

GAIT SYNTHESIS OF ABNORMAL GAITS IN CANINES

A Thesis

by

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ABSTRACT

When attempting to introduce new subjects or characters to a motion database, generating or capturing motions is particularly cumbersome, especially if the subject has some medical issue. This thesis describes techniques in which motion capture analysis is used to isolate the components of canine gait that are the direct result of poor health. These components are then synthesized with the healthy motion of a new dog to create the appearance of the unhealthy motion in that breed. Given two captured motions, one healthy A and one unhealthy A' , the goal of this work is to determine a mathematical method for finding the difference between A and A' and applying this difference to a third motion, B , to generate a new motion, B' , that carries the characteristics shown in A' . This motion analogy method is successfully implemented and validated using two case studies. This technique has applications in diagnosing the impact of treatments in medical studies and the development of training for veterinarians as it allows for multiple variations of motion to be applied to a new subject.

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1. INTRODUCTION

Current motion capture systems allow the richness of quadrupedal motion to be accurately recorded and analyzed. Current demand by the medical and entertainment industries for more precise data has led to the creation of robust databases of motion, for many applications, including medical and computer graphics. Though these databases contain various subjects and their subsequent motions, constructing such databases is laborious, time consuming and, when dealing with various medical conditions, often impossible due to (production) budget or a limited number of examples. When attempting to introduce new subjects or characters into a database, generating or capturing motions can prove particularly cumbersome. This is partially due to the consistency required for the motion capture marker placements and the fact that it is often easier to recapture a motion than deal with problematic data is also a factor.

However, discovering problems within the data is often impossible at the time of capture, leading to multiple sessions to get a workable piece of motion data. Also, some motions may or may not exist within the database already, particularly if the subject is undergoing medical intervention to improve their motion. To streamline this process, this thesis proposes a new method that uses existing motions and applies them to other motions, thereby creating a new motion with most of the characteristics of the source motions.

Describing motions procedurally is challenging because of the complex subtleties within the motions, such as conveying the weight, rhythm, and balance of the subject accurately. The objective of this thesis is to infer user-desired motion from example

motions. A mathematical model is developed by providing matching motions in an input and output pair. To learn the translation of a normal to a limping gait, for example, one would pair three strides of a normal gait to three strides of a limping one. The overall content (three strides) is identical but the characteristics of the motions comprise spatial and temporal variation.

Given two captured motions A (healthy) and A' (unhealthy) the goal of this work is to develop a mathematical model to determine the difference between A and A' and apply this difference to a third motion B to generate a new motion B' that encapsulates the characteristics shown in A'. The representation of this motion analogy is provided below:

$$\mathbf{A : A' :: B : B'} \quad \mathbf{(1)}$$

The goal of the motion analogies application is to synthesize new motions with the characteristics of the provided motions. By synthesizing abnormal gaits the user can use the synthesized gait for comparisons and predictions of health issues as they progress. For example, if starting out with a three-month progression of a disease and the subject goes on clinical trials to help with the diseases symptoms, at six months the user may want to compare what the subject would have been like without medical intervention compared to what that subject is now. By using previously captured data of the disease the system can synthesize a projection of how the disease would progress on the subject.

However, this system of motion analogies is not limited to just a clinical setting. This model can be used for any type of similar motions. While this paper specifically concentrated on dogs walking and the differences between healthy and unhealthy, the system can handle any type of similar motions and skeletons. As such this system can be used to apply variations of motions between various subjects. For example, the system could eventually be used to include other digitigrade subjects.

The key to this approach is to create a generic method that is anatomically apparent and can be easily transferred between morphologies. The generic algorithm used takes the two similar motions and establishes a correspondence between the two separate subjects. This correspondence along with an input motion for the first subject is optimized to create the new motion that exhibits the behavior of the input motion. Essentially, by treating motions as space-time signals and a problem of motion editing, the problem is converted to that of high-dimensional signal processing. The end result of this project is a mathematical system of motion analogies that can be implemented and validated by several synthesized example motions.

2. RELATED WORK

2.1 MOTION SYNTHESIS

Several approaches for synthesizing motion and motion characteristics exist. Retargeting approaches transfer entire motions from one character to another at varying skeletal sizes and proportions. Gleicher [1998] defined this problem as adapting the animation to transfer between characters. In this work motion is retargeted to similar skeletal structures with different bone proportions by solving space-time optimization problems. Such solutions give an infinite number of possible motions, many not in the realm of reality. Graph based approaches, such as Parametric Motion Graphs presented by Heck and Gleicher [2007] or Motion Graphs presented by Kovar et al. [2002a], search short clips that satisfy user determined constraints from a motion database and assemble them to synthesize a new, extended motion sequence. As such no synthesized motion is a true motion, but rather a collage of preexisting data. Likewise, motion blending approaches interpolate and extrapolate from examples and linearly combine them to synthesize new motion sequences that consist of multiple styles (Park et al. [2004]). There are several approaches that proceed by cutting and pasting skeleton elements, and their subsequent motions, from different subjects to combine separate elements into a new whole skeleton (Ikemoto and Forsyth [2004]). Parametric approaches extend possible output motions to allow users to adjust the motion with various predefined parameters (Kovar and Gleicher [2004]). However, for the application of this project, adapting any of these existing methods is challenging. This is because results produced by these methods are not plausible due to the fact that:

- Resulting motions are often outside the realm of real world possibilities
- There is the added challenge of acquiring new contents and characteristics effectively.
- There is no way of extracting the subject from the motion, which is necessary to extract just the components of the unhealthy motion.

2.2 WARPING MOTION CURVES

The closest methodology to that presented in this thesis are works that seek to modify motions and their styles by warping motion curves. Witkin and Popovic [1995] adjusted motion curves to create a desired curve using displacement mapping at key user-defined frames of existing curves while Wu et al. [2008] used the entire motion curve to eliminate user input. Amaya et al. [1996] extracted emotion from motion by comparing neutral and “emotional” motions and applying this emotion component to a different neutral motion to generate a new sequence with the same “emotion” component. The method presented in this thesis not only encompasses “emotion” but also rhythm and the semantics of the original motions to the target motion. Straight displacement mapping is tends to be an inflexible form of finding the difference. The difference defined in this thesis is more flexible than straight displacement mapping.

Several other methods have focused on extracting characteristics from one or more examples, similar to the method presented here. Bruderlin and Williams [1995] treated motion sequences as frequency bands and adjusted motion characteristics by adjusting those frequencies. Brand and Hertzmann [2000] based their approach on analyzing motion sequences with the Hidden Markov Model (HMM) to extract styles, which in turn can be interpolated, extrapolated and applied to new sequences. However,

each of these methods changes only the style of the motion rather than the content. In this thesis the content is modified.

2.3 EXAMPLE MOTIONS

Previous works have described methods to map between input and output motions by examining the correspondence between them. Dontcheva et al [2003] mapped low-dimensional performance to a high-dimensional motion using the Canonical Correlation Analysis method, a statistical method for finding linear correlations between cross-covariance matrices. He then drove the character animation by manipulating “widgets” movements. Hsu et al. [2005] treated motion mapping as a Linear Time Invariable (LTI) system and transferred motion characteristics by estimating dynamic metrics. Their system was limited in that it required the example motions to exist inside the example database while the intent of this system is to generate motion sequences for new characters that do not currently exist in the motion database.

2.4 VISUALIZATION IN CLINICAL GAIT ANALYSIS

In clinical research, motion analysis systems, force plate technology and electromyography can provide a detailed picture of the quadrupedal gait. However, much of this technology is labor intensive, time-intensive and often too expensive for clinical use. As such, much research has been devoted to classifying and describing gaits, but little has been done to organize data into useful diagnostic or therapeutic regimes. Gillette and Angle [2008] provided a review of recent developments in canine

locomotion, focusing on human perception of gait analysis of canines and the captured analysis of canine locomotion. With reviews conducted in current analytical techniques and current biomechanical technologies it is noted that 2D computer assisted video-graphic gait analysis systems were the most relevant to the general practitioner. This is due to the fact that 3D systems required more specialized laboratories. Current studies on biped and quadruped locomotion involve measurement and analysis of temporal characteristics, electromyographic signals, kinematics of limb segments and the kinematics of the foot-floor and joint resultants. Analysis of the latter half of these features require a voluminous amount of data with limited ability to process this data for later analysis, particularly when dealing with quadrupeds (Newton and Nunamaker [1985]).

2.4.1 EDUCATION

Visualization of clinical data, such as 3D animations, is used to highlight relevant data and link specific pieces of data together to allow users to quickly and easily identify underlying causes for health defects. These visualizations allow the clinician to give a more informed decision instead of being overwhelmed by the volumes of data. In education, 2D and 3D animations are used to supplement traditional teaching methods to allow for better understanding of injuries and procedures (Clements et al. [2013]). Scherzer et al. [2010] concluded that although interactive 3D media will never fully replace experimental learning, or learning by doing, it may prove as a useful tool in

aiding instructors to present complex material in a more understandable way, ultimately preparing students better.

2.4.2 THERAPEUTIC

Assessing the outcome of gait analysis is useful in the current evidence-based practice environment. There is a need to evaluate the effectiveness of rehabilitation interventions, such as therapeutic exercise, or drug studies (Steiss, [2007]). According to Steiss [2007], kinematics in a 2D/3D setting allows for detailed analysis of joint motions, such as joint angle differences, and analysis of various activities that can be tailored to specific areas of interest. 2D recordings are portable and can be sent elsewhere for a secondary opinion and there are numerous analytical tools already commercially available. However, these 2D analyses are often limited to the sagittal view of the recording camera, with 3D analysis being expensive in terms of motion capture and the equipment needed. Also, effective analysis requires breed specific normative data, e.g., a Greyhound varies greatly from a German Shepherd Dog.

3. APPROACH / METHOD

Given two captured motions A and A', the goal of this work is to determine a mathematical method for finding the difference between A and A' and applying this difference to a third existing motion B to generate a new motion B' that carries all characteristics shown in A'. When applying this to, for example, healthy and unhealthy motions, A becomes the healthy motion of a specific breed, A' becomes the unhealthy motion of that breed, B is the healthy motion of a new different breed, thus B' becomes the unhealthy motion of the new breed. The process synthesizes the unhealthy motion of a new breed based on the difference characteristics found between the healthy and unhealthy versions of the measured/captured breed.

This work proceeds by first retargeting captured motions of A and A' onto the target subject's skeleton (B) to eliminate any motion that is driven by proportions and ensure that the skeletons have the same topology. The next step is to align the example motions to the reference motion using a procedure called *time warping*. The method used is a linear model describing spatial differences between the aligned examples. This *spatial estimation stage* returns parameters that are then attached to the target motion B. This gives motion B the style of the example motions but not the timing. The procedure for finding the temporal estimation and adjusting the timing of the intermediate motion is done through the *inverse time warping* function. The resulting motion B' may contain artifacts. These artifacts can be corrected by one or more standard processes for post processing of motion capture.

3.1 MOTION REPRESENTATION

Animation curves, like the one shown in Figure 1 represent the x, y, and z position and/or rotation of a joint in Euclidian space as the positions or rotations change over time. Time is measured in sub-second measurements, typically 1/60th of a second for motion capture, called frames. For general use motions are represented as animation curves.

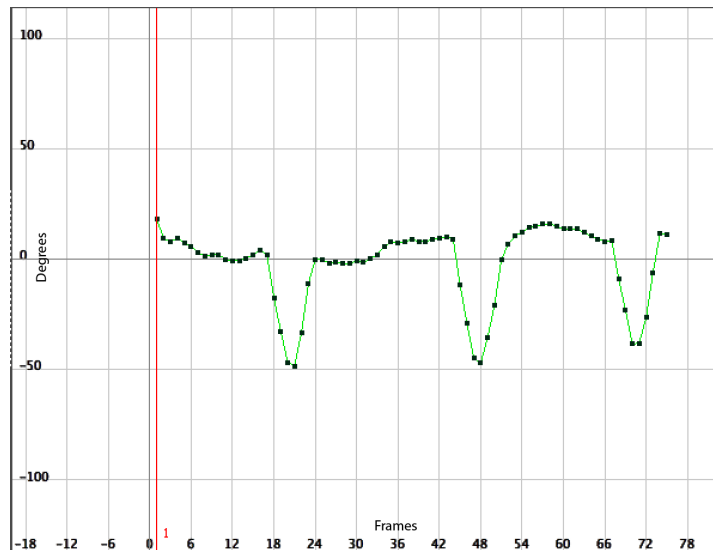


Figure 1 Animation Curve

A motion sequence $M = \{ M(t_i) \}$ is a set of frames which contains a motion curve in the time domain. $M(t_i) = (p_i^0 | q_i^0 | q_i^1 | \dots | q_i^{n-1})$ represents the configuration of joints at the i^{th} frame where p_i^0 is the global position of the root and q_i^0 is the orientation of the root in world space and q_i^1 is the orientation of the child joint in relation to its parent, in this case the root. Each component of M is one Degree Of

Freedom (DOF). A table of some of the symbols used throughout this paper is shown below.

t_i	<u>frame</u> at index i
M_A	<u>motion</u> curve of one DOF of A
$M_{A'}$	<u>motion</u> curve of one DOF of A'
M_B	<u>motion</u> curve of one DOF of B
\tilde{M}_A	<u>time-aligned</u> motion curve of one DOF of A
$\tilde{M}_{A'}$	<u>time-aligned</u> motion curve of one DOF of A'
$\tilde{M}_{B'}$	<u>time-aligned</u> resulting motion curve of one DOF of B'
$S_{A \rightarrow B}$	<u>time-alignment</u> function that aligns motion A to motion B
$S_{A' \rightarrow B}$	<u>time-alignment</u> function that aligns motion A' to motion B
$S_{B \rightarrow B'}$	<u>time-alignment</u> function that aligns motion B to motion B'

In this paper joints are defined as objects that can be translated and rotated in 3D space. They can also be linked together to form a hierarchy. The first joint in a hierarchy is known as the root joint. A skeleton is a complete hierarchy of joints in the form of an organism, in this case a canine, with joints that placed in their correct anatomical positions.

3.2 SUBJECT NORMALIZATION

Before aligning the motions and finding the differences between them it is necessary to normalize the skeleton proportions and topologies to the target motion. First, the position vectors are scaled and rotation vectors are directly transferred. The method presented in Kovar et al. [2002b] is used to cleanup any artifacts that may occur. Kovar's method uses defined footplant constraints assigned using an identifier algorithm to find the exact frames the foot is on the ground. Inverse kinematic solvers are used to reposition the leg joints to keep the foot in a single place.

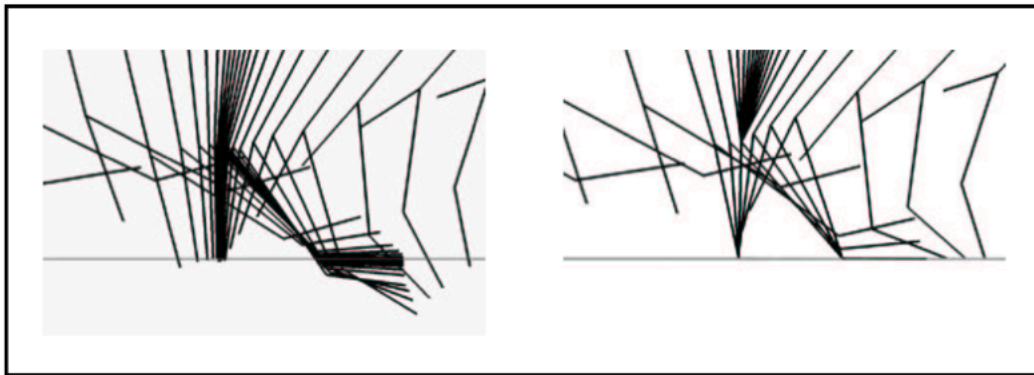


Figure 2 Example of Footskate on the Left and the Result of Kovar et al. [2002b] Algorithm on the Right

3.3 TIME ALIGNMENT

With the skeletons of the same topology and proportion, a frame by frame correspondence action is performed to temporally align the example motions M_A and $M_{A'}$ to M_B . Linear blending can fail if motions have different timing, i.e. when corresponding events, like foot plants, occur at different frames in the sequence. To overcome this issue a *time warp* solution is used to correctly align corresponding events.

To align two motions, a time-alignment curve is constructed, which maps frames from one motion to corresponding frames in another motion. This curve is represented as:

$$S_{A \rightarrow B} \triangleq \{(t_i, t_j) : \text{the } i^{\text{th}} \text{ frame of } A \text{ corresponds to the } j^{\text{th}} \text{ frame of } B\} \quad (2)$$

To obtain the most optimal alignment, the user selects appropriate starting and ending frames of each sequence to ensure good alignment exists at the boundaries. The time-alignment curve must also satisfy the constraints of continuity, causality and slope limitations, as seen in Kovar et al. [2003].

With the time-alignment curves and the subsequent correspondence the example motion can be warped to align with the target. Assuming that M_A corresponds to M_B , as shown below in Figure 2, I can warp the motion M_A , represented as \tilde{M}_A , based on three different correspondence criteria. The first is that one $M_A(t_i)$ corresponds to one $M_B(t_j)$, so $\tilde{M}_A(t_j) = M_A(t_i)$. The second is that multiple $M_A(t_i)$ correspond to one $M_B(t_j)$, so $\tilde{M}_A(t_j) = \frac{1}{m+1} \sum_{i+k+m}^{i+k} M_A(t_i)$. The last case is that one $M_A(t_i)$ corresponds to multiple $M_B(t_j)$. In this case a spline interpolation of $M_A(t_i)$ and its nearest before and after neighbors determines the values for $\tilde{M}_A(t_j)$. This warping procedure is performed on each DOF independently. A diagram of this process can be found in Figure 3 below.

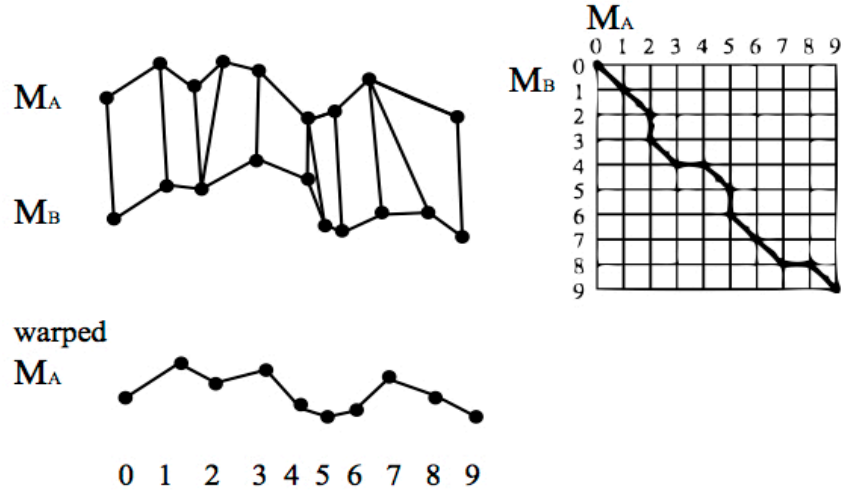


Figure 3 Time Alignment of M_A to M_B

3.4 ANALOGIES ALGORITHM

After M_A and $M_{A'}$ are warped and aligned to M_B , the three motions are of the same temporal length, eliminating any rhythm differences in the motions. The provided motions are then used to estimate parameters for the transformation from M_B to $M_{B'}$. Note that \tilde{M}_A and $\tilde{M}_{A'}$ are represented as the alignment motions and the alignment curves $\mathcal{S}_A \rightarrow \mathcal{B}$ and $\mathcal{S}_{A'} \rightarrow \mathcal{B}$ are respectively represented as well.

A motion sequence is treated as a space-time curve in motion-space. Since handling the entire motion sequence as an analogy problem is difficult due to the high-dimensionality of the entire motion sequence, projecting each DOF and processing them independently simplifies this issue. While some synchronization is lost there is greater

accuracy for the overall resulting motion. For each DOF the transformation is computed as:

$$\tilde{\mathbf{M}}_{A'}(t_i) = \mathbf{a}(t_i)\tilde{\mathbf{M}}_A(t_i) + \mathbf{b}(t_i) \quad (3)$$

where t_i is the frame index and the parameters \mathbf{a} and \mathbf{b} are vectors that measure scale and offset of a linear transformation. These two parameters are used to discover the differences between the two motions.

The original representation of this algorithm is from Witkin and Popovic [1995]. The main differences between their algorithm and the one presented in this paper is that the motions have been warped, so there is no need to include this warp factor into the equation at this time, and that they sample a few key poses defined by the user, while in this paper the entire motion is sampled.

3.5 ESTIMATION

Equation 3 can be solved directly, however \mathbf{a} and \mathbf{b} are sensitive to noise, resulting in a naïve solution. To improve the distributions of \mathbf{a} and \mathbf{b} , the following objective function (4) is minimized:

$$E(\mathbf{a}, \mathbf{b}) = \|\mathbf{a} * \tilde{\mathbf{M}}_{A'} + \mathbf{b} - \tilde{\mathbf{M}}_A\|^2 + \omega_a * \|\mathbf{S}\mathbf{a}\|^2 + \omega_b * \|\mathbf{S}\mathbf{b}\|^2 \quad (4)$$

where $\tilde{\mathbf{M}}_{A'}$ is the diag. ($\tilde{\mathbf{M}}_{A'}$) and \mathbf{S} is a diagonal matrix that approximates first derivatives as shown below.

$$\mathbf{S} = \frac{1}{2} \begin{bmatrix} -2 & 2 & & & & \\ -1 & 0 & 1 & & & \\ & \ddots & \ddots & \ddots & & \\ & & -1 & 0 & 1 & \\ & & & -2 & 2 & \end{bmatrix} \quad (5)$$

The smoothness terms $\|\mathbf{S}\mathbf{a}\|^2$ and $\|\mathbf{S}\mathbf{b}\|^2$ are normalized by the constants ωa and ωb . There is a tradeoff between the accuracy of the linear approximation and the smoothness of the two parameters. A higher ωa means more smoothness in the scale factor over time. This means that the difference function is sampled more for a better fit, making the resulting motion curve more accurate. A higher ωb means more smoothness in the overall gait, flattening the motion curve, and resulting in a loss of fidelity but filtering out any outliers in the data. In this thesis setting $\omega a = 2 \times 10^6$ and $\omega b = 2$ allows for a high level of fidelity while filtering out data noise. These parameter values were iteratively searched for and the above values were found to be the best fit for the system. To solve Eq. 4 setting $\delta E / \delta a = \delta E / \delta b = 0$ reformulates the equation to:

$$\begin{bmatrix} \tilde{\mathbf{M}}_{A'}^T \tilde{\mathbf{M}}_{A'} + \omega a \mathbf{S}^T \mathbf{S} & \tilde{\mathbf{M}}_{A'}^T \\ \tilde{\mathbf{M}}_{A'}^T & \mathbf{I} + \omega b \mathbf{S}^T \mathbf{S} \end{bmatrix} \begin{bmatrix} \mathbf{a} \\ \mathbf{b} \end{bmatrix} = \begin{bmatrix} \tilde{\mathbf{M}}_{A'}^T \tilde{\mathbf{M}}_A \\ \tilde{\mathbf{M}}_A \end{bmatrix} \quad (6)$$

Using Gaussian Elimination, the above linear system can be solved for \mathbf{a} and \mathbf{b} .

The above equation is identical to that used in Wu et al. [2008].

3.6 TRANSFORMATIONS ALGORITHM

In Section 3.5, transformation parameters \mathbf{a} and \mathbf{b} were found. Those parameters can then be applied directly to \mathbf{M}_B to generate a new motion. However, since the sequences are all aligned it is assumed that $\mathbf{M}_{B'}$ has also been aligned to \mathbf{M}_B as well and therefore is actually a warped motion, $\tilde{\mathbf{M}}_{B'}$. Again, each DOF is processed independently.

$$\tilde{\mathbf{M}}_{B'}(\mathbf{t}_i) = \mathbf{a}(\mathbf{t}_i)\mathbf{M}_B(\mathbf{t}_i) + \mathbf{b}(\mathbf{t}_i) \quad (7)$$

3.7 INVERSE TIME ALIGNMENT

Similar to the process described in Wu et al. [2008], the target motion $\tilde{\mathbf{M}}_{B'}$ is not the final desired result. As $\tilde{\mathbf{M}}_{B'}$ is aligned to motion \mathbf{M}_B like all other sequences, it is necessary to invert this alignment to get $\mathbf{M}_{B'}$.

The key to recovering the timing is in the time-alignment curve $S_B \rightarrow B'$ which aligns \mathbf{M}_B to $\mathbf{M}_{B'}$. However, such curve does not exist as it is impossible to find without first knowing $\mathbf{M}_{B'}$. By treating the time-alignment curves as an extra DOF of the motion, this problem can be solved. As earlier, \mathbf{a} and \mathbf{b} are solved for however this time replacing $S_{A'} \rightarrow B$ for $M_{A'}$ and $S_A \rightarrow B$ for M_A such that:

$$S_{A' \rightarrow B}(t_i) = a(t_i)S_{A \rightarrow B}(t_i) + b(t_i) \quad (8)$$

and

$$S_{B' \rightarrow B}(t_i) = a(t_i)S_{B \rightarrow B}(t_i) + b(t_i) \quad (9)$$

$S_{B' \rightarrow B}(t_i) \equiv t_i$ because there is a one to one ratio. By using the equations defined previously, (8) and (9), it is possible to solve for $S_{B' \rightarrow B}$. However, $S_{A \rightarrow B}(t_i)$ and $S_{A' \rightarrow B}(t_i)$ may not be uniformly sampled, or may have different lengths. To overcome this, $S_{A \rightarrow B}(t_i)$ is first aligned to $S_{A' \rightarrow B}(t_i)$ before determining the temporal transformation.

With $S_{B \rightarrow B'}$ found the inverse alignment curve can be obtained according to the following:

$$S_{B \rightarrow B'} = \{(t_i, t_j): \text{where } (t_j, t_i) \text{ is an element of } S_{B' \rightarrow B}\} \quad (10)$$

It is also important to ensure that the curve $S_{B \rightarrow B'}$ satisfies the constraints of continuity, causality, and slope limitation, similar to the constraints determined by Kovar et al. [2003]. By warping $\tilde{M}_{B'}$ with the inverse of $S_{B \rightarrow B'}$, $M_{B'}$ is produced.

3.8 POST PROCESSING

Given motions without any marker errors, occlusions or identity switching, and neutral gaits, a stylistic motion can be created. However, there may be a few artifacts that do not satisfy kinematic, or physical, constraints. The most common of these artifacts is foot skate, where the foot slides or skates around on the ground instead of staying in one place during a footplant. Kovar et al. [2002b] provided an efficient method to clean up this problem. Using his method any artifacts in the synthesized motion can be cleaned.

4. IMPLEMENTATION

4.1 MOTION CAPTURE

The motion analogy system described in this thesis is implemented in Python programming language and Autodesk Maya 2012, a 3D software package. Motion Capture data was obtained using Vicon Nexus, a motion capture system, and Autodesk MotionBuilder, an accompanying software package (Autodesk Inc.). These specific programming languages and software were used due to their ease of use and availability, but other choices of software could be substituted. The motion analogy method is designed such that it can be adapted to a variety of programming languages and implemented with most commercial 3D animation software packages. For more details, reference the program architecture and process in Appendix A.

The marker placement used in this thesis is only one of many possible combinations. However, for the use of this work and others a standard placement was developed. A marker placement for bipeds can be found in the Vicon 512 manual. Modifications to the placement and marker names were made to standardize the marker placement for canines (Woolard, 1995). A diagram of the marker set used in this thesis is available in Appendix B.

Markers (63) were necessary on each joint so that all three rotational DOFs were obtained and to compensate for occlusions that occur naturally during capturing. Certain physical attributes, such as the width of the stifle, were measured as well. These measurements serve as input to calculate the actual joint centers, as the markers

themselves were only placed on the skin. A complete list of these attributes can in Appendix B.

Vicon Nexus and Autodesk MotionBuilder enabled the extraction of raw motion capture data. This data came in the form of marker trajectories through 3D space, or x, y, and z positional values. Vicon Nexus allows for the capture and cleaning, of filling occlusions and assigning identities to the markers, of the marker trajectories, which are then exported as a .C3D file, a binary file format .C3D cannot be parsed so MotionBuilder converts the .C3D file to a .FBX file format, which can be read natively into Maya (Autodesk Inc.).

Once the marker trajectories are imported into Maya, a representation of the subject's skeleton is constructed using a python script. Using the measured attributes from before, mathematical approximations of the joint centers could be calculated. With these joint centers, the approximate skeleton and motion was constructed using built in Maya joint definitions and solvers. An example of the constructed skeleton is shown below in Figure 4.

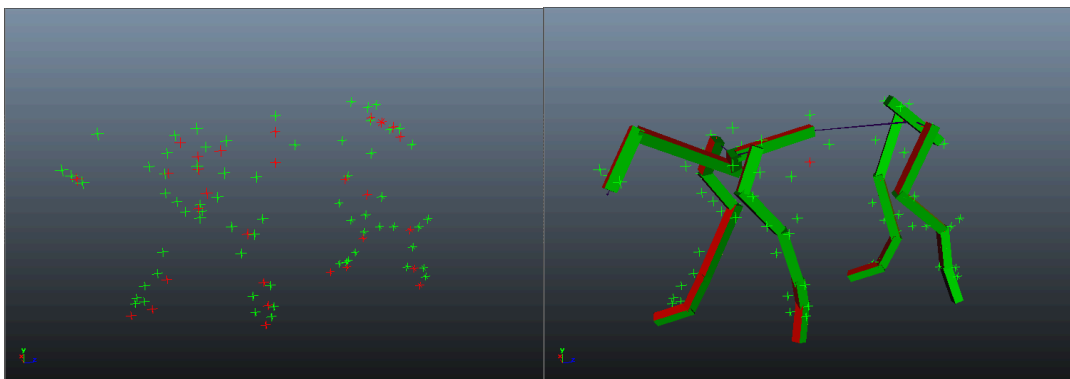


Figure 4 Skeleton Construction from Marker Trajectories

4.2 MOTION ANALOGY

Once the animation data is extracted it is assembled for the analogies operations, performed using Python in Autodesk Maya. Three full strides of data are ideal for comparison. Three strides are necessary to ensure that the middle stride is completely clean of any boundary noise. This middle stride can then be used for further analysis without fear of noise contamination. Sometimes it is impossible to get three full strides due to factors like immature subjects or compromising actions, such as transitioning gaits. When this is the case, the best solution is to overshoot the boundaries of a single stride to allow for an elimination of boundary noise and provide a single clean complete stride for comparison.

5. RESULTS

Motion capture data was collected and provided by the College of Veterinary Medicine at Texas A&M University using the capture method described in Section 4. Each canine skeleton comprises of 23 joints with 78 DOFs. Two sample cases of the differences between the healthy motion of a single breed (A) and an unhealthy motion of that same breed (A') are compared. The system developed in this thesis then allows the application those differences to the healthy motion of a new breed (B). The components of the motions differ in many ways, including style, speed and path. Full videos are provided as supplemental files to this paper.

Say we look at two case studies.

5.1 CASE STUDY 1: HIP DYSPLASIA

This case study demonstrates the application of motion analogies between a healthy Labrador, a Labrador with hip dysplasia, and a healthy German Shepherd to synthesize a German Shepherd with hip dysplasia. Clinical signs of hip dysplasia vary from dog to dog and may include hind limb lameness, “bunny hopping,” a swaying gait, a narrow stance, hip pain, atrophy of the thigh muscles, hypertrophy of the shoulder muscles and reduced hip joint motion (Demko and McLaughlin [2005]). This case study has a single subject for each motion, therefore the system operates on the assumption that each motion given is the standard for that motion, i.e. the hip dysplasia motion is the standard of hip dysplasia.

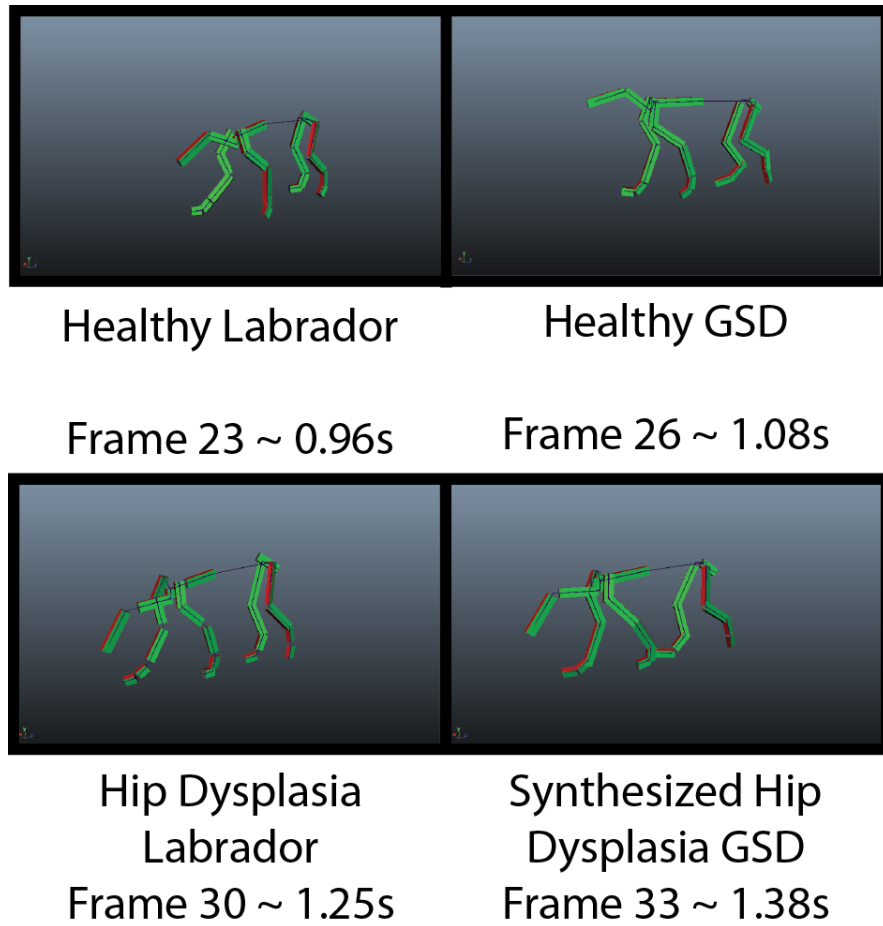


Figure 5 Hip Dysplasia Comparison

Figure 5 illustrates single motion capture frames of a normal Labrador dog, a Labrador (Lab) afflicted with hip dysplasia, a healthy German Shepherd dog (GSD) and a synthesized motion for a German Shepherd with hip dysplasia. Notice the common characteristics between the measured Labrador with hip dysplasia compared with the synthesized German Shepherd with hip dysplasia. For example the Labrador with hip dysplasia elevates the pelvis and lowers the front end. These characteristics are reflected in the synthesized German Shepherd with hip dysplasia.

The hip dysplasia synthesized is not the same as that on the Labrador because the analogies model only extracts the differences and eliminates the common features that appears in both the Labrador and the German Shepherd dog. Figure 6 shows the motion curves of a single DOF, in this case the left femur rotation x , or twist, DOF. As shown, the synthesized motion curve is not a copy of the Labrador's motion, but characterized by the differences between the healthy motion and the motion with hip dysplasia.

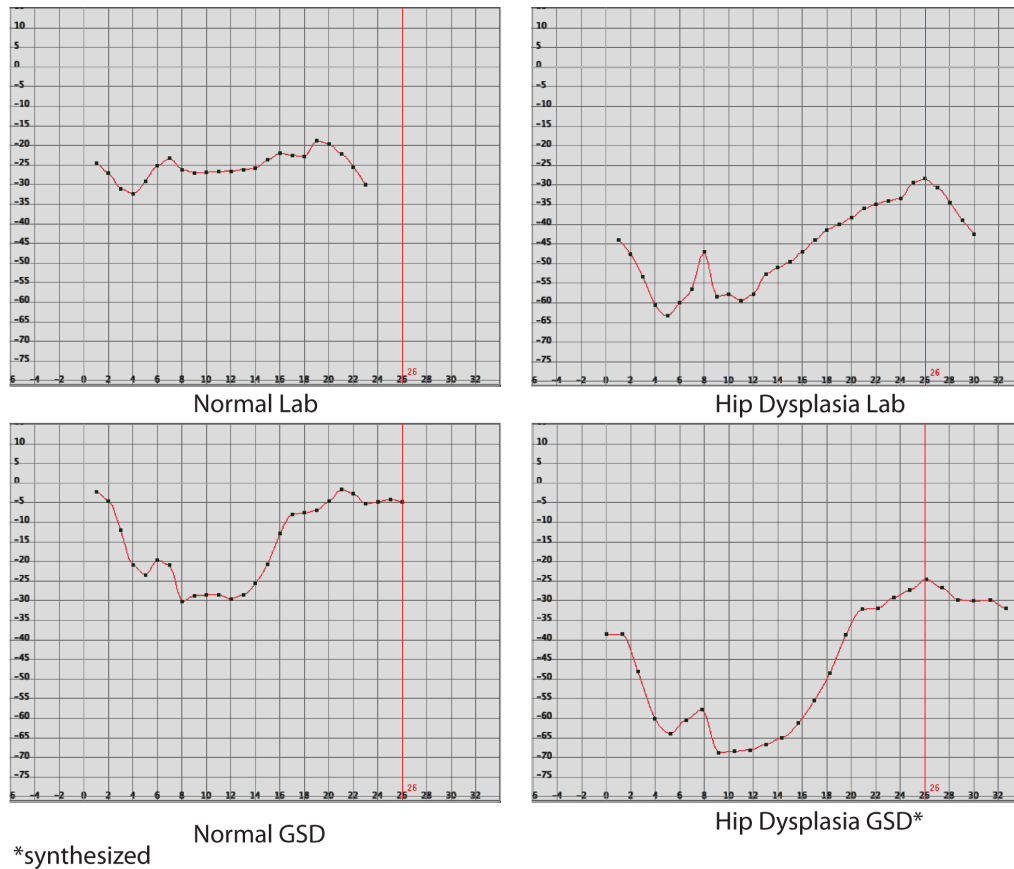


Figure 6 Left Femur Twist Animation Curve Diagram

5.2 CASE STUDY 2: MUSCULAR DYSTROPHY

Demonstrated here is a sample of analogies between a healthy Golden Retriever, a Golden Retriever with muscular dystrophy (MD), and a different Golden Retriever to synthesize that Golden Retriever with muscular dystrophy as if they follow the progression of the standard. MD is not diagnosed on an orthopedic level but some symptoms exhibit physically. Those include, but are not limited to, a slower gait, smaller stride length, increased stifle joint extension and decreased hock flexion with the hock joint being overall less mobile than healthy canines [Barthélémy et al., 2011]. This sample has multiple subjects for each motion or multiple motions for each subject and as such there is an assumption that each motion given is the standard of that motion. There are two healthy motions and three unhealthy motions for this sample. Since there is more than one motion the analogy is performed on all possible combinations.

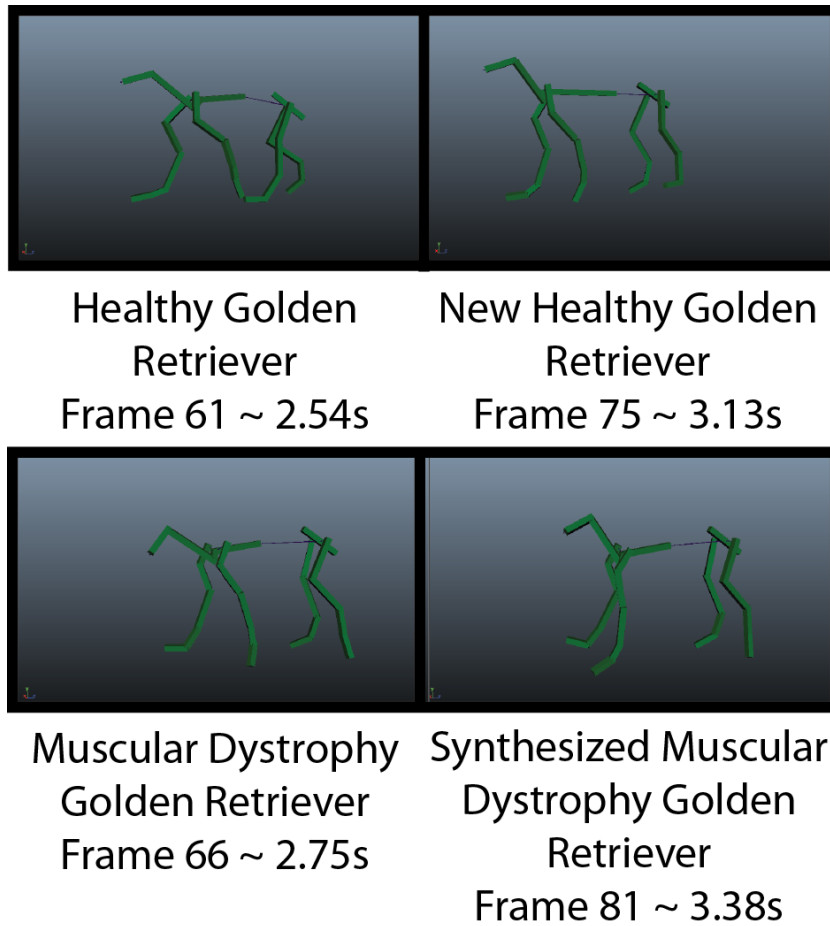


Figure 7 Muscular Dystrophy Comparison

Figure 7 above shows a single analogy combination. Notice that not only are the physical characteristics shown but that rhythm and temporal aspects are also prevalent. The lengths of the motion curves of the dogs with MD are longer than those without, however, the two MD motions, captured and synthesized, are not the same length. Figure 8 below shows this effect in the motion curves of a single rotation Z DOF.

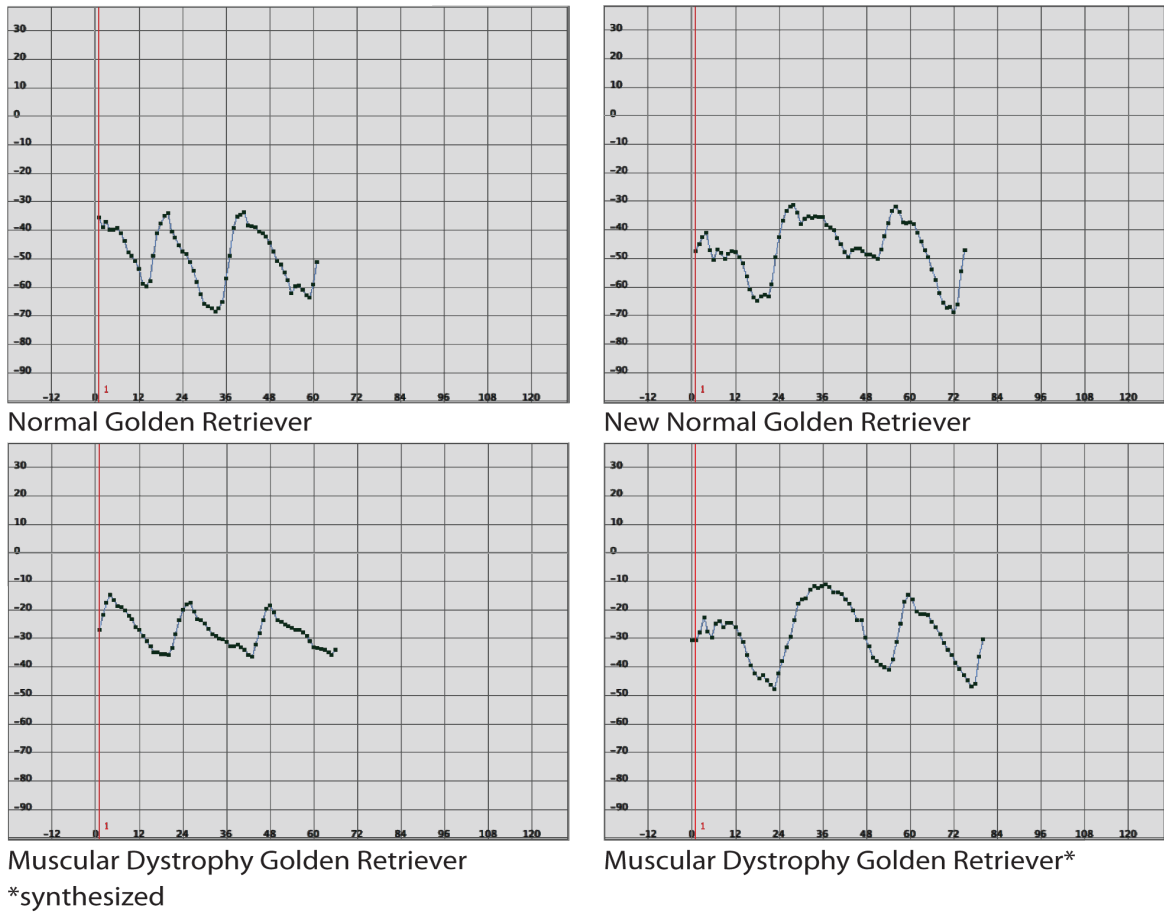


Figure 8 Left Femur Extension/Flexion (Rotation Z) Animation Curve

5.3 LIMITATIONS AND FUTURE WORK

The system has limitations. For example, motion analogies are dependent on providing accurate input data free of noise. This means that the captured data needs to be of good quality otherwise more and more artifacts appear. Also the current system is limited to performing analogies between similar motions and motions that have a common footfall pattern. For example, the system cannot perform an analogy between a

diagonal symmetrical gait and a transverse asymmetrical gait because the diagonal symmetrical gait has a footfall pattern of LH/LF/RH/RF while the transverse asymmetrical gait has a footfall pattern of LH/RH/LF/RF as shown below in Figure 9.

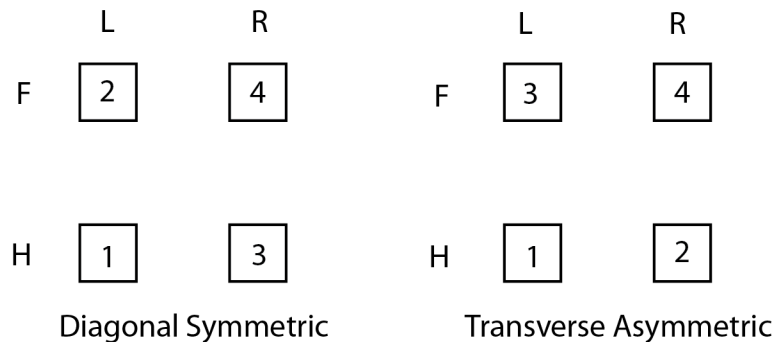


Figure 9 Diagonal Symmetric and Transverse Asymmetric Gait Footfall Pattern

This system also only takes a single motion for each of the healthy and unhealthy motions. With only a single motion per input it is difficult to get an accurate representation of the orthopedic disease or injury. However, if the goal is to compare a subject to multiple motions, the input motions of that disease or injury need to be normalized first. Further work is needed integrating an algorithm that could take multiple motions for a single input and output the standard.

Also, there is currently no user interface or easy access to this system for veterinarians as the system is currently implemented in Autodesk MAYA 2012. Making this system available and building a larger database of motions would serve as a good next step. While these extensions would result in a more robust system, they are out of the scope of the current project and are left for future work.

6. CONCLUSION

In this thesis, a motion analogy system was developed that specializes in synthesizing abnormal gaits and applying them to virtual canines. The methods developed are intended to be applicable to a wide range of abnormal gaits and breeds of dogs and eventually could be applied to other quadruped digitigrades. With the addition of new subjects and with a limited amount of capture work, this new system has the capability to generate new motions for that subject. The system successfully separated the characteristics of each motion in a just a few test cases and such parameters can be further analyzed.

This model is abstract enough that it can be used for any type of similar motions. While this thesis specifically concentrated on dogs walking and the differences between healthy and unhealthy, the system can handle any type of similar motions and skeletons. As such this system can be used to apply variations of motions between various subjects and with further work become even more robust.

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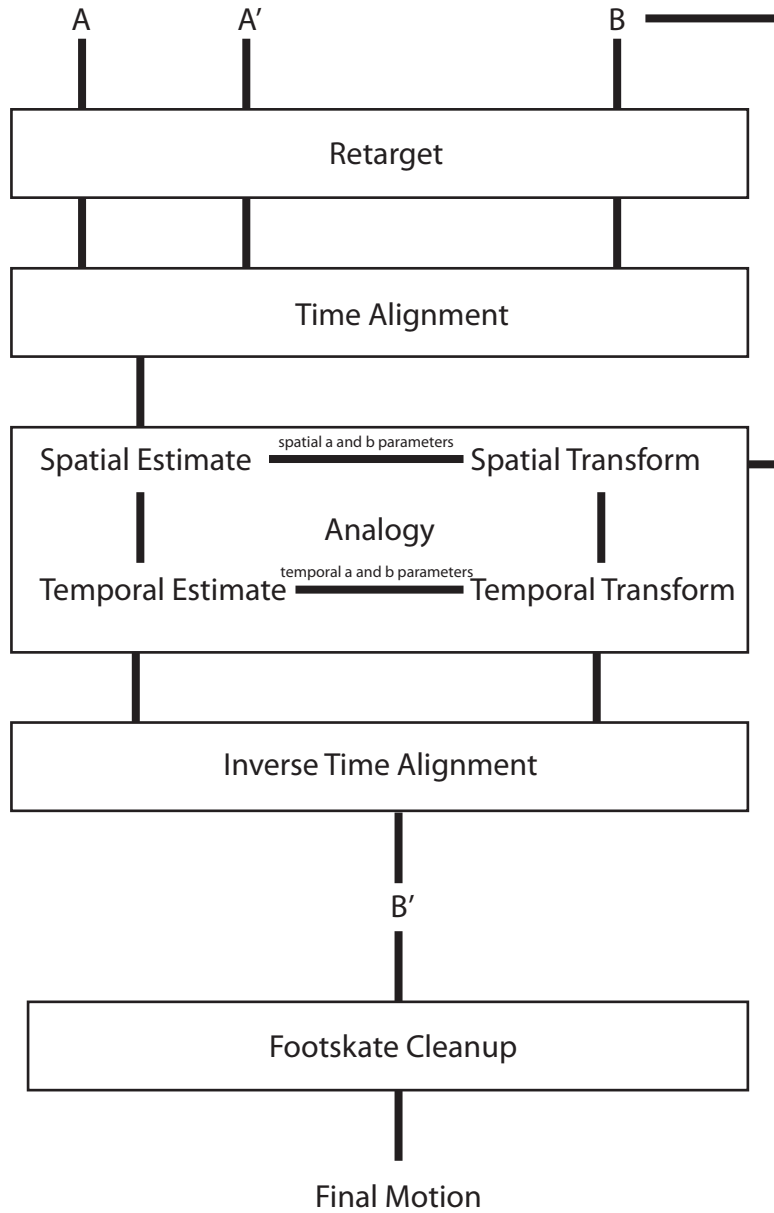
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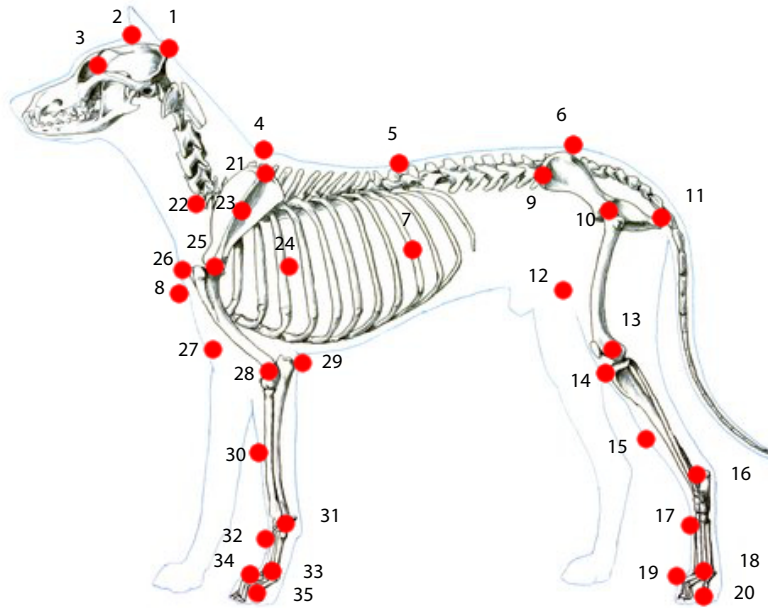
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APPENDIX A: PROCESS DIAGRAM AND SAMPLE CODE



APPENDIX B: MARKER SET AND MEASUREMENTS



Marker Diameter: 9.5 mm

Markers:

Medial

1. EOP
2. CRAN
3. L_EYE (R_EYE)
4. WITH
5. TL
6. SCRM
7. ASYM
8. MANU

Pelvic Limb

9. L_ILI (R_ILI)
10. L_GRTRO (R_GRTRO)
11. L_ISCH (R_ISCH)
12. L_MFEM (R_MFEM)
13. L_LEPIF (R_LEPIF)
14. L_TIBCR (R_TIBCR)
15. L_MTIB (R_MTIB)
16. L_LMAL (R_LMAL)
17. L_MTAR (R_MTAR)
18. L_L5MT (R_L5MT)
19. L_DRPAW (R_DRPAW)
20. L_LRDIG (R_LRDIG)

Thoracic Limb

21. L_DSCAP (R_DSCAP)
22. L_CLAV (R_CLAV)
23. L_MSCAP (R_MSCAP)
24. L_TRIC (R_TRIC)
25. L_ACRO (R_ACRO)
26. L_GRTUB (R_GRTUB)
27. L_MHUM (R_MHUM)
28. L_LEPIH (R_LEPIH)
29. L_OLE (R_OLE)
30. L_MRAD (R_MRAD)
31. L_STYL (R_STYL)
32. L_MCARP (R_MCARP)
33. L_L5MC (R_L5MC)
34. L_DFP AW (R_DFP AW)
35. L_LFDIG (R_LFDIG)

Physical Measurements (mm):

- Elbow Width
- Carpus Width
- Paw Width (Front and Back)
- Stifle Width
- Tarsus Width
- Paw Length (Front and Back)