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A Novel Algorithm for Creating Useful Hip Joint Center Location Estimates from Gait Motion

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UNIVERSITY OF MIAMI

A NOVEL ALGORITHM FOR CREATING USEFUL HIP JOINT CENTER
LOCATION ESTIMATES FROM GAIT MOTION

By

James Soutelle

A THESIS

Submitted to the Faculty
of the University of Miami
in partial fulfillment of the requirements for
the degree of Master of Science

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May 2013

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A NOVEL ALGORITHM FOR CREATING USEFUL HIP JOINT CENTER
LOCATION ESTIMATES FROM GAIT MOTION

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A Novel Algorithm for Creating Useful
Hip Joint Center Location Estimates From
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This document contains the results of an experiment conducted in the Biomechanics Research Laboratory at the University of Miami. A novel two sided hip joint center location algorithm was created and tested. The Vicon motion capture system located in the Biomechanics lab assisted in the testing of the algorithm. Both hip joint centers were successfully located during multiple gait trials. The hip location results were compared to the conventional predictive hip joint center techniques. A validation trial was also conducted. More validation testing is need to confirm the applicability of this hip joint center location technique.

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Chapter 1: Statement of Topic

Human movement, observed Pers, Bon, Kovacic, Sibila and Dezman, "can be observed at different levels of detail" (p. 295). Despite the significant advances that have been made in research and medicine which permit the study, diagnosis, and treatment of an array of physiological disorders, there remains a great deal of work to be done in the improvement of diagnostic and intervention techniques with respect to joint disorders. One of the reasons why more research is needed in this area is because individuals' bodies vary considerably, frustrating both researchers' and clinicians' attempts to develop a consistently efficient and effective joint center location algorithm. Conventional methods of joint center location are widely acknowledged to have a broad margin of error range, thereby complicating understanding and adequate treatment of joint-related disorders. Not surprisingly, the conventional techniques of using patients' self-reports and clinicians' observations to identify the location of a joint's center are increasingly being supplemented by technological instruments and electronically derived algorithms for research and direct use applications.

The need for accurate biomechanical motion analysis is clear for multiple applications. Geriatrics, athletic performance, ergonomics, and biomedical device evaluation are just a few applications for motion capture analysis. The location of the hip joint center is very important for lower body and full body biomechanical evaluations. "Location of the center of the hip joint is especially difficult because it is farther from palpable bony landmarks than are the centers of more distal joints." (Piazza et al., p. 967) Several methods have been developed to try to predict HJC location accurately, but have failed to produce an efficient, effective, and accurate method. Radiographic and anatomical landmarks are the usual methods to find the hip joint center, but they both have an undesirable margin of error.

Aims of Thesis

The aim of this thesis is to introduce a novel algorithm intended to find the hip joint center. It is very similar to the score algorithm proposed by Ehrig et al, (2006). The primary advantage of the score algorithm is the ability to find both hip joint centers in a moving frame. This algorithm has similar traits as the score algorithm in finding both hjc (hip joint centers) on a moving frame.

Validation takes place with using an analog equivalent, so the true hip joint center can be measured.

Chapter 2: Review of Literature

Research about the development and use of biomechanical motion analysis devices and practices is the subject of this review of the recent peer-reviewed scientific literature. A specific emphasis is placed on the way in which biomechanical motion analysis is used to identify joint locations, and, in particular, the location of the hip joint center. Historically, the hip joint center has been one of the most difficult among the joints to identify and assess accurately, efficiently, and effectively (Siston & Delp, 2006). Possible advantages and limitations of the use of the biomechanical motion analysis model for the location of the hip joint center will be examined.

Joint center location is an important task in clinical practice, particularly for orthopedists, because compromised joints serve as precipitating or exacerbating factors that contribute to a wide variety of medical ailments, ranging from arthritis and other inflammatory diseases (Cook, Pietrobon, & Hegedus, 2007) to chronic pain (Manchikanti, Pampati, Brandon, & Giordano, 2008), sciatica (Bujis, Visser, & Groen, 2007), and mobility and gait deficiencies (Brunner & Romkes, 2008). Despite the

importance of joint center location as a part of the diagnostic and treatment processes, however, identifying joint centers has historically been a challenging task due to the variation among the types of measurement techniques that are used and the constructs they are intended to measure (Holden & Stanhope, 1998). Joint center identification has also been frustrated by what Holden and Stanhope (1998) referred to as "uncertainty in joint movement patterns," which is caused, among other variables, by patients' individual physiological characteristics and conditions (p. 1).

Historically speaking, researchers and clinicians attempting to locate joint centers have utilized a process consisting of the observation and analysis of at least two tiers, also referred to in the literature as variables or constructs (Piazza, Erdemir, Okita, & Cavanagh, 2004). The types of variables conventionally used to locate joint centers have included behavioral observation of the patient, the patient's completion of a self-report questionnaire, and the researcher's or clinician's analysis of the patient's performance on a variety of tasks (Watzke, 2004). Among the tasks that patients are asked to perform and which researchers or clinicians observe are "walking,

sit-to-stand, stair ascent, [and] stair descent" (Piazza et al., 2004, p. 349). Although movements made while standing are the most popular assessments, additional motion measurements include movements made from a seated position using "three markers on the pelvis" (Bush & Gotowski, 2003, p, 1739). Bergmann, Graichen, Rolhmann, & Linke (1997) and Shea, Lenhoff, Otis, and Backus (1997) also added load-carrying tasks to the list of performance analysis variables that are examined as a means of assessing joint location and, in particular, hip-joint center location (Watzke, 2004). Collectively, these conventional methods of joint location are referred to as functional models (Camomilla, Cereatti, Vannozzi, & Capozzo, 2006).

Although most researchers and clinicians generally satisfy themselves with a two-tier analysis, the use of three or more tiers has not been uncommon. The underlying assumption made about a multiple construct measurement is that the more variables that are measured, the more accurate the identification of the joint center is likely to be (Camomilla et al., 2006). In their study on multiple construct measurements using a functional model, Camomilla et al. (2006) reported, for instance, that an optimized protocol for hip joint center location could be developed

by collecting multiple data streams. However, the derivation of the optimized protocol using the functional model as described by Camomilla et al. (2006) was complex and, therefore, inefficient, involving a multi-stepped process that included examining "the type and amplitude of the movement of the femur relative to the pelvis" in a number of subjects (p. 1096). The collection of these data was followed by the use of a "simulation approach which, in turn, was validated using experiments made on a physical analogue of the pelvis and femur system. The algorithm were then classified and, in some instances, modified and submitted to a comparative evaluation" (Camomilla et al., 2006, p. 1096). Although the researchers acknowledged that the process was time-consuming, they did not discuss how the inefficiency of their model could contribute to its impracticability in a clinical context, where the administrative pressure to diagnose and treat patients rapidly exerts an influence on the types of strategies that are used.

Over time, the assumption that more data equates to more informed diagnosis and practice, particularly with respect to joint location, has come to be questioned. Not only does the use of multiple constructs for measurement

decrease the efficiency of the clinical evaluation encounter, but multiple construct measurements have also failed to produce empirical data that confirms the validity of the assumption that more data produces richer and more accurate conclusions (Piazza et al., 2004).

In fact, the opposite appears to be true. Bush and Gotowski (2003) stated that identifying the hip joint center using the seated posture battery of motion assessments "has been difficult if not impossible" (p. 1739). Piazza et al. (2004) arrived at similar conclusions regarding the efficacy, efficiency, and accuracy of standing motion assessment data used to determine the hip joint center location, reporting that the measurements taken by conventional analysis of these tasks are highly prone to error, particularly in individuals who have a constricted or limited range of motion. In their own study, Piazza et al. (2004) reported "worst-case hip joint center location errors [ranging from] 26 [to 70] mm" (p. 349). Their findings are by no means different from within the large body of research literature that is available on the subject. Piazza, Okita, and Cavanagh (2001) asserted that such a broad margin of error is unacceptable. "Accurate location of the hip joint center is essential, for hip

kinematics and kinetics," as well as larger intervention and treatment considerations (p. 967).

Other approaches have been employed in addition to the functional class of task performance analyses that have traditionally been used to locate joint centers. One of the most common conventional hip joint center location techniques in this other category of predictive measures has involved the derivation of algorithms based on the examination of primate and human cadavers (John & Fisher, 1994; Seidel, Marchinda, Dijkers, & Soutas, 1995). This technique of gathering information to determine the location of joint centers is perhaps the most controversial among the conventional data-gathering and algorithm-generating strategies, for the quality of data it produces is as at least as questionable as that of the functional/observational analyses and techniques. The primary question that has been raised about cadaver study as a means of expanding knowledge about joint location alludes to a criticism that has been lodged against all of the conventional techniques: human movement is actually highly variable. Motion is dependent upon a range of factors, including the examined individual's height, weight, gender, degree of flexibility, and a number of

other anatomic parameter variables (Genda, Iwasaki, Li, & MacWilliams, 2001).

Because joint center location is increasingly being viewed as so individualistic, the relative value of measurements derived from one individual or study group is questionable because the degree to which such measurements can be generalized to a broader population is suspect. Understanding this limitation of existing methods of joint location research and clinical practice is crucial because it helps explain how and why biomechanical motion analysis emerged as a field of study, and what kinds of benefits it might be able to provide in the research and practice arenas.

Biomechanical Motion Analysis

The utility of the data collected using the functional and predictive models of joint location are further undermined by the fact that these data are used to generate two-dimensional models of joint location schema. As various researchers have pointed out, two-dimensional models possess inherent limitations for research and practice that revolve around matters of motion (Miller & Childress, 2005). Miller and Childress (2005) explained that the functional and predictive techniques producing two-

dimensional models are not particularly valuable. This is especially for certain types of research and practice, such as the preparation of prosthetic limbs, which require careful and precise joint location calculations (Miller & Childress, 2005). Other researchers have arrived at similar conclusions. Aminian, Mahar, Yassir, Newton, and Wenger (2005), for instance, noted that while x-rays have long been used to assist in the corroboration of joint-related data collected through observational means, even these powerful visual aids fail to provide the rich understanding of the rotational aspects of joints that must be understood to facilitate the development of best practices for the accurate, efficient, and efficacious identification of joint locations.

The development of biomechanical models of analysis can be attributed in part to the need for the research and clinical communities interested in joint location identification to begin developing more powerful models with greater explanatory and predictive accuracy. Specifically, given the clear limitations of two-dimensional models, it seemed obvious to many researchers that the next generation of joint locator framework practices needed to provide three-dimensionality (Sabel,

1996; Soechting & Flanders, 1992; Xue & Morrell, 2003). As Soechting and Flanders (1992) explained, "We move in a three-dimensional world"; therefore, it makes sense that researchers should be "studying a variety of movements in three-dimensional space" (p. 167). Biomechanical measurement and analysis systems have provided the mechanisms to study motion to locate joints from a more realistic, three-dimensional perspective.

Since the late 1990s, a number of "high-speed, high-accuracy" biomechanical measurement devices have become available on the commercial market (Pers et al., 2002, p. 295), and as research and clinical settings both incorporate new technologies, these types of devices have become more prevalent in both environments. Early research suggests that biomechanical measurement systems provide numerous advantages over conventional functional models with respect to the accuracy, efficacy, and efficiency of the joint location process. Among the specific benefits noted in the literature are spatial accuracy and temporal resolution (Pers et al., 2002), attributes that are critical to the location of joints. The core feature of biomechanical motion analysis is the evolution from a two-dimensional model to a three-dimensional model (Sabel,

1996), which is more comprehensive and, therefore, offers better opportunities for the diagnosis and treatment of joint disorders in particular.

Research on Biomechanical Motion Analysis

Research on biomechanical motion analysis has examined the application of a three-dimensional model in a variety of study populations. The populations fall into two broad categories. The use of biomechanical motion analysis has been used to study athlete performance and injury (Masahiro, 1999; Pers et al., 2002) and physiological stress caused by repetitive movements by workers in industrial settings and professional musicians (Crnivec, 2004; Fjellmann-Wiklund, Grip, Karlsson, Sundelin, 2004; Punnett & Keyserling, 1987; Shan & Visentin, 2003). While much of this research has focused on the application of biomechanical motion analysis to better understand athlete, worker, or musician performance, a growing body of research also documents the study of joint-related issues among these three study populations as well.

In their study of female athletes, Hewett, Myer, Ford, Heidt, Colosimo, McLean et al. (2005) assessed 205 female athletes involved in "high-risk sports," which were defined as soccer, basketball, and volleyball, to determine whether

increased load on the valgus joint predicts greater risk for anterior cruciate ligament injury. With respect to methodology, Hewett et al. (2005) proposed a research design that hybridized a functional conventional technique—the use of task performance variables—with a three-dimensional biomechanical assessment instrument. The researchers directed the athletes to perform a task that involved jumping and landing typical of the sports they played. Using three-dimensional kinematics and kinetics-based joint loads, the researchers evaluated the degree of stress that was borne by the valgus joints of the study participants. Hewett et al. (2005) confirmed their hypothesis, concluding that both motion and loading on the valgus joint are significant predictors of anterior cruciate ligament injury risk among the athletes who were studied.

The findings of Hewett et al. (2005) also reaffirmed the findings that some of the same researchers from that group had reported in an earlier study, in which the relationship between motion, load, and valgus joint injuries were compared in male and female basketball players (Ford, Myer, & Hewett, 2003). Using techniques similar to those employed in the 2005 study, the

researchers found that valgus joint injuries were more frequent among female athletes, who also demonstrated "greater total valgus knee motion and a greater valgus knee angle" compared to the male basketball players in the study (Ford et al., 2003, p. 1745). What was important about the Ford et al. (2003) study and the subsequent Hewett et al. (2005) study was that both pieces of research underscored the importance that biomechanical analysis can have on direct clinical practice. By building a body of knowledge about joint motion and joint injury, researchers are generating critical information about the best practices of prevention and intervention that can be used—and then confirmed—by clinicians in direct practice settings.

Although the study population differed from that of athletes, Punnett's and Keyersling's (1987) study of garment industry workers used techniques quite similar to those of Hewett et al. (2005). Combining performance tasks that were typical of the repetitive motions of their jobs, the garment workers were asked by the researchers to perform hand and wrist tasks that created occupational stress on their joints (Punnett & Keyserling, 1987). In addition to being repetitive, the tasks that the garment workers in the study were asked to perform were both fine,

requiring exceptional hand-eye coordination, and labor-intensive tasks were considered particularly stressful upon the joints (Punnett & Keyserling, 1987). By analyzing the three-dimensional stressors upon the hand joints, Punnett and Keyserling (1987) learned how joint location can be improved, how joint deterioration occurs, and how efficient and healthier work techniques can be developed.

In their study of professional violinists, Shan and Visentin (2003) explained how biomechanical motion analyses can be conducted to examine the ways in which asymmetrical repetitive movements affect the joints of musicians. Shan and Visentin (2003) set up nine cameras to record the movements of the violinists, each camera focused on an isolated area of the musician's body and a specific type of movement. The musicians were then directed to perform exercises that demonstrated a range of movements. The researchers then used "quantitative model comparison and statistical analysis" to generate results; in doing so, Shan and Visentin (2003) determined that while playing styles and posture varied considerably, the biomechanical assessment served as a reliable model that allowed the researchers to conclude that "highly consistent patterns"

of elbow joint motion existed between the subjects in the study (p. 3).

Current research that examines hip joint location using biomechanical motion assessment focuses on the accurate identification of segmental parameters, such as "mass, center-of-gravity, and moment-of-inertia," that are "necessary for biomechanical analyses of a species' locomotor behavior" (Vilensky, 2005, p. 57). Much of the recent research has focused on how these segmental parameters can be determined effectively and efficiently. Boudriot et al. (2006) determined the anatomic hip center by using the intersection between Koehler's line and a line between the foramina obutratatoria as a point of reference. While recognizing that a large measure of the value of biomechanical motion assessment is its ability to produce individualized data, what Boudriot et al. (2006) also posited was that biomechanical motion assessment is able to produce reliable averages of hip joint center location compared to conventional functional methods because of its extra layer of dimensionality.

Siston and Delp (2006) affirmed the necessity of establishing accurate, valid, and reliable segmental parameters. In their own study, in which the researchers

attempted to calculate a pivoting algorithm that could be used to locate the hip joint center, the researchers tested various motion patterns to determine which of the patterns would produce the smallest mean errors (Siston & Delp, 2006). Siston and Delp (2006) learned that the largest mean errors, ranging from 1.3 to 4.2 mm, occurred when a single plane motion was observed. By contrast, the smallest mean errors, ranging from 0.2 mm to 2.2 mm, were observed when a circumduction pattern of motion was analyzed. While they concluded that the pivoting algorithm works adequately in a research setting, they acknowledged that further research needs to be conducted before the model can be applied in a clinical setting (Siston & Delp, 2006).

The introduction of a third dimension of analysis provides the benefits that the conventional models of joint location are unable to provide, particularly with respect to accuracy. In each of the studies described here, the margins of error that were reported were far lower than margins of error reported in earlier studies in which two dimensions of functional observation and analysis were utilized.

Discussion

As Lemaire (2004) pointed out, "advances in Internet connectivity and personal multimedia computing have created opportunities for integrating simple [biomechanical] motion analysis into clinical practice" (Lemaire, 2004, p. 39). As the benefits of biomechanical motion analysis have become clearer, research and clinical interest has been stimulated in learning more about how this technology can be exploited. For this reason, more research is needed to understand the exact ways in which biomechanical measurement technology can be applied.

The research that has been conducted to date suggests that biomechanical motion analysis can serve as an important ancillary visual tool that can help the clinician explore and then corroborate the patient data collected through other common tools, such as the task performance measurements used in conventional functional motion analysis techniques. In terms of actual application in the clinical context, Kang, Sadri, Mocozet, Magnenat-Thalmann, and Hoffmeyer (2002) explained that joint related calculations—including calculations that facilitate the identification of the location of the hip center joint—are performed by constructing three dimensional bone surface

models based on computer tomography (CT) or magnetic resonance imaging (MRI) images. Computer tomography and magnetic resonance imaging are just two conventional techniques that can be used to identify joint locations.

What distinguishes the biomechanical motion analysis techniques from the conventional two-dimensional techniques is that the former not only demonstrates greater accuracy, they also fulfill the other three criteria that are vital to determining joint locations: efficiency, efficacy, and individualization of data. While the types of strategies that can be used to collect data using biomechanical motion analysis strategies vary widely, they all tend to generate data far more quickly than prediction techniques, which rely upon the clinician's observation or the individual patient's self-report, and they are easier to corroborate. What is perhaps most important and distinctive, however, is the ability of biomechanical motion analysis to produce an individualized portrait of the patient's joints. As Carrozza, Laschi, Micera, Dario, Roccella, and Carpaneto, et al. (2007) explained, one of the newest developments in the field of biomechanical motion research is the invention of wearable motion analysis devices that can monitor individual patients, both in the immediate clinical context

and over a longitudinal period. Wearable motion devices provide both researchers and clinicians with the ability to collect more useful data (Carrozza et al., 2007).

The method of using individualized dynamic stereo photogrammetric motion capture data made accessible by implementing wearable motion devices to find the hip joint center is called the dynamic functional method. There are various mathematical approaches to reach the hip joint center estimate. Different sets of assumptions distinguish the different categories of joint center estimations. One category of assumptions entails no geometric constraints between markers and imposes the each femoral marker lies on a spherical surface in which the center is the center of rotation during movement. These spherical methods have three analytical approaches: one is based on a quadratic best sphere fitting procedure (Cappozzo, 1984); second uses a quartic sphere fitting procedure (Gamage and Lasenby, 2002); the third is based on the Reuleaux Method and determines the center of rotation as the quasi-intersection between mid-orthogonal planes to vectors connecting each marker position in two arbitrarily chosen instants of time (Halvorsen et al., 1999). Within this class of joint determination approaches, it is also assumed that the

center of rotation is stationary therefore is only applicable if one segment is also at rest.

Another category of joint location algorithms is called the transformation techniques. One-sided transformation techniques also assume that the center of rotation and one segment are stationary. When at least one segment is defined by three markers, it is possible to define rigid body transformations and rotations. When the CoR (center of rotation) is stationary, all of the transformations map to a single point, the center of rotation. This approach can be calculated by defining a local coordinate system on the segment and calculating the CoR from the transformations. The Centre transformation technique computes transformations from the global to local coordinates then computes the minimal residual. This is computed as a linear least squares solution which is commonly called the pivoting algorithm (Siston and Delp, 2006). Another technique under this category is named the helical pivot technique which determines the CoR as the point closest to all instantaneous helical axes (Woltring, 1990). The original helical axis approach describes the movement of a rigid-body as a rotation around and a translation parallel to a unique helical axis. The Stoddart

approach is the only one sided transformation technique that does not require the assumption that one of the segments is at rest. Mean segment fixed systems are chosen on both segments and computed by averaging the coordinate systems over all time frames.

Two sided transformation techniques are another method for finding the CoR. The two sided transformation technique named the symmetrical center of rotation technique (SCoRE) does not need the general assumption of having one segment at rest and is capable of calculating a moving CoR (Ehrig et al., 2006). This technique does require a defined local coordinate system on each segment. The assumption of this approach "is that the coordinates of the CoR must remain constant relative to both segments." (Ehrig et al., 2006, p. 2803) Which leads to this objective function below (see fig. 1)

$$f_{\text{SCoRE}}(c_1, c_2) = \sum_{i=1}^n \|R_i c_1 + t_i - (S_i c_2 + d_i)\|^2$$

"Which needs to be minimized, in which c_1, c_2 are the centers of rotation in local coordinate systems." (Ehrig, 2006, p. 2803) This can be written as a linear least squares problem (see fig. 2)

$$\begin{pmatrix} R_1 & -S_1 \\ \vdots & \vdots \\ R_n & -S_n \end{pmatrix} \begin{pmatrix} c_1 \\ c_2 \end{pmatrix} = \begin{pmatrix} d_1 - t_1 \\ \vdots \\ d_n - t_n \end{pmatrix}$$





Where R_i is the right femur rotation matrix and d_i is right the location matrix with respect global origin. S_i is is the left femur rotation matrix and t_i is the left location matrix with respect to global origin.

Testing Methods

There are various algorithm testing methods to test the accuracy and applicability of the joint center prediction methods previously mentioned and the applicability in the clinical construct. One testing method uses computer generated motion data called simulation testing.

To run various movements at a high number of simulations, it is advantageous to run them through a numerical simulation. Ehrig et al.(2006) repeated "all simulations n=1000 times, each with 200 time frames, with random distribution of the marker positions within a specified range of motion with Gaussian noise attributed to each marker." (p.2804) Camomilla et al. (2006) also ran various algorithms through a mathematical simulation to test the output. The hip motion patterns for this study are shown below (see fig. 3)

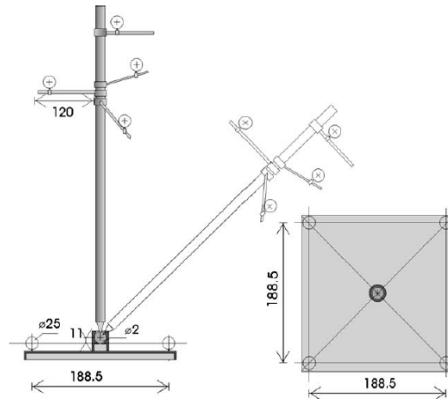
Table 1
Description of the lower limb movements relative to the pelvis

Movement		Description
<i>Cross</i>		Flexion of 30°, neutral position, extension of 30°, neutral position, abduction of 30°, neutral position.
<i>Arc</i>		Flexion of 30°, half circumduction to extension of 30°, neutral position.
<i>Star</i>		Seven flexion-extension/abduction-adduction combined movements from the neutral position within the perimeter drawn in the <i>Arc</i> movement.
<i>StarArc</i>		<i>Star</i> movement followed by <i>Arc</i> movement

Plots indicate the trajectory of the foot as seen from above. Angles are defined according to the convention described in Grood and Suntay, 1983. The internal-external rotation angle was given a null value.

Mechanical linkages also have been used in multiple studies to help validate and compare multiple algorithms. In Piazza et al., 2001, a manipulated a ball and socket linkage to test the spherical algorithm that determines “the center of rotation between the femur and pelvis by fitting a sphere to paths of markers followed by a femur-fixed point as motion occurs about the hip.” (p.967) In this setup, the center of rotation is stationary while the ball joint is manipulated. In another study, Sisten and Delp, 2006 used a mechanical linkage to manipulate the artificial ball and socket though the movement pattern table to test the “pivoting” algorithm. Again the center of the test apparatus is stationary and the joint center is calculated by manipulating a ball socket with a medal arm with markers attached. Camomilla et al. (2006) used a

similar mechanical linkage to test various algorithms through a motion pattern (see fig. 4).



The assumption again is that the center of rotation is stationary. The ultimate goal of the creating the location algorithms is to properly find the true hip joint center on a human subject. Some projects have used lower body cadavers to test the algorithms because the true center of rotation can be measured. Also, the joint mechanics will be more realistic if actual anatomy is used to test the various algorithms. A major source of error in motion analysis is the skin artifacts. This is an unavoidable error source and is very difficult to eliminate. An advantage of using cadavers is that a rigid reference frame can be implanted into the femur. The leg and attached frame are then manipulated through a particular pattern and

captured. The motion capture data is then ran though the various algorithms to find the hip joint center estimate.

As mentioned above testing on cadavers allows to rigidly attach a reference frame to the femur, but other characteristics make cadaveric testing conditions not ideal. The joint mechanics of a cadaver are not identical to the joint mechanics of a live person. Lopomo et al. (2009) used a stereo photogrammictracking system to test the sphere fit method and the pivoting algorithm on eight cadaveric hips. They tested the algorithm with a femoral tracker and without a femoral tracker. "The femur was passively circumducted approximately 12 times around the hip in order to perform the functional test." p.2 The results of the Lopomo et al., (2009) showed that the pivoting algorithm had a closer estimation than the sphere fit method without the pelvic tracker.

De Momi et al. (2009) introduces the Monti Carlo-pivoting algorithm with a similar experimental setup as in Lopomo et al. (2009) with a cadaveric pelvis and femur. DeMomi et al. (2009) concluded that the "MC-pivoting proved significantly better in 6 out of the 21 experiments performed".p 992 In these experimental setups the pelvis and hip joint center are stationary.

Cereatti et al. (2009) performed a study ex vivo with cadavers comparing the quartic sphere fit method and the symmetrical centre of rotation estimation (SCoRE) method. Two pins were implanted into the femur and two into the pelvis. Cadavers lie supine on a table while an operator rotated the right femur with respect to the pelvis. The analysis on the effect of hip movement amplitude revealed that a reduction of the amplitude does not improve the HJC location accuracy. Again the pelvis and hip joint center are stationary.

Live Human Testing

Some studies have tested multiple transformation methods using live human trials. Piazza et al. (2004) tested the pivoting algorithm on stair ascent, stair decent, and varied hip motion movements on subjects. "The hip motion sequence consisted of two circumduction, flexion, extension, abduction, adduction, and two more circumduction trials." (p. 350) The stair ascent and descent trials were conducted on a staircase with seven steps. Walking trials were conducted on a flat walkway. The results of the study suggested that functional methods would result in worst-case hip joint center location errors of 26 mm (comparable to the average errors previously reported for joint center location based on bony landmarks)

when available hip motion is substantially limited. Much larger errors (70 mm worst-case) resulted when hip joint centers were located from data collected during commonly performed motions, perhaps because these motions are, for the most part, restricted to the sagittal plane. It appears that the functional method can be successfully implemented when range of motion is limited, but still requires collection of a special motion trial in which hip motion in both the sagittal and frontal planes is recorded. Study found that functional methods found better results, but in walking trials created more error possibly due to pivoting algorithm not designed for a moving reference frame.

McGibbon et al.(1997) investigated hip center location methods by comparing in-vivo estimations to posthumous hip joint measurement in the same subject. The motion patterns used were a constrained sit-to-stand and axis of rotation movement method. In ex vivo, a linear least squares method was used to calculate the spherical algorithm to find CoR. "Results suggest that using anatomical scaling to locate the HJC may result in unsatisfactory subject-specific estimates of the HJC." (McGibbon et al., 1997, p. 491)

Leardini et al.(1999) tested the functional method by finding the center of the sphere made by hip rotations

described by the thigh markers. Other methods using regression equations and anthropometric measurements were also assessed.

“Prediction methods estimated the HJC location at an average rms distance of 25-30 mm. The functional method performed significantly better and estimated HJCs within a rms distance of 13 mm on average.” (Leardini et al., 1999, p.99)

The score algorithm has a number of advantages over other prediction methods. First, not much motion data is needed to come up with a HJC estimate. Quickly finding an accurate estimate is critical in a clinical environment. Another advantage is that a gait movement trial can be used as a motion pattern to find the HJC. In contrast to other movement patterns used in previous studies, gait is a fundamental human movement that has a moving HJC. Additionally, both HJCs can be located simultaneously using the SCoRE algorithm. Also, to find these points no initial guess is needed. Majority of location techniques need an initial guess to begin and a location is found through several iterations. This can create a source of error and create inconsistent results.

Conclusion

While more research is needed to determine precisely how biomechanical motion assessment can be used to determine hip joint location, initial evidence suggests that the functional methods provide numerous advantages when compared against conventional methods. The SCoRE algorithm provides numerous advantages over other transformation methods, specifically finding both moving joint centers in a gait trial.

Chapter 3: Theoretical Orientation

For two sided coordinate transformation techniques, no stationary CoR is required. Local coordinate systems are needed for each segment. The coordinates of the CoR must remain constant relative to both segments. This leads to the objective function which must be minimized (see fig. 5).

$$f_{\text{SCORE}}(c_1, c_2) = \sum_{i=1}^n \|R_i c_1 + t_i - (S_i c_2 + d_i)\|^2$$

c_1, c_2 are centers of rotation in the local coordinate systems. (R_i, t_i) , (S_i, d_i) are the local to global transformations. R_i and S_i are the rotation matrixes and t_i and d_i are the location matrixes. This can be written as a least linear squares problem (see fig. 6).

$$\begin{pmatrix} R_1 & -S_1 \\ \vdots & \vdots \\ R_n & -S_n \end{pmatrix} \begin{pmatrix} c_1 \\ c_2 \end{pmatrix} = \begin{pmatrix} d_1 - t_1 \\ \vdots \\ d_n - t_n \end{pmatrix}$$

This approach yields a joint position for each segment and each time instant, $R_i * c_1 + t_i$ and $S_i * c_2 + d_i$. The Score algorithm is a two sided transformation method. In initial testing, the Score algorithm produced very noisy HJC locations. To combat this issue, a one sided tranformation

method similar to the Center Transformations Technique (CTT) is implemented and modified. The center of rotation of the femur is found through the objective function (see fig. 7).

$$f_{\text{CTT}}(c, \tilde{c}) = \sum_{i=1}^n \|R_i \tilde{c} + t_i - c\|^2$$

Where $Rc + t$ is the global HJC location for a particular frame. This also can be solved as a least linear squares problem. (see fig. 8).

$$\begin{pmatrix} R_1 & -I \\ \vdots & \vdots \\ R_n & -I \end{pmatrix} \begin{pmatrix} \tilde{c} \\ c \end{pmatrix} = - \begin{pmatrix} t_1 \\ \vdots \\ t_n \end{pmatrix}$$

Where I is an identity matrix. The CTT is implemented with the assumption that the center of rotation is stationary. To be able to make a one sided transformation technique find a moving center of rotation, a virtual point located at the center of pelvis is created. The least linear squares problem is set up as (see fig. 9)

$$\begin{pmatrix} R_1 & -I \\ \vdots & \vdots \\ R_n & -I \end{pmatrix} \begin{pmatrix} \tilde{c} \\ c \end{pmatrix} = \begin{pmatrix} d_1 - t_1 \\ \vdots \\ d_n - t_n \end{pmatrix}$$

Where d is the center of the pelvis. t is the location of the femur at the hip marker (greater

trochanter) and R is the rotation matrix of the femur with respect to global coordinate axis. The subtraction of the location of the center of the pelvis with the femur segment, a moving center of rotation can be found for each femur for each frame. This approach is a combination of the Score algorithm and center transformation technique

Chapter 4: Methods

Model Creation

A custom model is written in the Vicon Bodybuilder language. The objective of the model is to output the position of the pelvis segment and the position and rotation of both femur segments. Body segments are created using a set of markers that are placed on the body. Pelvis and femur segments are created in this model. After the trail, the markers are labeled. The Vicon Bodybuilder program exports the location and orientation of the segments for each frame. The position and rotation data of the segments exported and opened in Microsoft Excel. For the data to be used in the objective function, rotation matrixes must be made from the data. Each frame of the trial produces a 3x3 rotation matrix for each segment. To create these particular matrixes, a custom macro is run in Microsoft Excel. One large rotation matrix and position matrix is created for each segment for the whole trial. After the matrix creation, the data is imported into Matlab. The purpose of this step is to solve for coefficient c in the objective function. The solution is found by using the Matlab backslash command. C is found by rotation matrix backslash position matrix. The Matlab backslash command is a least linear squares solution.

After solving for c , the value is then entered into Excel to multiply the rotation matrix by c and add it to the position vector. This process will find the hip joint center location for each segment for each frame. This process must be done for both femur segments. To visualize these locations in the trial, the positions are then imported into the particular trial in Vicon Nexus using the ASCII import command.

The standard Vicon model for biomechanical motion analysis is called Golem. Gait analysis and other biomechanical analysis are dependent on the location of the HJC that is calculated with following formula

$$\begin{aligned} \text{LHJC} = \{ & C \cdot \cos\theta \sin\beta - (\text{LATD} + \text{mm}) \cdot \cos\beta, \\ & -C \cdot \sin\theta + \text{aa}, \\ & -C \cdot \cos\theta \cos\beta - (\text{LATD} + \text{mm}) \cdot \\ & \sin\beta \} * \text{Pelvis} \end{aligned}$$

$$\begin{aligned} \text{RHJC} = \{ & C \cdot \cos\theta \sin\beta - (\text{RATD} + \text{mm}) \cdot \cos\beta, \\ & C \cdot \sin\theta - \text{aa}, \\ & -C \cdot \cos\theta \cos\beta - (\text{RATD} + \text{mm}) \cdot \\ & \sin\beta \} * \text{Pelvis} \end{aligned}$$

As shown above, it is a predictive model not a functional model. The hip joint centers are calculated

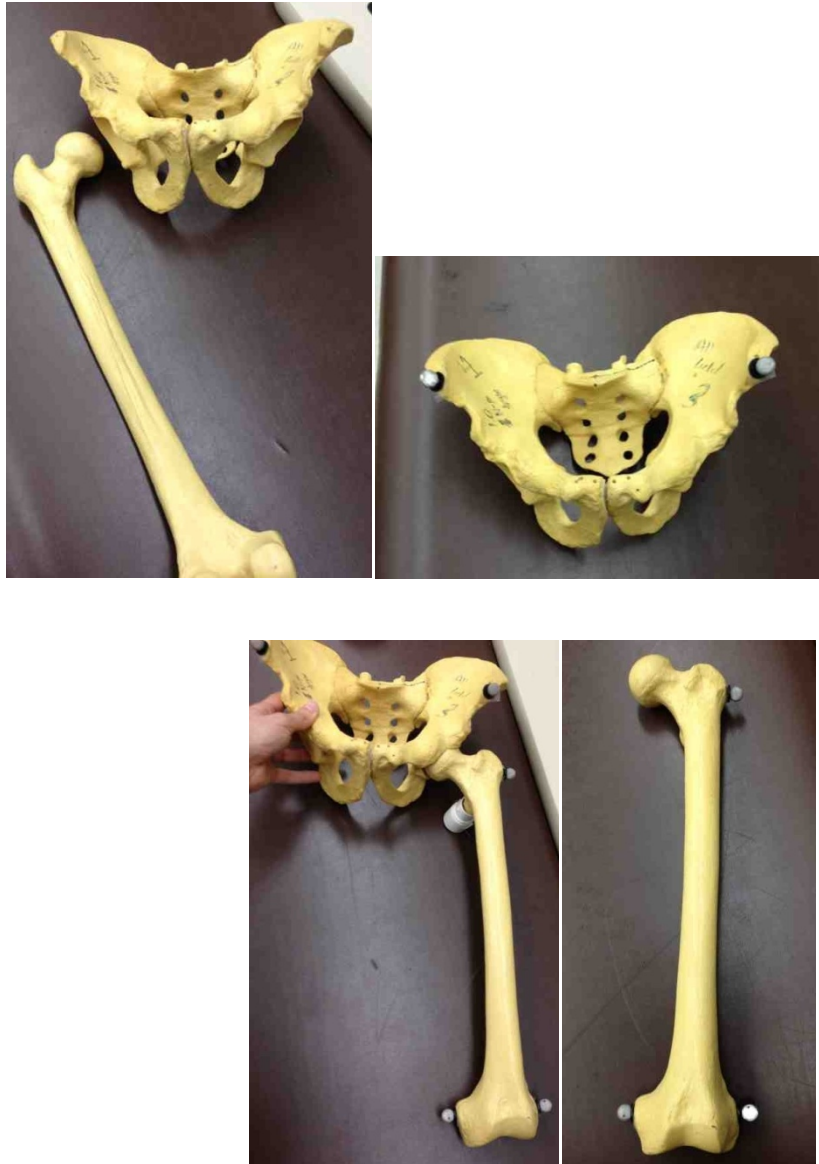
based on the position of the markers placed on the pelvis and values of the coefficients in the formula.

Gait Trials

Subjects' anatomical measurements were taken before the motion. The resources used in this motion capture session are the Vicon motion capture system and reflective markers. The motion capture system consists of 9 Vicon Mcams connected to Vicon MX Nexus system. All of the resources are located in the University of Miami Biomechanics Laboratory. The subject performed 15 gait trials at normal speed walking speed.

Validation

A life sized anatomically correct femur and pelvis bones were used in the validation of the algorithm as shown below.



Markers are placed on the same bony landmarks as the human trial. The pelvis and femur were moved through the capture space by hand to simulate a gait trial. The hip joint was held together by hand, and the femur was swung in a pendulum pattern similar to a gait pattern.

Chapter 5: Results

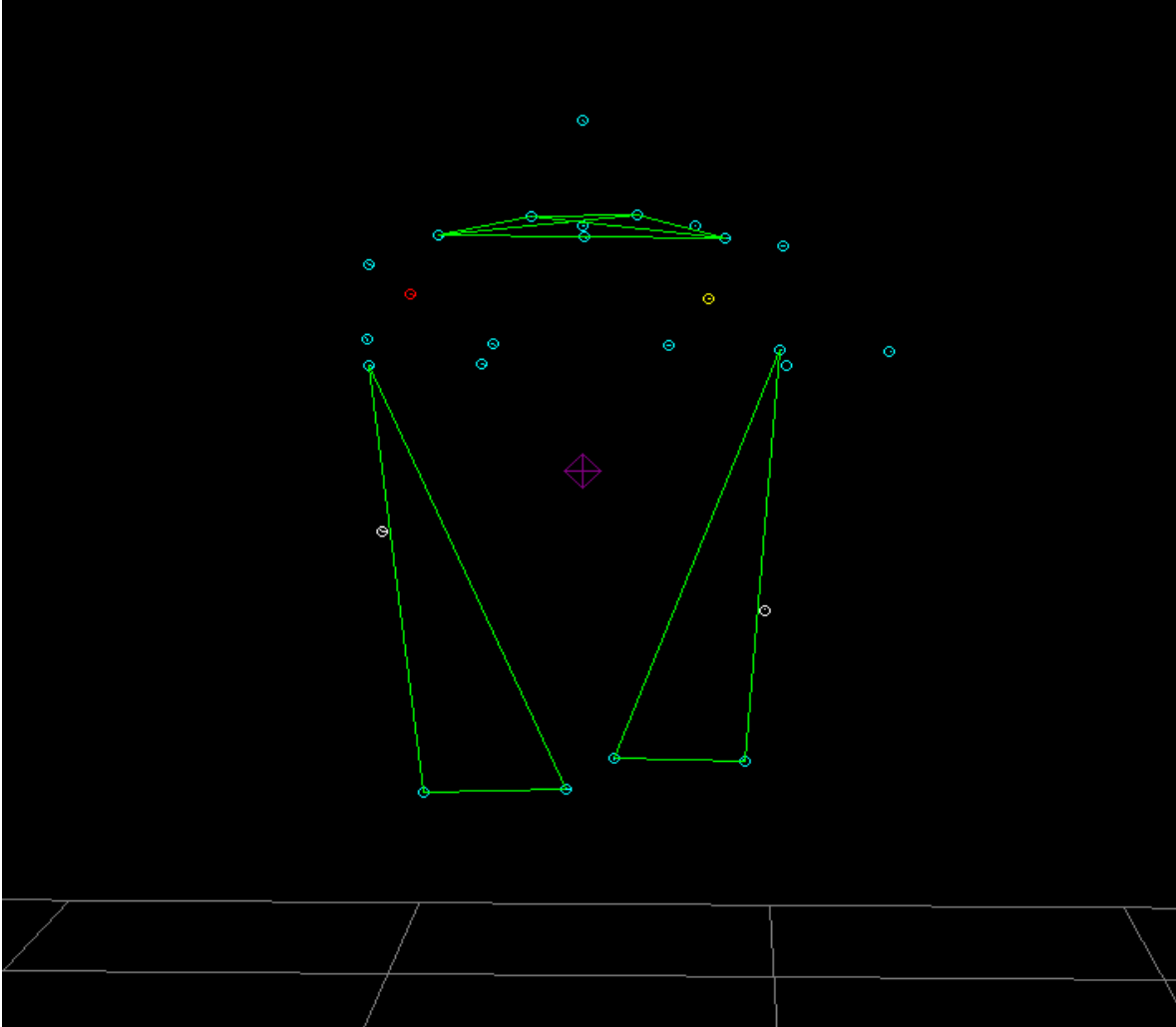
Gait Trials

LEFT				RIGHT			
trial	score	HIP golem	diff	trial	score	HIP golem	diff
1	95.97	118.10	-22.13	1	85.72	118.19	-32.47
2	91.81	117.22	-25.41	2	83.16	118.83	-35.66
3	100.24	118.81	-18.58	3	103.50	120.50	-17.00
4	93.63	116.54	-22.91	4	93.12	118.57	-25.45
5	89.41	116.01	-26.61	5	99.48	116.85	-17.36
6	91.25	116.45	-25.20	6	86.07	117.10	-31.03
7	96.25	116.02	-19.78	7	98.47	117.71	-19.23
8	96.88	116.48	-19.60	8	99.29	116.85	-17.55
9	96.12	116.33	-20.21	9	109.05	118.30	-9.25
10	89.91	116.86	-26.96	10	98.51	117.21	-18.71
11	71.61	117.12	-45.51	11	82.37	117.51	-35.14
12	92.46	117.10	-24.64	12	95.96	117.34	-21.38
13	87.43	117.24	-29.81	13	80.90	116.85	-35.96
14	84.09	117.27	-33.17	14	81.04	117.19	-36.15
15	98.64	117.35	-18.71	15	90.54	117.30	-26.76
16	94.43	116.82	-22.39	16	103.29	117.08	-13.79
17	78.11	117.23	-39.12	17	90.03	117.56	-27.53
18	70.56	116.77	-46.20	18	88.43	116.86	-28.43
19	92.98	117.14	-24.16	19	93.71	117.62	-23.91
20	93.79	116.68	-22.89	20	99.34	117.82	-18.49
MEANS	90.28	116.98			93.10	117.66	

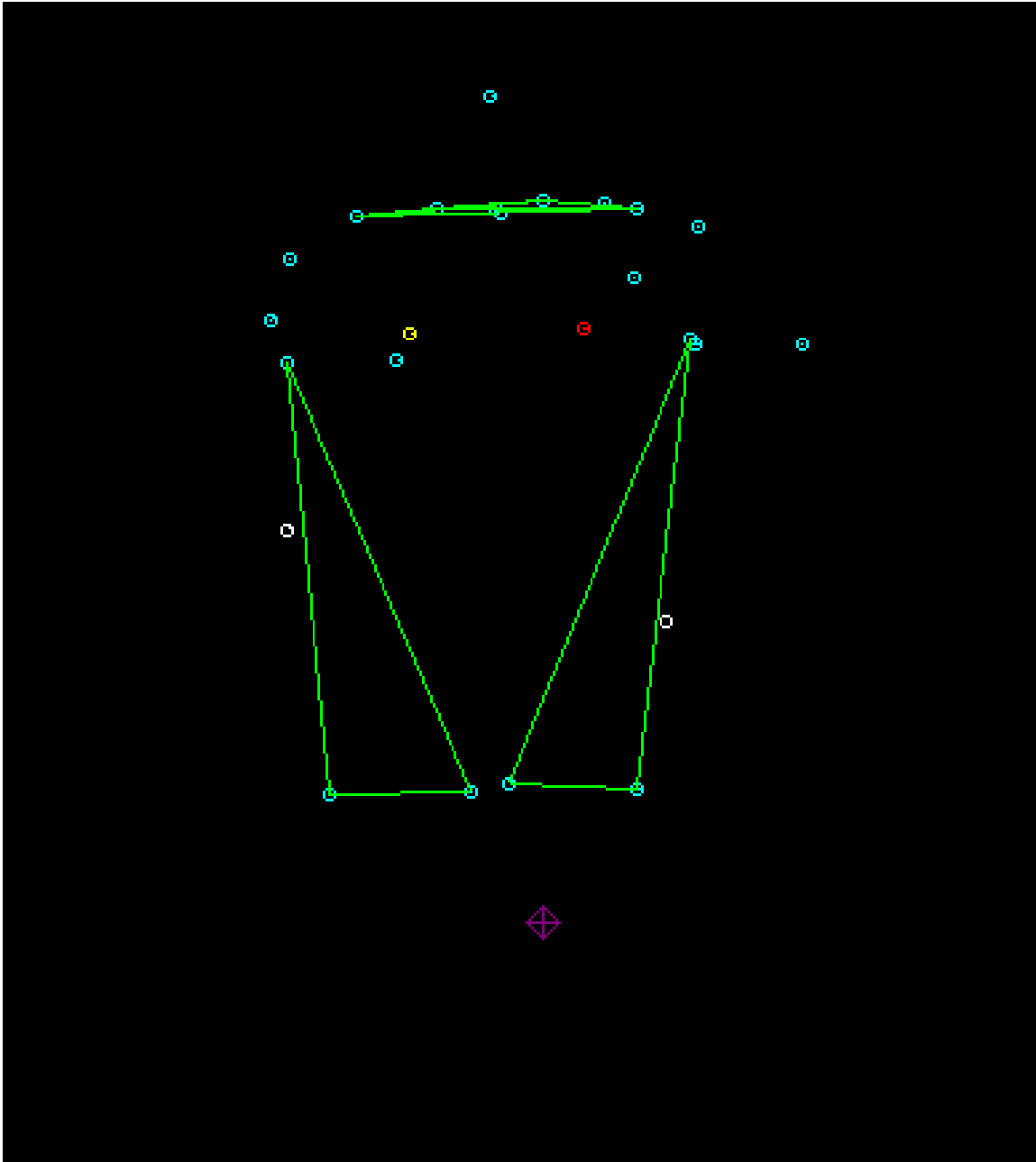
The algorithm outputs a global hip joint location for every frame. To measure the relative joint location, the vector distance from the hip marker located at the greater trochanter to the virtual center is measured. Below is a comparison of the calculated hip joint center for both methods for 20 gait trials in mm.

A paired T test for each side was performed to statistically show that there is a significant difference between score vector distance and golem vector distances. The null hypothesis of $H_0=H_i$ is rejected with an alpha of .05.

The visualization of the score HJC is shown below with the red and yellow markers.



A visualization of the golem model is shown below with red and yellow markers.



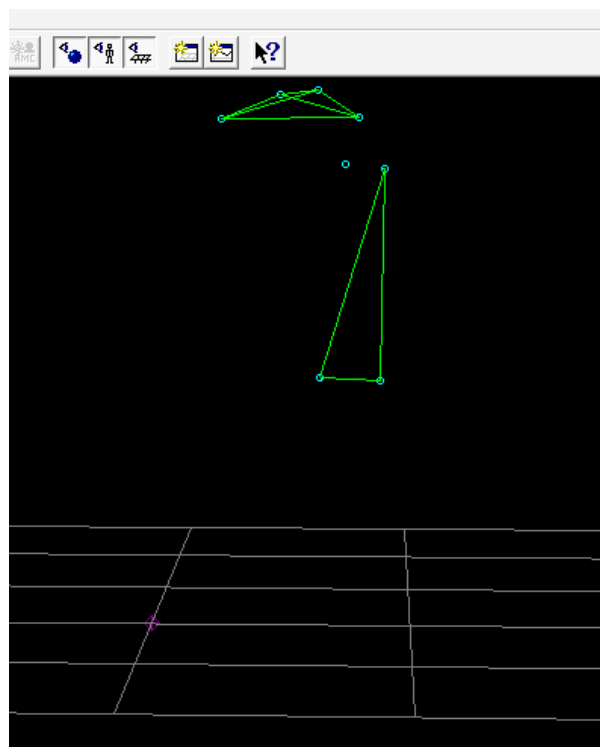
As seen in the above visualizations, the score virtual hip joint center location appears to be in correct

location. The golem model the virtual hip joint centers are located deeper into the pelvis.

Kickwood et al. (1999) digitized a frontal plane radiograph and reported the center of the femoral head to be an average of 90 mm medial to an external greater trochanter marker.

Validation Trial

As stated earlier, a validation trial was performed consisting of using life sized plastic bones. The distance from the center of the femur head to the edge of the femur was calculated at 77.8 mm from the motion capture trial. As shown in the picture below, the calculated width is consistent with the measured width of 78 mm.



Above is the virtual visualization of the validation trial showing the hip joint center being shown with the blue virtual marker.

Conclusion

The preliminary results of the hip joint center algorithm show promising results. As stated earlier, there's no way to validate live human subjects without invasive and expensive imaging techniques. Femur geometry and dimensions vary greatly in the human population. Kickwood et al. (1999) digitized a frontal plane radiograph and reported the center of the femoral head to be an average of 90 mm medial to an external greater trochanter marker. The subjects' calculated hip joint center distance from the left hip marker and right hip marker are 86.08 mm and 92.96 mm, respectively. In contrast to the golem model output of 110.6 mm and 114 mm for the left and right hip joint center, respectfully, it appears that the HJC center algorithm is producing more accurate results than the golem model. More trials and subjects will secure the validation of the HJC algorithm.

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Appendix

Score Bodybuilder Model

```
MACRO DisplayAxes( ASeg )

ASeg#O = ASeg(0)
ASeg#X = ASeg(0) + 100 * ASeg(1)
ASeg#Y = ASeg(0) + 100 * ASeg(2)
ASeg#Z = ASeg(0) + 100 * ASeg(3)
OUTPUT( ASeg#O, ASeg#X, ASeg#Y, ASeg#Z )

ENDMACRO

Parent = [{0,0,0}, {1,0,0}, {0,0,1}, 1]
DisplayAxes( Parent )

Gorigin = {0,0,0}
Global = [Gorigin, {1,0,0}, {0,0,1}, 1]

Lpelvis = (LASI+LPSI)/2
Rpelvis = (RASI+RPSI)/2
Bpelvis = (LPSI+RPSI)/2
Fpelvis = (LASI+RASI)/2

Cpelvis = (Lpelvis+Rpelvis)/2

Pelvis = [Cpelvis, Lpelvis-Rpelvis, Fpelvis-Bpelvis, 2]
DisplayAxes ( Pelvis )

LFemur=[LHIP,LKNE-LKNI,LKNE-LHIP,-2]
RFemur=[RHIP,RKNI-RKNE,RKNE-RHIP,-2]

DisplayAxes ( LFemur )
DisplayAxes ( RFemur )

LFemurang= <LFemur, 1>
RFemurang= <RFemur, 1>
Pelvisang= <Pelvis, 1>

OUTPUT (LFemurang, RFemurang, Pelvisang)
```

Golem Model

```

Gorigin = {0,0,0}
Global = [Gorigin, {1,0,0}, {0,0,1}, xyz]

SACR = (LPSI+RPSI)/2

LLegLength = DIST(LASI, LKNE)+DIST(LKNE, LANK)
RLegLength = DIST(RASI, RKNE)+DIST(RKNE, RANK)

MP_LegLength = (LLegLength+RLegLength)/2
PARAM(MP_LegLength)

PELF = (LASI+RASI)/2

Pelvis = [PELF, LASI-RASI, PELF-SACR, yzx]

LATD = 0.1288*MP_LegLength-48.56
RATD = LATD

C = MP_LegLength*0.115-15.3
InterASISDist=DIST(LASI, RASI)
aa = InterASISDist/2
mm = 10/2
COSBETA = 0.951
SINBETA = 0.309
COSTHETA = 0.880
SINTHETA = 0.476
COSTHETASINBETA = COSTHETA*SINBETA
COSTHETACOSBETA = COSTHETA*COSBETA

LHJC = {C*COSTHETASINBETA - (LATD + mm) * COSBETA,
        -C*SINTHETA + aa,
        -C*COSTHETACOSBETA - (LATD + mm) * SINBETA}*Pelvis

RHJC = {C*COSTHETASINBETA - (RATD + mm) * COSBETA,
        C*SINTHETA - aa,
        -C*COSTHETACOSBETA - (RATD + mm) * SINBETA}*Pelvis

OUTPUT (LHJC, RHJC)

```

Validation Score model-

```

MACRO DisplayAxes( ASeg )

ASeg#O = ASeg(0)
ASeg#X = ASeg(0) + 100 * ASeg(1)
ASeg#Y = ASeg(0) + 100 * ASeg(2)
ASeg#Z = ASeg(0) + 100 * ASeg(3)
OUTPUT( ASeg#O, ASeg#X, ASeg#Y, ASeg#Z )

ENDMACRO

Parent = [{0,0,0}, {1,0,0}, {0,0,1}, 1]
DisplayAxes( Parent )

Gorigin = {0,0,0}
Global = [Gorigin, {1,0,0}, {0,0,1}, 1]

Lpelvis = (LASI+LPSI)/2
Rpelvis = (RASI+RPSI)/2
Bpelvis = (LPSI+RPSI)/2
Fpelvis = (LASI+RASI)/2

Cpelvis = (Lpelvis+Rpelvis)/2

Pelvis = [Cpelvis, Lpelvis-Rpelvis, Fpelvis-Bpelvis, 2]
DisplayAxes ( Pelvis )

LFemur=[LHIP, LKNE-LKNI, LKNE-LHIP, -2]
{*RFemur=[RHIP, RKNI-RKNE, RKNE-RHIP, -2]*}

DisplayAxes ( LFemur )
{*DisplayAxes ( RFemur )*}
LFemurang= <LFemur, 1>
{*RFemurang= <RFemur, 1>*}
{*Pelvisang= <Pelvis, 1>*}

OUTPUT (LFemurang)

```

T-TEST PAIRS=scoreright WITH golemright (PAIRED)

/CRITERIA=CI(.9500)

T-Test

Paired Samples Statistics

	M ean	N	Std. Deviation	Std. Error Mean
scoreright	93 .1001	2 0	8.2756 0	1.8504 8
golemright	11 7.6620	2 0	.88658	.19824

Paired Samples Correlations

	N	Corr elation	S ig.
scoreright & golemright	2 0	.230	.3 28

Paired Samples Test

	Paired Differences			
	Me an	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference
				Lower
scoreright - golemright	- 24.56193	8.1172 5	1.8150 7	- 28.36092

Paired Samples Test

	Paired Differences	t	df	Sig. (2-tailed)
	95% Confidence Interval of the Difference			
	Upper			
air scoreright - golemright 1	-20.76294	- 13.532	19	.000

T-TEST PAIRS=scoreleft WITH golemleft (PAIRED)

/CRITERIA=CI(.9500)

T-Test

Paired Samples Statistics

	M ean	N	Std. Deviation	Std. Error Mean
sc	90	2	8.2827	1.8520
oreleft	.2778	0	3	7
air 1				
go	11	2	.65895	.14735
lemleft	6.9773	0		

Paired Samples Correlations

	N	Corr elation	S ig.
scoreleft & air 1 golemleft	2 0	.089	.7 10

Paired Samples Test

	Paired Differences			
	Me an	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference
				Lower
scoreleft - air 1 golemleft	- 26.69953	8.2504 7	1.8448 6	- 30.56088

Paired Samples Test

	Paired Differences	t	df	Sig (2-tailed)
	95% Confidence Interval of the Difference			
	Upper			
P scoreleft - air 1 golemleft	-22.83819	- 14.472	19	.00 0