

ANTHROPOMETRY FOR COMPUTER GRAPHICS

HUMAN FIGURES

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Contents

1	Introduction	1
2	Anthropometry Issues	1
3	Implementation of Anthropometric Scaling	2
4	Joints	5
4.1	Monaxial (or Uni-Axial) Joints (1 Degree of Freedom)	5
4.2	Bi-Axial Joints (2 Degrees of Freedom)	5
4.3	Tri-Axial (or Multi-Axial) Joints (3 Degrees of Freedom)	5
5	Joint Limits	6
6	Mass	6
7	Moment of Inertia	7
8	Segment/Body Volume	7
9	BODY.FIG	8
10	BODY DESCRIPTION FILES	8
10.1	Segment Variable Descriptions	8
10.2	Additional Measurements	13
10.3	Skin fold measurements	14
10.4	Somatotype	15
10.5	Mass	16
10.6	Joint Names	16
11	User Interface	20
11.1	GIRTHFUN	20
11.2	JACK Menus	21
11.3	MEX Window Menus	21
11.4	Spreadsheet Anthropometry Scaling System (SASS)	21
12	SASS: The Spreadsheet Anthropometry Scaling System	21
12.1	Getting Started	22
12.2	Anthropometric Spreadsheet	22
12.2.1	Anthropometric Group Status	22
12.2.2	Standard (Global) Data	22
12.2.3	Data Section for Girth, Joint Limits, and Center of Mass	24
12.2.4	Command Menu	25
12.3	Database Query Spreadsheet	29
12.3.1	Summary Data Section	29
12.3.2	Query/Selected List Section	29
12.3.3	Command Menu	29
12.4	Display Anthropometric Data for Real Person	37
12.5	Exit SASS	39
13	Biostereometric Data	39
13.1	Biostereometric body model	40
13.2	Biostereometric data tiling	40
13.3	Establishing joint centers in the biostereometric data	40

14 Open Issues	43
14.1 Joint motion for spherical joints	43
14.2 Field of view	44
14.3 Joint centers in complex human figure models	44
15 Results and examples of human figure model	44
16 Future Needs	47
16.1 Dynamics Related Factors	47
16.2 Anthropometry Related Factors	47
16.3 Biostereometric body model improvements and extensions	48
17 Appendices	50
A Body Segment and Joint List	50
B Male Girths	53
C Female Girths	54
D Figure definition file, BODY.FIG	55
E Segmented torso definition file	66
F Sample Figure Description File, MALE50.FIG	68
G Joint motion variable list	72
H Male Joint Limits	74
I Female Joint Limits	75
J JLIMITS.H	76
K Mass Values	79
L Center of Mass	80
L.1 Determination of the center of mass locations	80
L.2 The Database	82
M List of Psurfs – Skinnybody	84
N List of Psurfs – Polybody	85
O “An Anthropometric Database for Computer Graphics Human Figures”	86
P Biostereometric Figure File	89
Q Fields of the Anthropometric Database	95

List of Figures

1	Polybody model male and female 50 th %ile figures.	3
2	Polybody and skinnybody male 50 th %ile figures.	4
3	Sample Anthropometric Spreadsheet for Girth.	23
4	Anthropometric Spreadsheet Screen Layout.	24

5	Sample Anthropometric Spreadsheet for Strength.	26
6	Command Menu for Anthropometric Spreadsheet.	27
7	SASS Statistics Data File Format for Girth, Joint Limits, and Center of Mass.	28
8	SASS Statistics Data File Format for Strength.	28
9	Sample Database Query Spreadsheet.	30
10	Database Query Spreadsheet Screen Layout.	31
11	Command Menu for Database Query Spreadsheet.	31
12	Sample Database Input File for Girth.	34
13	The Sequence of Pop-up Menus Used in the Sample Query.	38
14	Biostereometric figures: female as contours (original data); male is tiled and given joint spheres.	41
15	Polybody model range of male figure sizes	45
16	Polybody model range of female figure sizes	46

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Abstract

Anthropometry as it applies to Computer Graphics is examined in this report which documents the Anthropometry work done in the Computer Graphics Research Laboratory at the University of Pennsylvania from 1986 to 1988. A detailed description of the basis for this work is given along with examples of the variability of computer graphics human figures resulting from this work. Also discussed is the unique and versatile user interface developed to allow easy manipulation of the data used to describe the anthropometric parameters required to define human figure models. The many appendices contain the specifics of our models as well as much of the data used to define the models.

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1 Introduction

This technical report is a compilation of the work done at the University of Pennsylvania's Computer Graphics Laboratory in anthropometry for computer graphics human figures and related areas since 1986. This report documents and explains the reasoning used and assumptions made during this work and when putting many of the pieces of data into place.

Detailed descriptions of the implementation and use of the many factors involved in anthropometric scaling are provided. These descriptions, hopefully, will provide a sound and clear basis for understanding the work which has been done and how the information is, can, and should be used. An itemized list of the required data is included. The specific details of the measurements used and the actual data values are found in the many appendices.

A unique and extremely useful user interface has been developed to work with this information. A brief introduction to this interface, the Spreadsheet Anthropometry Scaling System (**SASS**), developed by Richard Quach, is given here. **SASS** provides the ability to use, review, and modify the individual data items needed for the description and depiction of a human figure for computer graphics systems. Diagrams of human figures are included to show the variability of the human figures producible.

2 Anthropometry Issues

Anthropometry, the science of human body measurement, has been an area of interest throughout history [LOH88]:

In his authoritative book "A History of the Study of Human Growth," Professor Tanner writes that the ancient Greeks, as well as sculptors and painters of the Renaissance, measured the human body to estimate body proportions and, thus, reproduce life-like images of varying sizes. Interest in absolute size developed later in the 17th and 18th centuries out of military concerns. The European armies preferred taller soldiers, and recruiting officers became anthropometrists. Interest in scientific study of growth and in the relative importance of nature versus nurture in explaining human variability has been pronounced since the 19th century.

Thus, anthropometry as we know it today has been an active area of research since the 19th century. The vast majority of the work in "modern" anthropometry has been done by Anthropologists who were studying various populations of people and the effects of some environmental factor on the population. While there are studies dating back to the mid- to late- 1800's, more recent studies covering groups of adults (i.e. populations) from around the world are summarized in the *Anthropometry Source Book* [NAS78]. Its two volumes have become one of the foundation sources for contemporary anthropometry.

Anthropometric studies differ greatly in the number and kind of measurements selected. They all report a statistical analysis of the values of each measurement giving at least a median with standard deviation and the maximum and minimum values. The studies typically report the above values along with a breakdown at selected percentiles of the population, typically 1st, 5th, 25th, 50th, 75th, 95th and 99th percent of the population.

Some of the data found in these studies was used in the *NASA Man-Systems Integration Manual* [NAS87], as the basis for the estimated measurements for male and female astronauts in the year 2000, using the body dimensions of American males (both blacks and whites) and Japanese females. It is felt that these populations provide the maximum range in body sizes in the developed world today since the American male is among the largest of males and the Japanese female is the smallest of females. There is a growth rate factor⁴ which is used to adjust the values in projecting to the year 2000.

The measurements selected for inclusion in the *NASA Man-Systems Integration Manual* [NAS87], were chosen to meet the various needs of NASA and were not intended to be a complete set of measurements for all purposes or for all possible users. These measurements served as the basis for the human figure model we developed but are not complete enough to totally describe our human figure model. This is due to

⁴refer to Figure 3.2.3.3-1, Assumed Secular Growth Rate of Stature [NAS87]

either data missing from the *NASA Man-Systems Integration Manual* [NAS87] or to measurements which were not included in that report. Most of the missing values can be found in the *Anthropometry Source Book* [NAS78]. There are a number of measurements required for our model which were not found in any of the resources available to us. Where this occurred intelligent estimates have been made based upon data values from closely related measurements (possibly from a different population) or by calculating the values from other measurements. In no case were the undefined values set arbitrarily.

3 Implementation of Anthropometric Scaling

A computer program, **SASS** – Spreadsheet Anthropometry Scaling System – was written which will generate the dimensions of each segment of a human figure based upon population data supplied as input. The model we use currently consists of thirty-one (31) segments or body structures, of which twenty-four (24) have a geometrical representation (see Appendix A for the complete list). For each segment or body structure with geometrical representation, there are three measurements which are needed, the segment (or structure) length, width, and depth (or thickness). Therefore, we require a minimum of seventy-two (72) measurements be made to describe the physical dimensions of our human figure. The list of measurements upon which we base our human figure can be found in Appendix A. These measurements were compiled from the *NASA Man-Systems Integration Manual* [NAS87] and the *Anthropometry Source Book, Volume II* [NAS78].

The geometric primitive we use is a polyhedral surface (*psurf*). Using *psurfs* we can easily describe the nodes or vertices, edges, and faces which will result in a displayable shape to represent each segment. This representation of segments forms the foundation for the human figure models which we currently use. See Figures 1 and 2 for examples of the “polybody” and “skinnybody” models.

Each *psurf* for the various segments is stored in a Unix archive file, in normalized format where the Z (length) dimension ranges from zero (0) to positive one (+1), and the X (depth) and Y (width) dimensions range from negative one (−1) to positive one (+1). This normalized format is an integral part of the variability of human figures available.

In order to display these *psurfs*, using either real measurements for a person or percentile measurements for some specifiable population, the *psurfs* must be scaled. The scaling factors for each dimension, x, y, and z, can be specified for each *psurf*. These scaling factors will be used when the figures (and their *psurfs*) are displayed using **JACK**, an interactive interface to 3-D articulated models ([PHI88a], [PHI88b], and [PHI88c]). **JACK** uses the **PEABODY** language syntax to represent figures (human and any other geometrically definable, usually segmented) which are to be displayed or manipulated. **PEABODY** expects a file to be input which defines the relationships of each *psurf* and allows for the definition of joints, constraints, and sites (features or attachment points) for the figure. For the human figure the file “**BODY.FIG**” contains the required definitions. (See Section 9 and Appendix D for details). Since the **PEABODY** syntax is flexible and extensible, the human figure definition can be extended to include additional factors as they become needed or available. Segment dimensions (as *psurf* scale factors), segment masses, segment centers of mass, joint limits, and segment moments of inertia are currently defined in addition to joints, constraints, and sites. These items are identified by meaningful variable names within the “**BODY.FIG**” file. The addition of segment strength values is expected in the very near future. See Appendix D for the current “**BODY.FIG**” file.

The values for the **PEABODY** descriptors are input to **JACK** from a file, (“*.fig”), called a body definition file. Its name is typed by the user or else selected directly from a **JACK** menu. This latter option is good only for some predefined, default body models. An example of a body definition file is “**MALE50.FIG**” which contains the data representing a 50th percentile male figure for the NASA crewmember trainee population. The current “**MALE50.FIG**” file can be found in Appendix F. All such body definition files defining human figures will have structure identical to “**MALE50.FIG**” but with different values for the variable names listed. These body definition files also identify the *psurf* archive file to use (“**SKINNY.A**” for a skinny body figure), the **PEABODY** language file identifying how the *psurfs* relate to each other and other pertinent information, (i.e. “**BODY.FIG**” for a human figure), along with all values necessary for the human figure. Each of these values are assigned to a corresponding variable name which is found in the “**BODY.FIG**” file. In this way, the body is completely defined and stored in the data structures initialized when “**BODY.FIG**” is read in by **JACK**.

Figure 1: Polybody model male and female 50th percentile figures.

Figure 2: Polybody and skinnybody male 50th percentile figures.

Body definition files containing the desired values can be created in one of three ways:

1. by manually entering the variable names and values in the proper format (see Appendix F for the sample “**MALE50.FIG**” file),
2. by modifying (editing) an existing file to contain new values, or
3. by running the Spreadsheet Anthropometry Scaling System (**SASS**) which will be discussed in detail in Section 11.4.

In this way, a user can define and describe any number of human figures based upon the **PEABODY** language syntax for use with **JACK**.

4 Joints

At each articulation in the human body a physical joint is found. In order for an articulation to exist, there must be two segments (bones, actually) involved. The joints of the human body have all been named by Biologists (Anatomists) over the years. There often is more than one name for a given joint – the scientific name and the common name. This document uses the scientific name in all cases. In the instance where the scientific name is likely to be unfamiliar to the general public, the common name is mentioned or a description of the joint is given.

There are three different types of joints found in the human body [**TOR75**, page 162], Fibrous joints, Cartilaginous joints, and Synovial joints. Of these three types of joints we are only concerned with the synovial joints (joints with joint cavities). The synovial joints are categorized based upon the shape of the articulating surface of the joint. There are seven sub-types of synovial joints found in the human body ([**BAS76**], pages 78–79, and [**TOR75**], pages 165, 169). These subtypes are:

4.1 Monaxial (or Uni–Axial) Joints (1 Degree of Freedom):

- a. Hinge joints. A convex surface of one bone fits in a concave surface of another bone. This joint allows movement in only one plane, usually extension and flexion, similar to that of a door hinge. Examples are the elbow joint, knee joint, ankle joint, and interphalangeal joints (joints in the toes and fingers).
- b. Pivot joint. A rounded, pointed, or conical surface of one bone articulates with a shallow depression in another bone. The primary motion of this joint sub-type is rotation. Examples are shown by the supination and pronation of the palms, atlas–axis joint (Atlanto–Axial joints located at the very top of the spine), and radioulnar joint (between radius and ulna in forearm).

4.2 Bi–Axial Joints (2 Degrees of Freedom)

- a. Condylod Joints. These are the joints like those at the heads of the metacarpals (hand bones), i.e. the knuckles, which is the best example of this type of joint.
- b. Ellipsoidal joints. The oval-shaped condyle (end) of one bone fits into the elliptical cavity of another bone. This type of joint permits side-to-side and back-and-forth movements (in the principal axes of the ellipse). Examples are shown by the flexion and extension and abduction and adduction of the wrist (radiocarpal) joint.

4.3 Tri–Axial (or Multi–Axial) Joints (3 Degrees of Freedom)

- a. Saddle joint. Both bones in this joint are saddle-shaped, that is convex in one direction and concave in the other. This type of joint is essentially a modified ellipsoidal joint and has more freedom of movement. Saddle joints allow side-to-side and back-and-forth movements as well as rotation. An example is the joint between the trapezium and metacarpal bones of the thumb (carpometacarpal joint of the thumb).

- b. Ball and socket joints. A ball like surface of one bone fits into a cup-like depression of another bone. These joints permit flexion-extension, abduction-adduction, and rotation. Examples are the hip and shoulder joints.
- c. Gliding (or Plane) joints. Bones involved have flat or nearly flat articulating surfaces. Movement can occur in almost any plane, with side-to-side and back-and-forth movements the most common. The movements are always slight. Examples of this type of joint can be found between the carpal (wrist) bones (intercarpal joints), between the tarsal (foot/ankle) (intertarsal joints) bones, between the sacrum (lower end of the spine) and ilium (a hip bone) (the sacro-iliac joint), between the sternum (breast bone) and clavicle (collar bone), between the scapula (shoulder blade) and clavicle, between the individual vertebral arches, at the heads and at the tubercles of the ribs, and at the front ends of the costal (rib) cartilages.

5 Joint Limits

Each joint in the human body has a range of motion (ROM) over which it will allow movement to occur. A joint's range of motion is determined by a number of factors including joint type, muscle size at the joint, muscle tension (tonus) for the muscles at the joint (ie. fitness of the person), ligament stretchability or give, amount of fatigue, and training adaptations for the joint. The term flexibility is frequently used to describe the influence that each of the components listed above has on joint movement.

Joint range of motion (ROM), described in terms of angles, is measured in degrees for each degree of freedom (DOF), that is, each plane in which movement is allowed at a joint. When a joint has more than one degree of freedom, then the range of motion at the joint for each degree of freedom may be variable because one degree of freedom may influence the others. Also, for joints which are influenced by muscles crossing two joints (as in some muscles of the thigh, for example) there may be a two joint dependency on the joint limit.

Our human figure model allows motion at twenty (20) joints which have a total of forty-two (42) DOF. For each DOF two measurements are required, an upper limit and a lower limit, or eighty-four (84) joint measurements for each human figure. A complete list of joint motion variable names and an explanation of which motion each variable name represents can be found in Appendix H. We have chosen to model the joints as simply as possible therefore no two-joint dependency relationships are currently handled. Also, joints with three degrees-of-freedom, such as the shoulder and hip, are modeled using only the three one-plane joint limits which is not really an accurate representation of the joint limits and motions. More research will have to be done to determine the actual three dimensional joint limits for the shoulder and hip joints (for a discussion of this see Section 14. This data may be extractable from the reach data that can be found in Chapter 3 of the *NASA Man- Systems Integration Manual* [NAS87].

The current joint limits are listed in Appendix H for males and Appendix I for females.

6 Mass

Along with stature, mass is among the most common body measures taken. Mass is the sum of the mass of all body segments. There have been a number of studies which have determined that each of the various body segments contributes a certain percentage of the total body mass. In **SASS** a percentage value for each segment's contribution to the total mass is stored. This percentage is applied to the total mass of the figure being modeled to determine the mass of each individual segment. The mass percentages used are average percentile values for a fit male population as would be found in the NASA male crewmember trainees. For the average general population or a population which is skewed to either the small/light weight (like horse racing jockeys) or large/heavy weight (like American Football lineman) these percentages are likely to be different. The segment mass percentages are also likely to be different for female subjects as well.

SASS allows the user to change the mass of a human figure by providing a real mass value or by providing a percentile value based upon the current population.

The mass data listed in Appendix K is for male subjects only. Female segment mass data could not be determined due to insufficient data. The male data is therefore used for both sexes, without adjustment.

The determination of valid female values is an important future need, especially before valid dynamic studies can be performed.

7 Moment of Inertia

The concept of moment of inertia is important when attempting to describe the kinetic behavior of a human figure. These values are needed when determining the motion of a figure under the influence of forces (both external and internal), moments, and instantaneous transfers of momentum (i.e. collisions). When considering human figure modeling the common forces and moments effecting the human figure include, but are not limited to:

1. gravity, which acts at the center of mass of each segment with a magnitude proportional to the segment's mass.
2. internal forces generated by muscles, which in fact act as a distributed force along some length of the segments but can be modeled as a driving moment applied at the joint.
3. reaction forces, generated by the figure's surroundings, for example the normal forces and friction forces applied to the figure's hand by the counter it is leaning on.
4. external forces. For example, other people, weights lifted by the figure, levers the figure attempts to pull, etc.
5. collisions. This usually is modeled as an instantaneous change in velocity of the point on the figure being struck.

The influence of moment of inertia is frequently slight. When not in free fall, (i.e. no astronauts or spring board divers) the most important quantities are mass and center of mass. Gravity so dominates the calculations, that unless the figure is moving very rapidly or much accuracy is desired, rotational inertia effects are probably insignificant. This means we probably do not normally need any inertia information for the segments and can therefore treat them as point masses located at the corresponding center of mass.

In zero gravity situations, however, the inertia data may be very significant. In diving, for example, the actual distribution of mass in diver's arms and legs is crucial in determining rate of rotation and the simple point mass model is probably not an accurate enough estimate for most studies.

8 Segment/Body Volume

Data exists concerning the volume of the human figure. This data comes in two forms — the volume of the entire body and the volume of each segment of the body. Data for the individual segment volumes is found in the *NASA Man-Systems Integration Manual*, Chapter 3 [NAS87].

Our current system does not make use of volume data directly. Even though our model makes use of specific segment dimensions (length, width, and thickness) it does not realistically represent the segment shapes. The volumes theoretically displaced by each segment could be stored and manipulated in the same manner as the other segment attributes. It would also be easy to calculate the actual segment volumes for our models but these values would not accurately represent the real values expected for such volumes. If the use of stereometric data were included then the actual segment and whole body volumes could be accurately calculated from these figures.

The segment and whole body volumes become important when trying to determine space displacement of human figures and when trying to determine the amount of material required for clothing and special

suits. This information can also aid in determining the proper size of straps and spaces where the figures must reach into or move through. A good deal of this type of information can be readily gleaned directly from the segment dimensions.

9 BODY.FIG

Using the **PEABODY** language it is relatively easy to define the structure of any articulated (and segmented) figure. We use a standard human figure definition file using the **PEABODY** language, named “**BODY.FIG**”. “**BODY.FIG**” contains all of the fields required to describe a complete human figure: the segments, joints, constraints, and sites which are required for the human figure definition. “**BODY.FIG**” also provides for scaling the psurf primitives, as well as defining and setting joint limits and segment DOF, segment masses, and segment centers of mass. The current “**BODY.FIG**” file can be found in Appendix D.

10 BODY DESCRIPTION FILES

Segment lengths, segment masses, and joint limits are variable in nature and therefore are defined as variable fields within the figure definition file, “**BODY.FIG**.” The values for these variables are found a related file which also has the extension “**FIG**.” These files are called body description files, an example of which is “**MALE50.FIG**.” The filename proper is arbitrary. Current convention in use for statistically based figures has the filename identify the sex of the subject and the percentile represented, if applicable, when using the “skinnybody” model. For example, “**MALE50.FIG**” should contain a male figure with all 50th percentile values. When using the polybody figure, the name is prefixed with “**PB**” as in “**PBMALE50.FIG**,” which represents a male figure with all 50th percentile values using the polybody human figure model. When defining “real” people, that is creating body description files with values from actual individuals or values which are not all of one percentile, the filename should be as meaningful as possible.

The body description files can be created and stored by **SASS** in **PEABODY** syntax. The files all contain a list of variable names (all the variable names found in “**BODY.FIG**”) with each name set equal to a numeric value. The variable’s units are specified as well. The categories of values included are: segment dimensions (length, width, and depth or thickness), joint limits, segment masses, and segment centers of mass. The current “**MALE50.FIG**” body description file can be found in Appendix F.

The variable names in a body description file for the segment measurements indicate the segment name and the coordinate axis name for the measurement where

1. X is out of the body/segment (in the direction of the normal to the frontal plane) (i.e. depth or thickness),
2. Y is across the body/segment (in the direction of the normal to the saggital plane) (i.e. width), and
3. Z is in along the body/segment (in the direction of the normal to the transverse plane) (i.e. length).

Joint limit variable names contain the joint name, a coordinate axis name for the plane in which the joint measurement moves, and an indication of the direction, positive or negative, of the movement. For all joints a pair of angles are given, the upper limit and the lower limit, which represent movements in the positive and negative directions, respectively, from the standard anatomical neutral position. Joint centers use the same coordinate system as the segments.

10.1 Segment Variable Descriptions.

The measurements required for each segment or structure in our human figure model are described here. The actual body measurement which supplies the data used by our system is indicated. For some variables a choice of measurements is indicated and these options are listed in order of preference. The second or later choices would be used only if the preferred value is unavailable. Such measurements are not exact substitutes for the primary choice as they give values which are often (numerically) noticeably different from the primary. Problems with these alternative measures will usually not be visually noticeable but may be

seen when figures with a mixture of such values are in use. Normally this will not occur unless multiple populations are being used simultaneously since all members of a given population are based upon the same statistical values.

Note: The numbers given in parenthesis for each body measurement is the number used to identify the measurement in the *NASA Man-Systems Integration Manual* and the *Anthropometry Source Book*.

segment name	Variable Name	Body measurement used to supply value
HEAD	boheadx	head breadth (#427)
	boheady	head length (#441)
	boheadz	menton to top of head (#595)

The Top Head segment provides the ability to change the shape of the head and face.

Top Head	topheadx	head breadth (#427)
	topheady	sellion to wall (#741) or head length (#441)
	topheadz	sellion to top of head (#739)
Bottom Head	boheadx	face or bizygomatic breadth (#165)
	boheady	sellion to wall (#741) or head length (#441)
	boheadz	face or menton-sellion length (#586)
Eye Socket, Right	reyex	(biocular breadth (#138) - interocular breadth (#500)) / 2
	reyey	set to a constant value of 2.4cm
	reyez	set to a constant value of 2.4cm
Eye Socket, Left	leyex	(biocular breadth (#138) - interocular breadth (#500)) / 2
	leyey	set to a constant value of 2.4cm
	leyez	set to a constant value of 2.4cm
Eye Socket Location	eyelocx	sellion to wall (#741) - (1/2 of eye depth)
	eyelocy	interocular breadth (#500) / 2
	eyelocz	ectocanthus to top of head (#289)
Neck	neckx	neck depth (or thickness)
	necky	neck breadth
	neckz	posterior neck length

The sellion is located at the level of the eyebrows, the menton is the chin, and the ectocanthus is the skin fold of the eye at the side of the head.

The dimensions of the eye sockets was determined from various readings [BOF86]. The diameter of the eye, an approximate sphere, is known to be 2.4 centimeters therefore the eye socket depth and height is set to this value. The eye socket width is calculated by determining the difference between the interocular breadth (#138) and the biocular breadth (#500) divided by two. This allows the width of the eye sockets to vary with head size.

The location of the eye socket, which is roughly shaped as a three dimensional diamond designed to hold the eye ball, is identified by its medial most point. These medial points are equidistant from the bridge of the nose and calculated by determining one-half of the interocular breadth for the x-value. The inner and outer corners of the eyes are assumed to be at the same point above the ground so the location of the ectocanthus is used to determine the z-value for the eye socket location. The y-value is determined to be one-half of the eye depth from the front of the face.

Since the literature does not provide neck depth and neck breadth we had to devise a method by which these measurements could be found. Assuming that the cross-section of the neck is (roughly) circular, the diameter is computed from the circumference. The actual measurements would obviously be preferred.

This procedure would require the use of this additional measurement:

neck circumference (#639)

When the data was being put together for our figure there was no value for posterior neck length available in the *NASA Man-Systems Integration Manual*. Therefore, the diameter value was also used as the neck length. Clearly this situation should be corrected once the proper data becomes available.

TORSO		
Upper/Center	ctorsox	interscye (#506)
	ctorsoy	chest depth (male) (#236) or bust depth (female) (#169)
	ctorsoz	waist back (#921)
Center/Lower	ltorsox	hip breadth standing (#457)
	ltorsoy	abdominal extension depth (#10) or abdominal depth sitting (#6) or waist depth (#939)
	ltorsoz	waist height (#949) – crotch height (#249)

If a psurf is used to represent the upper torso then the following measurements should be used. An upper torso segment allows changing the shape of the torso thereby providing for more figure individuality and variability. It would be possible to provide for a model with variability due to body fat (as in the abdomen) increasing the overall value and reality of the model.

TORSO		
Upper	utorsox	interscye (#506)
	utorsoy	chest depth – males (#236) or bust depth – Females (#169)
	utorsoz	thorax length (C7 – L1 or T1 – T12 distance)
Center	ctorsox	waist breadth (#924)
	ctorsoy	abdominal extension depth (#10) or abdominal depth sitting (#6) or waist depth (#939)
	ctorsoz	abdomen length (L1 – L5 distance)
Lower	ltorsox	hip breadth – standing (#457)
	ltorsoy	buttock depth (#183)
	ltorsoz	pelvis length (S1 – crotch distance)
Clavicle, Right	rclavx	Shoulder Length (#754) (this is a very rough approximation)
	rclavy	set to a fixed value of 1 unit (cm)
	rclavz	set to a fixed value of 1 unit (cm)
Clavicle, Left	lclavx	Shoulder Length (#754) (this is a very rough approximation)
	lclavy	set to a fixed value of 1 unit (cm)
	lclavz	set to a fixed value of 1 unit (cm)

The clavicle measurements, other than length, are really incidental. Length could also be determined by upper torso (or center torso) width divided by two (ctorsoy/2 or utorso/2), depending whether a two or three segment torso is being used. There is no actual data provided in the literature for this length which is why the shoulder length approximation has been used.

Upper Right	Arm,	ruparmx	biceps depth
		ruparmy	biceps breadth
		ruparmz	acromion–radiale length (#751)
Upper Left	Arm,	luparmx	biceps depth
		luparmy	biceps breadth
		luparmz	acromion–radiale length (#751)

We had to devise a method for computing biceps depth and breadth. Starting with the assumption that the shape of the biceps is elliptical, we used the circumference measurement and found the size of the major and minor semi-axes. The following procedure uses an estimate of the ratio of the semi-axes⁵. The upper arm ratio used: $x/y = 17/20$.

Ellipse Axis Procedure:

Let C be the circumference of an ellipse with semi-axes A and B.

$$C = 2 * \text{PI} * \text{sqrt}((A^{**2} + B^{**2})/2) \text{ (approximately).}$$

In our case, C is known, so solving for A and B is possible if their ratio is known. If the ratio of the semi-axes is $K = A/B$, then

$$A = C * K * \text{sqrt}(2 / (K^{**2} + 1)) / (2 * \text{PI})$$

$$B = A / K$$

$K = x/y$ where $x =$ width of segment, $y =$ thickness of segment

This procedure requires the use of these additional measurements:

- biceps circumference, relaxed (#113)
- biceps circumference, flexed (#111)

The relaxed circumference was used in as variable C in the above procedure.

forearm, right	rlowarmx	forearm depth
	rlowarmy	forearm breadth
	rlowarmz	radiale–stylion (elbow–wrist) length (#324) or forearm–hand length (#381) – hand length (#420) or elbow height (#309) – wrist height (#973)
forearm, left	llowarmx	forearm depth
	llowarmy	forearm breadth
	llowarmz	radiale–stylion (elbow–wrist) length (#324) or forearm–hand length (#381) – hand length (#420) or elbow height (#309) – wrist height (#973)

As with the upper arm, the forearm depth and breadth measures are not normally found in the literature so we had to find an alternative method. The procedure outlined above for the upper arm was used for the forearm as well. The lower arm ratio used: $x/y = 3/2$.

This procedure requires the use of these additional measurements:

- forearm circumference, relaxed (#370)
- forearm circumference, flexed (#369)

The relaxed circumference was used as variable C in the above procedure.

⁵The ratio was determined empirically from measurements of members of the Graphics Lab.

Hand, right (palm only)	rhandx	hand breadth (#411)
	rhandy	hand thickness at metacarpal (knuckles) (#423)
	rhandz	palm length (#656)
Hand, Left (Palm only)	lhandx	hand breadth (#411)
	lhandy	hand thickness at metacarpal (knuckles) (#423)
	lhandz	palm length (#656)
Fingers, Right Hand	rfingersx	hand breadth (#411)
	rfingersy	hand thickness at metacarpal (knuckles) (#423)
	rfingersz	hand length (#420) – palm length (#656)
Fingers, Left hand	lfingersx	hand breadth (#411)
	lfingersy	hand thickness at metacarpal (knuckles) (#423)
	lfingersz	hand length (#420) – palm length (#656)
Thigh, right	ruplegx	thigh depth or thigh clearance (#856)
	ruplegy	thigh breadth
	ruplegz	femur length or trochanteric height (#894) – tibiale height (#873)
Thigh, left	luplegx	thigh depth or thigh clearance (#856)
	luplegy	thigh breadth
	luplegz	femur length or trochanteric height (#894) – tibiale height (#873)

Thigh depth and thigh breadth are based on the assumption that the shape of the thigh is (roughly) circular. Using the circumference measurement, we computed the diameter of the corresponding circle. The actual measurements would be preferred.

This procedure would require the use of this additional measurement:
thigh circumference

Lower Leg, Right	rlolegx	calf breadth
	rlolegy	calf depth (#212)
	rlolegz	tibiale length or tibiale height (#873) – ankle height (#64)
Lower Leg, Left	llolegx	calf breadth
	llolegy	calf depth (#212)
	llolegz	tibiale length or tibiale height (#873) – ankle height (#64)

As with the thigh, there was no information available for the depth and breadth of the calf. The algorithm used for the thigh was applied to the calf to compute calf depth and breadth. Clearly, the actual measurements would be preferred.

This procedure would require the use of this additional measurement:
calf circumference, standing (#207)

Foot, Right	rfootx	instep length (#496)
	rfooty	foot breadth at ball (#356)
	rfootz	ankle height (#64)
Foot, Left	lfootx	instep length (#496)
	lfooty	foot breadth at ball (#356)
	lfootz	ankle height (#64)
Toes, Right foot	rtoesx	foot length (#362) - instep length (#496)
	rtoesy	foot breadth at ball (#356)
	rtoesz	foot thickness (at metatarsophalangeal joint)
Toes, Left foot	ltoesx	foot length (#362) - instep length (#496)
	ltoesy	foot breadth at ball (#356)
	ltoesz	foot thickness (at metatarsophalangeal joint)

Since the geometric primitive for the feet have an orientation which is different from the other segments, the measurements are applied differently.

Location of body root off floor	flooroffset	<p>this is the sum of the right ankle height (rfootz), right lower leg length (rllegz), and right thigh length (rulegz). It takes the body root site, which is located at the bottom of lower torso segment, at a height which places the bottom of the feet on the ground plane (bottom of feet height = 0).</p> <p>The right and left sides are normally equal in length so the right side was picked for this task. In the event the right and left sides are unequal, it is possible for the feet to be at different heights, but the right foot will always be on the ground plane.</p>
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10.2 Additional Measurements

There are some additional measurements which are useful and may come in handy in certain situations. A list of these additional measurements follows. Included is a description of how this measurement can be used with our system.

height (stature) (#805)	the height of the subject. Used for the Heath–Carter Anthropmetric Somatotype method.
weight (mass) (#957)	the mass of the subject. Used for the Heath–Carter Anthropmetric Somatotype method.
anterior neck length (#72)	a possible alternative to posterior neck length
neck circumference (#639)	a possible alternative to neck depth and neck breadth if one is following the assumptions described above with the other neck measurements.
chest breadth (#223)	a possible alternative to interscye
waist–front (#949)	a possible alternative to waist back
elbow height (#309)	when used with acromial (shoulder) height (#23), a possible alternative to acromion–radiale length (#751)
acromial (shoulder) height (#23)	when used with elbow height (#309), a possible alternative to acromion–radiale length (#751)
waist height (#949)	used to determine the separation of the torso segments when using a two–segment torso geometry (as our current model does).
thigh clearance (#856)	a possible alternative to thigh depth.
femoral (femur) breadth or knee breadth (#334)	used for the Heath–Carter Anthropmetric Somatotype method or possibly as measure of distal end of thigh and/or proximal end of lower leg.
calf circumference (#207)	a possible alternative to calf depth and calf breadth as described above. Also used for the Heath–Carter Anthropmetric Somatotype method.
ankle breadth or bimalleolar breadth (#134)	Represents the size (width) of the distal end of the lower leg.
heel breadth (#450)	Represents the width of the back of the foot.
biceps circumference, relaxed (#113)	a possible alternative to biceps depth and biceps breadth as described above.
biceps circumference, flexed (#111)	a possible alternative to biceps depth and biceps breadth as described above. Also used for the Heath–Carter Anthropmetric Somatotype method.
elbow breadth or humerus breadth (#293)	used for the Heath–Carter Anthropmetric Somatotype method or possibly as measure of distal end of upper arm and/or proximal end of forearm.
forearm circumference, relaxed (#370)	a possible alternative to forearm depth and forearm breadth as described above.
forearm circumference, flexed (#369)	a possible alternative to forearm depth and forearm breadth as described above.
wrist breadth (#964)	Represents the width of the distal end of the forearm or the proximal width of the hand (palm). May be used when developing a more complete or complex figure.
hand breadth across thumb (#413)	A possible alternative to hand breadth. Valid only if the thumb will be included in the model. Currently, the thumb is not part of the model.

10.3 Skin fold measurements

These measurements are useful when determining body somatotype and body fat levels. The skin folds are standard measurements but were not reported in the literature which was used for the current model. Refer to Matthews and Fox ([MAT76]), pages 420–427, for a description on how these are used for body fat and

to pages 413–417 for their use in somatotype (after the Heath–Carter method). The Sloan–Weir body fat determination method is preferred over all others.

subscapular	Used for the Heath–Carter Anthropmetric Somatotype method. Also used for male body fat determination (Sloan–Weir method and Buskirk Method).
triceps	Used for the Heath–Carter Anthropmetric Somatotype method. Also used for female body fat determination (Sloan–Weir method) and for male body fat determination (Buskirk Method).
thigh	Used for male body fat determination (Sloan–Weir method).
abdomen	Used for male body fat determination (Buskirk Method).
suprailiac	Used for the Heath–Carter Anthropmetric Somatotype method. Also used for female body fat determination (Sloan–Weir method).
calf	Used for the Heath–Carter Anthropmetric Somatotype method.

10.4 Somatotype.

The subject of somatotype has often been discussed in the lab but its usefulness and applicability has never been clearly identified. Somatotype, devised by W. Sheldon in 1954 [**SHE54**], is a description of body type (build) or physical classification of an individual. There are three components of somatotype: endomorphy, mesomorphy, and ectomorphy. The somatotype of an individual is described in terms of all three components since research by Sheldon ([**MAT76**], pg 411–412) has shown that the pure type does not exist.

Each component is given a value from 1 to 7, with 7 being the maximal value. So, a somatotype of 117 would be an extreme ectomorph, 171 would be an extreme mesomorph, and 711 would be an extreme endomorph.

The Sheldon system of body typing required photographs of the subject in three planes and measurements taken from these photographs (by a properly trained person). These measurements would then be used with tables devised by Sheldon to determine the somatotype.

The Heath–Carter Anthropmetric Somatotype Method, developed in the late 1960’s [**HEA67**] makes use of certain anthropometric measurements and a special form to determine an individual’s somatotype. This scale has higher maximum values for the various components than the Sheldon method. An example of this procedure is given in ([**MAT76**], pages 413–417).

The Heath–Carter method uses the following measurements:

for endomorphy:	Triceps skinfold Subscapular skinfold Suprailiac skinfold
for mesomorphy:	stature (height) Humerus breadth Femur breadth biceps circumference, flexed triceps skinfold calf circumference calf skinfold
for ectomorphy:	mass (weight) stature (height)

The Heath–Carter method of classification does not require much training if the necessary data is provided so that measurements do not have to be made. These measurements should be made by a trained anthropometrist, as is always the case.

10.5 Mass

Following is a list of the mass values being used for our human figure model. A variable name is associated with each segment name. The masses which are set to zero are actually included in the mass of other segments. When data values are determined for these variables then they can be used in the same way as the others. The value of such numbers is unclear at present since the mass of the various segments are taken as point masses.

Body segment name	variable name
Top Head (cranium)	topheadmass = 0 ⁶
Right Eye Socket and eyeball	reyemass = 0
Left Eye Socket and eyeball	leyemass = 0
Bottom Head (face region)	botheadmass
Neck	neckmass
Right Clavicle	rclavmass = 0
Left Clavicle	lclavmass = 0
Upper Torso (thorax)	uptorsomass = 0
Right Sternum (breastbone)	rsternummass = 0
Left sternum (breastbone)	lsternummass = 0
Center Torso (abdomen)	ctorsomass
Right Upper Arm	ruparmmass
Left Upper Arm	luparmmass
Right Forearm	rlowarmmass
Left Forearm	llowarmmass
Right Hand and Fingers	rhandmass
Left Hand and Fingers	lhandmass
Right Fingers	rfingersmass = 0
Left Fingers	lfingersmass = 0
Lower Torso (pelvis)	ltorsomass
Right Hip Flap	rhipmass = 0
Left Hip Flap	lhipmass = 0
Bodyroot	bodyrootmass = 0
Right Thigh	ruplegmass
Left Thigh	luplegmass
Right Lower Leg	rlowlegmass
Left Lower Leg	llowlegmass
Right foot and toes	rfootmass
Left foot and toes	lfootmass
Right Toes	rtoesmass = 0
Left Toes	ltoesmass = 0

10.6 Joint Names

The following table contains the names of all body joints identified and used in our human figure model. Associated with each joint name is a joint variable name for the upper and lower limits of motion for each joint DOF and a description of the motion the variable defines.

Joint Name	variable name	joint motion
Neck Joint		
Lateral Alanto-Axial Joints	neck_z_ulimit	Neck, rotation right
	neck_z_llimit	Neck, rotation left
Alanto-Occipital Joints	neck_y_ulimit	Neck, Flexion
	neck_y_llimit	Neck, extension
Medial Alanto-Axial Joint	neck_x_ulimit	Neck, lateral right
	neck_x_llimit	Neck, lateral left
Sternoclavicular Joint, Right	right_clavicle_x_ulimit	clavicle, protract or pull shoulders forward
	right_clavicle_x_llimit	clavicle, retract or pull shoulders backward
	right_clavicle_y_ulimit	clavicle, elevate (raise) shoulders (shrugging)
	right_clavicle_y_llimit	clavicle, depress (drop) shoulders (drooping)
		very limited movement for this rotation , has been ignored until now
	right_clavicle_z_ulimit	clavicle, rotation
	right_clavicle_z_llimit	clavicle, rotation
Sternoclavicular Joint, Left	left_clavicle_x_ulimit	clavicle, protract or pull shoulders forward
	left_clavicle_x_llimit	clavicle, retract or pull shoulders backward
	left_clavicle_y_ulimit	clavicle, elevate (raise) shoulders (shrugging)
	left_clavicle_y_llimit	clavicle, depress (drop) shoulders (drooping)
		very limited movement for this rotation , has been ignored until now
	left_clavicle_z_ulimit	clavicle, rotation
	left_clavicle_z_llimit	clavicle, rotation

Shoulder Joint, Right	right_shoulder_x_ulimit	Shoulder, abduction
	right_shoulder_x_llimit	Shoulder, adduction
	right_shoulder_z_ulimit	Shoulder, rotation lateral
	right_shoulder_z_llimit	Shoulder, rotation medial
	right_shoulder_y_ulimit	Shoulder, flexion
	right_shoulder_y_llimit	Shoulder, (hyper) extension
Shoulder Joint, Left	left_shoulder_x_ulimit	Shoulder, abduction
	left_shoulder_x_llimit	Shoulder, adduction
	left_shoulder_z_ulimit	Shoulder, rotation lateral
	left_shoulder_z_llimit	Shoulder, rotation medial
	left_shoulder_y_ulimit	Shoulder, flexion
	left_shoulder_y_llimit	Shoulder, (hyper) extension
Elbow Joint, Right	right_elbow_y_ulimit	elbow, flexion
	right_elbow_y_llimit	elbow, extension
Elbow Joint, Left	left_elbow_y_ulimit	elbow, flexion
	left_elbow_y_llimit	elbow, extension
Superior Radio-Ulnar Joint, Right this joint actually shares the joint capsule of the elbow.	right_wrist_z_ulimit	forearm, pronation starting from Anatomically neutral position
	right_wrist_z_llimit	forearm, supination starting from Anatomically neutral position
Wrist Joint	right_wrist_x_ulimit	wrist, radial Abduction
	right_wrist_x_llimit	wrist, ulnar Adduction
	right_wrist_y_ulimit	wrist, flexion
	right_wrist_y_llimit	wrist, extension
Superior Radio-Ulnar Joint, Left this joint actually shares the joint capsule of the elbow.	left_wrist_z_ulimit	forearm, pronation starting in neutral position
	left_wrist_z_llimit	forearm, supination starting in neutral position
Wrist Joint	left_wrist_x_ulimit	wrist, (radial) Abduction
	left_wrist_x_llimit	wrist, (ulnar) Adduction
	left_wrist_y_ulimit	wrist, flexion
	left_wrist_y_llimit	wrist, extension

There is no individual joint providing for movement at the waist. These fields really represent the movement allowed by the flexible nature of the spinal or vertebral column. The combination of the movements allowed by the lumbar region of the spinal column provides the vast majority, if not all, of the movements at the waist. The data values used here are actually educated estimates (guesses) since no data was found for this area of the body, which obviously is flexible and should be treated as a jointed region (until a curvable spine model is implemented). The range of motion in this area is highly variable among (even otherwise healthy) people and can change for any individual due to body fat, fatigue, stress, and even time of day.

	waist_y_ulimit	waist, forward bend without hips moving
	waist_y_llimit	waist, backward bend without hips moving
	waist_x_ulimit	waist, bend to right
	waist_x_llimit	waist, bend to left
	waist_z_ulimit	waist, twist to left
	waist_z_llimit	waist, twist to right
Hip Joint, right	right_hip_y_ulimit	Hip, flexion
	right_hip_y_llimit	Hip, extension
	right_hip_x_ulimit	Hip, abduction
	right_hip_x_llimit	Hip, adduction
	right_hip_z_ulimit	Hip, rotation lateral
	right_hip_z_llimit	Hip, rotation medial
Hip Joint, Left	left_hip_y_ulimit	Hip, flexion
	left_hip_y_llimit	Hip, extension
	left_hip_x_ulimit	Hip, abduction
	left_hip_x_llimit	Hip, adduction
	left_hip_z_ulimit	Hip, rotation lateral
	left_hip_z_llimit	Hip, rotation medial

Knee Joint, Right	right_knee_y_ulimit	knee, flexion
	right_knee_y_llimit	knee, extension
Knee Joint, Left	left_knee_y_ulimit	knee, flexion
	left_knee_y_llimit	knee, extension
Talocrural or Ankle Joint, Right	right_ankle_y_llimit	ankle, plantar flexion
	right_ankle_y_ulimit	ankle, dorsi flexion
Due to mobility of calcaneus (heel bone)	right_ankle_x_llimit	ankle, pronation
	right_ankle_x_ulimit	ankle, supination
Knee Joint, right	right_ankle_z_llimit	knee, medial rotation
	right_ankle_z_ulimit	knee, lateral rotation
Talocrural or Ankle Joint, left	left_ankle_y_llimit	ankle, plantar flexion
	left_ankle_y_ulimit	ankle, dorsi flexion
Due to mobility of calcaneus (heel bone)	left_ankle_x_llimit	ankle, pronation
	left_ankle_x_ulimit	ankle, supination
Knee Joint, left	left_ankle_z_llimit	knee, medial rotation
	left_ankle_z_ulimit	knee, lateral rotation
Metatarsophalangeal joints The great toe generally gives the value to these limits	right_ball_of_foot_y_ulimit	flexion
	right_ball_of_foot_y_llimit	extension
Metatarsophalangeal joints The great toe generally gives the value to these limits	left_ball_of_foot_y_ulimit	flexion
	left_ball_of_foot_y_llimit	extension
Metacarpophalangeal joints ("knuckles")	right_knuckles_y_ulimit	flexion
	right_knuckles_y_llimit	extension
Metacarpophalangeal joints ("knuckles")	left_knuckles_y_ulimit	flexion
	left_knuckles_y_llimit	extension

11 User Interface

11.1 GIRTHFUN

The generation of a complete human figure model is a time consuming task if done by hand. Since the specification of all human figures based upon our model is identical in form, the processes of generation of such specifications was a prime subject for automation via a computer program.

The first program developed for this purpose, **GIRTHFUN** (girth function), was written by Marc R. Grosso and interactively generated desired dimensions for each segment: length, width, and depth or thickness. This program allowed the user to choose (and switch between) actual measurements and statistical measurements for each dimension. The user could generate a figure of either sex, male or female, and could use any one of the three body models currently available.

The program was independent of any other system and operated using an interactive, question and answer format which was rather inflexible and tedious to use. In its original form, the program was limited to working only with segment girths (dimensions).

11.2 JACK Menus

At the time **GIRTHFUN** was being developed the **JACK** interface program was under development as well. There was a desire to make **GIRTHFUN** able to run under the **JACK** interface since **GIRTHFUN** was viewed as being an integral part of the human figure modeling work being done in the lab.

In order for **GIRTHFUN** to be able to use the **JACK** interface a set of menus, compatible with the **JACK** menus, needed to be developed. This need required that **GIRTHFUN** be modified to run using the **JACK** menu system. Richard D. Quach made these modifications and developed the necessary **JACK** menus. The result was a much nicer user interface and a system which was much easier to use.

11.3 MEX Window Menus

Around the time that the **JACK** menu system version of **GIRTHFUN** was developed a change was made to **JACK**, due to the acquisition of new hardware and operating system software, such that the entire **JACK** menu system was converted to use the **MEX** window system on the Silicon Graphics IRIS workstation. This change to the **MEX** window system required that all software being developed be converted to the **MEX** window system as well. Thus, **GIRTHFUN** was converted to run under **MEX** windows and it was also decided that **GIRTHFUN** should be run as a stand-alone program instead of being incorporated directly into or absorbed by the **JACK** interface.

Meanwhile, our human figure model was extended to include eye sockets, fingers, and toes, so **GIRTHFUN** was extended to handle these. Since the original approach to storing and working with the necessary data was general in nature, it was a relatively simple task to make these extensions. Likewise, **GIRTHFUN**, soon incorporated joint limits and segment masses in a straightforward fashion.

11.4 Spreadsheet Anthropometry Scaling System (SASS)

As the system continued to develop and plans for necessary extensions were laid out, it became clear that the system in its current state was flexible enough to accommodate the expansion but the system became harder to use due to the increasing number of data items.

One of us (Quach) decided to change the **GIRTHFUN** program to a spreadsheet format so that the large number of data items could be manipulated in a clear and simple manner. The result is **SASS** – the Spreadsheet Anthropometry Scaling System.

The next section describes the scope and operation of **SASS**.

12 SASS: The Spreadsheet Anthropometry Scaling System

SASS (Spreadsheet Anthropometry Scaling System) is a spreadsheet-like system which allows flexible interactive access to all anthropometric variables needed to size a human figure described structurally by a **PEABODY** file. Data that may be accessed is organized into “groups”; currently these groups include segment dimensions (“girth”), joint limits, center of mass, and strength. **SASS** provides an interpolation function which can be used to estimate a strength value through a prediction equation if the desired strength data is not stored in the database.

Initially **SASS** used only population statistic (generic) data to generate generic human figures. Recently **SASS** was expanded by building an anthropometric database that stores anthropometric data for (real) individuals and provides an interactive query system for database access. The user does not need to know about the format of the database or its query language.

All **SASS** functions are accessed through pop-up menus or direct spreadsheet cell manipulations. In the case of database queries, the user requests the desired information through pop-up menus and **SASS** translates it into the query language that is recognized by the database system. The query results are displayed in the spreadsheet format.

This section consists of a User’s Guide describing how to use both new and previously existing commands in **SASS**. It includes instructions on how to run **SASS** on the IRIS workstations, how to execute commands from **SASS** spreadsheet command menus, and how to query the anthropometric database through pop-up menus.

12.1 Getting Started

To run **SASS** on one of the Silicon Graphics Iris 4D workstations, type “**SASS**” after the system prompt:

```
% SASS
```

A grid or frame will then appear on the screen. By moving the mouse, center the grid to the desired position on the screen, then press any mouse button. The Anthropometric spreadsheet screen will appear. At this time, the spreadsheet is filled with numbers. By default, it loads in test data for strength and the population statistics data of NASA crewmen for girth, joint limits, and center of mass. At the bottom of the spreadsheet is the **Command/Message** window which is used for entering data and displaying any important messages about what **SASS** is doing and what it is expecting. The first message that should appear in this window is:

Press left-mouse to select items.

Different operations and commands on the data in the spreadsheet may now be performed.

There are two types of **SASS** spreadsheet. One is the *Anthropometric Spreadsheet* which is used to display the anthropometric data for a generic person or a real individual in different anthropometric groups. This spreadsheet allows the user to browse and modify any anthropometric data. The other type of spreadsheet is the *Database Query Spreadsheet*. This spreadsheet is used to build queries for the anthropometric database and to display the results of the queries. Each of these spreadsheets is described in the following sections.

12.2 Anthropometric Spreadsheet

The anthropometric spreadsheet screen, as shown in Figure 3 and more diagrammatically in Figure 4, is divided into five main sections: anthropometric group status line, standard (global) data, command menu, data section, and command/message window. Each of these screen sections is described below.

12.2.1 Anthropometric Group Status

This section allows the user to select the desired anthropometric group or topic to browse or modify. The present version can handle four groups: girth, joint limits, center of mass, and strength. When a group has been selected, the color of the group’s cell will be changed and the desired group data file will be loaded and then displayed in the data section. The function to load in any desired group file will be explained in the **Command Menu** section.

12.2.2 Standard (Global) Data

This section of the spreadsheet is used to display the “summary” of the data being displayed. It is intended to allow the user to have a “global” view of the human figure that the user is working on. Currently, the eleven labels are: *population, figure type, gender, mass, stature, group percentile, strength type, motion speed, handedness, training level, and fatigue level*. Except for *group percentile*, the information displayed in this section will be the same for all groups. Therefore, modifying any one of these fields in any particular group or topic will change the corresponding fields in the other groups. A group percentile indicates the percentile of each anthropometric group. Changing the group percentile will cause the data for all segments or joints of the displayed group to be scaled to the newly specified percentile value. However, it will not change percentiles for the other three groups. The group percentile will allow the user to create a human figure with different percentiles in different anthropometric groups if desired.

The user cannot modify the label of the currently displayed population, because it is read from an input file. This label is used to indicate the current population data file that the user has selected. The definitions of other fields in the **Standard (Global)** section are summarized in the following.

- **Figure Type**

This indicates the type of human figure model which the user wants to create using the **Jack** interface after exiting **SASS**. Currently, there are two human figure models, skinny and polybody, which can be selected in **SASS**.

Figure 3: Sample Anthropometric Spreadsheet for Girth.

Anthropometric Group Status	
Standard (global) data	Command Menu
Data Section	
command/message window	

Figure 4: Anthropometric Spreadsheet Screen Layout.

- **Gender, Mass, and Stature**

These indicate the respective current values of the human figure (defaults are male with 50th percentile mass and 50th percentile stature).

- **Strength Type, Motion Speed, Handedness, Training Level, and Fatigue Level**

These are parameters that affect the human strength data, so modifying any one of these fields will only change strength and will not affect data in the other three groups. *Strength type* indicates the current type of the strength data that is displayed: isometric (default), isokinetic, and isotonic. *Motion speed* indicates the angular velocity (default 0) of the movement. *Handedness* indicates whether the defined human figure is to be considered as right- (default) or left- handed. *Training level* indicates the level of training (to increase the strength) of the defined figure. The default value, 0, means no training. *Fatigue level* indicates the figure’s level of fatigue. The default value, 0, means normal or not tired.

12.2.3 Data Section for Girth, Joint Limits, and Center of Mass

There are two different formats of the data section. One is for the anthropometric groups girth, joint limits, and center of mass, and the other is for strength.

The data section for girth, joint limits, and center of mass is reserved for the display of individual segment or joint data and their corresponding percentiles. The leftmost column is reserved for the segment or joint names, while the other six columns are used for the data and percentile display. The segment or joint name column cannot be modified. In the present version, the segment and joint names are *hard-coded* in an include file. The data are read from an input file. The default values represent 50th percentile data.

Data and its corresponding percentile can be modified by simply moving the mouse to the desired cell and pressing on the left-mouse button. The color of the selected cell is then changed and a new data value for the selected cell can be entered in the command/message window. Pressing the **RETURN** key without typing a new data value leaves the cell unchanged. Changing any segment percentile will change its corresponding value, and vice versa.

SASS keeps a current measurement unit type for each group. Values entered without measurement units are interpreted in the current units. Values with an explicit (appropriate) unit following (**in, cm, deg, rad, ft-lb, N-m**) are converted, if necessary, into the current measurement type: joint limits in degrees or radians, segment dimensions in inches or centimeters, and strength values in ft-lb or N-m.

The data section for strength is used to display strength data in terms of joint angles. As shown in Figure 5, the leftmost column is used for the names of the motion impetus. It is also hard-coded in an include file and therefore cannot be modified. Under the label of *motion impetus*, there is a label, *right*. It indicates that the current displayed strength data is for the *right* arm or the *right* leg. The middle column shows the body configuration in terms of joint angles. The rightmost column displays the resultant strength value of the corresponding motion impetus at the displayed body configuration. For example, the first row of the data section in Figure 5 shows that the *right* shoulder abduction strength at shoulder angle of x axis 30°, shoulder angle of y axis 45°, and elbow angle 90° is 17.98 *ft-lbs*. The user can change any joint angles by moving the mouse to the desired cell, pressing on the left-mouse button, and then entering the new angle

value in the command/message window. Changing any joint angle will change its corresponding strength value. However, if the user's input angle is not within joint limits, an error message will be displayed in the *Command/Message* window instead. The purpose of this data section is to provide the user a convenient way to find out the strength value of a given body configuration for a current defined figure. The strength value for a body configuration specified by the user is either retrieved from the database or calculated from a strength prediction equation by **SASS**.

12.2.4 Command Menu

The top right corner of the display contains commands for the manipulation of the spreadsheet. These commands allow the user to browse through the selected dataset, change the measurement units, read in different input data files, create **PEABODY** structure files, get to database query spreadsheet screen, and so on. The present **Command Menu** section is shown in Figure 6. The *Void* commands are empty slots for future expansion. In order to execute any desired command in this section, the **red box** is selected with the left-mouse button. Further instructions appear on the **Command/Message** window.

Commands included in the anthropometric spreadsheet for strength are slightly different than the ones for other anthropometric groups. For example, the command $ft-lb \rightarrow N-m$ or $N-m \rightarrow ft-lb$ is used for the conversion of strength measurement units. Therefore, these two commands appear only in the *Command Menu* of *Strength*. There are also some differences in the *Command menu* in the spreadsheets for displaying real (individual) and generic data. For example, the command *Disp. Pop.* is contained in the *Command menu* of individual display, that is, for real data. It is used to get back to the spreadsheet of population from the display of a real individual so, naturally, it is not included in the population display. The *Quit* command exits **SASS**. The functions of other commands are described in the following sections.

- **Next/Previous Page**

This command is used for changing pages within any selected group. Since the size of the spreadsheet is fixed to 14 lines of data display for strength and 25 lines for the other anthropometric groups, the program decides on the total number of pages it needs to fit all the data. If the selected group of data contains more than one page of data, then the commands *Next Page* and *Previous Page* will function accordingly.

- **Global Conversion of Measurement Unit**

Depending on the group that one has selected, the conversion units appearing on this command will be different. For example, if one is working on the joint limits and the measurement unit is in degrees, then the command will be $deg \rightarrow rad$. This implies that in the current group, one can only convert the measurement unit from degrees to radians. On the other hand, if the current unit is already in radians, then the command will be $rad \rightarrow deg$. If one is working on the girth, then the conversion unit will be centimeters to/from inches, and for joint limits it will be degrees to/from radians. As indicated earlier, the command $ft-lb \rightarrow N-m$ or $N-m \rightarrow ft-lb$ is used for the conversion of the strength measurement unit.

- **Right \rightarrow Left/Left \rightarrow Right**

Since each spreadsheet can only display the strength data for one limb (arm or leg), these commands are used for changing displays of the strength data from one side to another. We assume the strengths of the dominating limb are measured and the strengths of the nondominating limb are scaled from the strengths of the dominating limb. The user will be prompted to supply the scaling factor. Pressing the **RETURN** key without typing a new scaling factor causes the system to use the default scaling factor.

- **Input Data**

One of the most important features of this spreadsheet is its capability to display, modify and create generic human figures from different populations. This command allows the user to load different population statistic data files into the spreadsheet. These data files must have a syntax that is recognized by the input functions of the spreadsheet otherwise it will be rejected. The default input data files of

Figure 5: Sample Anthropometric Spreadsheet for Strength.

Next Page	Query <i>or</i> Disp. Pop.
Previous Page	Disp. Indv. <i>or</i> Disp. More
cm to in <i>or</i> deg to rad	void
Input Data <i>or</i> void	void
Create Figure	ft-lb \longrightarrow N-m <i>or</i> void
Quit <i>or</i> void	Right \longrightarrow Left <i>or</i> void

Figure 6: Command Menu for Anthropometric Spreadsheet.

girth, joint limits, center of mass, and strength are *girth.dat*, *jntlmt.dat*, *cmass.dat*, and *strength.dat*, respectively.

There are two different formats of input files. One is for anthropometric groups of girth, joint limits, and center of mass. The other is for strength. Each of these input file formats is described below.

– **The format of input file for girth, joint limits, and center of mass**

The present version of **SASS** accepts input files in the format shown in Figure 7. Lines starting with a capital ‘C’ in the first column are taken to be comment lines and are ignored by the program. The capital ‘T’ in the first column followed by the gender type *male* or *female* is used to identify the data type that it will be receiving next. Until it encounters the next ‘T’, it will assume that all the data read are of the same gender. The order of the data in the input file must agree with the order displayed in the spreadsheet. For example, the order of the girth data is *bottom head*, *neck*, *center torso*, and so on. The first comment line in the file will be taken, by default, as the title of the population file.

The user can choose to use other percentiles as long as there are three sets of data provided. The user must make sure that the files are in the proper format. Percentile files can be created for any population for which segment girths, joint limits, and figure masses are available.

– **The format of input file for strength**

Figure 8 shows the input file format of strength data that is accepted by **SASS**. Lines starting with a capital ‘C’ in the first column are still used to identify comment lines and are ignored by the input parser. However, the capital ‘G’ in the first column is now used to indicate the gender type of *male* or *female* for the strength input file. In addition, a capital ‘L’ in the first column followed by the limb side *right* or *left* indicates that the input strength data is for the *right* or the *left* limb. The order of the strength data in the input file should also follow the same order as displayed on the spreadsheet, that is, *shoulder abduction*, *shoulder adduction*, *shoulder flexion*, and so on. The line starting with a capital ‘P’ in the first column is used to identify the title of the strength population file.

• **Create Figure**

After specifying the girth, joint limits, center of mass, and strength data of a human figure, it can be constructed and displayed. The command *Create Figure* will create a **PEABODY** structure file that is recognized by **Jack**. Once this file is created, we can exit **SASS** and run **Jack** with the newly created figure file as follows:

```
% jack newfigure.fig
```

The file *newfigure.fig* is the file created by **SASS**.

The user has the choice of creating a **PEABODY** structure file with or without *strength* data using **SASS**. If the user chooses not to include the strength data in the **PEABODY** structure file, the strength input file need not be loaded into **SASS**. **SASS**, however, will not allow the creation of the **PEABODY** file if the data files have not been loaded for girth, joint limits, and center of mass.


```

C
C
T  MALE or FEMALE
C      x          y          z
C 05%  50%  95%  05%  50%  95%  05%  50%  95%  comment
   data  data  data  data  data  data  data  data  data  /*...*/
   ...  ...  ...  ...  ...  ...  ...  ...  ...  ...
   ...  ...  ...  ...  ...  ...  ...  ...  ...  ...

C
C
T  MALE or FEMALE
C      x          y          z
C 05%  50%  95%  05%  50%  95%  05%  50%  95%  comment
   data  data  data  data  data  data  data  data  data  /*...*/
   ...  ...  ...  ...  ...  ...  ...  ...  ...  ...
   ...  ...  ...  ...  ...  ...  ...  ...  ...  ...

```

Figure 7: SASS Statistics Data File Format for Girth, Joint Limits, and Center of Mass.

```

P
C
G  MALE or FEMALE
C  Shoulder Angle  Elbow Angle  Wrist Angle  Strength
C  x    y    z          y          x    y    z  Value  %  comment
   data  data  data      data      data  data  data  data  data  /*...*/
   ...  ...  ...      ...      ...  ...  ...  ...  ...  ...
   ...  ...  ...      ...      ...  ...  ...  ...  ...  ...

C
C
G  MALE or FEMALE
C  Shoulder Angle  Elbow Angle  Wrist Angle  Strength
C  x    y    z          y          x    y    z  Value  %  comment
   data  data  data      data      data  data  data  data  data  /*...*/
   ...  ...  ...      ...      ...  ...  ...  ...  ...  ...
   ...  ...  ...      ...      ...  ...  ...  ...  ...  ...

```

Figure 8: SASS Statistics Data File Format for Strength.

If one is generally satisfied with the overall dimensions of the human figure that **SASS** has created, but wishes some minor changes, then one can simply edit this figure file using a text editor. On the other hand, if one is very concerned with the percentile of the segments or is totally unsatisfied with the human figure dimensions, then one should re-run **SASS** and re-create another human figure file.

- **Query**

The *Query* command is used for changing spreadsheet screens from the *Anthropometric Scaling* to the *Database Query*. After the *Query* command is executed and the *Database Query* screen is displayed, one can then query the database. The details of the *Database Query* spreadsheet will be described later.

- **Display Individual, Display More**

These commands are used to retrieve and display the anthropometric data of an individual from the database. The user can execute commands from the **Command Menu** to manipulate this real data as one does for statistical data. The label *population* is changed to *person name* in the anthropometric spreadsheet for displaying individual data. The command *Disp. Indv.* is used to display the first individual and *Disp. More* is used to display more individuals in the *Selected List* after displaying the first one. The definition of *Selected List* will be given later.

12.3 Database Query Spreadsheet

This spreadsheet is used to build a query and display the result of the query. As shown in Figure 9 and Figure 10, this spreadsheet is divided into four sections: summary data, command menu, query/selected list, and command/message window. Each of these sections is described below.

12.3.1 Summary Data Section

This section displays the query requested by the user under the label “Query”. The typical query is to find the people that satisfy certain constraints on global or local anthropometric data. Example queries are: “find a person who has a right upper arm longer than 28 centimeters” or “list any right handed females who have elbow flexion strength greater than 20 ft-lbs.” The summary data section also displays the summary of the result of the requested query. The label, *Current Display List* indicates the type of list that is currently displayed in the **Query/Selected List** section. *Total Data in Query List*, specifies the number of individuals in the query list. *Total Data in Selected List* shows the number of individuals in the selected list.

12.3.2 Query/Selected List Section

This section displays the global data of individuals that satisfy the requested query. The global data of an individual includes the individual’s name, gender, mass, stature, strength type, motion speed, handedness, training level, and fatigue level. Each individual’s global data is listed on a row in this section. The individuals that satisfy the query and their global data are stored in a list called the query list. After examining the global information in the query list, the user can choose all or some of the individuals and store them in the selected list. The detailed anthropometric data of each individual in the selected list can be displayed on the anthropometric spreadsheet by the command *Disp. Indv.* as mentioned earlier. If desired, the user can also create the **PEABODY** structure files for those selected individuals and later display their figures on the screen with **JACK**.

12.3.3 Command Menu

As in the *Anthropometric* spreadsheet, the top right corner of the database query display contains commands for the manipulation of the spreadsheet. These commands allow the user to load in different data files to the database, query the database, examine the global information of individuals found in the query, and so on. The present **Command Menu** section of *Database Query Spreadsheet* is shown in Figure 11. Commands included in the *Command Menu* for *Query List* display are slightly different than the ones included in the

Figure 9: Sample Database Query Spreadsheet.

Summary Data	Command Menu
Query or Selected List	
command/message window	

Figure 10: Database Query Spreadsheet Screen Layout.

Next Page	Disp. Query List <i>or</i> Disp. Selected List
Previous Page	Input DB
Query DB	void
Select All <i>or</i> void	void
Select One <i>or</i> void	void
Delete One	Exit Query <i>or</i> void

Figure 11: Command Menu for Database Query Spreadsheet.

display of *Selected List*. The command listed first in Figure 11 is the one in the display of *Query List*. The function of each of these commands is described below.

- **Input Database (Input DB)**

This command allows the user to load in a different data file to the database for the query. The anthropometric database contains the data required for the graphical representation of human figure. These include general body attributes, segment information, joint information, center of mass, strength, and others. This database is a relational one. Each anthropometric characteristic of a human figure is represented as a relation in the database. Future expansion is therefore easy. For example, the somatotype attribute is not implemented now, but this can be incorporated later by simply adding a new relation to the database.

The following relations are implemented in the current version of **SASS**. The attributes (fields) of each relation are listed under the corresponding relation together with brief comments. For example, *Girth* relation contains the data of thickness, width, length, and mass of each segment in the body for an individual (person). It includes attributes of *id_num*, *seg_name*, *thickness*, *width*, *length*, and *mass*. *Id_num* is an identification number used to identify an individual uniquely. Every relation in the database has this attribute. It allows us to link two relations together and find all the data stored in the database for an individual if desired.

```

person = (
  id_num,           {identification number of the person}
  name,            {name of the person}
  gender,          {gender type of the person}
  stature,         {total body height}
  mass,            {total figure mass}
  handedness,     {left or right handed person}
  age,             {age of the person}
  source,         {source of data}
girth = (
  id_num,           {identification number of the person}
  seg_name,        {segment name}
  thickness,       {thickness of segment (x-axis)}
  width,           {width of segment (y-axis)}

```

```

    length,          {length of segment (z-axis)}
    mass             {mass of segment}
)
center of mass = (
    id_num,          {identification number of the person}
    seg_name,        {segment name}
    cmass_x,         {center of mass of x axis}
    cmass_y,         {center of mass of y axis}
    cmass_z,         {center of mass of z axis}
)
joint limits = (
    id_num,          {identification number of the person}
    seg_name,        {joint limit name}
    jlimit_x,        {joint limit of x axis}
    jlimit_y,        {joint limit of y axis}
    jlimit_z,        {joint limit of z axis}
)
strength_par = (
    id_num,          {identification number of the person}
    exp_num,         {experiment number}
    side_of_limb,    {left or right side of limb}
    strgh_type,      {type of strength}
    speed,           {speed of motion}
    fatigue,         {fatigue level}
    training,        {training level}
    angle_unit,      {unit of angle}
    strgh_unit,      {unit of strength}
    speed_unit,      {unit of motion speed}
)
shoulder_strgh = (
    id_num,          {identification number of the person}
    exp_num,         {experiment number}
    shoulder_ang_x,  {shoulder displacement about x axis}
    shoulder_ang_y,  {shoulder displacement about y axis}
    shoulder_ang_z,  {shoulder displacement about z axis}
    elbow_ang,       {elbow displacement}
    axis,            {joint axis of x, y, or z}
    pstrgh,          {strength value at positive direction of an axis}
    nstrgh,          {strength value at negative direction of an axis}
)

elbow_strgh = (
    id_num,          {identification number of the person}
    exp_num,         {experiment number}
    elbow_ang,       {elbow displacement}
    shoulder_ang_x,  {shoulder displacement about x axis}
    shoulder_ang_y,  {shoulder displacement about y axis}
    shoulder_ang_z,  {shoulder displacement about z axis}
    wrist_ang_x,     {wrist displacement about x axis}
    wrist_ang_y,     {wrist displacement about y axis}
    wrist_ang_z,     {wrist displacement about z axis}
    pstrgh,          {strength value at positive direction of an axis}
    nstrgh,          {strength value at negative direction of an axis}
)

wrist_strgh = (
    id_num,          {identification number of the person}
    exp_num,         {experiment number}
    wrist_ang_x,     {wrist displacement about x axis}
    wrist_ang_y,     {wrist displacement about y axis}
    wrist_ang_z,     {wrist displacement about z axis}
    elbow_ang,       {elbow displacement}
    axis,            {joint axis of x, y, or z}
    pstrgh,          {strength value at positive direction of an axis}
    nstrgh,          {strength value at negative direction of an axis}
)

```

Each relation is stored as a “flat” file. The order of the fields must follow the one in the corresponding relation. For example, *girth* relation is stored in the file *girth.db* shown partially in Figure 12. The first row of the file reads *id_num*, 1, *girth name*, *bottom_head*, width, 9.80, thickness, 7.75, length, 24.41, and mass, 1.40. This indicates that the person with identification number 1 has the width, thickness, length, and mass of bottom head of 9.80 *cm*, 7.75 *cm*, 24.41 *cm*, and 1.40 *kg*, respectively.

The files *person.db*, *girth.db*, *jntlmt.db*, *cmass.db*, *strgh_par.db*, *elbow_strgh.db*, *shoulder_strgh.db*, and *wrist_strgh.db* contain default data. The user can, however, create personalized files and then execute the command *Input DB* to load the files in the database. After the user selects the command *Input DB*, The following message will appear:

Enter File Name for *Person*

After the user keys in the file name for *Person*, similar messages will appear one by one to ask the user to enter the file names for *Girth*, *Joint Limits*, *Center of Mass*, *Strength Parameter*, *Shoulder Strength*, *Elbow Strength*, and *Wrist Strength*. If the user does not want to query strength data, typing the *< ESC >* key when asked to enter the file name for *Strength Parameter* will prevent the system from asking for other file names related to strength, that is, *Shoulder Strength*, *Elbow Strength*, and *Wrist Strength*. However, the user must load in all the files for *Girth*, *Joint Limits*, and *Center of Mass* if any are needed as data for a query.

Unfortunately, the current version of **SASS** does not have the capability of taking a person’s data and adding to or deleting from the database through a **SASS** command; the user will have to use a text editor to edit the data files. This editing job is tedious, time consuming, and also error prone, it will be eliminated in a later version of **SASS**.

- **Next/Previous Page**

These page commands are used to change pages for the display of the query/selected list. Based on size limitations in the *Database Query* spreadsheet – fixed to 25 lines (rows) of display – the program decides on the total number of pages needed to fit all the individuals in the list. If the current display list contains more than one page of individuals, then the commands *Next Page* and *Previous Page* function accordingly.

- **Select All, Select One, and Delete One**

After examining the global information for individuals that are in the query list, if the user wants to see more detailed anthropometric data of all or some of them, the command *Select All* or *Select One* is used to select all individuals or one individual at a time from the query list to the selected list, respectively. The individual that is selected from the query list will be deleted from the query list and added to the selected list. The command *Delete One* allows the user to delete one individual at a time from either the query or the selected list. The program keeps track of the number of individuals in the current query or selected list. This information is displayed in the **Summary Data** section as indicated earlier.

- **Display Query/Selected List**

These commands are used to display the query or selected list on the query database spreadsheet, respectively.

- **Query Database (Query DB)**

This command allows the user to make a query request and get the answer back from the database. After the user selects *Query DB* from the **Command Menu** section, the following message will show on the **Command/Message** window:

Press rightmouse to build query.

When this message disappears, another message will appear:

```

1,BOTTOM_HEAD, 9.80, 7.75, 24.41, 1.40
1,NECK, 5.46, 5.46, 9.18, 0.14
1,CENTER_TORSO, 8.55, 15.40, 30.81, 9.66
1,LOWER_TORSO, 9.04, 15.65, 11.65, 2.94
1,R_UPPER_ARM, 4.16, 3.54, 28.94, 1.96
1,L_UPPER_ARM, 4.16, 3.54, 28.94, 1.96
1,R_LOWER_ARM, 2.76, 4.15, 24.66, 1.12
1,L_LOWER_ARM, 2.76, 4.15, 24.66, 1.12
1,R_UPPER_LEG, 7.43, 7.43, 40.35, 7.00
1,L_UPPER_LEG, 7.43, 7.43, 40.35, 7.00
1,R_LOWER_LEG, 6.07, 6.07, 41.19, 3.22
1,L_LOWER_LEG, 6.07, 6.07, 41.19, 3.22
1,R_FOOT, 11.89, 4.26, 5.85, 0.88
1,L_FOOT, 11.89, 4.26, 5.85, 0.88
1,R_HAND, 1.45, 4.10, 10.80, 0.28
1,L_HAND, 1.45, 4.10, 10.80, 0.28
1,R_CLAVICLE, 0.50, 0.50, 13.92, 2.10
1,L_CLAVICLE, 0.50, 0.50, 13.92, 2.10
1,UPPER_TORSO,999.0,999.0,999.0, 11.97
1,R_EYE, 2.20, 2.75, 2.20, 0.00
1,L_EYE, 2.20, 2.75, 2.20, 0.00
1,EYE_LOCATION, 8.90, 2.70, 12.30,999.0
1,R_TOES, 4.60, 3.95, 1.46, 0.10
1,L_TOES, 4.60, 3.95, 1.46, 0.10
1,R_FINGERS, 1.03, 3.41, 7.20, 0.14
1,L_FINGERS, 1.03, 3.41, 7.20, 0.14
1,R_HIP,999.0,999.0,999.0, 2.94
1,L_HIP,999.0,999.0,999.0, 2.94
1,R_STERNUM,999.0,999.0,999.0, 0.14
1,L_STERNUM,999.0,999.0,999.0, 0.14
1,TOP_HEAD,999.0,999.0,999.0, 4.13
2,BOTTOM_HEAD, 9.80, 7.75, 24.54, 1.40
2,NECK, 5.46, 5.46, 10.03, 0.14
2,CENTER_TORSO, 8.55, 15.40, 34.13, 9.66
2,LOWER_TORSO, 9.04, 15.65, 9.23, 2.94
2,R_UPPER_ARM, 4.32, 3.67, 29.56, 1.96
2,L_FINGERS, 1.03, 3.41, 6.60, 0.14
.
.
.

```

Figure 12: Sample Database Input File for Girth.

Query:

This indicates that the user can press the right-mouse button to build a query from pop-up menus. The query that the user is building will be displayed on the **Command/Message** window. The user can edit the query anytime before the command *Done* on the pop-up menu is selected. Once the command *Done* is chosen, the query built by the user will be sent for execution. While the query is executing, the user will get a message saying:

Query on database, please wait...

When the execution is complete, the user will get the message saying:

Query execution is complete.

The result will then be displayed on the **Query/Selected List** and the **Summary Data** sections of the spreadsheet. If no person is found for the requested query, the following message will be given:

No data satisfied the query.

The new query list and the summary data will overwrite the old one. However, the selected list from the previous query will be kept and more individuals (persons) from the new query list can be selected and added to the existing list.

There are five types of pop-up menus for building a query. Each of them is described below.

– **Query Menu**

The present *Query Menu* looks like the following:

Query Menu
Global Information
Anthropometric Groups
Re_execute
Abort

This is the first pop-up menu which appears in building a query. The command *Global Information* or *Anthropometric Groups* allows the user to build a query on these data. Selecting either of these two commands will lead to the second type of pop-up menu. The command *Re_execute* allows the user to execute the previous query without building it again. The command *Abort* allows the user to get out the loop of *Query DB* without executing the query. This is useful for scrapping the query and starting over if the user does not like the one under construction.

– **Global Information or Anthropometric Group Menu**

This is the second pop-up menu that will show up when building a query. The present *Global Information Menu* looks like the following:

Global Information
Gender
Mass
Stature
Strength Type
Handedness
Motion Speed
Training Level
Fatigue Level
Previous Menu

This menu allows the user to query the global information listed. Selecting any item from this menu will lead to the selected global data menu which provides the user with the choice of values to be selected. For example, picking *Strength Type* will lead to the *Strength Type Menu* that

provides three possible strength types for the user to choose from. The *Strength Type Menu* looks like this:

Strength Type
Isokinetic
Isotonic
Previous Menu

The present *Anthropometric Group Menu* looks like the following:

Anthropometric Group
Girth
Joint Limit
Center of Mass
Strength
Previous Menu

This menu allows the user to choose an anthropometric group to query. After picking the group from this menu, the selected anthropometric group menu will appear. For example, picking *Girth* will lead to the *Girth Menu* which lists all the segments of a human figure. The user can choose any one of these segments to query. The present *Girth Menu* is shown below.

Girth Menu
Head
Neck
Center Torso
.
.
.
Left Toes
Right Fingers
Left Fingers
Previous Menu

– **Axis Menu**

In a human figure, segments are defined in terms of width (x axis), thickness (y axis), and length (z axis) and joint limits are defined in three different rotation axes. This menu allows the user to specify the segment or rotation axis. It is shown below.

Axis Menu
X Axis
Y Axis
Z Axis
Previous Menu

– **Relational Operation Menu**

This menu contains operations that are allowed in a query. The present *Relational Operation Menu* looks like the following:

Relational Operation Menu
Less Than (<)
Greater Than (>)
Less Than or Equal (\leq)
Greater Than or Equal (\geq)
Equal (=)
Not Equal (\neq)
Previous Menu

After an operation in this menu is selected, the user will get the following prompt:

Type in the constraint value:

The user is expected to enter a number and then hit the **RETURN** key to get to the next pop-up menu.

– **Conjunction Menu**

The *Conjunction Menu* is shown below.

Conjunction Menu
And
Or
Done
Previous Menu

The conjunctions *and* and *or* allow the user to build a more complicated query. If the conjunction *and* or *or* is selected, the first menu (the *Query Menu*) will appear again and the loop of building a query will be repeated. The command *Done* will stop the loop and send the query that was just built to be executed. Note that every menu except the *Query Menu* contains the command *Previous Menu*. This command allows the user to go back to the previous menu and erase the unwanted part of the query. This also enables the user to edit the query while building it. If the query is too messy to edit, the user can execute the command *Abort* in the *Query Menu* to scratch it and start over.

Figure 13 shows the sequence of the pop-up menus used in the sample query. The result of this query is shown in Figure 9.

Sample Query:

Find males that have a length of the right upper arm greater than 28 centimeters and also have the maximum elbow flexion strength greater than 20 *ft – lbs*.

• **Exit Query**

This command allows the user to get back to the *Anthropometric Spreadsheet* that is left before entering the *Database Query Spreadsheet*.

12.4 Display Anthropometric Data for Real Person

After the command *Exit Query* is executed, the user can select the command *Display Individual* to display the anthropometric data of the first individual in the selected list. After the red box of the command *Display Individual* is pressed, the following messages will appear.

Query on girth.db, please wait...

Query on jntlmt.db, please wait...

Query on cmass.db, please wait...

Query on strength.db, please wait...

This indicates that **SASS** is retrieving the anthropometric data from the database.

It will take about two minutes to get every group of anthropometric data for an individual. Presently we do not have a real database management system to retrieve and manage the data. Temporarily, we use the Prolog interpreter. The problem of speed can be solved once we have a real database management system.

If the user wants to display other individuals in the selected list, the command *Display More* may be used. After pressing the red box of *Display More*, the following pop-up menu will appear on the spreadsheet:

Figure 13: The Sequence of Pop-up Menus Used in the Sample Query.

More Menu
First
Last
Previous
Next
N^{th} Person

This menu provides the user a convenient way to select and display the desired individual in the selected list. If the user selects the command, N^{th} Person, the system will give the following prompt:

Enter the number:

The user is expected to type in a number and hit the **RETURN** key. The system will then query the database to retrieve the desired person’s anthropometric data, and display it on the spreadsheet.

12.5 Exit SASS

The command *Display Population* takes the user from the display of an individual’s real anthropometric data back to the display of population’s statistical data. The command *Quit* in the spreadsheet of statistical data exits **SASS**.

13 Biostereometric Data

One of the major problems with most geometric body models is their decidedly unrealistic appearance. This lack of realism is the result of a compromise in appearance to allow for faster display and manipulation of the figures. Note, however, that the unrealistic look of our human figure models does not mean that the figures are not properly sized.

In order to display figures with more realistic looking images one must use more detailed geometry for each segment. There are a number of methods by which such data can be collected more quickly and more accurately; for example, biostereometric techniques use manual processing of multiple camera images. Kathleen Robinette at Wright-Patterson Air Force Base has kindly provided us with biostereometric data for both male and female subjects.

The amount of data for each individual subject is quite large, having over 6,000 data points per subject. The computer resources required to display and manipulate such large amounts of data are significant and cause the figures to lose the real-time motion capability of simpler figures.

The bulk of the data for each subject consists of “slices” through the body. Each slice has a variable number of data points associated with it since the number of data points is dependent upon the size (circumference) of the body part. This data was preprocessed before we received it. This preprocessing grouped the slices based upon body segments allowing each body segment to be identified and manipulated.

The slices provided in the biostereometric data file for each subject are slightly different from the segment list which we normally use for our human figure models. In addition to our normal list of segments the biostereometric data provides the following additional ones:

- a. **Thigh Flaps:** Each upper leg segment attaches to the pelvis region. In our original model the connection was sharply defined (and straight across). In reality, the muscles controlling the movement of the legs (thighs) extend up into the pelvic region therefore, Anthropometrists define the thigh–pelvis connection to account for this. Some models simply extend the thigh into the pelvis (and making a matching cutout in the pelvis). The preferred model is to create hip flaps which are triangular slices located above the thigh which basically contain the hip joints. The slices cause the lower edge of the pelvis to be v-shaped.
- b. **Abdomen:** A third torso segment (abdomen or center torso). Our regular body model used only two torso segments which split the abdomen between them. The Center Torso segment in our regular model is equivalent to the Upper Torso in the biostereometric data and the Lower Torso in our regular model is equivalent to the Pelvis (or Lower) section in the biostereometric data.

13.1 Biostereometric body model

When the biostereometric data was received with large amounts of data for each figure a new body model was possible. The completeness of the data allows for a very realistic body model to be displayed and manipulated. As this very robust data is from actual people one could not ask for much greater reality.

Again the **PEABODY** language is used to display and manipulate the figures. The human figure description file used for the other body models, “**BODY.FIG,**” was modified to allow the display and manipulation of the biostereometric data. The human figure description file for the biostereometric data can be found in Appendix P. A number of changes had to be made to the original file. The primary changes were to accommodate the differences in body model structure including the hip flaps and abdomen as discussed above. By examination of the **PEABODY** file one can easily discern the other differences.

13.2 Biostereometric data tiling

In order to allow for fast manipulation of the biostereometric figures it was necessary to reduce the number of data points. It was also desirable to improve the visual image of the figure since a “stack” of slices tended to look very strange. Both of these goals was accomplished by the use of a “tiling” program written to process the slice verticies to produce a solid figure. The tiling routine connects the verticies of adjacent slices to produce a geometric surface between the slices. The number of data points skipped in each slice is a program parameter.

In addition, one or two spheres built of polygons were added at most joint centers to prevent the “splits” when the segments are moved relative to one another. By differentially coloring each segment, the figure may be made to appear clothed⁷. Present choices include underwear, short pants, half pants, long pants, sleeveless shirt, halfsleeve shirt, and fullsleeve shirt. Examples of the contour figure are shown in Figure 14.

13.3 Establishing joint centers in the biostereometric data

To make the biostereometric data usable we had to establish proper joint centers between the segments. Necessary for this task are the original files labeled tapefiles 1-6 and the psurf files for each segment of each body. Specifically, tapefile5 (male landmark data) and tapefile2 (female data) are mandatory. They contain the necessary information.

The data in these files are in the following format: a section containing the segment volume and principal moments, a section with principal axes origin and anatomical axis origin, a third section labeled ‘direction cosines principal with respect to global’ (by columns), a fourth section called ‘direction cosines anatomical with respect to global’ (by columns) and a fifth section containing all the landmarks and their global coordinates. Usable data for the joint centers are in the second and fifth sections. Anatomical axes will now be referred to as a.a., segment number ‘n’ and name are defined in section 1, and landmark ‘n’ and name are defined in section 5.

There are 18 joints. What follows is a description of the algorithms necessary to create these joints. It is necessary to create sites in the two segments of a joint that are equivalent to each other and to the result of the algorithm applied to the data. Note that these descriptions were applied to male subject 2. The same formulas applied to the female is necessary to compute her joint centers.

The limits of rotations present were determined by Marc Grosso and Richard Quach. The naming conventions were by Marc Grosso.

- **RIGHT_ANKLE_JOINT:** x (y) coordinate is average of the x (y) coordinate from landmarks 69 and 71 - the right medial and lateral malleolus, respectively, z coordinate is from z coordinate of landmark 36 - right sphyrion.
- **LEFT ANKLE JOINT:** x (y) coordinate is average of the x (y) coordinate from landmarks 68 and 70 - the left medial and lateral malleolus, respectively, z coordinate is from z coordinate of landmark 35 -left sphyrion.

⁷These enhancements were provided by Jiahe Lu.

Figure 14: Biostereometric figures: female as contours (original data); male is tiled and given joint spheres.

(Note: The Right and Left Medial Malleolus is not a landmark on the female. To create ankle joints, average the x coordinates of the lateral malleolus (landmark 66 and 67 of the female) with the x coordinates of the appropriate sphyrion (landmarks 68 and 69). The z coordinate of the joint is the same - i.e. the z from the sphyrion.)

- RIGHT KNEE JOINT: x (y) coordinate is average of the x (y) coordinate from landmarks 34 and 61 - the right lateral and medial femoral condyls respectively, z coordinate is from z coordinate of landmark 34 - right lateral femoral condyl.
- LEFT KNEE JOINT: x (y) coordinate is average of the x (y) coordinate from landmarks 33 and 60 - the left lateral and medial femoral condyls respectively, z coordinate is from z coordinate of landmark 33 - right lateral femoral condyl.
- RIGHT LEFT HIP-FLAP TO UPPER LEG: As there is no degree of rotation at these joints, any point on the plane of attachment of these two segments is permissible. Use landmarks 15 and 16 left and right gluteal folds as this joint.
- RIGHT HIP JOINT: x coordinate is from the right trochanterion - landmark 12; z is the average of the largest and smallest z coordinates in the right hipflap psurf file; y is the smallest negative y coordinate at the z (or approximate z) level in the psurf file.
- LEFT HIP JOINT: x coordinate is from the left trochanterion - landmark 11; z is the average of the largest and smallest z coordinates in the left hipflap psurf file; y is the smallest positive y coordinate at the z (or approximate z) level in the psurf file.
- RIGHT WRIST JOINT: x (y) coordinate is average of x (y) coordinates of landmarks 30 and 32 - the right radial and ulnar styloids; the z coordinate is from 32 - right ulnar styloid landmark.
- LEFT WRIST JOINT: x (y) coordinate is average of x (y) coordinates of landmarks 29 and 31 - the left radial and ulnar styloids; the z coordinate is from 31 - left ulnar styloid landmark.
- RIGHT ELBOW JOINT: x (y) coordinate is average of x (y) coordinates from landmarks 26 and 28 - right medial and lateral humerus epicondyls respectively. z is from the greatest z coordinate in the right lower arm.
- LEFT ELBOW JOINT: x (y) coordinate is average of x (y) coordinates from landmarks 25 and 27 - left medial and lateral humerus epicondyls respectively. z is from the greatest z coordinate in the left lower arm.
- RIGHT SHOULDER JOINT: x coordinate is 1/2 the distance between the x coordinates of landmarks 20 and 22 - the right anterior and posterior scyes respectively. z coordinate is 1/4 the distance from the z coordinate of landmark 18 - right acromiale - and the lesser of the z coordinates from landmarks 20 and 22 (see above). y coordinate is the smallest negative y coordinate at the z level just determined in the right upper arm psurf file.
- LEFT SHOULDER JOINT: x coordinate is 1/2 the distance between the x coordinates of landmarks 19 and 21 - the left anterior and posterior scyes respectively. z coordinate is 1/4 the distance from the z coordinate of landmark 17 - right acromiale - and the lesser of the z coordinates from landmarks 19 and 21 (see above). y coordinate is the smallest negative y coordinate at the z level just determined in the left upper arm psurf file.
- LTORSO TO CTORSO JOINT: x (y) coordinate is average x (y) coordinates of landmarks 9 and 10 - left and right iliocristales; z coordinate is the greater z coordinate of landmarks 9 and 10.
- CTORSO TO UTORSO JOINT: Use landmark 8 - the 10th ribmidspine.
- NECK TO UTORSO JOINT: Use landmark 3 - the cervicale.

- **HEAD TO NECK JOINT:** x coordinate is average of x coordinates from landmarks 42 and 43 - left and right tragions; y coordinate is from the y coordinate of landmark 41 - sellion; z coordinate is from the average of the z coordinates of landmarks 6 and 7 - left and right gonions respectively.

It is important to note that the z coordinate need not be computed as above. It may be read from psurf files as in some examples above. The z coordinate for a joint is the highest z value in the psurf file of the lower segment of a joint, or the lowest z value in the psurf file of the higher segment.

The spine values (those connecting the torso to the utorso and connecting the torso to ltorso) are not extremely precise. Work on a better spine model is in progress.

14 Open Issues

The real human body is an extremely complicated object having many parts and abilities. These parts and abilities are far more difficult to model than one might expect even following a careful study of the human body. Our human figure model accounts for all of the major body structures and parts but does not handle everything as completely as one would like. The issues which are currently receiving attention include:

1. the implementation of a curvable spine (this work is being done by Jianman Zhao and will be reported elsewhere),
2. finding the joints motion limits for spherical (ball-and-socket) joints such as the shoulder and hip, and
3. determining the dimensions and parameters for the human field of view.

There are other concerns which are related to a specific human figure model rather than the general concerns which apply to all body models. These concerns are:

1. determining the joint centers in the biostereometric data, and
2. determining the joint center motions in joints having complex geometry.

14.1 Joint motion for spherical joints

Motions for monaxial and bi-axial joints tend to be in strict circular or spherical sectors. The range-of-motions for these types of joints is easy to determine and model by measuring limits along the plane of the circle or on planes slicing the sphere. Spherical (ball-and-socket) joints, as found in the shoulder and hip of human beings have three degrees-of-freedom: adding twist (rotation) onto the range of spherical motions. Therefore slicing by planes is not as satisfactory since the limits vary as the twist changes for any given segment orientation.

Since it is easier to model joint motions in single planes we have implemented our model on this basis. This is accurate and works well for all joints except the shoulder and hip joints. For monaxial joints this is clearly sufficient. For bi-axial joints this generally works because any joint motion can be modeled as two orthogonal single plane motions (that is, ideally the limits are not coupled). Tri-axial joints allow flexion-extension, abduction-adduction, and rotation to occur at the same time. Joint movements for tri-axial joints cannot be completely and accurately modeled as independent one plane motions because of the joint shapes and the way in which the three DOFs interact. Our current model consists of independent single plane motions. While this works for much of the motion range near the principal rotation axes, it becomes increasingly inaccurate in the areas inbetween the planes. Korein's solution [KOR85] is slightly better in that it uses a spherical polygon rather than two fixed orthogonal angle limits, but it is still unable to handle the third DOF limit at all. A (continuous) series of spherical polygons paramertized by twist angle may be the only real solution.

Data to represent the actual shape of the shoulder joint's range-of-motion is difficult to find in the literature. This information may be represented in a different form and needs to be extracted or converted to a form which would be usable. For example, in the *NASA Man-Systems Intergration Manual* [NAS87] there is data describing the reach envelope of the same population of astronaut crewmember trainees that is

used throughout the manual. This data may contain the information needed to describe the actual shape of the joint limit envelope for the shoulder for that population. At present, it is unclear how to interpret and extract such information. For example, arm twist is not included in the determination of reach envelope.

14.2 Field of view

The field of view of a human being is a complex issue involving many components and problems. Some of the factors which can effect the field of view include: the size of the nose (bridge), the basic eyesight ability of the individual, the effect of any headgear that may be worn. In the normal human, not wearing anything which will cause an obstruction, the field of view has been studied and is rather clearly defined [CRO81]. Our human figure model currently does not make use of vision in any manner, but the model includes correct eye locations with the intent of further extending the model to include a field of view. The eye locations may be used as camera positions for dynamic monitoring of view direction during figure positioning or movement.

14.3 Joint centers in complex human figure models

The standard human figure models in use in our laboratory were constructed such that the segment connections were well known. As a result, these connections became the joint centers so there was no real question as to these locations. When the biostereometric data arrived it posed a new and interesting problem. Along with the nice displayable figure and the large number of data points representing the figures, the actual location of the joint centers and their path during movement were unknown. Joint centers are clearly located within the figure in the area where two segments meet. We have landmark locations available as well as segment lengths, however this does not actually tell us where the joint centers are located.

For example, if we examine the area around an elbow joint, we know the location of four landmarks near where the upper arm and forearm join as well as the lengths of both the upper arm and the forearm. One may want to take the naive approach and say that the joint center is located at the point equidistant from the four landmarks at the elbow and in line with the ends of the arm segments. However, this approach may not be suitable for all joints, even if it is suitable for a few. This approach may be good as a starting point. Work is in progress to determine where the actual joint centers are located.

15 Results and examples of human figure model

The human figure models which we can create using **SASS** for display using the Jack Interface are quite variable. Figure 15 (a series of figures from 1st to 99th percentile, polybody) shows the Polybody figure range that is possible for male figures (based upon NASA crewmember trainee data). Figure 16 (a series of figures from 1st to 99th percentile, polybody) shows the same range for the female figures. Figure 1 of the 50th percentile male and female shows that the female figure actually looks different from the male figure in body proportions. The female is thinner in the upper torso and the appendages, has a much higher waist, and has relatively wider hips than the male.

With the polybody figure the female's lower torso looks rather large. This is an artifact due to the lack of three segments in the torso. The torso should have an upper torso (the thorax region which includes the rib cage), a center torso (the abdomen region, stomach and intestines, etc.), and a lower torso region (the pelvis which includes the hips and the sacrum or lower end of the spine). Since there are only two torso segments used, the abdomen region is divided between the lower torso and center torso since there is no geometry for the upper torso currently in use. When geometry for the third torso region and data can be determined, then this artifact will disappear⁸.

The biostereometric data body model is based upon data from actual subjects. Both male and female subjects can be displayed and manipulated. See Figure 14 on page 41 for examples of a male and female biostereometric body model.

⁸See Appendix E for a description of a five segment upper torso.

Figure 15: Polybody model range of male figure sizes

Figure 16: Polybody model range of female figure sizes

16 Future Needs

There are a number of future extensions and much additional work which can be done to further improve and refine our human figure modeling system. The goal of all this work is to achieve a greater amount of reality for the models.

16.1 Dynamics Related Factors

In order to more completely support our dynamics modeling system we need to refine the data for our female human figure models so that they will be as accurate as the data used for the male. Due to data missing from our current literature sources the female models have been implemented using male data or modified male data in some instances. To correct this we need to:

1. Determine valid segment mass values for females.
2. Determine segment and whole body center of mass values for females.

With these corrections in place the female model will be as robust as the male model. Our data sources do not provide this data therefore either a new source for data has to be found or the current data sources need to be updated to include female data.

16.2 Anthropometry Related Factors

Due to decisions made when developing the skinnybody and polybody models a number of limitations were introduced into these models. These limitations were due to system design requirements and speed of display and manipulation requirements at the time of development. Improvements in hardware have allowed some of these limitations to be relaxed. Those design requirements based upon inaccurate, missing, or poorly understood data required additional investigation which can now be undertaken. The investigations should focus on:

1. The determination of valid segment and whole body volumes for females.
2. The addition of the third torso region (the abdomen or center torso) in the skinnybody and polybody models. This includes development of a psurf to represent the region for each model. The skinnybody model may require changes to the other two torso regions in order to get an acceptable visual representation but this is unclear at present. The addition of the third torso region will require that the data for the entire torso length be reworked. The three torso regions are best delineated by the sections of the vertebral columns with the upper torso (Thorax or chest region) going from the top of T1 (C7/T1 junction) to the T12/L1 junction, the center torso (Abdominal region) going from the T12/L1 junction to the L5/S1 junction, and the lower torso (Pelvic region) containing the section from L5/S1 and below (to the crotch).
3. The determination of lower torso length data. This data should be the measurement of the pelvis which is best represented by the region from the L5/S1 juncture in the spine and below.
4. The determination of actual neck dimensions: length (essentially the length from the base of the skull to the C7/T1 juncture), width, and depth (or thickness).
5. The determination of actual width and depth values for:
 - upper leg
 - lower leg
 - upper arm
 - forearm

6. The addition of a top head region (essentially separating the head into the cranium or skull) and the face region for all models. This would require the development of the necessary psurf for each model. The data for the current head region would have to be reworked to allow for the new region (only lengths would have to be adjusted. Refer to the explanation in Section 10.1 for the details.
7. The inclusion of somatotype parameters which would allow for greater variability of the models that could be displayed. Such parameters would bring the models much closer to reality since we would be able to create figures with varying amounts of body fat (a smoothening effect) that were algorithmically determined. This would allow for examining the effects of weight gain or weight loss for the the populations in use. The benefits of this are rather clear.

Adding the geometry for a third torso region and for the top head region makes the entire model more variable and therefore more valuable as well. The inclusion of somatotype can now be made because the body structure supported by such an extended model would contain the necessary components. The top head region would allow for more individualization of the figures since populational and individual skull and facial traits could be represented.

16.3 Biostereometric body model improvements and extensions

The skinnybody and polybody models currently in use have many aesthetic and visual limitations but are based upon valid data and produce reasonable and accurately sized human figure representations. Both of these models provide for very fast display and manipulation of the figures within the **JACK** interface due to the small amount of data required to represent these figures. In order to improve the look of the displayed human figures there would have to be an increased amount of geometric data stored for each figure. Depending upon how much of an increase is necessary, the performance of the system may become unacceptably slow. For example, the biostereometric data figures which contain in excess of 6000 data points produce very nice human figure displays but the amount of data is so large that the figure display is slow and any movement is all but impossible.

The clear need for some middle ground produced the biostereometric tiling routine described in Section 13.2 on page 40 which reduces the number of data points in the figure in order to speed the display and manipulation of these figures.

However, the biostereometric body model differs from the skinnybody and polybody models structurally as well. The biostereometric body has added segments (hip flaps and abdomen as discussed in Section 13.1 on page 39) but also lacks some segments and structures. The missing sections are fingers and toes and their related joints. The eye socket structures are also missing.

As it is desirable to have models which are compatible the differences between them must be rectified. These changes or additions must be carefully thought out since they involve complex representations and will not be as straightforward as with the simpler models.

The skinnybody and polybody models are quite variable since they use normalized psurfs as their geometric basis. The biostereometric bodies each represent actual individuals, that is, are a collection of data for a specific person. These are clearly not as general as is necessary. The normalized psurfs can be reliably scaled which is what provides the variability of the models. Normalizing the biostereometric body data for one individual would not result in universally usable and reliable segments, no matter how many data points were included. Since the shape of each segment would vary from person to person this approach must be refined. We are examining ways to scale and deform the actual data by population statistics and somatotype.

An approach which may allow for normalizing and scaling the biostereometric data would be to carefully select a representative individual in both sexes from the population in question for each somatotype. The data from these individuals would be normalized and stored in Unix archive files as psurfs as is done for the skinnybody and polybody models. The result would be six archive files for the biostereometric body primitives which would be selected as needed by the user – one each for male and female ectomorphic types, male and female mesomorphic types, and male and female endomorphic types. The ability to modify body types as discussed in Section 16.2 above should still be usable but this set of files would allow for selection of a body type without need for modification.

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17 Appendices

A Body Segment and Joint List

A complete list of the body segments, structures, and joints used by our human figure model is contained in this Appendix. Listed along with each segment/structure name is the psurf name (geometric primitive) used to represent the segment or structure. If no psurf is used for a segment or structure then the column is left blank. The variable names used for each segment/structure are also included. For each joint, the joint name, sites associated with the joint, and variable names used in the joint are listed. Joints with no variable names listed have no movements allowed, therefore no joint limits are needed. Most segment, structure, and joint names are self-explanatory so little additional explanation is provided here.

SEGMENT NAME	PSURF USED	ASSOCIATED VARIABLE NAMES
left_toes	ltoes.pss	ltoesx, ltoesy, ltoesz ltoesmass
right_toes	rtoes.pss	rtoesx, rtoesy, rtoesz rtoesmass
right_fingers	rfingers.pss	rfingersx, rfingersy, rfingersz rfingersmass
left_fingers	lfingers.pss	lfingersx, lfingersy, lfingersz lfingersmass
left_foot	lfoot.pss	lfootx, lfooty, lfootz lfootmass
right_foot	rfoot.pss	rfootx, rfooty, rfootz rfootmass
right_lower_leg	rlleg.pss	rlolegx, rlolegy, rlolegz rlolegmass
left_lower_leg	llleg.pss	llolegx, llolegy, llolegz llolegmass
right_upper_leg	ruleg.pss	ruplegx, ruplegy, ruplegz ruplegmass
left_upper_leg	luleg.pss	luplegx, luplegy, luplegz luplegmass
right_hip		rhipmass
left_hip		lhipmass
lower_torso	ltorso.pss	ltorsox, ltorsoy, ltorsoz ltorsomass
center_torso	ctorso.pss	ctorsox, ctorsoy, ctorsoz ctorsomass
upper_torso		uptorsomass
bottom_head	head.pss	botheadx, botheady, botheadz eyelocx, leyex, eyelocy, eyelocz, botheadmass
top_head		topheadmass
neck	neck.pss	neckx, necky, neckz neckmass
right_clavicle	rclav.pss	rclavx, rclavy, rclavz rclavmass
left_clavicle	lclav.pss	lclavx, lclavy, lclavz lclavmass
right_sternum		ctorsoy, rclavz rsternummass
left_sternum		ctorsoy, lclavz lsternummass
right_upper_arm	ruarm.pss	ruparmx, ruparmy, ruparmz ruparmmass
left_upper_arm	luarm.pss	luparmx, luparmy, luparmz luparmmass
right_lower_arm	rlarm.pss	rloarmx, rloarmy, rloarmz rloarmmass
left_lower_arm	llarm.pss	lloarmx, lloarmy, lloarmz lloarmmass
right_hand	rhand.pss	rhandx, rhandy, rhandz rhandmass
left_hand	lhand.pss	lhandx, lhandy, lhandz lhandmass
right_eyeball	reye.pss	reyex, reyey, reyez reyemass
left_eyeball	leye.pss	leyex, leyey, leyez leyemass
body_root		flooroffset

JOINT NAME	SITES INVOLVED	ASSOCIATED VARIABLE NAMES
right_shoulder	right_clavicle.lateral	right_shoulder_z_ulimit, right_shoulder_x_ulimit, right_shoulder_y_ulimit
	right_upper_arm.proximal	right_shoulder_z_llimit, right_shoulder_x_llimit, right_shoulder_y_llimit
right_elbow	right_upper_arm.distal	right_elbow_y_ulimit
	right_lower_arm.proximal	right_elbow_y_llimit
right_wrist	right_lower_arm.distal	right_wrist_z_ulimit, right_wrist_x_ulimit, right_wrist_y_ulimit
	right_hand.proximal	right_wrist_z_llimit, right_wrist_x_llimit, right_wrist_y_llimit
left_shoulder	left_clavicle.lateral	left_shoulder_z_ulimit, left_shoulder_x_ulimit, left_shoulder_y_ulimit
	left_upper_arm.proximal	left_shoulder_z_llimit, left_shoulder_x_llimit, left_shoulder_y_llimit
left_elbow	left_upper_arm.distal	left_elbow_y_ulimit
	left_lower_arm.proximal	left_elbow_y_llimit
left_wrist	left_lower_arm.distal	left_wrist_z_ulimit, left_wrist_x_ulimit, left_wrist_y_ulimit
	left_hand.proximal	left_wrist_z_llimit, left_wrist_x_llimit, left_wrist_y_llimit
right_hip_joint	right_hip.lateral	right_hip_z_ulimit, right_hip_x_ulimit, right_hip_y_ulimit
	right_upper_leg.proximal	right_hip_z_llimit, right_hip_x_llimit, right_hip_y_llimit
right_knee	right_upper_leg.distal	right_knee_y_ulimit
	right_lower_leg.proximal	right_knee_y_llimit
right_ankle	right_lower_leg.distal	right_ankle_z_ulimit, right_ankle_x_ulimit, right_ankle_y_ulimit
	right_foot.proximal	right_ankle_z_llimit, right_ankle_x_llimit, right_ankle_y_llimit
left_hip_joint	left_hip.lateral	left_hip_z_ulimit, left_hip_x_ulimit, left_hip_y_ulimit
	left_upper_leg.proximal	left_hip_z_llimit, left_hip_x_llimit, left_hip_y_llimit

left_knee	left_upper_leg.distal	left_knee_y_ulimit
	left_lower_leg.proximal	left_knee_y_llimit
left_ankle	left_lower_leg.distal	left_ankle_z_ulimit, left_ankle_x_ulimit, left_ankle_y_ulimit
	left_foot.proximal	left_ankle_z_llimit, left_ankle_x_llimit, left_ankle_y_llimit
right_clavicle_joint	right_sternum.distal	right_clavicle_x_ulimit, right_clavicle_y_ulimit
	right_clavicle.proximal	right_clavicle_x_llimit, right_clavicle_y_llimit
left_clavicle_joint	left_sternum.distal	left_clavicle_x_ulimit, left_clavicle_y_ulimit
	left_clavicle.proximal	left_clavicle_x_llimit, left_clavicle_y_llimit
waist	lower_torso.distal	waist_z_ulimit, waist_x_ulimit, waist_y_ulimit
	center_torso.proximal	waist_z_llimit, waist_x_llimit, waist_y_llimit
atlanto_occipital	neck.distal	neck_z_ulimit, neck_x_ulimit, neck_y_ulimit
(Head-neck joint)	bottom_head.proximal	neck_z_llimit, neck_x_llimit, neck_y_llimit
solar_plexus	center_torso.distal	
(Mid-torso location)	upper_torso.proximal	
right_knuckles	right_hand.distal	right_knuckles_y_ulimit
	right_fingers.proximal	right_knuckles_y_llimit
left_knuckles	left_hand.distal	left_knuckles_y_ulimit
	left_fingers.proximal	left_knuckles_y_llimit
right_ball_of_foot	right_foot.distal	right_ball_of_foot_y_ulimit
	right_toes.proximal	right_ball_of_foot_y_llimit
left_ball_of_foot	left_foot.distal	left_ball_of_foot_y_ulimit
	left_toes.proximal	left_ball_of_foot_y_llimit
base_of_neck	upper_torso.distal	
	neck.proximal	

right_sternoclavicular	upper_torso.right	
(Sternum - clavicle joint)	right_sternum.proximal	
left_sternoclavicular	upper_torso.left	
(Sternum - clavicle joint)	left_sternum.proximal	
right_eye	right_eyeball.point	
	bottom_head.rsochet	
left_eye	left_eyeball.point	
	bottom_head.lsochet	
root_torso	body_root.distal	
	lower_torso.proximal	
root_rhip	body_root.right	
	right_hip.proximal	
root_lhip	body_root.left	
	left_hip.proximal	

B Male Girths

Contained here is the table of male girth values, based upon the NASA Crewmember trainee data, used by our model. The table is in a format similar to the original include file for GIRTHFUN.C. It has columns for X dimension values (5th%, 50th%, and 95th%), Y dimension values (5th%, 50th%, and 95th%), and Z dimension values (5th%, 50th%, and 95th%) along with an identifier for the values.

MALE GIRTHS

X			Y			Z			
5%	50%	95%	5%	50%	95%	5%	50%	95%	
18.8,	20.0,	21.1,	14.8,	15.7,	16.5,	21.1,	22.7,	24.3,	/* bottom head */
11.3,	12.3,	13.3,	11.3,	12.3,	13.3,	7.7,	10.0,	12.6,	/* Neck */
21.8,	25.0,	28.2,	32.9,	39.2,	45.4,	43.7,	47.6,	51.6,	/* Center Torso */
20.3,	23.2,	27.8,	30.9,	33.9,	37.9,	12.0,	13.1,	13.7,	/* Lower Torso */
9.36,	10.70,	12.04,	7.95,	9.1,	10.23,	33.7,	36.6,	39.4,	/* r Upper Arm */
9.36,	10.70,	12.04,	7.95,	9.1,	10.23,	33.7,	36.6,	39.4,	/* l Upper Arm */
6.84,	7.52,	8.17,	10.20,	11.27,	12.25,	26.6,	30.1,	31.5,	/* r Lower Arm */
6.84,	7.52,	8.17,	10.20,	11.27,	12.25,	26.6,	30.1,	31.5,	/* l Lower Arm */
13.2,	15.2,	17.8,	13.2,	15.2,	17.8,	40.7,	43.4,	47.0,	/* r Upper Leg */
13.2,	15.2,	17.8,	13.2,	15.2,	17.8,	40.7,	43.4,	47.0,	/* l Upper Leg */
10.3,	11.4,	12.7,	10.3,	11.4,	12.7,	34.0,	36.8,	38.3,	/* r Lower Leg */
10.3,	11.4,	12.7,	10.3,	11.4,	12.7,	34.0,	36.8,	38.3,	/* l Lower Leg */
17.8,	19.4,	21.1,	9.0,	9.9,	10.7,	12.0,	13.9,	15.8,	/* r Foot */
17.8,	19.4,	21.1,	9.0,	9.9,	10.7,	12.0,	13.9,	15.8,	/* l Foot */
2.6,	3.0,	3.3,	8.2,	8.9,	9.6,	10.4,	11.5,	12.6,	/* r Hand */
2.6,	3.0,	3.3,	8.2,	8.9,	9.6,	10.4,	11.5,	12.6,	/* l Hand */
1.0,	1.0,	1.0,	1.0,	1.0,	1.0,	14.8,	17.2,	19.4,	/* r Clavicle */
1.0,	1.0,	1.0,	1.0,	1.0,	1.0,	14.8,	17.2,	19.4,	/* l Clavicle */
2.2,	2.2,	2.2,	2.75,	2.75,	2.75,	2.2,	2.2,	2.2,	/* r eye */
2.2,	2.2,	2.2,	2.75,	2.75,	2.75,	2.2,	2.2,	2.2,	/* l eye */
18.4,	19.6,	20.8,	2.7,	3.1,	3.6,	10.5,	11.6,	12.7,	/* eye location*/
x is the distance from the front of the head to the wall */									
6.9,	7.4,	7.8,	9.0,	9.9,	10.7,	5.2,	6.0,	6.6,	/* ball of right foot */
6.9,	7.4,	7.8,	9.0,	9.9,	10.7,	5.2,	6.0,	6.6,	/* ball of left foot */
2.6,	3.0,	3.3,	8.2,	8.9,	9.6,	7.7,	8.1,	8.7,	/* knuckles of right hand */
2.6,	3.0,	3.3,	8.2,	8.9,	9.6,	7.7,	8.1,	8.7,	/* knuckles of left hand */

C Female Girths

This appendix contains the table of female girth values, based upon the NASA Crewmember trainee data, used by our model. The table of data is in a format similar to the original include file for GIRTHFUN.C. It has columns for X dimension values (5th percentile, 50th percentile, and 95th percentile), Y dimension values (5th percentile, 50th percentile, and 95th percentile), and Z dimension values (5th percentile, 50th percentile, and 95th percentile) along with an identifier for the values.

FEMALE GIRTHS

	X			Y			Z			
	5%	50%	95%	5%	50%	95%	5%	50%	95%	
16.7,	18.2,	19.6,	13.5,	14.5,	15.5,	20.1,	21.9,	23.8,		/* Bottom Head */
11.0,	11.8,	12.6,	11.0,	11.8,	12.6,	11.0,	11.8,	12.6,		/* Neck */
17.4,	20.5,	24.3,	31.2,	35.0,	39.2,	35.2,	38.1,	41.0,		/* Center Torso */
18.4,	21.3,	24.3,	31.6,	34.8,	38.8,	24.9,	26.1,	27.3,		/* Lower Torso */
7.48,	8.75,	10.05,	6.36,	7.43,	8.54,	27.2,	29.8,	32.4,		/* r Upper Arm */
7.48,	8.75,	10.05,	6.36,	7.43,	8.54,	27.2,	29.8,	32.4,		/* l Upper Arm */
4.97,	5.49,	6.02,	7.45,	8.24,	9.03,	21.5,	24.5,	25.9,		/* r Lower Arm */
4.97,	5.49,	6.02,	7.45,	8.24,	9.03,	21.5,	24.5,	25.9,		/* l Lower Arm */
10.4,	12.4,	14.6,	10.4,	12.4,	14.6,	35.1,	37.4,	39.7,		/* r Upper Leg */
10.4,	12.4,	14.6,	10.4,	12.4,	14.6,	35.1,	37.4,	39.7,		/* l Upper Leg */
9.6,	10.8,	12.0,	9.6,	10.8,	12.0,	30.7,	33.2,	35.7,		/* r Lower Leg */
9.6,	10.8,	12.0,	9.6,	10.8,	12.0,	30.7,	33.2,	35.7,		/* l Lower Leg */
16.0,	17.3,	18.6,	8.6,	9.3,	10.0,	9.2,	11.1,	13.6,		/* r Foot */
16.0,	17.3,	18.6,	8.6,	9.3,	10.0,	9.2,	11.1,	13.6,		/* l Foot */
2.1,	2.5,	2.9,	6.9,	7.6,	8.2,	8.5,	8.8,	9.5,		/* r Hand */
2.1,	2.5,	2.9,	6.9,	7.6,	8.2,	8.5,	8.8,	9.5,		/* l Hand */
1.0,	1.0,	1.0,	1.0,	1.0,	1.0,	11.3,	13.1,	14.8,		/* r Clavicle */
1.0,	1.0,	1.0,	1.0,	1.0,	1.0,	11.3,	13.1,	14.8,		/* l Clavicle */
2.2,	2.2,	2.2,	2.75,	2.75,	2.75,	2.2,	2.2,	2.2,		/* r eye */
2.2,	2.2,	2.2,	2.75,	2.75,	2.75,	2.2,	2.2,	2.2,		/* l eye */
4.78,	5.38,	5.98,	1.0,	1.0,	1.0,	10.2,	11.0,	11.6,		/* eye location */
4.0,	4.0,	4.0,	2.7,	2.7,	2.7,	12.1,	12.3,	12.6,		/* eye location */
16.3,	17.8,	19.2,	2.7,	2.7,	2.7,	12.1,	12.3,	12.6,		/* eye location */
10.4,	11.7,	13.4,	8.0,	8.9,	9.8,	5.1,	5.3,	5.5,		/* ball of right foot */
10.4,	11.7,	13.4,	8.0,	8.9,	9.8,	5.1,	5.3,	5.5,		/* ball of left foot */
2.1,	2.5,	2.9,	6.9,	7.6,	8.2,	8.4,	8.8,	9.5,		/* knuckles of right hand */
2.1,	2.5,	2.9,	6.9,	7.6,	8.2,	8.4,	8.8,	9.5,		/* knuckles of left hand */

D Figure definition file, BODY.FIG

This is a copy of the current version of the **PEABODY** human figure definition file. The file is used to define the relationships required to create the data structures necessary to represent and display a human figure using the **JACK** interface.

```
/* Note : the commented sites are sites that are not used in defining
 * the humanoid figure. There are kept there for possible future
 * needs. If one were to use these sites, one has to enter the
 * new site POSITIONS, since the existing sites do not make any
 * sense.
 */
figure (arch) {
  archive = arch;
  segment left_toes {
    psurf = "ltoes.pss" * scale(ltoesx, ltoesy, ltoesz);
    site proximal->location = xyz(0,0,0) *
                                trans(-lfootx,0,ltoesz);
    site distal->location   = xyz(0,0,0)   * trans(0,0,ltoesz);
    site lateral->location  = xyz(-90deg,0,0) * trans(0,0,ltoesz);
    site medial->location   = xyz(90deg,0,0) * trans(0,0,ltoesz);
    mass = ltoesmass;
  }

  segment right_toes {
    psurf = "rtoes.pss" * scale(rtoesx,rtoesy,rtoesz);
    site proximal->location = xyz(0,0,0) *
                                trans(-rfootx,0,rtoesz);
    site distal->location   = xyz(0,0,0)   * trans(0,0,rtoesz);
    site medial->location   = xyz(-90deg,0,0) * trans(0,0,rtoesz);
    site lateral->location  = xyz(90deg,0,0) * trans(0,0,rtoesz);
    mass = rtoesmass;
  }

  segment right_fingers {
    psurf = "rfingers.pss" * scale(rfingersx,rfingersy,rfingersz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0)   * trans(0,0,rfingersz);
    site medial->location   = xyz(-90deg,0,0) * trans(0,0,rfingersz);
    site lateral->location  = xyz(90deg,0,0) * trans(0,0,rfingersz);
    mass = rfingersmass;
  }

  segment left_fingers {
    psurf = "lfingers.pss" * scale(lfingersx,lfingersy,lfingersz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0)   * trans(0,0,lfingersz);
    site lateral->location  = xyz(-90deg,0,0) * trans(0,0,lfingersz);
    site medial->location   = xyz(90deg,0,0) * trans(0,0,lfingersz);
    mass = lfingersmass;
  }
}
```

```

    segment left_foot {
psurf = "lfoot.pss" * scale(lfootx,lfooty,lfootz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location   = xyz(0,0,0) * trans(0,0,lfootz);
site lateral->location  = xyz(-90deg,0,0) * trans(0,0,lfootz);
site medial->location   = xyz(90deg,0,0) * trans(0,0,lfootz);
mass = lfootmass;
    }

    segment right_foot {
psurf = "rfoot.pss" * scale(rfootx,rfooty,rfootz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location   = xyz(0,0,0) * trans(0,0,rfootz);
site medial->location   = xyz(-90deg,0,0) * trans(0,0,rfootz);
site lateral->location  = xyz(90deg,0,0) * trans(0,0,rfootz);
mass = rfootmass;
    }

    segment right_lower_leg {
psurf = "rlleg.pss" * scale(rlowlegx,rlowlegy,rlowlegz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location   = xyz(0,0,0) * trans(0,0,rlowlegz);
/*
*     site medial->location   = xyz(-90deg,0,0) * trans(0,0,rlowlegz);
*     site lateral->location  = xyz(90deg,0,0) * trans(0,0,rlowlegz);
*/
mass = rlowlegmass;
    }

    segment left_lower_leg {
psurf = "llleg.pss" * scale(llowlegx,llowlegy,llowlegz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
/* here */
site distal->location   = xyz(0,0,0) * trans(0,0,llowlegz);
/*
*     site lateral->location  = xyz(-90deg,0,0) * trans(0,0,llowlegz);
*     site medial->location   = xyz(90deg,0,0) * trans(0,0,llowlegz);
*/
mass = llowlegmass;
    }

    segment right_upper_leg {
psurf = "ruleg.pss" * scale(ruplegx,ruplegy,ruplegz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location   = xyz(0,0,0) * trans(0,0,ruplegz);
/*
*     site medial->location   = xyz(-90deg,0,0) * trans(0,0,ruplegz);
*     site lateral->location  = xyz(90deg,0,0) * trans(0,0,ruplegz);
*/
mass = ruplegmass;
    }

```

```

}

segment left_upper_leg {
psurf = "luleg.pss" * scale(luplegx,luplegy,luplegz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location = xyz(0,0,0) * trans(0,0,luplegz);
/*
*      site lateral->location = xyz(-90deg,0,0) * trans(0,0,luplegz);
*      site medial->location = xyz(90deg,0,0) * trans(0,0,luplegz);
*/
mass = luplegmass;
}

segment right_hip {
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site lateral->location = xyz(90deg,0,0) *
trans(0,0,ltorsox * .5273);
/*
*      site distal->location = xyz(0,0,0) *
*                          trans(0,0,ltorsox * .5273);
*      site medial->location = xyz(-90deg,0,0) *
*                          trans(0,0,ltorsox * .5273);
*/
mass = rhipmass;
}

segment left_hip {
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site lateral->location = xyz(-90deg,0,0) *
trans(0,0,ltorsox * .5273);
/*
*      site distal->location = xyz(0,0,0) *
*                          trans(0,0,ltorsox * .5273);
*      site medial->location = xyz(90deg,0,0) *
*                          trans(0,0,ltorsox * .5273);
*/
mass = lhipmass;
}

segment lower_torso {
psurf = "ltorso.pss" * scale(ltorsox,ltorsoy,ltorsoz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location = xyz(0,0,0) * trans(0,0,ltorsoz);
/*
*      site left->location = xyz(-90deg,0,0) * trans(0,0,ltorsoz);
*      site right->location = xyz(90deg,0,0) * trans(0,0,ltorsoz);
*/
mass = ltorsomass;
}

```

```

    segment center_torso {
psurf = "ctorso.pss" * scale(ctorsox,ctorsoy,ctorsoz);
site proximal->location = xyz(0,0,0) * trans(0,0,0);
site distal->location   = xyz(0,0,0) * trans(0,0,ctorsoz);
/*
*     site left->location   = xyz(-90deg,0,0) * trans(0,0,ctorsoz);
*     site right->location  = xyz(90deg,0,0)  * trans(0,0,ctorsoz);
*/
    mass = ctorsomass;
}

segment upper_torso {
    site proximal->location = xyz(0,0,0)      * trans(0,0,0);
    site distal->location  = xyz(0,0,0)      * trans(0,0,0);
    site left->location    = xyz(-90deg,0,0) * trans(0,0,0);
    site right->location   = xyz(90deg,0,0)  * trans(0,0,0);
    mass = uptorsomass;
}

segment bottom_head {
    psurf = "head.pss" * scale(botheadx,botheady,botheadz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site lsochet->location  = xyz(0,0,0) *
        trans(eyelocx,eyelocy,eyelocz);
    site rsochet->location  = xyz(0,0,0) *
        trans(eyelocx,-eyelocy,eyelocz);
/*
*     site distal->location  = xyz(0,0,0) * trans(0,0,neckz * .4620);
*     site left->location    = xyz(0,-90deg,0) *
*         trans(0,0,neckz * .4620);
*     site right->location   = xyz(0,90deg,0) *
*         trans(0,0,neckz * .4620);
*/
    mass = botheadmass;
}
/*

segment top_head {
    site proximal->location = xyz(0,0,0)      * trans(0,0,0);
    site distal->location  = xyz(0,0,0)      * trans(0,0,0);
    site left->location    = xyz(-90deg,0,0) * trans(0,0,0);
    site right->location   = xyz(90deg,0,0)  * trans(0,0,0);
    mass = topheadmass;
}
*/

segment neck {
    psurf = "neck.pss" * scale(neckx,necky,neckz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0) * trans(0,0,neckz * .4620);

```

```

/*
 *   site left->location      = xyz(-90deg,0,0) *
 *                           trans(0,0,neckz * .4620);
 *   site right->location    = xyz(90deg,0,0) *
 *                           trans(0,0,neckz * .4620);
 */
    mass = neckmass;
}

segment right_clavicle {
    psurf = "rclav.pss" * scale(rclavx,rclavy,rclavz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site lateral->location  = xyz(90deg,0,0) * trans(0,0,rclavz);
/*
 *   site distal->location   = xyz(0,0,0) * trans(0,0,rclavz);
 *   site medial->location  = xyz(-90deg,0,0) * trans(0,0,rclavz);
 */
    mass = rclavmass;
}

segment left_clavicle {
    psurf = "lclav.pss" * scale(lclavx,lclavy,lclavz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site lateral->location  = xyz(-90deg,0,0) * trans(0,0,lclavz);
/*
 *   site distal->location   = xyz(0,0,0) * trans(0,0,lclavz);
 *   site medial->location  = xyz(90deg,0,0) * trans(0,0,lclavz);
 */
    mass = lclavmass;
}

segment right_sternum {
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location  = xyz(0,0,0) * trans(0,0,ctorsoy-rclavz);
/*
 *   site medial->location   = xyz(-90deg,0,0) *
 *                           trans(0,0,ctorsoy-rclavz);
 *   site lateral->location  = xyz(90deg,0,0) *
 *                           trans(0,0,ctorsoy-rclavz);
 */
    mass = rsternummass;
}

segment left_sternum {
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location  = xyz(0,0,0) * trans(0,0,ctorsoy-lclavz);
/*
 *   site lateral->location  = xyz(-90deg,0,0) *
 *                           trans(0,0,ctorsoy-lclavz);
 *   site medial->location  = xyz(90deg,0,0) *

```



```

*                                     trans(0,0,ctorsoy-lclavz);
*/
    mass = lsternummass;
}

segment right_upper_arm {
    psurf = "ruarm.pss" * scale(ruparmx,ruparmy,ruparmz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0) * trans(0,0,ruparmz);
/*
*     site medial->location   = xyz(-90deg,0,0) * trans(0,0,ruparmz);
*     site lateral->location  = xyz(90deg,0,0)  * trans(0,0,ruparmz);
*/
    mass = ruparmmass;
}

segment left_upper_arm {
    psurf = "luarm.pss" * scale(luparmx,luparmy,luparmz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0) * trans(0,0,luparmz);
/*
*     site lateral->location  = xyz(-90deg,0,0) * trans(0,0,luparmz);
*     site medial->location   = xyz(90deg,0,0)  * trans(0,0,luparmz);
*/
    mass = luparmmass;
}

segment right_lower_arm {
    psurf = "rlarm.pss" * scale(rlowarmx,rlowarmy,rlowarmz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0) * trans(0,0,rlowarmz);
/*
*     site medial->location   = xyz(0,-90deg,0,0) * trans(0,0,rlowarmz);
*     site lateral->location  = xyz(90deg,0,0)  * trans(0,0,rlowarmz);
*/
    mass = rlowarmmass;
}

segment left_lower_arm {
    psurf = "llarm.pss" * scale(llowarmx,llowarmy,llowarmz);
    site proximal->location = xyz(0,0,0) * trans(0,0,0);
    site distal->location   = xyz(0,0,0) * trans(0,0,llowarmz);
/*
*     site lateral->location  = xyz(-90deg,0,0) * trans(0,0,llowarmz);
*     site medial->location   = xyz(90deg,0,0)  * trans(0,0,llowarmz);
*/
    mass = llowarmmass;
}

segment right_hand {

```

```

    psurf = "rhand.pss" * scale(rhandx,rhandy,rhandz);
    site proximal->location = xyz(0,0,0)      * trans(0,0,0);
    site distal->location   = xyz(0,0,0)      * trans(0,0,rhandz);
    site medial->location   = xyz(0,-90deg,0) * trans(0,0,rhandz);
    site lateral->location  = xyz(90deg,0,0)  * trans(0,0,rhandz);
    mass = rhandmass;
}

segment left_hand {
    psurf = "lhand.pss" * scale(lhandx,lhandy,lhandz);
    site proximal->location = xyz(0,0,0)      * trans(0,0,0);
    site distal->location   = xyz(0,0,0)      * trans(0,0,lhandz);
    site lateral->location  = xyz(-90deg,0,0) * trans(0,0,lhandz);
    site medial->location   = xyz(90deg,0,0)  * trans(0,0,lhandz);
    mass = lhandmass;
}

segment right_eyeball {
    psurf = "reye.pss" * scale(reyex,reyey,reyez);
    site point->location = xyz(-90deg,0,90deg) *
        trans(-reyex,0,reyez * 0.5);
    site sight->location = xyz(0,0,0) * trans(0,0,0);
    mass = reyemass;
}

segment left_eyeball {
    psurf = "leye.pss" * scale(leyex,leyey,leyez);
    site point->location = xyz(90deg,0,90deg) *
        trans(leyex,0,leyez * 0.5);
    site sight->location = xyz(0,0,0) * trans(0,0,0);
    mass = leyemass;
}

segment body_root {
/*
*     site proximal->location = xyz(0,0,0)      * trans(0,0,0);
*/
    site distal->location   = xyz(0,0,0)      * trans(0,0,0);
    site left->location     = xyz(-90deg,0,0)  * trans(0,0,0);
    site right->location    = xyz(90deg,0,0)   * trans(0,0,0);
    site floor->location   = xyz(90deg,90deg,0) *
        trans(0,0,-flooroffset );
    mass = bodyrootmass;
}
joint right_shoulder {
    connect right_clavicle.lateral to
        right_upper_arm.proximal;
    type = R(0,0,-1) * R(-1,0,0) * R(0,1,0);
    ulimit = (right_shoulder_z_ulimit,right_shoulder_x_ulimit,right_shoulder_y_ulimit);
    llimit = (right_shoulder_z_llimit,right_shoulder_x_llimit,right_shoulder_y_llimit);
}

```

```

}
joint right_elbow {
    connect right_upper_arm.distal to
        right_lower_arm.proximal;
    type = R(0,1,0);
ulimit = (right_elbow_y_ulimit);
llimit = (right_elbow_y_llimit);
}

joint right_wrist {
    connect right_lower_arm.distal to
        right_hand.proximal;
    type = R(0,0,-1) * R(-1,0,0) * R(0,1,0);
ulimit = (right_wrist_z_ulimit,right_wrist_x_ulimit,right_wrist_y_ulimit);
llimit = (right_wrist_z_llimit,right_wrist_x_llimit,right_wrist_y_llimit);
}
joint left_shoulder {
    connect left_clavicle.lateral to
        left_upper_arm.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
    ulimit = (left_shoulder_z_ulimit,left_shoulder_x_ulimit,left_shoulder_y_ulimit);
    llimit = (left_shoulder_z_llimit,left_shoulder_x_llimit,left_shoulder_y_llimit);
}

joint left_elbow {
    connect left_upper_arm.distal to
        left_lower_arm.proximal;
    type = R(0,1,0);
ulimit = (left_elbow_y_ulimit);
llimit = (left_elbow_y_llimit);
}
joint left_wrist {
    connect left_lower_arm.distal to
        left_hand.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
ulimit = (left_wrist_z_ulimit,left_wrist_x_ulimit,left_wrist_y_ulimit);
llimit = (left_wrist_z_llimit,left_wrist_x_llimit,left_wrist_y_llimit);
}

joint right_hip_joint {
    connect right_hip.lateral to
        right_upper_leg.proximal;
    type = R(0,0,-1) * R(-1,0,0) * R(0,1,0);
ulimit = (right_hip_z_ulimit,right_hip_x_ulimit,right_hip_y_ulimit);
llimit = (right_hip_z_llimit,right_hip_x_llimit,right_hip_y_llimit);
}
joint right_knee {
    connect right_upper_leg.distal to
        right_lower_leg.proximal;
    type = R(0,-1,0);
ulimit = (right_knee_y_ulimit);
}

```

```

llimit = (right_knee_y_llimit);
}
joint right_ankle {
    connect right_lower_leg.distal to
        right_foot.proximal;
    type = R(0,0,-1) * R(-1,0,0) * R(0,1,0);
ulimit = (right_ankle_z_ulimit,right_ankle_x_ulimit,right_ankle_y_ulimit);
llimit = (right_ankle_z_llimit,right_ankle_x_llimit,right_ankle_y_llimit);
}

joint left_hip_joint {
    connect left_hip.lateral to
        left_upper_leg.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
ulimit = (left_hip_z_ulimit,left_hip_x_ulimit,left_hip_y_ulimit);
llimit = (left_hip_z_llimit,left_hip_x_llimit,left_hip_y_llimit);
}
joint left_knee {
    connect left_upper_leg.distal to
        left_lower_leg.proximal;
    type = R(0,-1,0);
ulimit = (left_knee_y_ulimit);
llimit = (left_knee_y_llimit);
}

joint left_ankle {
    connect left_lower_leg.distal to
        left_foot.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
ulimit = (left_ankle_z_ulimit,left_ankle_x_ulimit,left_ankle_y_ulimit);
llimit = (left_ankle_z_llimit,left_ankle_x_llimit,left_ankle_y_llimit);
}
joint right_clavicle_joint {
    connect right_sternum.distal to
        right_clavicle.proximal;
    type = R(-1,0,0) * R(0,1,0);
ulimit = (right_clavicle_x_ulimit,right_clavicle_y_ulimit);
llimit = (right_clavicle_x_llimit,right_clavicle_y_llimit);
}

joint left_clavicle_joint {
    connect left_sternum.distal to
        left_clavicle.proximal;
    type = R(1,0,0) * R(0,1,0);
ulimit = (left_clavicle_x_ulimit,left_clavicle_y_ulimit);
llimit = (left_clavicle_x_llimit,left_clavicle_y_llimit);
}
joint waist {
    connect lower_torso.distal to
        center_torso.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
}

```

```

ulimit = (waist_z_ulimit,waist_x_ulimit,waist_y_ulimit);
llimit = (waist_z_llimit,waist_x_llimit,waist_y_llimit);
}
joint atlanto_occipital { /* Head-neck joint */
    connect neck.distal to
        bottom_head.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
ulimit = (neck_z_ulimit,neck_x_ulimit,neck_y_ulimit);
llimit = (neck_z_llimit,neck_x_llimit,neck_y_llimit);
}

joint solar_plexus { /* Mid-torso location */
    connect center_torso.distal to
        upper_torso.proximal;
/* no joint movement for solar_plexus */
}
joint right_knuckles {
    connect right_hand.distal to
        right_fingers.proximal;
    type = R(0,1,0);
ulimit = (right_knuckles_y_ulimit);
llimit = (right_knuckles_y_llimit);
}
joint left_knuckles {
    connect left_hand.distal to
        left_fingers.proximal;
    type = R(0,1,0);
ulimit = (left_knuckles_y_ulimit);
llimit = (left_knuckles_y_llimit);
}

joint right_ball_of_foot {
    connect right_foot.distal to
        right_toes.proximal;
    type = R(0,1,0);
ulimit = (right_ball_of_foot_y_ulimit);
llimit = (right_ball_of_foot_y_llimit);
}
joint left_ball_of_foot {
    connect left_foot.distal to
        left_toes.proximal;
    type = R(0,1,0);
ulimit = (left_ball_of_foot_y_ulimit);
llimit = (left_ball_of_foot_y_llimit);
}

joint base_of_neck {
    connect upper_torso.distal to
        neck.proximal;
/* no joint movement for base of neck */
}

```

```

    joint right_sternoclavicular { /* Sternum - clavicle joint */
        connect upper_torso.right to
            right_sternum.proximal;
/* no joint movement for sternum-clavicle joint */
    }
    joint left_sternoclavicular { /* Sternum - clavicle joint */
        connect upper_torso.left to
            left_sternum.proximal;
/* no joint movement for sternum-clavicle joint */
    }

    joint right_eye {
        connect right_eyeball.point to
            bottom_head.rsocket;
/* no joint movement for eye socket */
    }
    joint left_eye {
        connect left_eyeball.point to
            bottom_head.lsocket;
/* no joint movement for eye socket */
    }
    joint root_ltorso {
        connect body_root.distal to
            lower_torso.proximal;
/* no joint movement for body root */
    }

    joint root_rhip {
        connect body_root.right to
            right_hip.proximal;
/* no joint movement for body root */
    }
    joint root_lhip {
        connect body_root.left to
            left_hip.proximal;
/* no joint movement for body root */
    }
}

```

E Segmented torso definition file

Although a rigid torso is acceptable in many applications, it is not really satisfactory. To have the torso more natural, Jianmin Zhao split the center torso (from lumbar to thorax) into 5 segments. Geometrically, the lumbar part is not so long as the thorax part, though it contributes more motion than the thorax part. So we split the lumbar part into 3 segments and the thorax part into 2 segments. Having split the torso into 5 segments, we choose the joint sites at the intersections of the spinal curve with the respective segments. Degrees of freedom and joint limits were given according to the contribution of each part — the lumbar part contributes significantly more motion than the thorax part. Data was not obtained from experiment but only estimated from anatomic qualitative descriptions. The result appears quite acceptable.

Following is the alternative 5-segmented torso peabody code that can be used instead of the rigid torso.

```
segment lumbar1_torso {
  psurf = "lumbar1.pss" * scale(ctorsox, ctorsoy, ctorsoz);
  site proximal->location = xyz(0,0,0) + trans(0, 0, 0);
  site distal->location = xyz(0,0,0) + trans(0.1402, 0, lumbar1);
}
segment lumbar2_torso {
  psurf = "lumbar2.pss" * scale(ctorsox, ctorsoy, ctorsoz);
  site proximal->location = xyz(0, 0, 0) + trans(0.1402, 0, 0);
  site distal->location = xyz(0,0,0) + trans(0.0700, 0, lumbar2);
}
segment lumbar3_torso {
  psurf = "lumbar3.pss" * scale(ctorsox, ctorsoy, ctorsoz);
  site proximal->location = xyz(0, 0, 0) + trans(0.0700, 0, 0);
  site distal->location = xyz(0,0,0) + trans(-0.0701, 0, lumbar3);
}
segment thorax1_torso {
  psurf = "thorax1.pss" * scale(ctorsox, ctorsoy, ctorsoz);
  site proximal->location = xyz(0, 0, 0) + trans(-0.0701, 0, 0);
  site distal->location = xyz(0, 0, 0) + trans(0.3854, 0, thorax1);
}
segment thorax2_torso {
  psurf = "thorax2.pss" * scale(ctorsox, ctorsoy, ctorsoz);
  site proximal->location = xyz(0, 0, 0) + trans(0.3854, 0, 0);
  site distal->location = xyz(0, 0, 0) + trans(0, 0, thorax2);
}
segment upper_torso {
  site proximal->location = xyz(0,0,0) + trans(0,0,0);
  site distal->location = xyz(0,0,0) + trans(0,0,0);
  site left->location = xyz(-90deg,0,0) + trans(0,0,0);
  site right->location = xyz(90deg,0,0) + trans(0,0,0);
  mass = uptorsomass;
}
joint waist {
  connect lower_torso.distal to
    lumbar1_torso.proximal;
  type = R(0,0,1) * R(1,0,0) * R(0,1,0);
  ulimit = (waist_z_ulimit,waist_x_ulimit,waist_y_ulimit);
  llimit = (waist_z_llimit,waist_x_llimit,waist_y_llimit);
}
joint vertebrae1 {
  connect lumbar1_torso.distal to
```

```

        lumbar2_torso.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
    ulimit = (vert1_z_ulimit,vert1_x_ulimit,vert1_y_ulimit);
    llimit = (vert1_z_llimit,vert1_x_llimit,vert1_y_llimit);
}
joint vertebrae2 {
    connect lumbar2_torso.distal to
        lumbar3_torso.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
    ulimit = (vert2_z_ulimit,vert2_x_ulimit,vert2_y_ulimit);
    llimit = (vert2_z_llimit,vert2_x_llimit,vert2_y_llimit);
}
joint vertebrae3 {
    connect lumbar3_torso.distal to
        thorax1_torso.proximal;
    type = R(0,0,1) * R(1,0,0) * R(0,1,0);
    ulimit = (vert3_z_ulimit,vert3_x_ulimit,vert3_y_ulimit);
    llimit = (vert3_z_llimit,vert3_x_llimit,vert3_y_llimit);
}
joint vertebrae4 {
    connect thorax1_torso.distal to
        thorax2_torso.proximal;
    type = R(1,0,0) * R(0, 1, 0);
    ulimit = (vert4_x_ulimit,vert4_y_ulimit);
    llimit = (vert4_x_llimit,vert4_y_llimit);
}

```


F Sample Figure Description File, MALE50.FIG

A sample figure description file which is used to supply the values to variables found in the “**BODY.FIG**” file is contained in this appendix. All the variable names used and their associated values are listed. This is the file which generated the male bodies in Figures 1 and 2. These files can be generated by **SASS**.

format: variable name = value;

```
    botheadx = 10.00cm;
botheady = 7.85cm;
botheadz = 22.70cm;
neckx = 6.15cm;
necky = 6.15cm;
neckz = 10.00cm;
ctorsox = 12.50cm;
ctorsoy = 19.60cm;
ctorsoz = 47.60cm;
ltorsox = 11.60cm;
ltorsoy = 16.95cm;
ltorsoz = 13.10cm;
ruparmx = 5.35cm;
ruparmy = 4.55cm;
ruparmz = 33.40cm;
luparmx = 5.35cm;
luparmy = 4.55cm;
luparmz = 33.40cm;
rlowarmx = 3.76cm;
rlowarmy = 5.63cm;
rlowarmz = 28.80cm;
llowarmx = 3.76cm;
llowarmy = 5.63cm;
llowarmz = 28.80cm;
ruplegx = 7.60cm;
ruplegy = 7.60cm;
ruplegz = 43.40cm;
luplegx = 7.60cm;
luplegy = 7.60cm;
luplegz = 43.40cm;
rlowlegx = 5.70cm;
rlowlegy = 5.70cm;
rlowlegz = 36.80cm;
llowlegx = 5.70cm;
llowlegy = 5.70cm;
llowlegz = 36.80cm;
rfootx = 14.55cm;
rfooty = 4.95cm;
rfootz = 13.90cm;
lfootx = 14.55cm;
lfooty = 4.95cm;
lfootz = 13.90cm;
rhandx = 1.50cm;
rhandy = 4.45cm;
rhandz = 11.50cm;
lhandx = 1.50cm;
```

lhandy = 4.45cm;
lhandz = 11.50cm;
rclavx = 0.50cm;
rclavy = 0.50cm;
rclavz = 17.20cm;
lclavx = 0.50cm;
lclavy = 0.50cm;
lclavz = 17.20cm;
reyex = 2.20cm;
reyey = 2.75cm;
reyez = 2.20cm;
leyex = 2.20cm;
leyey = 2.75cm;
leyez = 2.20cm;
eyelocx = 9.80cm;
eyelocy = 3.10cm;
eyelocz = 11.60cm;
rtoesx = 7.40cm;
rtoesy = 4.95cm;
rtoesz = 6.00cm;
ltoesx = 7.40cm;
ltoesy = 4.95cm;
ltoesz = 6.00cm;
rfingersx = 3.00cm;
rfingersy = 4.45cm;
rfingersz = 8.10cm;
lfingersx = 3.00cm;
lfingersy = 4.45cm;
lfingersz = 8.10cm;
flooroffset = 94.10cm;
mass variables

rfootmass = 1.15kg;
lfootmass = 1.15kg;
rlolegmass = 3.78kg;
llolegmass = 3.78kg;
ruplegmass = 8.22kg;
luplegmass = 8.22kg;
rhipmass = 3.45kg;
lhipmass = 3.45kg;
ltorsomass = 3.45kg;
ctorsomass = 11.34kg;
uptorsomass = 14.06kg;
botheadmass = 1.64kg;
topheadmass = 4.85kg;
neckmass = 0.16kg;
rclavmass = 2.47kg;
lclavmass = 2.47kg;
rsternummass = 0.16kg;
lsternummass = 0.16kg;
ruparmmass = 2.30kg;
luparmmass = 2.30kg;
rloarmmass = 1.32kg;

```

lloarmmass = 1.32kg;
rhandmass = 0.49kg;
lhandmass = 0.49kg;
reyemass = 0.00kg;
leyemass = 0.00kg;
bodyrootmass = 0.00kg;
rtoesmass = 0.00kg;
ltoesmass = 0.00kg;
rfingersmass = 0.00kg;
lfingersmass = 0.00kg;
joint variables

neck_z_ulimit = 99.6deg;
neck_z_llimit = -99.1deg;
neck_y_ulimit = 71.0deg;
neck_y_llimit = -103.0deg;
neck_x_ulimit = 63.5deg;
neck_x_llimit = -63.5deg;
/* the clavicle values are educated guesses */
right_clavicle_x_ulimit = 30.0deg;
right_clavicle_x_llimit = -15.0deg;
right_clavicle_y_ulimit = 45.0deg;
right_clavicle_y_llimit = -10.0deg;
left_clavicle_x_ulimit = 30.0deg;
left_clavicle_x_llimit = -15.0deg;
left_clavicle_y_ulimit = 45.0deg;
left_clavicle_y_llimit = -10.0deg;
right_shoulder_x_ulimit = 162.0deg;
right_shoulder_x_llimit = -63.0deg;
right_shoulder_z_ulimit = 96.7deg;
right_shoulder_z_llimit = -126.6deg;
right_shoulder_y_ulimit = 210.9deg;
right_shoulder_y_llimit = -83.3deg;
left_shoulder_x_ulimit = 162.0deg;
left_shoulder_x_llimit = -63.0deg;
left_shoulder_z_ulimit = 96.7deg;
left_shoulder_z_llimit = -126.6deg;
left_shoulder_y_ulimit = 210.9deg;
left_shoulder_y_llimit = -83.3deg;
right_elbow_y_ulimit = 159.0deg;
right_elbow_y_llimit = 0.0deg;
left_elbow_y_ulimit = 159.0deg;
left_elbow_y_llimit = 0.0deg;
right_wrist_z_ulimit = 26.1deg;
right_wrist_z_llimit = -215.8deg;
right_wrist_x_ulimit = 36.7deg;
right_wrist_x_llimit = -47.9deg;
right_wrist_y_ulimit = 94.8deg;
right_wrist_y_llimit = -78.0deg;
left_wrist_z_ulimit = 26.1deg;
left_wrist_z_llimit = -215.8deg;
left_wrist_x_ulimit = 36.7deg;
left_wrist_x_llimit = -47.9deg;

```

```

left_wrist_y_ulimit = 94.8deg;
left_wrist_y_llimit = -78.0deg;
/* the waist values are educated guesses */
waist_y_ulimit = 60.0deg;
waist_y_llimit = 0.0deg;
waist_x_ulimit = 50.0deg;
waist_x_llimit = -50.0deg;
waist_z_ulimit = 75.0deg;
waist_z_llimit = -75.0deg;
right_hip_y_ulimit = 148.0deg;
right_hip_y_llimit = -10.0deg;
right_hip_x_ulimit = 53.5deg;
right_hip_x_llimit = -51.0deg;
right_hip_z_ulimit = 51.0deg;
right_hip_z_llimit = -56.0deg;
left_hip_y_ulimit = 148.0deg;
left_hip_y_llimit = -10.0deg;
left_hip_x_ulimit = 53.5deg;
left_hip_x_llimit = -51.0deg;
left_hip_z_ulimit = 51.0deg;
left_hip_z_llimit = -56.0deg;
right_knee_y_ulimit = 145.6deg;
right_knee_y_llimit = 0.0deg;
left_knee_y_ulimit = 145.6deg;
left_knee_y_llimit = 0.0deg;
right_ankle_y_llimit = -79.6deg;
right_ankle_y_ulimit = 19.9deg;
right_ankle_x_llimit = -39.0deg;
right_ankle_x_ulimit = 35.0deg;
right_ankle_z_llimit = -55.0deg;
right_ankle_z_ulimit = 63.0deg;
left_ankle_y_llimit = -79.6deg;
left_ankle_y_ulimit = 19.9deg;
left_ankle_x_llimit = -39.0deg;
left_ankle_x_ulimit = 35.0deg;
left_ankle_z_llimit = -55.0deg;
left_ankle_z_ulimit = 63.0deg;
left_ball_of_foot_y_ulimit = 45.0deg;
left_ball_of_foot_y_llimit = 0.0deg;
right_ball_of_foot_y_ulimit = 45.0deg;
right_ball_of_foot_y_llimit = 0.0deg;
right_knuckles_y_ulimit = 90.0deg;
right_knuckles_y_llimit = 0.0deg;
left_knuckles_y_ulimit = 90.0deg;
left_knuckles_y_llimit = 0.0deg;

```

Figure Description File and Archive File

figure ["body.fig"] ("skinny.a");

G Joint motion variable list

The list of all of the joint motion field names and a brief description of the use/purpose for each of the variable names is contained in this appendix.

motion by degree of freedom	motion, English explanation
neck_z_ulimit	/* Neck, rotation right */
neck_z_llimit	/* Neck, rotation left */
neck_y_ulimit	/* Neck, Flexion */
neck_y_llimit	/* Neck, extension */
neck_x_ulimit	/* Neck, lateral right */
neck_x_llimit	/* Neck, lateral left */
right_clavicle_x_ulimit	/* clavicle, pull shoulders forward */
right_clavicle_x_llimit	/* clavicle, pull houlders backward */
right_clavicle_y_ulimit	/* clavicle, raise shoulders (shrug) */
right_clavicle_y_llimit	/* clavicle, drop shoulders */
left_clavicle_x_ulimit	/* clavicle, pull shoulders forward */
left_clavicle_x_llimit	/* clavicle, pull houlders backward */
left_clavicle_y_ulimit	/* clavicle, raise shoulders (shrug) */
left_clavicle_y_llimit	/* clavicle, drop shoulders */
right_shoulder_x_ulimit	/* Shoulder, abduction */
right_shoulder_x_llimit	/* Shoulder, adduction */
right_shoulder_z_ulimit	/* Shoulder, rotation lat */
right_shoulder_z_llimit	/* Shoulder, rotation med */
right_shoulder_y_ulimit	/* Shoulder, flexion */
right_shoulder_y_llimit	/* Shoulder, (hyper) extension */
left_shoulder_x_ulimit	/* Shoulder, abduction */
left_shoulder_x_llimit	/* Shoulder, adduction */
left_shoulder_z_ulimit	/* Shoulder, rotation lat */
left_shoulder_z_llimit	/* Shoulder, rotation med */
left_shoulder_y_ulimit	/* Shoulder, flexion */
left_shoulder_y_llimit	/* Shoulder, (hyper) extension */
right_elbow_y_ulimit	/* elbow, flexion */
right_elbow_y_llimit	/* elbow, extension */
left_elbow_y_ulimit	/* elbow, flexion */
left_elbow_y_llimit	/* elbow, extension */

right_wrist_z_ulimit	/* forearm, pronation starting in neutral position*/
right_wrist_z_llimit	/* forearm, supination starting in neutral position*/
right_wrist_x_ulimit	/* wrist, radial */
right_wrist_x_llimit	/* wrist, ulnar */
right_wrist_y_ulimit	/* wrist, flexion */
right_wrist_y_llimit	/* wrist, extension */
left_wrist_z_ulimit	/* forearm, pronation starting in neutral position*/
left_wrist_z_llimit	/* forearm, supination starting in neutral position*/
left_wrist_x_ulimit	/* wrist, radial */
left_wrist_x_llimit	/* wrist, ulnar */
left_wrist_y_ulimit	/* wrist, flexion */
left_wrist_y_llimit	/* wrist, extension */
waist_y_ulimit	/* waist, forward bend without hips moving */
waist_y_llimit	/* waist, backward bend without hips moving */
waist_x_ulimit	/* waist, bend to right */
waist_x_llimit	/* waist, bend to left */
waist_z_ulimit	/* waist, twist to left */
waist_z_llimit	/* waist, twist to right */
right_hip_y_ulimit	/* Hip, flexion */
right_hip_y_llimit	/* Hip, extension */
right_hip_x_ulimit	/* Hip, abduction */
right_hip_x_llimit	/* Hip, adduction */
right_hip_z_ulimit	/* Hip, rotation lateral */
right_hip_z_llimit	/* Hip, rotation medial */
left_hip_y_ulimit	/* Hip, flexion */
left_hip_y_llimit	/* Hip, extension */
left_hip_x_ulimit	/* Hip, abduction */
left_hip_x_llimit	/* Hip, adduction */
left_hip_z_ulimit	/* Hip, rotation lateral */
left_hip_z_llimit	/* Hip, rotation medial */
right_knee_y_ulimit	/* knee, flexion */
right_knee_y_llimit	/* knee, extension */
left_knee_y_ulimit	/* knee, flexion */
left_knee_y_llimit	/* knee, extension */
right_ankle_y_llimit	/* ankle, plantar */
right_ankle_y_ulimit	/* ankle, dorsi */
right_ankle_x_llimit	/* ankle, pronation */
right_ankle_x_ulimit	/* ankle, supination */
right_ankle_z_llimit	/* knee, medial rotation */
right_ankle_z_ulimit	/* knee, lateral rotation */
left_ankle_y_llimit	/* ankle, plantar */
left_ankle_y_ulimit	/* ankle, dorsi */
left_ankle_x_llimit	/* ankle, pronation */
left_ankle_x_ulimit	/* ankle, supination */
left_ankle_z_llimit	/* knee, medial rotation */
left_ankle_z_ulimit	/* knee, lateral rotation */

H Male Joint Limits

This appendix contains the joint limit values for males. The values are listed in C-include file format with comments indicating the joint and limit to which the numbers apply. The values are arranged in a 3 by 3 by (number of joints * 2) format.

```
/* Joint limits for human figure model. */
/* MALES: based upon the NASA Man--Systems Integration Standard Manual and */
/* tables (on pages 87 and 88) in Occupational Biomechanics by D. B. Chaffin */
/* and G. B. J. Andersson, 1984, Wiley and Sons, publisher */
/* values for the clavicles and waist were not found in the available */
/* literature so were estimated (i.e. are educated guesses) */

34.9, 49.2, 63.5, 34.5, 52.75, 71.0, 73.3, 86.45, 99.6, /* Neck ul */
-35.5, -49.5, -63.5, -65.4, -84.2, 103.0, -74.3, -86.7, -99.1, /* Neck ll */
20.0, 25.0, 30.0, 35.0, 40.0, 45.0, 999, 999, 999, /* R clavicle ul */
-9.0, -12.0, -15.0, -6.0, -8.0, -10.0, 999, 999, 999, /* R clavicle ll */
20.0, 25.0, 30.0, 35.0, 40.0, 45.0, 999, 999, 999, /* L clavicle ul */
-9.0, -12.0, -15.0, -6.0, -8.0, -10.0, 999, 999, 999, /* L clavicle ll */
173.2, 180.95, 188.7, 164.4, 187.65, 210.9, 46.3, 71.5, 96.7, /* R Shoulder ul */
-33.0, -48.0, -63.0, -39.6, -61.45, -83.3, 90.5, 108.55, 126.6, /* R shoulder ll */
173.2, 180.95, 188.7, 164.4, 187.65, 210.9, 46.3, 71.5, 96.7, /* L Shoulder ul */
-33.0, -48.0, -63.0, -39.6, -61.45, -83.3, 90.5, 108.55, 126.6, /* L shoulder ll */
999, 999, 999, 140.5, 149.75, 159.0, 999, 999, 999, /* R elbow ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R elbow ll */
999, 999, 999, 140.5, 149.75, 159.0, 999, 999, 999, /* L elbow ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L elbow ll */
16.9, 26.8, 36.7, 61.5, 78.15, 94.8, 78.2, 97.15, 116.1, /* R Wrist ul */
-18.6, -33.25, -47.9, -40.1, -59.05, -78.0, -83.4, -104.6, -125.8, /* R wrist ll */
16.9, 26.8, 36.7, 61.5, 78.15, 94.8, 78.2, 97.15, 116.1, /* L Wrist ul */
-18.6, -33.25, -47.9, -40.1, -59.05, -78.0, -83.4, -104.6, -125.8, /* L wrist ll */
30.0, 40.0, 50.0, 30.0, 45.0, 60.0, 65.0, 70.0, 75.0, /* waist ul */
-30.0, -40.0, -50.0, 0.0, 0.0, 0.0, -65.0, -70.0, -75.0, /* waist ll */
26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* R hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* R hip ll */
26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* L hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* L hip ll */
999, 999, 999, 118.4, 132.0, 145.6, 999, 999, 999, /* R knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knee ll */
999, 999, 999, 118.4, 132.0, 145.6, 999, 999, 999, /* L knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knee ll */
11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* R Ankle ul */
-9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* R Ankle ll */
11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* L Ankle ul */
-9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* L Ankle ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* R Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R Ball of Foot ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* L Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L Ball of Foot ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* R Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knuckles ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* L Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knuckles ll */
```

I Female Joint Limits

This appendix contains the joint limit values for females. The values are listed in C-include file format with comments indicating the joint and limit to which the numbers apply. The values are arranged in a 3 by 3 by (number of joints * 2) format.

```
/* Joint limits for human figure model. */
/* FEMALES: based upon the NASA Man--Systems Integration Standard Manual and */
/* tables (on pages 87 an 88) in Occupational Biomechanics by D. B. Chaffin */
/* and G. B. J. Andersson, 1984, Wiley and Sons, publisher */
/* values for the clavicles and waist were not found in the available */
/* literature so were estimated (i.e. are educated guesses) */

37.0, 50.1, 63.2, 46.0, 65.2, 84.4, 74.9, 91.85, 108.8, /* Neck ul */
-29.1, -53.15, -77.2, -64.9, -83.95, -103.0, -72.2, -90.6, -109.0, /* Neck ll */
20.0, 25.0, 30.0, 35.0, 40.0, 45.0, 999, 999, 999, /* R clavicle ul */
-9.0, -12.0, -15.0, -6.0, -8.0, -10.0, 999, 999, 999, /* R clavicle ll */
20.0, 25.0, 30.0, 35.0, 40.0, 45.0, 999, 999, 999, /* L clavicle ul */
-9.0, -12.0, -15.0, -6.0, -8.0, -10.0, 999, 999, 999, /* L clavicle ll */
172.6, 182.75, 192.9, 152.0, 184.5, 217.0, 53.8, 69.8, 85.8, /* R shoulder ul */
-33.0, -48.0, -63.0, -33.7, -60.8, -87.9, -95.8, -113.35, -130.9, /* R shoulder ll */
172.6, 182.75, 192.9, 152.0, 184.5, 217.0, 53.8, 69.8, 85.8, /* L shoulder ul */
-33.0, -48.0, -63.0, -33.7, -60.8, -87.9, -95.8, -113.35, -130.9, /* L shoulder ll */
999, 999, 999, 144.9, 155.4, 165.9, 999, 999, 999, /* R elbow ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R elbow ll */
999, 999, 999, 144.9, 155.4, 165.9, 999, 999, 999, /* L elbow ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L elbow ll */
16.1, 26.1, 36.1, 68.3, 83.2, 98.1, 82.3, 100.6, 118.9, /* R wrist ul */
-21.5, -32.25, -43.0, -42.3, -58.5, -74.7, -90.4, -113.15, -135.9, /* R wrist ll */
16.1, 26.1, 36.1, 68.3, 83.2, 98.1, 82.3, 100.6, 118.9, /* L wrist ul */
-21.5, -32.25, -43.0, -42.3, -58.5, -74.7, -90.4, -113.15, -135.9, /* L wrist ll */
30.0, 40.0, 50.0, 30.0, 45.0, 60.0, 65.0, 70.0, 75.0, /* waist ul */
-30.0, -40.0, -50.0, 0.0, 0.0, 0.0, -65.0, -70.0, -75.0, /* waist ll */
26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* R hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* R hip ll */
26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* L hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* L hip ll */
999, 999, 999, 125.2, 135.2, 145.2, 999, 999, 999, /* R knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knee ll */
999, 999, 999, 125.2, 135.2, 145.2, 999, 999, 999, /* L knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knee ll */
11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* R Ankle ul */
-9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* R Ankle ll */
11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* L Ankle ul */
-9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* L Ankle ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* R Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R Ball of Foot ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* L Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L Ball of Foot ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* R Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knuckles ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* L Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knuckles ll */
```


J JLIMITS.H

This is how the joint limit data were originally provided to the system, as a C language include file. This file has been separated above into a male and female listing of joint limits (Appendix H and I, respectively).

```

/*****
/*  jlimits.h
/*
/*      This file contains the male and female joint limits from
/*  the NASA Man--systems Integration Standards Manual (NASA--STD--3000) */
/*  and Occupational Biomechanics by D. Chaffin and B. Andersson.
/*
/*  There are some values which are unavailable in the literature so
/*  a series of resonable estimates were made. The segments/joints
/*  to which this applies are the clavicles, waist, knuckles of the
/*  hand, and balls of the feet.
/*
/*  The format of the data below is as follows:
/*
/*  lower limit of joint range of motion:  x, y, z (in degrees).
/*  upper limits of joint range of motion: x, y, z (in degrees).
/*
/*  For a joint which has no motion around an axis, the value 999 is
/*  entered in the array for that axis.
/*
*****/

/*  male joint limits  */

float malejlimits[maxjoints][3][3] =
/*      x              y              Z */
{
    34.9,  49.2,   63.5,  34.5,  52.75,  71.0,  73.3,   86.45,  99.6, /* Neck ul */
   -35.5, -49.5,  -63.5, -65.4, -84.2, -103.0, -74.3,  -86.7, -99.1, /* Neck ll */
    20.0,  25.0,   30.0,  35.0,  40.0,  45.0,  999,   999,   999, /* R clavicle ul */
   -9.0, -12.0,  -15.0,  -6.0,  -8.0, -10.0,  999,   999,   999, /* R clavicle ll */
    20.0,  25.0,   30.0,  35.0,  40.0,  45.0,  999,   999,   999, /* L clavicle ul */
   -9.0, -12.0,  -15.0,  -6.0,  -8.0, -10.0,  999,   999,   999, /* L clavicle ll */
   173.2, 180.95, 188.7, 164.4, 187.65, 210.9,  46.3,   71.5,   96.7, /* R Shoulder ul */
   -33.0, -48.0,  -63.0, -39.6, -61.45, -83.3,  90.5,  108.55, 126.6, /* R shoulder ll */
   173.2, 180.95, 188.7, 164.4, 187.65, 210.9,  46.3,   71.5,   96.7, /* L Shoulder ul */
   -33.0, -48.0,  -63.0, -39.6, -61.45, -83.3,  90.5,  108.55, 126.6, /* L shoulder ll */
    999,  999,   999,  140.5, 149.75, 159.0,  999,   999,   999, /* R elbow ul */
    999,  999,   999,   0.0,   0.0,   0.0,  999,   999,   999, /* R elbow ll */
    999,  999,   999,  140.5, 149.75, 159.0,  999,   999,   999, /* L elbow ul */
    999,  999,   999,   0.0,   0.0,   0.0,  999,   999,   999, /* L elbow ll */
    16.9,  26.8,   36.7,  61.5,  78.15,  94.8,  78.2,   97.15, 116.1, /* R Wrist ul */
   -18.6, -33.25, -47.9, -40.1, -59.05, -78.0, -83.4, -104.6, -125.8, /* R wrist ll */
    16.9,  26.8,   36.7,  61.5,  78.15,  94.8,  78.2,   97.15, 116.1, /* L Wrist ul */
   -18.6, -33.25, -47.9, -40.1, -59.05, -78.0, -83.4, -104.6, -125.8, /* L wrist ll */
    30.0,  40.0,   50.0,  30.0,  45.0,  60.0,  65.0,   70.0,   75.0, /* waist ul */
   -30.0, -40.0,  -50.0,   0.0,   0.0,   0.0, -65.0, -70.0, -75.0, /* waist ll */
    26.8,  40.15,  53.5, 116.5, 132.25, 148.0,  18.0,   34.0,   51.0, /* R hip ul */

```

```

-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* R hip ll */
 26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* L hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* L hip ll */
999, 999, 999, 118.4, 132.0, 145.6, 999, 999, 999, /* R knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knee ll */
999, 999, 999, 118.4, 132.0, 145.6, 999, 999, 999, /* L knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knee ll */
 11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* R Ankle ul */
 -9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* R Ankle ll */
 11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* L Ankle ul */
 -9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* L Ankle ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* R Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R Ball of Foot ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* L Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L Ball of Foot ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* R Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knuckles ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* L Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knuckles ll */
}

```

```
/* female joint limits */
```

```
float femalejlimits[maxjoints][3][3] =
```

```

/*      x              y              z */
{
 37.0, 50.1, 63.2, 46.0, 65.2, 84.4, 74.9, 91.85, 108.8, /* Neck ul */
-29.1, -53.15, -77.2, -64.9, -83.95, -103.0, -72.2, -90.6, -109.0, /* Neck ll */
 20.0, 25.0, 30.0, 35.0, 40.0, 45.0, 999, 999, 999, /* R clavicle ul */
 -9.0, -12.0, -15.0, -6.0, -8.0, -10.0, 999, 999, 999, /* R clavicle ll */
 20.0, 25.0, 30.0, 35.0, 40.0, 45.0, 999, 999, 999, /* L clavicle ul */
 -9.0, -12.0, -15.0, -6.0, -8.0, -10.0, 999, 999, 999, /* L clavicle ll */
172.6, 182.75, 192.9, 152.0, 184.5, 217.0, 53.8, 69.8, 85.8, /* R shoulder ul */
-33.0, -48.0, -63.0, -33.7, -60.8, -87.9, -95.8, -113.35, -130.9, /* R shoulder ll */
172.6, 182.75, 192.9, 152.0, 184.5, 217.0, 53.8, 69.8, 85.8, /* L shoulder ul */
-33.0, -48.0, -63.0, -33.7, -60.8, -87.9, -95.8, -113.35, -130.9, /* L shoulder ll */
999, 999, 999, 144.9, 155.4, 165.9, 999, 999, 999, /* R elbow ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R elbow ll */
999, 999, 999, 144.9, 155.4, 165.9, 999, 999, 999, /* L elbow ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L elbow ll */
 16.1, 26.1, 36.1, 68.3, 83.2, 98.1, 82.3, 100.6, 118.9, /* R wrist ul */
-21.5, -32.25, -43.0, -42.3, -58.5, -74.7, -90.4, -113.15, -135.9, /* R wrist ll */
 16.1, 26.1, 36.1, 68.3, 83.2, 98.1, 82.3, 100.6, 118.9, /* L wrist ul */
-21.5, -32.25, -43.0, -42.3, -58.5, -74.7, -90.4, -113.15, -135.9, /* L wrist ll */
 30.0, 40.0, 50.0, 30.0, 45.0, 60.0, 65.0, 70.0, 75.0, /* waist ul */
-30.0, -40.0, -50.0, 0.0, 0.0, 0.0, -65.0, -70.0, -75.0, /* waist ll */
 26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* R hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* R hip ll */
 26.8, 40.15, 53.5, 116.5, 132.25, 148.0, 18.0, 34.0, 51.0, /* L hip ul */
-33.0, -53.0, -73.0, 0.0, 0.0, 0.0, -39.0, -23.0, -56.0, /* L hip ll */
999, 999, 999, 125.2, 135.2, 145.2, 999, 999, 999, /* R knee ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knee ll */
999, 999, 999, 125.2, 135.2, 145.2, 999, 999, 999, /* L knee ul */
}

```

```

999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knee ll */
11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* R Ankle ul */
-9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* R Ankle ll */
11.0, 23.0, 35.0, 8.1, 14.0, 19.9, 23.0, 43.0, 63.0, /* L Ankle ul */
-9.0, -24.0, -39.0, -36.1, -58.3, -79.6, -15.0, -35.0, -55.0, /* L Ankle ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* R Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R Ball of Foot ll */
999, 999, 999, 35.0, 40.0, 45.0, 999, 999, 999, /* L Ball of Foot ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L Ball of Foot ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* R Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* R knuckles ll */
999, 999, 999, 70.0, 80.0, 90.0, 999, 999, 999, /* L Knuckles ul */
999, 999, 999, 0.0, 0.0, 0.0, 999, 999, 999, /* L knuckles ll */
}

```

K Mass Values

The values in this appendix represent the fraction of the total body mass which each segment contributes for the male NASA crewmember trainee population. Since female data was unavailable at this time, these male percentages are used for female human figure models as well.

```
lfootmass = .014;
rfootmass = .014;
rlegmass = .046;
llegmass = .046;
ruplegmass = .1;
luplegmass = .1;
rhipmass = .042;
lhipmass = .042;
ltorsomass = .042;
ctorsomass = .138;
uptorsomass = .171;
botheadmass = .02;
topheadmass = .059;
neckmass = .002;
rclavmass = .03;
lclavmass = .03;
rsternummass = .002;
lsternummass = .002;
ruparmmass = .028;
luparmmass = .028;
rloarmmass = .016;
lloarmmass = .016;
rhandmass = .006;
lhandmass = .006;
bodyrootmass = .00;
```

L Center of Mass

Locating Segment Centers of Mass In the Human Figure

-Ernest M. Otani (July, 1988)

This appendix was prepared by Ernest Otani. It contains a table of values for the locations of the center of mass for each segment of the body and the total body along with a description of how each of these values was determined. These values are used in dynamic analysis of the human figure's motion and/or position.

Ideally, each segment should have a mass and a center of mass site location associated with it. We define a simplified set of center of mass data with the mass of some segments lumped together and others ignored. The list below describes the details of the simplification.

- Each "toes" segment has no mass of its own. Instead, the mass of each "toes" segment is included in the mass of the corresponding "foot" segment. The center of mass site for the foot/toes combination is attached to the foot segment.
- Similarly, the masses of the "sternum", "clavicle", "hip", "upper torso", and "lower torso" segments are included in the mass of the "center torso" segment. The center of mass site for the whole combination is attached to the "center torso" segment.
- The masses of the "top head" and "bottom head" segments are lumped together, with the center of mass site and the mass of the combination attached to the "bottom head" segment.
- Each "fingers" segment's mass is lumped with the corresponding "hand" and the center of mass site of the combination is attached to the "hand" segment.

L.1 Determination of the center of mass locations

References to [NAS78] and [NAS87] in the following discussion indicate that data was taken or adapted from those sources.

(Male figure)

Foot/Toes combination:

distance(in direction of toes) from anklebone = $0.44 * (\text{footx} + \text{toesx}) - 0.2516 * (\text{footx})$
0.44 factor comes from [NAS78].
-0.2516 factor comes from psurf geometry.
Assume symmetry in y and z directions.

Hand/Fingers combination:

distance(in direction of fingers) from wrist = Z.
Z is given in [NAS87].
Assume symmetry in x and y directions.

Lower Leg:

distance(in direction of foot) from knee = $0.44 * \text{lowlegz}$.
0.44 factor comes from [NAS78].
Assume symmetry in x and y directions.

Upper Leg:

distance from top of leg = Z.
Z is given in [NAS87].
Assume symmetry in x and y directions.

Neck:

distance from base of neck = 0.5*neckz.
(this is an estimate)
Assume symmetry in x and y directions.

Upper Arm:

distance from top of arm= Z.
Z is given in [NAS87].
Assume symmetry in x and y directions.

Lower Arm:

distance from elbow = Z.
Z is given in [NAS87].
Assume symmetry in x and y directions.

Head:

distance (toward front of head) from center of head=X-botheadx.
Assume symmetry in y direction.
distance (toward top of head) from chin = eyelocz - Z.
X and Z given in [NAS87].

Center Torso:

distance (toward chest) from center of torso = X - ctorsox.
Assume symmetry in y direction.
distance (toward feet) from base of neck = ctorsoz - Z.
X and Z given in [NAS87].

(Female figure)

In the absence of empirical data for the female figure, I have estimated center of mass locations by scaling the male data in proportion to the female segment lengths. The resulting data set is very rough but may be accurate enough for some applications.

For most segments center of mass locations are based on the formula:

Female distance=(Male distance)*[(Female segment length)/(Male segment length)]

The exceptions are:

- Foot/Toes combination: Use same formula as for Male figure.
- Lower Leg: Use same formula as for Male figure.
- Hand/Fingers combination: Use (handz + fingerz) as segment lengths in Female distance formula.
- Center Torso:

Female CMctorsox=(Male X)*[(Female ctorsox)/(Male ctorsox)] - Female ctorsox
Female CMctorsoz=(Female ctorsoz)-1.1*(Male Z)*
[(Female ctorsoz)/(Male ctorsoz)]

Assume symmetry in y direction. Male X and Male Z are synonymous with X and Z and are given in [NAS87]. The 1.1 factor makes the female torso center of mass 10% lower than the male's. This is an estimate.

- Head:

Female CMbotheadx =(Male X)*[(Female botheadx)/(Male botheadx)]-Female botheadx

Assume symmetry in y direction. Use Female distance formula for z direction.

L.2 The Database

Shown below is a copy of the actual data file used by Richard Quach's SASS. All lengths are in centimeters.

```

C NASA Crewmen data
C
CC
C MALE CENTER OF MASS DATA
C float malegirths[MAXDATA][3][3] =
T MALE
C      x coord      y coord      z coord
C05%  50%  95%  05%  50%  95%  05%  50%  95%
C-----
  0.0  0.4  0.95  0.0  0.0  0.0  8.4  9.3 10.2 /* bottom head */
  0.0  0.0  0.0  0.0  0.0  0.0  3.85 5.0  6.3 /* Neck */
-2.5 -2.5 -2.6  0.0  0.0  0.0  22.7 25.8 29.0 /* Center Torso */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* Lower Torso */
  0.0  0.0  0.0  0.0  0.0  0.0  14.1 14.9 15.7 /* r Upper Arm */
  0.0  0.0  0.0  0.0  0.0  0.0  14.1 14.9 15.7 /* l Upper Arm */
  0.0  0.0  0.0  0.0  0.0  0.0  10.9 11.5 12.1 /* r Lower Arm */
  0.0  0.0  0.0  0.0  0.0  0.0  10.9 11.5 12.1 /* l Lower Arm */
  0.0  0.0  0.0  0.0  0.0  0.0  17.0 18.0 19.1 /* r Upper Leg */
  0.0  0.0  0.0  0.0  0.0  0.0  17.0 18.0 19.1 /* l Upper Leg */
  0.0  0.0  0.0  0.0  0.0  0.0  15.0 16.2 16.9 /* r Lower Leg */
  0.0  0.0  0.0  0.0  0.0  0.0  15.0 16.2 16.9 /* l Lower Leg */
  6.4  6.9  7.41 0.0  0.0  0.0  6.0  7.0  7.9 /* r Foot */
  6.4  6.9  7.41 0.0  0.0  0.0  6.0  7.0  7.9 /* l Foot */

  0.0  0.0  0.0  0.0  0.0  0.0  5.1  5.6  6.0 /* r Hand */
  0.0  0.0  0.0  0.0  0.0  0.0  5.1  5.6  6.0 /* l Hand */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* r Clavicle */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* l Clavicle */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* r eye */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* l eye */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* eye location */

C x is the distance from the front of the head to the wall */
C6.9  7.4  7.8  9.0  9.9 10.7  5.2  6.0  6.6 /* ball of right foot */
C6.9  7.4  7.8  9.0  9.9 10.7  5.2  6.0  6.6 /* ball of left foot */
C2.6  3.0  3.3  8.2  8.9  9.6  7.7  8.1  8.7 /* knuckles of right hand */
C2.6  3.0  3.3  8.2  8.9  9.6  7.7  8.1  8.7 /* knuckles of left hand */
C
C
C* female girths - depth (x) width (y) length (z) */
C
C femalegirths[MAXDATA][3][3] =
C
C FEMALE CENTER OF MASS DATA SCALED FROM MALE DATA
T FEMALE
C      x coord      y coord      z coord
C05%  50%  95%  05%  50%  95%  05%  50%  95%
C-----
  0.0  0.36 0.88 0.0  0.0  0.0  8.0  9.0 10.0 /* bottom head */
  0.0  0.0  0.0  0.0  0.0  0.0  5.5  5.9  6.3 /* Neck */
-2.0 -2.05 -2.19 0.0  0.0  0.0  16.5 18.7 21.3 /* Center Torso */
  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* Lower Torso */
  0.0  0.0  0.0  0.0  0.0  0.0  12.2 13.4 14.26 /* r Upper Arm */
  0.0  0.0  0.0  0.0  0.0  0.0  12.2 13.4 14.26 /* l Upper Arm */
  0.0  0.0  0.0  0.0  0.0  0.0  8.8  9.8 10.1 /* r Lower Arm */

```

```

0.0  0.0  0.0  0.0  0.0  0.0  8.8  9.8 10.1 /* l Lower Arm */
0.0  0.0  0.0  0.0  0.0  0.0 16.7 15.5 16.1 /* r Upper Leg */
0.0  0.0  0.0  0.0  0.0  0.0 16.7 15.5 16.1 /* l Upper Leg */
0.0  0.0  0.0  0.0  0.0  0.0 13.5 14.6 15.7 /* r Lower Leg */
0.0  0.0  0.0  0.0  0.0  0.0 13.5 14.6 15.7 /* l Lower Leg */
5.74 6.25 6.76 0.0  0.0  0.0  4.6  5.6  6.8 /* r Foot */
5.74 6.25 6.76 0.0  0.0  0.0  4.6  5.6  6.8 /* l Foot */
0.0  0.0  0.0  0.0  0.0  0.0  4.7  5.1  5.5 /* r Hand */
0.0  0.0  0.0  0.0  0.0  0.0  4.7  5.1  5.5 /* l Hand */
0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* r Clavicle */
0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* l Clavicle */
0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* r eye */
0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* l eye */
0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0 /* eye location */

```


M List of Psurfs – Skinnybody

The names of the psurfs used in the skinnybody figure model are listed in this appendix. This list was generated from the Unix archive verbose listing option since the actual psurfs are stored in the file skinny.a which is a Unix archive file. The date that the psurf was included in the archive file is also listed so that it will be possible to determine the current file to use and also to indicate the last time a psurf was modified or changed.

– skinny.a

psurf file creation date	psurf name
Dec 9 13:35 1987	ctorso.pss
Dec 9 13:35 1987	head.pss
Dec 9 13:36 1987	lclav.pss
Jan 19 13:47 1988	lfoot.pss
Jun 16 16:13 1988	lhand.pss
Dec 9 13:36 1987	llarm.pss
Dec 9 13:36 1987	llleg.pss
Dec 9 13:37 1987	ltorso.pss
Dec 9 13:37 1987	luarm.pss
Dec 9 13:37 1987	luleg.pss
Dec 9 13:37 1987	neck.pss
Dec 9 13:38 1987	rclav.pss
Jan 19 13:46 1988	rfoot.pss
Jun 16 16:16 1988	rhand.pss
Dec 9 13:38 1987	rlarm.pss
Dec 9 13:38 1987	rlleg.pss
Dec 9 13:38 1987	ruarm.pss
Dec 9 13:39 1987	ruleg.pss
Jun 16 15:56 1988	lfingers.pss
Jun 27 16:53 1988	ltoes.pss
Jun 16 15:56 1988	rfingers.pss
Jun 27 15:15 1988	rtoes.pss
Jun 17 16:47 1988	leye.pss
Jun 17 17:46 1988	reye.pss

N List of Psurfs – Polybody

The names of the psurfs used in the polybody figure model are listed in this appendix. This list was generated from the Unix archive verbose listing option since the actual psurfs are stored in the file `unsuit.a` which is a Unix archive file. The date that the psurf was included in the archive file is also listed so that it will be possible to determine the current file to use and also to indicate the last time a psurf was modified or changed.

- polybody.a			
Jan 20 10:08 1988	ctorso.pss		
Jan 20 10:28 1988	head.pss		
Jan 12 12:46 1988	lclav.pss		
Jan 20 11:39 1988	lfoot.pss		
Jan 12 12:46 1988	lhand.pss		
Jan 12 12:46 1988	llarm.pss		
Jan 12 12:46 1988	llleg.pss		
Jan 12 12:46 1988	ltorso.pss		
Jan 12 12:46 1988	luarm.pss		
Jan 12 12:46 1988	luleg.pss		
Jan 20 10:08 1988	neck.pss		
Jan 12 12:46 1988	rclav.pss		
Jan 20 11:41 1988	rfoot.pss		
Jan 12 12:46 1988	rhand.pss		
Jan 12 12:46 1988	rlarm.pss		
Jan 20 10:11 1988	rlleg.pss		
Jan 12 12:46 1988	ruarm.pss		
Jan 12 12:46 1988	ruleg.pss		
Jun 27 17:24 1988	lfingers.pss		
Jun 27 17:28 1988	ltoes.pss		
Jun 27 17:10 1988	rfingers.pss		
Jun 27 17:28 1988	rtoes.pss		
Jun 22 15:01 1988	leye.pss		
Jun 22 15:01 1988	reye.pss		

O “An Anthropometric Database for Computer Graphics Human Figures”

This appendix contains the text of the paper written by Marc R. Grosso, Rohinton S. Gonda, and Norman I. Badler which was presented at the 13th Annual Northeast Bioengineering Conference in March 1987. The paper has been reformatted and is included for completeness.

An Anthropometric Database for Computer Graphics Human Figures

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Abstract

A database of anthropometric characteristics is described for the graphical display of human figure models. This data is used in task analysis, reach and view assessment, and population studies. The information required for the graphical representation of realistic human figure models falls into three general groups - (1) general body attributes, such as name, and the Standard Anthropometric Measurements (SAMs) for the body, (2) body segment information, such as the segment name, length, and girth, and (3) body joint information, such as joint name, type, and limits in the range of motion about the joint. A review of human anatomy and physiology was undertaken to provide a guide to the contents of such a database. VAX Rdb/VMS, a relational database, was selected as the system to be used and each of the three categories were implemented as relations within the database.

1. Introduction: Study of the interaction of the human body with its environment has been an especially active in its use of computer graphics. The need for the simulation of these environmental interactions has led to the development of a number of specialized computer graphics systems for human figure modeling. Human figure modeling systems, based on anthropometric models, are used increasingly by human factors engineers and anthropometrists in many industries. The environmental interactions which have been modeled include task analysis, reach and view assessment, population studies, human factors, motion analysis, and ergonomic design of equipment and work areas. The ability to use computer graphics to evaluate the suitability and correctness human interactions with newly designed equipment for work areas, cockpits, space shuttles, etc., has resulted in significant savings of time, money, and effort as well as speeding up the various processes involved.

There are many human figure models currently available from different systems which provide the ability to display human figures in various positions and environments [DOO82]. Usually the human figure models are based upon Standard Anthropometric Measurements (SAMs) but actually only roughly approximate human form, tending to be somewhat limited and unrealistic. These systems make use of human figures ranging from simple stick figures to bodies formed by many polygons to bodies formed by a series of spheres (as in the **BUBBLEPEOPLE** developed at the University of Pennsylvania [BAD85]). Almost all of these forms require relatively low computer resources and, with current hardware capabilities, can be displayed and manipulated in real-time or near real-time.

2. Human Figure Modeling Tasks. Currently at the University of Pennsylvania there are two computer graphics systems which work in the realm of human figure modeling. These systems are **TEMPUS**, used for human figure positioning and display, and **POSIT**, used for general kinematic analysis. **DYSPAM**, a system used for dynamic simulations of human movement, can be linked to either system [LEE87].

Since all three of these systems ultimately work with the same human figure models they require a similar set of data to allow them to represent these figures and they must be able to exchange and share the data they have in common. Due to the specialized purpose and function of each of these systems there are a number differences in the actual data requirements, in terms of both format and content, which also must be considered. At one time the data requirements of each system were considered to be completely separate.

For example, **TEMPUS** uses a series of files as input of anthropometric data for specific individuals and statistically determined figures. Using Standard Anthropometric Measurements (**SAMs**) and regression equations based on the Crew Assessment of Reach (**CAR-II**) system [HAR80] the figures are displayed and can be manipulated. It is possible to select a “real” individual or a person consisting of desired statistical specifications. **POSIT** and **DYSPAM** have the ability to make use of some of the same anthropometric data when displaying human figures, but need to receive the data in slightly different formats. The two systems also make use of additional data which is of no concern of **TEMPUS**.

Originally there were data conversion routines in place to facilitate the exchange of common data between each of the three systems. This essentially required that the same data be stored three times, in three different formats, resulting in a great deal of wasted storage space on the computer system. The excess overhead and duplication of data caused by this need for converting the same data into three different formats for a single body model was determined to be an unnecessary expense.

2.1. Database Investigation and Description. In order to handle the consolidation and exchange of the common data and also to allow for future system enhancements the use of a common system database was investigated.

A database is a system of programs which allows for efficient storage and retrieval of data, reducing duplication, and improved data management. This data is stored as a series of items, called fields, and can be combined in many different ways depending upon the needs and desires of the user. For example, suppose one is storing information for individuals in a personnel file. The information typically found in such a file for a single individual would include: *First name, Last name, Address, City, State, and Zip Code*. Each item listed is referred to as a field (six fields in this example) and if combined together these fields would form a record. In a standard programming system, the record would have to be retrieved as stored, with little or no flexibility. In a database system, the fields can be selected and combined as needed. Such a system will also allow for specific records to be selected based upon the values stored within the fields without specialized programming.

This investigation determined the exact data requirements for each of the three systems. This data can be broken into two general categories — data common to all systems and data unique to a specific system. Also determined was what additional data would be required for possible future system additions and enhancements. The goal of this investigation was to determine the data requirements for a comprehensive body model and to include all fields that would be needed. Since the human body is a complicated structure with greatly varied abilities, a review of human anatomy and physiology references was undertaken [AST77, BAS76, FOX79, BAT76, HOL78] to serve as a guide for the information (fields) which would be of use in the present systems as well as in possible future extensions or additions to these systems.

2.2 Data Field Categories. The data required for the graphical representation of a realistic human figure model falls into three broad categories: 1) general body attributes, such as the Standard Anthropometric Measurements (**SAMs**) for the body, 2) body segment information, such as the segment name, length, and girth, and 3) body joint information, such as joint name, type, and limits in the range of motion about the joint.

These three categories are clearly distinct and describe the relationships between the data fields. Specifically, there is one set of general body attributes for each human figure model stored. For every human figure model there are many segments and many joints to be stored. A complete copy of the body segment information must be stored for each segment (23 segments in our model) in the entire body and similarly for body joint information (16 joints stored as 49 degrees of freedom in our model). So, for every individual body we need to store information about the general body characteristics, the 23 body segments, and the 49 joints (degrees of freedom). (Note that certain real joints, like the shoulder joint, are modeled as three separate degrees of freedom with movement limited in the direction of one coordinate, either X, Y, or Z). This results in very large data files for each individual stored.

3. The Anthropometric Database. The search for a tool which would provide the ability to store and manipulate the data described above led to the selection of the VAX Rdb/VMS database system (**RDB**), a relational database. It was felt that **RDB** would allow for the exchange of information as required as well as consolidating the data into a common format at a central location. This consolidation would also prevent data inconsistencies from developing as the data is used by the programming systems. **RDB** also provides

the flexibility to allow for future growth and changes in the data requirements and permits anthropometric information to be queried without resorting to new code or changes in **TEMPUS** (e.g. statistics, etc.).

Each of the three categories enumerated above were implemented as relations using **RDB** into a database which we call our Anthropometric Database (**ADB**)⁹.

Prior to the decision to implement the **ADB** there were a number of files in existence which were used by either **TEMPUS**, **POSIT**, or **DYSPAM**. Since we could not afford to simply discard these data files and therefore wanted to store the data in the newly formed **ADB** it was clear that conversion programs should be written to enable the data to be stored in the database. Data conversion programs were written, using an extended version of Pascal, part of the **RDB** system, which provided the necessary macro instructions for interfacing with **RDB**, to store these files in the **ADB**.

The introduction of the **ADB** required that an interface be built between the three programming systems, **TEMPUS**, **POSIT**, and **DYSPAM**, and the **ADB**. These additional interfacing programs were written, providing access from each system to the **ADB**, and allow previously stored body model data to be read from and new body model data to be added to the **ADB**. Future plans call for the development of an interactive system specifically designed for adding new body data to the **ADB**. Such a system would have to be very easy to use and “user friendly” so that the addition of data to the **ADB** would be a straightforward and unconfusing task.

4. Conclusion. **ADB**, an anthropometric database, is a valuable addition to the human figure modeling work being done in the Computer Graphics Laboratory at the University of Pennsylvania. It provides for flexible, expandable, and adaptable storage of the data required to graphically represent human figures.
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⁹See Appendix Q.

P Biostereometric Figure File

This appendix contains a copy of the current version of the **PEABODY** figure definition for the biostereometric contour people.

```
figure {
  attribute attribute3 {
    rgb = (0.50,0.60,1.00);
  }
  segment right_foot {
    psurf = "RFOOT.pss";
    attribute = attribute3;
    site proximal->location = trans(-11.85cm,-12.17cm,6.96cm);
/*
    site distal->location = trans(0.00cm,0.00cm,13.90cm);
    site medial->location = xyz(-90.00deg,0.00deg,0.00deg) *
                          trans(0.00cm,0.00cm,13.90cm);
    site lateral->location = xyz(90.00deg,0.00deg,0.00deg) *
                          trans(0.00cm,0.00cm,13.90cm);
*/
  }

  segment left_foot {
    psurf = "LFOOT.pss";
    attribute = attribute3;
    site proximal->location = trans(-11.85cm,12.17cm,6.96cm);
/*
    site distal->location = trans(0.00cm,0.00cm,13.90cm);
    site lateral->location = xyz(-90.00deg,0.00deg,0.00deg) *
                          trans(0.00cm,0.00cm,13.90cm);
    site medial->location = xyz(90.00deg,0.00deg,0.00deg) *
                          trans(0.00cm,0.00cm,13.90cm);
*/
  }

  segment right_lower_leg {
    psurf = "RLLEG.pss";
    attribute = attribute3;
    site proximal->location = trans(-14.06cm,-8.42cm,46.21cm);
    site distal->location = trans(-11.85cm,-12.17cm,6.96cm);
  }

  segment left_lower_leg {
    psurf = "LLLEG.pss";
    attribute = attribute3;
    site proximal->location = trans(-14.06cm,8.42cm,46.21cm);
    site distal->location = trans(-11.85cm,12.17cm,6.96cm);
/*
    site top->location = trans(-14.06cm,8.42cm,46.21cm);
*/
  }

  segment right_upper_leg {
```

```

    psurf = "RULEG.pss";
    attribute = attribute3;
    site proximal->location = trans(-6.11cm,-9.45cm,73.07cm);
    site distal->location = trans(-14.06cm,-8.42cm,46.21cm);
}
segment left_upper_leg {
    psurf = "LULEG.pss";
    attribute = attribute3;
    site proximal->location = trans(-6.11cm,9.45cm,73.07cm);
    site distal->location = trans(-14.06cm,8.42cm,46.21cm);
}
segment right_hipflap {
    psurf = "RHIPFLAP.pss";
    attribute = attribute3;
    site proximal->location = trans(-6.11cm,-9.45cm,80.67cm);
    site lateral->location = trans(-6.11cm,-9.45cm,73.07cm);
/*
    site lateral->location = xyz(90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,9.44cm);
*/
}

segment left_hipflap {
    psurf = "LHIPFLAP.pss";
    attribute = attribute3;
    site proximal->location = trans(-6.11cm,9.45cm,80.67cm);
    site lateral->location = trans(-6.11cm,9.45cm,73.07cm);
/*
    site lateral->location = xyz(-90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,9.44cm);
    site top->location = trans(-6.11cm,9.45cm,80.67cm);
*/
}
segment lower_torso {
    psurf = "LTORSO.pss";
    attribute = attribute3;
    site base->location =
trans(0,-100,0) *
xyz(90,0,0) * xyz(0,0,90) *
trans(-8.79cm,0.00cm,96.82cm);
    site proximal->location = trans(-8.79cm,0.00cm,96.82cm);
    site rdistal->location = trans(-6.11cm,-9.45cm,80.67cm);
    site ldistal->location = trans(-6.11cm,9.45cm,80.67cm);
/*
    site top->location = trans(-2.35cm,0.08cm,100.12cm);
*/
}

segment center_torso {
    psurf = "CTORSO.pss";
    attribute = attribute3;
    site proximal->location = trans(-8.79cm,0.00cm,102.10cm);

```

```

    site distal->location = trans(-8.79cm,0.00cm,96.82cm);
}
segment upper_torso {
    psurf = "UTORSO.pss";
    attribute = attribute3;
    site proximal->location = trans(-0.14cm,0.00cm,132.19cm);
    site distal->location = trans(-8.79cm,0.00cm,102.10cm);
    site left->location = trans(-13.58cm,17.48cm,125.54cm);
    site right->location = trans(-13.58cm,-17.48cm,125.54cm);

/*
    site gbras->location = trans(-13.58cm,17.48cm,125.54cm);
    site top->location = trans(-7.03cm,0.00cm,139.64cm);
*/
}

segment bottom_head {
    psurf = "HEAD.pss";
    attribute = attribute3;
    site proximal->location = trans(-10.38cm,0.00cm,146.61cm);
}
segment neck {
    psurf = "NECK.pss";
    attribute = attribute3;
    site proximal->location = trans(-0.14cm,0.00cm,132.19cm);
    site distal->location = trans(-10.38cm,0.00cm,146.61cm);
}
segment right_upper_arm {
    psurf = "RUARM.pss";
    attribute = attribute3;
    site proximal->location = trans(-13.58cm,-17.48cm,125.54cm);
    site distal->location = trans(-9.29cm,-27.88cm,105.31cm);
}
segment left_upper_arm {
    psurf = "LUARM.pss";
    attribute = attribute3;
    site proximal->location = trans(-13.58cm,17.48cm,125.54cm);
    site distal->location = trans(-9.29cm,27.88cm,105.31cm);
/*
    site top->location = trans(-10.95cm,26.28cm,104.35cm);
*/
}

segment right_lower_arm {
    psurf = "RLARM.pss";
    attribute = attribute3;
    site proximal->location = trans(-9.29cm,-27.88cm,105.31cm);
    site distal->location = trans(-3.95cm,-33.71cm,81.47cm);
}
segment left_lower_arm {
    psurf = "LLARM.pss";
    attribute = attribute3;

```



```

    site proximal->location = trans(-9.29cm,27.88cm,105.31cm);
    site distal->location = trans(-3.95cm,33.71cm,81.47cm);
}
segment right_hand {
    psurf = "RHAND.pss";
    attribute = attribute3;
    site proximal->location = trans(-3.95cm,-33.71cm,81.47cm);
/*
    site distal->location = trans(0.00cm,0.00cm,19.30cm);
    site medial->location = xyz(-90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,19.30cm);
    site lateral->location = xyz(90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,19.30cm);
*/
}

segment left_hand {
    psurf = "LHAND.pss";
    attribute = attribute3;
    site proximal->location = trans(-3.95cm,33.71cm,81.47cm);
/*
    site distal->location = trans(0.00cm,0.00cm,19.30cm);
    site lateral->location = xyz(-90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,19.30cm);
    site medial->location = xyz(90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,19.30cm);
*/
}

segment body_root {
    site proximal->location = xyz(90.00deg,0.00deg,0.00deg) *
        trans(0.00cm,0.00cm,0.00cm);
}

joint right_ankle {
    connect right_lower_leg.distal to right_foot.proximal;
    type = R(0.00,0.00,-1.00) * R(-1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}

joint left_ankle {
    connect left_lower_leg.distal to left_foot.proximal;
    type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}

joint right_knee {
    connect right_upper_leg.distal to right_lower_leg.proximal;
    type = R(0.00,-1.00,0.00);
}

joint left_knee {
    connect left_upper_leg.distal to left_lower_leg.proximal;
    type = R(0.00,-1.00,0.00);
}

joint right_hipflap_joint {

```

```

    connect right_hipflap.lateral to right_upper_leg.proximal;
    type = R(0.00,0.00,-1.00) * R(-1.00,0.00,0.00);
}
joint left_hipflap_joint {
    connect left_hipflap.lateral to left_upper_leg.proximal;
    type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00);
}
joint right_hip_joint {
    connect lower_torso.rdistal to right_hipflap.proximal;
    type = R(0.00,1.00,0.00);
}
joint left_hip_joint {
    connect lower_torso.ldistal to left_hipflap.proximal;
    type = R(0.00,1.00,0.00);
}

joint waist {
    connect lower_torso.proximal to center_torso.distal;
    type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}
joint solar_plexus {
    connect center_torso.proximal to upper_torso.distal;
    type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}
joint atlanto_occipital {
    connect neck.distal to bottom_head.proximal;
    type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}
joint base_of_neck {
    connect upper_torso.proximal to neck.proximal;
    displacement = trans(0.00cm,0.00cm,0.00cm);
}
joint right_shoulder {
    connect upper_torso.right to right_upper_arm.proximal;
    type = R(0.00,0.00,-1.00) * R(-1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}
joint right_elbow {
    connect right_upper_arm.distal to right_lower_arm.proximal;
    type = R(0.00,1.00,0.00);
}

joint right_wrist {
    connect right_lower_arm.distal to right_hand.proximal;
    type = R(0.00,0.00,-1.00) * R(-1.00,0.00,0.00) *
        R(0.00,1.00,0.00);
}
joint left_shoulder {
    connect upper_torso.left to left_upper_arm.proximal;

```

```

        type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00) *
                R(0.00,1.00,0.00);
    }
    joint left_elbow {
        connect left_upper_arm.distal to left_lower_arm.proximal;
        type = R(0.00,1.00,0.00);
    }
    joint left_wrist {
        connect left_lower_arm.distal to left_hand.proximal;
        type = R(0.00,0.00,1.00) * R(1.00,0.00,0.00) *
                R(0.00,1.00,0.00);
    }
    /*
    joint world_joint {
        connect body_root.proximal to lower_torso.proximal;
    }
    */
    root = lower_torso.base;
}

```

Q Fields of the Anthropometric Database

This appendix contains a description and explanation of all of the fields found in the Anthropometric database described in Appendix O. This description is included to allow others to understand the purpose and motivation behind each of the fields in the ADB and to aid in its extension.

```
! ANTHROPOMETRIC DATA BASE RELATION DEFINITIONS
!  
! Defining RELATION for BODY Attributes
!  
! BODY ATTRIBUTES
!
```

FIELD NAME	DATA TYPE	DATA SOURCE	DATA USE
person_type.	character	user choice	identify whether this data is for a real or statistical person
gender_type.	character	user choice	identify which sex the figure will represent
display_type.	character	user choice	identify which body type will be used – skinnybody, polybody, etc.
! bounding box			
bbox_min_x.	real	calculated from total body size	identifies the extent of the entire figure
bbox_min_y.	real	calculated from total body size	identifies the extent of the entire figure
bbox_min_z.	real	calculated from total body size	identifies the extent of the entire figure
bbox_max_x.	real	calculated from total body size	identifies the extent of the entire figure
bbox_max_y.	real	calculated from total body size	identifies the extent of the entire figure
bbox_max_z.	real	calculated from total body size	identifies the extent of the entire figure
stature.	real	actual measurement from figure	total body height
waist_height.	real	actual measurement from figure	
sitting_height.	real	actual measurement from figure	
eye_height_sitting.	real	actual measurement from figure	
popliteal_height.	real	actual measurement from figure	
buttock_knee_length.	real	actual measurement from figure	
shoulder_elbow_length.	real	actual measurement from figure	
forearm_hand_length.	real	actual measurement from figure	
bideltoid_diameter.	real	actual measurement from figure	
hip_breadth.	real	actual measurement from figure	
foot_length.	real	actual measurement from figure	
hand_length.	real	actual measurement from figure	
!			
spine_type.	integer	user selection	select between a curvable spine or rigid spine (default)
!			

! spine_tangents			
spine_tangent_1_x.	real	user set initially	program changeable for curved spine
spine_tangent_1_y.	real	user set initially	program changeable for curved spine
spine_tangent_1_z.	real	user set initially	program changeable for curved spine
spine_tangent_2_x.	real	user set initially	program changeable for curved spine
spine_tangent_2_y.	real	user set initially	program changeable for curved spine
spine_tangent_2_z.	real	user set initially	program changeable for curved spine
!			
somatotype.	real	user determined based on body characteristics	this should be a set of three numbers (reals). These identify certain body characteristics (i.e. build)
body_fat_percentage.	real	user determined	body characteristic identifies the amount of fat in the figure. Can be used to help determine somatotype, etc.
muscle_mass_percentage.	real	user determined	body characteristic - identifies the amount of muscle mass in the figure. Can be used to help determine somatotype, etc.
! center_of_mass			
center_of_mass_x.	real	program calculated	body characteristic the location of the center of mass of the total body
center_of_mass_y.	real	program calculated	body characteristic the location of the center of mass of the total body
center_of_mass_z.	real	program calculated	body characteristic the location of the center of mass of the total body
!			

total_body_mass.	real	figure characteristic		body characteristic the “weight” of the figure. This can either be user determined or generated by a program from statistical values.
total_body_volume.	real	figure characteristic		body characteristic this is calculated based upon the volumes of the figure segments. It may be based on statistical or real values as above.
girth_equations_filename.	character	user determined		This file was to contain a set of equations which generated the girth of each body segment based upon the segment values below. This concept has been replaced by GIRTHFUN and its successors (SASS).
overall_strength_percentage.	real	user determined		This data item was to identify the figure’s total body strength based upon an, as yet, unknown set of statistical values.
number_of_segments.	integer	figure determined	model	identifies the number of segments this figure has and is based upon the figure model in use.
number_of_joints.	integer	figure determined	model	identifies the number of joints this figure has and is based upon the figure model in use.
population_group.	character	user/data determined		identifies which population this figure belongs to (or for statistical figure, which population the values are based upon).
!				
END				
RELATION.				
!				

```

!
SEGMENT RELATION
!
person_name      based    on character    user determined    provides pointer back to
body_name.
segment_number.      integer    user determined or    identifies the segment which is
program generated    being described.
segment_name.        character    user determined or    identifies the segment which is
program generated    being described.
segment_length.      real    user
determined generated    the actual length for real figures
or program generated    a generated value for statistical
figures.
related_joint_1.     integer    program generated    pointer to the previous joint
related_joint_2.     integer    program generated    pointer to the next joint
! rtelement
translate_x.         real    program generated    joint translation from neutral po-
sition in x direction
translate_y.         real    program generated    joint translation from neutral po-
sition in y direction
translate_z.         real    program generated    joint translation from neutral po-
sition in z direction
!
rt_joint.           integer    user generated    indicates how the coordinate
frames of adjacent segments line
up
rt_type.            integer    program generated    used by internally DYSPAM
! selement
fake_segment_1.     integer    program generated    used by POSIT as one of
two segments surrounding each
degree-of-freedom at a joint.
Provides an interface between
POSIT and DYSPAM
fake_segment_2.     integer    program generated    used by POSIT as the sec-
ond of two segments surround-
ing each degree-of-freedom at a
joint. Provides an interface be-
tween POSIT and DYSPAM
!

```


joint_y.	real	program generated	joint location y
joint_x.	real	program generated	joint location x
joint_z.	real	program generated	joint location z
!			
segment_center_of_mass_x.	real	program generated	location of segment center of mass - x
segment_center_of_mass_y.	real	program generated	location of segment center of mass - y
segment_center_of_mass_z.	real	program generated	location of segment center of mass - z
!			
segment_moment_of_inertia_x.	real	program generated	location of segment moment of inertia - x
segment_moment_of_inertia_y.	real	program generated	location of segment moment of inertia - y
segment_moment_of_inertia_z.	real	program generated	location of segment moment of inertia - z
!			
segment_girth_x.	real	program generated or user determined	segment thickness
segment_girth_y.	real	program generated or user determined	segment width
segment_girth_z.	real	program generated or user determined	segment length
!			
segment_volume.	real	program generated or user determined	segment volume
!			
!bounding box			
!			
segment_bbox_min_x.	real	program generated	segment bounding box coordinate
segment_bbox_min_y.	real	program generated	segment bounding box coordinate
segment_bbox_min_z.	real	program generated	segment bounding box coordinate
segment_bbox_max_x.	real	program generated	segment bounding box coordinate
segment_bbox_max_y.	real	program generated	segment bounding box coordinate
segment_bbox_max_z.	real	program generated	segment bounding box coordinate
!			
segment_display_type.	real	user or program generated	identifies which body model is being used for display
!			
END SEGMENT_TO_BODY RELATION.			
!			

! JOINT RELATIONS

!				
person_name	based on character		user or program generated	identifies the figure to which joint this is belongs
body_name.				
joint_number.		integer	program generated or user determined	identifies the joint (as part of a linked list of joints)
joint_name.		character	program generated or user determined	identifies the joint
!				
connected_segment_1.		integer	program generated	identifies the segment to which this joint is associated
dir_segment_1.		integer	program generated	identifies the segment to which this joint is associated
connected_segment_2.		integer	program generated	identifies the segment to which this joint is associated
dir_segment_2.		integer	program generated	identifies the segment to which this joint is associated
!				
joint_type.		integer	program generated	identifies type of joint - revolute or prismatic
joint_velocity_max.		real	user determined	identifies the maximum speed at which the joint can move
joint_strength_max_positive.		real	user determined	identifies the maximum force which can be produced at the joint (usually in flexion motion)
joint_strength_max_negative.		real	user determined	identifies the maximum force which can be produced at the joint (usually in extension motion)
!				
joint_limit_max.		real	program generated or user determined	identifies the maximum angle for range of motion at the joint
joint_limit_min.		real	program generated or user determined	identifies the minimum angle for range of motion at the joint (usually zero or negative)
!				
stiffness_coefficient_1.		real	program generated	used in dynamics calculation of motion
stiffness_coefficient_2.		real	program generated	used in dynamics calculation of motion
stiffness_coefficient_3.		real	program generated	used in dynamics calculation of motion
stiffness_coefficient_4.		real	program generated	used in dynamics calculation of motion
!				
damping_coefficient_1.		real	program generated	used in dynamics calculation of motion
damping_coefficient_2.		real	program generated	used in dynamics calculation of motion
damping_coefficient_3.		real	program generated	used in dynamics calculation of motion
damping_coefficient_4.		real	program generated	used in dynamics calculation of motion
!				
END JOINT_TO_BODY RELATION.				