Estimating Anthropometric Marker Locations from 3-D LADAR Point Clouds

Matthew J. Maier

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ESTIMATING ANTHROPOMETRIC MARKER LOCATIONS FROM 3-D LADAR POINT CLOUDS

THESIS

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AFIT/GE/ENG/11-27

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ESTIMATING ANTHROPOMETRIC MARKER LOCATIONS FROM 3-D LADAR POINT CLOUDS

THESIS

Presented to the Faculty
Department of Electrical and Computer Engineering
Graduate School of Engineering and Management
Air Force Institute of Technology
Air University
Air Education and Training Command
in Partial Fulfillment of the Requirements for the
Degree of Master of Science in Electrical Engineering

Matthew J. Maier, BSEE
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June 2011

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ESTIMATING ANTHROPOMETRIC MARKER LOCATIONS FROM 3-D LADAR POINT CLOUDS

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Abstract

With a greater emphasis being placed on rapidly identifying non-conventional adversaries, the U.S. armed forces have placed a high priority on expanding and developing dismount detection capabilities. Current work in this area utilizes a multispectral imaging system to exploit spectral properties in order to detect areas of exposed skin and identify clothing properties.

An area of interest for improving the characterization portion of the system is in extracting anthropometric markers from a Laser Detection and Ranging (LADAR) point cloud. Analyzing anthropometric markers is a common means of studying how a human moves and has been shown to provide good results in determining certain demographic information about the subject. This research examines a marker extraction method utilizing principal component analysis (PCA), self-organizing maps (SOM), alpha hulls, and basic anthropometric knowledge. The data set is comprised of 3-D body scans and truth marker locations from the Civilian American and European Surface Anthropometry Resource (CAESAR) Project. The performance of the extraction algorithm is tested by performing gender classification with the calculated markers. Classification is performed using linear discriminant analysis. The measured classification accuracy using the estimated marker locations is approximately 78% whereas the classification accuracy using the truth marker locations is 88%. This indicates that the marker estimation algorithm developed in this research performs well and shows that fusing LADAR data with the multispectral detection system's data is a promising path for improving the dismount detection and identification problem.
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Matthew J. Maier
# Table of Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abstract</td>
<td>iv</td>
</tr>
<tr>
<td>Acknowledgements</td>
<td>v</td>
</tr>
<tr>
<td>List of Figures</td>
<td>viii</td>
</tr>
<tr>
<td>List of Tables</td>
<td>xiii</td>
</tr>
<tr>
<td>1. Introduction</td>
<td>1-1</td>
</tr>
<tr>
<td>1.1 Problem Statement</td>
<td>1-1</td>
</tr>
<tr>
<td>1.2 Scope</td>
<td>1-2</td>
</tr>
<tr>
<td>1.3 Document Organization</td>
<td>1-3</td>
</tr>
<tr>
<td>2. Background</td>
<td>2-1</td>
</tr>
<tr>
<td>2.1 The Nature of LADAR Point Cloud Data</td>
<td>2-1</td>
</tr>
<tr>
<td>2.2 Segmentation Approaches</td>
<td>2-3</td>
</tr>
<tr>
<td>2.2.1 Segmentation from Point Clouds</td>
<td>2-3</td>
</tr>
<tr>
<td>2.2.2 Segmentation From Surfaces</td>
<td>2-4</td>
</tr>
<tr>
<td>2.3 Conceptual Paradigm for the Marker Extraction Problem</td>
<td>2-5</td>
</tr>
<tr>
<td>2.3.1 Point Cloud Data Analysis</td>
<td>2-5</td>
</tr>
<tr>
<td>2.3.2 Projection Methods</td>
<td>2-6</td>
</tr>
<tr>
<td>2.3.3 Clustering Methods</td>
<td>2-9</td>
</tr>
<tr>
<td>2.3.4 Geometry Computation</td>
<td>2-20</td>
</tr>
<tr>
<td>2.3.5 Skeletonization</td>
<td>2-23</td>
</tr>
<tr>
<td>2.3.6 Extracting Marker Locations</td>
<td>2-26</td>
</tr>
<tr>
<td>2.4 Computing Truth Markers</td>
<td>2-29</td>
</tr>
<tr>
<td>2.4.1 Exploitation of the CAESAR LADAR Data</td>
<td>2-29</td>
</tr>
<tr>
<td>2.4.2 Truth Marker Processing</td>
<td>2-32</td>
</tr>
<tr>
<td>2.5 Evaluating the Marker Estimation Algorithm</td>
<td>2-36</td>
</tr>
<tr>
<td>2.5.1 Classification</td>
<td>2-36</td>
</tr>
<tr>
<td>2.5.2 Linear Discriminant Analysis</td>
<td>2-37</td>
</tr>
<tr>
<td>2.6 Summary</td>
<td>2-39</td>
</tr>
<tr>
<td>3. Methodology</td>
<td>3-1</td>
</tr>
<tr>
<td>3.1 Algorithm Overview</td>
<td>3-2</td>
</tr>
<tr>
<td>3.2 Projection</td>
<td>3-2</td>
</tr>
<tr>
<td>3.3 Marker Estimation Algorithm</td>
<td>3-3</td>
</tr>
<tr>
<td>3.3.1 Self-Organizing Map</td>
<td>3-4</td>
</tr>
<tr>
<td>3.3.2 Alpha Hull</td>
<td>3-5</td>
</tr>
<tr>
<td>3.3.3 Voronoi Skeleton</td>
<td>3-6</td>
</tr>
</tbody>
</table>
3.3.4 Incorporating Anthropometric Information into the Algorithm ........................................... 3-8
3.3.5 Post-processing ......................................................................................................................... 3-13
3.4 Summary .................................................................................................................................. 3-13

4. Experimental Results and Analyses .............................................................................................. 4-1
4.1 Data ........................................................................................................................................... 4-1
4.2 Experimentation Process ............................................................................................................. 4-2
4.2.1 Monte Carlo Simulations ........................................................................................................... 4-2
4.2.2 Classification Process ............................................................................................................. 4-3
4.2.3 Classification Evaluation Methods .......................................................................................... 4-5
4.3 Segmentation Algorithm Parameters .......................................................................................... 4-6
4.3.1 Principal Component Analysis ................................................................................................. 4-6
4.3.2 Self-Organizing Map ............................................................................................................... 4-7
4.3.3 Alpha Hull ............................................................................................................................... 4-11
4.3.4 Monte Carlo Simulation Numbers ........................................................................................... 4-12
4.4 Marker Estimation Error .............................................................................................................. 4-14
4.4.1 Multivariate Normality ............................................................................................................. 4-14
4.4.2 Discussion on Normality Testing Results ............................................................................... 4-18
4.4.3 Mahalanobis Distance ............................................................................................................ 4-19
4.5 Classification Results .................................................................................................................. 4-22
4.5.1 Case I - Truth Data versus Truth Data ..................................................................................... 4-22
4.5.2 Case II - Estimated Markers versus Truth Data ..................................................................... 4-23
4.5.3 Case III - Monte-Carlo Means versus Monte-Carlo Means .................................................. 4-23
4.5.4 Case IV - Estimated Markers versus Monte-Carlo Means ..................................................... 4-24
4.6 Analysis of Results and Summary .............................................................................................. 4-24

5. Conclusions and Future Work ....................................................................................................... 5-1
5.1 Summary of Methods and Conclusions ..................................................................................... 5-1
5.2 Future Work ............................................................................................................................... 5-2
5.3 Contributions .............................................................................................................................. 3

A. Mahalanobis Calculations for Another Subject ........................................................................... A-1

B. Software Acknowledgments ....................................................................................................... B-1

Bibliography ...................................................................................................................................... BIB-1
# List of Figures

<table>
<thead>
<tr>
<th>Figure</th>
<th>Description</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>An example of the results from the skin-cued dismount detection system with a bounding box placed around the detected dismount.</td>
<td>1-2</td>
</tr>
<tr>
<td>2</td>
<td>An example of the use of a LiDAR system to map terrain. The LiDAR transmits a light pulse which is reflected back to the receiver by the various surfaces in the path of the light pulse corresponding to the spikes in the waveform.</td>
<td>2-2</td>
</tr>
<tr>
<td>3</td>
<td>Fundamental diagram of the overall segmentation problem for the two approaches: segmenting from a point cloud and from a surface.</td>
<td>2-5</td>
</tr>
<tr>
<td>4</td>
<td>Example 3-D point cloud from the AFRL/RWPA Civilian American and European Surface Anthropometry Resource (CAESAR) Project database [72].</td>
<td>2-6</td>
</tr>
<tr>
<td>5</td>
<td>The results of transforming the data into PCA space while retaining all three principal components. The figure’s rotation changes since the axes of the body align with the principal component axes.</td>
<td>2-8</td>
</tr>
<tr>
<td>6</td>
<td>The transformed data using the first two principal components in the projection of the 3-D LADAR point cloud data.</td>
<td>2-9</td>
</tr>
<tr>
<td>7</td>
<td>The nomenclature and orientation of the primary planes associated with describing planar locations of anatomical features and views.</td>
<td>2-10</td>
</tr>
<tr>
<td>8</td>
<td>The 3-D point cloud data in the 3-D LLE domain.</td>
<td>2-11</td>
</tr>
<tr>
<td>9</td>
<td>The 3-D point cloud data projected into the 2-D LLE domain.</td>
<td>2-12</td>
</tr>
<tr>
<td>10</td>
<td>The results from the $K$-means algorithm. Notice that the two means near the subject’s armpits fall outside the region of the body.</td>
<td>2-13</td>
</tr>
<tr>
<td>11</td>
<td>The input data of 5 compact clusters each containing 50 data points for the Litinskii-Romanov algorithm with cluster centers highlighted in red.</td>
<td>2-15</td>
</tr>
<tr>
<td>Figure</td>
<td>Page</td>
<td></td>
</tr>
<tr>
<td>--------</td>
<td>------</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>The Litinskii-Romanov algorithm’s results of estimated number of clusters versus threshold radius plot for the 5 cluster data set. 2-16</td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>The Litinskii-Romanov algorithm’s estimated number of clusters versus threshold radius plot for the IRIS data set [25]. 2-17</td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>The Litinskii-Romanov algorithm’s estimated number of clusters versus threshold radius plot for the body scan data. 2-18</td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>The calculated cluster centers at a stage 20% through the Litinskii-Romanov algorithm with taxons marked and representative threshold radius circles drawn around the taxon. 2-19</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>A Voronoi diagram for a set of 20 random points. 2-21</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>A Delaunay triangulation for a set of 20 random points (Fig. 16). 2-22</td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>A convex hull for a set of 20 random points (Figs. 16, 17). 2-23</td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>An alpha hull with $\alpha = 0.25$ for a set of 20 random points (Figs. 16, 17, 18). 2-24</td>
<td></td>
</tr>
<tr>
<td>20</td>
<td>A standard representation of the generation of an alpha hull by rolling a disk of radius $\alpha$ around the set of points. 2-25</td>
<td></td>
</tr>
<tr>
<td>21</td>
<td>A standard depiction of the effect of varying the size of $\alpha$ on the resulting alpha hull from a set of points. 2-26</td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>A triangulated surface mesh applied to a 3-D point cloud. The mesh is derived using a Delaunay triangulation based algorithm. 2-27</td>
<td></td>
</tr>
<tr>
<td>23</td>
<td>A Reeb graph of a torus and a Reeb graph of a human body shape as produced in [89]. 2-27</td>
<td></td>
</tr>
<tr>
<td>24</td>
<td>A skeleton of the lower body derived from the triangulated surface mesh. It is based on a medial axis algorithm to find the central set of points equidistant from the surface. 2-28</td>
<td></td>
</tr>
</tbody>
</table>
A line segment depicting the relationship the points $A$, $B$, and $C$ and the lengths $M$ and $m$ for the purposes of illustrating the concept of the golden section as described in [63].

Plot of the markers placed on the subject. For clarity, the markers are depicted as red diamonds.

Line drawing depiction of the femoral epicondyle lateral (left and center) and medial (right) marker placement. The drawings are from [72].

Pelvic anatomical frame showing ASISs, PSISs, and the local reference system [10].

Line drawing depicting the location of the placement of the acromion marker prior to the body scan. Note its proximity to the shoulder joint center. Drawing is taken from [72].

Plot of the anthropometric truth markers calculated from the markers placed on the subject during the scan. Only 0.5% of the 3-D point cloud data is plotted to provide clarity.

Diagrams of (a) the fundamental flow introduced in Section 2.3 and (b) the overall segmentation process specific to the segmentation from a point cloud approach. The 3-D point cloud data is the input to the system, and the estimated marker locations are the product of the marker estimation algorithm.

Point cloud data from [72] projected into 2-D using the first two principal components.

Representative result of the SOM portion of the marker estimation algorithm.

Results of the alpha shape algorithm when $\alpha = 0.75$. The $\alpha$ is too large to provide fidelity to the outline shape of the subject.

Results of the alpha hull algorithm. The asterisks indicate the location of a lattice node from the SOM. Circles around the asterisk indicate nodes that lie inside the alpha hull based upon a positive result from a point-in-polygon test.
<table>
<thead>
<tr>
<th>Figure</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>36</td>
<td>A Voronoi diagram from the alpha hull obtained from the projected 3-D point cloud of a subject from [72].</td>
</tr>
<tr>
<td>37</td>
<td>The initial step in pruning the Voronoi diagram by removing the lines not contained within the alpha hull.</td>
</tr>
<tr>
<td>38</td>
<td>The skeleton from the Voronoi diagram results derived from the alpha hull of the projected point cloud for a subject from [72].</td>
</tr>
<tr>
<td>39</td>
<td>The medial axis results derived from the alpha hull of the projected point cloud for a subject from [72].</td>
</tr>
<tr>
<td>40</td>
<td>Results of the pruning and anthropometric adjustment portion of the algorithm.</td>
</tr>
<tr>
<td>41</td>
<td>The resulting alpha hull with $\alpha = 0.025$.</td>
</tr>
<tr>
<td>42</td>
<td>The resulting alpha hull with too much of the platform showing in the scan.</td>
</tr>
<tr>
<td>43</td>
<td>An example of the typical lattice node locations in the arms for the 1-D SOM.</td>
</tr>
<tr>
<td>44</td>
<td>The type of scanner used to obtain 3-D body scans in the CAESAR database.</td>
</tr>
<tr>
<td>45</td>
<td>An example of the distribution of calculated markers from the Monte Carlo simulation for a random subject.</td>
</tr>
<tr>
<td>46</td>
<td>Part 1 Histograms for anthropometric marker locations based on 100 Monte Carlo simulations.</td>
</tr>
<tr>
<td>47</td>
<td>Part 2 Histograms for anthropometric marker locations based on 100 Monte Carlo simulations.</td>
</tr>
<tr>
<td>48</td>
<td>An example of the 3-D histograms located at their respective marker locations.</td>
</tr>
<tr>
<td>49</td>
<td>SOMs of various lattice sizes shown in the projected data space.</td>
</tr>
<tr>
<td>50</td>
<td>The topographic error for a 1-D lattice SOM in data space.</td>
</tr>
<tr>
<td>51</td>
<td>The learning rate used in the SOM training.</td>
</tr>
</tbody>
</table>
Figure | Page
--- | ---
52 | The resulting alpha hull with $\alpha = 0.025$. 4-12
53 | The set of markers retained by the alpha hull routine. SOM nodes are denoted by an asterisk. Retained markers are denoted by a circle around the retained node. 4-13
54 | The resulting alpha hull with too much of the platform showing in the scan. 4-13
55 | The resulting alpha hull with too large of an $\alpha$ and too much of the platform showing in the scan. 4-14
56 | Histograms of Mahalanobis distances to mean estimated marker locations for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot. 4-20
57 | Histograms of Mahalanobis distances to truth markers for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot. 4-21
58 | An example of the distribution of calculated markers from the Monte Carlo simulation for a random subject. A-1
59 | Part 1 - Histograms of the 100 run Monte Carlo simulations. A-2
60 | Part 2 - Histograms of the 100 run Monte Carlo simulations. A-3
61 | Part 1 - Histograms of Mahalanobis distances to mean estimated marker locations for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot. A-4
62 | Part 2 - Histograms of Mahalanobis distances to mean estimated marker locations for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot. A-5
# List of Tables

<table>
<thead>
<tr>
<th>Table</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Significant measures for the gender classification problem in [27]. Values shown are the means (standard deviations) for the anthropometric measurements given in mm or kg.</td>
</tr>
<tr>
<td>2</td>
<td>Truth marker set.</td>
</tr>
<tr>
<td>3</td>
<td>Feature set used for classification.</td>
</tr>
<tr>
<td>4</td>
<td>Demographics for the test subjects.</td>
</tr>
<tr>
<td>5</td>
<td>Racial demographics for the North American subjects.</td>
</tr>
<tr>
<td>6</td>
<td>Nationalities of subjects from the Netherlands database.</td>
</tr>
<tr>
<td>7</td>
<td>Nationalities of subjects from the Italian database.</td>
</tr>
<tr>
<td>8</td>
<td>Platform offsets for the various data collection sites.</td>
</tr>
<tr>
<td>9</td>
<td>Statistics for the Euclidean distance of estimated markers from Monte Carlo simulation to truth markers.</td>
</tr>
<tr>
<td>10</td>
<td>Classification accuracy for the truth data using linear discriminant analysis (LDA).</td>
</tr>
<tr>
<td>11</td>
<td>Classification accuracy for the calculated marker locations versus the truth data.</td>
</tr>
<tr>
<td>12</td>
<td>Classification accuracy for the means of the Monte Carlo simulation as both training and testing data.</td>
</tr>
<tr>
<td>13</td>
<td>Classification accuracy for test data consisting of estimated marker locations classified against the training data consisting of the means of the Monte-Carlo simulation runs.</td>
</tr>
</tbody>
</table>
ESTIMATING ANTHROPOMETRIC MARKER LOCATIONS FROM 3-D LADAR POINT CLOUDS

1. Introduction

The United States Air Force Science & Technology Program continues to stress the importance of research into persistent surveillance capabilities that provide the warfighter with all-weather, around-the-clock, continuous tracking of dismounts. Dismount tracking is useful for inferring intent which can provide information about whether the dismount is exhibiting suspicious behavior [40].

Significant advancements in the area of dismount detection have been achieved by the Sensors Exploitation Research Group at the Air Force Institute of Technology [8, 14, 15, 45, 65, 67]. The work in [8, 15, 45, 65, 67] has focused on skin-cued dismount detection through the use of multispectral analysis. An example of the results from the skin-cued dismount detector is shown in Fig. 1. Another element in the overall dismount detection system is clothing detection and characterization [14].

An opportunity for new research of benefit to solve the dismount detection problem is the fusing of Laser Detection and Ranging (LADAR) data with the existing approaches to provide anthropometric information that can aid the characterization piece of the dismount detection system. The limited nature of the literature available on applying marker estimation techniques to LADAR data indicates the novelty of the concept of anthropometric marker extraction.

1.1 Problem Statement

The goal of this thesis is to advance the state-of-the-art dismount detection and characterization system. Focusing on the characterization component through the segmentation of 3-D LADAR point cloud data to build a human abstraction based on estimated anthro-
Figure 1. An example of the results from the skin-cued dismount detection system with a bounding box placed around the detected dismount.

pometric markers. Two methods of verification are employed in evaluating the performance of the marker estimation algorithm. The first is through the measured offset between the estimated and the actual marker location. The second method is a verification of the utility of the marker estimates through the use of a gender classification algorithm.

1.2 Scope

The scope of this thesis effort must be limited in order to accomplish the previously stated goals. Accordingly, the scope of the research centers on the following:

- Obtain anthropometric marker locations from 3-D LADAR data;
- Limit the classification process to that of gender; and
- Analyze the performance of the marker estimation algorithm through classification accuracy and error measurements.

The Civilian American and European Surface Anthropometry Resource (CAESAR) Project is the source for the 3-D scans [72]. Associated with this research, there are several challenges pertaining to the data. The first is that the available data set consists of only 3-D
scans of adults. Secondly, the scans are not racially diverse. The data set is comprised of only populations from North America, Italy, and the Netherlands. This limits the possibility of performing classification based on race/nationality characteristics. The demographics for the database are provided in Section 4.1.

The marker estimation algorithm is based on a conceptual framework presented in Chapter 3. The 3-D point cloud data is projected into a dimensionally reduced space and normalized. These steps are detailed in Section 3.2. Section 3.3.1 describes the Self-Organizing Map that is applied to the projected data and extracts cluster centers from the distribution of the projected data. The calculated cluster centers are then refined based on the projected data’s geometry which is discussed in Section 3.3.2. Further refinement of the cluster centers is performed using skeletal information, covered in Section 3.3.3, and anthropometric information, discussed in Section 3.3.4.

1.3 Document Organization

This thesis consists of five chapters. This first chapter motivates the research effort, states the problem, and presents the scope and limitations associated with the research.

The second chapter provides a discussion of literature related to problem of segmenting 3-D LADAR point cloud data. The chapter also contains the background information necessary to understand the structure and components of the developed marker extraction algorithm.

The third chapter presents the methodology by describing the marker estimation algorithm from the 3-D LADAR data through the various stages of processing to the resulting anthropometric marker estimates. This chapter specifically focuses on the algorithm’s primary components: Principal Component Analysis (PCA), Self-Organizing Maps (SOM), Alpha Hulls, and the process of marker refinement.

The fourth chapter provides the details of the parameters specific to each stage of the marker estimation algorithm. The performance of the algorithm based on gender classification is presented in this chapter as well.

The fifth chapter summarizes the results, discusses the impact of this thesis’ contribution
to current dismount detection and characterization efforts, and provides recommendations for areas of future work in improving the marker estimation algorithm.
2. Background

This chapter provides an overview of the problem of segmenting 3-D point clouds and how others have approached the problem. Additionally, this chapter provides the necessary background information on the pattern recognition, neural network, and classification tools implemented in this thesis.

The chapter begins with a brief overview of the notation and terminology conventions used in this thesis. This is followed by an overview of the nature of point cloud data and a review of current approaches to the segmentation problem. The next section deals with the tools used in this thesis to build the segmentation algorithm. The final portion of this chapter discusses previous related work and the issues with classification.

2.1 The Nature of LADAR Point Cloud Data

Light Detection and Ranging (LiDAR) systems, of which LADAR systems are a subset, are a common tool used to collect ranging information used in a myriad of fields, including terrestrial mapping and target tracking. LiDAR, LADAR, and RADAR are all ranging systems that transmit and receive electromagnetic information. In the case of LADAR, the transmitted energy falls into the frequency band associated with laser energy. A simplified view of how LADAR performs is presented in Fig. 2. It shows that a pulse is transmitted and an approximately co-located receiver detects the returned pulse. The time delay between the transmission and reception of the pulse determines the distance to the scanned object. This 1-D example can then be expanded to a 2-D array of receivers that can provide a 3-D representation of the scanned object. The output of the LADAR system used in the human body scans is a dense point cloud representing the location of the thresholded signal return.

Typical LiDAR segmentation can be classified into two categories: part-type segmentation and patch-type segmentation. Part-type segmentation is commonly used in terrestrial mapping to extract basic geometric shapes from the data [71]. Patch-type methods strive to segment the data into homogeneous regions based on similarities between local points or the proximity of the points [88]. The segmentation of the human body scans falls into the
latter category of segmentation.

3-D LiDAR segmentation has interest from a number of diverse fields. The geo-spatial and remote sensing community often look to segment data for terrestrial mapping applications [12, 61, 88]. The computer vision community uses segmentation in the area of vision-aided navigation [38]. Pertaining to the segmentation of LiDAR data from human body scans, there is significant interest from the perspective of the computer graphics field in order to develop more realistic computer models of humans for the entertainment and simulation industries [9, 31, 50]. Additionally, the desire to improve automated human identification and recognition has provided more avenues for further progress in the area of point cloud segmentation.

Current strategies that address the problem of segmenting 3-D point cloud data can be generalized into two basic methods: segmentation from the point cloud directly or surfacing the point cloud before segmentation. The former approach benefits from a reduction in the amount of algorithm preprocessing necessary to conduct segmentation, whereas the latter approach attempts to take advantage of the underlying curved nature and geometric properties of the object to aid in identification and segmentation [2]. With the end goal of extracting anthropometric markers from point cloud data, a part of this research examines the recent research into LiDAR segmentation.
2.2 Segmentation Approaches

Much of the published literature pertaining to the segmentation of 3-D point cloud data falls into two basic categories: segmenting point cloud data directly or segmenting a surfaced representation of the point cloud. Often, the decision of which method to use is based on the academic field using the information. Geo-spatial and vision-based navigation applications tend to utilize raw point cloud data processing methods whereas the computer graphics community focuses on surfacing based methods. One reason for this difference is due to the format of the data returned from the sensor. Typically, fielded LiDAR sensors for geo-sensing applications return either waveforms or point clouds; however, many 3-D scanners employed in computer graphics applications process the data and generate polygonally meshed surfaces. Whether it is with the intent of incorporating a surfacing algorithm into geo-sensing applications or an effort to improve the surfacing algorithms designed into the 3-D scanner software, there is significant research in the area of surfacing point cloud data [28, 47, 60, 66].

2.2.1 Segmentation from Point Clouds.

Based on the previously described distinctions, the literature pertaining to implementing clustering algorithms directly on point clouds from the remote sensing community generally addresses terrestrial mapping problems. A large portion of the research in this area is split into papers dealing with improvements or variations to the $K$-means algorithm [11, 12] with others focusing on research into implementing or adapting Iterative Self-Organizing Data Analysis Techniques (ISODATA) algorithms [61].

Direct segmentation from point cloud data is also addressed from the computer vision community, generally from the perspective of vision-aided navigation for robots but also in the area of human tracking and motion capture [13, 29]. Often, these methods focus on $K$-Nearest Neighbor (KNN) based approaches [44], such as Clustering Large Applications based on RANdomized Search (CLARANS) [64] and Density-Based Spatial Clustering of Applications with Noise (DBSCANS) algorithms [21].
A direct application of processing point cloud data of human body scans is addressed in [16] and builds upon the capability of spectral embeddings to map 3-D shapes into lower dimensional manifolds [3, 82]. Specifically, the author explores the capability of locally linear embedding (LLE) to reveal the intrinsic geometry of the articulated shape. Additionally, the author compares the performance of LLE to Isomap, a low-dimensional embedding method in which geodesic distances on a weighted graph are incorporated with metric multidimensional scaling [36].

### 2.2.2 Segmentation From Surfaces.

When approaching segmentation from the perspective of surfacing, the published work can be divided into at least three categories: graph theory based methods, extensions of image processing techniques, and perceptual segmentation. In general, approaches considering segmentation from a surface assume that the surface was provided as the output from the scanner or accomplished as a preprocessing step with the nature of the surfacing algorithm left as a separate area of research.

A popular graph theory method for segmenting a surfaced point cloud is the Reeb Graph [93]. The Reeb Graph, a mathematical construct based on Morse theory, represents the topological skeleton of a multi-dimensional object. A height function is used to calculate level-set curves which represent a vertex in a graph, producing a skeleton of the object [19]. Implementations of a basic Reeb Graph are generally sensitive to noise in the data. As such, the numerous adaptations of this approach include the following: examining various height functions [81], using a discrete Reeb Graph [86, 92], and affine invariant Reeb graphs [62].

A second approach to segmenting a surface extends 2-D image processing techniques to 3-D applications. This approach includes using the watershed algorithm for segmentation [52], extending binary morphologic transforms and filters [73], and applying the Medial Axis Transformation (MAT) to the problem [80]. The first approach involves examining the local curvature minima in order to derive the segmentation criterion. The latter two methods produce a skeleton which can be segmented through graph-based characterization methods.
similar to those used in Reeb Graph techniques.

The third approach draws on similarities to the way in which human perception segments objects [48, 91]. This approach is based on minima theory and how human perception decomposes an image. From the perspective of the literature, this appears to have been a popular approach in the initial stages of addressing the problem, but there has been little research in this direction in recent years.

2.3 Conceptual Paradigm for the Marker Extraction Problem

In approaching the problem of extracting anthropometric markers directly from point cloud data, the problem can be broken down into several fundamental processes. A representation of the approach is depicted in Fig. 3.

2.3.1 Point Cloud Data Analysis.

In exploring several of the algorithms developed from the background research, the 3-D point cloud data used in testing the developed algorithms is from the Civilian American and European Surface Anthropometry Resource (CAESAR) Project [72]. Each data set is large, on the order of hundreds of thousands of points. An example of the point cloud data is shown in Fig. 4. The data was randomly downsampled for the purpose of display. There are several challenges in dealing with the collected data. The scans were conducted in three separate locations: North America, Italy, and the Netherlands, using different scanners and different data collection teams, both resulting in inconsistency in the values for marker locations. Additionally, the fidelity of the scans varies with some scans having sparse data points in regions of the body or missing body parts entirely.
2.3.2 Projection Methods.

As part of the preprocessing phase, dimensionality reduction is often used with the goal of simplifying the complexity of the problem. There are a number of dimensionality reducing, or projection methods, used in the field of pattern recognition [24, 77] including Sammon’s nonlinear mapping, multidimensional scaling, independent component analysis, and even self-organizing maps. However, the focus from the background research is on principal component analysis and locally linear embedding, discussed in the following sections.

2.3.2.1 Principal Component Analysis.

Generally, principal component analysis (PCA) is employed in dimensionality reduction, data compression, and feature extraction problems. However, it can be useful in data analysis/visualization efforts. Applying PCA to the 3-D point cloud data can provide information about various angles of rotation and the eigenvectors derived from the covariance of the point cloud provides the principal axes of the data. In general, PCA is implemented...
using the following equation:

\[ Y = \Phi^H X, \]

where \( \Phi \) is the eigenvector matrix found from the covariance matrix of \( X \), \( X \) is the original data, and \( Y \) is the output data in the transformed space. In this case, the desired result is the eigenvectors from the decomposition of the covariance matrix. After projecting the 3-D data onto the first and second principal components, the eigenvectors of the autocorrelation matrix provide the two vectors that describe the major and minor axis of the data distribution.

Examining the data in the transform space using all three principal components, as shown in Fig. 5, does not provide much in the way of additional insight into the data. Using the first two principal components produces the results in Fig. 6. Since the principal components are ordered in descending order of variance, the first component corresponds to the subject’s height, the second component to the subject’s breadth, and the third component to the subject’s depth. The plane formed by the first and second principal components corresponds to the coronal plane as shown in Fig. 7. The coronal plane is likely sufficient for determining marker locations [26].

### 2.3.2.2 Locally Linear Embedding.

An interesting non-linear approach to the problem of segmenting a 3-D point cloud of a human subject is discussed in [16], in which locally linear embedding (LLE) is used. The rationale behind this approach is that, in general, multidimensional scaling (MDS) and PCA both fail to provide a method to reduce the dimensionality of non-linear point cloud data because they model linear variabilities over the entire data set. Due to the inherent nonlinearity of the human body scans, utilizing a dimensionality reduction tool designed to operate on nonlinear manifolds makes sense. LLE is such a tool. It is an unsupervised learning algorithm that “computes low dimensional, neighborhood preserving embeddings of high dimensional data” [74].

*Local Linear Embedding Description*
LLE makes use of the approximate linear relationship of a point set of nearest neighbors, assigning a set of weights to each point based on its linear relationship with its neighbors. An eigenvector optimization algorithm is used to find a lower dimensional embedding of the points, preserving the linear relationship of a point with its nearest neighbors [74]. The results of this transform can be seen in Fig. 8. As can be seen, the LLE transform improves upon the PCA transform in terms of providing more definitively segmentable regions. From Fig. 9 we can see that LLE also provides a means of reducing the 3-D point cloud dimensionality while maintaining a means to segment the data into natural groupings.

**Evaluation of Local Linear Embedding**

A big discriminator in evaluating the success of the various segmentation algorithms lies in their computational efficiency. The computational intensity of KNN determination and eigenvector decomposition results in the LLE algorithm being very slow. In order to achieve results, the data set was randomly downsampled, retaining only 2.5% of the original data set.
LLE provides a good method for segmenting the data as well as a way to provide dimensionality reduction. Using LLE, in conjunction with a point representation method such as the mean, may provide suitable results when extracting marker locations from the point cloud data. However, the computational intensity of the KNN portion of the algorithm is a drawback. Due to the KNN approach of most of the vision-navigation-based clustering algorithms, they suffer from similar problems when applied to the large human body scan data.

2.3.3 Clustering Methods.

Moving into the area of segmentation, there are a number of hierarchical and agglomerative clustering methods available. However, as part of this research the focus is on examining the $K$-means, formal element, and self-organizing map algorithms.
2.3.3.1 \textit{K}-Means.

\textit{K}-Means Description

In the \textit{K}-means approach, \textit{K} randomly generated points are chosen and the algorithm iteratively updates the location of the \textit{K} points to correspond to the density centers of the updated cluster regions. One of the problems with this method when applied to the human body scan data is that the natural anthropometric information is not taken into account when clustering the data. This may result in instances where a mean of a region falls outside the contained volume of the scanned human body.

Implementing an unsupervised \textit{K}-means algorithm with \textit{K} = 20 produces the results...
shown in Fig. 10. The algorithm was run using the entire data set but was randomly
downsamples in the plot to show where the means align within the data. As shown in
Fig. 10, there are two means that fall outside the volume of the human body.

Evaluation of K-Means

Due to the unsupervised nature of the K-Means algorithm, its ability to extract marker
locations from the data comes into question. However, if some anthropometric a priori
knowledge is used in conjunction with it, the K-Means algorithm could provide suitable
results.

2.3.3.2 Family of FOREL Clustering Algorithms.

Background

The formal element (FOREL) algorithm [69] is a taxonomy-based algorithm that falls
into the category of agglomerative clustering [32]. It was first used in statistical data processing of palaeontology data [32]. In recent years, it has seen increased use in data mining efforts in the medical field, specifically in genetic and cancer research [68].

The goal of the FOREL algorithm is to divide $m$ objects into $K$ taxons based on the criterion of cluster compactness, assuming that $K < m$. Each taxon is comprised of a cluster of relatively close data points and represented by a central data point. The other taxons are comprised of data points that are maximally separated from the other taxons. By growing the radius of the hypersphere from a minimal value to a maximum value corresponding to half of the maximal distance, the data can be explored and the decreasing number of taxons tracked.

Though there are several variations of the basic algorithm [49, 94, 95], the general scheme of a FOREL algorithm is as follows:

1. For a fixed threshold radius, $T$, place the cluster center at a random data point.

2. Determine which data points lie within the sphere defined by the radius, $T$. 

Figure 9. The 3-D point cloud data projected into the 2-D LLE domain.
3. Using all data points that fall within the sphere, calculate the center of gravity.

4. Move the center to this new location, determine the new set of internal points and calculate the new center.

5. Repeat steps 1-4 until the center of gravity ceases varying. The sphere is referred to as a taxon, and all of the enclosed data points are represented by the calculated center of gravity.

6. Perform this process for the rest of the input data points until all data points are included in a taxon.

Litinskii-Romanov Algorithm

In [49], the authors propose a variation of the FOREL algorithm in which only the between data point distances are used in a neural network algorithm to extract class centers.

An $N \times N$ matrix consisting of the Euclidean distances between the $m$-dimensional points is calculated. At the beginning of the algorithm, each data point is represented by a
neuron with initial activity, $S_i(0)$. The weight matrix is comprised of connections between the $i$th and $j$th neurons, $w_{ij}$, given by the following:

$$w_{ij} = \begin{cases} \frac{T^2}{D_{ij}^2 + T^2} & \text{when } D_{ij} \leq T, \\ 0 & \text{when } D_{ij} > T. \end{cases}$$

Eqn. 2 states that if the distance between points is greater than $T$ then there are no connections between the neurons. However, if the distance between points is less than the threshold radius, $T$, the weight for the associated neurons is defined as the ratio of the squared threshold radius to the sum of the squared inter-neuron distance and squared threshold radius. The initial neuron activity is given by the following:

$$S_i(0) = \sum_{j=1}^{N} w_{ij} \geq 1,$$

which results in large initial activities for neurons inside a dense region. The “transmitting” process is captured with the following learning rule:

$$S_i(t + 1) = S_i(t) + \alpha \sum_{j=1}^{N} w_{ij} (S_i(t) - S_j(t))$$

where $\alpha$ is the learning rate parameter, often a time-decreasing function. If the activity of a neuron becomes negative during the transmitting process, the activity for that neuron is defined by $S_i(t) = 0$, removing it from the solution. As the transmitting process continues, the neurons at the periphery of the agglomeration surrender their activities to more centralized neurons. As the process runs its course, $K$ neurons should remain distant from each other. The data points corresponding to these neurons are the cluster centers.

If the threshold is varied from a minimal value where each data point represents its own cluster center to a maximal value where all data points are contained in a single cluster, the algorithm explores the data set and provides insight into the number of clusters inherent to the data set.

One difference between the Litinskii-Romanov algorithm and the standard FOREL al-
algorithm is that the resultant cluster centers will always be drawn from the original data set, whereas in the standard FOREL algorithm the cluster centers are calculated based on the distribution of points within the threshold radius and can result in a cluster center that lies between the original data points.

**Evaluation of Litinskii-Romanov Clustering**

Due to the promising nature of the results, the Litinskii-Romanov clustering algorithm is evaluated for the point cloud segmentation problem. Its performance is first evaluated using common data sets and comparing the results of the developed implementation to those that Litinskii and Romanov report in [49].

The first data set used for comparison is comprised of 5 compact clusters, each with 50 data points. Each cluster of points is internally compact and the between cluster separation is large. The data for each cluster is generated using a Gaussian distribution. A plot of the data is provided in Fig. 11. A plot of the estimated number of classes versus threshold radius is shown in Fig. 12.

![Data with Calculated Cluster Centers](image.png)

Figure 11. The input data of 5 compact clusters each containing 50 data points for the Litinskii-Romanov algorithm with cluster centers highlighted in red.
The algorithm is also tested using the IRIS data set [25] to compare results with those published by Litinskii and Romanov in [49]. The resulting plot, shown in Fig. 13, shows some similarities with the published results; however, there are some significant differences. The published plot has a smoother and slower transition from 150 cluster centers to the expected 3 cluster centers (one for each of the three IRIS clusters), with the shape of the curve over this range of radii being concave down. The plateaus for 2 and 3 cluster centers are present in both plots, but the present results produce a plateau for 1 cluster at a much smaller radius than that in [49].

Applying the Litinskii-Romanov algorithm to the body scan data results in the cluster-vs-radius plot presented in Fig. 14. This plot shows the estimated number of clusters versus threshold radius. The terminal plateau of the plot indicates the data is comprised of two clusters. Though this is a viable result, it does not serve the intended purpose of correlating cluster centers to anthropometric marker locations. Since the goal is to locate the centers corresponding to the shoulders, hips, knees, ankles, elbows, wrists, and the head,
Figure 13. The Litinskii-Romanov algorithm’s estimated number of clusters versus threshold radius plot for the IRIS data set [25].

an intermediate result is extracted corresponding to 13 cluster centers. The plot in Fig. 15 captures the cluster centers approximately 20% through the algorithm.

The Litinskii-Romanov algorithm performs well when working with easily separable clusters, as shown in the duplication of Litinskii and Romanov’s results in [49]. The algorithm struggles in adequately providing anthropometrically useful cluster centers when applied to the body scan data. The general data exploration piece of the algorithm appears to find an appropriate number of clusters, but their class centers do not correspond to anthropometric marker locations.

2.3.3.3 Self-Organizing Map Clustering.

Though there is no literature directly addressing the application of applying a Self-Organizing Map (SOM) algorithm to 3-D body scan data, there is literature pertaining to the use of SOMs in reverse engineering mechanical components into CAD drawings. This is accomplished by taking LADAR scans of the object and then performing segmentation on
the scans in order to extract the regions that comprise a surface of the object [51]. As part of the reverse engineering effort, there is a strong emphasis on performing edge detection on the point clouds in order to aid the segmentation process [87].

The SOM, an unsupervised clustering method, was introduced by Kohonen in 1982 [46]. In general, the goal of a SOM is the derivation of a feature map that captures the essential characteristics of the input data in a lower dimensional representation. The SOM network is comprised of two components: a connected lattice of neurons and a weight vector associated with each neuron. The lattice has an inherent connectivity and is a means to provide neighborhood preservation. A key feature of an SOM is that it preserves the inherent topology of the input data. The weight vectors are the learned component of the network [46].

The SOM algorithm begins with weight initialization. The three basic processes that comprise the formation of a SOM are as follows [35]: (a) competition, (b) cooperation, and (c) adaptation.
In the competition phase, each neuron calculates a value based on a discriminant function. The node with the smallest resulting value is declared the winning neuron. Based on the location of the winning neuron and a predetermined neighborhood function, a neighborhood of spatially related neurons become excited. The results of this excitement produce the adaption process in which the synaptic weights are adjusted to increase their value based on the input. Thus, similar inputs will provide enhanced responses to those particular lattice nodes [23].

In many applications, the discriminant function used to find the winning neuron compares the Euclidean distances such that the best-matching neuron is found as:

$$c = \arg \min_i \{\|x - m_i\|\}$$

(5)

where $m_i$ is the weight of $i$th neuron. Updates to the winning neuron and neurons within
the neighborhood of the winner occur as:

\[ m_i(t+1) = m_i(t) + h_{ci}(t)|x(t) - m_i(t)|, \]  

(6)

where \( t \) is a discrete-time coordinate. The neighborhood function is given by \( h_{ci}(t) \) which converges to zero as \( t \) approaches \( \infty \) for Gaussian neighborhoods. Common neighborhood functions consist of a time diminishing Gaussian function and an \( n \)-connected components function in which 4- or 8- connected neighboring neurons are updated.

2.3.4 Geometry Computation.

The geometry computation section is a significant preprocessing step used in a segmentation from a surface approach. It is also a useful tool in evaluating the results of clustering algorithms. Presented here are discussions on Voronoi diagrams, Delaunay triangulations, and alpha hulls.

2.3.4.1 Voronoi Diagrams.

Voronoi tessellations are a common tool in computational geometry. In the simplest terms, a Voronoi region is defined in terms of its nearest neighbors in which the delineated region defines the region of points that are closer to that point than any other in the set of points [53].

More formally, given a set of points \( \mathcal{X} = \{x_1, ..., x_n\} \) in \( \mathbb{R}^d \), the Voronoi region of \( x_i \) is the set of points in \( \mathbb{R}^d \) which are closer to \( x_i \) than to the other points in \( \mathcal{X} \).

\[ V_i = V(x_i; \mathcal{X}) = \{ x \in \mathbb{R}^d : d(x, x_i) < \min_{j \neq i} d(x, x_j) \}. \]  

(7)

The distance \( d \) is usually the Euclidean distance. The Voronoi tessellation, or Voronoi diagram, of the points is the set of points in \( \mathbb{R}^d \) which have more than one nearest neighbor in \( \mathcal{X} \) [53]. An example of a Voronoi diagram for a set of 20 random points is shown in Fig. 16.
2.3.4.2 Delaunay Triangulation.

The Delaunay triangulation is the dual to the Voronoi tessellation. It is the graph whose vertices are $\mathcal{X}$, with an edge between $x_i$ and $x_j$ if and only if the Voronoi cells of $x_i$ and $x_j$ share an edge. The Delaunay triangulation theory dictates that for a set of points, $P$, there is a triangulation, $DT(P)$, such that no point in $P$ lies within the circumscribed circle of any triangle in $DT(P)$ thereby minimizing the size of each of the triangles. A couple of other important properties of the Delaunay triangulation are that a convex hull is a subgraph of the Delaunay triangulation and no elements of $\mathcal{X}$ are contained within a triangle [53]. The computation time of a Delaunay triangulation is $\mathcal{O}(n \log n)$ [53]. An example of a Delaunay triangulation on the set of 20 random points used in the Voronoi tessellation example (Section 2.3.4.1) is shown in Fig. 17.
2.3.4.3 Alpha Hulls.

Alpha hulls are a generalization of the convex hull of a point set [20]. A convex hull for the random 20 point example is shown in Fig. 18. Marchette’s definition of an alpha hull is presented as the following: for \( \alpha > 0 \), the alpha hull (also called the alpha shape) of a set of points \( \mathcal{X} = \{x_1, \ldots, x_n\} \) is the graph with vertices \( V = \mathcal{X} \) and edge set \( E = \{v_i v_j : \exists D_\alpha \text{ with } v_i, v_j \in \partial D_\alpha \text{ and } \mathcal{X} \cap D_\alpha = \emptyset\} \), where \( D_\alpha \) is a disk of radius \( \alpha \) and \( \partial S \) denotes the boundary of the set \( S \). For \( \alpha < 0 \), we require that the disk be of radius \( \alpha \), and \( \mathcal{X} \cap D_\alpha = \mathcal{X} \). Finally, for \( \alpha = 0 \), the graph is the empty graph on \( \mathcal{X} \) [53]. An example of an alpha hull for the set of 20 random points used in the Voronoi tessellation and Delaunay triangulation examples (Sections 2.3.4.1 and 2.3.4.2) is shown in Fig. 19.

A common description of the alpha hull process is to imagine rolling a disk of radius \( \alpha \) around the set of points and the point pairs that can be touched by the disc of radius \( \alpha \).
become a constituent line segment of the boundary that forms the shape of the data set. This concept is shown in Fig. 20. The effects of different values of $\alpha$ can be seen in Fig. 21 in which the appearance of the resulting alpha hull varies greatly based on the selected $\alpha$. The result of $\alpha = \infty$ is the convex hull.

2.3.5 Skeletonization.

In segmentation from a surface approaches, skeletonization acts as the segmentation method whereas it serves as a post-processing step for segmentation from point cloud approaches. Discussed here are the concepts of Reeb graphs and medial axes.

2.3.5.1 Skeletonization from a Surface.

Background on Skeletonization

Due to the significant number of papers that addressed segmentation from a polygo-
nally meshed surface, the approach by [92] is described. There are a variety of methods available to generate a polygonal mesh from a point cloud, but Delaunay triangulation is a common method used in computational geometry, mathematics, and computer graphics and is selected for evaluation. It is a similar algorithm to the Voronoi tessellation algorithm used for creating equidistant decision boundaries for classification problems [1]. A Delaunay triangulation mesh extracted from the 3-D point cloud data is shown in Fig. 22.

Once a surface is generated, the skeleton is derived. A method drawn from 2-D image processing is the Medial Axis Transform [41]. It was formalized by Harry Blum of the Air Force Research Laboratories in Cambridge, Massachusetts, in which he defined a medial axis for computing a 2-D skeleton using a “grass field fire propagation” model to describe the resultant line segment generated if a fire was set at the boundary of a shape and was allowed to run to the center of the shape [7]. This description serves as a basic understanding for the analogous mathematical definitions further developed under Reeb graph and contour
Figure 20. A standard representation of the generation of an alpha hull by rolling a disk of radius $\alpha$ around the set of points.

tree theory in computational geometry and topology [4].

The Reeb Graph, a mathematical construct based on Morse theory, represents the topological skeleton of a multi-dimensional object. A height function is used to calculate level-set curves which represent a vertex in a graph, producing a skeleton of the object [19]. Implementations of a basic Reeb Graph are generally sensitive to noise in the data. As such, the numerous adaptations of this approach include the following: examining various height functions [81], using a discrete Reeb Graph [86, 92], and affine invariant Reeb graphs [62].

A simplified description of Reeb graph theory is that for a surface, $DT(P)$, such as produced from a Delaunay triangulation, a height function, $f$, can be defined such that the contour of the surface is described by a skeleton, the reduction of the shape to its minimal form. The skeleton is derived in such a way that it connects all of the critical points of the object. An example of the output of a Reeb graph algorithm is shown in Fig. 23 (from [89]).

An example of a skeleton derived from a 3-D point cloud is shown in Fig. 24 for the lower body portion (waist and below) of the point cloud data. In this example, a medial axis calculation is used. The medial axis is found by minimizing the Euclidean distance of each point on the surface with those contained within the surface.

*Evaluation of a Skeletonization from a Surface Algorithm*
Computational adversities, similar to those faces in the LLE implementation, are encountered with the skeletonization process. In part, this increased processing time is due to the additional step of generating a surface from the point cloud, though the skeletonization algorithms are computationally intensive unto themselves.

The published results for skeletonization from a meshed surface show promising results for extracting a skeleton from the point cloud data [9, 31, 89, 92]. However, attempts to duplicate those efforts did not produce satisfactory results. Additionally, once a skeleton is obtained, marker estimation would need to be extrapolated from the critical points of the surface as per the Reeb graph theory approach, or some other method of marker extraction would need to be developed.

### 2.3.6 Extracting Marker Locations.

#### 2.3.6.1 Incorporating Anthropometric Information.

A topic that is not addressed in the available literature on segmenting human body scans is how to extract anthropometric markers from the resulting segmentation. An interesting approach to the problem is based on historical research into the proper proportioning of the human body. A famous example of this research is Leonardo da Vinci’s classic Vitruvian
Figure 22. A triangulated surface mesh applied to a 3-D point cloud. The mesh is derived using a Delaunay triangulation based algorithm.

Figure 23. A Reeb graph of a torus and a Reeb graph of a human body shape as produced in [89].

Man drawing from approximately 1487 [17]. The accompanying text, known as the Canon of Proportions delineated a series of proportions for body parts. This work was brought to fruition in the 19th century by the German scientist, Adolf Zeising [63]. His work was based on the principle of the golden section. Given a line segment, shown in Fig. 25, defined by endpoints $A$ and $B$, there exists some point $C$ on this line segment that divides the line...
Figure 24. A skeleton of the lower body derived from the triangulated surface mesh. It is based on a medial axis algorithm to find the central set of points equidistant from the surface.

such that:

\[
\frac{AB}{AC} = \frac{AC}{CB} \quad (8)
\]

\[
(AC)^2 = (AB)(CB). \quad (9)
\]

If the length of line segment \(AC\) is defined as \(M\) and the length of line segment \(CB\) is defined as \(m\) and substituted into Eqns. 9, then

\[
\frac{M + m}{M} = \frac{M}{m} \quad (10)
\]

\[
M^2 = m(M + m) \quad (11)
\]

Solving the resulting quadratic equation for the ratio, \(M/m\), provides a single positive root of 1.6180. From this result, and the proper selection of the points, the location of body markers are obtained. The initial step is to let \(AB\) represent the total height of the individual and point \(C\) represent the location of the umbilicus. This golden section ratio
can then be used to further partition the body into subsequently smaller sections [63].

![Figure 25. A line segment depicting the relationship the points A, B, and C and the lengths M and m for the purposes of illustrating the concept of the golden section as described in [63].](image)

Unfortunately, in practice this systematic proportioning of the human body fails. The length of the upper arms is greater than that predicted by the model, the arms are longer than expected, the biacromial diameter is greater than predicted, the length of the bust is lower than calculated, and the lower limbs are completely different from expected. Furthermore, the height of the leg is longer than expected, the shank is longer and the knee is located higher than expected. In the end, the golden section ratio may provide a rough estimate of marker locations, but the true locations of the markers are not accurately predicted by the golden section ratio method. Or rather, the “ideal” proportions do not provide a good prediction of the wide variance of human proportions [63]. However, incorporating such information may prove useful in locating markers in the LADAR data.

### 2.4 Computing Truth Markers

#### 2.4.1 Exploitation of the CAESAR LADAR Data.

Work accomplished by the Air Force Research Laboratory’s 711th Human Performance Wing in gender classification is based on the goal of “identifying anthropometric measurement combinations that best distinguish between genders in order to address issues related to apparel and workstation design and performance [27].” The results from this research serve as the baseline performance measures used in evaluating the segmentation algorithm developed in this work. The research in [27] combined traditional 1-D measurements with additional information obtained from the 3-D body scans. This combination provides 97 anthropometric measures from which to discriminate gender. In the final analysis, only 16
Table 1. Significant measures for the gender classification problem in [27]. Values shown are the means (standard deviations) for the anthropometric measurements given in mm or kg.

<table>
<thead>
<tr>
<th>anthropometric measure</th>
<th>North America</th>
<th></th>
<th></th>
<th>Italy</th>
<th></th>
<th></th>
<th>The Netherlands</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>males</td>
<td>females</td>
<td></td>
<td>males</td>
<td>females</td>
<td></td>
<td>males</td>
<td>females</td>
<td></td>
</tr>
<tr>
<td>a) waist back</td>
<td>481 (35)</td>
<td>399 (28)</td>
<td></td>
<td>468 (30)</td>
<td>405 (30)</td>
<td></td>
<td>475 (36)</td>
<td>401 (29)</td>
<td></td>
</tr>
<tr>
<td>b) bustpt brth</td>
<td>236 (27)</td>
<td>187 (23)</td>
<td></td>
<td>217 (20)</td>
<td>183 (21)</td>
<td></td>
<td>230 (25)</td>
<td>206 (26)</td>
<td></td>
</tr>
<tr>
<td>c) hip brth, sitting</td>
<td>382 (36)</td>
<td>408 (46)</td>
<td></td>
<td>359 (25)</td>
<td>375 (29)</td>
<td></td>
<td>382 (29)</td>
<td>416 (38)</td>
<td></td>
</tr>
<tr>
<td>d) ankle circ</td>
<td>269 (15)</td>
<td>240 (15)</td>
<td></td>
<td>263 (13)</td>
<td>238 (12)</td>
<td></td>
<td>267 (16)</td>
<td>246 (16)</td>
<td></td>
</tr>
<tr>
<td>e) bi-lat fem epi brth sit</td>
<td>463 (55)</td>
<td>361 (64)</td>
<td></td>
<td>449 (46)</td>
<td>350 (48)</td>
<td></td>
<td>427 (59)</td>
<td>340 (53)</td>
<td></td>
</tr>
<tr>
<td>f) chest circ</td>
<td>1040 (109)</td>
<td>958 (124)</td>
<td></td>
<td>958 (79)</td>
<td>890 (80)</td>
<td></td>
<td>1015 (102)</td>
<td>998 (119)</td>
<td></td>
</tr>
<tr>
<td>g) chest grth at scye</td>
<td>1055 (96)</td>
<td>921 (100)</td>
<td></td>
<td>978 (71)</td>
<td>854 (60)</td>
<td></td>
<td>1022 (85)</td>
<td>943 (88)</td>
<td></td>
</tr>
<tr>
<td>h) neck base circ</td>
<td>468 (30)</td>
<td>410 (27)</td>
<td></td>
<td>475 (21)</td>
<td>425 (21)</td>
<td></td>
<td>489 (36)</td>
<td>441 (33)</td>
<td></td>
</tr>
<tr>
<td>i) weight</td>
<td>86 (18)</td>
<td>69 (18)</td>
<td></td>
<td>73 (11)</td>
<td>58 (9)</td>
<td></td>
<td>84 (16)</td>
<td>73 (16)</td>
<td></td>
</tr>
<tr>
<td>j) triceps skinfold</td>
<td>13 (7)</td>
<td>24 (10)</td>
<td></td>
<td>13 (7)</td>
<td>21 (7)</td>
<td></td>
<td>10 (5)</td>
<td>19 (8)</td>
<td></td>
</tr>
<tr>
<td>k) bi-lat hum epi brth sit</td>
<td>561 (53)</td>
<td>475 (57)</td>
<td></td>
<td>557 (45)</td>
<td>469 (39)</td>
<td></td>
<td>562 (49)</td>
<td>496 (49)</td>
<td></td>
</tr>
<tr>
<td>l) shoulder brth</td>
<td>496 (36)</td>
<td>430 (35)</td>
<td></td>
<td>459 (27)</td>
<td>405 (23)</td>
<td></td>
<td>472 (29)</td>
<td>431 (31)</td>
<td></td>
</tr>
<tr>
<td>m) radiale-styliion lth rt</td>
<td>265 (17)</td>
<td>237 (15)</td>
<td></td>
<td>265 (14)</td>
<td>239 (14)</td>
<td></td>
<td>265 (17)</td>
<td>239 (16)</td>
<td></td>
</tr>
<tr>
<td>n) waist circ (pref)</td>
<td>914 (125)</td>
<td>789 (135)</td>
<td></td>
<td>843 (83)</td>
<td>752 (78)</td>
<td></td>
<td>918 (109)</td>
<td>845 (131)</td>
<td></td>
</tr>
<tr>
<td>o) knee height</td>
<td>562 (31)</td>
<td>509 (28)</td>
<td></td>
<td>541 (26)</td>
<td>497 (24)</td>
<td></td>
<td>558 (35)</td>
<td>514 (28)</td>
<td></td>
</tr>
<tr>
<td>p) sitting height</td>
<td>926 (40)</td>
<td>865 (36)</td>
<td></td>
<td>908 (35)</td>
<td>855 (30)</td>
<td></td>
<td>945 (41)</td>
<td>887 (38)</td>
<td></td>
</tr>
</tbody>
</table>

measures were significant to the discriminant functions as listed in Table 1.

Based on the use of the above features, the authors in [27] achieved classification accuracy of 99.5% for the North American and Italian databases and 98.5% for the Netherlands database. Further evaluation of the discriminators indicated that two measures were of greater significance. These are the sitting hip breadth and the sitting bi-lateral femoral epicondyle breadth, or more commonly, the sitting knee breadth. These measures cause a problem when attempting to apply a classification algorithm based on those features to a data set consisting entirely of standing subjects. It is impossible to accurately calculate these features from a scan of a standing subject. The benefit of being able to use these two features in discriminating gender is that there are distinct differences between males and females in these two areas. The female’s pelvis is larger and broader than that of a male’s. A male’s pelvis is taller, narrower, and more compact than a female’s [78]. Women tend to be proportionately larger in the hips and smaller in knee breadth than men [27]. A contributing factor to this observation is that women tend to store more adipose tissue in the gluteal-femoral region, whereas men tend to store fat around the abdomen [6].
Table 2. Truth marker set.

<table>
<thead>
<tr>
<th>Set of Calculated Truth Markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Left ankle center</td>
</tr>
<tr>
<td>Right ankle center</td>
</tr>
<tr>
<td>Left knee center</td>
</tr>
<tr>
<td>Right knee center</td>
</tr>
<tr>
<td>Left hip center</td>
</tr>
<tr>
<td>Right hip center</td>
</tr>
<tr>
<td>Left wrist center</td>
</tr>
<tr>
<td>Left elbow center</td>
</tr>
<tr>
<td>Left shoulder center</td>
</tr>
<tr>
<td>Right wrist center</td>
</tr>
<tr>
<td>Right elbow center</td>
</tr>
<tr>
<td>Right shoulder center</td>
</tr>
<tr>
<td>Head center</td>
</tr>
</tbody>
</table>

Table 3. Feature set used for classification.

<table>
<thead>
<tr>
<th>Feature Set</th>
</tr>
</thead>
<tbody>
<tr>
<td>Left shank length</td>
</tr>
<tr>
<td>Right shank length</td>
</tr>
<tr>
<td>Left thigh length</td>
</tr>
<tr>
<td>Right thigh length</td>
</tr>
<tr>
<td>Left lower arm length</td>
</tr>
<tr>
<td>Right lower arm length</td>
</tr>
<tr>
<td>Left upper arm length</td>
</tr>
<tr>
<td>Right upper arm length</td>
</tr>
<tr>
<td>Shoulder breadth</td>
</tr>
<tr>
<td>Hip breadth</td>
</tr>
<tr>
<td>Hip height</td>
</tr>
<tr>
<td>Height</td>
</tr>
</tbody>
</table>

The marker set calculated by the segmentation algorithm consists of the markers presented in Table 2. Since the problem addressed in this thesis contains only the 3-D LADAR data, the feature set was restricted to only those measurements obtainable from the calculated anthropometric markers. Therefore, measurements of weight, triceps skinfold, and measurements obtained from sitting subjects are removed from the feature set. This results in a reduced feature set used for the classification process. The reduced feature set is presented in Table 3.
2.4.2 Truth Marker Processing.

The CAESAR data set consists of a 3-D LADAR body scan file as well as a landmark file that consists of the locations of 72 markers affixed to the subject’s body. The markers that the tester places on the subject is shown in Fig. 26. As is the nature of obtaining true marker locations, there are some errors associated with placing the markers on the skin since the flesh is not tightly attached to the bone. Additionally, the tester’s skill in placing the markers is important since many of the markers are attached to either side of the desired marker location. For example, in determining the knee center location markers are affixed at the femoral epicondyle medial and femoral epicondyle lateral locations as shown in Fig. 27 [72]. The desired marker thus becomes the average of those two markers. Of course, if one of the markers is placed too high or too low, the resulting calculated knee center will not correspond with the true knee center location.

Figure 26. Plot of the markers placed on the subject. For clarity, the markers are depicted as red diamonds.
2.4.2.1 Hip Joint Center (HJC) Calculation.

Finding the location of the hip joint center (HJC) is a difficult problem since by its location it is impossible to place a marker on the skin to completely describe the location of the HJC. In general, the only sure method of accurately locating the HJC is through x-ray or MRI scans [42]. Significant research in calculating the HJC exists in the medical, anthropometry, and kinesiology communities. Several methods with a high degree of HJC accuracy rely on placing the markers at the anterior superior iliac spines (ASISs) and the posterior superior iliac spines (PSISs), as shown in Fig. 28 [10].

Figure 27. Line drawing depiction of the femoral epicondyle lateral (left and center) and medial (right) marker placement. The drawings are from [72].

Figure 28. Pelvic anatomical frame showing ASISs, PSISs, and the local reference system [10].
As seen in Fig. 28, the z-axis is defined as the line passing through the ASISs. The HJC lies on the vector $\vec{c}$. To produce the HJC, the process begins by creating the z-axis for a coordinate system local to the hips by subtracting the midpoint between the left and right ASIS markers from the right ASIS marker location:

$$\vec{z} = p_{ASIS_R} - p_{ASIS_C}. \quad (12)$$

A temporary vector that lies in the plane depicted in Fig. 28 is created by subtracting the midpoint between the left and right ASIS markers from the midpoint between the left and right PSIS markers:

$$\vec{t}_a = p_{PSIS_C} - p_{ASIS_C}. \quad (13)$$

The y-axis of the coordinate system is found by taking the cross product of the two vectors:

$$\vec{y} = \vec{t}_a \times \vec{z}. \quad (14)$$

The x-axis of the right-handed coordinate system is found by taking the cross product of the first two axes:

$$\vec{x} = \vec{y} \times \vec{z}. \quad (15)$$

In the defined local coordinate system, the HJC can be found as [10].

$$RHJC_{Local} = [0.36PW, -0.22PW, 0.3PW], \quad (16)$$

$$LHJC_{Local} = [-0.36PW, -0.22PW, 0.3PW], \quad (17)$$

where $PW$ is the pelvic width defined as the Euclidean distance between the ASIS markers. Once the HJC is computed, it is transformed into the global coordinate system.

The axis vectors constitute a rotation matrix used to associate the location of the HJC in the local coordinate system to its location in the global coordinate system. The rotation
The joint center (JJC) calculation is addressed in a similar manner to that described for the HJC [90]. However, in practice good results can be achieved by calculating the SJC based on a standard offset from the acromion marker location [26, 70]. The correspondence of the acromion marker to the SJC can be seen in Fig. 29 [72].

In order to examine the results of the joint center calculations, the combination of all of the markers is presented in Fig. 30. Only 0.5% of the 3-D body scan data points are shown to provide sufficient clarity to see the marker locations while retaining the scanned subject’s body structure. The landmark file is used in conjunction with the marker determination algorithm described in Sec. 2.4 to calculate the standard set of anthropometric markers.

\[
\begin{bmatrix}
  z_1 & y_1 & x_1 \\
  z_2 & y_2 & x_2 \\
  z_3 & y_3 & x_3
\end{bmatrix}
\]

\[
\mathbf{R}_{\text{HJC}} = \begin{bmatrix}
  z_1 & y_1 & x_1 \\
  z_2 & y_2 & x_2 \\
  z_3 & y_3 & x_3
\end{bmatrix}
\]

(18)

The HJC in the global coordinate system is then described as:

\[
\mathbf{HJC}_{\text{Global}} = \mathbf{p}_{\text{ASIS}} + \mathbf{HJC}_{\text{Local}} \mathbf{R}_{\text{HJC}}^T.
\]

(19)

### 2.4.2.2 Shoulder Joint Center (SJC) Calculation.

The shoulder joint center (SJC) calculation is addressed in a similar manner to that described for the HJC [90]. However, in practice good results can be achieved by calculating the SJC based on a standard offset from the acromion marker location [26, 70]. The correspondence of the acromion marker to the SJC can be seen in Fig. 29 [72].
used in this research as listed in Table 2.

![Calculated anthropometric markers.](image)

Figure 30. Plot of the anthropometric truth markers calculated from the markers placed on the subject during the scan. Only 0.5% of the 3-D point cloud data is plotted to provide clarity.

### 2.5 Evaluating the Marker Estimation Algorithm

In order to evaluate how well the marker estimation algorithm performs, we need a method to quantify performance. One way of doing this is to use the classification results described in [27].

#### 2.5.1 Classification.

The classification problem can be accomplished through a variety of methods, and through the course of this research effort several methods were explored and tested. However, since the sponsor obtained the performance benchmark using linear discriminant analysis, it is the method applied to the results presented in this thesis.
2.5.2 Linear Discriminant Analysis.

Linear discriminant analysis (LDA) is a method to find a linear combination of features with which to characterize two or more classes. Define the prior probability of class $k$ as $\pi_k$ with $\sum_{k=1}^{K} \pi_k = 1$. The class-conditional probability density function of $X$ in class $G = k$ is $f_k(x)$. From decision theory, optimal classification is based on the class posteriors $Pr(G|X)$. Calculating the posterior probability based on an application of Bayes theorem results in

$$Pr(G = k|X = x) = \frac{f_k(x)\pi_k}{\sum_{l=1}^{K} f_l(x)\pi_l}. \quad (20)$$

By maximum a posteriori decision theory, the optimal classification is based on the class posteriors:

$$\hat{G}(x) = \arg \max_k Pr(G = k|X = x)$$

$$= \arg \max_k f_k(x)\pi_k. \quad (21)$$

If each class density is modeled as a multivariate Gaussian having the form:

$$f_k(x) = \frac{1}{(2\pi)^{p/2}|\Sigma_k|^{1/2}} e^{-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k)}. \quad (22)$$

then

$$\hat{G}(x) = \arg \max_k Pr(G = k|X = x)$$

$$= \arg \max_k f_k(x)\pi_k. \quad (23)$$

When it is assumed that the classes have a common covariance matrix, $\Sigma_k = \Sigma, \forall k$, the
special case of linear discriminant analysis (LDA) is obtained.

\[
\hat{G}(x) = \arg \max_k \log(f_k(x)\pi_k) \\
= \arg \max_k [-\log((2\pi)^{p/2}|\Sigma|^{1/2}) - \frac{1}{2}(x - \mu_k)^T \Sigma^{-1}(x - \mu_k) + \log(\pi_k)] \\
= \arg \max_k [-\frac{1}{2}(x - \mu_k)^T \Sigma^{-1}(x - \mu_k) + \log(\pi_k)] \\
= \arg \max_k [x^T \Sigma^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k - \frac{1}{2} x^T \Sigma^{-1} x + \log(\pi_k)] \\
= \arg \max_k [x^T \Sigma^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k + \log(\pi_k)].
\] (24)

The linear discriminant function is defined as:

\[
\delta_k(x) = x^T \Sigma^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k + \log(\pi_k),
\] (25)

resulting in the following classification rule:

\[
\hat{G}(x) = \arg \max_k \delta_k(x).
\] (26)

Looking at the two class case where the classes are represented by \(k\) and \(l\), the decision boundary is described by

\[
\{x : \delta_k(x) = \delta_l(x)\}
\] (27)

and the following holds:

\[
\log \frac{\pi_k}{\pi_l} - \frac{1}{2} (\mu_k + \mu_l)^T \Sigma^{-1}(\mu_k - \mu_l) + x^T \Sigma^{-1}(\mu_k - \mu_l) = 0.
\] (28)

This results in a decision boundary linear in \(x\). In practice, the parameters for the Gaussian distribution are unknown, so the parameters can be estimated from the training data as

2-38
follows:

$$\hat{n}_k = \frac{N_k}{N}, \quad (29)$$

$$\hat{\mu}_k = \sum_{g_i=k} x_i \frac{N_k}{N}, \quad \text{and} \quad (30)$$

$$\hat{\Sigma} = \sum_{k=1}^{K} \sum_{g_i=k} (x_i - \hat{\mu}_k)(x_i - \hat{\mu}_k)^T / (N - K), \quad (31)$$

where $N_k$ is the number of class-k observations [34].

If the covariance matrices are not assumed to be equal, then the quadratic elements in $x$ remain. This establishes the quadratic discriminant function (QDA) [5] as:

$$\delta_k(x) = -\frac{1}{2} \log |\Sigma_k| - \frac{1}{2} (x - \mu_k)^T \Sigma_k^{-1} (x - \mu_k) + \log \pi_k. \quad (32)$$

The classification rule is

$$\hat{G}(x) = \arg \max_k \delta_k(x) \quad (33)$$

and the decision boundaries are quadratic in $x$.

### 2.6 Summary

This chapter reviewed related literature dealing with segmenting point cloud data, introduced a conceptual paradigm in which to approach the marker estimation problem, and described various tools that will be used in the next chapter to describe the segmentation algorithm’s flow. The next chapter goes into depth on the particular process used to estimate marker locations. Based on promising concepts in approaches from the literature review and preliminary algorithm evaluation, research into the development of the segmentation algorithm focuses on building it around the Self-Organizing Map. A description of the theory behind the individual components is provided in this section beginning with a few computational geometry concepts. The integrating of these methods to produce anthropometric markers is covered in Chapter 3.
3. Methodology

This chapter provides the methodology that serves as the initial foray into extracting marker locations from 3-D LADAR point cloud data. The segmentation directly from the point cloud (Section 2.2.1) is chosen for the general approach and a description of the overall process is depicted in Fig. 31.

The decision to proceed with the segmentation from point cloud approach vice the segmentation from a surface approach is based on several factors. The primary reason is that, since the end goal is to derive anthropometric markers, the surfacing approach would

![Diagram of the fundamental flow and segmentation process](image)

**Figure 31.** Diagrams of (a) the fundamental flow introduced in Section 2.3 and (b) the overall segmentation process specific to the segmentation from a point cloud approach. The 3-D point cloud data is the input to the system, and the estimated marker locations are the product of the marker estimation algorithm.
require an additional step to appropriately locate the markers. Furthermore, segmenting from a point cloud is more computationally efficient. The surfacing and medial axis of a 3-D point cloud are more computationally intensive than projection and clustering often used in segmenting point clouds.

In relating Fig. 31b to the conceptual paradigm shown in Fig. 31a, the preprocessing block in the current diagram consists of two steps: (a) scaling and (b) projection. The segmentation block of Fig. 31a is clustering in Fig. 31b. The post-processing step of Fig. 31a consists of (a) computation of the geometry, (b) skeletonization, and (c) marker refinement.

3.1 Algorithm Overview

The general concept of the segmentation from point cloud approach is to project the 3-D point cloud data into a meaningful dimensionally reduced space on which a clustering algorithm extracts cluster centers from the distribution of the projected data. The calculated cluster centers are then refined to better estimate anthropometric marker locations. Based on the background research discussed in Sections 2.3.4, 2.3.5, and 2.3.6, the cluster center refinements depend on incorporating anthropometric information into the algorithm. The rest of the chapter details the choices made for each of the blocks in Fig. 31b.

3.2 Projection

Due to the nature of the feature set used in the classification problem, namely a feature set of body segment lengths as described in Sec. 2.4.1, the dimensionality of the data is reduced to simplify the complexity of the problem. A good choice for dimensionality reduction is one that provides a coronal plane view of the subject as shown in Fig. 7. The coronal plane provides a complete view of the markers we are trying to calculate since, for a standing subject, the anthropometric marker set we desire is roughly situated in a single plane. As discussed in Section 2.3.2.1, PCA provides such a result. An example of the resulting projection is shown in Fig. 32. The data is projected into two dimensions using the first two principal components.
In the data preprocessing phase, the data are also scaled. The primary reason for scaling the data is to make use of the results found in Section 2.3.6 about locating a region in which we can expect a marker to lie based on the golden section ratio. Working in a scaled space minimizes the effects of the wide variations in human physiques, standardizing the region in which markers are expected to exist. The calculated markers are rescaled at the end of the marker extraction algorithm.

![Point cloud data from [72] projected into 2-D using the first two principal components.](image)

**Figure 32.** Point cloud data from [72] projected into 2-D using the first two principal components.

### 3.3 Marker Estimation Algorithm

The marker estimation phase of the methodology consists of four parts: (a) clustering, (b) computing a bounding geometry, (c) skeletonization, and (d) marker refinement. This section describes the methods employed and the reasons for their selection.
3.3.1 Self-Organizing Map.

The clustering method chosen is the Self-Organizing Map (SOM). The first reason for this choice is its performance in mapping the distribution of the projected point cloud data. Secondly, the connectivity of the lattice structure is capable of imparting more information than the K-Means or FOREL approaches. A detrimental aspect of both the SOM and K-Means approaches is the possibility of neurons or means falling outside the projected data set. The FOREL method on the other hand constrains its taxons to an actual data point, hence avoiding the problem. A method for dealing with the dead neurons, as the outlying neurons are called in SOMs, is presented in the next section.

The algorithm starts with the 2-D projected point set. From this set of points, the SOM algorithm is run. The algorithm uses a 22-node 1-D lattice. This lattice size was determined empirically through the analysis of the quantization and topographic errors. A representation of the typical output of the SOM portion of the segmentation algorithm is shown in Fig. 33. The rationale behind these selections is provided in Chapter 4.

![Figure 33. Representative result of the SOM portion of the marker estimation algorithm.](image)
3.3.2 Alpha Hull.

Geometry computation is accomplished through the use of the alpha hull. As described in Sec. 2.3.4.3, the choice of disk radius has a significant impact on the resultant shape. So, in selecting an appropriate radius is an area where trade offs are weighed to provide the best results. If too large of a radius is selected, then the resultant shape becomes a convex hull as in Fig. 34; whereas, if the radius is too small, areas of missing data may cause discontinuities and gaps in the shape. The appropriate value for the alpha hull radius was found using empirical methods. The output of the alpha hull portion of the algorithm is shown in Fig. 35.

![Figure 34. Results of the alpha shape algorithm when $\alpha = 0.75$. The $\alpha$ is too large to provide fidelity to the outline shape of the subject.](image)

The resulting alpha hull serves as the initial step in pruning the SOM lattice. The nodes are compared to the alpha hull, and if the node falls outside of the alpha hull, that node is eliminated from the marker set. Further, the alpha hull provides connectivity information based on testing whether the midpoint of each lattice connection falls within the alpha hull. If the midpoint falls outside the alpha hull, that connection is discarded. A final reason
Figure 35. Results of the alpha hull algorithm. The asterisks indicate the location of a lattice node from the SOM. Circles around the asterisk indicate nodes that lie inside the alpha hull based upon a positive result from a point-in-polygon test.

for employing an alpha hull is that it is the initial step in developing a skeleton for the projected data set.

3.3.3 Voronoi Skeleton.

The medial axis, or pruned Voronoi tessellation [22], is used to find the optimized skeleton based on the alpha hull. The resultant skeleton provides a refinement to the centralized markers: ankle, knee, wrist, elbow and shoulder. A typical output from a basic Voronoi skeletonization is shown in Fig. 36. The results are first pruned based on what is inside the alpha hull, as shown in Fig. 37. Since the general shape of the desired skeleton is known, further refinement is done by pruning the Voronoi diagram based on removing lines that have a slope inconsistent with $slope \approx 0$ as shown in Fig. 38. In practice, the pruning portion of the algorithm is not as successful as desired and does not reliably provide the skeleton information desired which is the mid line of the alpha hull for specific areas: the legs, arms, and head. These are the areas needed to refine the anthropometric markers to
the final location. With this goal in mind, the algorithm simplifies the Voronoi process by scanning through all of the points along the x-axis and noting the points of intersection with the alpha hull. Each pair of intersections is averaged to find the midpoint which then becomes a constituent component in the skeletal object. An example of the output from the described revised medial axis algorithm is shown in Fig. 39. The lines connecting the legs to the torso are not computed since they do not follow the skeletal structure. The simplified method of computing the medial axis is used since the Voronoi diagram fails to provide desirable information around the hips; therefore, using the more complex method does not improve the results.

Figure 36. A Voronoi diagram from the alpha hull obtained from the projected 3-D point cloud of a subject from [72].
3.3.4 Incorporating Anthropometric Information into the Algorithm.

Due to the potential for misalignments of the SOM neurons as estimates for the anthropometric marker locations, we exploit the structure of the human body to derive the estimated markers. The next portion of the algorithm utilizes anthropometric information to refine the final marker locations. Part of this component of the algorithm uses basic anthropometric information to assign locations and labels to the markers, e.g. the next connected marker away from the ankle will be the knee, etc. This provides the labels for the markers. The locations get refined based on empirically determined results. Typical results for this stage of the algorithm are presented in Fig. 40.

Based on the converged SOM map and the resulting output of the alpha hull, the anthropometric pruning refines the location of the final markers. There are a number of checks that need to be considered based upon the available information, such as (a) whether the platform is included in the scan necessitating the incorporation of internal alpha hulls, (b) whether the 3-D body scan is corrupt or missing parts, and (c) whether there are
erroneously excluded SOM lattice nodes. If the scanned data are too sparse to fully connect
the subject, the algorithm makes some assumptions to fully flesh out the marker set. One
assumption made is that if one ankle marker is found, there will be a corresponding marker
in the other leg. Similarly, if the scan did not completely capture parts of the arm, then the
algorithm assumes that there is a wrist or elbow marker in an expected location, e.g. near
the end of the arm or between the wrist and shoulder markers. There are also instances
when the alpha hull excludes an SOM lattice node that appears to be inside the resulting
polygon. Once again, on these occasions, the anthropometric algorithm places a marker
in the missing location corresponding to the one found in the other appendage. (The
omission of some elements inside the alpha shape is likely an error in the specific MATLAB®
implementation. However, adapting to the MATLAB® issue is useful in the case when there
are missing/incomplete portions of the scan.)

Based on the shape resulting from the alpha hull, anthropometric pruning may perform
differently. If the alpha hull is of the expected format where the scan is complete and there is
distinct separation between the arms and the torso and between both legs as that presented in Fig. 41, then anthropometric pruning relies on the Voronoi based skeletal results to center the markers in the appendages. If the result of the alpha hull is similar to that in Fig. 42 where the definition between the legs is not captured, then the algorithm looks to incorporate an internal alpha hull piece that removes the section between the subject’s legs that does not correspond to data. If the result is not available, then the algorithm relies on the initial placement of the nodes from the SOM mapping.

For the knee and hip markers, the final marker location is determined by averaging the location of the two lattice nodes that fall closest to the anticipated marker locations based on the golden section results in Section 2.3.6.1 [63]. As noted in Section 2.3.6.1, the experimental results disproved the validity of basing body measurements solely on the golden segment principle. However, general estimates for where a marker may lie can be made. In this case, in the normalized space in which the algorithm works, knees are expected to be found around the $x = 0.25$ mark and hips around the $x = 0.45$ lines. These values.
Figure 40. Results of the pruning and anthropometric adjustment portion of the algorithm.

Figure 41. The resulting alpha hull with $\alpha = 0.025$. 
do not directly factor into the calculation of the stated markers, but only serve as the initialization point for searching for the two nearest neurons to use. Based on the number of nodes used in the SOM portion of the algorithm, the location of the markers along the skeletal line for the knees is found by averaging the two nearest nodes to the $x = 0.25$ line which results in finding $x_{knee}$. The process is done for both knees. The $x$-axis location of the hips is found by averaging the two nodes closest to the $x = 0.45$ line. This results in $x_{hip}$ for one of the hips. This process is repeated for the other hip as well which results in a pair of $x$-axis locations for both the knees and hips.

Having found the ankle and knee markers, the hip marker refinement process begins by finding the intersection of the line formed by the ankle-knee markers and the vertical line associated with the averaged hip marker location. This intersection point becomes the y-axis location for the hip. This process is repeated for the other leg.

The anthropometric refinement process for the arms is minimal. The results from the SOM process provide three markers located in each arm as seen in Fig. 43. The results from the skeletal representation is used to center the marker along the width of the arm.
Occasionally, the results of the SOM place two nodes in the head. In these instances, the algorithm averages the locations of the two markers and projects the results onto the skeleton.

Figure 43. An example of the typical lattice node locations in the arms for the 1-D SOM.

3.3.5 Post-processing.

The resulting set of markers is rescaled using the retained scaling factors from the original preprocessing step. The feature set used in the classification phase is then calculated based on calculating the distance between the appropriate markers to obtain the body segment lengths.

3.4 Summary

This chapter described the various components of the marker estimation algorithm and the methodology used in selecting those components. In the next chapter the specific details of the implemented algorithm are provided and the results from the classification are presented and analyzed.
4. Experimental Results and Analyses

This chapter documents the simulation process, the parameter choices made for each phase, and the results of the point cloud segmentation algorithm developed in this thesis and depicted in Fig. 31b. Additionally, the results of the gender classification are presented. The chapter begins by discussing of each part of the segmentation algorithm and describes and justifies parameter choices followed by the results obtained through classification. The final section of this chapter presents an analysis of the results to include computational efficiency comparing those methods discussed in the literature.

4.1 Data

The 3-D LADAR point clouds come from the CAESAR database [72]. The point cloud is generated by the body scanner’s four scanning heads which provide a 360° scan of the subject as can be seen in Fig. 44. Each subject’s point cloud consists of approximately 250,000 data points. The overall CAESAR database consists of 4,426 subjects. However, due to missing data and markers, a small subset of those scans are not used in this research.

Table 4 provides the basic demographic information for the CAESAR database in total including the number of subjects from each country and a breakout of the gender distribution. Tables 5, 6, and 7 provide the make up of each country’s database separately.

<table>
<thead>
<tr>
<th>Scan Location</th>
<th>Males</th>
<th>Females</th>
<th>Totals</th>
<th>Percentages</th>
</tr>
</thead>
<tbody>
<tr>
<td>North America</td>
<td>1120</td>
<td>1255</td>
<td>2375</td>
<td>53.7%</td>
</tr>
<tr>
<td>Italy</td>
<td>410</td>
<td>386</td>
<td>796</td>
<td>18.0%</td>
</tr>
<tr>
<td>Netherlands</td>
<td>564</td>
<td>691</td>
<td>1255</td>
<td>28.3%</td>
</tr>
<tr>
<td>Totals</td>
<td>2094</td>
<td>2332</td>
<td>4426</td>
<td></td>
</tr>
<tr>
<td>Percentages</td>
<td>47.3%</td>
<td>52.7%</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

A total of 3825 subjects are used in the classification process to evaluate the segmentation algorithm. The distribution of the test set is approximately equally distributed between male and female subjects.
4.2 Experimentation Process

4.2.1 Monte Carlo Simulations.

A Monte Carlo simulation on each subject is conducted with the segmentation algorithm. This is done for 100 runs on 40 of the subjects to determine the distribution of the calculated markers. An example of the distribution of the calculated markers for a random subject...
Table 7. Nationalities of subjects from the Italian database.

<table>
<thead>
<tr>
<th>Nationality</th>
<th>Males</th>
<th>Females</th>
<th>Totals</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Italian</td>
<td>388</td>
<td>376</td>
<td>764</td>
<td>96.0%</td>
</tr>
<tr>
<td>Other</td>
<td>22</td>
<td>10</td>
<td>32</td>
<td>4.0%</td>
</tr>
<tr>
<td>Totals</td>
<td>410</td>
<td>386</td>
<td>796</td>
<td></td>
</tr>
</tbody>
</table>

is shown in Fig. 45. Histograms for a representative sample of marker points is presented below in Figs. 46 and 47. Laying the 3-D histograms over the projection of the point cloud data is shown in Fig. 48. Due to processing time considerations, it is necessary to reduce the number of simulations. This is possible if the data are approximately normally distributed. In that case 10 simulations would suffice. The subject of multivariate normality is explored in further detail in Section 4.4.

4.2.2 Classification Process.

For the classification process, three approaches are used. When a separate test set is available, it is used. If a separate test set is not available, then the training data set is used
Figure 46. Part 1 Histograms for anthropometric marker locations based on 100 Monte Carlo simulations.

As both the training and the testing data through the use of resubstitution and $K$-fold cross validation. In resubstitution, the entire data set is used for training and testing. In $K$-fold cross-validation, the training data is divided into $K$ approximately equally sized groupings. One of the subdivided groups is withheld from the training step and is used as the test set. The other $K - 1$ groups are used to train the classifier. This process is repeated for each of the other $K - 1$ groups. This provides an estimate for the true generalization error.

Classification is done for four separate cases in which the test data and truth data are comprised of the following data sets, respectively: Case I, truth markers versus truth markers; Case II, estimated markers versus truth markers; Case III, Monte Carlo mean markers versus Monte Carlo mean markers; and Case IV, estimated markers versus Monte Carlo mean markers. In Cases I and III, resubstitution and $K$-fold cross validation are used in the classification. In Cases II and IV, separate test data are available and used in the classification process.
4.2.3 Classification Evaluation Methods.

The first step in reporting the classification results is to recreate the results from the sponsor’s paper on gender classification [27]. This is discussed in Section 2.4.1. Using the entire 16-measurement feature set shown in Table 1, the developed classifier duplicated the 98.5% classification accuracy for the Netherlands database and 99.5% classification accuracy for the North American and Italian databases through the use of resubstitution. When the feature set used for classification is reduced to the distance measures listed in Table 3, the classification accuracy dropped to 88.7% for the truth data when performing resubstitution.

In each of the four cases described in Section 4.2.2, the performance of the classification process is reported for the entire CAESAR database as well as for the database subsets
Figure 48. An example of the 3-D histograms located at their respective marker locations.

consisting of the scans for North America, Italy, and the Netherlands. For each of the subsets, the testing and training data are constrained to come from that subset alone, e.g. the North American truth markers are classified versus North American truth markers.

4.3 Segmentation Algorithm Parameters

Many of the marker estimation algorithm components depicted in Fig. 31b rely on specific parameter choices. Those parameters and results are discussed here.

4.3.1 Principal Component Analysis.

The 3-D body scan data is processed through the principal component analysis (PCA) algorithm retaining the first two principal components. At this stage, the data are also scaled. The results of these two steps are shown in Fig. 32.
4.3.2 Self-Organizing Map.

When using the Self-Organizing Map (SOM), there are several parameters that need to be determined. Namely, the dimension of the lattice, the number of nodes in the lattice, the neighborhood function, and the learning rate are all available to be adjusted based on the application.

4.3.2.1 Lattice Dimension.

Initial exploration of both 1-D and 2-D lattices were explored early in the research. Some examples of the initial explorations using a 2-D lattice on the data in 2-D PCA space and mapping the lattice to data space results in the plot shown in Fig. 49a. The SOM is comprised of an 8 x 8 lattice of neurons. Looking at different lattice sizes results in the mappings presented in Fig. 49b for a 5 x 5 lattice and Fig. 49c for a 10 x 10 lattice. Applying a 1-D lattice to the 2-D data results in the mapping shown in Fig. 49d for a 20 neuron lattice. A 30 neuron lattice is presented in Fig. 49e and a 40 neuron lattice is presented in Fig. 49f. The 1-D lattice is selected based upon the desired end results. Since the goal is to determine anthropometric markers that align to a human skeleton and much of the skeletal framework of interest is a linear entity, the 1-D lattice is used.

4.3.2.2 Number of Neurons.

The number of lattice nodes is initially explored empirically with a routine utilized to determine the number of nodes that best fit the data. The result of sweeping through a range of nodes and calculating the average topographic error [39, 85] is shown in Fig. 50. The quantization and topographic errors are a significant factor in determining the appropriate number of nodes selected since the desire is to minimize both errors.

A widely used metric to determine the quality of the resulting SOM is the quantization error. This error measures the average distance between each data vector and its best
Figure 49. SOMs of various lattice sizes shown in the projected data space.
matching unit (BMU) [46]. The quantization error is calculated as:

\[
\varepsilon_q = \frac{1}{N} \sum_{i=1}^{N} || \vec{x}_i - m_{\vec{x}_i} || \tag{34}
\]

where \( N \) is the number of data vectors and \( m_{\vec{x}_i} \) is the BMU of the corresponding \( \vec{x}_i \). This error evaluates how well the neural map fits the data. Therefore, the smaller the quantization error, the closer the data vectors are to the prototype vectors [85]. Quantization error decreases as the number of lattice nodes increase.

An error measure used to quantify the topological preservation of the map is the topographic error. For a given \( \vec{x}_k \), the SOM finds the BMU \( (w_i) \) and the second-BMU \( (w_j) \). Input vectors between \( \vec{x}_k \) and \( w_i \) are mapped to \( w_i \) or \( w_j \). The mapping is called locally continuous if the associated nodes for \( w_i \) and \( w_j \) are adjacent. If they are not adjacent, then there is a discontinuity which is captured as a local topographic error. The overall topographic error is defined as the proportion of local topographic errors that exist in the
map and is formalized as:

\[ \epsilon_t = \frac{1}{N} \sum_{k=1}^{N} u(\tilde{x}_k) \text{ where } u(\tilde{x}_k) = \begin{cases} 1, & \text{if best and second BMUs are non-adjacent} \\ 0, & \text{otherwise} \end{cases} \]  

(35)

A noted failing, or feature, of this measure is that it does not account for the closeness of the local topographic error. It does not matter if two data vectors that are close to one another in the data space get mis-mapped to nodes that are close, but not adjacent, or to the extreme opposite ends of the map [43].

4.3.2.3 Neighborhood Function.

The utilized neighborhood function is a time-decaying Gaussian (exponential) of the form:

\[ h_{j,i}(x)(n) = \exp \left( -\frac{d_{j,i}^2}{2\sigma(n)^2} \right) \]  

(36)

where \(d_{j,i}\) is the distance between the winning neuron \(i\) and the excited neuron \(j\) (in lattice units, not weight vectors).

The size of the neighborhood shrinks over time so that the width (\(\sigma\)) takes the form:

\[ \sigma(n) = \sigma_0 \exp \left( -\frac{n}{\tau_1} \right) \quad n = 0, 1, 2, ... \]  

(37)

where \(\sigma_0\) is the initial value for \(\sigma\), \(\tau_1\) is a time constant, and \(n\) are discrete time units.

4.3.2.4 Learning Rate.

The learning rate is a stepped, decaying exponential as shown in Fig. 51. The learn rate is held constant for an initial period of time and then decayed exponentially. A common form for the learning rate is [35]:

\[ \eta(n) = \eta_0 \exp \left( -\frac{n}{\tau_2} \right) \]  

(38)
where $\eta_0$ is the initial value, $\tau_2$ is another time constant, and $n$ are discrete time units. According to [35], the learning rate should begin with a value close to 0.1, decrease gradually from this initial point, but remain above 0.01. Based on these guidelines, it was found that in practice, learning rates of the form prescribed in Eq. 38 decayed too rapidly, so the learning rate used in the marker estimation algorithm is:

$$\eta(n) = \eta_0 n^{-0.1}$$

(39)

where $\eta_0 = 0.1$.

4.3.3 Alpha Hull.

A representative alpha hull result, when applied to projected data, is shown in Fig. 52. Here, a radius of $\alpha = 0.025$ is used. The alpha hull combined with the converged SOM lattice nodes is shown in Fig. 53. In this example, one node located near the crotch of the subject is excluded by the alpha hull, as indicated by the red asterisk without a blue circle.
around it. Based on how some of the scans were conducted, there is a wide variation in whether the platform is included in the scanned volume or not. In the North American scans, a large portion of the scanner’s platform appears in the scans. This presents a challenge when generating the alpha hull (Fig. 54). If the radius of the alpha hull disk is too large and the platform is in the scan, we get results similar to those shown in Fig. 55. Table 8 provides a listing of the measured platform offsets at the various scanning locations. For some of the data sets, it is necessary to remove the platform offset from the data prior to projecting it. This alleviates the inconvenience associated with the platform.

![Resulting alpha shape](image)

**Figure 52.** The resulting alpha hull with \( \alpha = 0.025 \).

### 4.3.4 Monte Carlo Simulation Numbers.

A Monte Carlo simulation on each subject is performed using the segmentation algorithm. Due to processing time considerations, as mentioned in Section 4.2.1, a Monte Carlo simulation consists of 10 runs of the marker estimation algorithm on each subject. The 10 runs are averaged to generate a set of mean marker locations for use as training data in the classification process.
Figure 53. The set of markers retained by the alpha hull routine. SOM nodes are denoted by an asterisk. Retained markers are denoted by a circle around the retained node.

Figure 54. The resulting alpha hull with too much of the platform showing in the scan.
4.4 Marker Estimation Error

In addition to evaluating the functional performance of the marker estimation algorithm through gender classification, the estimated marker locations are examined for multivariate normality, and their distance from the mean estimated marker and truth marker locations is calculated using the Mahalanobis distance.

4.4.1 Multivariate Normality.

In order to justify the reduction in the number of runs in the Monte Carlo simulation, the distribution of markers is tested for normality using various methods. An initial empirical graphical method served to indicate the likelihood of normality. Based on positive results from the empirical analysis, further tests are performed to confirm normality, specifically, the Mardia’s, Royston’s, and Henze-Zirkler’s tests for normality [58, 59].
Table 8. Platform offsets for the various data collection sites.

<table>
<thead>
<tr>
<th>Data Collection Site</th>
<th>Subject Numbers</th>
<th>Platform Offset (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Los Angeles, CA</td>
<td>0001-0321</td>
<td>1000</td>
</tr>
<tr>
<td>2. Detroit, MI</td>
<td>0324-0671</td>
<td>992</td>
</tr>
<tr>
<td>3. Ames, IA</td>
<td>1031-1173</td>
<td>998</td>
</tr>
<tr>
<td>4. WPAFB1, OH</td>
<td>1174-1261</td>
<td>994</td>
</tr>
<tr>
<td>5. Greensboro, NC</td>
<td>1262-1346</td>
<td>998</td>
</tr>
<tr>
<td>6. Marlton, NJ</td>
<td>1350-1480</td>
<td>1000</td>
</tr>
<tr>
<td>7. Ottawa, Ontario, Canada</td>
<td>1481-1713</td>
<td>1000</td>
</tr>
<tr>
<td>8. Minneapolis, MN</td>
<td>1715-2119</td>
<td>998</td>
</tr>
<tr>
<td>9. Houston, TX</td>
<td>2120-2343</td>
<td>998</td>
</tr>
<tr>
<td>10. Portland, OR</td>
<td>2344-2592</td>
<td>998</td>
</tr>
<tr>
<td>11. WPAFB2, OH</td>
<td>2593-2618</td>
<td>996</td>
</tr>
<tr>
<td>12. San Francisco, CA</td>
<td>2619-2788</td>
<td>998</td>
</tr>
<tr>
<td>13. Atlanta, GA</td>
<td>2789-3028</td>
<td>998</td>
</tr>
<tr>
<td>14. Genoa1, Italy</td>
<td>4000-4394</td>
<td>1000</td>
</tr>
<tr>
<td>15. Genoa2, Italy</td>
<td>4395-4800</td>
<td>1000</td>
</tr>
<tr>
<td>16. Soesterberg, Netherlands</td>
<td>11001-17079</td>
<td>993.1</td>
</tr>
</tbody>
</table>

4.4.1.1 Mardia Test.

If a set of variables is multivariate normally distributed, then each variable must be normally distributed. However, the reverse is not necessarily true as the set of variables may not be multivariate normally distributed just because all of the individual variables are normally distributed. Hence, testing each variable only for univariate normality is not sufficient. Mardia proposed tests of multivariate normality based on sample measures of multivariate skewness and kurtosis [54].

For a random variable \( \mathbf{x} = (x_1, ..., x_n) \) from a \( p \)-variate distribution with a sample mean, \( \bar{x} \), and sample covariance matrix, \( S \), Mardia defines the \( p \)-variate skewness and kurtosis statistics by the following

\[
b_{1,p} = \frac{1}{n^2} \sum_{i=1}^{n} \sum_{j=1}^{n} [(x_j - \bar{x})^T S^{-1} (x_i - \bar{x})]^3, \tag{40} \]

\[
b_{2,p} = \frac{1}{n} \sum_{i=1}^{n} [(x_i - \bar{x})^T S^{-1} (x_j - \bar{x})]^2. \tag{41} \]

Given that the data is multivariate-normally distributed, the expected value of the...
multivariate skewness statistic is given by
\[
E[b_{1,p}] = \frac{p(p + 2)(n + 1)(p + 1) - 6}{(n + 1)(n + 3)},
\]
and the expected value of the multivariate kurtosis statistic is
\[
E[b_{2,p}] = \frac{p(p + 2)(n - 1)}{(n + 1)},
\]
where \( p \) is the number of variables and \( n \) is the number of samples \([55]\). If the data is in fact multivariate normally distributed, then the \( E[b_{1,p}] = 0 \) and \( E[b_{2,p}] = p(+2) \) \([57]\). From \([54]\), a function of multivariate skewness is asymptotically distributed as a \( \chi^2 \) random variable with \( \frac{p(p+1)(p+2)}{6} \) degrees of freedom and the multivariate kurtosis is asymptotically distributed as a standard normal random variable with a mean of \( p(p + 2) \) and a variance of \( \frac{8p(p+2)}{n} \).

### 4.4.1.2 Royston’s H Test.

Common tests for univariate normality are the Shapiro-Wilk test \([79]\) and the Kolmogorov-Smirnov test \([56]\). Royston extended the Shapiro-Wilk W test in such a way as to provide good results \([58]\) when applied to the multivariate case \([76]\).

Royston's H test begins by using Shapiro-Wilk univariate normality test on each of the \( n \) variates. The second part of the test combines the dependent tests into one test statistic for multivariate normality which is approximately a \( \chi^2 \) random variable.

Letting \( W_i \) be the Shapiro-Wilk statistic for the \( i \)th variable in a \( p \)-variate distribution, and then define
\[
R_i = \left\{ \Phi^{-1} \left[ \frac{1}{2} \Phi \left\{ -((1 - W_i)^{\lambda} - \mu)/\sigma \right\} \right] \right\}^2,
\]
where \( \lambda, \mu, \) and \( \sigma \) are calculated from polynomial approximations that Royston gives in \([75]\). The variables \( \Phi^{-1} \) and \( \Phi \) are the inverse and standard normal cumulative distribution function, respectively.
If the data are from a multivariate normal distribution, then

\[ H = \xi \sum_{i=1}^{p} R_i/p \]  

approximates a \( \chi^2 \) distribution, where the equivalent degrees of freedom are

\[ \hat{\xi} = \frac{p}{1 + (p - 1)\hat{c}} \]

\( \hat{c} \) is an estimate of the average correlation among the \( R_j \)'s [76]. This \( \chi^2 \) distribution is used to obtain the \( p \)-values for the multivariate normal test [76].

### 4.4.1.3 Henze-Zirkler Test.

Another powerful multivariate normal test is the Henze-Zirkler test. It is based on a nonnegative functional distance that measures the distance between two distribution functions: the characteristic function of the multivariate normality and the empirical characteristic function.

The Henze-Zirkler test statistic is defined as follows. Let \( \mathbf{X}_1, \mathbf{X}_2,...\mathbf{X}_n \) be a set of \( n \) independent data samples (i.e., the \( \mathbf{X}_1, \mathbf{X}_2,...\mathbf{X}_n \) are obtained from \( n \) independent records) each of dimension \( d \) (i.e., \( \mathbf{X}_i = \{x_{i1}, x_{i2}, ..., x_{id}\} \)). A closed form of the test statistic is given as:

\[
T_{n,b} = \frac{1}{n} \sum_{k=1}^{n} \sum_{j=1}^{n} \left[ \exp \left( -\frac{\beta^2}{2} ||Y_j - Y_k||^2 \right) \right] \\
-2(1 + \beta^2)^{-d/2} \sum_{j=1}^{n} \left[ \exp \left( -\frac{\beta^2}{2(1 + \beta^2)} ||Y_j||^2 \right) \right] + n(1 + 2\beta^2)^{-d/2}
\]

where

\[
\beta = \frac{1}{\sqrt{2}} \left( \frac{2d + 1}{4} \right)^{\frac{1}{\\pi+4}} n^{\frac{1}{\\pi+4}},
\]

\[
||Y_j - Y_k||^2 = (\mathbf{X}_j - \mathbf{X}_k)^T \mathbf{S}^{-1} (\mathbf{X}_j - \mathbf{X}_k),
\]

\[
||Y_j||^2 = (\mathbf{X}_j - \bar{\mathbf{X}}_n)^T \mathbf{S}^{-1} (\mathbf{X}_j - \bar{\mathbf{X}}_n),
\]

4-17
$T_{n,\beta}$ is the test statistic, $\bar{X}_n$ is the sample mean vector of the $n$ realizations $X_1, X_2, \ldots, X_n$, and $S$ is the sample covariance matrix defined as

$$S = \frac{1}{n} \sum_{j=1}^{n} (X_j - \bar{X}_n) (X_j - \bar{X}_n)^T \quad (48)$$

The Henze-Zirkler statistic is approximately distributed as a log-normal. The log-normal distribution is used to compute the null hypothesis probability.

According to Henze-Wagner [37], their test has the following desirable properties: (a) affine invariant; (b) consistency against each fixed non-normal alternative distribution; (c) asymptotic power against contiguous alternatives of order $n^{-1/2}$; and (d) feasibility for any dimension and any sample size.

### 4.4.2 Discussion on Normality Testing Results.

A note about all of the multivariate tests that use the $p$-value. If the $p$-value of any of the tests is small, then multivariate normality will be rejected. However, the univariate Shapiro-Wilk W test is a very powerful test and is capable of detecting small departures from univariate normality with relatively small sample sizes, thus causing the test to reject univariate normality (and therefore multivariate normality) unnecessarily, because the results upon which the multivariate test is being done may be from a robust system insensitive to small departures from normality [58].

Based on the nature of the algorithm’s design for the multivariate tests, each test returns a true or false value based upon whether the null hypothesis of multivariate normality is a reasonable assumption based on a specified significance level, often 5%. When these tests are conducted on the results of a Monte-Carlo simulation, there is high confidence that the distributions for the head, hips, shoulders, ankles and elbows are generally multivariate normal. However, the tests indicate that, in general, the knee and wrist markers are not multivariate normal with the distributions for those markers often indicating bimodality. Fig. 45 provides the histograms for a random subject. For this subject, the distributions of both knees, the left hip, and the left wrist are clearly bimodal.
4.4.3 Mahalanobis Distance.

A useful measure often employed to evaluate multivariate data is the Mahalanobis distance. Its power derives from the fact that it takes into account the covariance of the distribution for the variables in question, eliminating the problems that may arise from using the Euclidean distance, namely scale and correlation. A multivariate normal distribution’s isocontours might not be spherical nor might the principal axes of the formed hyperellipsoid coincide with the axes of the Cartesian coordinate system, thus assuming the Euclidean distance from the mean holds the same importance throughout the data set may be erroneous. Since the Mahalanobis distance relies on the distribution of the data, it becomes an extremely useful determinant in detecting outlying points and judging classification [34]. The standard equation for the squared Mahalanobis distance between $x$ and $\mu$ [18] is defined as:

$$r^2 = (x - \mu)^T \Sigma^{-1} (x - \mu).$$

(49)

Calculating the Mahalanobis distance for each set of estimated marker locations to the means of the estimated marker set from the Monte Carlo simulation and looking at the histograms of the distances provides the results shown in Fig. 56. The calculation is only valid for distributions that are multivariate normal; therefore, bimodal marker distributions are not presented in Fig. 56. Each plot also has vertical lines representing the $\sigma$, $2\sigma$, and $3\sigma$ distances.

Examining the histograms of the Mahalanobis distances indicates that there are outlying points for most of the sets of markers. However, in the case of the distribution for the left knee markers, which was shown by the Mardia, Royston, and Henze-Zirkler tests as not being multivariate normal, the outlying point seems to be just that, an outlier. Whereas, the majority of the calculated left knee markers fall within the bounds of a multivariate normal distribution indicating that assuming a multivariate normal distribution is not a bad assumption.

We can also look at the Mahalanobis distance for each set of estimated marker locations to the set of truth markers which provides an idea of the performance of the algorithm at
Figure 56. Histograms of Mahalanobis distances to mean estimated marker locations for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot.

estimating each marker. Calculating the Mahalanobis distances and plotting the histograms of the distances provides the results shown in Fig. 57. Each plot also has vertical lines representing the $\sigma$, $2\sigma$, and $3\sigma$ distances.

Examining the Mahalanobis distances shown in Fig. 57 provides information about the systematic biases produced by the marker estimation algorithm. Additionally, insight into how well a multivariate normal distribution fits the estimated markers is gained by examining the distribution of the Mahalanobis distances. As with univariate normal distributions, we expect a majority of the Mahalanobis distances to fall within $1\sigma$ of the truth marker. When this is not the case, a systematic bias is observed.
Another measure worth examining is the mean Euclidean distance. The mean Euclidean distance provides information about the accuracy of the estimates as well as insight into the systematic biases. Table 9 provides the mean Euclidean distances, in the re-scaled space, of the estimated markers from the Monte Carlo simulations to the truth marker. Additionally, Table 9 provides the span of the distances, the median distance, and the consistency of the distances as indicated by the variance. Examining these results, we see that the estimated hip markers have the largest average distance from the truth markers. The largest variances correspond to the hip and knee centers, which is an expected result based on the distribution of estimated markers shown in Fig. 45.
Table 9. Statistics for the Euclidean distance of estimated markers from Monte Carlo simulation to truth markers.

<table>
<thead>
<tr>
<th>Marker Set</th>
<th>Mean (mm)</th>
<th>Minimum (mm)</th>
<th>Maximum (mm)</th>
<th>Median (mm)</th>
<th>Variance (mm²)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Right Ankle</td>
<td>37.40</td>
<td>15.75</td>
<td>68.82</td>
<td>33.52</td>
<td>202.91</td>
</tr>
<tr>
<td>Left Ankle</td>
<td>39.51</td>
<td>9.70</td>
<td>73.05</td>
<td>36.20</td>
<td>197.66</td>
</tr>
<tr>
<td>Right Knee</td>
<td>38.45</td>
<td>0.64</td>
<td>66.92</td>
<td>44.35</td>
<td>290.40</td>
</tr>
<tr>
<td>Left Knee</td>
<td>38.34</td>
<td>1.83</td>
<td>65.82</td>
<td>43.53</td>
<td>281.34</td>
</tr>
<tr>
<td>Right Wrist</td>
<td>20.59</td>
<td>10.74</td>
<td>37.68</td>
<td>18.78</td>
<td>44.38</td>
</tr>
<tr>
<td>Right Hip</td>
<td>75.09</td>
<td>42.67</td>
<td>134.31</td>
<td>69.47</td>
<td>443.65</td>
</tr>
<tr>
<td>Left Hip</td>
<td>63.72</td>
<td>10.11</td>
<td>128.80</td>
<td>57.56</td>
<td>544.97</td>
</tr>
<tr>
<td>Left Wrist</td>
<td>16.65</td>
<td>2.91</td>
<td>37.73</td>
<td>14.21</td>
<td>91.28</td>
</tr>
<tr>
<td>Right Elbow</td>
<td>28.46</td>
<td>12.73</td>
<td>53.72</td>
<td>26.42</td>
<td>70.64</td>
</tr>
<tr>
<td>Left Elbow</td>
<td>29.17</td>
<td>12.79</td>
<td>66.29</td>
<td>26.71</td>
<td>136.39</td>
</tr>
<tr>
<td>Right Shoulder</td>
<td>32.99</td>
<td>16.11</td>
<td>76.10</td>
<td>32.08</td>
<td>120.76</td>
</tr>
<tr>
<td>Left Shoulder</td>
<td>32.27</td>
<td>15.35</td>
<td>51.38</td>
<td>31.36</td>
<td>54.82</td>
</tr>
<tr>
<td>Head Center</td>
<td>21.73</td>
<td>3.49</td>
<td>39.60</td>
<td>21.37</td>
<td>65.33</td>
</tr>
<tr>
<td>All Distances</td>
<td>36.49</td>
<td>0.64</td>
<td>134.31</td>
<td>31.66</td>
<td>444.99</td>
</tr>
</tbody>
</table>

4.5 Classification Results

4.5.1 Case I - Truth Data versus Truth Data.

Here, the truth data is used as the training data and the testing data for the classification algorithm. The results are provided in Table 10 for the classification accuracy using resubstitution and 10-fold cross validation. As discussed in Sections 4.2.2 and 4.2.3, classification is done on the entire database and also on the three countries separately. As expected, the classification results for the reduced feature set are worse than the results obtained in [27], where the 16-measurement feature set is used. Furthermore, 10-fold cross validation produces a lower classification accuracy than resubstitution. The reduction in classification accuracy for K-fold cross validation is consistent with the expected results from classification theory [34]. An additional observation is that the reported results in [27] show a diminished classification accuracy for the Netherlands portion of the CAESAR database which holds true when using the reduced feature set. In [27], the cause for this reduction in accuracy for the Netherlands database is surmised to be due to differences in the scanner’s calibration, resolution, and processing.
Table 10. Classification accuracy for the truth data using linear discriminant analysis (LDA).

<table>
<thead>
<tr>
<th>Scan Location</th>
<th>Resubstitution</th>
<th>10-fold Cross-Validation</th>
</tr>
</thead>
<tbody>
<tr>
<td>North America</td>
<td>89.5%</td>
<td>89.3%</td>
</tr>
<tr>
<td>Italy</td>
<td>94.8%</td>
<td>86.0%</td>
</tr>
<tr>
<td>Netherlands</td>
<td>87.3%</td>
<td>87.1%</td>
</tr>
<tr>
<td>Entire Database</td>
<td>88.7%</td>
<td>88.57%</td>
</tr>
</tbody>
</table>

4.5.2 Case II - Estimated Markers versus Truth Data.

Using the truth data as the training set for the LDA classification and the estimated markers as the test set produces a classification accuracy of 60.8%. The test set consists of an approximately equal number of male and female subjects from each separate section of the database. Some further insight into the problem is seen when looking at the classification accuracy of each nation’s database separately. As shown in Table 11, the result of a lower classification accuracy for the Netherlands portion of the CAESAR database is consistent with the baseline results established in Case I.

Table 11. Classification accuracy for the calculated marker locations versus the truth data.

<table>
<thead>
<tr>
<th>Scan Location</th>
<th>Classification Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>North America</td>
<td>62.9%</td>
</tr>
<tr>
<td>Italy</td>
<td>69.3%</td>
</tr>
<tr>
<td>Netherlands</td>
<td>55.2%</td>
</tr>
<tr>
<td>Entire Database</td>
<td>60.8%</td>
</tr>
</tbody>
</table>

4.5.3 Case III - Monte-Carlo Means versus Monte-Carlo Means.

In this case, the test and training data come from the same data set, the mean marker locations produced from the Monte Carlo simulation of each subject. Similar to the classification results shown in Table 10, the classification process calculates the resubstitution accuracy and estimates the true generalization error through $K$-fold cross-validation. The results are provided in Table 12.
Table 12. Classification accuracy for the means of the Monte Carlo simulation as both training and testing data.

<table>
<thead>
<tr>
<th>Scan Location</th>
<th>Resubstitution</th>
<th>10-fold Cross Validation</th>
</tr>
</thead>
<tbody>
<tr>
<td>North America</td>
<td>83.9%</td>
<td>83.1%</td>
</tr>
<tr>
<td>Italy</td>
<td>85.2%</td>
<td>83.2%</td>
</tr>
<tr>
<td>Netherlands</td>
<td>82.3%</td>
<td>81.3%</td>
</tr>
<tr>
<td>Entire Database</td>
<td>77.1%</td>
<td>77.2%</td>
</tr>
</tbody>
</table>

4.5.4 Case IV - Estimated Markers versus Monte-Carlo Means.

The test data consists of a set of estimated marker locations from a single run of the marker estimation algorithm, and the training data is comprised of the mean marker locations produced by the Monte Carlo simulation using ten runs of the marker estimation algorithm for each subject. The test set consists of an approximately equal number of male and female subjects drawn from each subsection of the database. The results are presented in Table 13. As opposed to the results in Table 11, the reduction in classification accuracy when using a separate test set versus resubstitution and \( K \)-fold cross validation is minimal.

Table 13. Classification accuracy for test data consisting of estimated marker locations classified against the training data consisting of the means of the Monte-Carlo simulation runs.

<table>
<thead>
<tr>
<th>Scan Location</th>
<th>Classification Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>North America</td>
<td>79.6%</td>
</tr>
<tr>
<td>Italy</td>
<td>79.7%</td>
</tr>
<tr>
<td>Netherlands</td>
<td>74.2</td>
</tr>
<tr>
<td>Entire Database</td>
<td>74.3%</td>
</tr>
</tbody>
</table>

4.6 Analysis of Results and Summary

The performance of the LDA classification algorithm itself is confirmed as a suitable method for this problem by the duplication of the results from [27]. The low classification accuracy of the calculated markers versus the truth data in Case II is indicative of systematic errors the methodology injects into the calculated markers. This supposition is supported by improved classification accuracy obtained when classifying calculated markers against the average marker locations of the Monte Carlo simulations in Case IV. The consistently reduced classification accuracies for the Netherlands database are an interesting observation,
but there are no further insights to be added to those mentioned in [27]. Overall, the 74.3% classification accuracy presented in Table 13 indicates that the novel approach developed in this thesis for anthropometric marker estimation performs well in segmenting the 3-D LADAR point cloud data.

In this chapter, the simulation process, parameter selection, and segmentation results are presented. The gender classification results are provided, indicating that the algorithm is a promising method for gender classification from point cloud data. In the next chapter, the results are summarized and areas for future work are described.
5. Conclusions and Future Work

This chapter begins with a discussion of methods used to achieve the research’s goal, followed by a summary of the results, and conclusions. The final section covers the potential for future work to improve the algorithm inspected here.

5.1 Summary of Methods and Conclusions

The goal of this thesis is to describe an innovative segmentation algorithm that extracts anthropometric markers from a 3-D LADAR point cloud. The algorithm is built on the dimensionality reduction tool, principal component analysis (PCA), as the initial step. Clustering is performed using a Self-Organizing Map (SOM) to explore the distribution of the data. Anthropometric knowledge in conjunction with a skeletal framework obtained by the use of an alpha hull is incorporated to refine the location of the markers obtained from the SOM map. The validity of the marker locations is then tested using linear discriminant analysis (LDA) as the classification tool, following [27].

The quality of the estimation algorithm is measured by performing gender classification on the resulting marker set. The performance of the algorithm was compared to the true marker location with limited success, with an accuracy of 61%. However, this is not entirely indicative of how well the algorithm performs since truth data is not available in real-world scenarios. When a set of average marker locations, obtained from Monte Carlo simulations, is used as the training set, the classification accuracy increases to approximately 74%, a significant accuracy for the first algorithm to extract anthropometric markers from 3-D point cloud data. This result indicates that the algorithm may show promising results when applied to a more realistic data set, lending credence to the notion that the avenue of marker extraction developed in this thesis will serve as a useful addition to the research group’s dismount detection system when the sensor fusion effort grows to include a LADAR system.
5.2 Future Work

This research effort indicates the feasibility of successfully extracting anthropometric markers from a 3-D LADAR point cloud. Despite the evidence of this success, there are still a variety of avenues in which the performance of the marker extraction algorithm may be improved.

Certainly, a major area for improvement is in developing a richer data set for training the system. A data set that contains subjects from more diverse backgrounds would help in determining if other demographic factors can be determined from the markers extracted from a 3-D point cloud. Additionally, a data set comprised of different poses would prove beneficial in examining the performance of the algorithm and discovering where modifications need be made.

Directly related to the decisions made in implementing the algorithm, further research should be done to examine the effects of hip marker placement to the overall classification accuracy. Specific decisions were made during the algorithm development process in linking the location of the hip markers linearly to the ankle-knee marker line. This decision may not accurately predict marker locations for subjects who are knock-kneed or bow-legged. A comparison study should be between allowing the hip centers to remain tied to the results of the SOM with minimal anthropometric refinement and using the current slope-adjusted method.

Similarly, a comparison study could be conducted using a modified marker estimation algorithm. Near the end of the research effort, work was begun on a method that removed the SOM step from the algorithm, replacing it with an approximate marker estimate along the x-axis based on the golden segment principles and snapped to the alpha hull derived skeleton. The resulting algorithm is significantly faster. However, its performance was not evaluated using the developed classification algorithm. Conducting this performance evaluation may provide some insight into the importance of the SOM in the developed approach.

An additional area for further investigation is in comparing the performance of the
marker extraction algorithm using other classification methods. For example, one may consider a backpropogation neural network, support vector machines, or other statistical methods.

An intriguing and vital area for future work is in exploring the performance of the algorithm when the data comes from a Flash LADAR system and when confusers are added to the scene. This may not be practical until the data fusion step occurs since the process may need to trigger off of a valid skin detection from the previous work into dismount detection using the multispectral camera system [8, 14, 15, 45, 65, 67].

5.3 Contributions

The research addressed in this thesis proposes a new approach to the problem of segmenting 3-D LADAR point cloud data. The classification results indicate the marker estimation algorithm successfully locates anthropometric markers, and the resulting gender information is a valid addition to dismount characterization. The lasting results from this thesis are that extracting anthropometric markers from point cloud data is possible with a great deal of success and the results are significant enough to warrant incorporation into the research group’s dismount detection and characterization system.
Appendix A. Mahalanobis Calculations for Another Subject

This appendix shows the multivariate analysis results for another subject in Fig. 58, Fig. 59, Fig. 60, Fig. 61, and Fig. 62.

Figure 58. An example of the distribution of calculated markers from the Monte Carlo simulation for a random subject.

Since none of the histograms clearly indicate bimodality, all of the Mahalanobis distance computations for the subject are presented in Figs. 61 and 62.
Figure 59. Part 1 - Histograms of the 100 run Monte Carlo simulations.
Figure 60. Part 2 - Histograms of the 100 run Monte Carlo simulations.
Figure 61. Part 1 - Histograms of Mahalanobis distances to mean estimated marker locations for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot.
Figure 62. Part 2 - Histograms of Mahalanobis distances to mean estimated marker locations for 100 Monte Carlo simulations with the $\sigma$, $2\sigma$, and $3\sigma$ bounds indicated as vertical lines on the plot.
Appendix B. Software Acknowledgments

In the course of performing some of the multivariate tests in this research effort several MATLAB scripts that implemented the MVN tests were used. Among these are the mar-diatest [33], HZmvntest [83], and Roystest [84]. The ply file reader developed by Pascal Getreur [30] was used to easily read in the 3-D LADAR body scans.
Bibliography


BIB-1


[40] Jaggers, T.J. “Presentation to the House Armed Forces Committee Subcommittee on Terrorism, Unconventional Threats and Capabilities”, 2009.


BIB-6


BIB-7


Estimating Anthropometric Marker Locations from 3-D LADAR Point Clouds

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An area of interest for improving the identification portion of the system is in extracting anthropometric markers from a Laser Detection and Ranging (LADAR) point cloud. Analyzing anthropometrics markers is a common means of studying how a human moves and has been shown to provide good results in determining certain demographic information about the subject. This research examines a marker extraction method utilizing principal component analysis (PCA), self-organizing maps (SOM), alpha hulls, and basic anthropometric knowledge. The performance of the extraction algorithm is tested by performing gender classification with the calculated markers.

Anthropometric marker extraction, LADAR, SOM, CAESAR database, dismount characterization

Security Classification:
- Report: U
- Abstract: U
- This Page: U

Limitation of Abstract:
UU

Number of Pages:
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