern, other transition patterns within the first ten trials were also common. These included the moving point mean lines that began on one side of the bandwidth prior to transitioning across to the other side before stabilising as well as those that began within the bandwidth before moving to either side then stabilising. While the patterns did vary, the consistent element was that the magnitude of the transition (slope of the curve) was greatest in the early trials and around the 10<sup>th</sup> trial fluctuations in the moving point mean generally became less severe. After the point of stability (trial 15 in this example), and even slightly before, the mean tended to be robust to fluctuations in raw data (dash-dot grey line), illustrating the concept of sequential analysis score and mean stability.

\*\*\*\*Figure 3 near here\*\*\*\*

Of the 15 relative sequential analysis scores of time series variable ANOVAs, 12 (excluding T10 in X and Y axes, Finger in Y axis) displayed significance,  $F(3, 57) \geq 4.78$ ,  $p < 0.05$ ,  $\eta^2 \geq 0.20$ . In 11 of 12 significant time series variables, the first 10 condition was significantly greater than the other main conditions. Same sized conditions formed homogenous groups based on sample size. Results for discrete relative sequential analysis score group mean marker variables displayed significance,  $F(1, 11) \geq 3304.52$ ,  $p < 0.05$ ,  $\eta^2 \geq 0.99$ . Group mean discrete variable relative sequential analysis scores between the three main conditions can be seen in Figure 4.

\*\*\*\*Figure 4 near here\*\*\*\*

Comparisons of the criterion mean values showed no significant difference in 12 of the 15 variables,  $F(2, 38) \leq 2.35$ ,  $p > 0.05$ ,  $\eta^2 \leq 0.11$ . Of the three significant time series comparisons (T10 in Z axis, Upper Arm in X axis and Finger in Y axis),  $F(2, 38) \geq 3.56$ ,  $p < 0.05$ ,  $\eta^2 \geq 0.16$  post hoc tests showed the first 10 condition to be different from the first 20 and 30 conditions for Upper Arm in X axis and different to the first 30 condition for T10 in Z axis and Finger in Y axis. Discrete group mean marker results reflected the time series results with non-significant ANOVA results for marker minimum and release values,  $F(1, 11) \leq 2.94$ ,  $p > 0.05$ ,  $\eta^2 \leq 0.21$ . While the ANOVA for marker maximum displayed significance,  $F(1, 11) = 15.55$ ,  $p < 0.05$ ,  $\eta^2 = 0.59$  post hoc analyses showed no difference between conditions.

### 3.2 Sequential Analysis Results

Group mean sequential analysis scores (95% CI), of the first 20 condition, for discrete marker variables and for maximum group mean (95% CI) time series marker variables are reported in Tables 2 and 3 respectively. Repeated measures ANOVA results on first 20 time series were significant for

Upper Arm, Elbow and Finger markers (in Z axes),  $F(100, 1900) \geq 1.33$   $p \leq 0.02$ ,  $\eta^2 = 0.07$ . However, post hoc analyses revealed no recurring pattern of results across time series and a consistent trend of all 101 points forming one homogenous group. As a result, it was determined that a single group mean value and associated confidence interval should be reported for all time series results. The maximum group mean value was therefore selected for this purpose as a decision based on this value would ensure that all points along the time series were accounted for. Group mean (95% CI) data for discrete joint angle variables and maximum group mean (95% CI) data for time series joint angle variables are reported in Table 4. Group mean (95% CI) results for release height, velocity and angle were 11.5 (1.8), 12.7 (1.9) and 10.5 (2.0) respectively.

\*\*\*\*Table 2 near here\*\*\*\*

\*\*\*\*Table 3 near here\*\*\*\*

\*\*\*\*Table 4 near here\*\*\*\*

#### **4. Discussion**

Sequential analysis score results showed that the outcome of this technique is affected by the total trial number from which criterion mean and SD values are drawn (Figures 2 and 4). Yet, results were not dependent on the position in the total sample where the subsample was drawn (e.g. first, mid or last 10). Qualitative assessment of the sequential analysis plots suggests that the results from the first 10 condition are affected by the 'transition' phase of the moving point mean (Figure 3). This transition appeared most commonly due to the mean of the first two trials lying above or below the criterion bandwidth as in the most regular pattern illustrated in Figure 3. There were of course instances where the transition phase did not exist and these data generally resulted in low sequential analysis scores. That the transition phase still existed in data from the mid 10 and last 10 conditions indicate it is not related to any warm up decrement or familiarisation with the task. Results of relative sequential analysis scores support the qualitative assessment (Figure 4), showing

that the first 10 condition often produces a relative score higher (65.6%) than the first 20 and 30 conditions (59.0% and 56.9% respectively). Similar differences in relative sequential analysis scores can be calculated from the data reported by James et al. (2007) when comparing their 10 (72%) and 20 (58%) trial conditions. These results are sufficient to exclude the first 10 condition as a supply of valid sequential analysis results to determine the number of trials to stable means.

With the first 10 condition excluded, it must also be considered whether to accept sequential analysis values from either the first 20 or 30 trial number conditions. Despite the evidence showing the different behaviour of the first 10 trials (mean 'transition' and higher relative sequential analysis score) analyses showed that there were few differences (5 of 36 pairwise time series comparisons) between the criterion mean values derived at the 10<sup>th</sup>, 20<sup>th</sup> and 30<sup>th</sup> trial. As the kinematic mean does not vary statistically from the 10<sup>th</sup> trial to 20<sup>th</sup> and 30<sup>th</sup>, nor are relative sequential analysis scores consistently different between the 20<sup>th</sup> to 30<sup>th</sup> trial conditions, collecting 20 trials appears sufficient to estimate stable means. This will ensure that the mean has passed the 'transition' phase illustrated in Figure 3 and avoided the different relative sequential analysis score behaviour of the first 10 condition. It is worth noting that this is the recommendation for the current population and task based on the process determining the optimal condition from which to report sequential analysis results described previously and summarised in Figure 5. Limitations such as time, budget or technological factors, learning and/or fatigue may stipulate modification of this process within other research projects or applied settings. Qualitatively, change in some participants' throwing technique was noted, perhaps attributable to fatigue or learning, within the final ten throws of this study. These perceived changes included decreased ball velocity, wrist and humerus height at release and changes in the release angle, altering the path of the ball in flight. In the present investigation this provided further justification for the use of the 20 trials condition, however, it is possible that the 30 trials condition may be more appropriate for estimating stable mean values in other tasks and populations.

\*\*\*\*Figure 5 near here\*\*\*\*

The reported sequential analysis results of marker displacement, ball release and joint angle data from this study (Tables 3–5) allow guidance in the determination of trial size for other studies of the same or similar design. While ball release and joint angle results may be of more impact in an applied setting than that of marker displacement, these data have been included as they are the direct measure of body movement, and all joint angle data are derived from these. When applying these results readers may choose to employ either the mean or the upper bound of the confidence interval, depending on how conservative they wish to be with this decision. While values are reported to one decimal place in order to provide a degree of precision, it is recommended that these values be rounded up when determining trials sizes from them. If discrete marker displacement data were to be analysed alone the reported results suggest that a trial size of 14–16 throws should provide mean stability in the selected variables. If discrete joint angle or ball release data are the only consideration then a trial size in the range of 13–15 is advised. From the results, the recommended trials sizes for analysing only complete marker or joint angle time series are 15–17 and 13–15 throws respectively. However, as these values were derived from the maximum group mean across all 101 time series data points, there is an element of conservativeness about the results which researchers and practitioners may wish to consider when utilising them.

This study has attempted to address the selection of trial number condition size by comparing results across different conditions. The selection of an arbitrary size for the SD bandwidth (0.25 SD) allows for the creation of a conservative test which is a strength of the sequential analysis technique. Yet the inherent subjectivity makes it less objective than other tests such as intraclass correlation (ICC) which has also been used for the same purpose (James, et al., 2007; Racic, et al., 2009). Stability results from ICC analysis from these studies, admittedly addressing different variables, are however lower (4 trials). Results from this study show that a trial size of four risks reporting mean

values from within the 'transition' phase which have not yet achieved stability as determined using the sequential analysis technique. As such, ICC may risk underestimation of a trial size which approximates stability in the mean compared to sequential analysis applied conservatively as in the current study, despite its objectivity. However, as James et al. (2007) reported, widening the SD bandwidth used in sequential analysis can yield similar results to ICC analyses. Researchers and practitioners should be aware of the strengths and weaknesses of the two techniques when choosing to use one over the other.

While differences exist between results from this study and from ICC analysis in other research, the current trial size recommendations are closer to those reported elsewhere based on sequential analysis. This includes 11 trials for continuous jumping (Racic, et al., 2009) and 12 trials for drop landing, vertical jumps and cricket bowling (James, et al., 2007; Rodano & Squadrone, 2002; Stuelcken & Sinclair, 2009). The higher results from this current study may be due to the different task, different data types (kinematic versus kinetic) or associated differences in data collection; it may also be related to the practice of using a range between the (rounded up) group mean and 95% confidence interval employed in the current study.

## **5. Conclusion**

The aims of this research were to investigate the effect of applying different trial numbers on the results of sequential analysis applied to kinematic data of an overarm throwing task, in order to determine the optimal trial number for conducting sequential analysis, and to report trial size recommendations from this sample for future research. Based on the results, performing sequential analysis on a sample of 20 trials or more to ascertain an acceptable estimate of mean stability in kinematic data from an overarm throwing task is recommended. Furthermore, the use of similar methods presented here to determine the required trial number for sequential analysis in other populations and tasks are suggested. Researchers may choose to implement this method on pilot samples of the target population to guide data collection and trial size decisions in studies with



larger samples. Practitioners may be able to use the technique to justify the number of trials collected during regular testing and/or servicing of athletes. Depending on the data type, the sequential analysis results suggest that collecting between 13 and 17 trials will provide stability in the mean of the targeted variables from the overarm throwing task.

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Table 1: Discrete and time series variables included in sequential analysis

<b>Marker Variables</b>	<b>Joint Angle Variables</b>	<b>Ball Release Variables</b>
Maximum value	Peak angle value	Release height
Minimum value	Time of peak angle value	Release velocity
Value at release	Value at release	Release angle
Normalised time series	Normalised time series	

*Note: Peak angle value represents relevant maximum or minimum value, occurring near wind up completion. Joint angles were shoulder external/internal rotation, elbow and wrist flexion/extension. Marker data was analysed in X, Y and Z axes.*

Table 2: Group mean (95% CI) sequential analysis results for marker maximum, minimum and release values

	<b>Maxima</b>			<b>Minima</b>			<b>Release</b>		
	<b>X</b>	<b>Y</b>	<b>Z</b>	<b>X</b>	<b>Y</b>	<b>Z</b>	<b>X</b>	<b>Y</b>	<b>Z</b>
<b>T10</b>	13.9 (1.7)	13.2 (1.8)	10.0 (1.8)	13.4 (1.6)	13.5 (1.2)	12.7 (1.5)	13.1 (2.0)	13.1 (1.4)	11.5 (1.7)
<b>UPA</b>	13.2 (1.8)	12.9 (1.6)	9.3 (2.0)	12.6 (1.5)	11.7 (1.8)	11.2 (2.0)	12.0 (1.7)	12.2 (1.3)	9.9 (1.9)
<b>ELB</b>	12.6 (1.6)	11.8 (2.1)	12.2 (1.7)	13.3 (1.6)	12.0 (1.5)	10.8 (1.6)	11.4 (1.7)	12.0 (1.5)	11.9 (1.8)
<b>FIN</b>	12.1 (1.9)	11.3 (1.9)	12.2 (1.8)	12.6 (1.7)	11.1 (2.3)	11.8 (1.7)	11.0 (2.0)	10.6 (1.9)	12.3 (1.8)

*Note: Markers were T10 (10<sup>th</sup> thoracic vertebra), Upper Arm (UPA), Elbow (ELB) and Finger (FIN)*

Table 3: Group mean (95% CI) sequential analysis results for marker time series

	<b>X</b>	<b>Y</b>	<b>Z</b>
<b>T10</b>	14.5 (1.6)	14.0 (1.4)	13.1 (2.1)
<b>UPA</b>	14.1 (1.3)	12.9 (1.2)	14.3 (1.5)
<b>ELB</b>	13.4 (1.5)	13.6 (1.3)	13.8 (1.7)
<b>FIN</b>	13.7 (1.5)	13.0 (1.5)	13.3 (1.4)

*Note: Markers were T10 (10<sup>th</sup> thoracic vertebra), Upper Arm (UPA), Elbow (ELB) and Finger (FIN)*

Table 4: Group mean (95% CI) sequential analysis results for discrete and time series (maximum group mean) joint angle variables

	<b>Peak</b>	<b>Release</b>	<b>Time of Peak</b>	<b>Time Series</b>
<b>Shoulder</b>	12.1 (2.2)	10.1 (2.2)	9.6 (2.1)	13.0 (1.9)
<b>Elbow</b>	12.2 (1.6)	11.3 (1.9)	11.3 (2.0)	12.4 (1.6)
<b>Wrist</b>	12.1 (1.5)	10.2 (1.8)	10.2 (1.7)	12.5 (2.1)

*Note: Joint angles were shoulder internal/external rotation, elbow and wrist flexion/extension*

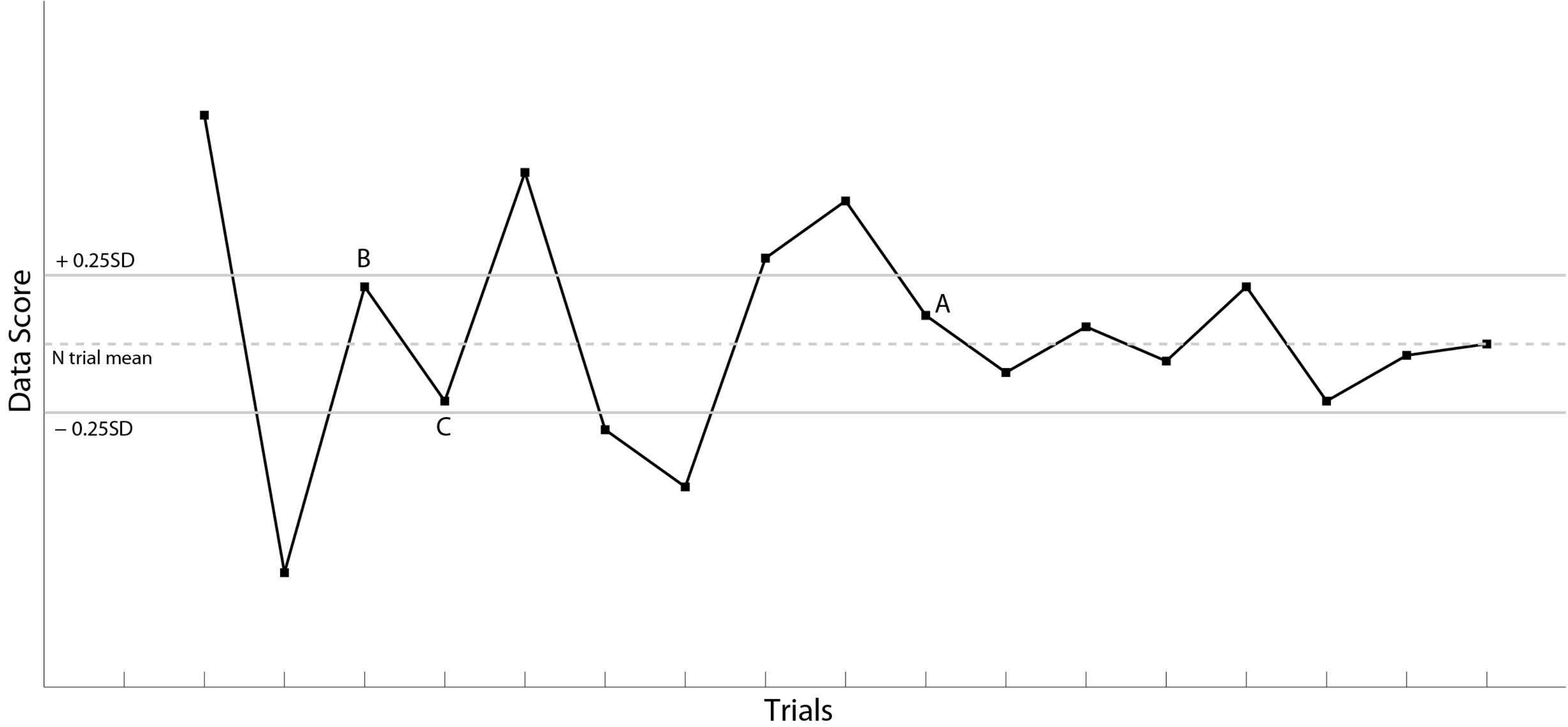
Figure 1: Example of sequential analysis technique applied to a trial size of N. Illustrated are the criterion elements of the total (trials 1 to N) mean (dashed grey line) and the  $\pm 0.25$  SD bandwidth (two solid grey lines). Assessed against this criterion is the moving point mean, starting at trial two (black line). The point of stability is represented by the letter A. Points B and C do not represent stability as the mean deviates outside the bandwidth between these points and point A.

Figure 2: Comparison of the three main condition group mean sequential analysis scores for marker maximum, minimum and release values. All conditions were significantly different ( $p < 0.05$ ) from other conditions within their marker variable.

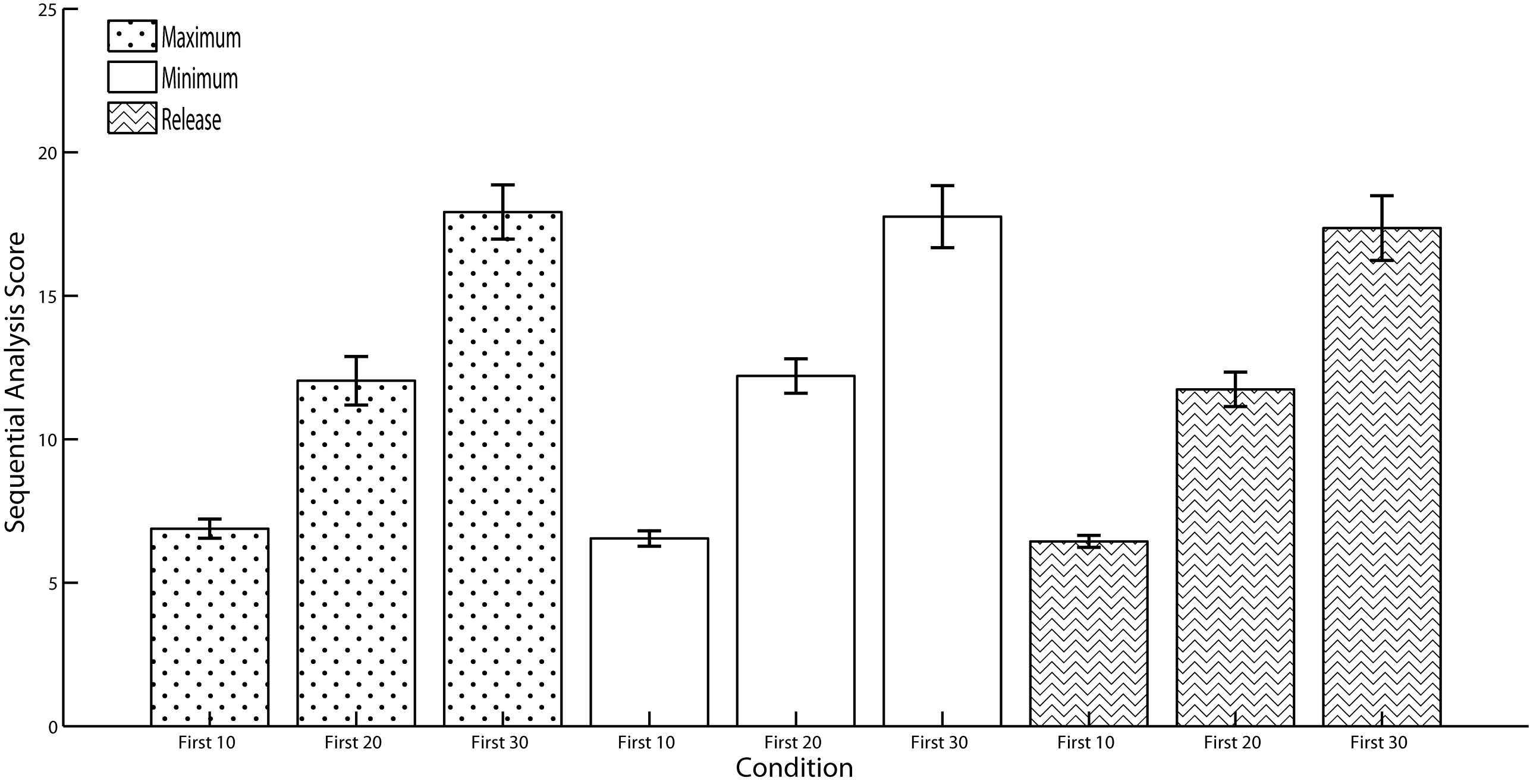
Figure 3: Example of sequential analysis of a finger marker (X axis) minimum value in 30 trial condition from one participant showing the relationship between raw kinematic data (dash-dot grey), moving point mean (solid black) and 0.25 standard deviation (SD) bandwidth (dash grey). Stability point (sequential analysis score = trial 15) is indicated by an arrow.

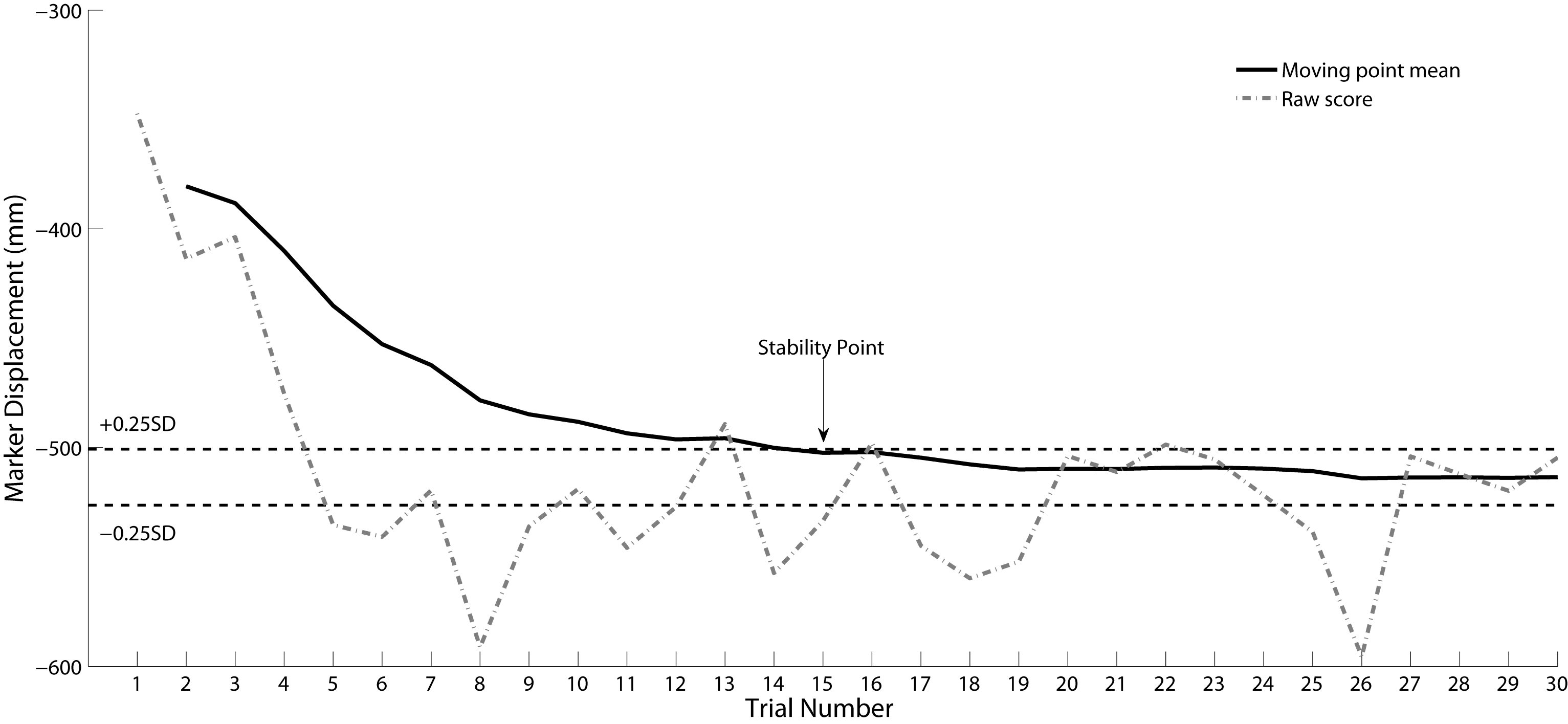
Figure 4: Comparison of the three main condition group mean relative sequential analysis scores for marker maximum, minimum and release values. Asterisk (\*) indicates significant difference ( $p < 0.05$ ) from the first 20 and first 30 conditions.

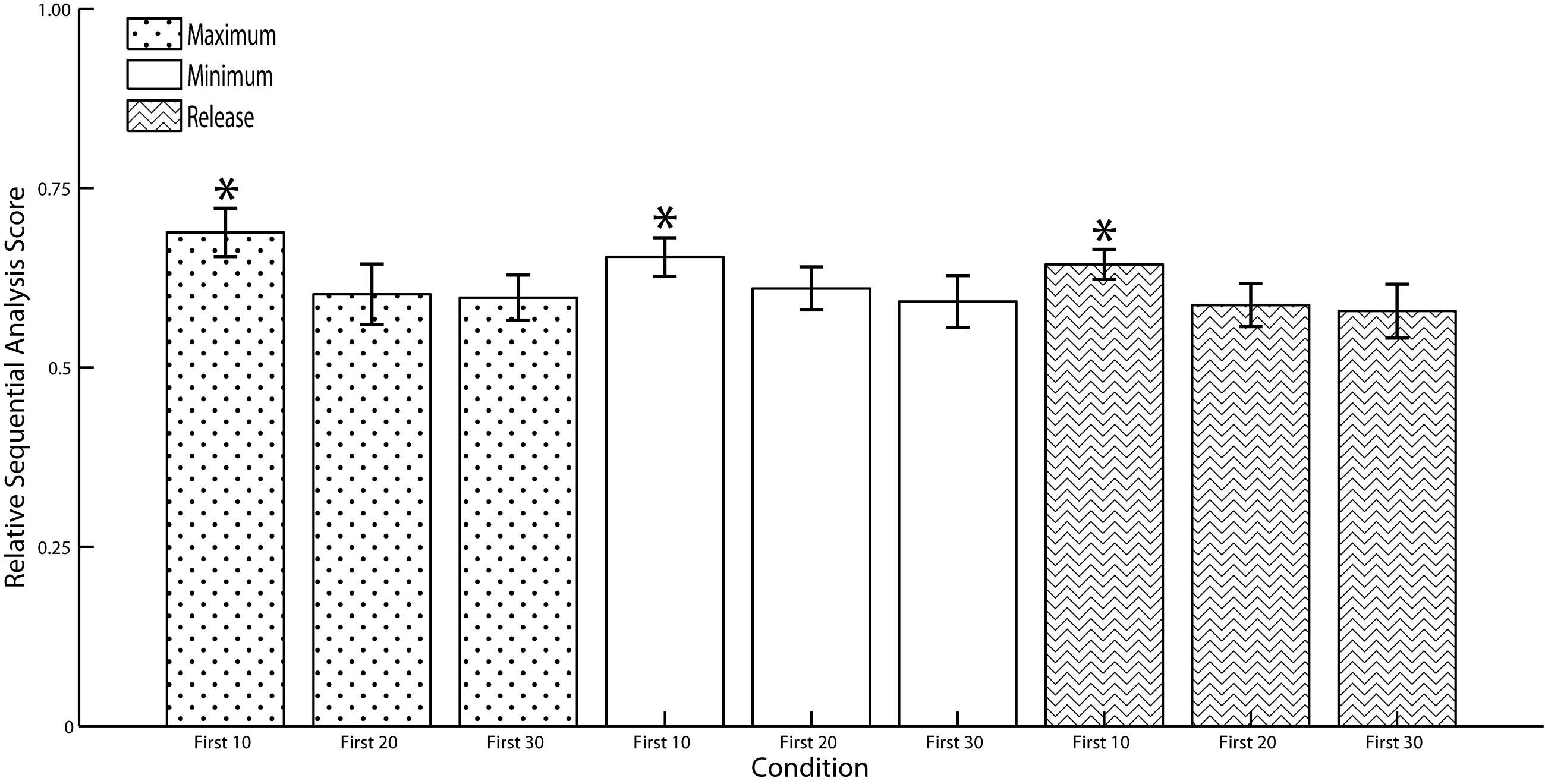
Figure 5: Flowchart of the aim, evidence and subsequent decisions/conclusion on which condition to report sequential analysis results from.











## Aim

To determine the effect of applying different trial numbers on the results of the sequential analysis



Sequential analysis result is reliant on the trial size of the sample from which it is derived



The first 10 throws do not provide a valid trial number on which to conduct sequential analyses



## Conclusion

A minimum of 20 and up to 30 trials may be employed as a trial size upon which to conduct sequential analyses

## Evidence

Sequential analysis score is significantly different between 10, 20 and 30 trial number conditions

Moving point mean undergoes a 'transition' phase during the first 10 throws. Sequential analysis results from the first 10 condition take a higher percentage of the maximum to reach stability, compared to first 20 and 30 conditions

Despite 'transition' phase and higher relative sequential analysis score there is no statistical difference between mean values (kinematic data) at the 10th, 20th and 30th trial