USING INVERSE KINEMATICS
TO POSITION ARTICULATED FIGURES

by

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We accept this thesis as conforming
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Abstract

Computer-assisted animation is an active research area in computer graphics. Within this field, many systems are being developed that allow traditional animators to utilize computers in the animation process. The ability to position articulated figures is of particular interest. A method called inverse kinematics allows the user to position a figure by specifying a desired goal location for a particular segment of the figure. An algorithm is employed to compute the required changes to the joint angles of the figure in order to move the segment to the desired location.

This thesis describes an experiment that was conducted to compare three different inverse kinematic methods: the Jacobian method, the CCD method and the 1DOF method. Subjects used the methods to manipulate the pose of a given articulated figure in an attempt to match a specified goal pose. Results from the experiment indicate that overall, the 1DOF method produced the best matches (in terms of speed and accuracy). However, no single method had superior performance for all of the positioning tasks that were studied. Consequently, an animation system should offer the user the choice of at least two of the positioning methods.

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Chapter 1

Introduction

Computer systems are increasingly being used to generate animations. Some systems are designed for people who are familiar with traditional animation techniques. In general, these animation systems attempt to assist an animator in the task of producing an animation. The systems try to facilitate the animation process while allowing the animator to apply skills from traditional animation. This thesis explores the portion of a computer-assisted animation system that allows an animator to produce animations of characters.

1.1 Character Animation

Many animations involve characters such as humans and animals. To produce satisfactory animated sequences, animators must be able to finely position and move all parts of the character. In most computer systems, characters are modelled as articulated (jointed) figures. Many of the current computer animation systems use a skeletal approximation of a jointed figure for positioning and motion purposes and assume that overlying muscle and tissue can be added to the figure once the skeletal positioning has been determined.

The skeletal approximation is normally modelled as a rooted tree with nodes representing pieces of the skeleton and arcs representing joints between the skeletal pieces. A limb, such as an arm or leg, is generally described as a chain of links. Figure 1.1 is an example of a typical chain.

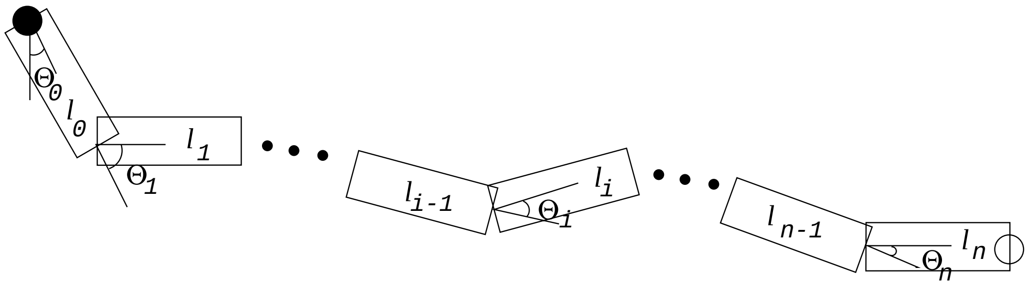

Figure 1.1: A typical chain with the i^{th} link labelled l_i and the angle of rotation of the i^{th} joint labelled θ_i. The link l_0 is at the proximal end of the chain and the link l_n is at the distal end of the chain. The set of links l_{i-1}, l_i, ..., l_{n-1}, l_n is an example of a distal subchain. The filled circle on link l_0 represents the inherent root of the chain and the open circle on link l_n represents the location of the end-effector if the entire chain is to be manipulated.

1.1.1 Terminology

The fixed end of a chain, where the limb attaches to the torso, is referred to as the *proximal end.* The free end that can be moved around in space is referred to as the *distal end.* A *distal subchain* is a subset of a larger chain sharing the same distal end. The *end-effector* is the distal link in the chain. The *free space* refers to the region in space that the end-effector can occupy. For a chain consisting of only 1 link, the free space is the circle in 2D (or sphere in 3D) centered at the proximal end of the link with a radius equal to the length of the link.

1.1.2 Joints and Joint Limits

The joints involved in articulated figures are generally classified as *revolute*, having one degree of freedom, or *prismatic*, having three degrees of freedom (such as a ball-and-socket joint). Joints with more than one degree of freedom are often modelled as several one degree of freedom revolute joints. For most articulated figures, joint limits must be taken into account as these restrict the possible ranges of motion.

The interaction between joints when manipulating an articulated figure requires another assumption to be made. It is assumed that the allowable angle of rotation of a given joint is independent of the other joints. This is an unrealistic assumption when modelling a human figure because the position of one joint can constrain the free space available to the end-effector. For instance, for some orientations of the upper arm given by the rotation of the shoulder joint, normally valid rotations of the elbow will result in the hand being embedded in the torso. Although the assumption of independent joints is not entirely realistic, a fairly accurate approximation of motion can be obtained with the assistance of joint limits. In a reasonable animation system, the animator can either compensate for these types of situations or ignore them. In general, it is necessary to allow the animator to override controls that prevent unrealistic situations from occurring so that s/he is not prevented from achieving a desired unrealistic configuration as might be required for a cartoon character.

1.1.3 Keyframing

Traditional animators often use a process called *keyframing*, in which various key poses of the figure are drawn (the *keyframes*), and then the remaining *inbetween* frames containing the interpolated motion are filled in by assistant animators known as *inbetweeners*. One required component of a computer graphics animation system that uses keyframing is the ability to place the parts of a figure at various positions in space. The motion between keyframes is generated later. One method of producing the inbetween frames involves the automatic generation of the motion path from the interpolation of the joint angles between keyframes using splines. This approach can generate very good smooth motion between keyframes, but the animator often has to make many adjustments to the initially generated motion in order to produce the desired motion. By changing the interpolated motion, the animator may inadvertently change the position of the figure in a keyframe.

This can cause undesired side effects, such as the foot of a character penetrating the floor. Animators desire better methods for controlling the generated motion and researchers continue to develop these methods.

The interpolation process uses *forward kinematics* to determine the positions of the parts of the figure. Forward kinematics refers to the calculation of the locations of the links in a chain from the position of the root of the chain, the joint angles of all of the links and the lengths of the links. These positions, which can be calculated using simple trigonometry, are unique.

The positioning problem involves solving the inverse kinematics of the figure. The solution determines the angles of revolution of the joints that position the end-effector of the figure in the desired location in space, given the position of the root and the lengths of the links. The inverse kinematic solution is not, in general, unique. For example, in two dimensions, a chain consisting of two links of the same length will have two mirror image solutions for all attainable end-effector positions except for the case when the chain is stretched out straight. In three dimensions this same chain would have an infinite number of solutions for these cases, with the joint between the two links lying anywhere on a circle. Figure 1.2 illustrates an instance of the given example.

Articulated figures used by animators typically consist of chains having many links and many degrees of freedom; for example, a simplified human figure will have at least 20 degrees of freedom. For most given positions of the end-effector, there will be multiple possible configurations of the chain.

1.1.4 Specifying the Position of the Figure

Some animation systems require the animator to describe the position of the figure by typing in the various joint angles. This can be a tedious process as animators do not generally think in terms of the values of joint angles. Rather, they draw something

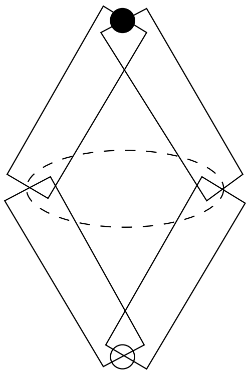

Figure 1.2: Multiple inverse kinematic solutions for a chain composed of two links. The black circle at the top indicates the root and the outlined circle at the bottom indicates the desired location for the end-effector. The two valid solutions in two dimensions are both shown. In three dimensions the valid solutions are represented by the dashed circle which indicates the position of the joint between the two links.

at whatever angle looks right. Therefore, describing positions by specifying joint angles tends to be an iterative process where an animator uses trial and error to adjust the joint angles until the figure appears as desired.

Direct manipulation, where the animator selects a part of the figure and indicates the desired location for the end-effector using an input device such as a mouse, provides a highly interactive user interface. The correspondence between the motion of the mouse and the motion of the figure on the screen gives the animator the impression of manipulating the figure itself. According to Shneiderman's taxonomy of interaction styles [Shn91], direct manipulation is preferred over all other interaction styles in situations where there is a "natural visual representation." User interfaces that employ direct manipulation are easy to learn and have high subjective satisfaction. Direct manipulation interfaces also encourage exploration because the results are shown immediately and actions are reversible.

In order to facilitate the direct manipulation of multiple links at a time, the system must determine the inverse kinematics of the figure. Real-time or near real-time solutions to this positioning problem are desired so that animators can interactively use the system to keyframe animated sequences of articulated figures.

1.2 Preview of the Thesis

This thesis describes an experiment that was designed and conducted to compare three methods for positioning articulated figures. Chapter 2 describes background work in the area of inverse kinematics. Chapter 3 presents the design of the experiment that was used to compare the three different positioning methods. Chapter 4 presents and discusses the results of the experiment. Chapter 5 contains the conclusions of the research and provides suggestions for future related research.

Chapter 2

Background material

The forward kinematic problem can be expressed as the calculation of the position vector $\vec{X}$, given a vector of joint angles $\vec{q}$

$$\vec{X} = f(\vec{q})$$

where the function f is nonlinear, continuous and differentiable and it depends upon the lengths of the links. This function has a unique solution. The inverse kinematic problem, that of solving for the joint angles given the positions of the root and end-effector and the lengths of the links

$$\vec{q} = f^{-1}(\vec{X})$$

does not in general have a unique solution.

The inverse kinematic equations can be solved using either direct or iterative techniques. Iterative techniques generally involve the computation of several steps before converging to a solution. As a result, direct solutions are usually faster to compute than iterative ones.

Some direct techniques calculate all of the possible solution configurations whereas iterative methods converge to only one solution at a time. If the solution found by an iterative method has to be discarded (for example, if a joint limit is violated), the method generally needs to be started from the beginning again in order to calculate another solution. An iterative method also requires an initial estimate of the solution in order to start the first iteration. The current position of the figure is generally used as the initial estimate of the solution, but if the two configurations are far apart, the algorithm may not converge. In this case, the user must specify intermediate goals.

Direct solutions are known for many six or fewer degree of freedom industrial robots. However, for most articulated figures used in animation, such as human figures and animals, there are more degrees of freedom to be calculated than there are constraining equations. Direct solutions do not exist for these underconstrained systems and thus iterative methods must be used instead. Generally, the calculation involving a iterative solution involves a user-defined degree of tolerance and the solution obtained is an approximation of the actual solution, within the specified degree of tolerance.

Solving the inverse kinematics of a figure gives positional information but it does not actually specify a motion path for moving the figure from one position to another. The intermediate solutions from the steps of the iteration process could be used to generate motion, but the resulting motion would most likely not be realistic or desired. If all of the iterations were used for motion generation, jerky motion could result as various steps in the iterative process may actually be converging on different solutions. Even if the iterations were filtered and only those that led to the particular solution were used, unrealistic motion might still result as the iteration process does not necessarily converge smoothly on the final solution. To avoid these problems and produce smooth motion, splines are typically used to define a motion path that interpolates between the starting and ending joint angles.

2.1 Implemented Methods

A system for exploring various positioning algorithms was created. Three different positioning algorithms were implemented in the system. The method that will be referred to as the cyclic coordinate descent or CCD method [WC91] is an inverse kinematic algorithm from the field of robotics that is based on combined optimization techniques. It is an iterative technique that is a combination of two gradient based non-linear programming techniques and forward recursion formulae. This method first uses the cyclic coordinate descent (CCD) method to quickly find a feasible point that is close to the actual solution and then uses the Broyden-Fletcher-Shanno (BFS) variable metric method to find the actual solution to the specified degree of precision. Wang and Chen [WC91] claim that this method is numerically stable and is not sensitive to singular configurations. They also state that the method is computationally efficient and can be applied to serial manipulators (simple chains) having any number of degrees of freedom.

The method that will be referred to as the Jacobian method [SS88, GW91] is also an inverse kinematic algorithm from the field of robotics. This iterative technique involves the linearization of a non-linear problem. This method looks at the problem in terms of the relationship between joint velocities $\dot{\vec{q}}$ and position velocities $\dot{\vec{X}}$

$$\dot{\vec{X}} = J(\vec{q})\dot{\vec{q}}$$

where $J(\vec{q})$ is the Jacobian matrix $\partial f / \partial \vec{q}$. This relationship can be inverted to obtain

$$\dot{\vec{q}} = J^{\dagger}(\vec{q})\dot{\vec{X}}$$

where $J^{\dagger}$ is the Moore-Penrose pseudoinverse defined by $J^{\dagger} = J^{T}(JJ^{T})^{-1}$. This relationship can be further modified to obtain solutions in cases where there are more degrees of freedom than coordinates in the position vector.

The method referred to as the 1DOF method is a degenerate version of the other two methods. In the 1DOF method, the only joint angle that can change is the one at the currently defined root, independent of the proximity of the root and end-effector. All of the links that are between the root and the end-effector are treated as a single solid object. In the case that the root and the end-effector are chosen to be adjacent links, all three methods will produce the same results.

The term *true inverse kinematic methods* will be used to refer to the CCD and Jacobian methods because they may change the joint angles at any of the joints between the root and the end-effector. This term does not apply to the 1DOF method because it only adjusts the joint at the root, independent of the placement of the end-effector.

2.1.1 Implementation Issues

All three methods use the same user interface to avoid having the user interface bias the results of the experiment. To indicate the desired location of the end-effector, the user first presses the left mouse button to select the end-effector and then holds the button down while moving the mouse. The system tracks the mouse cursor. It performs each iteration of the inverse kinematic algorithm using the current mouse position at that time as the desired end-effector location. Because users do not move the mouse very quickly in relation to the speed of calculation of an iteration, there is a relatively small difference in the mouse positions used in consecutive iterations. As a consequence, the CCD method and the Jacobian method calculate similar configurations and appear almost identical to the user unless the mouse is moved very rapidly.

A translation feature, that allowed the user to translate the entire chain in space, was built into the system. This feature was disabled for the experiment as it was decided to only use configurations where translations were not necessary. This decision simplified the subjects' task and also allowed the user interface to be simplified.

The CCD method [WC91] and the Jacobian method [SS88] are described in the context of robotics. As a result, these methods assume that the chains being manipulated are simple chains and that these chains are rooted at a fixed end. When implemented, these methods were modified to deal with complex chains that had a branching point.

They were also modified to allow for the placement of the root anywhere on the chain, including situations where the orientation of the chain is reversed (e.g. when the root is "below" the end-effector).

Both the CCD method and the Jacobian method have the ability to handle joint limits. The Jacobian method can also find solutions that avoid obstacles. These aspects of these two methods were not implemented as it was known at the time of implementation that they were not going to be necessary in the experiment.

The 1DOF method was implemented as a version of the Jacobian method rather than as a version of the CCD method. This choice was made because the Jacobian method was easier to implement than the CCD method. This was partly because an iteration step is a one-part process in the Jacobian method and a two-part process in the CCD method.

All three of these methods include a *weighting factor* for each joint that controls the joint's resistance to change in position. This weighting factor is used to modify the step size taken at each iteration. In the paper by Sciavicco and Siciliano [SS88], the term *gain* is used in place of the term weighting factor.

The CCD method [WC91] gives an equation for calculating the weighting factor but this equation includes a sizing factor that is dependent upon the length of the link. No information quantifying this dependency is provided in the paper. Similarly, Sciavicco and Siciliano [SS88] state that an adequate choice for the gain in the CCD method is related to the inverse of the sampling period but no quantification of this relation is given.

For the experiment, a weighting factor of 10.0 was used for all of the joints in all of the chains for all of the methods. The value of 10.0 was chosen after experimentation by an experienced user of the system as it provided a balance between controllability and sensitivity. A constant weighting factor was chosen in order make all chains react the same and to avoid introducing a possible bias into the experiment.

2.2 Shape-Matching

The goal of this thesis is to compare the capabilities of the three positioning methods. One approach would involve asking animators to position a figure based on a verbal or written description of the desired final configuration. This approach mimics the normal creative process in which the animator has an initial mental image of the desired configuration. Animators could be asked to rank the different positioning methods after using each of them to perform a variety of positioning tasks.

A weakness of this approach relates to the specification of the final configuration. A verbal or written description can be interpreted differently by different people. If the subjects are not actually trying to attain the same final configurations, their experiences with the different positioning methods may not be comparable and thus their rankings may not be comparable. In addition, an individual subject may change his or her interpretation of the desired final configuration. The interpretation may be biased by the positioning method itself. In this case, it would be difficult for a subject to objectively rank the positioning methods.

In addition, this approach relies on the subjective data of rankings by the subjects in order to compare the positioning methods. It is preferable to have a design that allows for the collection of objective data and for the comparison of results for the same task performed using the different positioning methods and by different subjects. In such an experiment, subjects can be asked to manipulate a chain from an initial given configuration to a specified final configuration. The time taken by the subject to perform the manipulation and the accuracy of the final configuration attained can be measured and analysed.

To allow comparisons of user performance, all subjects must have the same goal for a particular trial. One way of ensuring this is to change the task from one of creating a configuration from a written or verbal description to one of matching a displayed configuration. The subject has to manipulate the chain from a given initial configuration to match the given goal configuration as accurately as possible in as little time as possible. This chain-matching approach was used in the experiment. Results from this experiment should carry over to an animator's task of designing and creating a final configuration.

A similar application of the shape-matching paradigm has been used to compare formulations for manipulating splines in both two and three dimensions [Rue89, Jan92].

Chapter 3

Experiment Design

An experiment was conducted to compare the performance of subjects on a series of chain matching tasks using the three positioning methods described in Section 2.1. The hypothesis for the experiment was

> Inverse kinematics provides a faster and more accurate way of positioning articulated figures with many degrees of freedom than manipulating these figures one degree of freedom at a time.

The null hypothesis for the experiment was

> There is no advantage to using inverse kinematics for positioning articulated figures with many degrees of freedom.

3.1 Design

The experiment consisted of a series of 15 trials that were repeated by each subject for each of the three positioning methods. A Latin square design was used to determine the order in which the 30 subjects encountered the three different methods. This design ensures that all methods will be evenly affected by learning effects.

3.1.1 Ordering of Methods

The subjects were split into three groups. All of the subjects within each group started with the same method first. Subjects within the same group had a common second and third method as well. Details regarding the placement of individual subjects into a particular group are in Section 3.2.

The subjects were numbered after the experiment was completed. The numbering of the subjects was not related to the order in which they did the experiment. The first group, consisting of subjects 1 through 9, used the Jacobian method as their first method, the CCD method as their second method and the 1DOF method as their third method. The second group of subjects, consisting of subjects 10 through 18, used the CCD method as their first method, the 1DOF method as their second method and the Jacobian method as their third method. Finally, subjects 19 through 27 made up the third group. They used the 1DOF method as their first method, the Jacobian method as their second method and the CCD method as their third method. Subjects 28, 29 and 30 were grouped separately due to problems with their sessions. These problems are described in Section 4.2.

3.1.2 Ordering of Trials

The order of the 15 trials was the same for all of the subjects and it was the same for all of the methods. The same trials were presented for each of the methods in order to allow the comparison of a subject's results from the three methods. The order of the trials was kept constant in an attempt to minimize learning effects. The same trials were presented to all of the subjects to enable the comparison of results from various subjects.

In each trial the subject was presented with a chain in a given initial configuration (with the links drawn in alternating light and dark blue and the joints drawn in white) and a given given goal configuration (drawn in yellow). The subject's task was to manipulate the chain representing the initial configuration to match the goal configuration as closely as possible in as little time as possible.

3.1.3 Configurations Used in Trials

With the assistance of our on-staff animator, several classes of positioning configurations were identified. Four of the classes were: smoothly curved objects, zig-zags, branching structures and a torso with an attached pair of legs. Example chains belonging to these four classes were constructed. These chains had between 5 and 10 links. Configurations to be used in the experiment were chosen from the example chains.

Figures 3.1 through 3.4 each show an example of one of the four classes. In these figures, the goal configuration is displayed in medium gray. The links of the initial configuration are drawn in alternating light and dark gray and the joints are represented by white circles that are outlined in black.

Appendix C contains the specifications of all of the chains used in the experiment. It includes diagrams showing the initial and goal configurations for each trial.

An attempt was made to choose a set of initial/goal pairs where various manipulation techniques would be required. For some of the initial/goal pairs, it was anticipated that single degree of freedom manipulation would be required (i.e. where the capability of an inverse kinematic algorithm to adjust more than one degree of freedom at a time would be of little or no use). It was expected that adjusting many links at a time with an inverse kinematic algorithm would allow a subject to perform a more efficient manipulation for other selected initial/goal pairs. Yet other initial/goal pairs were chosen where there was no advance expectation of the optimal movement technique.

To simplify the matching tasks, all of the initial/goal pairs of chain configurations were created with one coincident joint. In all of the trials, this is the joint closest to the top of the screen, which is the inherent root of the chain. The experiment system allows subjects to select other joints as the root for purposes of moving the chain and in effect even allows subjects to reverse the orientation of the chain by having the end-effector

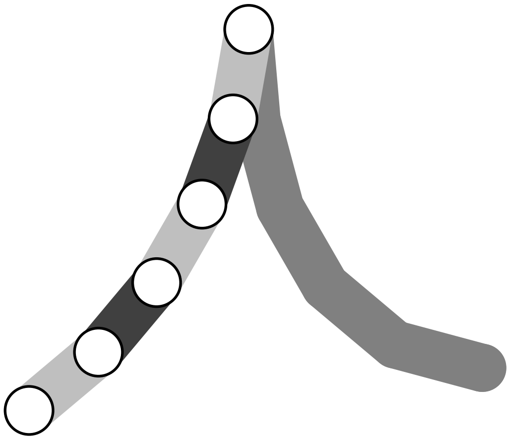

Figure 3.1: Example of a Smoothly Curved Object

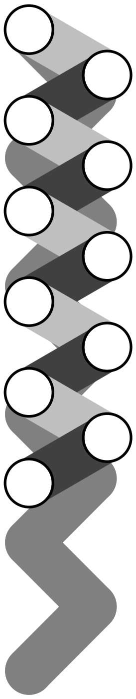

Figure 3.2: Example of a Zig-zag

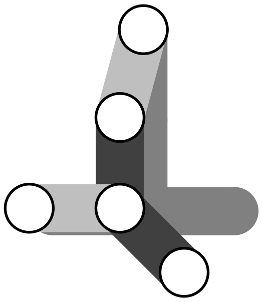

Figure 3.3: Example of a Branching Structure

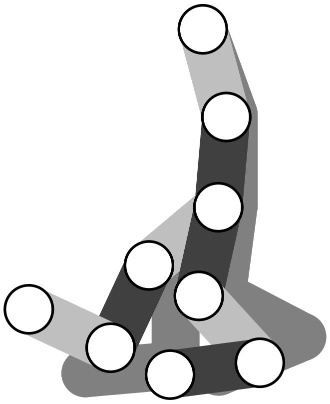

Figure 3.4: Example of a Torso with an Attached Pair of Legs

“above” the root. This reversal is not actually necessary to complete any of the trials but the functionality was left in the system to allow for greater flexibility.

The trials were ordered in terms of increasing difficulty. The ordering was done subjectively by an experienced user of the system after she used each of the methods to complete each of the trials several times. There are three trials involving a torso with an attached pair of legs that form a walking sequence. These three trials were treated as one trial for the purposes of ordering the trials and were presented in the experiment in the walking sequence order.

The first twelve trials except for trial 10 use simple chains (with no branching points). Trial 10 and the last three trials use complex chains (with a branching point). Some configurations are used in more than one trial.

Trials 1 through 5, 8 and 11 involve chains that belong to the class of smoothly shaped objects. The same initial configuration is used for trials 1, 5 and 8. This configuration is identical to the goal configuration for trial 4. The configurations used in trials 4 and 8 are reversals of each other. The initial configuration of trial 4 is the goal configuration of trial 8 and vice versa. Trials 2 and 11 also use configurations that are reversals of each other.

Trials 6, 7, 9 and 12 utilize chains that belong to the zig-zag class. Trials 6 and 7 use chains with the same initial configuration. The chains in trials 9 and 12 have the same goal configuration. Trials 7 and 9 are reversals of each other as are trials 6 and 12.

The chain used in trials 13, 14 and 15 represents a torso with an attached pair of legs. The configurations in these three trials form a series that can be used to keyframe a walk cycle. The goal configuration for trial 13 is the initial configuration for trial 14 and the goal configuration for trial 14 is the initial configuration for trial 15.

3.2 Subjects

Subjects were solicited from three groups: i) students taking a first year undergraduate computer science course, ii) senior undergraduate students working in the computer science department and iii) graduate students or post doctoral students either in the computer science department or with ties to the computer science department. All subjects volunteered to participate and were not compensated for their participation.

A total of 30 subjects participated in the experiment. Of these, 19 were male and 11 were female. All of the subjects had prior experience using a mouse. Background information was collected from these subjects and is summarized in Appendix A.

The subjects were assigned to one of three groups. Each subject's gender and background (first year undergraduate, senior undergraduate or graduate/post doctoral student) were known before the subjects came for their first experiment session. The subjects were placed into the three groups so that they were evenly divided across the groups along gender lines and along background lines.

3.3 Equipment

The experiment was run on an IRIS 4D/240 VGX computer. The subject was the sole user of the computer and all processing took place locally in order to avoid the impact of any network delays.

The experiment was conducted in an isolated office. The CPU of the computer was located in another room. The 19" computer monitor was centered on a computer table. A height-adjustable chair on casters was located in front of the table directly in front of the monitor. Subjects were allowed to adjust the height of the chair and position it as they desired. Typical viewing distances for subjects while doing the experiment was between 18 and 24 inches. The keyboard was moved off to the left side of the monitor as it was not used during the experiment. A mechanical mouse and foam mouse pad were on the table in front of the monitor. The overhead lights were off. A desk lamp was located on the back right-hand corner of the computer table and it was initially switched on.

3.4 Procedure

The remainder of this chapter details the procedure that each subject followed when performing the experiment.

In an attempt to minimize fatigue, the experiment was split into two sessions. During the first session the subject was asked to fill out a consent form and a subject information form that collected the background information referred to previously (sample forms are in Appendix B).

After filling out the two forms, the subject was escorted into the experiment room and was told to adjust the chair and the location of the mouse and mouse pad as desired. Subjects were advised that they could leave the desk lamp on or turn it off. Subjects were also told that they could come out of the room to ask questions.

When the subject was comfortable, a black curtain was drawn around the subject and computer and the subject was left alone in the room. The curtain isolated the subject from distractions from other objects in the room and also blocked out daylight.

The session started with the subject going through an IRIS Showcase (TM) slide show that served as a tutorial. More details about the tutorial are in Section 3.4.1.

After completing the tutorial, the subject performed the series of 15 trials using one of the three positioning methods. At the end of each trial, the subject rated the match attained. More details about the procedure followed to complete a trial are in Section 3.4.2. After completing the set of trials using a particular positioning method, the display showed a message that instructed the subject to advise the person supervising the experiment that s/he was finished. The subject then filled out a questionnaire about the particular method just used (copies of the questionnaires are in Appendix B). This completed the first session. The date and time of the subject's second session was verified before the subject left.

In the second session the subject was immediately escorted into the experiment room. The subject used the tutorial to become familiar with the second positioning method and then completed the series of 15 trials using the second method. The subject then completed a questionnaire. This questionnaire included questions that asked the subject to compare this positioning method to the positioning method used in the first session. The subject then returned to the experiment room, used the tutorial to become familiar with the third method and performed the series of 15 trials for the last time. The final questionnaire that the subject filled out asked the subject to compare all three positioning methods.

3.4.1 Tutorial

The tutorial was an introduction to the study and the system used in the experiment. Screen dumps of the tutorial pages are in Appendix D.

The tutorial defined and illustrated the concepts of links, joints, pivot points and manipulation points. The terms pivot point and manipulation point were used in the tutorial and questionnaires in place of the terms root and end-effector respectively since the former are more familiar to people who do not have prior knowledge of inverse kinematics.

The tutorial explained how to choose the pivot point and manipulation point and how to move the chain around. The subject was given the opportunity to practice each step as it was presented. Three complete sample trials were presented at the end of the tutorial.

The sample trials were labelled 1, 2 and 3 and increased in difficulty. The sample trials included rating the match. Subjects were asked to do each of the three sample trials at least once but they were told that they could do each sample trial as many times as they desired. Subjects were asked to experiment with the sample trials and were advised to not worry about the amount of time being taken to do the sample trials. The tutorial asked the subject to pick different combinations of pivot and manipulation points to see how the particular method reacted under various circumstances. At the end of the tutorial, subjects were prompted to click on a button when they were ready to start the experiment.

A slightly different version of the tutorial was used for a subject's second and third positioning methods. This version told the subject that pivot points and manipulation points were selected as before and that the mouse was used to move the chain as before, but that the computer would move the chain differently in response to movements of the mouse. The subject was then given the option of reviewing the instructions or going directly to the sample trials. In either case, the screen with the three sample trials was eventually displayed and the subject was asked to complete each of the three sample trials at least once. The same three sample trials were presented for each of the three methods. The same sample trials were presented each time so that the subjects could explore the differences between the three methods.

3.4.2 Procedure for a Trial

During each trial the subject first used the middle mouse button to choose a root. Then the subject used the left mouse button to choose an end-effector. The subject kept the left mouse button down while moving the mouse to indicate the desired location for the end-effector. The subject continued adjusting the chain, picking a different root and/or end-effector as desired until s/he wished to terminate the matching process (either the match was completed to the subject's satisfaction or the subject was unable to improve upon the match). The subject indicated that the match was completed by clicking on a button labelled "DONE" at the bottom of the screen. After a match was completed, the chains were removed from the screen and the subject was asked to rate the match just completed. The subject was presented with a screen with five large yellow buttons. The row of buttons was displayed in the middle of the screen.

. The buttons were labelled "Perfect Match", "Almost Perfect", "Pretty Good", "Satisfactory" and "Unsatisfactory" from left to right. Rating categories with a bias towards a good match were used as it was assumed that most subjects would continue manipulating the figure until a good match was attained. The "Unsatisfactory" rating category allowed a subject to indicate that s/he was not happy with a match but could not improve upon it.

Once a rating button was selected, the buttons were removed from the screen and the experiment paused until the subject indicated that s/he was ready to continue by clicking on a green button labelled "NEXT TRIAL".

Chapter 4

Data Collection and Analysis

4.1 Data Collection

At the start of each trial, the subject's name, the positioning method being used, the trial number, the goal configuration and the initial configuration of the chain used during the trial were written to a file. The sequence of joint angles of the chain was used to record each configuration. The data file was written onto the local disk of the computer being used to run the experiment to ensure that the writing of the data and the timing of the trials would not be affected by network delays.

Each joint in the chain was assigned an identification number when the chain was initially constructed. During the trial, the joint's identification number was recorded in the data file each time the subject chose it as a root or an end-effector. Each time the subject released the left mouse button and thereby reset the end-effector, the current configuration of the chain was also written to the data file. The final configuration of the chain attained by the subject was recorded when the "DONE" button was pressed.

Timing information, in tens of milliseconds, was recorded along with each of the events mentioned. The timing of a trial started when the goal and initial configurations of the chain were displayed on the screen and ended when the subject pressed the "DONE" button. As a result, the time taken for a trial included any time that the subject spent looking at the match considering what to do next (including time at the beginning of the trial, at the end before hitting the "DONE" button and during the trial when choosing a root, end-effector or moving the chain around). The time involved in moving the mouse cursor from its initial position centered in the window to the desired spot on the chain and from its final position on the chain to the "DONE" button centered at the bottom of the screen was also included.

4.2 Excluded Subjects

Results from three of the 30 initial subjects were not used in the analysis. The data analysis was done with subjects 1 through 27. Data from these subjects appears in Appendix E.

Subject 28 was unable to get the sample trials to appear on the screen. Rather than seeking help with this problem, she continued on to the experiment trials. The tutorial did not force subjects to complete all three sample trials before starting the experiment trials, but the instructions did tell subjects to try each one at least once before continuing. Since subject 28 did not have any practice before starting the experiment trials using her first method, her results from the first session included learning effects that were not present in her second session or in the first sessions of the other subjects. As a consequence, subject 28's data was unsuitable for inclusion in the data analysis.

During subject 29's first session, the computer crashed in the middle of the sixth experiment trial. After a delay of several minutes while the machine rebooted, the subject resumed the session starting at the beginning of the sixth trial. Since all of the other subjects completed all 15 trials using a particular method without such a delay, this disruption was considered significant enough exclude subject 29's data.

Subject 30 started her second session but was unable to stay to complete the entire second session. She completed the first part of the second session and filled out the corresponding questionnaire but then could not stay to do the second part of the second session at that time. She completed the portion of the experiment involving her third method in a third session which was held four days later. Since all of the other subjects completed the entire experiment in only two sessions which were at most three days apart, this subject's participation was considered unusual enough to exclude her data.

The problems with these three subjects arose early enough in the experiment cycle that it was possible to maintain the balance of the three groups according to gender and background category. For each of these three subjects, another subject of the same gender from the same background category who had not yet started the experiment was chosen as a replacement and was put in the appropriate group.

4.3 Initial Analysis

Initial analysis of the data included the calculation of two error metrics for determining the "closeness" of the configuration attained by the subject to the goal configuration. One error metric is the sum of the squares of the differences in joint angles between the goal position of the chain and the position attained by the subject. This error metric, henceforth referred to as the *angle error*, has units of degrees squared. The second error metric is the sum of the squares of the Euclidean distances between endpoints of the corresponding links of the goal configuration and the configuration attained by the subject. This error metric is called the *positional error*. The Euclidean distances are calculated in world coordinates and therefore the positional error metric has units of world coordinates squared. For reference purposes, the links in each chain were rectangles that were 10 units wide and 20 units high in world coordinates.

The same scale for measuring errors was used for each trial. This allowed data from various trials to be grouped even though the trials were not all of the same difficulty. Table 4.1 summarizes the values of the angle error metric and the positional error metric

Trial	Angle Error	Positional Error
1	100.00	153.83
2	150.00	97.15
3	3375.00	225.63
4	750.00	128.12
5	1200.00	88.19
6	8325.00	229.85
7	133200.00	571.32
8	750.00	128.12
9	133200.00	571.32
10	5850.00	439.19
11	150.00	97.15
12	8325.00	229.85
13	11506.25	63.71
14	550.00	71.87
15	1375.00	38.46

Table 4.1: Initial Error Metric Values

at the beginning of each trial (rounded to two decimal places).

Trials 13, 14 and 15 use the chain that represents a torso with an attached pair of legs. The subchains that make up the two legs of this chain are interchangeable. When calculating the values of the error metrics for these three trials, the data was tested to check if the subject had interchanged the two legs. This check was made to ensure that the error metrics would not be inflated by a subject swapping the legs. None of the subjects interchanged the legs so no corrections for this needed to be made.

Also determined during the initial analysis were counts of the number of joints chosen to be roots and end-effectors during each trial. This is an upper bound on the number of roots and end-effectors actually used for positioning as the data was not filtered. If, for example, a subject picked one joint as the root and then decided to pick another joint as the root without choosing an end-effector or moving the chain in between, both occurrences would increase the count of the number of roots selected.

In addition, the *distance* between the root and end-effector was calculated for each root/end-effector pair. The distance between the root and the end-effector is the number of links separating the two joints. The values for the distance can range from 0, when the root and the end-effector are chosen to be the same joint, to the number of links in a simple chain having no branches, when the root and end-effector are at opposite ends of the chain. The distance is negative if the end-effector is "above" the root.

The system did not actually prevent the subject from choosing the same joint for the end-effector that s/he had already chosen for the root. If, however, the root and the end-effector were chosen to be coincident, the configuration of the chain was not affected by any mouse movements.

The data was sorted by the time taken for a match and by each of the final values of the two error metrics. The data was sorted in order to check for outliers, where an outlier was considered to be any value that was anomalous when compared to the main group of data.

Subject 10

Sorting the data revealed outlying error values corresponding to trials 2 through 15 for subject 10 when using the 1DOF method. She ranked 13 of these 14 matches as Unsatisfactory. She had ranked all of the sample matches in the tutorial for the 1DOF method as Unsatisfactory as well.

This subject did not appear to understand the general strategy required to attain a match using the 1DOF method. She always set the root to be the top joint of the chain and then proceeded to position the chain by picking various joints as the end-effector and moving the mouse cursor. Selecting different end-effectors does not change the fact that the 1DOF method only modifies the joint angle at the root. Thus, it is impossible to adjust any angles other than the top one using subject 10's strategy with the 1DOF method.

It is possible to use this strategy with the 1DOF method to attain a match for trial 1 as the only difference between the initial configuration and the final configuration for trial 1 is the joint angle at the top of the chain. It is also possible to attain a reasonable match using this strategy with either of the true inverse kinematic methods.

For trial 1, subject 10's strategy did not preclude exact matches for any of the three positioning methods and other subjects used a similar strategy for this trial. However, for the remaining trials, subject 10's strategy could not be used to attain a reasonable match for the 1DOF positioning method. As a consequence, subject 10's data for trials 2 through 15 using the 1DOF method was not analysed along with the data from all of the other subjects.

Subject 12

Sorting the data for the two error metrics revealed that subject 12 did not improve upon the initial match given for trial 11 using his second method, which was the 1DOF method. The trace data for this match showed that subject 12 did not attempt to adjust the initial match given. He did not pick a root or an end-effector but just looked at the match and then clicked on the "DONE" button. He rated this match as Pretty Good so it does not appear as if he accidentally hit the "DONE" button before completing the match. The completed questionnaire filled out by subject 12 after finishing the set of trials using the 1DOF method mentioned that one trial during this session "was already done" for him. According to the trace data, trial 11 was displayed properly and thus was not already completed. If this trial was the trial that the subject claimed was already completed, it is puzzling why he only gave the match a rating of Pretty Good as this is the middle rating category.

Since this trial was not actually attempted by subject 12 when using the 1DOF method, it was removed from further analysis. Subject 12's 44 other trials (all 15 Jacobian trials, all 15 CCD trials and trials 1 through 10 and 12 through 15 using the 1DOF method) were used in the remaining analyses.

4.4 Further Analysis

Additional analysis involved the data as a complete set, split by subject group, by trial category, by the number of links in the chain and by trial. In addition, the data was thresholded based on the positional error and the analyses were repeated with the thresholded data.

The additional analysis involved a statistical analysis of variance (ANOVA) calculation using the data for the time, angle error metric and positional error metric at the end of each trial. A 95% confidence interval was used in the calculation of the ANOVA. For each ANOVA, an F value and a p value are reported. The F value is a ratio of the differences between groups to the differences within a group. A value higher than 1.0 indicates more of a difference between groups than within groups. The p value is a measure of the probability that this difference is due to random chance.

A Fisher's protected least significant difference (PLSD) post hoc analysis of significant results was used to determine the cause(s) of the significance. The significance level was set at 5%. This test uses a t statistic to evaluate all pairwise differences in the data.

More thorough explanations of these statistical tests can be found in introductory statistics books [Kep91, Moo85].

4.4.1 Summary of Statistically Significant Results

When all of the trials were grouped together, the data indicated that subjects took significantly more time to complete trials using the Jacobian method as compared to the 1DOF method. Significantly smaller positional errors were attained when using the 1DOF method than when using either of the other two methods. Complete results of the statistical analyses are in Table 4.2 and the discussion of the significant results is in Section 4.4.2.

The data was split according to the subject group (which determined the ordering of the methods used). The group that started with the Jacobian method first took significantly longer to complete the trials using the Jacobian method as compared to the CCD method and the 1DOF method. The group that started with the CCD method took significantly longer to complete the trials using the CCD method as compared to the other two methods. Results from the group that started with the 1DOF method first showed that these subjects made significantly more accurate matches (according to the positional error metric) with the 1DOF method than with the Jacobian method. Table 4.3 contains the results of the analyses and Section 4.4.3 contains the discussion of the significant results.

When the trials were grouped according to the method that was expected to generate accurate matches in the shortest period of time, there was a significant difference in the times and positional errors for the trials in the 1DOF category. These trials, for which the 1DOF method was expected to produce the best results, were done significantly faster when the 1DOF method was used than when the Jacobian method was used. The positional errors attained for the trials in this category were significantly less when the 1DOF method was used as compared to the Jacobian method as well. The results of the analyses are in Table 4.4 and a discussion of the significant results is in Section 4.4.4.

The trials were also grouped according to the number of links in the chain used in the trial. For trials using a chain with 6 links, the matches made with the CCD method were significantly faster than those made with the 1DOF method. For trials involving a chain with 9 links, the positional error values attained using the 1DOF method were significantly less than those attained using either of the other two methods. The matches made with the 1DOF method were significantly faster than those made with the Jacobian method for the trials involving chains with 10 links. The positional errors for these trials done using the 1DOF method were significantly less than those done with the CCD method. The complete set of results from the analyses are in Table 4.5 and a discussion of the significant differences appears in Section 4.4.5.

The data was also analysed separately for each trial. The trial 1 matches that were made with the 1DOF method were significantly more accurate (according to the angle error metric) than those made with the CCD method. The trial 9 matches that were performed using the 1DOF method were completed in significantly less time than those performed with either the Jacobian method or the CCD method. A complete listing of the results is in Table 4.6 and a discussion of the significant results is in Section 4.4.6.

The data was thresholded based on the positional error metric (more information on the thresholding process is in Section 4.5). The same analyses were repeated on the thresholded data. Since the data was thresholded using the positional error value, it is not surprising that several analyses that showed statistically significant differences in positional errors when using the original data no longer showed statistically significant differences when using the thresholded data.

In the analysis of the entire set of thresholded data treated as one group, the trials done with the Jacobian method once again took significantly longer than those done with the 1DOF method. Table 4.8 displays the results for the thresholded data and Section 4.5.1 contains the discussion of the statistically significant result.

The thresholded data split according to subject group showed statistically significant differences in the time taken for the trials completed by the group of subjects who used the Jacobian method first. These subjects once again took significantly longer to perform trials using the Jacobian method than they took when using either of the other two methods. The results of the analyses are in Table 4.9 and the discussion of the significant result is in Section 4.5.2.

When the thresholded data was grouped according to the method that was expected to generate accurate matches in the shortest period of time, there was at least one statistically significant difference in each of the four categories. Table 4.10 contains the results of the analyses for all of the categories and Section 4.5.3 contains the discussion of all of the significant results.

In the category consisting of trials for which the 1DOF method was expected to have the best performance, the matches were made in significantly less time when the 1DOF method was used than when either of the other two methods were used.

The category containing trials for which the two true inverse kinematic methods were expected to have the best performance had two significant results. The matches attained when using the 1DOF method were less accurate than those attained with the CCD method when measured by both the angle error metric and the positional error metric. The matches made with the 1DOF method were also less accurate than those made with the Jacobian method, according to the positional error metric.

It was expected that using either of the two true inverse kinematic methods to manipulate sections of the chain at once would produce the best results for the trials in the third category. For these trials, the matches made with the 1DOF method were significantly faster than those made with the Jacobian method.

The last category consisted of the trials that did not fit into any of the first three categories. There was no advance expectation of which positioning method would work best for these trials. For trials in this category, the matches made with the 1DOF method were significantly less accurate (in terms of the positional error metric) than those made with either of the other two methods.

Statistically significant results were also found when the trials were grouped according to the number of links in the chains. For the group of trials with 6 links, the matches made with the 1DOF method were less accurate (according to both error metrics) than those made with either of the two other methods. For the group of trials with 10 links, the matches made using the 1DOF method were significantly faster than those made with either of the other two methods. The results of the analyses are in Table 4.11 and the discussion of the significant results is in Section 4.5.4.

The analysis of the thresholded data split by trial showed at least one statistically significant result for trials 1, 2, 3, 7, 8, 9 and 11. Table 4.12 contains complete results of the analyses for all of the trials and Section 4.5.5 contains the discussion of the statistically significant results.

The trial 1 matches that were made with the 1DOF method were more accurate (according to the angle error metric) than those made with the CCD method.

The trial 2 matches made with the 1DOF method were less accurate (according to both error metrics) than those made with the CCD method.

When the matches made for trial 3 were examined, those trials performed using the 1DOF method were less accurate (according to the angle error metric) than those performed using either of the other two methods. According to the positional error metric, the trial 3 matches made with the CCD method were more accurate than those made with either of the other two methods.

The trial 7 matches made with the 1DOF method were significantly more accurate (according to both error metrics) than the matches made with either the CCD method or the Jacobian method.

When the data from the trial 8 matches was analysed, the matches made with the 1DOF method were found to be less accurate (according to the positional error metric) than those made with the Jacobian method.

The trial 9 matches were found to have been done faster with the 1DOF method than

Experiment Variables	F Value	p Value
Time and method	4.200	**0.0152**
Angle error and method	2.771	0.0630
Positional error and method	6.064	**0.0024**

Table 4.2: Results of ANOVA with All Data

with either of the other two methods.

The trial 11 matches that were made with the 1DOF method were found to be less accurate (according to the angle error metric) than the matches made with either the Jacobian method or the CCD method.

4.4.2 Data from All Trials

An initial ANOVA was done using all of the data from subjects 1 through 27 except for subject 12's trial 11 using the 1DOF method and subject 10's trials 2 through 15 using the 1DOF method. A summary of the results of the ANOVA are in Table 4.2 with the significant results shown in bold face.

The post hoc analysis showed that subjects generally took longer when using the Jacobian method than when using the 1DOF method. The matches attained with the 1DOF method were significantly more accurate (in terms of the positional error metric) than those made with either of the other two methods.

Additional analyses were done to explore and account for the various differences. As the data is split in various ways, there are fewer values in each individual group and thus differences within the groups are magnified.

Group	Experiment Variables	F Value	p Value
Jacobian Method First	Time and method	14.000	< **0.0001**
	Angle error and method	1.648	0.1937
	Positional error and method	1.339	0.2633
CCD Method First	Time and method	6.052	**0.0026**
	Angle error and method	1.889	0.1527
	Positional error and method	1.192	0.3047
1DOF Method First	Time and method	1.879	0.1541
	Angle error and method	0.953	0.3864
	Positional error and method	4.247	**0.0150**

Table 4.3: Results of ANOVA Split by Group

4.4.3 Data Split by Group

As part of the additional analysis, the data for the three groups of subjects was analysed separately. A summary of the results of the ANOVA using the data split by subject group is in Table 4.3.

The data was split by group to see if the order in which the subjects encountered the various methods had any effect on their results. The data for the group who used the Jacobian method first included the data from subjects 1 through 9. The data for the group who used the CCD method first included the data from subjects 10 through 18. The data for the group who used the 1DOF method first consisted of the data from subjects 20 through 27.

Group Using Jacobian Method First

The group of subjects who used the Jacobian method first took significantly longer to complete the trials using the Jacobian method as compared to the other two methods. This group of subjects started with the Jacobian method, used the CCD method second and the 1DOF method third. The mean time for their trials using the Jacobian method was 48.72 seconds. It was 35.79 seconds for their trials done with the CCD method and 31.05 seconds for the trials that they completed with the 1DOF method. The decrease in times across the three sets of trials was probably caused by learning effects due to the subjects becoming more familiar with the system as they performed the set of trials for the second and third times. In addition, when using the system for the first time, subjects may have found that taking extra time did not necessarily result in much improvement in the quality of the match. As a consequence, subjects may have not tried to make matches that were as perfect the second and third times. This supposition is explored in Section 4.5.

Group Using CCD Method First

For the group of subjects who used the CCD method first, the trials done using the CCD method took significantly longer than those done using either of the other two methods. This group of subjects started with the CCD method. They used the 1DOF method second and the Jacobian method last. The mean time for their trials using the CCD method was 40.63 seconds. It was 33.76 seconds for their trials using the 1DOF method and 32.60 seconds for their trials using the Jacobian method. Once again the decrease in the times could be attributed to learning effects.

Group Using 1DOF Method First

For the group of subjects who used the 1DOF method first, the trials done using the 1DOF method were significantly more accurate (in terms of positional error) than those done using the Jacobian method, with no significant differences in the time taken. The mean positional error using the 1DOF method was 3.833. It was 4.907 for the trials using the CCD method and 5.421 for the trials using the Jacobian method. This group of subjects used the 1DOF method first, the Jacobian method second and the CCD method third. In this case, the first method used by these subjects produced the most accurate matches. The mean positional error was highest for the matches made with the second method used by these subjects.

It was surprising that this group of subjects did not exhibit learning effects similar to the other two groups. Reviewing the link distance data for these subjects showed that these subjects did not just use the strategy of adjusting one link at a time with their second and third methods. They actually did take advantage of the ability of the Jacobian method and the CCD method to move more than one link at a time. It is possible that there was actually a learning effect but that the increased familiarity with the system was offset by the increased difficulty in using the true inverse kinematic methods as compared to the 1DOF method and thus no significant difference was evident.

4.4.4 Data Split by Category

The initial/goal configuration pairs had been chosen so that some were expected to be easier to match using the true inverse kinematic methods and others were expected to require manipulation of one link at a time. The data was split into categories according to these expectations for further analysis.

The trials were placed in one of four categories according to the expectation of which method would be easiest to use to complete the match. This expectation was based in part on the perception of an experienced user using all of the methods to try to attain an accurate match in a short period of time.

Trials 1, 9, 10, 13, 14 and 15 were placed in the *1DOF* category as it was expected that the manipulation of one link at a time would be required in order to achieve an accurate match. The *IK* category contained trials 2, 3 and 11. It was possible to attain an accurate match in a very short period of time for each of these three trials using either of the true inverse kinematic methods to manipulate the entire chain at once. Trials 6,

Category	Experiment Variables	F Value	p Value
1DOF	Time and method	4.039	**0.0182**
	Angle error and method	0.642	0.5267
	Positional error and method	3.049	**0.0483**
IK	Time and method	1.721	0.1812
	Angle error and method	1.686	0.1875
	Positional error and method	1.025	0.3605
IK Pieces	Time and method	2.545	0.0807
	Angle error and method	2.421	0.0911
	Positional error and method	2.230	0.1098
Unknown	Time and method	0.258	0.7729
	Angle error and method	0.853	0.4274
	Positional error and method	2.050	0.1310

Table 4.4: Results of ANOVA Split by Category

7 and 12 were placed in the *IK Pieces* category. For these three trials it was possible to attain an accurate match in a short period of time using one of the inverse kinematic methods if the chain was treated as several groups of links and the groups were matched one at a time. The remaining trials (4, 5 and 8) were placed in the *Unknown* category as there was not an apparently optimal way of making a match in these trials.

The results of the analyses of the data grouped by category are in Table 4.4.

The only significant results were in the 1DOF category. Subjects took longer to complete trials when using the Jacobian method than when using the 1DOF method. The trials performed using the Jacobian method were less accurate (in terms of the positional error metric) than those performed using the 1DOF method. It is not surprising that faster and more accurate results were obtained when using the 1DOF method as this group contained trials for which the 1DOF method was expected to give the best performance. It is surprising that there was not a significant difference between the CCD method and the 1DOF method for these trials. These differences (and lack thereof) are

Links	Experiment Variables	F Value	p Value
6	Time and method	3.655	**0.0282**
	Angle error and method	2.459	0.0890
	Positional error and method	0.259	0.7721
8	Time and method	0.711	0.4920
	Angle error and method	0.261	0.7705
	Positional error and method	0.956	0.3858
9	Time and method	1.353	0.2597
	Angle error and method	1.494	0.2257
	Positional error and method	4.704	**0.0096**
10	Time and method	4.671	**0.0100**
	Angle error and method	2.134	0.1201
	Positional error and method	3.508	**0.0312**

Table 4.5: Results of ANOVA Split by Number of Links

further explored in Section 4.5.3.

4.4.5 Data Split by Number of Links

Chains with similar ranges of motion have similar possible values for both the angle error metric and the positional error metric. The trials were grouped according to the number of links in the chain used in each trial in order to compare chains with similar ranges of motion. This grouping also compensated for possible differences in task complexity due to the number of links in the chain.

Trials 2 and 11 used chains with 6 links. The chains in trials 13, 14 and 15 each had 8 links. Trials 1, 4, 5, 8 and 10 utilized chains with 9 links. Chains with 10 links were used in trials 6, 7, 9 and 12. Trial 3 was the only trial that used a 5-link chain. The results of the analyses with the trials grouped by number of links are in Table 4.5. Analysis for trial 3 was not included in this section as all trials are analysed separately in Section 4.4.6.

For the group of trials using chains with 6 links, the matches made with the CCD method were significantly faster than those made with the 1DOF method. The true inverse kinematic methods were expected to have superior performance for both of the trials in this group so it is not surprising that the matches made with the 1DOF method took longer. It is surprising that the matches made with the Jacobian method were not significantly faster than those made with the 1DOF method.

The matches made with the 1DOF method were significantly more accurate (in terms of the positional error metric) than those made with either of the other two methods for the group of trials using chains with 9 links. The trials using chains with 9 links were either in the category of trials for which the 1DOF method was expected to have superior performance or in the category of trials where it was unknown which method would have superior performance. Given that the times taken when using the three methods were not significantly different and that the 1DOF method was expected to have superior performance for some of the trials in this group, it is not surprising that in similar amounts of time, the 1DOF method produced results that were more accurate in terms of the positional error metric.

For the trials using chains with 10 links, the matches made with the 1DOF method took significantly less time than those made with the Jacobian method. These trials were all ones for which either the 1DOF method was expected to give faster performance or for which the true inverse kinematic methods needed to be used to manipulate sections of the chain rather than the entire chain at once. The difference in time can be partly attributed to the fact that many subjects reported trying to manipulate the entire chain at once in trials 6 and 7 and then giving up on that strategy after it did not produce quick results.

The trials using chains with 10 links also had significant differences in the positional errors attained when using the various methods. The trials completed using the 1DOF method were more accurate than those completed using the CCD method. This difference can also be attributed to the nature of the trials involved. If similar amounts of time are taken when using both methods and the approach of manipulating the entire chain at once is taken with the CCD method, the final error attained will be greater for the CCD method as this method tends to not make adjustments evenly along the chain.

4.4.6 Data Split by Trial

The data for each trial was also analysed individually in case significant differences for particular trials were being masked by the various groupings of the data. The results of the analyses are in Table 4.6.

The data from trial 1 showed a significant difference in the angle errors attained. The matches made with the 1DOF were more accurate than those made with the CCD method.

Given the construction of the initial and goal configurations for trial 1, this result is not surprising. The only difference between the initial and goal configuration for trial 1 is at the top joint. The initial configuration has a joint angle of 10 degrees and the goal configuration has a joint angle of 20 degrees. The rest of the joint angles are identical, so only the top angle needs to be adjusted in order to make a match. Using the 1DOF method, as long as the top link is chosen as the root, only the joint angle at the top of the chain will be adjusted, independent of which joint is chosen to be the end-effector. Thus, other joint angles that do not need to be changed will not be affected. Most subjects reported a matching strategy that involved starting at the top of chain and this strategy would work favourably for this trial with the 1DOF method.

On the other hand, since the CCD method is a true inverse kinematic method, all joints between the root and the end-effector may be adjusted. If a subject picked the root to be the top joint and the end-effector to be the second joint, the performance would

Trial	Experiment Variables	F Value	p Value
1	Time and method	0.646	0.5272
	Angle error and method	3.607	**0.0317**
	Positional error and method	2.565	0.0834
2	Time and method	1.783	0.1751
	Angle error and method	1.035	0.3603
	Positional error and method	0.824	0.4428
3	Time and method	0.082	0.9218
	Angle error and method	0.003	0.9972
	Positional error and method	1.951	0.1493
4	Time and method	0.120	0.8869
	Angle error and method	0.478	0.6222
	Positional error and method	0.557	0.5754
5	Time and method	0.048	0.9535
	Angle error and method	0.367	0.6941
	Positional error and method	0.909	0.4075
6	Time and method	0.791	0.4573
	Angle error and method	0.765	0.4690
	Positional error and method	0.685	0.5071
7	Time and method	2.162	0.1223
	Angle error and method	1.667	0.1958
	Positional error and method	1.578	0.2131
8	Time and method	1.595	0.2097
	Angle error and method	0.084	0.9195
	Positional error and method	1.338	0.2685
9	Time and method	5.616	**0.0053**
	Angle error and method	0.033	0.9674
	Positional error and method	1.259	0.2899
10	Time and method	1.640	0.2008
	Angle error and method	0.218	0.8048
	Positional error and method	0.926	0.4006
11	Time and method	1.823	0.1687
	Angle error and method	1.452	0.2408
	Positional error and method	0.105	0.9007
12	Time and method	0.506	0.6052
	Angle error and method	0.254	0.7762
	Positional error and method	0.591	0.5562
13	Time and method	1.576	0.2135
	Angle error and method	0.012	0.9879
	Positional error and method	0.670	0.5149
14	Time and method	0.057	0.9448
	Angle error and method	0.238	0.7887
	Positional error and method	1.070	0.3482
15	Time and method	0.252	0.7779
	Angle error and method	0.229	0.7960
	Positional error and method	0.178	0.8376

Table 4.6: Results of ANOVA Split by Trial

be similar to the 1DOF method. If any other root/end-effector pair was chosen, angles that did not need to be adjusted to make the match would be adjusted and thus a less accurate match would be attained in the same amount of time.

It is surprising that a similar difference between the 1DOF method and the Jacobian method was not evident, as the Jacobian method is also a true inverse kinematic method.

The trial 9 matches made with the 1DOF method were significantly faster than those made with either of the other two methods. This trial involved straightening a chain that was initially in a zig-zag configuration. Many subjects tried to put the root at one end of the chain and the end-effector at the other end and “pull” on the chain to get it to straighten. Since the true inverse kinematic methods tended to not make adjustments evenly along the chain, but rather tended to adjust angles closer to the end-effector (in part due to the user interface for indicating the desired position of the end-effector) this strategy was very time consuming. The direct approach of moving one or two links at a time was faster. Subjects often abandoned the “pulling” strategy in favour of moving a small number of links at a time, starting at the top of the chain.

Trials 2 through 8 and 10 through 15 did not show any significant differences.

4.5 Analysis of Intermediate Data

In addition to the data obtained at the end of each trial (when the subject clicked on the “DONE” button), data was also collected during each trial whenever the subject released the left mouse button (and thereby reset the end-effector).

The data for each trial was sorted to determine the value of the greatest final positional error that was not an outlier. The greatest final positional error for the trial was divided by the number of links in the chain used in the trial to obtain a per link positional error. The greatest of the fifteen per link positional errors was used to calculate a threshold value for each trial. The threshold value for a trial was set equal to the greatest per link positional error multiplied by the number of links in the trial. Table 4.7 indicates the greatest final value obtained for the positional error metric, the per link positional error and the threshold value used for each trial. The threshold value is also shown (rounded to two decimal places) as a percentage of the trial's initial positional error for reference purposes.

The experiment data was cut off for three reasons. First, thresholding the values meant that the data from subjects who spent time near the end of a trial trying to perfect a match could be compared more equally with subjects who did not try to make matches that were as precise. Second, there were trials in which some subjects ended up with a final match that was not as accurate as one of their intermediate matches for that trial. In trying to improve the match, the subject actually made the match worse (according to the error metrics) and did not attain the same level of accuracy by the end of the trial. Third, in other cases the subject did end the trial with the most accurate match of the trial, but s/he spent a considerable amount of time to produce a final match that was only marginally better than an intermediate match.

The data was filtered and the first time at which the positional error was less than or equal to the cutoff value was recorded. The value of the angle error metric was also recorded. Out of the 1215 total trials, there were 11 trials for which this filtering caused a change and 16 trials that were outliers. The 11 filtered trials and the 16 outlier trials are identified as such in the data in Appendix E.

The 16 outlier trials all belonged to one of three subjects (subject 10, subject 12 or subject 19). All remaining analyses did not include the 16 trials that were identified as outliers.

The results of the analyses of the thresholded data for the remaining 1199 trials are shown in Table 4.8.

Trial	Max. Error	Per Link Error	Threshold Error	% of Initial Error
1	15.00	$1.\dot{6}$	26.46	17.20
2	7.29	1.215	17.64	18.16
3	6.20	1.24	14.70	6.52
4	9.93	1.10	26.46	20.65
5	26.46	2.94	26.46	30.00
6	23.55	2.355	29.40	12.79
7	20.00	2.0	29.40	5.15
8	11.22	$1.24\dot{6}$	26.46	20.65
9	22.85	2.285	29.40	5.15
10	13.18	$1.46\dot{4}$	26.46	6.02
11	8.50	$1.41\dot{6}$	17.64	18.16
12	17.24	1.724	29.40	12.79
13	11.15	1.39375	23.52	36.92
14	13.65	1.70625	23.52	32.73
15	19.81	2.47625	23.52	61.15

Table 4.7: Threshold Positional Error Values

Experiment Variables	F Value	p Value
Time and method	4.891	**0.0077**
Angle error and method	0.268	0.7647
Positional error and method	0.409	0.6644

Table 4.8: Results of ANOVA with Thresholded Data

Group	Experiment Variables	F Value	p Value
Jacobian	Time and method	7.369	**0.0007**
Method	Angle error and method	0.032	0.9689
First	Positional error and method	0.070	0.9326
CCD	Time and method	2.499	0.0844
Method	Angle error and method	0.908	0.4042
First	Positional error and method	0.007	0.9935
1DOF	Time and method	0.603	0.5475
Method	Angle error and method	0.182	0.8339
First	Positional error and method	0.673	0.5105

Table 4.9: Results of ANOVA Split by Group (Thresholded Data)

4.5.1 Thresholded Data from All Trials

As with the original data, there was a significant difference in the time taken to make matches using the different positioning methods. The mean time for all of the matches was 26.21 seconds. For the individual methods, the mean times were 28.28 seconds for matches made with the Jacobian method, 26.58 seconds for matches made with the CCD method and 23.71 seconds for matches made with the 1DOF method. The difference in times for the matches made with the Jacobian method and those made with the 1DOF method was significant.

Since the data was thresholded based on an error value, it is not surprising that there was not a significant difference for either of the two error values, even though the original data showed a significant difference in the positional error.

4.5.2 Thresholded Data Split by Group

Once again the data was split into the three groups according to the method that the subjects first used. The results from the analyses are in Table 4.9.

Group Using Jacobian Method First

As before, the group of subjects who used the Jacobian method first took significantly longer to complete matches when using the Jacobian method as compared to either of the other two methods. This difference could, once again, be attributed to learning effects as these subjects were least familiar with the system when using the Jacobian method.

Group Using CCD Method First

There were no statistically significant results in the thresholded data from the group of subjects who used the CCD method first. The time was no longer significant, as it had been in the analysis using the original data. The mean trial times with the original data were 40.63 seconds for trials using the CCD method, 33.76 seconds for trials using the 1DOF method and 32.60 seconds for trials using the Jacobian method. With the thresholded data, the mean trial times were 28.26 seconds for trials using the CCD method, 23.63 seconds for trials using the 1DOF method and 23.94 seconds for trials using the Jacobian method. It appears as if the significant difference in the original data was due to subjects spending more time trying to perfect a match when using their first method (the CCD method). When the data was thresholded and this extra effort was removed, the trials did not show statistically significant differences between the three methods.

Group Using 1DOF Method First

There were no statistically significant results in the data from the group of subjects who used the 1DOF method first. The only significant result in the original data for this group was in the positional error analysis. Because the data was thresholded based on the positional error, in some trials the final small value for the positional error was

Category	Experiment Variables	F Value	p Value
1DOF	Time and method	3.757	**0.0241**
	Angle error and method	0.410	0.6642
	Positional error and method	0.578	0.5617
IK	Time and method	1.224	0.2960
	Angle error and method	3.705	**0.0260**
	Positional error and method	10.05	$<$ **0.0001**
IK Pieces	Time and method	4.801	**0.0090**
	Angle error and method	1.309	0.2720
	Positional error and method	0.429	0.6519
Unknown	Time and method	0.463	0.6302
	Angle error and method	0.835	0.4353
	Positional error and method	3.744	**0.0251**

Table 4.10: Results of ANOVA Split by Category (Thresholded Data)

replaced by an earlier, larger value and thus, overall, the positional error data was more homogeneous. As a result, the positional error no longer had significant differences in it.

4.5.3 Thresholded Data Split by Category

As before, the data was split according to the four categories (1DOF, IK, IK Pieces and Unknown). The results of the analyses of the thresholded data grouped by trial category are in Table 4.10.

Results for Trials in the 1DOF Category

In the original data, there were statistically significant differences in the time taken using the three methods for the trials in the 1DOF category (trials 1, 9, 10, 13, 14 and 15). In the thresholded data, there were still statistically significant differences in the time taken using the three methods. With the thresholded data, the mean times for the trials in the 1DOF category were 21.58 seconds for trials using the 1DOF method, 26.04 seconds for trials using the CCD method and 26.69 seconds for trials using the Jacobian method. The differences between the 1DOF method and the other two methods were significant. This analysis supports the categorization of these trials as ones for which the 1DOF method produces accurate matches in the shortest period of time.

There was also a statistically significant difference in the positional error in the original data for the trials in the 1DOF category. Once again, the lack of such a difference in the analysis using the thresholded data is explained by the fact that the data was thresholded based on the positional error.

Results for Trials in the IK Category

Analyses of the error metric data from trials in the IK category (trials 2, 3 and 11) indicated statistically significant differences. In terms of the angle error, the matches made with the CCD method were more accurate than those made with the 1DOF method. In terms of the positional error, the matches made with the 1DOF method were less accurate than those made with either of the other two methods.

These differences were not statistically significant in the original data. The significant results in the thresholded data can be attributed to the thresholding process itself. With the two true inverse kinematic methods, multiple links can be adjusted at once. Large changes in both error metrics can result from one choice of root and end-effector. In particular, these trials can be done in one step with the true inverse kinematic methods if the root is placed at the top, the end-effector is placed at the bottom and the chain is swung smoothly.

With the 1DOF method, it is necessary to move the links one at a time. If subjects start at the top of these chains and work down to the bottom, the threshold value can be passed before the bottom links have been adjusted at all. For example, in trials 2 and 11, the threshold can be passed after matching the top three links, without manipulating the bottom three links. Thus, the thresholding process will cut off the latter sections of trials performed using the 1DOF method in which continued improvement is still being made. This can result in statistically significant differences in the error metrics between the 1DOF method and the two true inverse kinematic methods with the 1DOF method having the least accurate matches.

Results for Trials in the IK Pieces Category

There was a statistically significant difference in the times taken to perform the matches using the various positioning methods for the trials in the IK Pieces category (trials 6, 7 and 12). The mean time for the trials done using the 1DOF method was 35.66 seconds. It was 41.54 seconds for the trials done using the CCD method and 49.79 seconds for the trials done using the Jacobian method. The difference between the 1DOF method and the Jacobian method was statistically significant.

These three trials all involved chains that had an initial zig-zag configuration. Trial 6 involved uncompressing a tight zig-zag into a looser one. Trial 7 involved straightening out the same zig-zag and trial 12 involved compressing a looser zig-zag into a tighter one. The angle adjustments that were necessary to match the goal configuration were spread evenly along the chain.

These trials were put in the IK Pieces category because the optimal movement strategy involved manipulating a small number of links at a time. Many subjects reported trying to "pull" down on the end of the chain for these configurations. If subjects used the capability of the true inverse kinematic methods to attempt to manipulate the entire chain at once, the trial would take longer as the true inverse kinematic methods did not adjust the links evenly along the chain. Subjects would need to further adjust the links to attain an accurate match. As a consequence, the direct strategy of moving one link at a time would be faster than the strategy of trying to move a large number of links at a time.

Results for Trials in the Unknown Category

For the trials in the Unknown category (trials 4, 5 and 8), the trials done with the 1DOF method were significantly less accurate (in terms of the positional error) than those done with either of the other two methods. The trials done using the 1DOF method had a mean positional error of 16.957. Those done using the CCD method had a mean positional error of 15.217 and those done using the Jacobian method had a mean positional error of 15.126.

As with the trials in the IK category, it is possible to cross the threshold for the positional error metric without adjusting all of the links in the chain. The thresholding process will cut off latter sections of trials performed using the 1DOF method in which continued improvement is still being made. This can result in statistically significant differences in the error metrics between the 1DOF method and the two true inverse kinematic methods with the 1DOF method having the least accurate matches.

4.5.4 Thresholded Data Split by Number of Links

As in the original analysis, the trials using chains with the same number of links were grouped together and the thresholded data was analysed. The results of the analyses are in Table 4.11. Once again, trial 3 was not included in any group in this section as it is the only trial with a chain composed of 5 links.

Trials Using Chains With 6 Links

Trials 2 and 11 both involve chains with 6 links. The matches made with the 1DOF method were significantly less accurate in terms of both error metrics than those made

Links	Experiment Variables	F Value	p Value
6	Time and method	2.08	0.1283
	Angle error and method	6.451	**0.0020**
	Positional error and method	5.685	**0.0041**
8	Time and method	0.169	0.8442
	Angle error and method	0.666	0.5146
	Positional error and method	0.136	0.8728
9	Time and method	1.400	0.2470
	Angle error and method	0.873	0.4186
	Positional error and method	0.432	0.6493
10	Time and method	7.867	**0.0005**
	Angle error and method	1.537	0.2167
	Positional error and method	0.931	0.3951

Table 4.11: Results of ANOVA Split by Number of Links (Thresholded Data)

with either of the other two methods. These two trials were both in the IK category. Both of the error metrics were also significant in the IK category analysis and the thresholding explanation presented in that section also applies here.

Trials Using Chains with 8 Links

Trials 13, 14 and 15 all involve a chain with 8 links. There were no statistically significant differences shown in the analyses done using the thresholded data from these three trials. The analyses done using the original data did not have any significant differences either.

Trials Using Chains with 9 Links

Chains with 9 links are used in trials 1, 4, 5, 8 and 10. There were no statistically significant differences for the analyses done using the thresholded data from these trials. In the original data, there were significant differences in the positional errors attained using the various methods for these trials. Since the data was thresholded based on the positional error, it is not surprising that the analysis with the thresholded data did not show a statistically significant difference in the positional error metric.

Trials Using Chains with 10 Links

Trials 6, 7, 9 and 12 all use chains with 10 links. There was a statistically significant difference in the time taken to complete these trials. The mean time for the trials using the 1DOF method was 36.38 seconds. It was 44.88 seconds for the trials using the CCD method and 50.95 seconds for the trials using the Jacobian method. The differences in times between the 1DOF method and each of the other two methods were significant. In the original data, the difference between the Jacobian method and the 1DOF method was significant and it was more significant in the thresholded data. The difference between the CCD method and the 1DOF method was not significant in the original data but it was significant in the thresholded data. The explanation for the difference between the 1DOF and the Jacobian methods in the original data also explains the differences in the thresholded data.

The analysis of the original data for the group of trials using chains with 10 links showed a statistically significant difference in the positional error. This error was not significant in the thresholded data and once again the lack of significant difference is attributed to the fact that the data was thresholded based on the positional error.

4.5.5 Thresholded Data Split by Trial

Once again, the data was split by trial in order to see if there were statistically significant differences for particular trials. As before, trials 4, 5, 6, 10, 12, 13, 14 and 15 did not have any statistically significant differences. Table 4.12 contains the results of the analyses.

Trial	Experiment Variables	F Value	p Value
1	Time and method	2.850	0.0639
	Angle error and method	4.007	**0.0221**
	Position error and method	2.341	0.1030
2	Time and method	0.602	0.5502
	Angle error and method	3.534	**0.0340**
	Position error and method	4.783	**0.0110**
3	Time and method	0.038	0.9629
	Angle error and method	7.321	**0.0012**
	Position error and method	6.934	**0.0017**
4	Time and method	0.915	0.4050
	Angle error and method	0.564	0.5712
	Position error and method	0.645	0.5276
5	Time and method	0.103	0.9020
	Angle error and method	1.071	0.3476
	Position error and method	1.121	0.3313
6	Time and method	2.692	0.0741
	Angle error and method	0.516	0.5989
	Position error and method	2.837	0.0647
7	Time and method	2.549	0.0847
	Angle error and method	9.048	**0.0003**
	Position error and method	10.00	**0.0001**
8	Time and method	0.040	0.9609
	Angle error and method	1.492	0.2314
	Position error and method	3.253	**0.0440**
9	Time and method	6.742	**0.0020**
	Angle error and method	2.343	0.1028
	Position error and method	2.616	0.0796
10	Time and method	0.560	0.5737
	Angle error and method	0.475	0.6234
	Position error and method	0.697	0.5014
11	Time and method	1.85	0.1637
	Angle error and method	3.224	**0.0453**
	Position error and method	1.646	0.1996
12	Time and method	1.300	0.2791
	Angle error and method	1.566	0.2154
	Position error and method	0.462	0.6318
13	Time and method	2.790	0.0675
	Angle error and method	1.797	0.1728
	Position error and method	1.078	0.3453
14	Time and method	0.074	0.9289
	Angle error and method	0.501	0.6080
	Position error and method	0.098	0.9064
15	Time and method	1.000	0.3727
	Angle error and method	1.288	0.2818
	Position error and method	0.250	0.7797

Table 4.12: Results of ANOVA Split by Trial (Thresholded Data)

Trials with Significant Time and Method Results Only

Results from the analysis showed statistically significant differences in time for trial 9. The trials done using the 1DOF method took a mean time of 38.53 seconds. The mean time for the trials done using the Jacobian method was 54.45 seconds and it was 54.95 seconds for the trials done using the CCD method. Similar results also appeared in the original data but both results are more significant in the thresholded data. The same explanation of this result applies to both the thresholded data and the original data.

Trials with Significant Angle Error and Method Results Only

Trials 1 and 11 showed statistically significant differences in the angle error for the matches made using the various methods. For trial 1, the mean angle error for the trials done using the 1DOF method was 2.294 degrees squared. It was 74.646 degrees squared for the trials done using the Jacobian method and 142.410 degrees squared for the trials done using the CCD method. The difference between the 1DOF method and the CCD method was statistically significant. This difference was also significant in the original data, but it is more significant in the thresholded data. The same explanation presented in the section discussing the difference in the original data also applies to the thresholded data.

The analyses using the original data for trial 11 did not reveal any statistically significant results. The analysis of the thresholded data showed that there was a significant difference in the angle errors using the three positioning methods. The mean angle error for the trials using the 1DOF method was 83.719 degrees squared. It was 59.617 degrees squared for the trials using the CCD method and 57.772 degrees squared for the trials using the Jacobian method. The differences between the 1DOF method and the other two methods were statistically significant.

The initial configuration of the chain used in trial 11 is a gentle curve to the right with each link being rotated 5 degrees more than the previous one. The goal configuration has the chain hanging straight down with joint angles of zero. With the CCD and Jacobian methods, it is possible to complete this trial by putting the root at the top of the chain and the end-effector at the bottom and manipulating the all of the joint angles at the same time. This is not an option with the 1DOF method as only one joint angle can be adjusted at a time. Once again the thresholding process can explain the significance as the threshold can be reached for this trial after positioning only the top three links in the chain.

Trials with Significant Positional Error and Method Results Only

In the data from trial 8, the mean positional error for the trials that were completed using the 1DOF method was 17.490 units squared. It was 15.263 units squared for the trials that were completed using the CCD method and 14.414 units squared for the trials that were completed using the Jacobian method. The difference in the errors between the 1DOF method and the Jacobian method was statistically significant.

This trial involved straightening an s-shaped curve, where more adjustment was required at the bottom than at the top. The strategy of putting the root at the top of the chain and the end-effector at the bottom of the chain would be moderately successful. Once again it is possible to cross the threshold before adjusting all of the links in the chain when the 1DOF method is used to adjust the chain from top to bottom. The thresholding process will cut off the latter sections of a trial in which continued improvements were made to the match by adjusting the bottom links in the chain.

Trials with Significant Results for Both Error Metrics

Results from the analysis of the two error metrics and the method were statistically significant for trials 2, 3 and 7.

The mean angle error for the trial 2 matches made using the 1DOF method was 96.786 degrees squared. The mean angle error for these matches made using the Jacobian method was 70.739 degrees squared. For the matches made with the CCD method, the mean angle error was 56.964 degrees squared. The mean positional error was 12.441 units squared for the trials performed using the 1DOF method, 10.009 units squared for the trials performed using the Jacobian method and 8.284 units squared for the trials performed using the CCD method. The differences between both of the errors for matches made with the 1DOF method and those made with the CCD method were significant.

The chain used in trial 2 is straight in its initial configuration and smoothly curved to the right in its goal configuration. Using either of the true inverse kinematic methods, it is possible to make the match choosing only one root and one end-effector. This could be accomplished by putting the root at the top of the chain and the end-effector at the bottom of the chain and moving the mouse to the right. The match could also be performed by manipulating smaller chunks of the chain at a time. With the 1DOF method, each link needs to be moved separately. The thresholding process could once again account for the poor performance of the 1DOF method as the threshold can be crossed when only the top three links in the chain have been positioned. As a consequence, the thresholding process removes the latter portions of the trial during which continued improvements occur.

The mean angle error for the trial 3 matches performed using the 1DOF method was 1109.19 degrees squared. It was 568.394 degrees squared for the matches made using the CCD method and 821.726 degrees squared for those made using the Jacobian method. The mean positional error for the trials completed using the 1DOF method was 11.849 units squared. It was 10.733 units squared for the trials that were done with the Jacobian method and 8.170 units squared for the trials that were done using the CCD method. The differences in both of the error metrics between the 1DOF method and the other two methods were significant.

All of these differences can once again be attributed to the thresholding process. Trial 3 uses a chain with an initial configuration that is curved to the left and a goal configuration that is curved to the right. The differences in the angles between the initial configuration and the goal configuration increase from the top of the chain to the bottom of the chain. It is possible to cross the threshold for this trial before all of the links have been adjusted. In particular, the last link, with the greatest difference in angles between the initial configuration and the goal configuration, does not need to be adjusted. As a consequence, the thresholding process may cut off the final section of a trial using the 1DOF method during which adjustments are made to the last link thereby improving the final match.

In the data from trial 7, the differences between the values attained for both error metrics using the 1DOF method and the other two methods were statistically significant. The mean angle error for the matches made using the 1DOF method was 86.085 degrees squared. It was 555.824 degrees squared for the matches made using the Jacobian method and 947.248 degrees squared for the matches completed using the CCD method. As with the angle error, the mean positional error was smallest for the matches made using the 1DOF method (5.629 units squared). It was 13.081 units squared for matches made using the CCD method and 13.567 units squared for matches made using the Jacobian method.

Trial 7 uses the same initial configuration as trial 6 (a compressed zig-zag chain with 120 degree angles). The final configuration for trial 7 is a straight chain. Once again, when using the two true inverse kinematic methods, the strategy of putting the root at the top of the chain and the end-effector at the bottom of the chain and “pulling” on the chain would not be very effective as the bottom part of the chain would straighten more quickly than the top part. For this trial, a faster and more accurate match would result if the chain was adjusted one or two links at a time. Since the 1DOF method has this constraint built in, it is not surprising that in similar amounts of time, the matches made using the 1DOF method were more accurate than those made with either the CCD method or the Jacobian method which do not have this restriction.

Chapter 5

Conclusions and Future Research

5.1 Conclusions

This thesis presented an experiment that compared the 1DOF, CCD and Jacobian methods for positioning articulated figures. The analysis of the data collected during the experiment yielded several statistically significant differences between various pairings of the positioning methods under various conditions. Thresholding the data based on the positional error metric enhanced some of the results found in the initial data.

Overall, it appears to be possible to use the one degree of freedom (1DOF) method to produce better matches (faster and/or more accurate) than can be produced with either the CCD method or the Jacobian method. However, this is not the case for several particular categories of matches. In general, the CCD and Jacobian methods had superior performance when used for matches involving only smoothly shaped curves. The 1DOF method was superior in cases where a configuration involved a large change in the orientation of adjacent links. Thus it seems necessary to include both a 1DOF positioning method and a true inverse kinematic method in an animation system as the most effective positioning method will depend upon the desired configuration.

The task of adjusting a given chain to match a target chain was shown to have biases related to the configurations of the two chains. For example, if the roles of the given chain and the target chain are reversed (as in trials 4 and 8) different results were obtained. The trial 8 matches made with the 1DOF method were significantly less accurate than those made with the Jacobian method. For trial 4, there were no significant differences between the matches made with the three positioning methods.

Learning effects appeared to be present as the order in which the subjects used the three methods had an impact on the quality of the matches that they made.

Given that many subjects could not distinguish between the CCD method and the Jacobian method, it is surprising that there are several cases where there are statistically significant differences between the CCD method and the 1DOF method but not between the Jacobian method and the 1DOF method. Similarly, there are other cases where the differences between the Jacobian method and the 1DOF method are statistically significant but the differences between the CCD method and the 1DOF method are not. It is possible that some of the differences are not actually significant but that random chance made one significant. Similarly, other differences might actually be significant but random chance made them not significant.

5.2 Future Research

Further experimentation could be done to investigate the significant differences revealed by this experiment and to further delineate performance differences between the methods under various circumstances.

Currently there is no common time at which data is collected for all subjects, other than at the start of the trial. The system could be modified so that information about a trial was recorded on a regular basis in addition to it being recorded in response to a specific action by the subject. If the current configuration of the chain was recorded every second, for example, it would be easier to compare trials. This additional data logging must not adversely affect the response time of the system.

Interpolation of the collected data could be used to generate this information, but due to the nature of the nature of the subject's task, it could be very misleading. Currently the data is collected when the subject releases the end-effector and temporarily stops moving the chain. However, there is no guarantee that the subject reached the current configuration in a manner that could be approximated by any type of interpolation. For example, a subject could swing the entire chain back and forth and end in a position that was unchanged from the starting position. In this case, interpolation would miss the entire action of the subject.

The user interface for picking the final position could be modified. Currently the user presses the left mouse button to select the end-effector and then holds the button down while moving the mouse. The system tracks the mouse cursor and does each iteration of the inverse kinematic algorithm using the mouse position at that time. Alternatively, the user could click with the left mouse button to select the end-effector, move the mouse cursor to the desired location for end-effector and then click there. In this case, the path of the mouse cursor to the new end-effector location would not be used. This user interface could be compared to the current user interface with particular attention paid to initial/goal configurations where the chain needs to be straightened.

The experiment could be modified to use different trials, including more complex chains and configurations. Some of these trials could involve chains where the initial and goal configurations do not have an initial coincident link. If trials involving chains without an initial coincident link are used, the translation feature of the system should be enabled to facilitate the matching process.

If configurations are used that have branching structures with overlapping parts (as in trial 13), the trials should be constructed so that it is possible to position the left branch without moving the right branch out of the way. Most people reported using a top-to-bottom and left-to-right strategy for matching and did not react favourably when this strategy had to be modified.

The experiment could be extended to use 3-Dimensional chains. In this case, either three orthogonal views of the chain would be needed (with the ability to manipulate the chain in any of the three views) or else a simple method of rotating the chain/view would be required, such as the one used in the 3-Dimensional shape-matching experiment by Jang [Jan92].

Additional inverse kinematic methods, such as the one used by Zhao and Badler [ZB89] could be implemented and compared to the three methods used in the initial experiment. In addition, various methods of utilizing joint limits and constraints could be compared.

In order to make it possible to do a statistical analysis of the ratings given by each subject at the end of each trial, an initial calibration step could be done. A series of matches would be presented to each subject at the beginning of the two sessions and the subjects would be asked to rank the accuracy of the matches. The same matches would be presented at the start of both sessions so that the results could be compared to see if the subject had changed his or her rating criteria after doing the first part of the experiment. The subject would have to base the rating of these matches solely on the accuracy of the match itself, and this should increase the likelihood that each subject would use only that criteria for rating the matches attained during the experiment trials.

As the complexity of the trials increases, the possibility of subject fatigue also increases. Care must be taken to ensure that the overall number and difficulty of the trials does not increase the length of a subject's session to beyond 30 to 45 minutes.

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Appendix A

Subject Background Information

In this table, the names of the subjects have been replaced by subject numbers. The numbers do not reflect the sequence in which subjects did the experiment; rather, subjects were grouped by the first of the three methods used.

No.	Program	Gender	Age	Hand	Mouse	Anim.	IK
1	BASc NM	F	18	R	E	L (1)	N
2	—	M	28	R	E	L (2)	N
3	BASc EE	M	20	R	M	N	N
4	BSc CS	M	21	L	M	L (3)	N
5	BSc NM	M	18	R	E	E (4)	N
6	BSc CS	F	25	R	M	N	H
7	MSc CS	M	25	R	E	L (5)	N
8	BSc CS	F	18	R	L	N	N
9	BSc NM	M	28	R	M	N	N
10	BSc NM	F	21	R	M	L (6)	N
11	PhD CS	M	31	R	E	N	H
12	BSc CS	M	18	R	M	L (7)	N
13	BSc CS/Physics	M	22	R	E	L (8)	H
14	BSc NM	M	19	R	E	M (9)	H
15	BSc NM	F	19	R	M	N	N
16	PhD Physiology	M	25	R	M	M (10)	H
17	BSc NM	F	18	R	E	N	N
18	BSc CS	M	19	R	E	M (11)	N
19	BSc NM	F	18	R	L	N	N
20	PhD CS	M	31	R	E	N	H
21	BSc Bio	M	22	R	E	E (12)	N
22	MSc CS	M	22	R	E	N	N
23	BSc Physics	M	19	R	E	L (13)	H
24	MSc MIS	F	33	R	E	N	N
25	BSc CS	M	20	R	E	L (14)	N
26	BSc CS	F	20	R	M	N	N
27	BSc CS	M	18	R	E	E (15)	N
28	BSc CS	F	26	R	E	N	N
29	BASc EE	M	18	R	M	L (16)	N
30	MSc CS	F	26	R	E	N	N

- Program — a combination of a program and a department (for students only)
  - Program

    BASc Bachelor of Applied Science (Engineering)

    BSc Bachelor of Science

    MSc Master of Science

    PhD Doctor of Philosophy
  - Department

    Bio Biology

    CS Computer Science

    EE Electrical Engineering

    MIS Management Information Systems

    NM no major (students who do not yet have a declared major)
- Gender

  M Male

  F Female
- Hand — predominant hand used

  L Left-handed

  R Right-handed
- Mouse — experience using a mouse

  N None

  L Limited

  M Moderate

  E Extensive

- Anim. — experience using animation software

  N None

  L Limited

  M Moderate

  E Extensive

- Animation software used (names are as provided by subjects)

  1. Mario Paint
  2. PC based package (subject forgot name of package)
  3. Sprite World
  4. Animator, Animator Pro, DPaint, 3D Studio and others
  5. Alias, Wavefront
  6. Lion King Screen Saver
  7. has written animation software
  8. Alias Sketch, Stratavision 3D
  9. Lightwave 3D, 3D Studio
  10. Alias, Wavefront, Vertigo
  11. has programmed animations
  12. Disney Animation Studio, Deluxe Paint, Light Wave, Imagine
  13. Autodesk Animator
  14. Apple IIc program (subject forgot name of program)
  15. Autodesk Animator, AAPro, Autodesk 3D-studio, shareware programs
  16. a Windows drawing package (subject forgot name of package)

- IK — familiarity with inverse kinematics

  N Never heard of it

  H Have some idea about it

  K Know all about it

Notes: For IK familiarity, subject 6 put in the extra field "Heard of it, but don't really know what it is". This was recorded as "have some idea about it".

Subject 28 writes with her left hand and uses the mouse with her right hand.

Appendix B

Sample Forms

The following forms were filled out by each subject who participated in the experiment. The "Consent Form" and "Subject Information Form" were filled out by the subject at the beginning of his or her first session. The first "Comments Form" was filled out by the subject after completing the trials using his or her first method (the only method used in his or her first session). The second "Comments Form" was filled out by the subject midway through the second session, after completing his or her second method (the first method used in his or her second session). The third and final "Comments Form" was filled out by the subject at the end of his or her second session after completing his or her third method. The version of the last "Comments Form" given to the subjects was printed double-sided on one page.

Inverse Kinematic Chain Matching Experiment

Consent Form

I agree to participate in the study entitled *Inverse Kinematic Chain Matching Experiment* being conducted by the Imager Laboratory of the Department of Computer Science at the University of British Columbia.

I understand that the data gathered by the computer program will only be seen by the researchers. The results which will be summarized in the experiment supervisor's Master's thesis will be stripped of all identifying codes.

I understand that my participation is voluntary and that I may withdraw from the study at any time.

Signature: ______________________________

Date: ______________________________

Inverse Kinematic Chain Matching Experiment

Subject Information Form

Please provide the information requested below. This information will be held in strict confidence by the researchers.

Name: ____________________

Program and department (if student): ____________________

Sex: ____________________

Current Age: ____________________

Are you primarily left-handed or right-handed? ____________________

Indicate your experience using a mouse:

none ________ limited ________ moderate ________ extensive ________

Indicate your experience using animation software:

none ________ limited ________ moderate ________ extensive ________

List any animation software that you have used: ____________________

____

____

____

Indicate your familiarity with inverse kinematics:

never heard of it ______ have some idea about it ______ know all about it ______

Inverse Kinematic Chain Matching Experiment

Comments Form

Please complete this form after using the first method.

Name: ______________________________

How many of the different sample trials did you try? ______________

What specific strategy did you use in moving links to achieve a match?

____

____

____

____

What criteria did you use in rating your satisfaction with each match?
(i. e. accuracy of match, time taken, difficulty, etc.)

____

____

____

____

Please list any problems with or comments on the tutorial.

____

____

____

____

Please list any other problems with or comments about this session.

____

____

____

Thank you. Please verify the time and date for your next session.

Inverse Kinematic Chain Matching Experiment

Comments Form

Please complete this form after using the second method.

Name:

Did you review the tutorial instructions?

How many of the different sample trials did you try?

What specific strategy did you use in moving links to achieve a match?
(indicate any differences in strategy from last time)

What criteria did you use in rating your satisfaction with each match?
(i. e. accuracy of match, time taken, difficulty, same as last time etc.)

Did you find it easier to manipulate the chains with this method or the last one? Why?

Do you think that you were more successful with your matches this time or last time?

Which time did you prefer?

Please list any other comments about or problems with this session.

Inverse Kinematic Chain Matching Experiment

Comments Form

Please complete this form after using the final method.

Name:

Did you review the tutorial instructions?

How many of the different sample trials did you try?

What specific strategy did you use in moving links to achieve a match?
(indicate any differences in strategy from the previous times)

What criteria did you use in rating your satisfaction with each match?
(i. e. accuracy of match, time taken, difficulty, same as previous etc.)

Did you find it easier to manipulate the chains with this method, the first method or the second one? Why?

Do you think that you were more successful with your matches using this method, the first method or the second method? (please rank the 3 methods)

(please turn over)

Which time did you prefer? (please rank the 3 methods)

Please list any other comments about or problems with this session.

Thank you very much for participating in the study.

Appendix C

Chain Configurations

During the experiment, all of the chains were displayed with the inherent root at the same point on the screen. This initial inherent root position was centered horizontally on the monitor and was near the top of the screen. On the screen, goal chains were displayed in yellow and user manipulated chains were displayed in alternating light and dark blue links with the joints drawn on top in white. These chains were displayed against a black background. In this appendix, goal chains are drawn in a 50 percent gray level. The links of the user manipulated chains are drawn in alternating light and dark gray and the joints have been outlined in black.

The tables in this appendix contain the angles for the initial and goal configurations for the chains used in the three sample trials (in the tutorial) and the 15 experiment trials. All of the values for the angles are in degrees and represent the z rotation of the corresponding joint. The angles are expressed relative to the rotation of the previous joint and thus are cumulative.

The joints have been numbered with the inherent root of each chain being joint number 1. For chains with branches, joint numbers are reused in this numbering to indicate the branching points. The repeated joint number is the joint at which a branch occurs. The first value for that number and all values for increasing joint numbers until the joint number is repeated are the values for the "left" branch. The second value of the repeated joint number and all values following it are values for the "right" branch.

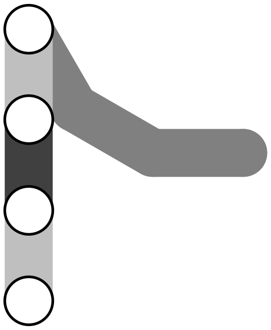


Figure C.1: Sample Trial #1

Joint	1	2	3
Initial	0.0	0.0	0.0
Goal	30.0	30.0	30.0

Table C.1: Sample Trial #1

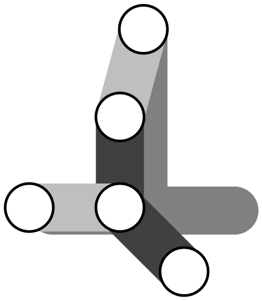


Figure C.2: Sample Trial #2

Joint	1	2	3	3
Initial	-15.0	15.0	-90.0	45.0
Goal	0.0	0.0	-90.0	90.0

Table C.2: Sample Trial #2

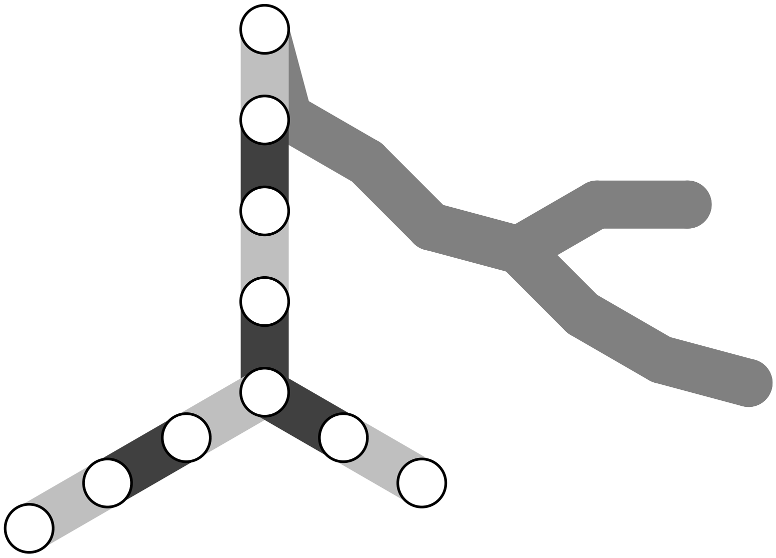


Figure C.3: Sample Trial #3

Joint	1	2	3	4	5	6	7	5	6
Initial	0.0	0.0	0.0	0.0	-60.0	0.0	0.0	60.0	0.0
Goal	15.0	45.0	-15.0	30.0	-30.0	15.0	15.0	45.0	-30.0

Table C.3: Sample Trial #3

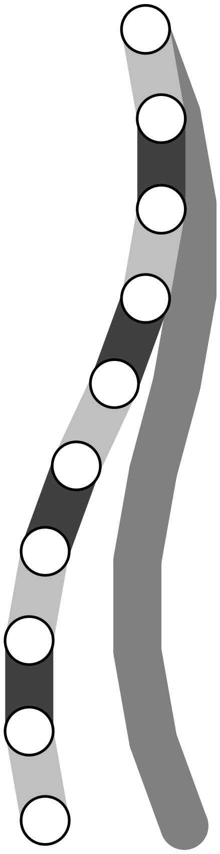


Figure C.4: Experiment Trial #1

Joint	1	2	3	4	5	6	7	8	9
Initial	10.0	-10.0	-10.0	-10.0	-5.0	5.0	10.0	10.0	10.0
Goal	20.0	-10.0	-10.0	-10.0	-5.0	5.0	10.0	10.0	10.0

Table C.4: Experiment Trial #1

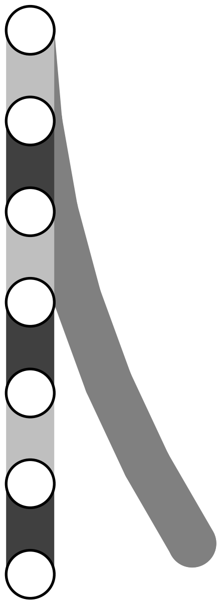


Figure C.5: Experiment Trial #2

Joint	1	2	3	4	5	6
Initial	0.0	0.0	0.0	0.0	0.0	0.0
Goal	5.0	5.0	5.0	5.0	5.0	5.0

Table C.5: Experiment Trial #2

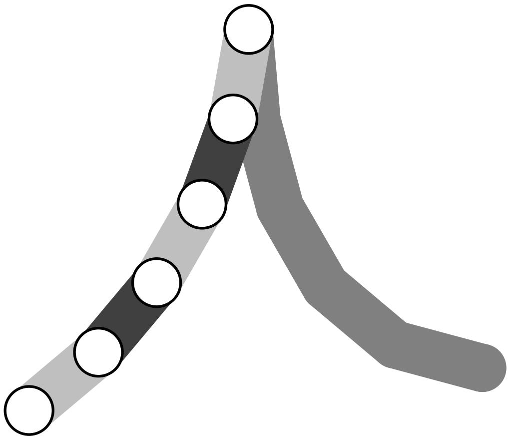


Figure C.6: Experiment Trial #3

Joint	1	2	3	4	5
Initial	-10.0	-10.0	-10.0	-10.0	-10.0
Goal	5.0	10.0	15.0	20.0	25.0

Table C.6: Experiment Trial #3

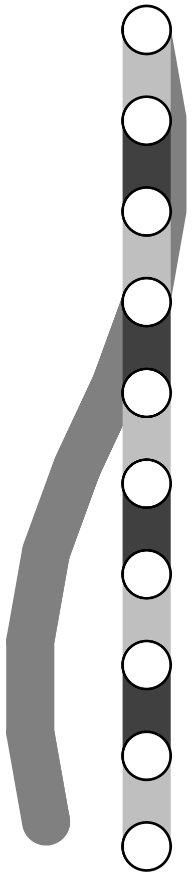


Figure C.7: Experiment Trial #4

Joint	1	2	3	4	5	6	7	8	9
Initial	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Goal	10.0	-10.0	-10.0	-10.0	-5.0	5.0	10.0	10.0	10.0

Table C.7: Experiment Trial #4

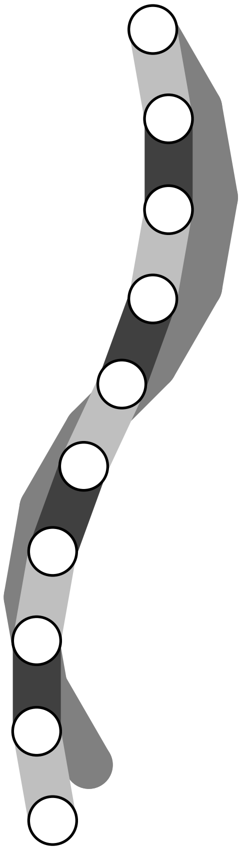


Figure C.8: Experiment Trial #5

Joint	1	2	3	4	5	6	7	8	9
Initial	10.0	-10.0	-10.0	-10.0	-5.0	5.0	10.0	10.0	10.0
Goal	30.0	-20.0	-20.0	-20.0	-15.0	15.0	20.0	20.0	20.0

Table C.8: Experiment Trial #5

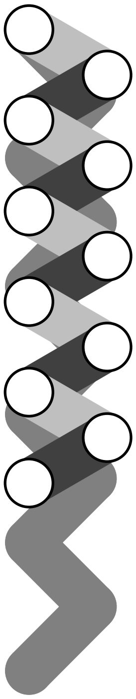


Figure C.9: Experiment Trial #6

Joint	1	2	3	4	5	6	7	8	9	10
Initial	60.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0
Goal	45.0	-90.0	90.0	-90.0	90.0	-90.0	90.0	-90.0	90.0	-90.0

Table C.9: Experiment Trial #6

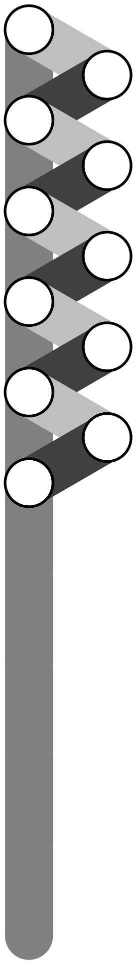


Figure C.10: Experiment Trial #7

Joint	1	2	3	4	5	6	7	8	9	10
Initial	60.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0
Goal	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Table C.10: Experiment Trial #7

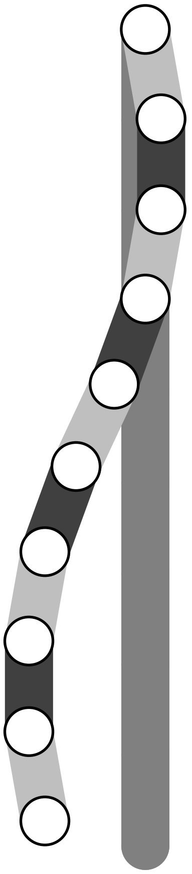


Figure C.11: Experiment Trial #8

Joint	1	2	3	4	5	6	7	8	9
Initial	10.0	-10.0	-10.0	-10.0	-5.0	5.0	10.0	10.0	10.0
Goal	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Table C.11: Experiment Trial #8

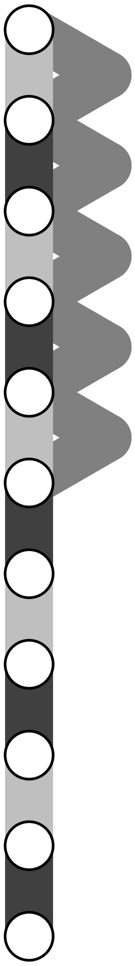


Figure C.12: Experiment Trial #9

Joint	1	2	3	4	5	6	7	8	9	10
Initial	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Goal	60.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0

Table C.12: Experiment Trial #9

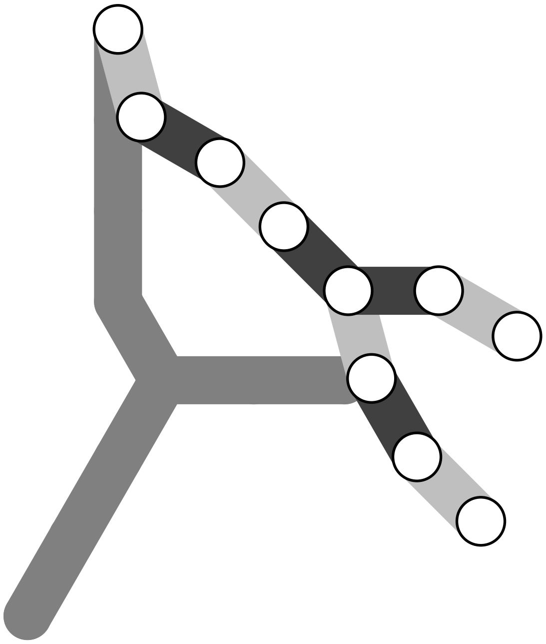


Figure C.13: Experiment Trial #10

Joint	1	2	3	4	5	6	7	5	6
Initial	15.0	45.0	-15.0	0.0	-30.0	15.0	15.0	45.0	-30.0
Goal	0.0	0.0	0.0	30.0	-60.0	0.0	0.0	60.0	0.0

Table C.13: Experiment Trial #10

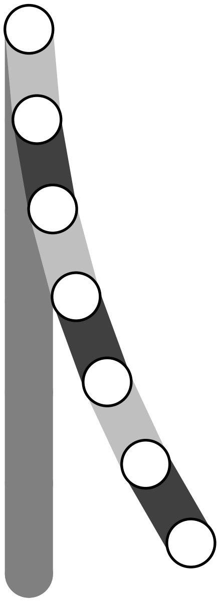


Figure C.14: Experiment Trial #11

Joint	1	2	3	4	5	6
Initial	5.0	5.0	5.0	5.0	5.0	5.0
Goal	0.0	0.0	0.0	0.0	0.0	0.0

Table C.14: Experiment Trial #11

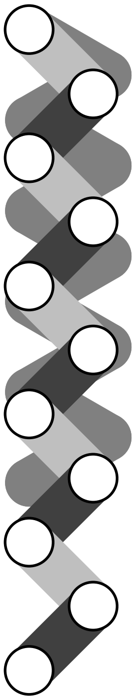


Figure C.15: Experiment Trial #12

Joint	1	2	3	4	5	6	7	8	9	10
Initial	45.0	-90.0	90.0	-90.0	90.0	-90.0	90.0	-90.0	90.0	-90.0
Goal	60.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0	120.0	-120.0

Table C.15: Experiment Trial #12

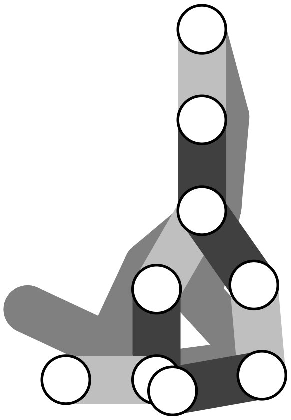


Figure C.16: Experiment Trial #13

Joint	1	2	3	4	5	3	4	5
Initial	0.0	0.0	-30.0	30.0	-90.0	35.0	-30.0	-85.0
Goal	15.0	-20.0	-45.0	25.0	-90.0	-7.5	55.0	-125.0

Table C.16: Experiment Trial #13

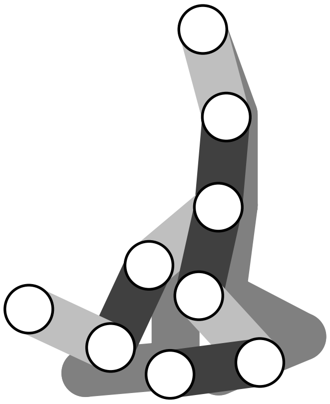


Figure C.17: Experiment Trial #14

Joint	1	2	3	4	5	3	4	5
Initial	15.0	-20.0	-45.0	25.0	-90.0	-7.5	55.0	-125.0
Goal	20.0	-20.0	-40.0	40.0	-85.0	-7.5	70.0	-130.0

Table C.17: Experiment Trial #14

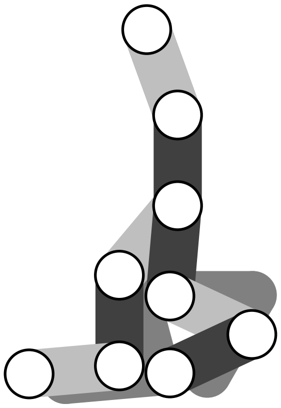


Figure C.18: Experiment Trial #15

Joint	1	2	3	4	5	3	4	5
Initial	20.0	-20.0	-40.0	40.0	-85.0	-5.0	70.0	-130.0
Goal	20.0	-20.0	-30.0	45.0	-100.0	-10.0	100.0	-120.0

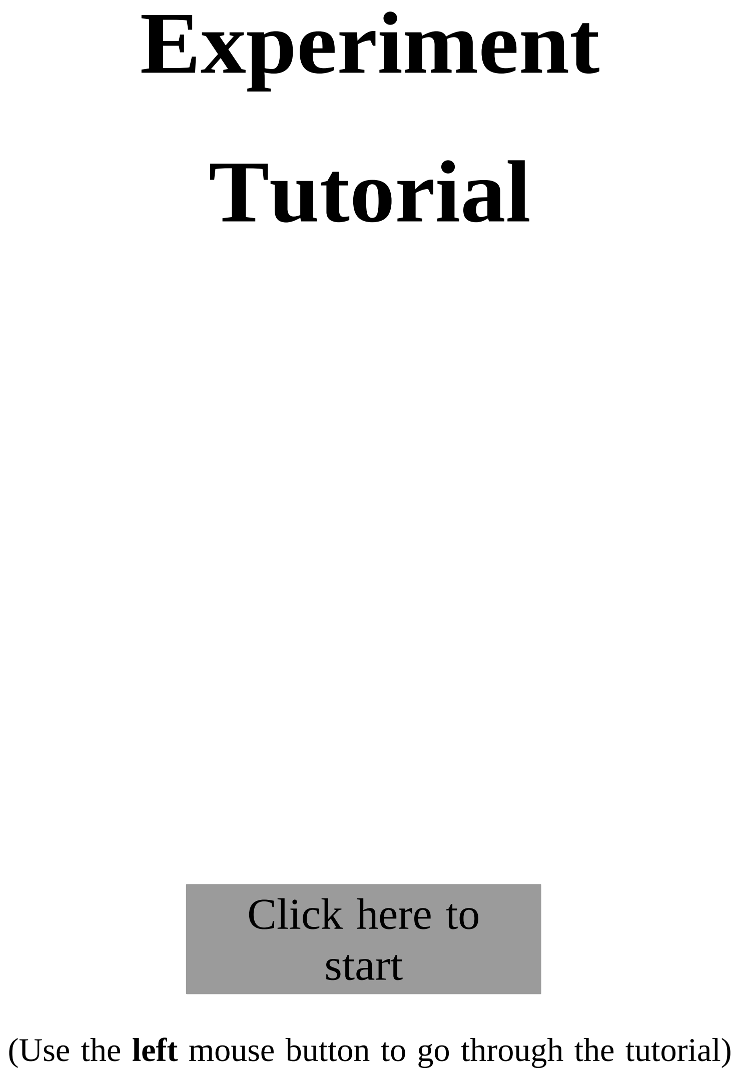
Table C.18: Experiment Trial #15

Appendix D

Tutorial Pages

The following pages are printouts of the IRIS Showcase tutorial that subjects went through before doing the experiment trials. The pages have been reduced and turned sideways in order to fit on the page. The pages in the actual tutorial are displayed in landscape mode and fill the entire screen.

The first nine pages of this appendix form the initial tutorial that each subject sees. The last page of this appendix is from the version of the tutorial that the subject sees before doing the set of experiment trials for the second and third times. Only the first page of text from this version of the tutorial is included as all of the other pages are identical to those in the initial tutorial.

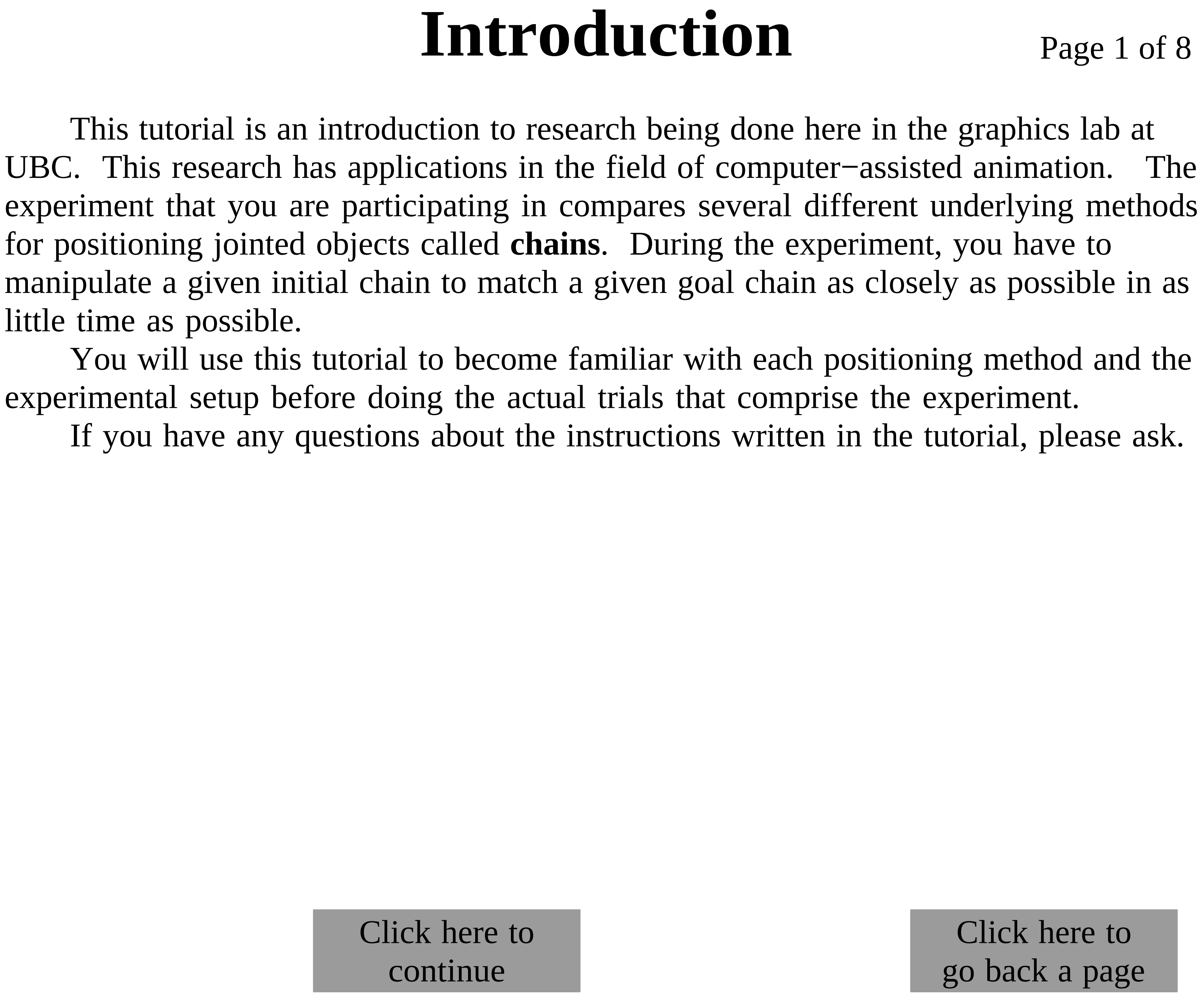


Experiment

Tutorial

Click here to start

(Use the **left** mouse button to go through the tutorial)



Introduction

Page 1 of 8

This tutorial is an introduction to research being done here in the graphics lab at UBC. This research has applications in the field of computer−assisted animation. The experiment that you are participating in compares several different underlying methods for positioning jointed objects called **chains**. During the experiment, you have to manipulate a given initial chain to match a given goal chain as closely as possible in as little time as possible.

You will use this tutorial to become familiar with each positioning method and the experimental setup before doing the actual trials that comprise the experiment.

If you have any questions about the instructions written in the tutorial, please ask.

The Chain

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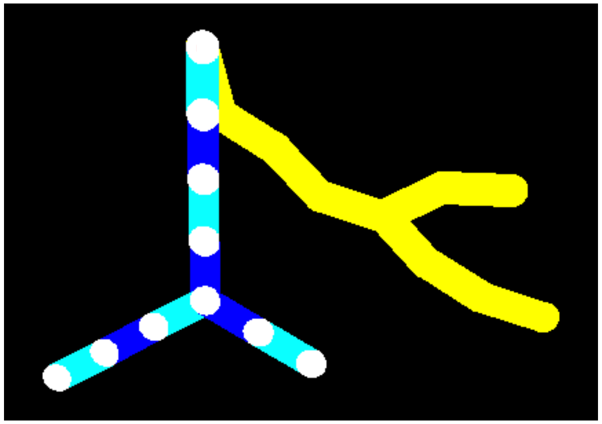
A chain is composed of a number of rectangles (called **links**) that are joined together. The point where two links connect is called a **joint**. Each chain that you will manipulate is made up of alternating *light blue* and *dark blue* links. The joints are represented by *white* circles. Each goal chain that you are trying to match is drawn in *yellow*.

A pair of chains that appear in the sample trials is shown below. The chain to manipulate is on the left and the goal chain is on the right. Both of these chains are composed of 9 links and 10 joints.



Click here to continue

Click here to go back a page

Moving the Chain

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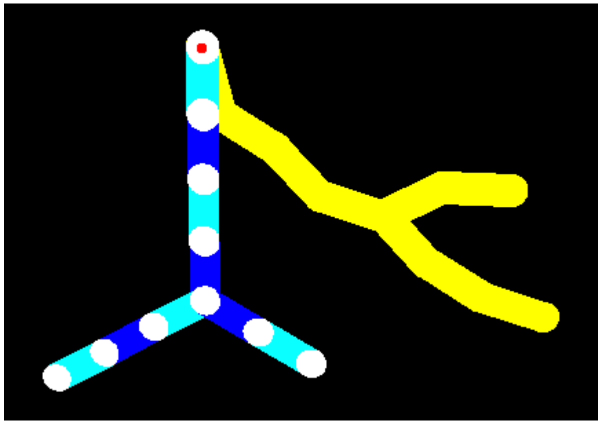
(NOTE: the picture below is just for illustration; the instructions do NOT work on this picture − click on the button at the bottom left to try out the instructions)

1) Select a joint to be the **pivot point**. This point will remain in place while you are manipulating the chain. To make your selection:

a) move the *red* mouse cursor on top of the white circle at the desired joint
b) press and release the **middle** mouse button
c) a *red* circle will appear in the middle of the selected pivot point
− to pick a different joint to be the pivot point, move the red mouse cursor to the new joint and press and release the middle mouse button there

The picture below illustrates a chain with the topmost joint selected as the pivot point.



Click here to try out instructions

Click here to continue

Click here to go back a page

Moving the Chain (con't)

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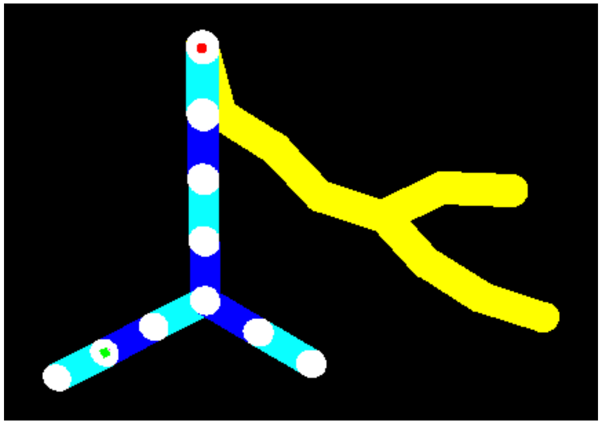
(NOTE: the picture below is just for illustration; the instructions do NOT work on this picture − click on the button at the bottom left to try out the instructions)

2) Choose a **manipulation point**. To make your selection:

a) move the red mouse cursor on top of the white circle at the desired joint
b) press and **hold** the **left** mouse button
c) a *green* square will appear in the middle of the selected manipulation point
− to pick a different manipulation point, release the mouse button, move the red mouse cursor to the new joint and press and hold the left mouse button there
− you must have a pivot point selected before you choose a manipulation point

The picture below illustrates a chain with the topmost joint selected as the pivot point and the second joint on the left branch selected as the manipulation point.



Click here to try out instructions

Click here to continue

Click here to go back a page

Moving the Chain (con’t)

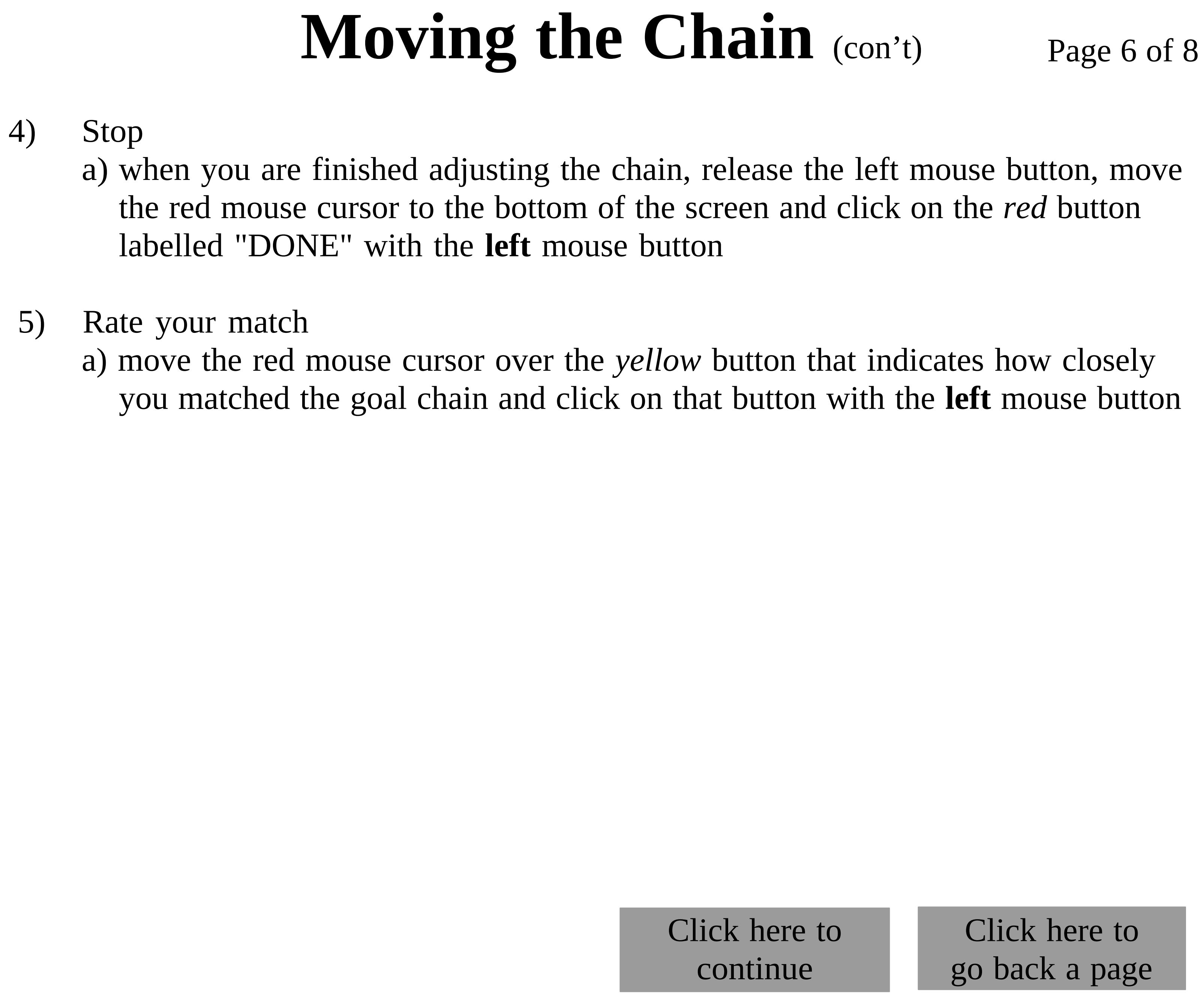
3) Move the chain

a) continue to **hold** the **left** mouse button while moving the mouse

- the chain will adjust to move the green square on the manipulation point to a position as close as possible to the red mouse cursor by moving some or all of the links between the selected manipulation point and the selected pivot point
- any links on the "other side" of the pivot point will not move
- the relative angles of the links that are not between the pivot point and the manipulation point will not change but the links on the "other side" of the manipulation point may be dragged along
- you can select the manipulation point to be at an end of the chain, adjacent to the pivot point, or anywhere inbetween
- if the pivot point and the manipulation point are on the same joint, the chain will not move
- to adjust a different part of the chain, choose a different pivot point and/or manipulation point

Click here to continue

Click here to go back a page



Moving the Chain (con’t)

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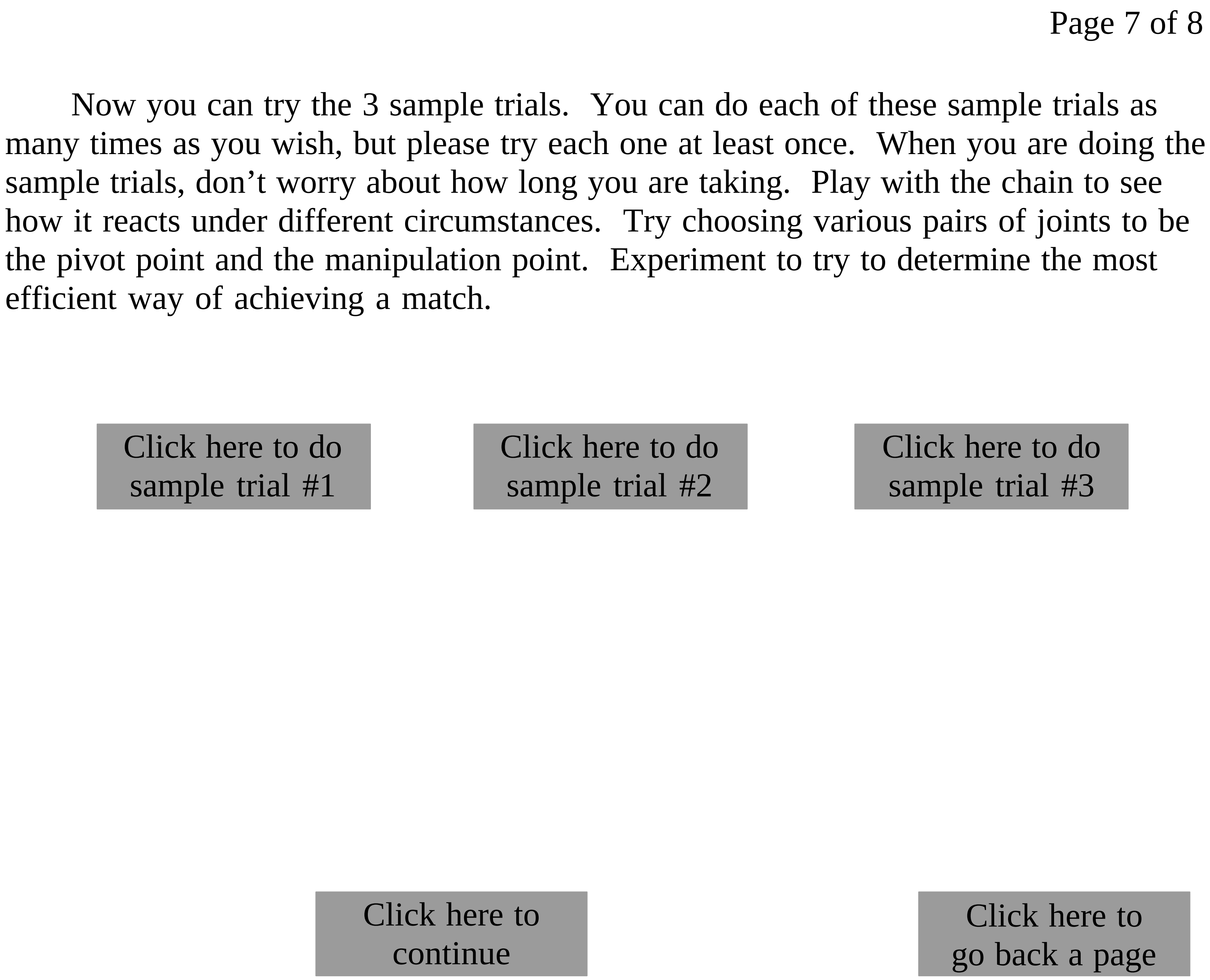
4) Stop
   a) when you are finished adjusting the chain, release the left mouse button, move the red mouse cursor to the bottom of the screen and click on the *red* button labelled "DONE" with the **left** mouse button

5) Rate your match
   a) move the red mouse cursor over the *yellow* button that indicates how closely you matched the goal chain and click on that button with the **left** mouse button



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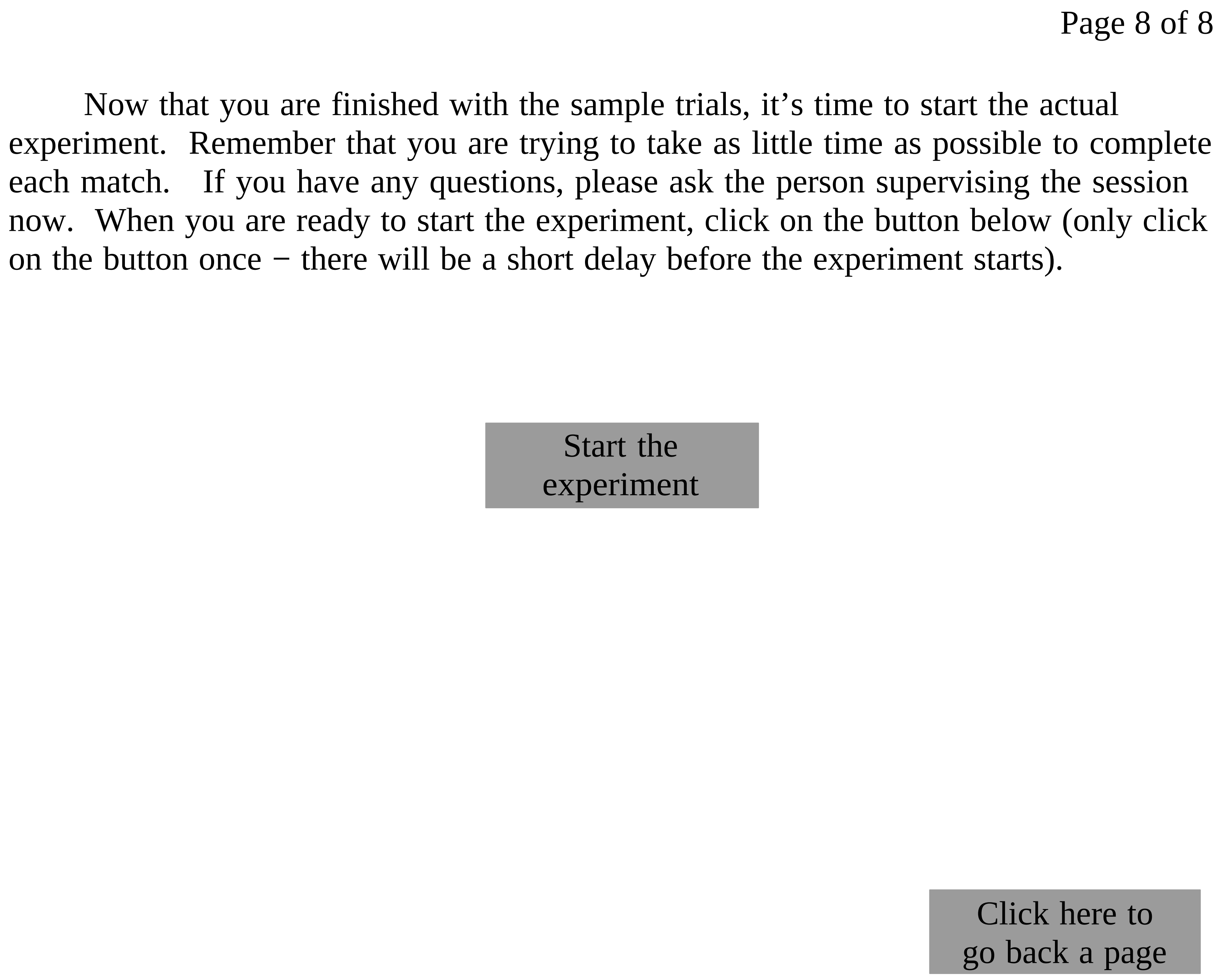
Now you can try the 3 sample trials. You can do each of these sample trials as many times as you wish, but please try each one at least once. When you are doing the sample trials, don't worry about how long you are taking. Play with the chain to see how it reacts under different circumstances. Try choosing various pairs of joints to be the pivot point and the manipulation point. Experiment to try to determine the most efficient way of achieving a match.



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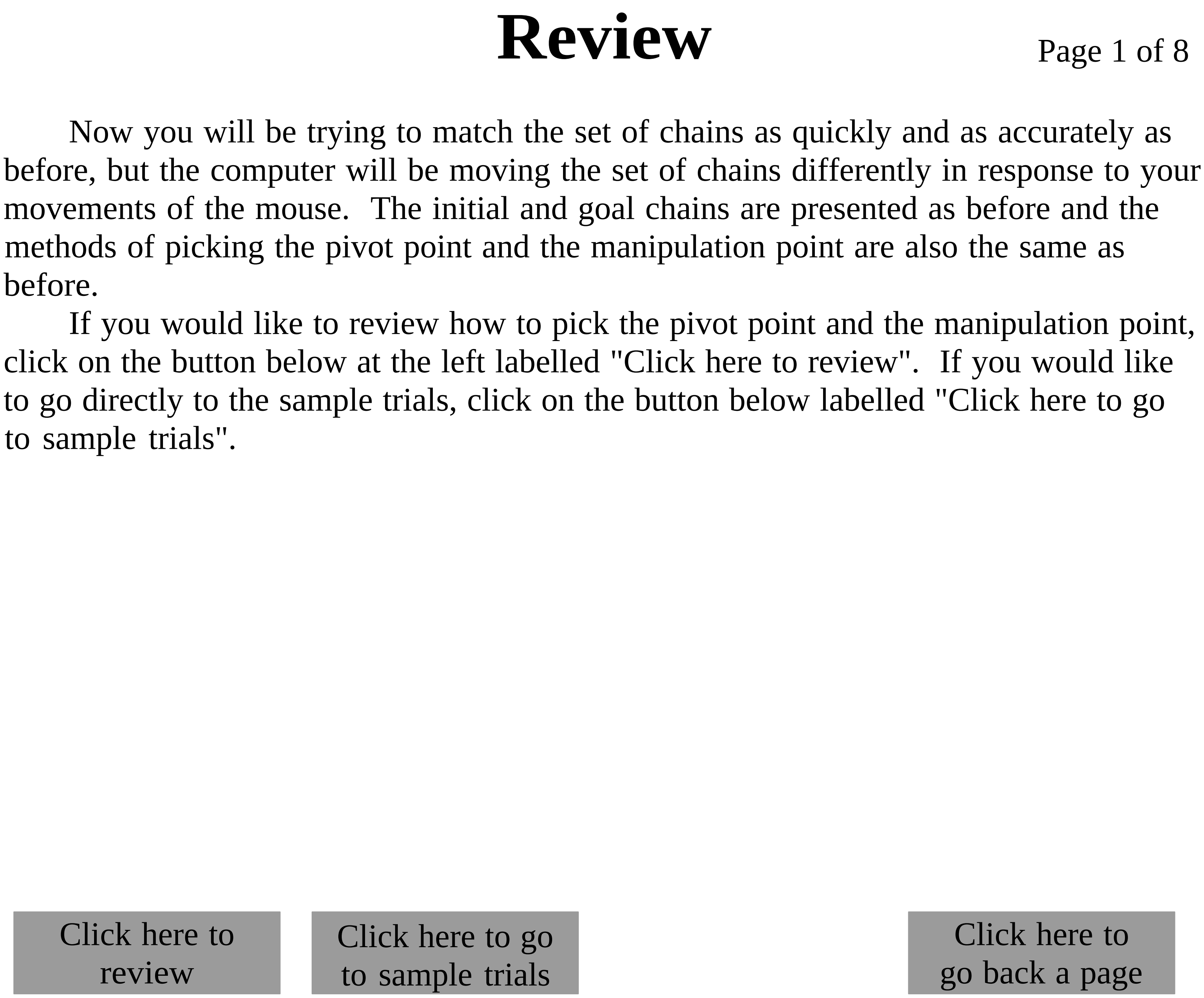
Now that you are finished with the sample trials, it’s time to start the actual experiment. Remember that you are trying to take as little time as possible to complete each match. If you have any questions, please ask the person supervising the session now. When you are ready to start the experiment, click on the button below (only click on the button once − there will be a short delay before the experiment starts).



Review

Page 1 of 8

Now you will be trying to match the set of chains as quickly and as accurately as before, but the computer will be moving the set of chains differently in response to your movements of the mouse. The initial and goal chains are presented as before and the methods of picking the pivot point and the manipulation point are also the same as before.

If you would like to review how to pick the pivot point and the manipulation point, click on the button below at the left labelled "Click here to review". If you would like to go directly to the sample trials, click on the button below labelled "Click here to go to sample trials".

Appendix E

Experiment Data

The following tables summarize the results of all of the trials for subjects 1 through 27.

The Type column classifies the trial. A value of “Unchanged” indicates that the positional error value at the end of the trial was below the cutoff threshold and that this was the first time in the trial that the positional error value went below the threshold value for that trial. A trial with types of “Final”, “Cutoff” and “Difference” was affected by the thresholding. The “Final” line displays the values at the end of the trial and the “Cutoff” line displays the values corresponding to the first time that the positional error was below the threshold value. The “Difference” line displays the differences between the “Final” data line and the “Cutoff” data line. A trial with a type of “Outlier” never had a positional error that was below the threshold value.

The times have been converted to seconds. The values for the angle error metric and the positional error metric have been rounded to 5 decimal places. These values have also been expressed as a percentage of the initial errors of the trial. The percentages have been rounded to 2 decimal places.

The R and E columns indicate the number of roots and end-effectors that were chosen by the subject during the trial. For trials that were affected by the thresholding, the “Final” line displays the total number of roots and end-effectors chosen during the trial and the “Cutoff” line displays the number of roots and end-effectors chosen to the point at which the trial was cutoff by the thresholding process. The “Difference” line indicates the number of root and end-effector choices that were made after the threshold value for the trial was obtained.

The data in the column labelled “Avg. Dist. ” is the average distance between roots and end-effectors in a trial. These values have been rounded to two decimal places. For trials that were affected by thresholding, the value in the “Cutoff” line is the average distance value for roots and end-effectors that were chosen before the threshold was reached. The value in the “Difference” line is the difference between the average distance for the entire trial and the average distance for the trial until the threshold was reached.

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Final	32.46141	10.47716	10.48	3.71389	2.41	3	5	2.20	Almost Perfect
1	Cutoff	8.67849	0.05693	0.06	3.67499	2.39	1	1	1.00	-
1	Difference	23.78292	10.42023	10.42	0.03890	0.02	2	4	1.20	-
2	Unchanged	27.22965	12.34629	8.23	1.31819	1.36	9	9	1.00	Almost Perfect
3	Unchanged	25.65794	1.13614	0.03	0.59380	0.26	5	5	1.00	Almost Perfect
4	Unchanged	31.03388	99.68097	13.29	3.72107	2.90	9	10	1.00	Perfect Match
5	Unchanged	60.70439	233.17042	19.43	5.55036	6.29	12	18	0.05	Almost Perfect
6	Unchanged	134.12319	134.19186	1.61	9.01849	3.92	28	44	1.36	Almost Perfect
7	Unchanged	63.09027	39.03083	0.03	4.93381	0.86	12	29	2.14	Almost Perfect
8	Unchanged	29.05134	84.82028	11.31	3.73818	2.92	11	10	0.90	Pretty Good
9	Unchanged	45.48078	22.55190	0.02	5.59596	0.98	10	12	1.00	Perfect Match
10	Unchanged	39.27485	63.10144	1.08	7.24810	1.65	9	13	1.62	Perfect Match
11	Unchanged	15.89195	59.08469	39.39	2.52619	2.60	6	6	1.00	Perfect Match
12	Unchanged	52.89593	37.99235	0.46	6.64471	2.89	14	16	1.13	Almost Perfect
13	Unchanged	37.07067	18.72409	0.16	3.65993	5.74	10	13	1.31	Perfect Match
14	Unchanged	21.89706	62.03894	11.28	5.09099	7.08	10	6	0.67	Pretty Good
15	Unchanged	28.77967	14.75073	1.07	2.13058	5.54	9	8	1.13	Almost Perfect

Table E.1: Subject 1 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	7.89846	0.24382	0.24	7.60518	4.94	1	1	1.00	Pretty Good
2	Unchanged	14.73939	34.57385	23.05	1.81469	1.87	6	7	1.00	Almost Perfect
3	Unchanged	21.14531	7.10196	0.21	1.67985	0.74	5	8	1.00	Perfect Match
4	Unchanged	29.42879	4.54204	0.61	1.06644	0.83	11	11	1.00	Perfect Match
5	Unchanged	34.54551	33.01946	2.75	2.03653	2.31	11	12	1.00	Perfect Match
6	Unchanged	54.68250	8.26426	0.10	2.28111	0.99	9	13	1.38	Almost Perfect
7	Unchanged	81.12456	23.26788	0.02	1.77342	0.31	18	42	1.76	Almost Perfect
8	Unchanged	31.10214	10.83309	1.44	2.86125	2.23	9	13	1.00	Perfect Match
9	Unchanged	50.91993	36.82016	0.03	5.40862	0.95	14	14	1.00	Perfect Match
10	Unchanged	27.07207	28.32816	0.48	3.71335	0.85	9	9	1.22	Almost Perfect
11	Unchanged	23.86703	5.73250	3.82	1.16762	1.20	9	13	1.00	Perfect Match
12	Unchanged	32.36632	57.44891	0.69	4.94886	2.15	10	10	1.00	Perfect Match
13	Unchanged	39.70560	84.00989	0.73	4.58422	7.19	9	21	2.23	Almost Perfect
14	Unchanged	24.26036	17.25434	3.14	2.92935	4.08	9	10	0.70	Perfect Match
15	Unchanged	39.13060	19.65193	1.43	3.38639	8.80	11	27	1.59	Perfect Match

Table E.2: Subject 1 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	6.17678	0.02712	0.03	2.53644	1.65	1	1	1.00	Almost Perfect
2	Unchanged	16.19692	10.16335	6.78	0.96982	1.00	6	6	1.00	Perfect Match
3	Unchanged	16.63694	8.34125	0.25	0.80502	0.36	5	5	1.00	Almost Perfect
4	Unchanged	26.25458	40.86652	5.45	2.36035	1.84	13	10	1.00	Perfect Match
5	Unchanged	23.48704	31.18840	2.60	1.50304	1.70	9	10	1.00	Perfect Match
6	Unchanged	39.81563	42.40014	0.51	3.92678	1.71	10	14	2.36	Perfect Match
7	Unchanged	43.18811	29.07081	0.02	2.53973	0.44	12	15	1.67	Perfect Match
8	Unchanged	22.47867	56.03222	7.47	2.11711	1.65	9	9	1.00	Almost Perfect
9	Unchanged	33.54547	12.01706	0.01	3.72825	0.65	12	13	1.00	Perfect Match
10	Unchanged	30.61959	26.07167	0.45	2.39043	0.54	11	12	1.33	Almost Perfect
11	Unchanged	11.00933	46.94238	31.29	1.93714	1.99	5	5	1.00	Almost Perfect
12	Unchanged	25.71704	20.47196	0.25	5.76228	2.51	10	10	1.00	Almost Perfect
13	Unchanged	24.41784	42.65621	0.37	2.64828	4.16	5	8	1.25	Almost Perfect
14	Unchanged	23.98783	1.51355	0.28	1.61532	2.25	8	7	0.86	Perfect Match
15	Unchanged	26.40119	7.65879	0.56	1.69836	4.42	12	9	0.22	Perfect Match

Table E.3: Subject 1 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	40.19399	22.13714	22.14	4.03058	2.62	10	14	1.36	Perfect Match
2	Unchanged	19.48781	18.57525	12.38	2.29315	2.36	6	6	1.00	Perfect Match
3	Unchanged	27.70128	10.32920	0.31	1.57104	0.70	7	7	1.00	Perfect Match
4	Unchanged	40.42898	21.31876	2.84	1.85195	1.45	11	11	1.00	Perfect Match
5	Unchanged	33.58221	36.28994	3.02	2.16679	2.46	9	10	1.00	Perfect Match
6	Unchanged	56.68924	7.06718	0.08	3.46361	1.51	12	17	1.53	Perfect Match
7	Unchanged	73.04369	35.41966	0.03	4.64187	0.81	14	17	1.94	Almost Perfect
8	Unchanged	33.45556	14.72688	1.96	10.23946	7.99	11	12	0.83	Perfect Match
9	Unchanged	63.11602	72.41050	0.05	7.29125	1.28	15	14	1.43	Almost Perfect
10	Unchanged	38.59480	19.01146	0.32	4.10599	0.93	9	13	0.92	Perfect Match
11	Unchanged	23.24288	36.43952	24.29	1.48179	1.53	6	6	1.00	Perfect Match
12	Unchanged	37.28228	64.80186	0.78	8.74529	3.80	10	14	1.00	Almost Perfect
13	Unchanged	33.07638	57.01338	0.50	4.05890	6.37	9	8	0.88	Almost Perfect
14	Unchanged	15.37027	114.95462	20.90	5.28875	7.36	3	4	1.25	Almost Perfect
15	Unchanged	35.42641	116.26361	8.46	6.37049	16.56	8	8	0.75	Perfect Match

Table E.4: Subject 2 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	6.54428	0.00607	0.01	1.20008	0.78	1	2	1.00	Perfect Match
2	Unchanged	8.22597	0.51034	0.34	1.11566	1.15	1	1	6.00	Perfect Match
3	Unchanged	11.43937	108.68795	3.22	4.27469	1.89	1	1	5.00	Almost Perfect
4	Unchanged	20.31951	131.44102	17.53	5.12024	4.00	3	4	4.25	Almost Perfect
5	Unchanged	43.38322	63.50136	5.29	4.51580	5.12	8	13	1.69	Perfect Match
6	Unchanged	41.10735	30.04922	0.36	6.19645	2.70	8	10	2.30	Perfect Match
7	Unchanged	48.71166	173.52420	0.13	4.76389	0.83	10	13	2.00	Perfect Match
8	Unchanged	20.64533	21.94130	2.93	2.79090	2.18	9	9	1.00	Perfect Match
9	Unchanged	38.84565	95.20087	0.07	10.14635	1.78	10	12	1.58	Perfect Match
10	Unchanged	34.66310	9.73437	0.17	4.13860	0.94	7	11	1.27	Perfect Match
11	Unchanged	18.16614	4.86940	3.25	0.95866	0.99	4	7	2.14	Perfect Match
12	Unchanged	35.17976	62.42075	0.75	8.12902	3.54	10	12	1.00	Perfect Match
13	Unchanged	31.41971	270.13791	2.35	7.02343	11.02	7	8	2.25	Almost Perfect
14	Unchanged	23.71289	106.17661	19.30	5.33977	7.43	4	8	2.00	Perfect Match
15	Unchanged	24.99709	90.77515	6.60	7.13586	18.55	6	8	0.50	Perfect Match

Table E.5: Subject 2 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	15.88778	24.67226	24.67	4.34398	2.82	3	3	1.00	Perfect Match
2	Unchanged	16.48612	12.77827	8.52	1.17829	1.21	6	6	1.00	Perfect Match
3	Unchanged	14.80276	5.36807	0.16	1.91661	0.85	5	5	1.00	Perfect Match
4	Unchanged	23.23042	58.89884	7.85	3.29121	2.57	9	9	1.00	Perfect Match
5	Unchanged	24.09709	39.01920	3.25	3.63853	4.13	9	9	1.00	Perfect Match
6	Unchanged	35.78813	98.86772	1.19	8.74857	3.81	12	13	1.00	Perfect Match
7	Unchanged	40.19906	220.66545	0.17	4.65920	0.82	10	12	1.00	Perfect Match
8	Unchanged	22.44457	9.26887	1.24	2.43839	1.90	9	10	1.00	Perfect Match
9	Unchanged	28.78218	58.18318	0.04	7.70390	1.35	10	11	1.00	Perfect Match
10	Unchanged	22.86874	65.35336	1.12	2.82969	0.64	9	9	0.89	Perfect Match
11	Unchanged	13.49606	7.43565	4.96	2.52693	2.60	6	6	1.00	Perfect Match
12	Unchanged	27.34631	13.09866	0.16	4.54105	1.98	10	10	1.00	Perfect Match
13	Unchanged	19.60034	36.37531	0.32	5.41074	8.49	5	6	1.33	Perfect Match
14	Unchanged	26.74798	11.66183	2.12	2.24421	3.12	7	6	0.50	Perfect Match
15	Unchanged	18.12699	121.70213	8.85	6.66070	17.32	4	4	0.50	Perfect Match

Table E.6: Subject 2 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	12.39602	0.00795	0.01	1.37297	0.89	2	1	1.00	Satisfactory
2	Unchanged	19.08945	54.69664	36.46	2.98045	3.07	5	5	1.00	Satisfactory
3	Unchanged	23.06118	21.06660	0.62	4.02615	1.78	5	7	1.00	Satisfactory
4	Unchanged	35.04803	168.59958	22.48	3.80447	2.97	8	10	1.00	Satisfactory
5	Unchanged	33.08467	76.75273	6.40	5.25981	5.96	11	12	1.00	Satisfactory
6	Unchanged	63.65262	66.55936	0.80	5.67510	2.47	12	13	1.69	Unsatisfactory
7	Unchanged	60.07673	44.80741	0.03	4.41444	0.77	10	11	1.09	Unsatisfactory
8	Unchanged	32.66050	23.74783	3.17	4.17708	3.26	9	9	1.00	Satisfactory
9	Unchanged	42.44397	132.91225	0.10	7.86435	1.38	10	11	1.00	Satisfactory
10	Unchanged	27.65124	61.53510	1.05	6.94783	1.58	8	9	1.22	Satisfactory
11	Unchanged	28.41127	4.84868	3.23	1.53199	1.58	6	7	1.00	Unsatisfactory
12	Unchanged	36.94306	43.97812	0.53	6.91858	3.01	10	11	1.00	Satisfactory
13	Unchanged	28.35876	161.43557	1.40	7.15325	11.23	7	7	1.29	Satisfactory
14	Unchanged	28.96961	41.34789	7.52	3.66062	5.09	7	8	1.00	Satisfactory
15	Final	103.39405	573.65999	41.72	17.84284	46.39	22	20	1.15	Unsatisfactory
15	Cutoff	18.98362	770.52148	56.04	17.77153	46.20	4	3	1.00	-
15	Difference	84.41043	-196.86148	-14.32	0.07131	0.19	18	17	0.15	-

Table E.7: Subject 3 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	9.30516	0.10637	0.11	5.02319	3.27	1	1	1.00	Satisfactory
2	Unchanged	14.29356	59.17740	39.45	1.72310	1.77	5	5	1.00	Satisfactory
3	Unchanged	15.51026	53.54346	1.59	2.41842	1.07	5	5	1.00	Satisfactory
4	Unchanged	31.71051	135.30557	18.04	4.76965	3.72	11	11	1.00	Satisfactory
5	Unchanged	31.83133	196.29357	16.36	11.56942	13.12	6	10	1.50	Satisfactory
6	Unchanged	37.20894	61.20065	0.74	6.76164	2.94	5	6	2.00	Satisfactory
7	Unchanged	88.21975	178.60788	0.13	5.04987	0.88	14	18	2.89	Satisfactory
8	Unchanged	31.07633	104.69993	13.96	3.82586	2.99	9	11	1.18	Satisfactory
9	Unchanged	43.20986	58.59931	0.04	8.20857	1.44	12	10	1.00	Satisfactory
10	Unchanged	27.24377	88.70246	1.52	6.05313	1.38	9	9	1.22	Satisfactory
11	Unchanged	12.01770	28.01077	18.67	2.80454	2.89	4	4	1.50	Satisfactory
12	Unchanged	23.16787	142.75082	1.71	8.90533	3.87	7	5	2.00	Satisfactory
13	Unchanged	30.02048	36.45002	0.32	3.67756	5.77	9	7	2.00	Satisfactory
14	Unchanged	28.02878	34.70604	6.31	6.70745	9.33	5	6	1.83	Satisfactory
15	Unchanged	18.43530	84.96803	6.18	4.26410	11.09	4	5	1.20	Satisfactory

Table E.8: Subject 3 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	8.88929	0.35602	0.36	9.18991	5.97	1	1	1.00	Satisfactory
2	Unchanged	16.82776	25.62851	17.09	3.48549	3.59	5	5	2.00	Satisfactory
3	Unchanged	19.94781	19.94536	0.59	2.05349	0.91	5	5	3.00	Satisfactory
4	Unchanged	35.34888	192.69125	25.69	6.54988	5.11	10	10	2.40	Satisfactory
5	Unchanged	32.80551	92.36855	7.70	11.19115	12.69	9	10	2.60	Satisfactory
6	Unchanged	41.05980	9.53979	0.11	3.89170	1.69	10	12	1.67	Satisfactory
7	Unchanged	57.79339	54.41654	0.04	5.89881	1.03	12	13	1.92	Satisfactory
8	Unchanged	27.86042	113.09761	15.08	4.34848	3.39	10	9	1.33	Satisfactory
9	Unchanged	35.55803	10.13948	0.01	2.91643	0.51	10	11	2.64	Satisfactory
10	Unchanged	36.41471	136.94211	2.34	4.12287	0.94	9	10	1.40	Satisfactory
11	Unchanged	16.45525	41.96014	27.97	1.84970	1.90	5	5	1.40	Satisfactory
12	Unchanged	33.45550	36.30442	0.44	7.37945	3.21	10	11	2.00	Satisfactory
13	Unchanged	30.84881	272.96719	2.37	6.77783	10.64	8	11	2.09	Satisfactory
14	Unchanged	17.76944	78.06156	14.19	4.27332	5.95	5	5	1.00	Satisfactory
15	Unchanged	17.08943	117.21693	8.52	7.51732	19.54	5	4	1.00	Satisfactory

Table E.9: Subject 3 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	5.81924	7.70997	7.71	8.18943	5.32	3	2	1.00	Almost Perfect
2	Unchanged	11.82851	43.47221	28.98	2.44760	2.52	6	6	1.00	Almost Perfect
3	Unchanged	17.11275	16.46224	0.49	1.67568	0.74	7	6	1.00	Pretty Good
4	Unchanged	16.37524	73.99228	9.87	4.63724	3.62	9	8	1.00	Almost Perfect
5	Unchanged	17.81609	122.90557	10.24	4.32377	4.90	9	11	1.00	Pretty Good
6	Unchanged	34.74215	310.92738	3.73	10.71007	4.66	10	11	1.00	Satisfactory
7	Unchanged	47.11736	878.45699	0.66	10.54614	1.85	9	18	2.78	Satisfactory
8	Unchanged	42.81481	202.20105	26.96	5.25973	4.11	12	13	1.92	Pretty Good
9	Unchanged	37.40806	67.78563	0.05	4.49282	0.79	10	10	1.00	Pretty Good
10	Unchanged	32.99965	67.36084	1.15	4.17991	0.95	7	15	0.87	Pretty Good
11	Unchanged	13.62438	44.08578	29.39	2.21778	2.28	4	5	2.40	Almost Perfect
12	Unchanged	26.75540	94.03919	1.13	5.81751	2.53	10	13	1.00	Pretty Good
13	Unchanged	27.51875	115.86965	1.01	5.17492	8.12	8	14	1.14	Pretty Good
14	Unchanged	19.27613	80.40963	14.62	3.76584	5.24	6	8	1.13	Pretty Good
15	Unchanged	27.58958	83.56979	6.08	5.18299	13.47	11	8	0.63	Satisfactory

Table E.10: Subject 4 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	16.88611	17.00385	17.00	7.30101	4.75	6	5	3.00	Pretty Good
2	Unchanged	12.16187	24.10202	16.07	1.82507	1.88	6	6	1.00	Almost Perfect
3	Unchanged	14.70025	51.77898	1.53	2.34073	1.04	5	6	1.00	Pretty Good
4	Unchanged	17.71945	23.84738	3.18	2.59781	2.03	9	9	1.00	Almost Perfect
5	Unchanged	17.44279	22.91778	1.91	3.50556	3.98	9	9	1.00	Almost Perfect
6	Unchanged	27.56297	358.18397	4.30	14.54488	6.33	10	10	1.80	Pretty Good
7	Unchanged	42.88323	1085.79459	0.82	12.96602	2.27	9	14	2.07	Satisfactory
8	Unchanged	20.48118	111.61803	14.88	5.65526	4.41	7	7	1.29	Pretty Good
9	Unchanged	38.11397	155.78668	0.12	13.63368	2.39	10	11	1.73	Pretty Good
10	Unchanged	19.30783	183.77866	3.14	4.11701	0.94	8	9	1.22	Pretty Good
11	Unchanged	6.67512	2.16993	1.45	2.29070	2.36	1	1	6.00	Almost Perfect
12	Unchanged	33.06555	68.89006	0.83	4.99868	2.17	11	15	1.93	Pretty Good
13	Unchanged	26.99545	59.41186	0.52	4.82907	7.58	7	10	1.40	Almost Perfect
14	Unchanged	15.88277	77.19956	14.04	5.67815	7.90	6	5	1.20	Pretty Good
15	Unchanged	15.32276	112.21201	8.16	7.10798	18.48	5	6	1.00	Almost Perfect

Table E.11: Subject 4 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	9.30348	0.00391	0.00	0.96354	0.63	1	2	5.00	Perfect Match
2	Unchanged	14.10439	15.97151	10.65	2.61127	2.69	6	6	1.17	Almost Perfect
3	Unchanged	18.93780	81.73030	2.42	2.83528	1.26	5	5	2.20	Almost Perfect
4	Unchanged	23.57870	45.25148	6.03	4.18996	3.27	9	12	1.58	Almost Perfect
5	Unchanged	19.33948	63.79510	5.32	3.56668	4.04	9	9	1.11	Almost Perfect
6	Unchanged	40.27980	41.96106	0.50	4.12327	1.79	10	12	3.33	Pretty Good
7	Unchanged	33.19635	85.57678	0.06	6.85123	1.20	10	11	1.91	Satisfactory
8	Unchanged	16.10192	38.44521	5.13	2.96631	2.32	9	9	1.00	Almost Perfect
9	Unchanged	33.88720	12.26140	0.01	2.94057	0.51	10	10	1.90	Pretty Good
10	Unchanged	21.44784	34.12715	0.58	3.10035	0.71	8	9	1.22	Almost Perfect
11	Unchanged	10.57432	8.76010	5.84	1.11842	1.15	6	6	1.00	Almost Perfect
12	Unchanged	21.85449	28.37800	0.34	4.66181	2.03	10	10	1.00	Pretty Good
13	Unchanged	17.78776	61.74235	0.54	4.17790	6.56	7	7	1.29	Pretty Good
14	Unchanged	19.98531	55.61558	10.11	4.00502	5.57	6	8	1.25	Pretty Good
15	Unchanged	22.78535	214.35658	15.59	9.35011	24.31	7	9	0.33	Pretty Good

Table E.12: Subject 4 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	84.09377	75.42240	75.42	2.95414	1.92	8	9	2.78	Almost Perfect
2	Unchanged	21.13616	49.53798	33.03	2.22699	2.29	6	7	1.00	Almost Perfect
3	Unchanged	25.93957	20.89426	0.62	1.60817	0.71	5	5	1.00	Almost Perfect
4	Unchanged	32.07050	46.19889	6.16	2.04563	1.60	9	9	1.00	Almost Perfect
5	Unchanged	31.05048	40.81033	3.40	3.65150	4.14	9	10	1.00	Almost Perfect
6	Unchanged	40.37896	7.14975	0.09	5.21288	2.27	10	10	1.00	Almost Perfect
7	Unchanged	50.47162	9.13428	0.01	1.76177	0.31	10	9	2.22	Almost Perfect
8	Unchanged	27.97876	74.06513	9.88	3.04462	2.38	9	9	1.00	Almost Perfect
9	Unchanged	44.04236	12.31272	0.01	5.18012	0.91	10	10	1.00	Almost Perfect
10	Unchanged	48.85991	122.06942	2.09	12.34971	2.81	15	15	0.60	Pretty Good
11	Unchanged	15.23689	17.29232	11.53	2.06206	2.12	6	6	1.00	Almost Perfect
12	Unchanged	29.53046	65.66918	0.79	4.92610	2.14	11	11	1.09	Almost Perfect
13	Unchanged	22.92703	47.66941	0.41	3.03825	4.77	9	7	1.29	Almost Perfect
14	Unchanged	21.47117	64.78407	11.78	2.92932	4.08	10	8	1.25	Almost Perfect
15	Unchanged	32.68135	10.37681	0.75	2.76039	7.18	11	8	0.75	Almost Perfect

Table E.13: Subject 5 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	22.29365	8.35966	8.36	2.84791	1.85	10	6	0.83	Almost Perfect
2	Unchanged	14.91439	22.05400	14.70	1.93038	1.99	7	7	1.00	Almost Perfect
3	Unchanged	12.10851	42.78168	1.27	1.76235	0.78	5	5	1.00	Pretty Good
4	Unchanged	28.19208	24.76367	3.30	1.49350	1.17	13	11	0.91	Perfect Match
5	Unchanged	22.23199	54.25394	4.52	4.95648	5.62	10	9	1.00	Almost Perfect
6	Unchanged	30.96296	68.86722	0.83	6.80756	2.96	11	11	1.64	Almost Perfect
7	Unchanged	36.29387	48.76657	0.04	3.61331	0.63	10	10	1.00	Pretty Good
8	Unchanged	16.92692	36.14893	4.82	2.39166	1.87	10	9	1.00	Pretty Good
9	Unchanged	26.21039	41.97043	0.03	4.39872	0.77	10	10	1.00	Almost Perfect
10	Unchanged	21.62782	98.41423	1.68	4.22068	0.96	11	9	1.55	Pretty Good
11	Unchanged	10.49433	18.66390	12.44	3.81198	3.92	7	6	1.00	Almost Perfect
12	Unchanged	25.49120	61.98484	0.74	5.02365	2.19	13	11	1.09	Almost Perfect
13	Unchanged	18.13110	63.21913	0.55	4.36008	6.84	9	8	1.25	Pretty Good
14	Unchanged	30.60129	11.78969	2.14	1.90380	2.65	13	10	1.10	Almost Perfect
15	Unchanged	28.21291	5.24582	0.38	1.51721	3.94	16	7	0.86	Almost Perfect

Table E.14: Subject 5 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	17.42610	9.93041	9.93	2.40295	1.56	8	5	1.00	Almost Perfect
2	Unchanged	13.99271	6.45423	4.30	0.77246	0.80	7	6	1.00	Almost Perfect
3	Unchanged	18.22028	3.05795	0.09	0.62912	0.28	5	5	1.00	Perfect Match
4	Unchanged	20.03365	37.82422	5.04	2.63532	2.06	9	9	1.00	Almost Perfect
5	Unchanged	22.11450	20.23914	1.69	2.83746	3.22	10	9	1.00	Almost Perfect
6	Unchanged	35.18054	70.57762	0.85	5.15813	2.24	12	12	1.17	Almost Perfect
7	Unchanged	25.68539	48.48206	0.04	2.84158	0.50	10	10	1.00	Almost Perfect
8	Unchanged	17.02109	89.71129	11.96	3.49971	2.73	11	9	1.00	Pretty Good
9	Unchanged	21.73200	9.69727	0.01	2.87436	0.50	10	10	1.00	Pretty Good
10	Unchanged	19.61280	12.14356	0.21	3.92331	0.89	9	9	1.22	Pretty Good
11	Unchanged	13.26187	17.63129	11.75	2.06347	2.12	9	6	1.00	Almost Perfect
12	Unchanged	18.06611	65.60421	0.79	5.84172	2.54	11	10	1.00	Pretty Good
13	Unchanged	13.75938	126.88252	1.10	4.66688	7.32	9	7	1.29	Pretty Good
14	Unchanged	14.63940	58.48382	10.63	4.60707	6.41	9	8	1.13	Pretty Good
15	Unchanged	28.58292	8.67810	0.63	2.54390	6.61	11	11	1.27	Pretty Good

Table E.15: Subject 5 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Final	51.15329	2.18280	2.18	0.86577	0.56	9	6	1.00	Almost Perfect
1	Cutoff	9.16180	0.00128	0.00	0.55012	0.36	1	1	1.00	-
1	Difference	41.99149	2.18153	2.18	0.31565	0.20	8	5	0.00	-
2	Unchanged	30.10964	4.55040	3.03	1.04121	1.07	6	6	1.00	Almost Perfect
3	Unchanged	84.49715	1.40361	0.04	0.56377	0.25	13	13	1.00	Almost Perfect
4	Unchanged	78.84790	27.09436	3.61	2.05537	1.60	15	16	1.00	Almost Perfect
5	Unchanged	95.31316	8.37202	0.70	3.00124	3.40	15	19	1.00	Pretty Good
6	Unchanged	87.46135	9.65399	0.12	3.10729	1.35	12	12	1.00	Almost Perfect
7	Unchanged	419.97988	34.31785	0.03	1.63661	0.29	11	20	3.35	Perfect Match
8	Unchanged	97.40569	5.39707	0.72	0.96629	0.75	21	18	1.44	Perfect Match
9	Unchanged	103.56995	46.74631	0.04	5.29673	0.93	21	18	1.50	Satisfactory
10	Unchanged	58.57091	10.37120	0.18	2.84445	0.65	11	11	1.45	Pretty Good
11	Unchanged	21.28700	11.17589	7.45	1.33514	1.37	6	7	1.00	Almost Perfect
12	Unchanged	46.63072	41.56527	0.50	4.47643	1.95	10	10	1.00	Satisfactory
13	Unchanged	49.12578	27.21818	0.24	2.35989	3.70	12	9	1.56	Pretty Good
14	Unchanged	33.16303	36.90114	6.71	3.24273	4.51	9	6	0.50	Pretty Good
15	Unchanged	73.83949	10.74457	0.78	1.81034	4.71	13	12	0.83	Pretty Good

Table E.16: Subject 6 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	17.19611	2.53624	2.54	1.63105	1.06	4	3	1.00	Almost Perfect
2	Unchanged	38.68061	9.82612	6.55	0.88851	0.91	7	7	1.00	Almost Perfect
3	Unchanged	24.21204	0.54815	0.02	0.20745	0.09	5	5	1.00	Perfect Match
4	Unchanged	53.77502	46.48330	6.20	2.48574	1.94	15	15	1.00	Almost Perfect
5	Unchanged	37.03892	49.67685	4.14	4.50280	5.11	9	9	1.00	Pretty Good
6	Unchanged	53.62835	55.40492	0.67	5.25825	2.29	10	11	1.82	Pretty Good
7	Unchanged	76.23037	50.91407	0.04	2.44656	0.43	17	16	1.00	Almost Perfect
8	Unchanged	37.08059	46.62221	6.22	2.13561	1.67	9	10	1.00	Almost Perfect
9	Unchanged	51.82833	26.49096	0.02	4.82198	0.84	11	10	1.00	Almost Perfect
10	Unchanged	48.01576	25.11879	0.43	4.08659	0.93	12	13	1.15	Pretty Good
11	Unchanged	17.61527	20.53897	13.69	3.36321	3.46	7	6	1.00	Almost Perfect
12	Unchanged	35.98558	5.97379	0.07	2.09600	0.91	10	10	1.00	Almost Perfect
13	Unchanged	52.33667	19.20750	0.17	2.43806	3.83	11	8	1.25	Almost Perfect
14	Unchanged	45.00656	18.95419	3.45	2.26443	3.15	11	9	0.89	Almost Perfect
15	Unchanged	46.63493	13.77278	1.00	2.35577	6.12	11	11	1.36	Pretty Good

Table E.17: Subject 6 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	25.48626	0.68843	0.69	1.02240	0.66	5	4	1.00	Pretty Good
2	Unchanged	18.87780	7.51838	5.01	1.40713	1.45	7	6	1.00	Pretty Good
3	Unchanged	32.49221	5.96989	0.18	1.48651	0.66	7	7	1.00	Pretty Good
4	Unchanged	36.66644	45.26257	6.04	4.01064	3.13	11	11	1.00	Pretty Good
5	Unchanged	45.19407	26.82859	2.24	2.52029	2.86	15	15	1.00	Pretty Good
6	Unchanged	30.66718	17.45590	0.21	3.56799	1.55	10	10	1.00	Almost Perfect
7	Unchanged	108.56512	58.63699	0.04	3.44532	0.60	24	26	1.69	Almost Perfect
8	Unchanged	51.02167	38.81158	5.17	2.35959	1.84	10	12	3.00	Perfect Match
9	Unchanged	37.69979	43.94577	0.03	9.49162	1.66	10	10	1.00	Satisfactory
10	Unchanged	29.57548	41.39500	0.71	3.53283	0.80	9	9	1.22	Pretty Good
11	Unchanged	29.63716	8.97455	5.98	3.26407	3.36	11	12	0.83	Pretty Good
12	Unchanged	31.20303	42.43294	0.51	7.23070	3.15	10	10	1.00	Pretty Good
13	Unchanged	52.41338	10.38928	0.09	3.31018	5.20	15	15	1.67	Satisfactory
14	Unchanged	42.56820	50.05180	9.10	4.38379	6.10	12	12	1.17	Pretty Good
15	Unchanged	86.79561	20.93164	1.52	3.88975	10.11	20	20	1.35	Satisfactory

Table E.18: Subject 6 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	53.83917	32.52789	32.53	2.64882	1.72	7	6	3.17	Almost Perfect
2	Unchanged	7.83263	1.09852	0.73	2.52719	2.60	1	1	6.00	Almost Perfect
3	Unchanged	13.11604	41.84835	1.24	2.89916	1.28	1	2	5.00	Almost Perfect
4	Unchanged	36.22807	123.25140	16.43	5.35849	4.18	4	5	2.40	Almost Perfect
5	Unchanged	31.92800	53.91648	4.49	4.03920	4.58	5	7	1.86	Almost Perfect
6	Unchanged	58.15676	59.26108	0.71	5.87377	2.56	10	10	2.20	Almost Perfect
7	Unchanged	71.14613	33.06993	0.02	2.78887	0.49	6	6	4.00	Almost Perfect
8	Unchanged	42.20379	45.42280	6.06	2.91815	2.28	4	5	2.20	Almost Perfect
9	Unchanged	74.41340	41.47538	0.03	4.96673	0.87	6	6	1.67	Almost Perfect
10	Unchanged	54.19240	25.85674	0.44	2.23891	0.51	6	9	1.67	Almost Perfect
11	Unchanged	15.87212	16.36252	10.91	1.72584	1.78	3	3	2.00	Almost Perfect
12	Unchanged	45.28882	13.31492	0.16	3.09536	1.35	5	5	2.00	Perfect Match
13	Unchanged	55.99330	63.62375	0.55	2.99520	4.70	3	6	2.17	Almost Perfect
14	Unchanged	39.45617	30.94094	5.63	3.10166	4.32	5	5	2.60	Almost Perfect
15	Unchanged	45.26129	70.34269	5.12	5.07911	13.20	6	6	1.00	Perfect Match

Table E.19: Subject 7 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	27.34205	3.43208	3.43	5.08529	3.31	2	2	2.50	Almost Perfect
2	Unchanged	13.11185	17.57399	11.72	1.69961	1.75	2	2	3.00	Almost Perfect
3	Unchanged	22.62866	14.14983	0.42	1.63108	0.72	4	3	3.33	Almost Perfect
4	Unchanged	47.80984	24.65831	3.29	3.57899	2.79	4	5	2.40	Almost Perfect
5	Unchanged	43.37228	6.79141	0.57	2.57384	2.92	4	8	2.50	Perfect Match
6	Unchanged	40.77059	34.64257	0.42	5.00999	2.18	5	7	2.00	Perfect Match
7	Unchanged	87.95458	15.91877	0.01	3.08470	0.54	4	8	4.50	Perfect Match
8	Unchanged	32.45545	35.30307	4.71	2.38014	1.86	8	8	1.13	Perfect Match
9	Unchanged	60.82586	21.02617	0.02	4.31760	0.76	5	7	1.86	Almost Perfect
10	Unchanged	43.19646	17.45427	0.30	4.17193	0.95	9	9	1.22	Almost Perfect
11	Unchanged	12.01934	27.75381	18.50	3.62335	3.73	1	2	4.00	Almost Perfect
12	Unchanged	41.00059	12.06001	0.14	4.24963	1.85	5	6	2.00	Almost Perfect
13	Unchanged	56.05081	9.47954	0.08	1.70852	2.68	6	8	2.88	Almost Perfect
14	Unchanged	37.44220	114.54642	20.83	5.85122	8.14	3	4	2.25	Almost Perfect
15	Unchanged	21.75114	32.12180	2.34	3.52587	9.17	3	4	1.25	Almost Perfect

Table E.20: Subject 7 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	12.58767	0.00366	0.00	0.93204	0.61	2	1	1.00	Perfect Match
2	Unchanged	17.58691	4.97229	3.31	1.05590	1.09	6	6	1.00	Almost Perfect
3	Unchanged	30.24712	7.85059	0.23	1.12621	0.50	7	6	1.00	Almost Perfect
4	Unchanged	33.81383	63.09034	8.41	4.77620	3.73	7	7	1.00	Pretty Good
5	Unchanged	24.26868	56.25109	4.69	3.05497	3.46	9	9	1.00	Almost Perfect
6	Unchanged	42.75146	37.28121	0.45	4.87869	2.12	10	11	1.00	Pretty Good
7	Unchanged	53.13244	41.10095	0.03	2.51127	0.44	10	11	1.82	Perfect Match
8	Unchanged	29.61627	14.29425	1.91	2.92699	2.28	9	9	1.00	Perfect Match
9	Unchanged	37.37304	15.43476	0.01	2.55262	0.45	10	10	1.00	Almost Perfect
10	Unchanged	41.95727	5.05876	0.09	3.47957	0.79	9	9	1.22	Perfect Match
11	Unchanged	30.66212	5.15928	3.44	1.78236	1.83	8	8	1.00	Perfect Match
12	Unchanged	36.08803	13.34053	0.16	3.04609	1.33	12	12	1.00	Almost Perfect
13	Unchanged	47.06903	14.96897	0.13	2.05400	3.22	9	9	1.22	Almost Perfect
14	Unchanged	37.42890	17.91376	3.26	2.30307	3.20	9	9	0.67	Almost Perfect
15	Unchanged	37.70306	62.02580	4.51	4.93704	12.84	9	9	0.56	Almost Perfect

Table E.21: Subject 7 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	57.06565	2.29892	2.30	1.21910	0.79	6	9	2.33	Pretty Good
2	Unchanged	34.38707	19.37924	12.92	1.05646	1.09	6	8	1.13	Almost Perfect
3	Unchanged	36.32041	1.54940	0.05	0.71933	0.32	5	13	1.00	Perfect Match
4	Unchanged	40.19797	22.60817	3.01	1.63436	1.28	11	24	1.00	Almost Perfect
5	Unchanged	62.74824	4.92551	0.41	1.59397	1.81	21	41	1.00	Almost Perfect
6	Unchanged	102.74874	7.54717	0.09	2.03769	0.89	28	75	1.00	Almost Perfect
7	Unchanged	83.49354	42.95833	0.03	2.01830	0.35	10	57	1.60	Almost Perfect
8	Unchanged	50.13812	8.77922	1.17	1.31321	1.02	11	24	1.96	Pretty Good
9	Unchanged	107.94554	6.30557	0.00	2.27339	0.40	22	79	1.00	Pretty Good
10	Unchanged	56.75240	1.77520	0.03	1.14858	0.26	15	43	1.51	Almost Perfect
11	Unchanged	62.20332	6.60069	4.40	0.86297	0.89	17	52	0.96	Almost Perfect
12	Unchanged	68.11757	8.62863	0.10	2.08692	0.91	19	55	1.00	Almost Perfect
13	Unchanged	66.84923	6.67799	0.06	1.55912	2.45	20	50	0.50	Satisfactory
14	Unchanged	29.32206	9.45769	1.72	1.69718	2.36	9	20	0.85	Pretty Good
15	Unchanged	143.37696	23.36166	1.70	3.31499	8.62	30	88	0.90	Pretty Good

Table E.22: Subject 8 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	77.35035	2.32399	2.32	0.58185	0.38	21	57	1.00	Perfect Match
2	Unchanged	55.19418	6.44030	4.29	0.69592	0.72	18	44	0.98	Perfect Match
3	Unchanged	48.73962	0.71168	0.02	0.28910	0.13	14	29	1.28	Perfect Match
4	Unchanged	100.56154	9.29886	1.24	1.15607	0.90	32	89	1.01	Perfect Match
5	Unchanged	50.79663	5.22234	0.44	1.34133	1.52	14	38	1.00	Perfect Match
6	Unchanged	84.57298	4.57126	0.05	1.26846	0.55	17	82	1.26	Almost Perfect
7	Unchanged	83.16670	41.64370	0.03	2.26050	0.40	14	58	1.51	Almost Perfect
8	Unchanged	33.47630	16.43886	2.19	1.30961	1.02	9	24	1.00	Perfect Match
9	Unchanged	103.84583	9.37124	0.01	2.33568	0.41	28	89	1.00	Almost Perfect
10	Unchanged	34.72709	12.84917	0.22	1.86967	0.43	12	25	1.64	Almost Perfect
11	Unchanged	27.12650	3.45711	2.30	0.48284	0.50	12	28	1.00	Perfect Match
12	Unchanged	66.91571	9.31372	0.11	3.68261	1.60	20	62	1.00	Satisfactory
13	Unchanged	35.40818	9.95929	0.09	2.06019	3.23	8	34	1.82	Pretty Good
14	Unchanged	60.33225	5.52042	1.00	1.46735	2.04	19	68	0.81	Almost Perfect
15	Unchanged	86.45357	6.93903	0.50	2.09693	5.45	24	64	1.52	Almost Perfect

Table E.23: Subject 8 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	100.38361	24.93786	24.94	1.56157	1.02	22	108	1.00	Unsatisfactory
2	Unchanged	20.00336	1.28737	0.86	0.74159	0.76	6	6	1.00	Almost Perfect
3	Unchanged	38.58118	0.25086	0.01	0.75539	0.33	10	19	1.00	Satisfactory
4	Unchanged	37.81464	21.06036	2.81	1.53326	1.20	15	35	1.00	Almost Perfect
5	Unchanged	46.24382	7.74339	0.65	1.38584	1.57	12	44	1.00	Perfect Match
6	Unchanged	43.12654	4.93891	0.06	2.55163	1.11	12	53	1.00	Pretty Good
7	Unchanged	62.76172	36.67701	0.03	2.27648	0.40	13	63	1.00	Pretty Good
8	Unchanged	46.03376	6.81274	0.91	1.25619	0.98	21	44	1.02	Perfect Match
9	Unchanged	43.59176	18.52978	0.01	3.49930	0.61	15	43	1.00	Unsatisfactory
10	Unchanged	50.29220	23.13008	0.40	2.71168	0.62	17	38	1.05	Unsatisfactory
11	Unchanged	20.34507	5.99622	4.00	0.71294	0.73	8	20	1.00	Perfect Match
12	Unchanged	52.84215	17.90572	0.22	4.53832	1.97	20	38	0.50	Unsatisfactory
13	Unchanged	40.32010	11.62735	0.10	2.36790	3.72	14	30	1.27	Pretty Good
14	Unchanged	39.23472	13.23336	2.41	1.97896	2.75	15	35	1.06	Satisfactory
15	Unchanged	79.18168	2.83942	0.21	1.16191	3.02	25	72	1.42	Pretty Good

Table E.24: Subject 8 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	52.77252	13.81418	13.81	1.57341	1.02	12	29	1.00	Almost Perfect
2	Unchanged	35.08556	19.05421	12.70	1.30653	1.34	8	40	0.98	Perfect Match
3	Unchanged	35.63307	4.90524	0.15	1.14921	0.51	7	9	1.00	Perfect Match
4	Unchanged	56.32009	67.38092	8.98	3.31472	2.59	9	13	1.00	Perfect Match
5	Unchanged	53.43504	50.90355	4.24	1.99244	2.26	11	20	1.00	Perfect Match
6	Unchanged	71.81198	14.46001	0.17	2.84168	1.24	10	33	1.00	Perfect Match
7	Unchanged	157.53084	50.43365	0.04	1.97043	0.34	17	28	1.46	Perfect Match
8	Unchanged	37.71393	46.55132	6.21	2.36062	1.84	12	20	0.85	Perfect Match
9	Unchanged	55.16172	29.12430	0.02	3.14514	0.55	10	16	1.00	Perfect Match
10	Unchanged	52.53835	33.90449	0.58	1.62404	0.37	14	20	1.20	Perfect Match
11	Unchanged	39.10645	25.91874	17.28	1.90643	1.96	12	40	0.93	Perfect Match
12	Unchanged	42.04151	4.76953	0.06	1.62352	0.71	10	11	0.91	Perfect Match
13	Unchanged	50.15663	7.05679	0.06	2.00266	3.14	14	26	0.96	Perfect Match
14	Unchanged	53.41418	54.80143	9.96	9.42091	13.11	17	26	0.88	Perfect Match
15	Unchanged	110.28594	137.82152	10.02	5.87426	15.27	26	25	1.16	Almost Perfect

Table E.25: Subject 9 1st method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	40.89639	4.07651	4.08	1.64283	1.07	11	25	1.00	Perfect Match
2	Unchanged	22.74031	22.41020	14.94	1.59928	1.65	7	24	1.00	Perfect Match
3	Unchanged	26.95537	11.16723	0.33	1.00182	0.44	7	12	1.00	Perfect Match
4	Unchanged	42.10309	34.94026	4.66	2.11613	1.65	11	31	1.00	Perfect Match
5	Unchanged	40.55891	11.26009	0.94	2.58190	2.93	9	34	1.00	Perfect Match
6	Unchanged	35.59717	36.42207	0.44	3.28716	1.43	10	21	1.00	Perfect Match
7	Unchanged	56.74749	62.90362	0.05	3.18508	0.56	10	23	1.00	Perfect Match
8	Unchanged	37.36054	17.09397	2.28	1.92772	1.50	13	31	1.00	Perfect Match
9	Final	62.36258	22.78850	0.02	6.75301	1.18	13	31	1.03	Perfect Match
9	Cutoff	55.91666	22.18874	0.02	5.80586	1.02	12	28	1.04	-
9	Difference	6.44592	0.59975	0.00	0.94715	0.16	1	3	-0.01	-
10	Unchanged	51.58798	16.22525	0.28	2.74094	0.62	9	27	1.93	Perfect Match
11	Unchanged	24.78939	12.68540	8.46	1.51438	1.56	8	37	1.00	Perfect Match
12	Unchanged	38.48282	15.46270	0.19	4.22533	1.84	10	21	1.00	Perfect Match
13	Unchanged	42.60621	1.16391	0.01	1.59048	2.50	10	33	1.58	Perfect Match
14	Unchanged	46.54712	3.44820	0.63	2.63713	3.67	12	48	1.17	Perfect Match
15	Unchanged	60.06479	29.88924	2.17	3.89557	10.13	14	40	0.20	Perfect Match

Table E.26: Subject 9 2nd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	45.72558	45.29135	45.29	2.05555	1.34	14	51	1.00	Perfect Match
2	Unchanged	17.95522	16.24530	10.83	1.15778	1.19	7	25	1.00	Perfect Match
3	Unchanged	24.32114	3.00247	0.09	0.86988	0.39	7	41	1.00	Perfect Match
4	Unchanged	32.62627	37.00775	4.93	2.94580	2.30	9	55	1.00	Perfect Match
5	Unchanged	28.20204	22.03617	1.84	2.70492	3.07	9	65	1.00	Perfect Match
6	Unchanged	39.43971	56.37188	0.68	4.64976	2.02	12	60	1.00	Almost Perfect
7	Unchanged	44.55397	10.75274	0.01	2.22218	0.39	14	40	1.00	Perfect Match
8	Unchanged	28.17374	25.77472	3.44	2.55487	1.99	11	42	1.00	Perfect Match
9	Unchanged	50.12739	43.44295	0.03	5.14014	0.90	12	56	1.05	Perfect Match
10	Unchanged	47.85570	14.01455	0.24	1.32401	0.30	13	64	1.45	Perfect Match
11	Unchanged	20.97614	19.79465	13.20	1.21899	1.25	8	33	1.00	Perfect Match
12	Unchanged	41.39979	8.77605	0.11	2.97421	1.29	12	58	1.00	Perfect Match
13	Unchanged	40.47651	16.35174	0.14	2.42834	3.81	12	33	1.33	Perfect Match
14	Unchanged	32.62732	49.80172	9.05	2.48331	3.46	10	34	1.03	Perfect Match
15	Unchanged	35.33156	18.38519	1.34	2.61066	6.79	7	30	0.93	Perfect Match

Table E.27: Subject 9 3rd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	23.49454	108.34635	108.35	9.02755	5.87	1	11	4.82	Almost Perfect
2	Unchanged	14.96024	64.26150	42.84	5.22616	5.38	1	8	3.88	Almost Perfect
3	Unchanged	28.51461	113.75332	3.37	4.21166	1.87	1	15	3.53	Almost Perfect
4	Unchanged	39.52812	176.34813	23.51	6.21164	4.85	1	23	4.57	Almost Perfect
5	Unchanged	36.66557	145.68806	12.14	8.25223	9.36	1	26	5.42	Almost Perfect
6	Unchanged	45.55573	255.32430	3.07	14.80776	6.44	1	22	4.95	Almost Perfect
7	Unchanged	82.23462	443.23662	0.33	7.15043	1.25	1	39	5.51	Almost Perfect
8	Unchanged	59.89345	128.69535	17.16	4.13081	3.22	1	43	4.56	Pretty Good
9	Unchanged	145.47648	136.59843	0.10	7.27230	1.27	1	96	5.19	Almost Perfect
10	Unchanged	63.50350	152.92853	2.61	6.68905	1.52	1	86	4.26	Almost Perfect
11	Unchanged	13.08020	14.14039	9.43	1.85947	1.91	1	29	3.41	Almost Perfect
12	Unchanged	55.87506	98.34481	1.18	6.85119	2.98	1	62	3.98	Almost Perfect
13	Unchanged	55.35420	97.01948	0.84	5.00367	7.85	1	31	3.35	Almost Perfect
14	Unchanged	47.10909	83.84015	15.24	5.59314	7.78	1	35	3.74	Perfect Match
15	Unchanged	34.87889	119.30007	8.68	8.04185	20.91	1	19	4.00	Almost Perfect

Table E.28: Subject 10 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	3.81172	0.26725	0.27	7.96229	5.18	1	1	1.00	Almost Perfect
2	Outlier	13.46187	282.03591	188.02	32.04190	32.98	1	5	4.60	Unsatisfactory
3	Outlier	29.48211	3223.42713	95.51	118.96730	52.73	1	7	2.71	Unsatisfactory
4	Outlier	27.75625	981.19286	130.83	54.20923	42.31	1	11	6.82	Unsatisfactory
5	Outlier	12.03268	1204.94604	100.41	88.53731	100.40	1	5	5.60	Unsatisfactory
6	Outlier	19.04612	8256.44651	99.18	226.39104	98.50	1	8	7.13	Unsatisfactory
7	Outlier	19.04029	132744.43949	99.66	563.53191	98.64	1	7	4.86	Unsatisfactory
8	Outlier	7.04010	936.80848	124.91	58.83767	45.92	1	2	2.00	Unsatisfactory
9	Outlier	14.10688	133157.98733	99.97	570.43188	99.84	1	4	3.50	Unsatisfactory
10	Outlier	10.31348	6052.49574	103.46	97.34277	22.16	1	3	4.00	Unsatisfactory
11	Outlier	5.04507	253.16214	168.77	27.24965	28.05	1	1	6.00	Unsatisfactory
12	Outlier	8.53097	8315.34239	99.88	229.20332	99.72	1	3	3.33	Unsatisfactory
13	Outlier	6.00259	11660.36458	101.34	59.78954	93.84	1	2	4.50	Unsatisfactory
14	Outlier	10.97099	525.35225	95.52	30.68166	42.69	1	4	2.75	Satisfactory
15	Outlier	9.79764	1377.51982	100.18	33.72110	87.67	1	2	2.50	Unsatisfactory

Table E.29: Subject 10 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	8.21430	0.02263	0.02	2.31698	1.51	1	8	1.00	Perfect Match
2	Unchanged	18.83946	47.52644	31.68	4.58375	4.72	1	14	2.93	Perfect Match
3	Unchanged	23.12869	20.51205	0.61	1.77301	0.79	1	22	3.50	Perfect Match
4	Unchanged	30.86965	118.74590	15.83	6.67666	5.21	1	27	5.00	Almost Perfect
5	Unchanged	41.93648	92.94853	7.75	5.23058	5.93	1	51	5.43	Perfect Match
6	Unchanged	58.29340	144.86647	1.74	13.10806	5.70	1	40	5.03	Perfect Match
7	Unchanged	101.62824	69.45638	0.05	6.51068	1.14	1	146	5.64	Almost Perfect
8	Unchanged	46.54156	150.86496	20.12	8.52143	6.65	1	72	4.97	Pretty Good
9	Unchanged	108.43419	66.26060	0.05	6.79040	1.19	1	94	6.33	Pretty Good
10	Unchanged	39.32728	56.33494	0.96	5.79071	1.32	1	57	4.89	Perfect Match
11	Unchanged	17.05693	49.86706	33.24	4.50791	4.64	1	25	3.32	Almost Perfect
12	Unchanged	184.23701	165.97053	1.99	11.51512	5.01	1	123	5.63	Unsatisfactory
13	Unchanged	62.90681	259.87925	2.26	11.00624	17.27	1	46	3.33	Unsatisfactory
14	Unchanged	24.29704	77.88081	14.16	8.64082	12.02	1	59	3.51	Pretty Good
15	Unchanged	23.11704	245.17912	17.83	10.47554	27.23	1	35	4.09	Almost Perfect

Table E.30: Subject 10 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	36.67655	54.49675	54.50	6.05535	3.94	5	5	3.00	Perfect Match
2	Unchanged	12.09470	10.83200	7.22	1.45128	1.49	2	2	3.00	Perfect Match
3	Final	27.29950	3.73846	0.11	1.00214	0.44	5	5	1.60	Perfect Match
3	Cutoff	13.38391	3.40418	0.10	0.91253	0.40	3	3	3.00	-
3	Difference	13.91559	0.33428	0.01	0.08961	0.04	2	2	-1.40	-
4	Unchanged	38.05670	50.25036	6.70	4.80698	3.75	6	6	2.67	Almost Perfect
5	Unchanged	29.79716	100.33191	8.36	5.32651	6.04	6	7	2.00	Almost Perfect
6	Unchanged	48.07808	65.74861	0.79	5.58002	2.43	9	11	2.09	Pretty Good
7	Unchanged	47.61906	104.78396	0.08	6.08233	1.06	9	15	1.93	Pretty Good
8	Unchanged	28.37806	21.95326	2.93	3.77634	2.95	9	13	1.15	Almost Perfect
9	Unchanged	41.50335	33.79300	0.03	4.73534	0.83	10	13	0.85	Almost Perfect
10	Unchanged	29.97773	75.45330	1.29	3.77692	0.86	11	11	1.73	Almost Perfect
11	Unchanged	21.20548	20.81624	13.88	1.62580	1.67	4	3	2.00	Almost Perfect
12	Unchanged	27.25087	25.16368	0.30	5.15179	2.24	10	12	1.00	Almost Perfect
13	Unchanged	31.61120	60.55153	0.53	4.97052	7.80	9	10	1.00	Pretty Good
14	Unchanged	34.20733	23.28658	4.23	3.98165	5.54	11	12	1.08	Almost Perfect
15	Unchanged	32.05971	246.75702	17.95	10.28691	26.74	13	9	0.88	Satisfactory

Table E.31: Subject 11 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	9.18097	0.03015	0.03	2.67455	1.74	1	1	1.00	Almost Perfect
2	Unchanged	24.94121	26.18777	17.46	1.80629	1.86	7	8	1.50	Almost Perfect
3	Unchanged	21.14448	5.07366	0.15	0.61755	0.27	5	5	1.60	Almost Perfect
4	Unchanged	25.91123	51.26145	6.83	4.11886	3.21	10	11	1.00	Almost Perfect
5	Unchanged	27.48208	36.66297	3.06	3.31173	3.76	10	9	1.00	Almost Perfect
6	Unchanged	34.72634	71.68499	0.86	5.49847	2.39	10	10	1.90	1Almost Perfect
7	Unchanged	42.14980	61.63646	0.05	3.33578	0.58	10	13	1.69	Pretty Good
8	Unchanged	24.93371	15.86919	2.12	4.17419	3.26	9	9	1.00	Pretty Good
9	Unchanged	34.06385	19.09830	0.01	3.01856	0.53	10	10	1.30	Almost Perfect
10	Unchanged	32.18799	37.63174	0.64	3.58473	0.82	10	9	1.22	Almost Perfect
11	Unchanged	16.98776	8.99841	6.00	2.83272	2.92	7	6	1.00	Almost Perfect
12	Unchanged	29.12210	106.01375	1.27	7.57775	3.30	10	11	1.09	Almost Perfect
13	Unchanged	32.01465	136.62344	1.19	8.89760	13.96	9	8	1.63	Pretty Good
14	Unchanged	45.13653	56.24053	10.23	4.07237	5.67	15	10	0.80	Almost Perfect
15	Unchanged	43.77316	63.69761	4.63	2.76445	7.19	15	11	0.64	Almost Perfect

Table E.32: Subject 11 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	9.18347	0.00791	0.01	1.37000	0.89	2	1	1.00	Almost Perfect
2	Unchanged	12.42935	4.58686	3.06	2.23781	2.30	2	2	4.50	Almost Perfect
3	Unchanged	14.24272	21.99374	0.65	3.20371	1.42	1	2	5.00	Almost Perfect
4	Unchanged	28.41045	32.13318	4.28	3.44694	2.69	9	10	1.30	Almost Perfect
5	Unchanged	18.46363	198.44420	16.54	7.32523	8.31	5	7	1.86	Pretty Good
6	Unchanged	32.55135	86.42823	1.04	4.90451	2.13	10	12	1.75	Almost Perfect
7	Unchanged	53.01916	114.73257	0.09	3.40894	0.60	10	17	0.88	Almost Perfect
8	Unchanged	22.14201	29.75624	3.97	2.17642	1.70	11	10	1.00	Almost Perfect
9	Unchanged	33.95220	21.41103	0.02	4.00151	0.70	10	10	1.00	Almost Perfect
10	Unchanged	30.93298	156.14072	2.67	3.59362	0.82	10	11	1.18	Almost Perfect
11	Unchanged	12.75602	33.84195	22.56	1.23203	1.27	6	6	1.00	Almost Perfect
12	Unchanged	29.00378	80.81351	0.97	6.28644	2.74	8	10	1.20	Almost Perfect
13	Unchanged	28.50628	89.93145	0.78	8.48839	13.32	9	9	1.56	Pretty Good
14	Unchanged	24.96039	31.79643	5.78	3.90365	5.43	9	9	1.00	Almost Perfect
15	Unchanged	29.47379	89.73076	6.53	4.71635	12.26	8	6	0.67	Almost Perfect

Table E.33: Subject 11 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	27.80045	33.65890	33.66	3.51315	2.28	7	9	2.67	Pretty Good
2	Unchanged	18.52447	32.07069	21.38	2.25156	2.32	4	6	1.83	Pretty Good
3	Unchanged	31.05133	1.95714	0.06	1.10602	0.49	7	8	1.25	Pretty Good
4	Unchanged	29.98965	18.39273	2.45	2.52700	1.97	9	12	2.33	Pretty Good
5	Unchanged	32.66551	81.03461	6.75	3.27884	3.72	10	10	1.80	Pretty Good
6	Unchanged	54.20337	85.77076	1.03	6.84209	2.98	12	12	1.75	Pretty Good
7	Unchanged	59.15093	300.05674	0.23	6.51105	1.14	15	15	2.20	Pretty Good
8	Unchanged	21.14949	29.30308	3.91	3.87231	3.02	9	9	1.00	Pretty Good
9	Unchanged	44.58153	27.12041	0.02	5.07204	0.89	11	13	0.92	Pretty Good
10	Unchanged	40.19146	41.31434	0.71	3.08632	0.70	8	11	0.82	Pretty Good
11	Unchanged	14.71857	3.91542	2.61	1.43860	1.48	6	6	1.00	Pretty Good
12	Unchanged	26.01957	9.87891	0.12	3.98946	1.74	10	11	1.00	Pretty Good
13	Unchanged	28.96545	76.79292	0.67	4.65600	7.31	8	7	1.29	Pretty Good
14	Unchanged	20.44615	197.13058	35.84	6.83077	9.50	5	4	1.00	Pretty Good
15	Unchanged	50.98997	16.19492	1.18	2.57357	6.69	12	10	1.20	Pretty Good

Table E.34: Subject 12 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	7.23344	0.00364	0.00	0.92925	0.60	1	1	1.00	Almost Perfect
2	Unchanged	17.67777	15.39054	10.26	1.50993	1.55	6	7	1.00	Pretty Good
3	Unchanged	22.09117	5.93508	0.18	1.39623	0.62	6	6	1.17	Almost Perfect
4	Unchanged	21.25115	80.92529	10.79	2.94133	2.30	9	9	1.00	Pretty Good
5	Unchanged	22.33786	95.93714	7.99	3.46182	3.93	9	9	1.00	Pretty Good
6	Unchanged	29.04211	135.00250	1.62	8.26630	3.60	10	10	1.00	Pretty Good
7	Unchanged	38.47891	23.61919	0.02	5.52189	0.97	10	11	1.00	Pretty Good
8	Unchanged	24.25702	54.82053	7.31	4.07174	3.18	9	10	1.00	Pretty Good
9	Unchanged	34.57635	24.74930	0.02	4.93377	0.86	11	11	0.91	Pretty Good
10	Unchanged	36.14305	17.13838	0.29	4.74424	1.08	9	11	1.55	Pretty Good
11	Outlier	6.15676	150.00000	100.00	97.15083	100.00	0	0	0.00	Pretty Good
12	Unchanged	27.61708	55.79409	0.67	6.22740	2.71	11	10	1.00	Pretty Good
13	Unchanged	24.93705	10.47580	0.09	3.35214	5.26	6	7	1.29	Pretty Good
14	Unchanged	25.77456	35.75609	6.50	3.58324	4.99	8	8	-0.13	Pretty Good
15	Unchanged	45.27485	98.64525	7.17	6.30734	16.40	10	12	0.92	Pretty Good

Table E.35: Subject 12 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	7.79762	0.19836	0.20	6.85977	4.46	1	1	1.00	Pretty Good
2	Unchanged	9.49015	40.16882	26.78	3.70904	3.82	2	2	3.00	Pretty Good
3	Unchanged	18.74612	101.96150	3.02	3.06056	1.36	5	5	1.00	Pretty Good
4	Unchanged	33.77467	110.24707	14.70	5.77370	4.51	6	10	2.40	Pretty Good
5	Unchanged	33.75800	65.07753	5.42	4.26057	4.83	8	7	1.71	Pretty Good
6	Unchanged	33.66717	156.28349	1.88	9.83704	4.28	11	13	0.85	Pretty Good
7	Unchanged	65.88265	206.45716	0.15	5.59580	0.98	12	13	2.00	Satisfactory
8	Unchanged	17.68610	73.20307	9.76	3.14743	2.46	9	10	1.00	Pretty Good
9	Unchanged	45.07650	87.40659	0.07	6.85027	1.20	12	13	0.85	Pretty Good
10	Unchanged	24.37613	121.86924	2.08	5.58211	1.27	9	9	1.22	Pretty Good
11	Unchanged	10.36430	4.20137	2.80	3.29948	3.40	1	1	6.00	Pretty Good
12	Unchanged	32.17124	69.43135	0.83	7.57158	3.29	11	13	1.00	Pretty Good
13	Unchanged	25.00032	73.26414	0.64	4.46738	7.01	5	7	1.43	Pretty Good
14	Unchanged	27.39868	172.20300	31.31	6.42961	8.95	10	9	1.22	Pretty Good
15	Unchanged	16.53854	108.11096	7.86	7.23603	18.81	3	3	0.67	Pretty Good

Table E.36: Subject 12 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	10.56182	2.33441	2.33	2.43195	1.58	2	3	1.33	Almost Perfect
2	Unchanged	13.78355	15.19236	10.13	1.45647	1.50	3	3	2.00	Almost Perfect
3	Unchanged	16.58943	22.47040	0.67	1.69082	0.75	4	5	1.40	Pretty Good
4	Unchanged	22.80286	104.68522	13.96	3.07389	2.40	6	7	1.71	Almost Perfect
5	Unchanged	35.18303	41.60816	3.47	3.87766	4.40	10	10	1.60	Almost Perfect
6	Unchanged	34.07803	27.80505	0.33	3.63263	1.58	6	9	2.56	Pretty Good
7	Unchanged	77.35961	228.58064	0.17	9.20828	1.61	11	21	3.05	Satisfactory
8	Unchanged	33.40224	39.46693	5.26	2.42916	1.90	10	11	1.55	Pretty Good
9	Unchanged	62.48938	45.85254	0.03	4.87614	0.85	12	21	1.81	Pretty Good
10	Unchanged	39.74650	96.57976	1.65	4.96504	1.13	7	14	1.29	Almost Perfect
11	Unchanged	16.21612	8.78572	5.86	1.27068	1.31	6	6	1.00	Almost Perfect
12	Unchanged	39.17901	34.45209	0.41	8.96724	3.90	8	9	1.78	Pretty Good
13	Unchanged	42.47407	58.42257	0.51	3.33744	5.24	12	12	1.50	Almost Perfect
14	Unchanged	28.95800	1.91301	0.35	2.32194	3.23	8	9	1.56	Almost Perfect
15	Unchanged	24.68127	76.19172	5.54	6.59659	17.15	8	6	0.83	Pretty Good

Table E.37: Subject 13 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	7.35428	0.00171	0.00	0.63780	0.41	1	1	1.00	Almost Perfect
2	Unchanged	21.70201	10.11424	6.74	1.38544	1.43	6	7	1.71	Almost Perfect
3	Unchanged	17.64862	10.06747	0.30	1.07748	0.48	5	5	1.00	Almost Perfect
4	Unchanged	21.17033	24.55105	3.27	3.55652	2.78	9	10	1.00	Pretty Good
5	Unchanged	21.00617	73.45895	6.12	3.33866	3.79	9	9	1.00	Almost Perfect
6	Unchanged	56.46422	120.01070	1.44	6.63591	2.89	20	21	1.86	Almost Perfect
7	Unchanged	50.50746	54.38040	0.04	3.06139	0.54	22	22	0.91	Almost Perfect
8	Unchanged	28.88379	25.77432	3.44	1.92273	1.50	10	10	1.00	Pretty Good
9	Unchanged	46.15489	6.38410	0.00	3.09611	0.54	12	13	1.00	Almost Perfect
10	Unchanged	26.03791	22.17610	0.38	2.57405	0.59	9	9	1.22	Almost Perfect
11	Unchanged	14.12522	5.07503	3.38	0.58388	0.60	6	6	1.00	Almost Perfect
12	Unchanged	45.91573	26.10064	0.31	3.65668	1.59	17	17	1.00	Almost Perfect
13	Unchanged	29.55298	0.73019	0.01	0.80055	1.26	8	9	1.11	Perfect Match
14	Unchanged	26.77625	29.42140	5.35	2.99794	4.17	9	8	1.00	Almost Perfect
15	Unchanged	23.37789	66.57374	4.84	6.43654	16.73	7	6	0.50	Pretty Good

Table E.38: Subject 13 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	24.58039	33.51567	33.52	2.96010	1.92	9	11	1.91	Almost Perfect
2	Unchanged	9.27016	3.52139	2.35	1.58016	1.63	2	2	3.50	Almost Perfect
3	Unchanged	22.40037	11.45033	0.34	0.72994	0.32	7	8	1.50	Pretty Good
4	Unchanged	30.79715	47.62455	6.35	2.95393	2.31	5	9	2.22	Almost Perfect
5	Unchanged	32.04135	8.57610	0.71	2.64097	2.99	11	12	1.58	Pretty Good
6	Unchanged	33.58805	13.09021	0.16	3.51937	1.53	10	12	2.42	Pretty Good
7	Unchanged	51.31916	133.77775	0.10	4.09056	0.72	12	18	2.83	Pretty Good
8	Unchanged	42.90984	7.43266	0.99	1.69708	1.32	18	15	1.47	Almost Perfect
9	Unchanged	61.42016	38.78366	0.03	5.29936	0.93	22	20	1.20	Almost Perfect
10	Unchanged	26.16544	28.00112	0.48	2.45960	0.56	9	10	1.20	Almost Perfect
11	Unchanged	13.92690	0.52440	0.35	2.14550	2.21	1	1	6.00	Almost Perfect
12	Unchanged	32.98470	42.83527	0.51	5.45302	2.37	8	8	2.13	Pretty Good
13	Unchanged	37.78146	49.76826	0.43	3.12407	4.90	12	13	1.54	Satisfactory
14	Unchanged	28.00546	43.99353	8.00	4.60283	6.40	5	10	1.60	Almost Perfect
15	Unchanged	17.91196	70.39961	5.12	5.89393	15.32	7	5	1.00	Pretty Good

Table E.39: Subject 13 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	8.74430	0.02195	0.02	2.28216	1.48	1	1	1.00	Perfect Match
2	Unchanged	21.18281	18.71432	12.48	1.52403	1.57	6	6	1.00	Almost Perfect
3	Unchanged	27.49958	42.89700	1.27	2.63755	1.17	5	6	1.00	Perfect Match
4	Unchanged	58.08753	73.39079	9.79	5.53089	4.32	15	17	0.76	Perfect Match
5	Unchanged	39.85058	16.44355	1.37	3.34426	3.79	12	11	1.00	Perfect Match
6	Unchanged	67.01848	22.45957	0.27	4.63943	2.02	10	14	2.29	Almost Perfect
7	Unchanged	61.42255	77.53080	0.06	3.05301	0.53	14	11	1.00	Almost Perfect
8	Unchanged	37.25220	79.37660	10.58	2.76686	2.16	9	10	1.00	Almost Perfect
9	Unchanged	43.92981	4.47903	0.00	2.54803	0.45	10	11	0.91	Perfect Match
10	Unchanged	37.00721	33.77009	0.58	4.61123	1.05	9	9	1.22	Almost Perfect
11	Unchanged	17.77109	55.47488	36.98	1.77811	1.83	6	6	1.00	Almost Perfect
12	Unchanged	46.16150	41.24228	0.50	4.58000	1.99	12	16	1.06	Perfect Match
13	Unchanged	44.36395	19.27728	0.17	2.03159	3.19	9	12	0.66	Almost Perfect
14	Unchanged	45.50229	52.37710	9.52	3.28915	4.58	13	15	0.53	Perfect Match
15	Unchanged	40.12722	202.48561	14.73	8.02713	20.87	9	9	1.33	Perfect Match

Table E.40: Subject 14 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	5.02010	0.04805	0.05	3.37619	2.19	1	1	1.00	Perfect Match
2	Unchanged	33.35058	38.58043	25.72	1.88258	1.94	7	11	2.00	Almost Perfect
3	Unchanged	18.13449	6.94860	0.21	0.92977	0.41	5	6	1.67	Perfect Match
4	Unchanged	21.10786	44.95184	5.99	2.77744	2.17	9	9	1.00	Perfect Match
5	Unchanged	23.67710	78.96757	6.58	4.11473	4.67	9	10	1.00	Perfect Match
6	Unchanged	35.88063	36.65330	0.44	4.54376	1.98	10	11	1.00	Perfect Match
7	Unchanged	53.11510	47.96728	0.04	3.11390	0.55	11	14	1.93	Almost Perfect
8	Unchanged	27.07548	37.18269	4.96	2.15985	1.69	10	11	1.09	Perfect Match
9	Unchanged	31.68556	65.14228	0.05	7.17802	1.26	10	11	1.00	Almost Perfect
10	Unchanged	27.15881	139.26935	2.38	6.56363	1.49	9	9	1.22	Almost Perfect
11	Unchanged	25.01543	8.67259	5.78	1.07408	1.11	9	7	1.71	Perfect Match
12	Unchanged	31.34721	69.32061	0.83	5.59403	2.43	10	10	1.00	Perfect Match
13	Unchanged	25.82712	92.78482	0.81	4.28650	6.73	7	7	0.86	Perfect Match
14	Unchanged	23.16374	35.40606	6.44	3.65964	5.09	8	6	0.50	Almost Perfect
15	Unchanged	36.28146	285.89318	20.79	9.18018	23.87	11	10	1.50	Almost Perfect

Table E.41: Subject 14 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	27.75291	35.93690	35.94	5.70038	3.71	3	5	6.00	Almost Perfect
2	Unchanged	31.50965	4.51229	3.01	1.32255	1.36	2	5	4.00	Perfect Match
3	Unchanged	7.72929	56.65203	1.68	3.19199	1.41	1	1	5.00	Perfect Match
4	Unchanged	33.08634	82.29343	10.97	3.97030	3.10	5	8	3.00	Perfect Match
5	Unchanged	35.82055	87.08068	7.26	3.30059	3.74	10	10	1.30	Almost Perfect
6	Unchanged	45.75071	101.97397	1.22	5.83974	2.54	8	11	2.18	Almost Perfect
7	Unchanged	47.69823	33.93265	0.03	4.03161	0.71	8	7	1.71	Almost Perfect
8	Unchanged	32.54468	72.73222	9.70	2.59176	2.02	7	8	1.88	Almost Perfect
9	Unchanged	37.94225	34.29553	0.03	4.54123	0.79	10	11	1.00	Perfect Match
10	Unchanged	35.41555	42.81940	0.73	2.65447	0.60	5	7	2.14	Perfect Match
11	Unchanged	9.34264	34.43655	22.96	2.21588	2.28	3	3	2.33	Almost Perfect
12	Unchanged	55.82670	18.45976	0.22	3.88133	1.69	9	12	1.58	Perfect Match
13	Unchanged	24.51872	183.44850	1.59	4.45673	6.99	6	7	1.29	Perfect Match
14	Unchanged	29.73713	20.95333	3.81	3.80585	5.30	8	7	0.86	Almost Perfect
15	Unchanged	26.47125	54.86882	3.99	5.10604	13.27	8	7	1.29	Almost Perfect

Table E.42: Subject 14 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	53.70756	229.24058	229.24	4.27668	2.78	11	9	3.22	Pretty Good
2	Unchanged	9.72432	0.13730	0.09	0.94513	0.97	1	1	6.00	Almost Perfect
3	Unchanged	27.91296	17.03906	0.50	3.13680	1.39	2	3	3.00	Almost Perfect
4	Unchanged	41.57985	280.73453	37.43	6.57339	5.13	5	6	2.67	Pretty Good
5	Unchanged	31.69386	118.66038	9.89	11.03073	12.51	4	4	2.25	Satisfactory
6	Unchanged	53.74172	153.90979	1.85	8.61954	3.75	7	8	3.75	Pretty Good
7	Unchanged	119.29946	71.14666	0.05	4.17819	0.73	6	14	2.93	Pretty Good
8	Unchanged	25.22625	38.58001	5.14	3.63789	2.84	2	3	6.00	Pretty Good
9	Unchanged	59.24764	101.17269	0.08	8.47660	1.48	8	7	1.71	Pretty Good
10	Unchanged	35.20058	26.80464	0.46	2.74055	0.62	3	5	3.60	Almost Perfect
11	Unchanged	9.52933	1.36063	0.91	1.94434	2.00	1	1	6.00	Almost Perfect
12	Unchanged	53.28754	17.42090	0.21	6.70292	2.92	8	11	1.82	Almost Perfect
13	Unchanged	57.19261	28.77374	0.25	3.88241	6.09	6	11	1.91	Pretty Good
14	Unchanged	21.59203	118.86171	21.61	6.75883	9.40	2	3	2.33	Pretty Good
15	Unchanged	26.20126	102.35348	7.44	6.65804	17.31	1	5	3.60	Pretty Good

Table E.43: Subject 15 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	16.09529	0.11089	0.11	5.12891	3.33	1	5	9.00	Almost Perfect
2	Unchanged	22.65621	36.45799	24.31	2.07144	2.13	5	6	2.17	Pretty Good
3	Unchanged	22.98957	48.89267	1.45	1.37568	0.61	5	6	1.67	Pretty Good
4	Unchanged	33.85399	68.16882	9.09	2.40595	1.88	8	10	2.90	Pretty Good
5	Unchanged	41.65167	111.44250	9.29	5.25628	5.96	11	11	1.55	Satisfactory
6	Unchanged	59.81211	128.88328	1.55	8.55362	3.72	10	13	2.23	Satisfactory
7	Unchanged	68.93653	84.28816	0.06	4.60276	0.81	10	14	2.00	Pretty Good
8	Unchanged	50.14629	76.23598	10.16	2.13397	1.67	11	11	2.18	Pretty Good
9	Unchanged	44.59695	11.25709	0.01	3.18517	0.56	10	12	1.17	Pretty Good
10	Unchanged	46.17120	105.86347	1.81	4.80371	1.09	9	11	2.91	Pretty Good
11	Unchanged	29.51823	88.30762	58.87	2.58985	2.67	6	8	-1.25	Satisfactory
12	Unchanged	34.95170	38.39967	0.46	4.82857	2.10	10	10	1.10	Almost Perfect
13	Unchanged	27.17905	137.75550	1.20	5.35124	8.40	7	7	1.29	Pretty Good
14	Unchanged	26.18483	36.12608	6.57	3.10453	4.32	6	9	0.67	Almost Perfect
15	Unchanged	33.09917	92.06324	6.70	6.15959	16.01	8	6	1.17	Pretty Good

Table E.44: Subject 15 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	28.16748	78.73323	78.73	3.45252	2.24	7	8	2.63	Almost Perfect
2	Unchanged	16.91215	51.73455	34.49	2.30003	2.37	3	4	3.25	Almost Perfect
3	Unchanged	22.82649	35.37085	1.05	2.40655	1.07	5	5	2.00	Pretty Good
4	Unchanged	29.84251	105.48705	14.06	4.88643	3.81	4	6	2.00	Pretty Good
5	Unchanged	32.14410	105.17453	8.76	6.00146	6.81	7	8	1.75	Satisfactory
6	Unchanged	41.05343	65.49407	0.79	5.06432	2.20	8	9	2.67	Pretty Good
7	Unchanged	52.52784	42.61727	0.03	3.35996	0.59	6	7	2.43	Pretty Good
8	Unchanged	32.93155	5.55514	0.74	4.52852	3.53	4	4	4.75	Almost Perfect
9	Unchanged	61.90574	10.98066	0.01	3.91228	0.68	6	8	3.00	Almost Perfect
10	Unchanged	55.18668	35.56606	0.61	8.42149	1.92	7	10	2.20	Pretty Good
11	Unchanged	8.58862	0.27729	0.18	0.39406	0.41	1	1	6.00	Almost Perfect
12	Unchanged	37.81636	24.09291	0.29	5.38180	2.34	5	7	4.14	Pretty Good
13	Unchanged	30.23108	67.98894	0.59	5.60571	8.80	6	6	1.50	Pretty Good
14	Unchanged	29.94375	72.09423	13.11	6.55898	9.13	5	5	0.80	Pretty Good
15	Unchanged	24.66099	19.64811	1.43	3.35376	8.72	3	4	1.50	Almost Perfect

Table E.45: Subject 15 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	6.13343	0.02878	0.03	2.61291	1.70	2	1	1.00	Almost Perfect
2	Unchanged	16.10444	64.44345	42.96	1.67872	1.73	5	5	1.00	Almost Perfect
3	Unchanged	16.86278	13.59189	0.40	2.96161	1.31	5	5	1.00	Almost Perfect
4	Unchanged	23.32122	397.40842	52.99	6.48103	5.06	7	7	1.00	Pretty Good
5	Unchanged	29.23550	241.34564	20.11	6.08256	6.90	11	12	0.83	Pretty Good
6	Unchanged	42.65572	53.78507	0.65	5.02494	2.19	14	12	0.92	Almost Perfect
7	Unchanged	45.84575	29.22240	0.02	4.60805	0.81	13	10	1.00	Pretty Good
8	Unchanged	25.62625	12.24958	1.63	2.69519	2.10	9	14	1.07	Almost Perfect
9	Unchanged	45.03659	37.57294	0.03	6.64012	1.16	10	12	0.83	Almost Perfect
10	Unchanged	26.20710	19.42929	0.33	2.80396	0.64	8	9	1.22	Almost Perfect
11	Unchanged	12.92687	18.55812	12.37	1.40841	1.45	7	6	1.00	Almost Perfect
12	Unchanged	27.75714	74.79405	0.90	6.64816	2.89	10	10	1.00	Almost Perfect
13	Unchanged	27.54378	82.21768	0.71	6.30820	9.90	9	7	1.29	Pretty Good
14	Unchanged	27.04796	149.77252	27.23	5.97751	8.32	8	9	1.22	Pretty Good
15	Unchanged	27.94547	923.49675	67.16	19.64705	51.08	7	7	2.00	Satisfactory

Table E.46: Subject 16 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	5.12840	0.00135	0.00	0.56501	0.37	1	1	1.00	Almost Perfect
2	Unchanged	14.91766	11.07703	7.38	2.16616	2.23	8	6	1.00	Almost Perfect
3	Unchanged	11.35178	65.75036	1.95	2.37502	1.05	5	5	1.00	Almost Perfect
4	Unchanged	18.79769	60.90662	8.12	4.53390	3.54	9	9	1.00	Pretty Good
5	Unchanged	17.27101	193.89741	16.16	5.97550	6.78	9	8	1.00	Pretty Good
6	Unchanged	29.07615	115.56283	1.39	14.87172	6.47	12	13	0.69	Satisfactory
7	Unchanged	30.48532	100.08593	0.08	5.91128	1.03	10	11	1.00	Pretty Good
8	Unchanged	20.35022	55.11288	7.35	3.28327	2.56	9	9	1.00	Almost Perfect
9	Unchanged	28.18280	35.85260	0.03	6.14510	1.08	10	10	1.00	Almost Perfect
10	Unchanged	22.85942	5.39521	0.09	2.62609	0.60	8	9	1.22	Pretty Good
11	Unchanged	12.65345	27.70701	18.47	2.17867	2.24	6	6	1.00	Pretty Good
12	Unchanged	23.73693	29.21824	0.35	6.47485	2.82	10	10	1.00	Pretty Good
13	Unchanged	17.55019	55.95444	0.49	4.37290	6.86	5	6	1.33	Pretty Good
14	Unchanged	18.64354	13.93378	2.53	3.28725	4.57	7	7	1.00	Almost Perfect
15	Unchanged	17.87770	114.38901	8.32	7.37957	19.19	6	6	0.50	Pretty Good

Table E.47: Subject 16 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	4.60839	0.10118	0.10	4.89924	3.18	1	1	1.00	Almost Perfect
2	Unchanged	13.05269	33.44352	22.30	2.03657	2.10	6	7	1.00	Almost Perfect
3	Unchanged	13.06269	4.37602	0.13	1.31367	0.58	5	5	1.00	Pretty Good
4	Unchanged	17.40609	86.00001	11.47	3.68251	2.87	8	8	1.00	Almost Perfect
5	Unchanged	20.35030	156.69540	13.06	4.45818	5.06	9	9	1.00	Almost Perfect
6	Unchanged	29.24375	51.82811	0.62	7.58883	3.30	11	11	0.91	Pretty Good
7	Unchanged	40.25141	221.80705	0.17	7.25447	1.27	10	11	1.00	Satisfactory
8	Unchanged	18.55776	15.10291	2.01	3.75143	2.93	9	10	1.00	Pretty Good
9	Unchanged	28.73126	39.05527	0.03	5.70209	1.00	10	10	1.00	Almost Perfect
10	Unchanged	24.07618	70.41877	1.20	3.85604	0.88	9	11	1.09	Almost Perfect
11	Unchanged	10.32848	6.12978	4.09	2.23681	2.30	6	6	1.00	Almost Perfect
12	Unchanged	22.60616	89.93709	1.08	7.36143	3.20	10	11	1.00	Pretty Good
13	Unchanged	19.45945	123.54493	1.07	5.26380	8.26	7	8	1.63	Pretty Good
14	Unchanged	19.56278	86.42982	15.71	6.21365	8.65	9	8	1.00	Pretty Good
15	Unchanged	17.56943	71.87987	5.23	7.19164	18.70	6	5	0.40	Satisfactory

Table E.48: Subject 16 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	9.08183	0.00979	0.01	1.52382	0.99	1	4	1.00	Pretty Good
2	Unchanged	27.21378	0.81408	0.54	0.39069	0.40	7	24	1.00	Pretty Good
3	Unchanged	26.11378	0.11732	0.00	0.42048	0.19	6	15	1.00	Pretty Good
4	Unchanged	41.21317	22.52542	3.00	2.07277	1.62	11	22	0.91	Pretty Good
5	Unchanged	76.26792	8.87296	0.74	1.44718	1.64	24	39	0.64	Satisfactory
6	Unchanged	46.84577	6.23834	0.07	3.20424	1.39	10	22	1.00	Pretty Good
7	Unchanged	87.67811	32.06300	0.02	4.50403	0.79	23	47	0.91	Almost Perfect
8	Unchanged	52.67421	13.72240	1.83	1.14466	0.89	11	37	0.86	Almost Perfect
9	Unchanged	89.38564	21.00445	0.02	4.92918	0.86	23	51	1.00	Pretty Good
10	Unchanged	62.88271	6.57650	0.11	6.59854	1.50	14	49	0.69	Pretty Good
11	Unchanged	16.58859	6.40135	4.27	1.60188	1.65	6	10	1.00	Pretty Good
12	Unchanged	60.49351	34.28173	0.41	4.21738	1.83	16	45	1.13	Almost Perfect
13	Unchanged	72.98787	7.81315	0.07	2.07681	3.26	19	60	1.18	Perfect Match
14	Unchanged	29.35465	11.10847	2.02	3.58106	4.98	9	14	0.36	Perfect Match
15	Unchanged	77.07711	227.22979	16.53	8.50026	22.10	18	56	0.71	Satisfactory

Table E.49: Subject 17 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	41.66186	5.45699	5.46	2.09361	1.36	13	34	0.88	Satisfactory
2	Unchanged	40.93672	7.34088	4.89	1.22921	1.27	10	57	0.86	Pretty Good
3	Unchanged	27.08275	7.98923	0.24	1.97902	0.88	8	24	1.00	Almost Perfect
4	Unchanged	30.69955	17.59160	2.35	2.76886	2.16	9	25	1.00	Almost Perfect
5	Unchanged	60.89722	38.16754	3.18	3.44672	3.91	19	45	0.98	Pretty Good
6	Unchanged	53.36765	50.29463	0.60	6.37225	2.77	17	23	1.00	Pretty Good
7	Unchanged	71.03560	22.30471	0.02	2.60314	0.46	22	38	1.00	Almost Perfect
8	Unchanged	36.66112	23.66026	3.15	1.80249	1.41	13	30	1.00	Almost Perfect
9	Unchanged	41.03286	35.00288	0.03	4.96283	0.87	12	15	1.07	Almost Perfect
10	Unchanged	57.31743	50.29571	0.86	3.00144	0.68	15	50	1.34	Almost Perfect
11	Unchanged	23.35395	4.73529	3.16	1.07788	1.11	8	11	1.00	Perfect Match
12	Unchanged	43.42364	10.49153	0.13	3.93390	1.71	12	21	1.00	Almost Perfect
13	Unchanged	49.15379	15.14952	0.13	1.82075	2.86	13	31	1.35	Perfect Match
14	Unchanged	45.63203	33.14355	6.03	3.47778	4.84	17	49	0.84	Pretty Good
15	Unchanged	85.15715	6.31674	0.46	1.60487	4.17	16	82	0.90	Satisfactory

Table E.50: Subject 17 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	55.05959	5.38768	5.39	1.59710	1.04	21	60	1.00	Pretty Good
2	Unchanged	19.61046	2.19256	1.46	0.78756	0.81	10	10	1.00	Almost Perfect
3	Unchanged	18.48375	3.70512	0.11	0.74906	0.33	7	10	1.00	Almost Perfect
4	Unchanged	36.50084	11.70895	1.56	1.74221	1.36	11	20	1.00	Almost Perfect
5	Unchanged	37.21586	7.25658	0.60	1.41902	1.61	11	28	1.00	Perfect Match
6	Unchanged	45.14523	83.05261	1.00	6.17430	2.69	16	38	0.94	Almost Perfect
7	Unchanged	114.06459	109.91269	0.08	4.27564	0.75	25	45	1.44	Unsatisfactory
8	Unchanged	35.85446	22.91977	3.06	1.76906	1.38	13	22	1.00	Perfect Match
9	Unchanged	90.94705	23.82760	0.02	4.32586	0.76	28	49	1.08	Pretty Good
10	Unchanged	53.69671	48.40258	0.83	3.12202	0.71	11	46	1.52	Perfect Match
11	Unchanged	11.66871	4.00571	2.67	0.92010	0.95	6	6	1.00	Perfect Match
12	Unchanged	42.68634	9.95627	0.12	2.73630	1.19	15	29	1.00	Perfect Match
13	Unchanged	51.72828	3.75945	0.03	2.14422	3.37	16	41	1.37	Perfect Match
14	Unchanged	20.29733	6.79521	1.24	1.47477	2.05	6	16	0.25	Perfect Match
15	Unchanged	60.55524	43.29397	3.15	3.89305	10.12	17	48	1.44	Almost Perfect

Table E.51: Subject 17 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	77.06776	6.15818	6.16	1.61735	1.05	13	11	1.00	Almost Perfect
2	Unchanged	38.32930	1.81518	1.21	1.53811	1.58	8	8	1.00	Almost Perfect
3	Unchanged	53.32718	1.22995	0.04	0.41815	0.19	9	9	1.00	Almost Perfect
4	Unchanged	49.79703	14.99318	2.00	2.39634	1.87	11	11	1.00	Almost Perfect
5	Unchanged	49.41451	19.60718	1.63	2.87685	3.26	11	11	1.00	Almost Perfect
6	Unchanged	78.76195	62.22799	0.75	4.88673	2.13	14	14	1.57	Almost Perfect
7	Unchanged	143.69909	21.67203	0.02	4.32391	0.76	14	18	1.17	Pretty Good
8	Unchanged	74.26549	13.21597	1.76	1.74922	1.37	11	10	1.10	Almost Perfect
9	Unchanged	65.71274	13.62535	0.01	4.06481	0.71	12	12	1.00	Almost Perfect
10	Unchanged	68.20323	28.64081	0.49	3.84164	0.87	12	11	1.36	Almost Perfect
11	Unchanged	50.26117	18.32541	12.22	2.41034	2.48	7	9	0.00	Perfect Match
12	Unchanged	67.51867	22.94167	0.28	3.94744	1.72	10	11	1.00	Pretty Good
13	Unchanged	86.17373	5.18600	0.05	1.65662	2.60	14	13	1.38	Almost Perfect
14	Unchanged	36.07984	1.82295	0.33	1.13955	1.59	8	6	0.50	Perfect Match
15	Unchanged	73.33821	4.04678	0.29	1.03476	2.69	12	9	0.89	Almost Perfect

Table E.52: Subject 18 1st method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	49.62502	8.74634	8.75	1.40150	0.91	12	10	1.00	Almost Perfect
2	Unchanged	38.58566	8.43488	5.62	0.77440	0.80	10	10	0.90	Almost Perfect
3	Unchanged	26.46629	5.87278	0.17	0.97080	0.43	5	5	1.00	Almost Perfect
4	Unchanged	72.76706	37.69828	5.03	2.56798	2.00	18	17	1.00	Almost Perfect
5	Unchanged	34.36727	7.95680	0.66	1.82375	2.07	9	9	1.00	Perfect Match
6	Unchanged	90.60823	49.01204	0.59	3.25813	1.42	18	18	1.00	Pretty Good
7	Unchanged	91.05989	12.18977	0.01	1.97825	0.35	20	19	1.68	Almost Perfect
8	Unchanged	49.34334	12.27212	1.64	1.35892	1.06	11	12	1.67	Perfect Match
9	Unchanged	86.40482	29.17742	0.02	4.40670	0.77	16	16	1.00	Pretty Good
10	Unchanged	55.36927	22.66580	0.39	3.50928	0.80	13	13	0.92	Almost Perfect
11	Unchanged	64.40861	33.57082	22.38	1.46363	1.51	16	17	0.65	Perfect Match
12	Unchanged	36.61230	8.37771	0.10	2.66437	1.16	10	10	1.00	Almost Perfect
13	Unchanged	37.94315	15.13414	0.13	2.27444	3.57	10	10	1.50	Almost Perfect
14	Unchanged	32.22721	7.11621	1.29	2.31444	3.22	6	6	0.50	Almost Perfect
15	Unchanged	52.66090	4.35681	0.32	1.40991	3.67	8	8	0.88	Perfect Match

Table E.53: Subject 18 2nd method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	52.59919	14.54181	14.54	1.56923	1.02	11	11	1.00	Almost Perfect
2	Unchanged	46.78993	0.95834	0.64	0.76991	0.79	10	9	1.00	Almost Perfect
3	Unchanged	35.14974	6.03827	0.18	0.67201	0.30	7	7	1.00	Perfect Match
4	Unchanged	47.96743	37.75949	5.03	2.85425	2.23	13	13	1.00	Pretty Good
5	Unchanged	40.01731	23.69451	1.97	1.90801	2.16	9	20	1.00	Almost Perfect
6	Unchanged	52.83669	19.80348	0.24	3.95848	1.72	13	20	1.45	Pretty Good
7	Unchanged	82.46215	19.56233	0.01	1.41123	0.25	15	19	1.47	Perfect Match
8	Unchanged	52.40919	5.43396	0.72	3.10517	2.42	7	9	1.89	Perfect Match
9	Unchanged	45.32655	3.06416	0.00	3.85690	0.68	10	11	0.91	Almost Perfect
10	Unchanged	56.31089	37.68023	0.64	3.03974	0.69	13	14	1.14	Pretty Good
11	Unchanged	25.53458	4.21674	2.81	1.30185	1.34	8	8	1.00	Perfect Match
12	Unchanged	35.27473	18.51398	0.22	4.82296	2.10	10	10	1.00	Almost Perfect
13	Unchanged	43.45237	4.79608	0.04	5.81360	9.12	12	17	1.65	Almost Perfect
14	Unchanged	44.96238	26.15754	4.76	2.57262	3.58	8	13	1.46	Almost Perfect
15	Unchanged	50.43332	12.65071	0.92	2.31611	6.02	9	13	1.69	Almost Perfect

Table E.54: Subject 18 3rd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	37.15725	39.99255	39.99	3.89165	2.53	3	7	5.86	Pretty Good
2	Unchanged	19.02447	295.33020	196.89	7.28864	7.50	7	5	1.00	Satisfactory
3	Unchanged	16.50860	148.92063	4.41	3.88130	1.72	5	5	1.00	Satisfactory
4	Unchanged	29.37546	493.81644	65.84	7.69073	6.00	8	10	1.10	Pretty Good
5	Unchanged	22.66868	550.11224	45.84	8.72157	9.89	7	6	1.17	Pretty Good
6	Unchanged	41.62983	181.14843	2.18	12.00041	5.22	10	13	1.69	Pretty Good
7	Unchanged	46.29741	148.11834	0.11	6.47486	1.13	13	12	1.00	Pretty Good
8	Unchanged	35.49055	252.45361	33.66	9.87432	7.71	11	14	-0.07	Pretty Good
9	Unchanged	38.38145	949.48638	0.71	20.47120	3.58	10	13	1.00	Satisfactory
10	Unchanged	38.48895	731.08669	12.50	10.41849	2.37	9	10	1.50	Satisfactory
11	Unchanged	12.64520	252.33936	168.23	5.80528	5.98	2	2	4.50	Satisfactory
12	Unchanged	22.82870	342.60841	4.12	11.29571	4.91	10	10	1.00	Satisfactory
13	Unchanged	36.83892	700.97961	6.09	21.57232	33.86	7	10	0.90	Satisfactory
14	Unchanged	13.54272	488.49303	88.82	12.64091	17.59	3	3	3.00	Satisfactory
15	Unchanged	13.78272	512.43836	37.27	13.78523	35.84	6	3	1.00	Pretty Good

Table E.55: Subject 19 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	17.34362	195.06988	195.07	14.75223	9.59	3	3	4.33	Satisfactory
2	Unchanged	12.58855	88.20453	58.80	6.02583	6.20	3	3	1.67	Satisfactory
3	Unchanged	17.36527	53.53620	1.59	4.33957	1.92	3	4	1.75	Satisfactory
4	Unchanged	13.48273	271.26807	36.17	9.50907	7.42	5	5	1.80	Satisfactory
5	Unchanged	28.50544	517.83204	43.15	26.30547	29.83	10	9	0.78	Satisfactory
6	Unchanged	40.44730	560.09126	6.73	16.41741	7.14	5	11	3.36	Satisfactory
7	Unchanged	49.85163	1886.72724	1.42	19.71768	3.45	6	11	2.91	Unsatisfactory
8	Unchanged	23.97787	235.16865	31.36	11.13890	8.69	8	8	1.13	Unsatisfactory
9	Unchanged	37.60476	714.95466	0.54	21.66894	3.79	10	11	1.00	Satisfactory
10	Unchanged	25.21789	213.12633	3.64	11.34897	2.58	4	7	2.14	Satisfactory
11	Unchanged	8.37847	36.27009	24.18	8.35599	8.60	1	1	6.00	Satisfactory
12	Unchanged	35.57305	274.42181	3.30	11.89885	5.18	5	6	3.33	Satisfactory
13	Outlier	31.25131	606.81238	5.27	57.13842	89.68	8	9	1.33	Satisfactory
14	Unchanged	20.88866	144.50748	26.27	10.25495	14.27	5	5	2.00	Satisfactory
15	Unchanged	11.96602	452.88409	32.94	14.81651	38.52	3	3	2.00	Satisfactory

Table E.56: Subject 19 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	40.36063	131.85145	131.85	13.66623	8.88	8	11	2.82	Unsatisfactory
2	Unchanged	9.20514	1.16456	0.78	2.13841	2.20	1	1	6.00	Satisfactory
3	Unchanged	15.78858	38.62582	1.14	3.06138	1.36	2	3	3.33	Satisfactory
4	Unchanged	19.30447	212.79348	28.37	8.21421	6.41	5	5	2.00	Satisfactory
5	Unchanged	23.33285	199.40171	16.62	15.80202	17.92	5	7	2.00	Satisfactory
6	Unchanged	28.81626	206.03648	2.47	14.27493	6.21	5	7	2.43	Satisfactory
7	Unchanged	60.11425	697.67822	0.52	8.54298	1.50	6	17	3.29	Satisfactory
8	Unchanged	20.35447	84.52888	11.27	8.21264	6.41	3	3	3.00	Satisfactory
9	Unchanged	45.78570	532.62842	0.40	17.52763	3.07	13	15	1.00	Satisfactory
10	Unchanged	23.68453	136.53822	2.33	7.59724	1.73	5	4	2.75	Satisfactory
11	Unchanged	6.73509	1.67404	1.12	3.82359	3.94	1	1	6.00	Satisfactory
12	Unchanged	36.65390	397.28624	4.77	16.86173	7.34	4	8	2.63	Satisfactory
13	Unchanged	21.20198	171.30669	1.49	9.93897	15.60	5	6	1.67	Satisfactory
14	Unchanged	26.93207	211.11415	38.38	13.51885	18.81	6	7	1.71	Satisfactory
15	Unchanged	13.66605	138.10192	10.04	7.51955	19.55	2	4	1.00	Satisfactory

Table E.57: Subject 19 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	135.03713	29.63100	29.63	2.53139	1.65	14	21	2.57	Almost Perfect
2	Unchanged	108.31338	33.16407	22.11	1.88321	1.94	14	16	1.69	Almost Perfect
3	Unchanged	136.01884	8.78227	0.26	1.36041	0.60	24	22	1.77	Almost Perfect
4	Unchanged	157.08001	3.69732	0.49	1.41742	1.11	30	28	1.57	Almost Perfect
5	Unchanged	224.84360	31.91434	2.66	2.85073	3.23	38	34	1.06	Almost Perfect
6	Unchanged	189.79889	67.53406	0.81	5.29905	2.31	31	37	0.97	Pretty Good
7	Unchanged	175.90367	69.64070	0.05	4.06264	0.71	37	41	1.07	Almost Perfect
8	Unchanged	72.66366	21.45931	2.86	2.75771	2.15	21	17	1.65	Pretty Good
9	Unchanged	59.78513	9.59057	0.01	3.18172	0.56	15	15	1.00	Almost Perfect
10	Unchanged	92.64901	12.93405	0.22	7.89294	1.80	16	19	0.84	Almost Perfect
11	Unchanged	55.32340	39.04667	26.03	2.40526	2.48	12	12	1.25	Pretty Good
12	Unchanged	91.52398	19.57032	0.24	4.97575	2.16	24	24	0.96	Pretty Good
13	Unchanged	68.06111	12.96938	0.11	3.39984	5.34	13	16	1.50	Pretty Good
14	Unchanged	91.63650	8.55736	1.56	2.92974	4.08	16	18	1.22	Almost Perfect
15	Unchanged	59.21347	97.04393	7.06	5.50089	14.30	16	9	0.56	Almost Perfect

Table E.58: Subject 20 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	109.86499	29.51033	29.51	2.03018	1.32	17	18	1.50	Almost Perfect
2	Unchanged	35.38803	8.44433	5.63	0.88700	0.91	6	6	1.00	Almost Perfect
3	Unchanged	62.95179	19.84643	0.59	1.08676	0.48	6	7	1.43	Almost Perfect
4	Unchanged	101.02903	37.85206	5.05	2.65119	2.07	17	18	1.67	Almost Perfect
5	Unchanged	57.83754	12.82926	1.07	3.01008	3.41	18	16	1.00	Almost Perfect
6	Unchanged	106.44245	9.91145	0.12	2.70800	1.18	20	20	2.20	Almost Perfect
7	Unchanged	141.28296	13.42072	0.01	3.30902	0.58	17	16	4.63	Pretty Good
8	Unchanged	48.20239	8.16056	1.09	1.23089	0.96	4	6	2.17	Perfect Match
9	Unchanged	81.21039	24.76725	0.02	5.28899	0.93	10	16	1.44	Almost Perfect
10	Unchanged	93.07473	39.55984	0.68	2.81805	0.64	8	15	1.40	Pretty Good
11	Unchanged	22.20534	9.03313	6.02	0.73654	0.76	3	3	2.00	Perfect Match
12	Unchanged	86.84631	12.01864	0.14	2.65230	1.15	11	15	0.20	Perfect Match
13	Unchanged	69.63354	14.71919	0.13	2.57033	4.03	10	10	1.70	Pretty Good
14	Unchanged	64.46098	14.50383	2.64	2.77029	3.85	14	16	1.56	Almost Perfect
15	Unchanged	33.45134	20.79870	1.51	3.21448	8.36	4	4	1.25	Almost Perfect

Table E.59: Subject 20 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	52.90416	21.61430	21.61	1.43482	0.93	11	10	1.80	Almost Perfect
2	Unchanged	22.63202	5.96269	3.98	0.95361	0.98	3	3	2.00	Almost Perfect
3	Unchanged	41.49900	0.54924	0.02	0.23029	0.10	6	7	1.29	Almost Perfect
4	Unchanged	61.92598	79.11929	10.55	2.48137	1.94	13	12	1.00	Almost Perfect
5	Unchanged	56.22672	31.17005	2.60	2.43428	2.76	9	13	1.31	Perfect Match
6	Unchanged	67.96358	55.76235	0.67	4.86852	2.12	11	17	3.06	Pretty Good
7	Final	99.64823	45.40262	0.03	5.41874	0.95	9	15	1.93	Almost Perfect
7	Cutoff	94.15065	50.34583	0.04	5.39328	0.94	8	15	1.27	-
7	Difference	5.49758	-4.94321	-0.01	0.02546	0.01	1	1	0.66	-
8	Unchanged	45.58905	51.67652	6.89	3.14931	2.46	12	10	1.80	Almost Perfect
9	Unchanged	91.83312	8.95192	0.01	3.43581	0.60	12	11	1.36	Pretty Good
10	Unchanged	53.48419	33.77693	0.58	3.02645	0.69	8	11	1.27	Pretty Good
11	Unchanged	24.27705	11.61886	7.75	1.18659	1.22	3	3	2.00	Almost Perfect
12	Unchanged	46.50823	3.78857	0.05	2.16829	0.94	5	5	2.00	Almost Perfect
13	Unchanged	69.24694	2.39386	0.02	1.65514	2.60	12	13	1.08	Pretty Good
14	Unchanged	69.89361	18.09424	3.29	2.75336	3.83	11	10	1.40	Perfect Match
15	Unchanged	69.45693	6.41518	0.47	2.19611	5.71	12	11	1.45	Almost Perfect

Table E.60: Subject 20 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	62.74629	4.93704	4.94	1.17444	0.76	7	11	1.18	Perfect Match
2	Unchanged	26.17470	24.92066	16.61	1.51716	1.56	8	9	1.00	Perfect Match
3	Unchanged	18.14204	18.25760	0.54	1.23705	0.55	5	5	1.00	Perfect Match
4	Unchanged	36.47576	129.57847	17.28	3.42532	2.67	12	11	1.00	Perfect Match
5	Unchanged	44.07593	99.84495	8.32	3.14143	3.56	14	14	1.00	Perfect Match
6	Unchanged	34.73990	30.92261	0.37	3.54161	1.54	11	11	0.91	Perfect Match
7	Final	48.54351	27.88438	0.02	1.68802	0.30	14	15	0.93	Perfect Match
7	Cutoff	38.71832	28.81009	0.02	1.63133	0.29	11	12	0.92	-
7	Difference	9.82519	-0.92571	0.00	0.05669	0.01	3	3	0.01	-
8	Unchanged	22.36963	19.96011	2.66	1.43061	1.12	9	9	1.00	Perfect Match
9	Unchanged	42.80090	13.80120	0.01	2.92635	0.51	10	14	1.00	Perfect Match
10	Unchanged	43.80923	20.74520	0.35	2.05657	0.47	17	20	1.15	Perfect Match
11	Unchanged	25.88469	6.22806	4.15	1.20629	1.24	8	11	0.55	Perfect Match
12	Unchanged	24.73776	12.43067	0.15	2.85970	1.24	10	10	1.00	Perfect Match
13	Unchanged	28.58616	3.00199	0.03	1.66958	2.62	11	11	0.82	Perfect Match
14	Unchanged	41.01629	26.08475	4.74	6.69750	9.32	20	16	0.94	Perfect Match
15	Unchanged	45.19300	24.24945	1.76	5.47253	14.23	19	18	1.28	Perfect Match

Table E.61: Subject 21 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	44.47565	17.18871	17.19	1.60661	1.04	12	16	0.94	Perfect Match
2	Unchanged	18.77278	3.31577	2.21	0.47421	0.49	7	6	1.00	Perfect Match
3	Unchanged	22.90951	2.23519	0.07	0.49047	0.22	5	5	1.00	Perfect Match
4	Unchanged	30.63045	3.77110	0.50	1.39365	1.09	9	10	1.00	Perfect Match
5	Unchanged	31.70464	15.22882	1.27	1.68052	1.91	9	10	1.00	Perfect Match
6	Unchanged	58.51836	29.69230	0.36	3.31590	1.44	8	17	1.48	Perfect Match
7	Unchanged	63.56927	15.91537	0.01	2.23161	0.39	13	23	1.96	Almost Perfect
8	Unchanged	29.91545	29.77340	3.97	2.23615	1.75	11	14	1.00	Perfect Match
9	Unchanged	52.38660	34.98001	0.03	5.29644	0.93	11	10	1.00	Perfect Match
10	Unchanged	45.25485	15.78879	0.27	3.04657	0.69	14	16	1.19	Perfect Match
11	Unchanged	20.15362	17.58574	11.72	2.12625	2.19	8	7	1.00	Perfect Match
12	Unchanged	32.16465	38.76604	0.47	4.76632	2.07	10	10	1.00	Perfect Match
13	Unchanged	27.70124	5.29356	0.05	1.82115	2.86	7	11	1.36	Perfect Match
14	Unchanged	17.40776	84.55546	15.37	3.81637	5.31	6	8	0.88	Almost Perfect
15	Unchanged	25.74872	108.31185	7.88	5.60587	14.57	10	12	0.50	Perfect Match

Table E.62: Subject 21 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Final	50.46407	201.01171	201.01	9.55532	6.21	9	9	2.67	Almost Perfect
1	Cutoff	39.04308	148.98617	148.99	9.54275	6.20	7	7	3.14	-
1	Difference	11.42099	52.02554	52.02	0.01257	0.01	2	2	-0.47	-
2	Unchanged	17.51443	95.13086	63.42	3.32392	3.42	5	4	1.50	Almost Perfect
3	Unchanged	18.76195	0.89024	0.03	0.56246	0.25	5	6	1.00	Perfect Match
4	Unchanged	43.74398	82.87053	11.05	2.50302	1.95	12	14	1.79	Perfect Match
5	Unchanged	28.85293	60.15488	5.01	2.97867	3.38	9	11	1.00	Perfect Match
6	Unchanged	37.11637	36.55657	0.44	4.33513	1.89	12	18	1.50	Perfect Match
7	Unchanged	64.10094	41.18273	0.03	1.85798	0.33	16	28	3.14	Perfect Match
8	Unchanged	22.31282	25.12448	3.35	1.64960	1.29	9	15	1.00	Perfect Match
9	Unchanged	65.53097	40.16803	0.03	7.28175	1.27	10	26	1.77	Perfect Match
10	Unchanged	38.29891	21.42190	0.37	2.78031	0.63	13	21	1.95	Perfect Match
11	Unchanged	12.10103	27.11045	18.07	1.40352	1.44	4	9	1.22	Perfect Match
12	Unchanged	30.61213	26.78589	0.32	4.52254	1.97	12	26	1.00	Perfect Match
13	Unchanged	19.09861	16.99708	0.15	3.23080	5.07	7	10	1.40	Almost Perfect
14	Unchanged	22.49366	14.19495	2.58	2.22322	3.09	9	11	0.64	Perfect Match
15	Unchanged	16.43275	85.79549	6.24	4.81492	12.52	7	11	1.18	Perfect Match

Table E.63: Subject 21 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Final	14.29189	0.20332	0.20	6.94496	4.51	2	2	1.00	Almost Perfect
1	Cutoff	5.09509	0.08050	0.08	4.37007	2.84	2	1	1.00	-
1	Difference	9.19680	0.12282	0.12	2.57489	1.67	0	1	0.00	-
2	Unchanged	22.27283	52.35726	34.90	1.84804	1.90	10	7	0.86	Almost Perfect
3	Unchanged	15.20356	27.30232	0.81	1.67147	0.74	5	5	1.00	Almost Perfect
4	Unchanged	37.51308	28.89808	3.85	2.32983	1.82	17	12	1.00	Almost Perfect
5	Unchanged	25.61372	60.98479	5.08	4.84552	5.49	10	12	1.00	Almost Perfect
6	Unchanged	43.82483	23.09994	0.28	4.50261	1.96	17	11	1.82	Almost Perfect
7	Unchanged	39.41476	21.60398	0.02	3.63712	0.64	14	11	1.00	Almost Perfect
8	Unchanged	24.38287	21.50818	2.87	2.80564	2.19	9	9	1.00	Almost Perfect
9	Unchanged	36.25305	45.92051	0.03	5.10115	0.89	11	10	1.00	Pretty Good
10	Unchanged	33.89968	8.78419	0.15	2.85311	0.65	11	12	1.17	Almost Perfect
11	Unchanged	27.00958	7.43979	4.96	0.80844	0.83	8	9	0.89	Perfect Match
12	Unchanged	30.94047	42.87628	0.52	3.63558	1.58	10	10	1.00	Pretty Good
13	Unchanged	28.39043	73.87267	0.64	5.48400	8.61	7	7	1.57	Almost Perfect
14	Unchanged	30.83881	10.72516	1.95	3.19581	4.45	14	8	0.25	Almost Perfect
15	Unchanged	21.05116	79.73452	5.80	5.05343	13.14	8	5	0.40	Almost Perfect

Table E.64: Subject 22 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	21.14951	29.57689	29.58	5.92627	3.85	9	7	2.29	Pretty Good
2	Unchanged	12.91438	0.91745	0.61	0.91385	0.94	3	2	6.00	Perfect Match
3	Unchanged	21.12702	54.05844	1.60	3.65922	1.62	4	5	3.00	Almost Perfect
4	Unchanged	35.45058	104.18167	13.89	4.25820	3.32	13	9	1.22	Almost Perfect
5	Unchanged	38.40146	82.14331	6.85	3.39944	3.85	17	12	1.25	Almost Perfect
6	Unchanged	38.24229	43.05748	0.52	5.87448	2.56	9	7	2.86	Pretty Good
7	Unchanged	59.47680	120.96588	0.09	4.42184	0.77	7	12	3.58	Pretty Good
8	Unchanged	33.74306	49.78598	6.64	3.67782	2.87	8	7	1.71	Pretty Good
9	Unchanged	36.12726	26.87274	0.02	4.48917	0.79	11	13	0.85	Perfect Match
10	Unchanged	26.91378	73.55939	1.26	5.81798	1.32	11	10	1.20	Pretty Good
11	Unchanged	13.98523	24.69867	16.47	2.42516	2.50	7	7	1.00	Almost Perfect
12	Unchanged	31.11217	40.17586	0.48	5.30612	2.31	13	14	1.00	Pretty Good
13	Unchanged	25.93542	108.58099	0.94	3.62895	5.70	12	6	1.33	Almost Perfect
14	Unchanged	21.86952	41.61641	7.57	3.61666	5.03	10	7	0.57	Perfect Match
15	Unchanged	14.36524	74.07766	5.39	6.21930	16.17	6	5	0.40	Almost Perfect

Table E.65: Subject 22 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	34.98389	20.72138	20.72	2.71750	1.77	10	10	2.30	Pretty Good
2	Unchanged	9.00764	1.33198	0.89	1.42732	1.47	1	1	6.00	Perfect Match
3	Unchanged	17.16361	13.93836	0.41	1.48988	0.66	4	5	2.00	Almost Perfect
4	Unchanged	28.19711	98.48664	13.13	4.08605	3.19	16	11	1.09	Almost Perfect
5	Unchanged	26.91793	40.39303	3.37	2.68234	3.04	17	13	0.69	Almost Perfect
6	Unchanged	39.54145	74.99373	0.90	7.44181	3.24	14	13	1.15	Almost Perfect
7	Unchanged	44.36155	141.00966	0.11	3.58646	0.63	12	15	0.40	Almost Perfect
8	Unchanged	19.23196	37.37221	4.98	3.33804	2.61	10	9	1.00	Perfect Match
9	Unchanged	43.10651	15.71211	0.01	6.16232	1.08	12	11	1.00	Almost Perfect
10	Unchanged	22.19202	80.20293	1.37	4.85801	1.11	11	9	1.22	Almost Perfect
11	Unchanged	18.74613	22.63993	15.09	2.46682	2.54	11	8	1.00	Perfect Match
12	Unchanged	23.64619	20.02438	0.24	4.70096	2.05	11	10	1.00	Almost Perfect
13	Unchanged	47.97992	37.15212	0.32	5.35978	8.41	16	14	0.29	Almost Perfect
14	Unchanged	23.86036	92.71296	16.86	4.30143	5.99	11	8	1.00	Almost Perfect
15	Unchanged	22.50786	195.12184	14.19	8.45687	21.99	10	7	0.57	Almost Perfect

Table E.66: Subject 22 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	14.62110	0.73306	0.73	1.67710	1.09	3	2	1.00	Almost Perfect
2	Unchanged	17.38615	46.06505	30.71	2.20748	2.27	6	6	1.00	Almost Perfect
3	Unchanged	16.21361	8.78589	0.26	1.10680	0.49	5	5	1.00	Almost Perfect
4	Unchanged	35.37313	14.99633	2.00	1.75071	1.37	11	12	1.00	Almost Perfect
5	Unchanged	38.83735	9.75852	0.81	2.78181	3.15	11	11	0.91	Almost Perfect
6	Unchanged	44.32161	82.30812	0.99	6.25063	2.72	10	11	1.00	Almost Perfect
7	Unchanged	53.02008	17.65497	0.01	2.37524	0.42	12	16	1.50	Pretty Good
8	Unchanged	37.48232	16.09514	2.15	2.29017	1.79	13	13	1.00	Almost Perfect
9	Unchanged	35.32310	14.34722	0.01	2.62678	0.46	11	10	1.00	Almost Perfect
10	Unchanged	36.67978	23.25257	0.40	5.71386	1.30	11	11	1.36	Almost Perfect
11	Unchanged	33.61056	9.75285	6.50	2.48004	2.55	9	8	1.00	Pretty Good
12	Unchanged	28.61381	19.87957	0.24	4.36184	1.90	10	10	1.00	Pretty Good
13	Unchanged	34.54809	29.99530	0.26	4.09068	6.42	10	9	1.56	Almost Perfect
14	Unchanged	25.88711	24.07596	4.38	2.62602	3.65	9	7	0.86	Almost Perfect
15	Unchanged	26.02877	61.15086	4.45	6.47045	16.82	8	6	0.33	Pretty Good

Table E.67: Subject 23 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	40.26646	41.87543	41.88	6.05582	3.94	8	7	-0.57	Almost Perfect
2	Unchanged	10.28183	1.08089	0.72	1.13416	1.17	1	1	6.00	Almost Perfect
3	Unchanged	14.19606	4.80331	0.14	3.02740	1.34	1	1	5.00	Pretty Good
4	Unchanged	28.59545	49.20613	6.56	4.72220	3.69	7	7	1.86	Almost Perfect
5	Unchanged	31.02632	48.83001	4.07	3.83459	4.35	5	6	1.83	Pretty Good
6	Unchanged	35.00305	121.74453	1.46	6.96504	3.03	6	7	2.86	Pretty Good
7	Unchanged	70.85110	52.35144	0.04	2.02689	0.35	3	8	5.38	Almost Perfect
8	Unchanged	49.21410	5.68484	0.76	3.07934	2.40	4	6	4.17	Pretty Good
9	Unchanged	46.16989	17.74639	0.01	5.48432	0.96	10	10	1.00	Almost Perfect
10	Unchanged	47.90158	39.08421	0.67	5.01179	1.14	6	12	0.83	Pretty Good
11	Unchanged	12.36852	0.88665	0.59	1.13474	1.17	1	1	6.00	Almost Perfect
12	Unchanged	29.96547	77.28875	0.93	6.50781	2.83	5	5	2.00	Almost Perfect
13	Unchanged	53.86001	45.97729	0.40	5.66731	8.89	9	13	2.00	Pretty Good
14	Unchanged	21.93368	18.98063	3.45	3.16147	4.40	8	7	0.42	Pretty Good
15	Unchanged	28.61377	53.39716	3.88	4.31136	11.21	6	7	1.71	Almost Perfect

Table E.68: Subject 23 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	19.89112	98.27385	98.27	7.99705	5.20	2	4	4.00	Pretty Good
2	Unchanged	8.55262	1.99360	1.33	2.06400	2.12	1	1	6.00	Almost Perfect
3	Unchanged	29.10377	28.27420	0.84	1.60322	0.71	3	8	2.88	Pretty Good
4	Unchanged	39.52727	124.42845	16.59	5.19806	4.06	5	7	2.14	Pretty Good
5	Unchanged	40.24562	56.89646	4.74	5.22670	5.93	8	8	1.75	Pretty Good
6	Unchanged	28.65543	100.31325	1.20	5.31789	2.31	5	6	3.33	Almost Perfect
7	Unchanged	94.91310	80.10503	0.06	5.44339	0.95	14	20	2.20	Satisfactory
8	Unchanged	38.13723	41.22014	5.50	2.33172	1.82	7	6	3.00	Almost Perfect
9	Unchanged	63.33177	30.15727	0.02	5.22639	0.91	11	15	1.33	Pretty Good
10	Unchanged	39.97059	34.84136	0.60	3.09142	0.70	6	14	0.64	Almost Perfect
11	Unchanged	9.83765	6.30646	4.20	1.27103	1.31	1	1	6.00	Pretty Good
12	Unchanged	35.08802	32.13164	0.39	5.85429	2.55	5	7	3.43	Pretty Good
13	Unchanged	21.93866	67.65952	0.59	4.45870	7.00	4	5	2.00	Almost Perfect
14	Unchanged	19.23528	37.14635	6.75	3.44195	4.79	4	6	1.83	Almost Perfect
15	Unchanged	22.62533	91.51062	6.66	5.40053	14.04	4	5	1.80	Pretty Good

Table E.69: Subject 23 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	10.12192	0.00343	0.00	0.90208	0.59	1	2	1.00	Almost Perfect
2	Unchanged	20.86719	61.26629	40.84	3.28220	3.38	6	6	1.00	Almost Perfect
3	Unchanged	19.16382	82.08095	2.43	1.92312	0.85	5	5	1.00	Almost Perfect
4	Unchanged	24.31726	65.20595	8.69	3.99031	3.11	8	7	1.00	Almost Perfect
5	Unchanged	29.91240	66.88235	5.57	3.81322	4.32	9	9	1.00	Perfect Match
6	Unchanged	36.00505	20.78724	0.25	3.71566	1.62	10	11	1.00	Almost Perfect
7	Unchanged	48.70951	52.67261	0.04	2.89885	0.51	10	13	1.92	Almost Perfect
8	Unchanged	29.21986	8.91211	1.19	1.39364	1.09	9	9	1.89	Perfect Match
9	Unchanged	34.36996	14.51441	0.01	3.21819	0.56	10	11	1.00	Almost Perfect
10	Unchanged	31.26488	25.79933	0.44	2.05477	0.47	8	9	1.22	Perfect Match
11	Unchanged	16.60369	25.09363	16.73	1.39456	1.44	6	7	1.00	Almost Perfect
12	Unchanged	27.12477	46.76123	0.56	7.15479	3.11	10	11	0.91	Almost Perfect
13	Unchanged	25.12138	8.45344	0.07	2.87176	4.51	7	7	1.29	Almost Perfect
14	Unchanged	27.17892	87.23544	15.86	5.08909	7.08	8	7	0.86	Almost Perfect
15	Unchanged	26.91891	51.26154	3.73	4.19257	10.90	6	6	0.83	Almost Perfect

Table E.70: Subject 24 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	28.93874	390.19545	390.20	11.27746	7.33	2	3	4.67	Pretty Good
2	Unchanged	10.67764	8.59673	5.73	4.58514	4.72	1	1	6.00	Almost Perfect
3	Unchanged	6.05759	13.28653	0.39	5.62597	2.49	1	1	5.00	Pretty Good
4	Unchanged	21.20446	571.22268	76.16	9.69029	7.56	2	2	4.50	Pretty Good
5	Unchanged	32.89964	579.05875	48.25	14.29146	16.21	3	5	3.20	Satisfactory
6	Unchanged	48.04904	98.40227	1.18	7.33017	3.19	12	13	1.85	Almost Perfect
7	Unchanged	69.74683	480.67546	0.36	8.48020	1.48	2	11	6.27	Pretty Good
8	Unchanged	23.41033	55.49460	7.40	8.23729	6.43	1	1	9.00	Pretty Good
9	Unchanged	34.83051	165.09017	0.12	9.53604	1.67	10	11	1.00	Almost Perfect
10	Unchanged	58.30836	56.25475	0.96	3.93276	0.90	12	11	1.27	Almost Perfect
11	Unchanged	7.46093	2.33354	1.56	2.79604	2.88	1	1	6.00	Perfect Match
12	Unchanged	31.36879	71.37227	0.86	6.82848	2.97	5	6	3.33	Almost Perfect
13	Unchanged	42.37227	144.78219	1.26	5.18517	8.14	9	8	1.88	Pretty Good
14	Unchanged	30.19211	104.70546	19.04	5.47022	7.61	5	6	2.67	Almost Perfect
15	Unchanged	24.43702	117.28600	8.53	6.10453	15.87	5	4	1.00	Almost Perfect

Table E.71: Subject 24 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	27.58042	354.51894	354.52	10.29514	6.69	2	3	5.33	Almost Perfect
2	Unchanged	8.31931	6.41672	4.28	1.46631	1.51	1	1	6.00	Perfect Match
3	Unchanged	8.06596	20.40975	0.60	5.96176	2.64	1	1	5.00	Pretty Good
4	Unchanged	18.58278	202.13143	26.95	7.62952	5.96	2	3	3.67	Pretty Good
5	Unchanged	41.24065	686.86155	57.24	17.91336	20.31	6	9	3.00	Pretty Good
6	Final	33.10801	672.86620	8.08	23.07462	10.04	7	9	3.00	Pretty Good
6	Cutoff	23.15035	1491.45201	17.92	17.43410	7.59	4	6	4.00	-
6	Difference	9.95766	-818.58580	-9.84	5.64052	2.45	3	3	-1.00	-
7	Unchanged	68.20940	252.25465	0.19	6.95174	1.22	6	14	3.14	Satisfactory
8	Unchanged	15.70858	127.10961	16.95	6.17876	4.82	3	3	3.33	Pretty Good
9	Final	36.66223	39.05132	0.03	6.75781	1.18	11	14	1.07	Almost Perfect
9	Cutoff	31.83382	46.28668	0.03	5.96046	1.04	10	13	1.08	-
9	Difference	4.82841	-7.23536	0.00	0.79735	0.14	1	1	-0.01	-
10	Unchanged	21.57534	45.23317	0.77	5.07605	1.16	4	5	2.20	Almost Perfect
11	Unchanged	9.08180	2.13810	1.43	2.76877	2.85	1	1	6.00	Almost Perfect
12	Unchanged	25.20956	73.31453	0.88	6.83414	2.97	5	5	2.00	Almost Perfect
13	Unchanged	28.50793	452.30914	3.93	6.78872	10.65	6	6	2.17	Pretty Good
14	Unchanged	20.29033	137.24059	24.95	8.70344	12.11	5	4	1.50	Almost Perfect
15	Unchanged	13.52103	90.65641	6.59	7.12505	18.52	4	3	0.67	Almost Perfect

Table E.72: Subject 24 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	15.31531	0.00171	0.00	0.63678	0.41	1	1	1.00	Perfect Match
2	Unchanged	43.52337	18.05857	12.04	2.87885	2.96	10	10	0.80	Almost Perfect
3	Unchanged	24.24715	3.11399	0.09	0.53563	0.24	5	5	1.00	Perfect Match
4	Unchanged	47.41512	20.74798	2.77	1.62181	1.27	15	14	1.00	Almost Perfect
5	Unchanged	81.84583	18.51188	1.54	1.73752	1.97	26	25	0.92	Almost Perfect
6	Unchanged	72.96388	10.56102	0.13	2.41644	1.05	19	20	1.00	Almost Perfect
7	Unchanged	55.23785	26.56966	0.02	1.69864	0.30	11	14	1.14	Perfect Match
8	Unchanged	33.01455	13.88286	1.85	1.42141	1.11	9	9	1.00	Perfect Match
9	Unchanged	84.00644	12.51900	0.01	2.46007	0.43	21	24	0.96	Perfect Match
10	Unchanged	34.45883	11.04196	0.19	1.46807	0.33	11	10	0.90	Perfect Match
11	Unchanged	18.32821	19.19860	12.80	1.13225	1.17	6	7	1.00	Perfect Match
12	Unchanged	91.44617	20.68788	0.25	2.65448	1.15	26	21	0.81	Almost Perfect
13	Unchanged	54.65150	8.69791	0.08	1.94090	3.05	13	13	1.08	Pretty Good
14	Unchanged	39.84101	10.87141	1.98	1.95686	2.72	10	11	0.55	Almost Perfect
15	Unchanged	52.68252	17.92927	1.30	2.87218	7.47	13	13	1.31	Almost Perfect

Table E.73: Subject 25 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	18.92611	0.00170	0.00	0.63592	0.41	1	1	1.00	Almost Perfect
2	Unchanged	40.26977	2.62590	1.75	0.48326	0.50	9	8	1.00	Perfect Match
3	Unchanged	46.85819	0.21452	0.01	1.65176	0.73	10	10	1.00	Almost Perfect
4	Unchanged	72.40522	29.02475	3.87	1.75385	1.37	20	22	1.00	Pretty Good
5	Unchanged	49.48905	15.25271	1.27	2.11893	2.40	12	11	1.00	Pretty Good
6	Unchanged	80.76285	42.32581	0.51	4.59482	2.00	18	17	1.00	Pretty Good
7	Unchanged	66.18430	20.69000	0.02	3.35614	0.59	10	11	1.00	Pretty Good
8	Unchanged	130.65525	13.59692	1.81	2.68497	2.10	29	32	0.69	Pretty Good
9	Unchanged	61.16089	14.37358	0.01	2.59899	0.45	11	12	0.92	Almost Perfect
10	Unchanged	65.73013	16.19154	0.28	1.96872	0.45	16	14	1.43	Almost Perfect
11	Unchanged	56.04417	14.06376	9.38	1.56341	1.61	14	15	1.00	Almost Perfect
12	Unchanged	58.46502	15.96869	0.19	6.34199	2.76	10	10	1.00	Almost Perfect
13	Unchanged	150.68056	23.30043	0.20	4.49949	7.06	39	36	0.83	Pretty Good
14	Unchanged	47.32986	2.47181	0.45	1.90034	2.64	13	13	1.54	Almost Perfect
15	Unchanged	60.81088	7.61794	0.55	1.80344	4.69	17	14	1.50	Perfect Match

Table E.74: Subject 25 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	23.61368	0.00029	0.00	0.26151	0.17	1	1	1.00	Almost Perfect
2	Unchanged	24.99454	0.69371	0.46	0.47924	0.49	6	6	1.00	Perfect Match
3	Unchanged	52.28911	15.33386	0.45	0.92060	0.41	8	12	1.67	Almost Perfect
4	Unchanged	54.52247	7.80227	1.04	0.93343	0.73	11	12	1.00	Almost Perfect
5	Unchanged	52.14660	18.96152	1.58	2.77568	3.15	15	17	0.94	Almost Perfect
6	Unchanged	70.19104	26.09921	0.31	5.31409	2.31	13	13	0.92	Pretty Good
7	Unchanged	57.73502	15.64487	0.01	2.67518	0.47	11	15	2.33	Almost Perfect
8	Unchanged	52.86579	35.30984	4.71	2.70157	2.11	15	16	1.00	Almost Perfect
9	Unchanged	55.92583	34.85145	0.03	4.82007	0.84	10	11	1.00	Almost Perfect
10	Unchanged	49.34656	12.71993	0.22	1.61230	0.37	14	14	1.36	Perfect Match
11	Unchanged	20.93115	11.58389	7.72	1.34283	1.38	8	8	1.00	Perfect Match
12	Unchanged	66.86184	9.35233	0.11	4.09515	1.78	17	18	1.00	Almost Perfect
13	Unchanged	60.67175	12.34005	0.11	2.44800	3.84	16	15	1.33	Pretty Good
14	Unchanged	48.44573	7.18010	1.31	2.10244	2.93	15	14	1.14	Almost Perfect
15	Unchanged	95.25058	14.50761	1.06	4.80166	12.48	23	24	0.95	Pretty Good

Table E.75: Subject 25 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	14.68606	6.13351	6.13	4.22993	2.75	4	2	1.00	Pretty Good
2	Unchanged	20.24949	15.88638	10.59	1.50347	1.55	6	6	1.00	Satisfactory
3	Unchanged	22.30368	12.63310	0.37	1.67089	0.74	5	5	1.00	Satisfactory
4	Unchanged	26.34376	13.29605	1.77	2.24541	1.75	9	9	1.00	Pretty Good
5	Unchanged	25.77041	12.96746	1.08	3.06876	3.48	9	9	1.00	Pretty Good
6	Unchanged	44.13486	2.44393	0.03	3.01214	1.31	10	12	1.08	Pretty Good
7	Unchanged	54.39920	20.56413	0.02	2.75369	0.48	12	13	1.54	Pretty Good
8	Unchanged	25.62208	19.92992	2.66	1.28700	1.00	10	9	1.00	Satisfactory
9	Unchanged	39.03645	4.68642	0.00	1.60631	0.28	10	11	0.91	Pretty Good
10	Unchanged	36.27307	50.09370	0.86	3.10137	0.71	10	9	0.89	Satisfactory
11	Unchanged	21.05700	15.96003	10.64	2.22216	2.29	6	7	1.00	Satisfactory
12	Unchanged	29.37797	23.02169	0.28	4.07793	1.77	10	11	1.00	Satisfactory
13	Unchanged	30.95799	69.20018	0.60	5.42849	8.52	9	10	1.30	Satisfactory
14	Unchanged	26.09458	15.23076	2.77	3.61498	5.03	8	7	1.00	Satisfactory
15	Unchanged	51.08497	11.31815	0.82	2.50280	6.51	11	11	0.72	Pretty Good

Table E.76: Subject 26 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	15.15101	44.95451	44.95	2.83091	1.84	7	6	1.17	Satisfactory
2	Unchanged	15.64101	27.60979	18.41	1.73884	1.79	10	7	1.00	Pretty Good
3	Unchanged	31.29204	109.20971	3.24	4.54923	2.02	9	10	0.60	Unsatisfactory
4	Unchanged	27.59199	125.34905	16.71	4.82817	3.77	11	12	1.00	Pretty Good
5	Unchanged	28.88952	63.90276	5.33	5.09939	5.78	15	16	0.56	Satisfactory
6	Unchanged	34.91626	99.23502	1.19	6.36518	2.77	10	10	1.00	Satisfactory
7	Unchanged	64.01079	12.73430	0.01	1.81561	0.32	11	13	3.85	Satisfactory
8	Unchanged	19.35107	51.33755	6.85	2.51913	1.97	4	4	2.25	Satisfactory
9	Unchanged	99.52206	59.97799	0.05	7.39341	1.29	12	23	1.70	Satisfactory
10	Unchanged	29.87955	81.54047	1.39	5.33823	1.22	5	7	1.43	Satisfactory
11	Unchanged	9.73012	44.34592	29.56	2.05245	2.11	4	3	2.00	Satisfactory
12	Unchanged	34.91377	139.24653	1.67	10.06899	4.38	11	13	0.85	Unsatisfactory
13	Unchanged	35.22293	70.27706	0.61	5.35303	8.40	9	9	1.78	Satisfactory
14	Unchanged	43.10722	85.00034	15.45	12.71896	17.70	10	9	1.56	Unsatisfactory
15	Unchanged	46.40059	69.70434	5.07	4.57755	11.90	9	11	1.18	Satisfactory

Table E.77: Subject 26 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	35.43882	348.23987	348.24	6.84741	4.45	6	7	2.43	Satisfactory
2	Unchanged	7.39676	19.62059	13.08	3.96455	4.08	1	1	6.00	Satisfactory
3	Unchanged	27.22538	130.32913	3.86	3.26576	1.45	2	2	3.50	Satisfactory
4	Unchanged	53.40322	65.53685	8.74	5.70462	4.45	6	9	2.78	Satisfactory
5	Unchanged	48.58733	173.85165	14.49	5.05977	5.74	6	7	2.29	Satisfactory
6	Unchanged	50.64318	111.77914	1.34	10.39783	4.52	8	8	3.00	Satisfactory
7	Unchanged	73.68767	124.35738	0.09	3.94162	0.69	5	18	4.28	Satisfactory
8	Unchanged	19.74110	82.14971	10.95	2.91529	2.28	4	5	2.20	Pretty Good
9	Unchanged	68.66929	29.81570	0.02	4.24188	0.74	16	13	1.46	Pretty Good
10	Unchanged	30.37542	49.03111	0.84	5.25935	1.20	5	4	2.75	Pretty Good
11	Unchanged	10.71181	31.41769	20.95	2.98406	3.07	2	2	3.00	Pretty Good
12	Unchanged	44.52646	93.71502	1.13	7.56163	3.29	9	12	1.67	Pretty Good
13	Unchanged	31.47628	178.24116	1.55	4.89601	7.68	4	9	2.44	Pretty Good
14	Unchanged	15.79356	70.34399	12.79	7.06606	9.83	2	3	3.33	Pretty Good
15	Unchanged	22.78366	41.38818	3.01	3.10595	8.08	1	6	1.50	Satisfactory

Table E.78: Subject 26 3rd method (CCD)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	6.01761	0.00010	0.00	0.15191	0.10	1	1	1.00	Perfect Match
2	Unchanged	18.47365	32.11598	21.41	2.68193	2.76	6	5	2.00	Almost Perfect
3	Unchanged	19.56366	43.45378	1.29	2.77463	1.23	8	7	0.71	Pretty Good
4	Unchanged	24.59460	39.51156	5.27	2.85784	2.23	11	12	0.92	Almost Perfect
5	Unchanged	30.32719	35.70955	2.98	2.54702	2.89	13	16	0.88	Almost Perfect
6	Unchanged	36.64812	71.61550	0.86	5.84693	2.54	14	13	0.92	Almost Perfect
7	Unchanged	41.10904	19.23417	0.01	2.40932	0.42	14	13	1.00	Almost Perfect
8	Unchanged	29.65468	14.49373	1.93	2.72700	2.13	13	12	1.42	Almost Perfect
9	Unchanged	41.76239	9.18421	0.01	4.79854	0.84	12	14	0.93	Almost Perfect
10	Unchanged	45.07660	12.03189	0.21	2.69393	0.61	20	18	1.33	Almost Perfect
11	Unchanged	17.67612	6.31623	4.21	1.31525	1.35	8	11	1.00	Almost Perfect
12	Unchanged	30.71969	23.12310	0.28	5.18579	2.26	13	13	1.00	Perfect Match
13	Unchanged	36.98396	41.60622	0.36	4.62152	7.25	17	15	0.47	Pretty Good
14	Unchanged	26.14544	42.97850	7.81	3.63502	5.06	9	8	0.88	Almost Perfect
15	Unchanged	45.65827	36.24655	2.64	3.73990	9.72	18	13	0.46	Almost Perfect

Table E.79: Subject 27 1st method (1DOF)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	8.53929	0.11603	0.12	5.24651	3.41	2	1	1.00	Almost Perfect
2	Unchanged	13.84685	16.56038	11.04	1.24240	1.28	8	6	1.00	Almost Perfect
3	Unchanged	51.45074	18.42212	0.55	2.47676	1.10	8	8	2.38	Pretty Good
4	Unchanged	20.24780	9.96442	1.33	1.87420	1.46	10	12	1.00	Almost Perfect
5	Unchanged	17.13774	64.11565	5.34	4.68139	5.31	5	5	1.80	Almost Perfect
6	Unchanged	38.22137	95.32860	1.15	6.03453	2.63	7	11	2.27	Almost Perfect
7	Unchanged	81.58284	84.79937	0.06	8.60460	1.51	10	13	4.00	Satisfactory
8	Unchanged	19.18611	35.97112	4.80	2.89837	2.26	4	3	4.33	Almost Perfect
9	Unchanged	70.26191	27.54450	0.02	6.57366	1.15	5	7	1.86	Pretty Good
10	Unchanged	32.85469	40.74987	0.70	3.18664	0.73	9	9	1.44	Almost Perfect
11	Unchanged	9.09097	0.79608	0.53	1.65011	1.70	1	1	6.00	Almost Perfect
12	Unchanged	30.18464	48.04988	0.58	6.82243	2.97	6	6	2.00	Almost Perfect
13	Unchanged	50.20912	5.66146	0.05	1.17630	1.85	8	7	2.43	Perfect Match
14	Unchanged	37.53225	40.84705	7.43	4.14704	5.77	7	10	2.00	Almost Perfect
15	Unchanged	34.03637	53.54287	3.89	4.26328	11.08	4	7	0.43	Almost Perfect

Table E.80: Subject 27 2nd method (Jacobian)

Trial	Type	Time (seconds)	Angle Error	%	Pos. Error	%	R	E	Avg. Dist.	Rating
1	Unchanged	34.18969	50.55890	50.56	2.62385	1.71	11	13	1.54	Almost Perfect
2	Unchanged	16.21526	8.00545	5.34	0.84971	0.87	6	9	1.00	Almost Perfect
3	Unchanged	37.13474	12.36086	0.37	1.33284	0.59	8	10	1.70	Almost Perfect
4	Unchanged	16.19193	78.73480	10.50	2.70238	2.11	10	9	1.00	Almost Perfect
5	Unchanged	27.44209	44.15148	3.68	3.09496	3.51	5	5	1.80	Almost Perfect
6	Unchanged	30.66629	71.49978	0.86	6.53393	2.84	7	5	2.00	Almost Perfect
7	Unchanged	57.98423	50.97590	0.04	2.93802	0.51	5	5	2.00	Perfect Match
8	Unchanged	30.39132	24.24441	3.23	1.75077	1.37	5	5	2.00	Almost Perfect
9	Unchanged	52.82165	88.12786	0.07	6.42404	1.12	7	9	1.78	Almost Perfect
10	Unchanged	30.34796	13.96807	0.24	3.83863	0.87	6	6	1.83	Almost Perfect
11	Unchanged	13.20853	11.11403	7.41	1.70220	1.75	3	3	2.00	Almost Perfect
12	Unchanged	33.96636	73.94806	0.89	7.31527	3.18	11	11	1.18	Almost Perfect
13	Unchanged	24.77539	179.67932	1.56	6.57039	10.31	6	7	1.71	Almost Perfect
14	Unchanged	19.12864	105.63788	19.21	4.87681	6.79	3	5	2.80	Almost Perfect
15	Unchanged	24.69705	33.20312	2.41	3.80696	9.90	5	6	1.33	Almost Perfect

Table E.81: Subject 27 3rd method (CCD)