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Prediction of Root Form Using Crown Data: Mandibular Left First Premolar

Matthew E. Durschlag

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Prediction of Root Form Using Crown Data: Mandibular Left First Premolar

by

Matthew E. Durschlag

A thesis submitted in partial satisfaction of
the requirements for the degree
Master of Science in Orthodontics and Dentofacial Orthopedics

September 2017
Each person whose signature appears below certifies that this thesis in his opinion is adequate, in scope and quality, as a thesis for the degree Master of Science.

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ACKNOWLEDGEMENTS

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## ABBREVIATIONS

<table>
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<th>Description</th>
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<tr>
<td>SSM</td>
<td>Statistical Shape Model</td>
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<tr>
<td>CBCT</td>
<td>Cone-Beam Computed Tomography</td>
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<tr>
<td>EDMA</td>
<td>Euclidean Distance Matrix Analysis</td>
</tr>
<tr>
<td>3D</td>
<td>Three-Dimensional</td>
</tr>
<tr>
<td>2D</td>
<td>Two-Dimensional</td>
</tr>
<tr>
<td>AAO</td>
<td>American Association of Orthodontics</td>
</tr>
<tr>
<td>IRB</td>
<td>Institutional Review Board</td>
</tr>
<tr>
<td>LLU</td>
<td>Loma Linda University</td>
</tr>
<tr>
<td>FOV</td>
<td>Field of View</td>
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<tr>
<td>DICOM</td>
<td>Digital Imaging and Communications in Medicine</td>
</tr>
<tr>
<td>ICC</td>
<td>Intraclass Correlation Coefficient</td>
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<tr>
<td>FDM</td>
<td>Form Difference Matrix</td>
</tr>
<tr>
<td>CEJ</td>
<td>Cemento-Enamel Junction</td>
</tr>
<tr>
<td>W</td>
<td>Regularization Weight</td>
</tr>
<tr>
<td>V</td>
<td>Landmark Variance</td>
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<td>PCA</td>
<td>Principle Component Analysis</td>
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ABSTRACT OF THE THESIS

Prediction of Root Form Using Crown Data: Mandibular Left First Premolar

by

Matthew E. Durschlag

Master of Science Graduate Program in Orthodontics and Dentofacial Orthopedics
Loma Linda University, September 2017
Dr. Joseph Caruso, Chairperson

Introduction: The purpose of this study was to determine if a statistical shape model (SSM) of the lower left first premolar, consisting of both crown and root data, could adequately describe the root form from a surface scan consisting of only crown data. Secondly, it tested if there were any angles or measurements on the tooth crown that correlate with any aspects of root morphology. The average orthodontist practicing today or in the near future is likely to use or own a digital intraoral scanner in their office. Yet optical scans only allow visualization of the crowns of teeth and external structures. We know that the orthodontic profession and the published literature support treatment of the teeth crowns and their roots in all three planes of space.1-7 Data acquired through CBCT imaging provides an accurate representation of the teeth and their roots, but it comes at a cost of relatively high radiation exposure.22-38 For this reason, the use of CBCT and other radiographic modalities to analyze orthodontic treatment is generally limited to the least use necessary.8 This study set out to find if statistical shape modeling could provide the practitioner with root form and/or positional data that could aid in patient care.

Materials and Methods: Surface scans of 76 extracted mandibular first premolar teeth were entered into statistical software that created a statistical shape model from the population data and select landmark points. Then, using only the optical surface scans of
16 real patient crowns, the statistical model predicted a root form. Real patient roots, after being segmented from CBCT’s, were compared to the predicted roots and agreement was measured. Statistical analysis was performed using intraclass correlation tests and Euclidean Distance Matrix Analysis (EDMA), a technique used to compare biologic shapes using landmark points, to compare the 3D root shapes and dimensions. Spearman’s rho test was used to determine relationships within the 76 teeth population crown and root measurements.

**Results:** The comparison between averaged real and predicted root forms using EDMA showed no significant differences. However, when an intraclass correlation coefficient test compared linear and angular measurements between individual real and predicted teeth forms, the agreement was weak or non-existent. For the population of 76 extracted mandibular first premolars, there were several different measurements and angles that showed moderate or weak agreement to each other. None of the tested measurements within the population showed strong, predictive correlation between crown and root measurements.

**Conclusions:** For the mandibular first premolar, we were able to accurately predict root form from only optical crown scans when we averaged the real and predicted comparisons. On an individual level, the real and predicted teeth forms were statistically different. There were several moderate and weak agreements between measurements in the population of 76 extracted mandibular first premolars.
CHAPTER ONE
REVIEW OF THE LITERATURE

Intraoral Scanning

An emerging trend in dentistry and orthodontics is the use of digital intraoral scanners. Three-dimensional, optical scanning was introduced over 30 years ago but its use in orthodontics only began in 1999 with Cadent’s OrthoCAD scanner. Whether used in conjunction with a prosthesis milling component or diagnostically as a supplement or replacement for traditional plaster study models, various authors believe that it is very likely to become a routine clinical practice in the move towards paperless, high-technology offices. Numerous recent studies have been performed on the efficiency and accuracy of optical scans. A 2014 study by Gjelvold et al. compared traditional impression techniques to digital impressions and found that the digital technique was more efficient and convenient. Aragon et al., however, found that they are currently still more expensive and time consuming. For orthodontic use, digital impression accuracy must be present throughout the entire upper and lower dental arches and in the way they occlude. Grauer et al. found that optically scanned digital models can reliably be occluded. A study by Guth et al. confirmed that not only are the intraoral scanning systems highly accurate over the entire arch, but they also show the same or even higher accuracy when compared to traditional impressions. A systematic review by Aragón et al. concluded that optically-scanned digital models were as reliable and accurate as conventional impressions. Additionally, the digital intraoral scanner has been found to be more accurate than impression negative scanning technology due to the difficulty in recording data in undercuts. However, a 2014 study by Vogel et al. concluded that
optical scanners face limitations when capturing undercuts and are not reliable for routine orthodontic diagnostics.\(^\text{15}\) A systematic review by Goracci et al. found that few studies showed adequate scientific evidence on their accuracy, reproducibility, and practicality.\(^\text{16}\) Overall, the majority of the literature supports the use of intraoral optical scanners\(^\text{9,16-21}\) and with rapid progress in this area, evidence for their use as a replacement to plaster models is accumulating.\(^\text{22}\)

Optical scan technology presents opportunity for a wide range of uses in orthodontics. An article by Martin et al. explains the growing use of scanners in orthodontic offices for treatment planning, diagnosis, indirect bonding tray fabrication, appliance construction, monitoring of treatment progress and outcome, and much more.\(^\text{9}\)

Additionally, optical impressions eliminate most of the accuracy shortcomings present with traditional impressions such as material shrinkage, mixing, storage, temperature sensitivity, etc.\(^\text{9}\) Some believe that in the near future, optical scanned digital models may replace plaster altogether.\(^\text{23}\) Recent applications include the use of machine-made appliances using wire bending robots and 3D acrylic printing.\(^\text{24}\) Optical scan data is also being used for diagnostic tooth setups and predicted treatment outcomes. 3D orthodontic digital tooth setups, however, do not show good reliability among users.\(^\text{23}\) Diagnostic setups are limited to crown data only, with no root position consideration.\(^\text{25,26}\) A visualization of root structure and position during diagnostic setup could ensure root parallelism in three planes of space and avoidance of dehiscence or fenestration.\(^\text{27}\) A study by Hou et al. found that digital diagnostic tooth setups based only on crown data cannot ensure good root alignment or avoid root exposure. They concluded that integrated root models were a necessity during diagnostic tooth arrangement.\(^\text{27}\) The
suresmile® system has been already been using cone-beam computed tomography (CBCT) technology to provide root data for digital treatment planning. While incredibly useful in many applications, the use of optical impressions in orthodontic diagnosis and progress analysis still require radiograph induced radiation exposure as they lack root form information.

**CBCT Technology**

Cone-beam computed tomography is a modern technology that has gained popularity in orthodontics and many other dental fields. It utilizes a low-energy, fixed anode tube that produces a cone-shaped beam directed at various intensifiers and sensors that capture the image in one rotational sweep. Among its various uses, the technology has the ability to identify the true 3D form and position of roots that was previously evaluated in only two dimensions. In today’s marketplace, there are a wide range of CBCT machines available, with a majority outputting highly accurate 3D image files. An analysis of the 3D Accuitomo 170 and CS 9500 machines, for example, concluded that the machines were capable of high levels of accuracy in vertical linear measurements. However, the 3D reconstruction accuracy of CBCT scanners is dependent upon the spatial resolution and voxel size of the field of view used in the scan. Voxel size ranges from 0.1 to 0.4 mm in x,y, and z planes. A large field of view provides less accurate information than a small field, for example, so it is important to note the parameters used in any given scan and its effect on the detail and accuracy of the data collected. In orthodontics and other applications that require detailed roots analysis, CBCT can be utilized as a reliable method. In two studies on the detection of apical root resorption...
from orthodontic treatment and other simulated factors, it was found that CBCT was effective in meticulous 3D analysis of small degrees of apical root resorption that would be difficult to find with other technologies.\textsuperscript{36,37} CBCT technology has been compared directly to other root visualization methodologies and has consistently shown superiority. In orthodontics, the accurate location of impacted canines and the resulting root resorption on adjacent teeth is essential information for treatment planning and diagnosis. Traditionally, this has been analyzed using 2D panoramic and periapical radiographs. In a study comparing the accuracy of panoramic radiographs to CBCT scans for cuspid 3D location and adjacent root resorption detection, it was found that on panoramic radiographs, resorption was undetectable until advanced stages. The cuspid crown dimensions and root angulation were statistically different in the two methods. It was concluded that CBCT was more sensitive and accurate for localization of impacted canines and adjacent resorption.\textsuperscript{38}

Several other studies have looked into analyzing the accuracy of mesiodistal root angulation on 2D panoramic films versus 3D CBCT images. The issue with panoramic films is that they are 2D representations of 3D structures. There is a significant amount of distortion due to variable amounts of vertical and horizontal magnification.\textsuperscript{39} Authors assessing panoramic image accuracy in detecting root angulation found that the panoramic image was a poor representation of the true root angulations compared to the CBCT.\textsuperscript{33,40,41} A study by Owens et al. recommended that clinicians use caution when using panoramic images to make clinical decisions.\textsuperscript{40} Despite the evidence, a 2008 paper on orthodontic trends found that 67.4% and 80.1% of orthodontists take progress and posttreatment panoramic radiographs, respectively.\textsuperscript{42} Additionally, studies have found
that when comparing root position accuracy of traditional panoramic images to the CBCT pan-like images, the CBCT images were closer to the true mesiodistal root angulation and were a more reliable measure.\textsuperscript{43} However, the use of routine CBCT images for orthodontic diagnosis has been questioned by some.\textsuperscript{44} The 2013 official clinical recommendation from the American Academy of Oral and Maxillofacial Radiology states that the selection of CBCT imaging should be justified by individual need, the benefit must outweigh the risk, and exposure to the patient must never be considered ‘routine’.\textsuperscript{8} Even with low-dose scan protocols, patients must be subjected to typical exposure doses of about 40-135μSv for each CBCT scan.\textsuperscript{30} While it provides much more information, this is about a 5-10 times higher effective dose than a panoramic radiograph.\textsuperscript{30} Since most orthodontic patients are children, considered to be the most sensitive to ionizing radiation, risk versus benefit must be considered.\textsuperscript{44} While CBCT technology is currently the best method for evaluation of many conditions including skeletal discrepancies, airway, unerupted teeth, impacted teeth, root resorption, root shape, and root position,\textsuperscript{30,45} some have concluded that it should not be used as a routine substitute for conventional orthodontic radiographs at this time.\textsuperscript{39}

**Importance of Root Alignment**

The orthodontic literature has always emphasized the benefits of properly aligned teeth,\textsuperscript{1,2} but it is important to also consider the position of the roots. According to the American Association of Orthodontics (AAO) Clinical Practice Guidelines, “The goals of orthodontic treatment are optimum dentofacial function, health, stability, and esthetics.”\textsuperscript{46} In order to maintain function, health, and stability, control of root alignment in three
dimensions is critical.³ Proper axial inclination and parallelism with consistent bone distribution between each tooth helps maintain stability and periodontal health.³ Root correction is integral in positioning teeth over basal bone and achieving ideal occlusal relationships.³,⁴ According to Nanda’s textbook “Esthetics and Biomechanics in Orthodontics,” there are three main reasons to achieve root parallelism; forces from the occlusal load will be transmitted across the longitudinal axis of the tooth, tipped teeth with angled roots have a greater chance of relapse, and root proximity may possibly lead to periodontal problems.⁵,⁶ Proper root position assures a good long-term prognosis and is a vital part of optimal treatment results.³ Root position importance is also emphasized by the American Board of Orthodontics (ABO). In their Objective Grading System (OGS), the ABO states that, “Generally, the roots of maxillary and mandibular teeth should be parallel to one another and oriented perpendicular to the occlusal plane.” If an ABO examinee presents a treated case that does not meet this root position criteria, points will be deducted.⁷

**Statistical Shape Modeling**

Statistical shape modeling (SSM) can be described as a method used to determine the primary modes of variation in shape among a set of specimens.⁴⁷ To build a SSM, a large sample population or training set and a set of common landmark points that can be found on all of the samples is necessary.⁴⁸ The mean shape of the sample population is extracted with different levels of variation⁴⁹ and can then be manipulated with a Gaussian process to widen the variation possibilities. Each SSM has a selected regularization weight (W) and landmark variance (V). The weight (W) is a number that describes how
much the user allows the model parameters to deviate from the mean shape. A high value indicates that the parameters are constrained closer to the mean and vice versa. The variance (V) is a numerical description of an estimate of landmark accuracy. Both W and V can affect the shape model predictions. SSM has shown potential for application in various fields such as biomechanics and medicine.\textsuperscript{49,50} It can aid in the study of anatomical shape changes and the effects of disease processes.\textsuperscript{51} Additionally, frequent issues in medical imaging such as low-quality images, background clutter, insufficient object boundaries, and image noise, make segmentation of anatomical images a challenging endeavor.\textsuperscript{52} With the use of SSM, the speed and accuracy of image segmentation can potentially be improved. SSM has thus far been employed in finite element modeling and segmentation involving the knee, tibia, femur, radius, pelvis, brain, cardiac structures, soft tissue organs, and the lumbar spine.\textsuperscript{49,53} It has been used to analyze and correlate the shape of a structure to other attributes as well as extrapolate shapes from limited 3D data.\textsuperscript{49} In the dental field, SSM has only been applied in limited ways. In a 2014 thesis by Jud at the University of Basel, it was shown that the implementation of a SSM with CBCT segmentations of third molars resulted in improved segmentation accuracy.\textsuperscript{52} In another study, an active SSM was used in an attempt to automatically identify cephalometric landmarks. While the shape model did not provide sufficient accuracy, it was deemed useful as a time-saving step in landmark identification.\textsuperscript{54} Since the SSM technology has not yet made its way into standard medical practice or clinical research, some believe it has not yet lived up to its true potential.\textsuperscript{51}
Current Research

Andrews’ devised 6 keys or guidelines used to judge ideal alignment and occlusion, a standard by which orthodontists treat their cases.² Two of the six keys (tooth angulation and tooth inclination), however, are difficult to judge clinically and must be visualized by seeing the tooth roots.⁵⁵,⁵⁶ Knowing the shortcomings of the panoramic radiograph and the risks of multiple CBCT exposures, two studies evaluated new methods to track root and crown position in three dimensions. In 2014, a paper by Robert J. Lee et al. developed a technique to monitor root and crown positions with a single CBCT volume and multiple intraoral optical scans. Lee proposed that using this technique could limit the amount of radiation exposure to the patient while providing the orthodontist with valuable root position data predicted from the data acquired before treatment.⁵⁷ The study obtained a CBCT scan and digital crown scans of a typodont in a simulated malocclusion. They stitched the crown data from the digital scan with the root data from the CBCT scan with a registration process. This generated composite digital teeth models that could then be registered with digital scans of the teeth at a second time point. This meant that at any point during simulated orthodontic treatment on this typodont, a simple, radiation-free optical scan of the teeth could be used to visualize the crowns and their roots. They found a high degree of accuracy with this method.⁵⁷ A 2015 follow-up study was performed by the same authors. In an effort to make the study more clinically relevant, the methodology was changed. A real patient’s pre-treatment CBCT scan was superimposed with a digital scan performed on a post-treatment plaster model. Predicted root positions from this superimposition was then compared to the patient’s actual post-treatment CBCT root positions. It was found that this was an accurate and
reliable approach to obtaining 3D data on a patient’s root positions at any point in their
treatment.58 However, several limitations remain in these studies on root position through
registration. These techniques are presently too technique sensitive and time consuming
for actual clinical application. Current technology and software do not support easy or
automatic tooth segmentation.58 Additionally, these methodologies still require a fair
amount of radiographic exposure to the patient which would not be indicated for
everyone.59 The need for clinically applicable, highly-accurate, and low radiation
exposure root visualization remains.58
CHAPTER TWO
PREDICTION OF ROOT FORM USING CROWN DATA:
MANDIBULAR LEFT FIRST PREMOLAR

Introduction

The average orthodontist practicing today or in the near future is likely to use or own a digital intraoral scanner in their office. A survey conducted in 2008 showed that use of digital models acquired from optical scans or other means increased from 6.6% in 2002 to 18% in 2008 and has surely increased since then. Current intraoral optical scanners have the ability to visualize only the crowns of teeth and external structures. We know that the orthodontic profession and the published literature support treatment of the teeth crowns and their roots in all three planes of space.\textsuperscript{1-7} Data acquired through CBCT imaging provides an accurate representation of the teeth and their roots, but it comes at a cost of relatively high radiation exposure.\textsuperscript{22-38} For this reason, the use of CBCT and other radiographic modalities to analyze orthodontic treatment is generally limited to the least use necessary\textsuperscript{8}.

Due to the ease and affordability of capturing 3D data in dentistry and medicine, there exists a profusion of information available. Databases can be utilized my machine learning algorithms to output statistical properties and to find representative variations within populations or classes of objects. These statistical shape models have the ability to predict future instances of input data and can fill in missing areas under learned boundary constraints. The medical community has already utilized this technology in areas like human faces, organs, and skeletal structures in various applications\textsuperscript{61}. Dentistry has yet to bring statistical shape modeling into mainstream practice.
In all areas of dentistry, radiographs are relied upon to visualize subgingival anatomical structures. If the x-ray isn’t absolutely essential, the practitioner is left with past records or guesswork. In orthodontics, the crowns of the patient’s teeth are readily available for assessment throughout treatment. However, the root form and position are generally assumed or guessed based on available information, which oftentimes is not current or accurate\textsuperscript{39,40}. Thus, the possibility of gaining valuable root form data makes statistical shape modeling a worthwhile avenue to explore.

In 2017, the trend continues towards an all-digital workflow. With several computerized treatment planning, bracket positioning, and monitoring options, practitioners could benefit greatly from additional information about the teeth they are treating. Three-dimensional visualization of the crowns and their roots would allow a more accurate assessment of tooth root position before and during the course of treatment, thus leading to a better result. If routine intraoral optical scanning could track both crown and root position, treatment progress could be monitored and adjustments made with more precision and frequency than is commonly achieved today.

The purpose of the current retrospective study, comparing real and predicted root forms, was to determine if a statistical shape model of the lower left first premolar could adequately describe the root form from a 3D surface image of the patient's crown. Secondly, the study evaluated if there were any measurements within the population of 76 extracted teeth that would show correlation between crown and root.
Null Hypothesis

1. The first null hypothesis states that there are no statistically significant differences in form between the actual root form and statistically modeled root form of the lower first premolar.

2. The second null hypothesis states that there are no statistically significant relationships between the crown and root measurements within a population of 76 extracted first mandibular premolars.

Materials and Methods

Part A: Building a Statistical Shape Model and Predicting Root Form

Specimen Selection

This study was deemed exempt from the Institutional Review Board (IRB) of Loma Linda University (LLU), Loma Linda, CA. 76 extracted permanent mandibular first premolar teeth from either side of the mouth were collected from various private practitioners and graduate dental departments at Loma Linda University. To meet the inclusion criteria, the teeth had to be intact, without restoration, without disease, and exhibiting minimal wear. The specimens contained no patient identifiers. Each tooth was cleaned with an ultrasonic and hand scaler, and stored in a 1:10 diluted bleach solution.

Optical Image Acquisition

The 76 clean, extracted teeth were each blot dried with gauze and mounted on a rotating platform attached to a size 15, endodontic K file which was inserted into the apex
opening. The specimens were optically scanned using a 3M™ True Definition scanner in the Graduate Orthodontics Clinic at Loma Linda School of Dentistry. The scan protocol consisted of lightly coating the teeth with 3M™ contrast patterning powder (titanium dioxide, amorphous silica, aluminum hydroxide, and synthetic amorphous silica) which was distributed from a battery powered delivery device. The scanning wand captured high-resolution video images in real time and transferred them to the connected computer for viewing. Each tooth file was saved and subsequently exported from the scanner as a .ply file.

**Statistical Shape Model Preparation**

All .ply files were then imported into Meshlab v2016.12 and the endodontic file was digitally removed from the mesh and patched closed. Right-sided teeth were mirrored to appear as left-sided teeth. The samples were then imported into Landmark v3.0 and 22 landmark points (Figure 1) were carefully identified on the 3D mesh. The 22 points on each tooth were saved as .pts files and both the .pts and .ply files for all 76 specimens were inputted into the Statismo command line interface to create a statistical shape model of this sample population. The resultant .hdf file contained the average mesh and the principle components of variation which could be individually visualized ±3 standard deviations with the Statismo viewer (Figure 9).

**Shape Model Construction**

The shape model was constructed using the Statismo command line interface. Correspondence was established between all of the inputted shapes (extracted teeth
specimens) by fitting a Gaussian process model to each. Known correspondences in the form of landmark points were added to the algorithm, giving it multiple points on the sample meshes that it knew were denoting the same anatomical points. A principle component analysis (PCA) model was fitted and then converted the sets of observations into sets of linearly uncorrelated variables called principle components. A regularization weight \( W \) of 0.005 and landmark variance \( V \) of 0.25 was used. Since only a sample of the real population of teeth were used to build the model, the model could not explain all possible shape variations encountered. A Gaussian process was used to enlarge the variation possibilities in the PCA model. The averaged tooth form (Figure 2) was used as a starting point and was adapted and deformed to fit each inputted crown form to a best fit within the model parameters (see Part 2 of Materials and Methods).
Figure 1. This figure shows the 22 landmark points that were carefully placed using Landmark v3.0 software. Each point was put on each individual sample according to the best approximation of the anatomical feature as shown in Table 1.

Table 1. This table describes the anatomical feature used to place the 22 landmarks on each sample mesh.

<table>
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Figure 2. The statistical shape model mean tooth mesh derived from the 76 extracted first bicuspids (Scalismo UI v0.10.0-RC1).

Part B: Acquisition of Real Patient Teeth and Comparisons to SSM Predictions

CBCTs and Optical Scans of Patients

CBCT and intraoral optical scans of 16 randomly selected patients who finished treatment between January and March 2016 were obtained from the Loma Linda University (LLU) Graduate Orthodontics Clinic. All CBCT images were taken at LLU, Graduate Orthodontics Clinic using the NewTom 5G™ (Verona, Italy). Images were taken with a 15 cm x 18 cm field of view (FOV) and a pulsed exposure time of 5 seconds set to 110kV. All patients were instructed to occlude into maximum intercuspation, hold
their tongue in resting position, and avoid swallowing, breathing or moving their head or tongue during image acquisition. Images captured were exported in Digital Imaging and Communications in Medicine (DICOM) format. The CBCT records were taken the day of appliance removal at the end of orthodontic treatment. On the same day, full arch intraoral optical scans were captured on the 16 patients. The scanning protocol for the 3M™ True Definition scanner consisted of drying and lightly coating the patient’s teeth with 3M™ contrast patterning powder. As stated earlier, the intraoral wand captured high-resolution video images of the teeth and processed them in real time on the connected computer. The final output produced was 3D .ply files of the 16 patient’s teeth, gingiva, and occlusion.

Segmentation and Reconstruction of Real Patient Teeth from the CBCT and Optical Data

To complete the comparison between real and predicted teeth, the optical crown data and subgingival root structure data from the CBCTs were combined. The segmented CBCT data was at a much lower resolution than the SSM due to differing imaging physics (leading to improper fitting) and so to remedy resolution differences, the higher resolution intraoral scan data containing the clinical crowns were registered and fused to the CBCT roots (Figure 3). First, the root forms of the teeth of interest (left, first mandibular premolars) were segmented (or mirrored right premolar if the left tooth was missing or did not meet inclusion criteria) using Simpleware ScanIP 2016.09-SP1 Build 519. The premolar clinical crowns were segmented from the optical arch scans and the
roots were segmented from the segmented CBCT premolars (just below the estimated CEJ) using Meshlab v2016.12. Next, five landmark points were placed using Landmark v3.0 on the optical mandibular arch and the corresponding CBCT mandibular arch to calibrate the differing coordinate systems associated with each mesh. Custom software (Appendix C) converted the two into a common coordinate system which allowed accurate placement of the optical clinical crown onto the CBCT root in three dimensions. The resultants were merged, real patient teeth. From here, the shape model was fit to each of the individual 16 patient crowns and best fit, predicted root forms were obtained. The predicted root meshes and the actual root meshes were then compared in various ways (Figure 4, 5, 6; Appendix A).

![Figure 3](image_url)

*Figure 3.* Example of the merged optical, high resolution tooth crowns and the CBCT segmented roots. The two meshes were registered using a calculated common coordinate system. Missing data between the two meshes represents space taken up by soft tissue and other teeth.

**Part C: Statistical Analysis**

**Comparison of Mean Root Forms, Real vs. Predicted**

For statistical testing, the root landmarks (a 9 landmark subset of the aforementioned 22 landmarks, Table 2) were identified on the 16 CBCT root meshes and the
16 predicted root meshes, and subjected to Euclidean Distance Matrix Analysis (EDMA)\textsuperscript{62,63} using 90\% confidence intervals (\(\alpha=0.10\)). Bootstrapping was performed to obtain model independent confidence intervals\textsuperscript{64}. This test was used to compare mean form similarities and/or differences.

**Comparison of Individual Teeth Measurements, Real vs. Predicted**

Next, we wanted to examine the similarities and/or differences of dimension and angulation between the individual samples (16 real and predicted sample population). Various linear measurements and angles were identified using crown and root landmark points (Table 3) on both the 16 real and 16 predicted crowns and roots. An intraclass correlation coefficient (ICC) test was used to check for agreement between individual real and predicted root measurements.

**Correlation Within the 76 Extracted Teeth Population**

For the population of 76 extracted teeth, the Shapiro-Wilk test was performed to check for distribution normality. Since some of the measurement distributions deviated from normal, a non-parametric Spearman’s rho test was performed to check for predictive correlation between crown and root measurements and angles.

**Reliability Tests**

One examiner performed all segmentations and placed all landmarks. A reliability test was run at least one month apart on 31\% of the samples for segmentation accuracy using both EDMA and ICC tests. The calculated ICC was 0.967 (\(p<0.001\)) indicating
very little discordance between segmentations. For the EDMA test of reliability, the form difference matrix (FDM) ratio, represented by a horizontal line slightly above 1.0, indicated that some factor caused a minor scaling difference between the segmentation measurements. We did not deem this significant. All tests were performed using custom software and SPSS™ 23.0 software (SPSS Inc., Chicago, IL, USA).

Results

Part 1: Shape Modeled Roots vs. Real Roots (EDMA)

The Euclidean Distance Matrix Analysis (EDMA), used to compare real and predicted mean root forms in the 16-sample group, showed a consistent form difference matrix (FDM) ratio value of 1.0 or very close to 1.0 (t(16) = 1.15, p = 0.226) (Figure 4). This indicates that the overall mean forms of both real and predicted roots were statistically similar and there is weak evidence to reject the null. However, there were several areas where the confidence intervals displayed extreme values indicating a large degree of variability within the samples for those particular measurements. A tight confidence interval width would be indicative of more consistent measurement ratios. The majority of the landmarks involved with wide confidence intervals were located around the middle/ lower third junction on the root and measurements involving lingual root landmarks.

Part 2: Shape Modeled Teeth vs. Real Teeth (ICC)

An intraclass correlation coefficient test was utilized to compare non-averaged real and predicted teeth forms among the 16-sample group. This test looked at 7 angular
and linear distance measurements of the entire tooth form, including the crown. The results showed that the agreements were non-existent or weak (Table 3). The strongest agreement was distance S8-S10, the sagittal buccolingual dimension 1/3 of the distance down the root with an intraclass correlation coefficient of 0.344 (p< 0.05). The scatterplot comparing the measurement values (x-axis) of real teeth to the difference of real and predicted measurement values (y-axis), showed an interesting vertical linear relationship. This indicates that as measurement values increased, the differences between the tooth forms grew larger. Hence, there was likely some standardized bias or factor that may have had an effect on the difference of real and predicted tooth form dimensions.

**Part 3: Correlation Within 76 Extracted Teeth Population (Spearman’s Rho)**

Using the spearman’s rho test to assess measurement and angle correlations within the 76 extracted teeth population, several moderately significant associations were found (Table 5). The mesiodistal and buccolingual widths at the cemento-enamel junctions (CEJ) showed a moderate agreement (rs= 0.697, p< 0.01). The distance from the buccal cusp tip to the facial axis of the anatomic crown was moderately correlated with the mesiodistal width at the CEJ (rs= 0.517, p< 0.01). The coronal crown to root angle S0-S20-S7 was moderately correlated with buccolingual width at the CEJ (rs= 0.501, p< 0.01). The mesiobuccal crown angle S0-S16-S4 was moderately correlated with the distobuccal crown angle S0-S17-S5 (rs= 0.485, p< 0.01). The coronal crown to root angle S0-S20-S14 was moderately correlated with buccolingual width at the CEJ (rs= 0.480, p< 0.01). The distance from the buccal cusp tip to the facial axis of the anatomic crown was moderately correlated with the buccolingual width at the CEJ (rs= 0.485, p< 0.01).
0.449, *p < 0.01*). Lastly, the sagittal crown to root angle S4-S9-S7 was moderately correlated with the coronal crown to root angle S0-S20-S7 (*r* = 0.443, *p < 0.01*). There were no other stronger, significant agreements. Overall, there did not appear to be any crown measurements that were strongly predictive of root size or angle.

**Table 2.** Nomenclature used to identify 9 landmarks on real and predicted root shapes.

<table>
<thead>
<tr>
<th>Root Comparison Landmarks</th>
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<tbody>
<tr>
<td>S0</td>
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<tr>
<td>S1</td>
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<tr>
<td>S2</td>
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<tr>
<td>S3</td>
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<td>S4</td>
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<td>S5</td>
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<td>S6</td>
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<tr>
<td>S7</td>
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<td>S8</td>
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</table>
Figure 4. This graph shows the EDMA FDM ratio comparing real (numerator) to predicted (denominator) roots. The distance measure along the x-axis are particular linear distances. The red and blue lines are the upper and lower confidence intervals. Wider confidence intervals indicate more variability within the samples for particular distances.
Figure 5. This graph shows the bootstrapped T-value frequencies used to calculate the EDMA confidence intervals.
Table 3. Intraclass correlation coefficient test between real and predicted teeth forms, with significant coefficients highlighted in cyan. Only distance S8-S10 showed a significantly weak agreement of 0.344.

<table>
<thead>
<tr>
<th>Measurement</th>
<th>Intraclass Correlation</th>
<th>95% Confidence Interval</th>
<th>F Test with True Value = 0</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Lower Bound</td>
<td>Upper Bound</td>
</tr>
<tr>
<td>Angle s0-s10</td>
<td>-.024</td>
<td>-.526</td>
<td>.473</td>
</tr>
<tr>
<td>Angle s4-s9-s7</td>
<td>-.192</td>
<td>-.549</td>
<td>.283</td>
</tr>
<tr>
<td>Distance s0-s7</td>
<td>-.156</td>
<td>-.616</td>
<td>.363</td>
</tr>
<tr>
<td>Distance s12-s14</td>
<td>.265</td>
<td>-.276</td>
<td>.668</td>
</tr>
<tr>
<td>Distance s13-s15</td>
<td>.074</td>
<td>-.457</td>
<td>.547</td>
</tr>
<tr>
<td>Distance s8-s10</td>
<td>.344</td>
<td>-.083</td>
<td>.692</td>
</tr>
<tr>
<td>Distance s9-s11</td>
<td>-.042</td>
<td>-.562</td>
<td>.466</td>
</tr>
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</table>

a. The estimator is the same, whether the interaction effect is present or not.

b. Type A intraclass correlation coefficients using an absolute agreement definition.

c. df=15
Figure 6. This scatterplot comparing real teeth measurement values in mm and degrees (x-axis) to the difference between real and predicted teeth measurements (y-axis), shows a vertical linear pattern of relationship. This indicates that there was likely some type of standardized error causing differences of form.

Table 4. Normality test using Shapiro-Wilk shows multiple p-value less than 0.05 indicating that the measurement differs from a normal distribution.
Table 5. Spearman rho test of correlation between measurements in the 76 extracted mandibular first premolar population. Moderate agreements are highlighted in dark cyan, and weak agreements are highlighted in light cyan.

<table>
<thead>
<tr>
<th>Measurement</th>
<th>Angle S0-S16-S4</th>
<th>Angle S0-S17-S5</th>
<th>Angle S0-S20-S7</th>
<th>Distance S0-S7</th>
<th>Distance S20-S18</th>
<th>Distance S4-S9-S7</th>
<th>Distance S19-S21</th>
<th>Distance S50-S6</th>
<th>Angle S0-S26-S14</th>
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<tbody>
<tr>
<td></td>
<td>Correlation</td>
<td>Coefficient</td>
<td>Sig. (2-tailed)</td>
<td>Correlation</td>
<td>Coefficient</td>
<td>Sig. (2-tailed)</td>
<td>Correlation</td>
<td>Coefficient</td>
<td>Sig. (2-tailed)</td>
</tr>
<tr>
<td>Angle S0-S16-S4</td>
<td>1.000</td>
<td>.485&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.000</td>
<td>1.19</td>
<td>.495</td>
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<tr>
<td>Angle S0-S17-S5</td>
<td>.485&lt;sup&gt;**&lt;/sup&gt;</td>
<td>1.000</td>
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<tr>
<td>Angle S0-S20-S7</td>
<td>.163</td>
<td>.119</td>
<td>.000</td>
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<tr>
<td>Distance S0-S7</td>
<td>-.059</td>
<td>.122</td>
<td>.000</td>
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<tr>
<td>Distance S20-S18</td>
<td>.014</td>
<td>.295</td>
<td>.000</td>
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<tr>
<td>Angle S4-S9-S7</td>
<td>.209</td>
<td>.483&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.000</td>
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<tr>
<td>Distance S19-S21</td>
<td>.142</td>
<td>.103</td>
<td>.364&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.379&lt;sup&gt;**&lt;/sup&gt;</td>
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<tr>
<td>Distance S0-S6</td>
<td>.065</td>
<td>.027</td>
<td>-.184</td>
<td>.335&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.445&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.000</td>
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<tr>
<td>Angle S0-S26-S14</td>
<td>.233&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.009</td>
<td>.729&lt;sup&gt;**&lt;/sup&gt;</td>
<td>.000</td>
<td>.000</td>
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</tbody>
</table>
**Table 6.** Overall intraclass correlation coefficient used to test agreement between segmentations.

<table>
<thead>
<tr>
<th>Intra-class Correlation</th>
<th>95% Confidence Interval</th>
<th>F Test with True Value 0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single Measures</td>
<td>.967 ( ^b )</td>
<td>.912 to .986</td>
</tr>
<tr>
<td>Average Measures</td>
<td>.983</td>
<td>.954 to .993</td>
</tr>
</tbody>
</table>

a. The estimator is the same, whether the interaction effect is present or not.
b. Type A intraclass correlation coefficients using an absolute agreement definition.

---

**Table 7.** Intraclass correlation coefficient for segmentation reliability, stratified by measure. In bold, the ICC for distance S6-S8, the only measure showing difference.

<table>
<thead>
<tr>
<th>Intra-class Correlation</th>
<th>95% Confidence Interval</th>
<th>F Test with True Value 0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Distance s0-s1</td>
<td>Single Measures</td>
<td>.575 ( ^b )</td>
</tr>
<tr>
<td>Distance s0-s7</td>
<td>Single Measures</td>
<td>.595 ( ^b )</td>
</tr>
<tr>
<td>Distance s1-s3</td>
<td>Single Measures</td>
<td>.851 ( ^b )</td>
</tr>
<tr>
<td>Distance s2-s4</td>
<td>Single Measures</td>
<td>.595 ( ^b )</td>
</tr>
<tr>
<td>Distance s5-7</td>
<td>Single Measures</td>
<td>.682 ( ^b )</td>
</tr>
<tr>
<td>Distance s6-s8</td>
<td>Single Measures</td>
<td>-.028 ( ^b )</td>
</tr>
</tbody>
</table>

Two-way random effects model where both people effects and measures effects are random.

a. The estimator is the same, whether the interaction effect is present or not.
b. Type A intraclass correlation coefficients using an absolute agreement definition.
c. df= 4
Figure 7. EDMA test used to verify reliability of root segmentation dimensions.
Figure 8. Bootstrapped T-value frequencies used to calculate the reliability EDMA confidence intervals.
Discussion

With the modern trend towards a paperless, digital workflow, it is no surprise that intraoral optical scanning in orthodontics has made its way into the mainstream. A 2015 study in the Journal of Clinical Orthodontics found that 42% of respondent orthodontists in private practice were using an optical scanner.\textsuperscript{65} It has been two years since that data was collected and based on the market influx of new scanner options and increasing ease of use, it seems very likely that there are more orthodontists with scanners today. The features included with scanner software have also advanced. It is now possible to simulate treatment outcomes such as interproximal reduction, extractions, and anterior-posterior corrections quickly and easily after a scan of a patient’s dentition. The orthodontist can gain an in-depth evaluation of case analytics from the 3D models and digital files can be instantly sent to labs or in-house 3D printers for appliance fabrication. One of the newest abilities of scanners, such as the iTero Element\textsuperscript{®}, is the ability to compare patient progress over time with a technology they call “TimeLapse.” The practitioner can accurately compare previous scan records to the present-day scan to distinguish and measure orthodontic tooth movement, gingival recession, and tooth wear. If undergoing Invisalign\textsuperscript{®} treatment, this feature allows the practitioner to evaluate any mid-treatment deviations from the prescribed tooth movement.

Subgingival intraoral structures can currently only be visualized with the use of x-rays. CBCT provides an accurate method for evaluation of root form and position, but its use is generally limited to the least necessary due to radiation exposure to patients.\textsuperscript{8,33,41} In 2015, it was reported that only 21% of orthodontists routinely utilized CBCT data.\textsuperscript{65} This means that many cases are being treated using 2D radiographs which have been
shown to be unreliable when evaluating root position.\textsuperscript{40} The current CBCT radiation dose is always improving, but is still too high to use more frequently.\textsuperscript{8} Therefore, a radiation-free method to accurately visualize whole teeth could solve the problem of missing treatment data and provide more information than is typically available when planning and treating orthodontic patients.

\textit{Part 1: Shape Modeled Roots vs. Real Roots (EDMA)}

The Euclidean Distance Matrix Analysis (EDMA) was developed in the early 1990’s to compare the forms of averaged biologic samples.\textsuperscript{64} EDMA is useful because it allows comparison of form without the constraints of factoring in translation, rotation, and reflection.\textsuperscript{64} It essentially eliminates the need for comparison using superimposition and works by using common 3D landmark points from the object surfaces to compare multiple averaged linear distances. EDMA was used in this research to test the null hypothesis of equality of forms. This test also contains information about shape variability in the form of confidence intervals which were obtained by bootstrapping.

The form difference matrix (FDM) value represents a ratio between averaged population measurements. If one population (numerator) is larger on average than the other (denominator), then one would expect to see a FDM ratio above 1.0, and vice versa. In our EDMA analysis of shape modeled roots vs. real roots, the averaged real root measurements were in the numerator of the FDM and the averaged modeled root measurements were in the denominator. Our results displayed a consistent FDM ratio value of 1.0, indicating that when comparing averaged real and modeled root forms, there were no differences. Bootstrapped T-values were used to estimate the sample distribution
and create 90% confidence intervals with a p-value of 0.226, showing no significant
difference between real and predicted root form. Looking at the upper and lower
confidence intervals, however, it is apparent that there were several measurements of
high variability. Ideally, similar forms with less measurement variability would show a
tight confidence interval around a 1.0 FDM ratio. The widest confidence intervals in our
test tended to be around the lower 1/3 of the root and measurements involving the lingual
root landmarks.

Figure 9. The three most significant components of variation in the
sample population from the statistical shape model. There were 74
total principal components of variation. Component 1 accounted for
39% of the variation; Component 2= 13%; Component 3= 8%.
Our evaluation of the reasoning behind the measurements of high variability stems from several factors. The first and likely largest factor was a limitation in the statistical shape model (SSM) that we created. When we visualize the differences in the root forms between real and predicted roots (Appendix A), it is apparent that the lingual root surfaces seemed to be the most divergent over the most samples. We believe that due to a scarcity of landmark points around the crown lingual surface used in model building, the SSM did not have enough information to accurately predict form in this area. The error seems to have manifested throughout the entirety of the lingual root surfaces in several samples. Additionally, the 76 specimens used to make the SSM were highly variable in form. When we look through the top three components of variation out of a total of 74 (Figure 9), it is clear that the population of teeth were diverse in anatomical configuration. Component 1, accounting for 39% of the population variation, involved both root length and general crown shape (round vs. grooved). Component 2, accounting for about 13% of the variation, involved variation in buccolingual root dimension and lingual cusp location. Finally, component 3 accounted for 8% of the variation and involved both root shape (tapered vs. rounded) and buccal and lingual cusp location. Perhaps a larger sample would have resulted in different principle components and standard deviations in the model. Lastly, there is the possibility of measurement variation caused by landmark placement error. The landmarks used to make up the SSM and the points of comparison in the EDMA test were all placed by hand and subject to human error.
Part 2: Shape Modeled Teeth vs. Real Teeth (ICC)

Since the EDMA test compared the averaged forms, we next wanted to evaluate agreement between the individual real and predicted teeth forms. The intraclass correlation coefficient (ICC) test was used to compare two angles and five linear measurements on the 16 real and statistically modeled teeth (Table 3). Instead of only using root measurements, we chose to compare the entire teeth, including both crown and root. This allowed the comparison of things like crown to root angle and cusp to apex measurements without trying to segment the samples at the cementoenamel junctions. The shape model used the real patient optical crowns as a starting point, and was augmented in various ways to best fit the input. As shown in the overlaid real and predicted teeth forms (Appendix A), there are small differences between the crown forms due to this imperfect fitting process. We do not believe that the variation in crowns lead to significant comparison differences, but it is one potential source of error. Additionally, our real patient teeth were missing data in areas that the optical scan could not visualize, such as the contact points and areas of buccal/lingual gingival coverage. Our measurements did not include these areas and because we were most concerned with comparison of root forms and we did not believe these areas were critical to our study. The optical scans could not image these areas of covered anatomical crown and it was therefore important to leave this data out when testing the shape model results.

The results of the ICC test were quite different from the EDMA comparison. Of the seven measurements tested, there were six correlation coefficients showing no agreement, and one exhibiting a weak agreement. There was a weak 0.344 correlation coefficient ($p<0.05$) between real and predicted distance S8-S10, the buccolinguial
distance 1/3 down the root. We believe that this signifies an important difference in our study outcome. When evaluating the results in averages, the real and predicted root forms were statistically similar. However, when considering any particular individual, there was a high level of variation in forms. Visual evaluation of the 3D registered samples (Appendix A), further confirms this. There are some predicted samples that did quite well in projection of root length, root curves, mesiodistal width, buccolingual width etc. However, the range of variability was large, and the form dimensions did not agree strongly. Again, we attribute these differences most notably to deficiencies in the SSM for the reasons noted previously.

We also evaluated the differences between real and predicted teeth measurements by plotting the differences of measurements on a scatterplot (Figure 6). The scatterplot revealed that as the measurement values grew larger (for linear or angular measurements), the error or difference between samples also grew larger and more spread out. This is graphically depicted as widening vertical lines. A pattern like this is indicative of some specific factor that caused a predictable effect on measurement differences between the groups. It may be possible to statistically remove the effect but we believe that the issue came from the SSM. We found that as the SSM was morphed to fit the various real sample crowns, the resultants were likely too constrained and appeared too similar. Perhaps with the addition of more landmark points or population data, the model would have had more information and been more adaptable. Varying the regularization weight (w) and the landmark variance (v) parameters may have also affected the outcome of our results.
Part 3: Correlation Within 76 Extracted Teeth Population (Spearman’s Rho)

Previous studies that have looked at relationships between crowns and roots in various teeth have had differing conclusions. A 1980 study looking at correlation between five mandibular teeth crowns, roots and mandible length, found only weak correlations and determined the existence of a low-order generalized size relationship. They did not find strong predictive characteristics between crown and root dimensions. On the other hand, a 2013 study of relationship between maxillary incisor crowns and roots found statistically significant correlations between crown and root widths at different points. For angulation predication, a previous study had looked at the correlation between maxillary incisor root column angle and crown in various malocclusions. They found that only interincisal angle and overjet were correlated with specific column angles and that other factors showed non-predictive variation. Because we had a large population of mandibular first premolars, we thought it would be interesting to examine measurement relationships.

In our study, spearman’s rho test was used to determine correlation coefficients between nine linear and angular measurements. The results showed several moderate and weak agreements amongst some of the measurements (Table 5). These associations appeared to generally agree with the previously mentioned study conclusions. There seemed to be a weak generalized size or proportional trend among some of the measurements. The strongest agreements were found between the mesiodistal and buccolingual root width at the CEJ ($r_s = 0.697, p < 0.01$) and the distance from cusp tip to facial axis of the crown and the mesiodistal CEJ root width ($r_s = 0.517, p < 0.01$). While it was interesting to find several moderate and weak agreements, none could be considered
strong. This suggests that for the measurements and population specimens used in our study, no measurements were truly useful for prediction of root dimensions or angles from the crown. Perhaps if we had examined different tooth dimensions and/or different landmark points, our conclusions may have turned out differently.

Limitations of Study and Recommendations for Future Studies

In our study, we were able to conclude different outcomes based on the way in which we analyzed the data. The averaged form comparison between real and shape modeled teeth resulted in no significant differences. Yet with the individual sample comparison of linear and angular measurements, the statistics showed a lack of agreement. When visually comparing the 16 specimens used in this study (Appendix A), the differences are readily apparent. As mentioned earlier, we believe that the major limitation in prediction of root form from optical crown data was most likely the way in which we constructed the statistical shape model (SSM). The model was dependent on population data in the form of extracted teeth structures, as well as user-defined landmark points. The following issues were likely contributing factors to the deficiencies of our SSM: a shortage of landmark points around the lingual aspect of the crown, an inadequate population size of 76 teeth with high variability in form, error associated with hand-placing the landmark points on all of the samples, and error in the Gaussian process deformation used to fit the model to the optical crowns. Additionally, the regularization weight (W) and the landmark variance (V) parameters in the SSM may not have been optimal and could have led to over-constraint of the model.
An additional possible limitation of our study may be found in the registration and construction of the real patient teeth. First, the segmentations from the CBCT data may have been prone to error. Selecting only the root structure from surrounding bone of similar density was challenging in some cases and the resolution of 0.3mm voxel size reduced image sharpness. While the segmentation reliability was quite high, one distance (S6-S8, distance from mesial to distal points at the intersection of the middle and lower root third) showed an ICC of -0.028 ($p= 0.525$), indicating some variability in segmentation accuracy (Table 7). This area of the root tended to be difficult to cleanly segment due to the similar densities of root structure and bone. The reliability EDMA test displayed a horizontal FDM ratio line slightly over 1.0 with a consistently large confidence interval (Figure 7). This may indicate a scaling error between the segmentation instances, but may also hint at a source of error in the data. Next, the segmented crowns were positioned and registered to their roots by relating the optical crown and CBCT root coordinate systems using custom software (Appendix C). The process involved picking five precisely corresponding landmark points on structures found on both optical and CBCT scans and an iterative closest point algorithm was used to fine tune them. The software used the 3D coordinate positions of each data source and linked them into a common system. Then, the crown and root structures could be merged and a reconstructed real patient tooth could be used in the study. Again, this process was subject to human error with the hand-placement of landmark points and use of the iterative closest point algorithm, but we do not believe this was a significant limitation to the outcome.
In future studies, there are several areas where the methodologies presented here could be improved upon. For enhancement of the SSM, additional landmark points in the lingual aspect of the crowns and a modification of model parameters used to augment the model could result in a more accurate outcome. We believe that a better model to crown fit could be obtained with these additional landmark references and a larger pool of population specimen data. The model prediction would likely improve in accuracy with this added information. Additionally, alteration of the W and V parameters in the model may lead to a more optimal level of constraint and lead to better root form prediction.

Another study could use the root form predictions and analyze them to compare the volumetric accuracy of the shape model. If the root volumes are fairly accurate, then that data can be used to estimate force values needed for individual teeth when treatment planning different types of movement. Additionally, the predicted root form data that we collected could be visualized differently by extracting 2D skeletons or medial axes. This data may be more accurate and just as useful as visualizing the entire surface structure of the roots. In another future study, the missing data region on the segmented optical crowns at the contact points and subgingival regions could be filled in with CBCT data, and the model can be tested again to check for improved prediction capabilities.

If the procedures in this study are improved upon and refined, we believe the outcomes may be quite useful. Based on the results of this study, the SSM that we constructed was accurate when assessing averages, but not when looking at individual cases. For this reason, it is not currently at the stage of clinical relevancy or usefulness unless developed further in future studies. SSM has yet to be utilized to its full potential in dentistry and orthodontics and more research is needed to find its best application. One
area with potential is its use as an enhancement in segmentation of 3D images. Intimate knowledge of the region of interest when undergoing a segmentation would save time and could possibly lead to automated segmentation technology. Furthermore, automatic forecast of accurate root form and position at the beginning or middle of treatment from only optical intraoral crown images would be highly beneficial to the orthodontic practitioner and the patient. The precision of treatment planning and analysis would potentially be significantly improved. There are currently no substitutes or more accurate methods than using x-ray technology, but hopefully in the future we can supplement radiography with shape model derived data that will lead to improved orthodontic treatment.

**Conclusions**

1. Among a population of 16 randomly selected patients, there was no statistically significant difference in form between the averaged shape modeled root forms and the averaged real patient root forms ($p=0.226$). Therefore, we fail to reject the null that there is no difference in form.

2. Among a population of 16 randomly selected patients, there was very weak agreement when comparing individual, non-averaged linear and angular measurements between shape modeled teeth and real patient teeth ($-0.024 \leq \rho \leq 0.344$). Therefore, we must reject the null that there is no difference in form.

3. Among a population of 76 extracted mandibular first premolars, there were multiple moderately strong agreements between measurements ($0.443 \leq \rho \leq 0.843$).
Therefore, we must reject our null that there are no significant relationships between crown and root measurements.

4. We must reject both of our null hypotheses.
References


63. Sardarian T. Evaluation of Apical, Coronal and Occlusal Form Differences with Conventional Orthodontic Treatment Orthodontics and Dentofacial Orthopedics Loma Linda University 2012.


APPENDIX A

VISUAL COMPARISON OF REAL AND PREDICTED ROOT FORMS, REGISTERED AT THE CROWN

These figures show a comparison of real and predicted root forms registered at the crown. The red structures represent the stitched optical crowns and CBCT segmented root forms of 16 real patients. The grey, 3D registered structures represent the SSM teeth, best fit to the optical crown data.

Sample 1

Sample 2
APPENDIX B

RAW DATA

Linear distances (mm) and angles (°) measured from landmark points on the population of 76 extracted teeth.

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Segmentation reliability test data. Various measurements (mm) measured from landmark points on the root surfaces of randomly selected samples to test for accuracy of segmentation data.

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import os
import string
import vtk
import numpy as np

def NumpyToVTKPoints(numpyPoints):
    vtkPoints = vtk.vtkPoints()
    if (np.shape(numpyPoints) == (4,1)):
        vtkPoints.InsertNextPoint(numpyPoints[0], numpyPoints[1], numpyPoints[2])
    else:
        for i in range(len(numpyPoints)):
            vtkPoints.InsertNextPoint(numpyPoints[i][0], numpyPoints[i][1], numpyPoints[i][2])
    return vtkPoints

def VTKToNumpyPoints(vtkPoints):
    numPoints = vtkPoints.GetNumberOfPoints()
    numpyPoints = np.zeros([numPoints, 3])
    for i in range(numPoints):
        numpyPoints[i][0] = vtkPoints.GetPoint(i)[0]
        numpyPoints[i][1] = vtkPoints.GetPoint(i)[1]
        numpyPoints[i][2] = vtkPoints.GetPoint(i)[2]
    return numpyPoints

def doDisplay2Points(points, points2, norm_vec, msg = ''):
    ren = vtk.vtkRenderer()
    ren.AutomaticLightCreationOff()
    renWin = vtk.vtkRenderWindow()
    renWin.AddRenderer(ren)
    renWin.SetSize(1000, 800)
iren = vtk.vtkRenderWindowInteractor()
iren.SetInteractorStyle(vtk.vtkInteractorStyleTrackballCamera())
iren.SetRenderWindow(renWin)

polydata = vtk.vtkPolyData()
polydata.SetPoints(points)
sphereSource = vtk.vtkSphereSource()
glyph3D = vtk.vtkGlyph3D()
glyph3D.SetSource(sphereSource.GetOutput())
glyph3D.SetInput(polydata)
glyph3D.Update()
pointMapper = vtk.vtkPolyDataMapper()
pointMapper.SetInput(glyph3D.GetOutput())
pointActor = vtk.vtkActor()
pointActor.SetMapper(pointMapper)
pointActor.GetProperty().SetPointSize(5)
pointActor.GetProperty().SetColor(152./255., 109./255., 87./255.0)
#pointActor.GetProperty().SetColor(1.0, 0, 0)
ren.AddActor(pointActor)

polydata2 = vtk.vtkPolyData()
polydata2.SetPoints(points2)
sphereSource2 = vtk.vtkSphereSource()
glyph3D2 = vtk.vtkGlyph3D()
glyph3D2.SetSource(sphereSource2.GetOutput())
glyph3D2.SetInput(polydata2)
glyph3D2.Update()
pointMapper2 = vtk.vtkPolyDataMapper()
pointMapper2.SetInput(glyph3D2.GetOutput())
pointActor2 = vtk.vtkActor()
pointActor2.SetMapper(pointMapper2)
pointActor2.GetProperty().SetPointSize(5)
pointActor2.GetProperty().SetColor(38./255., 41./255., 112./255.0)
#pointActor2.GetProperty().SetDiffuse(100)
#pointActor2.GetProperty().SetColor(0, 1.0, 0)
ren.AddActor(pointActor2)

textActor = vtk.vtkTextActor()
textActor.SetInput ( msg )
textActor.SetDisplayPosition ( 20, 20 )
textActor.GetTextProperty().SetFontSize ( 24 )
textActor.GetTextProperty().SetColor ( 1.0, 1.0, 1.0 )
ren.AddActor2D( textActor )

axesActor = vtk.vtkAxesActor()
axesActor.SetTotalLength(20.0, 30.0, 20.0)
axesActor.AxisLabelsOff()
axesActor.SetTipTypeToSphere()
axesActor.SetSphereRadius(.01)
ren.AddActor(axesActor)

line_source = vtk.vtkLineSource()
line_source.SetPoint1(0,0,0)
line_source.SetPoint2(norm_vec[0], norm_vec[1], norm_vec[2])
line_source.Update()
line_actor = vtk.vtkActor()
line_mapper = vtk.vtkPolyDataMapper()
line_mapper.SetInput(line_source.GetOutput())
line_actor.SetMapper(line_mapper)
line_actor.GetProperty().SetLineWidth(4)
ren.AddActor(line_actor)

angleWidget = vtk.vtkAngleWidget()
angleWidget.SetInteractor(iren)
angleWidget.CreateDefaultRepresentation()

lightKit = vtk.vtkLightKit()
lightKit.AddLightsToRenderer(ren)
lightKit.MaintainLuminanceOn()
lightKit.SetKeyLightWarmth(.60)
lightKit.SetKeyLightIntensity(.75)
lightKit.SetKeyLightElevation(50)
lightKit.SetKeyLightAzimuth(10)

lightKit.SetFillLightWarmth(.4)
lightKit.SetKeyToFillRatio(3.)
lightKit.SetFillLightElevation(-75)
lightKit.SetFillLightAzimuth(-10)

lightKit.SetBackLightWarmth(.5)
lightKit.SetKeyToBackRatio(3.5)
lightKit.SetBackLightElevation(0)
lightKit.SetBackLightAzimuth(110)

lightKit.SetHeadLightWarmth(.5)
lightKit.SetKeyToHeadRatio(1)

ren.SetBackgroundColor(94./255., 98./255., 122./255.0)
renWin.Render()
iren.Initialize()
renWin.Render()
# angleWidget.On()
iren.Start()

def doDisplayPointsPoly(points,corticalBone):
    ren = vtk.vtkRenderer()
    renWin = vtk.vtkRenderWindow()
    renWin.AddRenderer(ren)
    renWin.SetSize(800, 800)
    iren = vtk.vtkRenderWindowInteractor()
    iren.SetInteractorStyle(vtk.vtkInteractorStyleTrackballCamera())
    iren.SetRenderWindow(renWin)
    polydata = vtk.vtkPolyData()
polydata.SetPoints(points)
sphereSource = vtk.vtkSphereSource()
glyph3D = vtk.vtk Glyph3D()
glyph3D.SetSource(sphereSource.GetOutput())
glyph3D.SetInput(polydata)
glyph3D.Update()
pointMapper = vtk.vtkPolyDataMapper()
pointMapper.SetInput(glyph3D.GetOutput())
pointActor = vtk.vtkActor()
pointActor.SetMapper(pointMapper)
pointActor.SetProperty().SetPointSize(3)
pointActor.SetProperty().SetColor(1.0, 0, 0)
ren.AddActor(pointActor)

boneMapper = vtk.vtkPolyDataMapper()
boneMapper.SetInput(corticalBone)
boneMapper.ScalarVisibilityOff()
boneProperty = vtk.vtkProperty()
boneProperty.SetColor(1.0, 1.0, 0.9)
boneProperty.SetOpacity(.25)
boneActor = vtk.vtkActor()
boneActor.SetMapper(boneMapper)
boneActor.SetProperty(boneProperty)
ren.AddActor(boneActor)

axesActor = vtk.vtkAxesActor()
axesActor.SetTotalLength(50.0, 50.0, 50.0)
axesActor.AxesLabelsOn()
ren.AddActor(axesActor)

renWin.Render()
iren.Start()

def doDisplay2Poly(poly1, poly2):
    ren = vtk.vtkRenderer()
renWin = vtk.vtkRenderWindow()
renWin.AddRenderer(ren)
renWin.SetSize(800, 800)
iren = vtk.vtkRenderWindowInteractor()
iren.SetInteractorStyle(vtk.vtkInteractorStyleTrackballCamera())
iren.SetRenderWindow(renWin)

boneMapper = vtk.vtkPolyDataMapper()
boneMapper.SetInput(poly1)
boneMapper.ScalarVisibilityOff()
boneProperty = vtk.vtkProperty()
boneProperty.SetColor(1.0,1.0,0.9)
#boneProperty.SetColor(0,.5,1.0)
boneProperty.SetOpacity(.5)
boneActor = vtk.vtkActor()
boneActor.SetMapper(boneMapper)
boneActor.SetProperty(boneProperty)
ren.AddActor(boneActor)

boneMapper2 = vtk.vtkPolyDataMapper()
boneMapper2.SetInput(poly2)
boneMapper2.ScalarVisibilityOff()
boneProperty2 = vtk.vtkProperty()
boneProperty2.SetColor(.5,.1,.1)
#boneProperty2.SetColor(1.0,1.0,0.9)
boneProperty2.SetOpacity(.5)
boneActor2 = vtk.vtkActor()
boneActor2.SetMapper(boneMapper2)
boneActor2.SetProperty(boneProperty2)
ren.AddActor(boneActor2)

axesActor = vtk.vtkAxesActor()
axesActor.SetTotalLength(50.0, 50.0, 50.0)
axesActor.AxisLabelsOn()
ren.AddActor(axesActor)
def GetPtsList(directory):
    pts_list = []
    for file in os.listdir(directory):
        if file.endswith('.pts'):
            pts_list.append(file)
    return pts_list

def ReadPoints(file_name):
    points = []
    names = []
    f = open(file_name, 'r')
    for line in f.readlines():
        words = string.split(line)
        if len(words) == 4:
            #.InsertNextPoint(float(words[1]), float(words[2]), float(words[3]))
            points.append([float(words[1]), float(words[2]), float(words[3])])
            names.append(words[0])
    return points

def GetTransformMatrix(target_points, source_points):
    landmarkTransform = vtk.vtkLandmarkTransform()
    landmarkTransform.SetSourceLandmarks(source_points)
    landmarkTransform.SetTargetLandmarks(target_points)
    landmarkTransform.SetModeToRigidBody()
    landmarkTransform.Update()
    matrix = landmarkTransform.GetMatrix()
    return matrix

def DoTransformPoints(matrix, vtk_points):
    transform = vtk.vtkTransform()
    transform.SetMatrix(matrix)
transform.Update()

points_poly = vtk.vtkPolyData()
points_poly.SetPoints(vtk_points)
transformed_model_filter = vtk.vtkTransformPolyDataFilter()
transformed_model_filter.SetInput(points_poly)
transformed_model_filter.SetTransform(transform)
transformed_model_filter.Update()
aligned_model = transformed_model_filter.GetOutput()
aligned_points = aligned_model.GetPoints()
return aligned_points

def DoTransformPoly(matrix, poly_data):
    transform = vtk.vtkTransform()
    transform.SetMatrix(matrix)
    transform.Update()

    transformed_model_filter = vtk.vtkTransformPolyDataFilter()
    transformed_model_filter.SetInput(poly_data)
    transformed_model_filter.SetTransform(transform)
    transformed_model_filter.Update()
    aligned_model = transformed_model_filter.GetOutput()
    return aligned_model

def DoTransformPolyTwoMatrices(matrix1, matrix2, poly_data):
    transform = vtk.vtkTransform()
    transform.Premultiply()
    transform.SetMatrix(matrix1)
    transform.Concatenate(matrix2)
    transform.Update()

    transformed_model_filter = vtk.vtkTransformPolyDataFilter()
    transformed_model_filter.SetInput(poly_data)
    transformed_model_filter.SetTransform(transform)
    transformed_model_filter.Update()
aligned_model = transformed_model_filter.GetOutput()
return aligned_model

def GetResidualError(vtk_points_1, vtk_points_2):
    sum_error = 0
    errors = []
    for i in range(vtk_points_1.GetNumberOfPoints()):
        v1 = np.array(vtk_points_1.GetPoint(i))
        v2 = np.array(vtk_points_2.GetPoint(i))
        dist = np.linalg.norm(v2-v1)
        errors.append(dist)
    means = []
    avg = np.mean(errors)
    for error in errors:
        means.append(avg-error)
    return means

def GetMeanDistance(vtk_points_1, vtk_points_2):
    errors = []
    for i in range(vtk_points_1.GetNumberOfPoints()):
        v1 = np.array(vtk_points_1.GetPoint(i))
        v2 = np.array(vtk_points_2.GetPoint(i))
        dist = np.linalg.norm(v2-v1)
        errors.append(dist)
    avg = np.mean(errors)
    return avg

def main():
    root_dir = "~/Users/m Batesole/PycharmProjects/MattsResearch/sample60805/"
    files = os.listdir(root_dir)
    pts_list = GetPtsList(root_dir)
# print pts_list
matrix = None

for i in range(len(pts_list)):
    print pts_list[i].split()
    if pts_list[i].split()[1] == 'cbct':
        base_name = pts_list[i].split()[0]
        print base_name
        np_target_points = ReadPoints('./' + pts_list[i])
        vtk_target_points = NumpyToVTKPoints(np_target_points)
        if pts_list[i+1].split()[0] == base_name:
            np_source_points = ReadPoints('./' + pts_list[i+1])
            vtk_source_points = NumpyToVTKPoints(np_source_points)
        else:
            print "Something is wrong with the names or order of the files" 
            exit()
        matrix = GetTransformMatrix(vtk_target_points, vtk_source_points)
        print matrix
        vtkAligned_points = DoTransformPoints(matrix, vtk_source_points)
    # doDisplay2Points(vtk_target_points, vtk_source_points, [0,0,1])
    # doDisplay2Points(vtk_target_points, vtkAligned_points, [0,0,1])
    residual_errors = GetResidualError(vtk_target_points, vtkAligned_points)
    mean_error = GetMeanDistance(vtk_target_points, vtkAligned_points)
    print "Error is: ", mean_error
    print "Residual Errors: ", residual_errors

for file in files:
    if file.endswith("cbct.pts"):
        target_points_name = root_dir+file
    if file.endswith("optical.pts"):
        source_points_name = root_dir+file
    if file.endswith("cbct.ply"):
        cbct_model_fn = root_dir+file
    if file.endswith("optical.ply"):
optical_model_fn = root_dir+file

groups = file.split('_')
if len(groups) == 3:
    base_name = '_'.join(groups[:2]), '_'.join(groups[2:])[0]
    base_name = base_name[0]
eelif len(groups) == 2:
    base_name = groups[0]

root_name = root_dir+base_name+'_segroot.ply'
crown_name = root_dir+base_name+'_crown.ply'

ply_filename = root_dir+base_name+'_tooth.ply'
vtk_filename = root_dir+base_name+'_crown_to_test.vtk'

#target_points_name = ""/Users/mbatesole/PycharmProjects/MattsResearch/10-788 cbct arch land.pts"
#target_points_name = ""/Users/mbatesole/PycharmProjects/MattsResearch/10-788 cbct1.pts"
#source_points_name = ""/Users/mbatesole/PycharmProjects/MattsResearch/10-788 optical arch land.pts"
#source_points_name = ""/Users/mbatesole/PycharmProjects/MattsResearch/10-788_optical1.pts"

np_target_points = ReadPoints(target_points_name)
vtk_target_points = NumpyToVTKPoints(np_target_points)

np_source_points = ReadPoints(source_points_name)
vtk_source_points = NumpyToVTKPoints(np_source_points)

matrix_1 = GetTransformMatrix(vtk_target_points, vtk_source_points)
#print matrix

#cbct_model_fn =""/Users/mbatesole/PycharmProjects/MattsResearch/10-788 cbct.ply"
ply_reader_cbct = vtk.vtkPLYReader()
ply_reader_cbct.SetFileName(cbct_model_fn)
ply_reader_cbct.SetFileName(cbct_model_fn)
ply_reader_cbct.Update()
#optical_model_fn = "/Users/mbatesole/PycharmProjects/MattsResearch/10-788_optical.ply"
ply_reader_optical = vtk.vtkPLYReader()
ply_reader_optical.SetFileName(optical_model_fn)
ply_reader_optical.Update()

transformed_optical_1 = DoTransformPoly(matrix_1, ply_reader_optical.GetOutput())

#doDisplay2Poly(ply_reader_cbct.GetOutput(), transformed_optical_1)

## perform ICP surface to surface
icpTransform = vtk.vtkIterativeClosestPointTransform()
icpTransform.SetSource(transformed_optical_1)
icpTransform.SetTarget(ply_reader_cbct.GetOutput())
icpTransform.GetLandmarkTransform().SetModeToRigidBody()
#icpTransform.StartByMatchingCentroidsOn()
icpTransform.Modified()
icpTransform.Update()
print icpTransform.GetMeanDistance()

matrix_2 = icpTransform.GetLandmarkTransform().GetMatrix()
transformed_optical_2 = DoTransformPoly(matrix_2, transformed_optical_1)
#doDisplay2Poly(ply_reader_cbct.GetOutput(), transformed_optical_2)

#exit()

#vtk_aligned_points = DoTransformPoints(matrix, vtk_source_points)
#doDisplay2Points(vtk_target_points, vtk_source_points, [0,0,1])
#exit()
#doDisplay2Points(vtk_target_points, vtk_aligned_points, [0,0,1])
#exit()
# residual_errors = GetResidualError(vtk_target_points, vtk_aligned_points)
# mean_error = GetMeanDistance(vtk_target_points, vtk_aligned_points)
# print "Error is: ", mean_error
# print "Residual Errors: ", residual_errors
# exit()

# root_name = "~/Users/mbatesole/PycharmProjects/MattsResearch/10-788_root_only.stl"
# stl_reader = vtk.vtkSTLReader()
# stl_reader.SetFileName(root_name)
# stl_reader.Update()

root_reader = vtk.vtkPLYReader()
root_reader.SetFileName(root_name)
root_reader.Update()

# crown_name = "~/Users/mbatesole/PycharmProjects/MattsResearch/10-788_crown.ply"
ply_reader = vtk.vtkPLYReader()
ply_reader.SetFileName(crown_name)
ply_reader.Update()

root_poly = root_reader.GetOutput()
crown_poly = ply_reader.GetOutput()

# transformed_crown = DoTransformPoly(matrix, crown_poly)
transformed_crown = DoTransformPolyTwoMatrices(matrix_1, matrix_2, crown_poly)

whole_tooth = vtk.vtkAppendPolyData()
whole_tooth.AddInput(root_poly)
whole_tooth.AddInput(transformed_crown)
whole_tooth.Update()

poly_writer = vtk.vtkPLYWriter()
poly_writer.SetFileName(ply_filename)
poly_writer.SetInput(whole_tooth.GetOutput())
poly_writer.Write()
vtk_writer = vtk.vtkPolyDataWriter()
vtk_writer.SetFileName(vtk_filename)
vtk_writer.SetInput(transformed_crown)
vtk_writer.Write()

doDisplay2Poly(root_poly, transformed_crown)

arch_name = "/Users/mbatesole/PycharmProjects/MattsResearch/10-788_optical.ply"
ply_reader = vtk.vtkPLYReader()
ply_reader.SetFileName(arch_name)
ply_reader.Update()
doDisplayPointsPoly(vtk_source_points, ply_reader.GetOutput())

if __name__ == "__main__":
    main()
File 2. Python script used to calculate angles and distances between landmark points.

```python
import os
import string
import numpy as np
import csv

def GetPtsList(directory):
    pts_list = []
    for file in os.listdir(directory):
        if file.endswith(('.pts')):
            pts_list.append(file)
    return pts_list

def ReadPoints(file_name):
    points = []
    names = []
    f = open(file_name, 'r')
    for line in f.readlines():
        words = string.split(line)
        if len(words) == 4:
            #.InsertNextPoint(float(words[1]), float(words[2]), float(words[3]))
            points.append([float(words[1]), float(words[2]), float(words[3])])
            names.append(words[0])
    return points

def AngleFromPoints(p1, p2, p3):
    a = np.array(p1)
    b = np.array(p2)
    c = np.array(p3)
    ba = a - b
    bc = c - b
    cosine_angle = np.dot(ba, bc) / (np.linalg.norm(ba) * np.linalg.norm(bc))
    angle = np.arccos(cosine_angle)
    return np.degrees(angle)

def DistanceFromPoints(p1, p2):
    a = np.array(p1)
    b = np.array(p2)
    distance = np.linalg.norm(a - b)
    return distance

def main():
    angle1s = []
    angle2s = []
    distance1s = []
    distance2s = []
    distance3s = []
    distance4s = []
    distance5s = []
    distance6s = []
    pts_list = GetPtsList('/Users/mbatesole/PycharmProjects/MattsResearch/Angles/data')
    for i in range(len(pts_list)):
        points = ReadPoints('/Users/mbatesole/PycharmProjects/MattsResearch/Angles/data/' + pts_list[i])
        #distance1s.append(DistanceFromPoints(points[0], points[7]))
        #distance2s.append(DistanceFromPoints(points[8], points[10]))
        #distance3s.append(DistanceFromPoints(points[9], points[11]))
        #distance4s.append(DistanceFromPoints(points[12], points[14]))
        #distance5s.append(DistanceFromPoints(points[13], points[15]))
        #angle1s.append(AngleFromPoints(points[0], points[10], points[7]))
        #angle2s.append(AngleFromPoints(points[4], points[9], points[7]))
```

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```python
distance1s.append(DistanceFromPoints(points[1], points[3]))
distance2s.append(DistanceFromPoints(points[2], points[4]))
distance3s.append(DistanceFromPoints(points[5], points[7]))
distance4s.append(DistanceFromPoints(points[6], points[8]))
distance5s.append(DistanceFromPoints(points[0], points[1]))
distance6s.append(DistanceFromPoints(points[0], points[7]))

#labels = ['Specimin Label', 'Distance S0-S7', 'Distance S8-S10', 'Distance S9-S11', 'Distance S12-S14', 'Distance S13-S15', 'Angle S0-S10-S7', 'Angle S4-S9-S7']
#data = [pts_list, distance1s, distance2s, distance3s, distance4s, distance5s, angle1s, angle2s]

labels = ['Specimin Label', 'S1-S3', 'S2-S4', 'S5-S7', 'S6-S8', 'S0-S1', 'S0-S7']
data = [pts_list, distance1s, distance2s, distance3s, distance4s, distance5s, distance6s]
data = zip(*data)

file = open('./angles_distances.csv', "wb")
writer = csv.writer(file)
writer.writerow(labels)
for row in data:
    writer.writerow(row)
file.close()

if __name__ == "__main__":
    main()
```
import vtk
import numpy as np
import os
import subprocess
from utility import *

def ReadPLY(filename):
    reader = vtk.vtkPLYReader()
    reader.SetFileName(filename)
    reader.Update()
    return reader.GetOutput()

def ReadVTK(filename):
    reader = vtk.vtkPolyDataReader()
    reader.SetFileName(filename)
    reader.Update()
    return reader.GetOutput()

def SaveCSVFile(points, count, save_dir):
    num_points = points.GetNumberOfPoints()
    csv_file = open(save_dir + '/' + str(count) + '.csv', 'wt')
    writer = csv.writer(csv_file)
    for i in range(num_points):
        writer.writerow([i, points.GetPoint(i)[0], points.GetPoint(i)[1], points.GetPoint(i)[2]])

def main():
    root_dir = "Subjects/sample50664/"
    files = os.listdir(root_dir)
    groups = files[1].split('_') # take second file in case .DS_Store is in the directory
    if len(groups) == 3:
        base_name = '_'.join(groups[2:2]), '_'.join(groups[2:2])
        base_name = base_name[0]
    elif len(groups) == 2:
        base_name = groups[0]

    point_subset_index = [0, 1, 2, 3, 4, 5, 6, 16, 17]
    # load the mean shape model points
    target_points = vtk.vtkPoints()
    # get the number of points
    count = len(open(root_dir + 'mean.pts').readlines()) - 1 # minus 2 because landmark.exe adds 2 line returns at the end
    pts_file = open(root_dir + "mean.pts", 'r')
    lines = pts_file.readlines()
    lines = np.array(lines)
    i = 0
    for line in lines[2:count]:
        if i in point_subset_index:
            # print line.split()[1:4]
            x = float(line.split()[1])
            y = float(line.split()[2])
            z = float(line.split()[3])
            target_points.InsertNextPoint(x, y, z)
        i += 1

File 3. Python script used to align the shape model and fit the Gaussian process augmented model to each test tooth.

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num_points = target_points.GetNumberOfPoints()
csv_file = open(root_dir + "mean.csv", 'wt')
writer = csv.writer(csv_file)
for i in range(num_points):
    writer.writerow([i, target_points.GetPoint(i)[0], target_points.GetPoint(i)[1], target_points.GetPoint(i)[2]])

# load the subject points
source_points = vtk.vtkPoints()
# get the number of points
count = len(open(root_dir + base_name + "_tooth.pts").readlines()) - 1  # minus 2 because landmark.exe adds 2 line returns at the end

pts_file = open(root_dir + base_name + "_tooth.pts", 'r')
lines = pts_file.readlines()
lines = np.array(lines)
i = 0
for line in lines[2:count]:
    if i in point_subset_index:
        # print line.split()[1:4]
        x = float(line.split()[1])
        y = float(line.split()[2])
        z = float(line.split()[3])
        source_points.InsertNextPoint(x, y, z)
i += 1

# get transform from subject to model
doDisplay2Points(target_points, source_points)

# Landmark Transform
landmarkTransform = vtk.vtkLandmarkTransform()
landmarkTransform.SetSourceLandmarks(source_points)
landmarkTransform.SetTargetLandmarks(target_points)
landmarkTransform.SetModeToRigidBody()
landmarkTransform.Update()

# apply that transform to the subject poly

source_ply = ReadVTK(root_dir + base_name + "_crown_to_test.vtk")
transformFilter = vtk.vtkTransformPolyDataFilter()
transformFilter.SetInput(source_ply)
transformFilter.SetTransform(landmarkTransform)
transformFilter.Update()
source_transformed_ply = transformFilter.GetOutput()

writer = vtk.vtkPolyDataWriter()
writer.SetInput(source_transformed_ply)
writer.SetFileName(root_dir + base_name + "_crown_to_test_aligned.vtk")
writer.Update()

source_points_poly = vtk.vtkPolyData()
source_points_poly.SetPoints(source_points)
transformFilter = vtk.vtkTransformPolyDataFilter()
transformFilter.SetInput(source_points_poly)
transformFilter.SetTransform(landmarkTransform)
transformFilter.Update()
source_transformed_points = transformFilter.GetOutput().GetPoints()

csv_file = open(root_dir + base_name + "_source_points.csv", 'wt')
writer = csv.writer(csv_file)
for i in range(num_points):
writer.writerow([i, source_transformed_points.GetPoint(i)[0], source_transformed_points.GetPoint(i)[1], source_transformed_points.GetPoint(i)[2]])

doDisplay2Points(target_points, source_transformed_points)

whole_tooth = ReadPLY(root_dir + base_name + "_tooth.ply")
transformFilter = vtk.vtkTransformPolyDataFilter()
transformFilter.SetInput(whole_tooth)
transformFilter.SetTransform(landmarkTransform)
transformFilter.Update()

writer = vtk.vtkPolyDataWriter()
writer.SetInput(transformFilter.GetOutput())
writer.SetFileName(root_dir+base_name + "_tooth.vtk")
writer.Update()

command = "statismo-fit-surface -i augmentedpcamodel.h5 -t '%s' -o '%s' -f '%s' -m '%s' -p -w .005 -v .25" % (
    root_dir + base_name + "_crown_to_test_aligned.vtk",
    root_dir + base_name + "_fitted-mesh.vtk",
    root_dir + base_name + "_source_points.csv",
    "mean.csv")

subprocess.call(command, shell=True)
print "nRun this from the top level directory: 'n"

print command+""n"
print "Then open _fitted-mesh.vtk and tooth.vtk in paraview"
if __name__ == '__main__':
    main()