MeshMonk: open-source large-scale intensive 3D phenotyping

Julie D. White1\*, Alejandra Ortega-Castrillón2,3, Harry Matthews4,5,6, Arslan A. Zaidi1,7, Omid Ekrami8, Jonatan Snyders9, Yi Fan4,5,10, Tony Penington4,5,6, Stefan Van Dongen8, Mark D. Shriver1, Peter Claes2,3\*

1Department of Anthropology, The Pennsylvania State University, University Park, PA, USA.

2Department of Electrical Engineering, ESAT/PSI, KU Leuven, Leuven, Belgium

3Medical Imaging Research Center, MIRC, UZ Leuven, Leuven, Belgium

4Mudoch Children’s Research Institute, Melbourne, Australia

5Royal Children’s Hospital, Melbourne, Australia

6Department of Pediatrics, University of Melbourne, Melbourne Australia

7Department of Biology, The Pennsylvania State University, University Park, PA, USA.

8Department of Biology, University of Antwerp, Antwerp, Belgium

9WebMonks, Hasselt, Belgium

10Melbourne Dental School, University of Melbourne, Melbourne Australia

**\* Correspondence:**jdw345@psu.edu; peter.claes@kuleuven.be

Keywords: Automated landmarking1, automated phenotyping2, non-rigid registration3, phenomics4, genomics5, morphometrics6, 3D7, facial variation8.

Abstract

Introduction

In the post-genomics era, emphasis has been placed on disentangling ‘genotype-phenotype’ connections so that the biological basis of complex phenotypes can be understood. However, our ability to efficiently and comprehensively characterize phenotypes lags behind our ability to characterize genomes. Anthropometric studies of morphology have traditionally relied on sparse sets of landmarks manually placed on images, from which linear distances and angles are calculated to be used in genetic association studies. This requires the tedious placement of landmarks on many images and is error prone and sensitive to individual differences among observers. Here, we report a toolbox for fast and reproducible high-throughput phenotyping of 3D images. While we demonstrate the utility of this method using 3D facial images, the procedure can also be applied to 3D scans of other complex morphological structures, such as the human brain and skeletal bones.

Methods

Given a facial image (target) with five crude positioning landmarks, a rigid registration is first used to orient an anthropometric mask (reference) to the target scan. Then, using a weighted k-nearest neighbors and a visco-elastic transformation model, the reference is transformed to fit the specific shape of the target. For facial scans, this results in homologous spatially dense (N=7,160) quasi-landmark configurations for all 3D images. As validation, a dataset (N=41) with 19 manually-placed landmarks was superimposed onto the reference in a leave-one-out approach to identify the closest barycentric coordinate on the mask. These coordinates were then projected back onto the training faces and the manual and automatic landmark placements were compared.

Results and Conclusion

We demonstrate that this method is highly accurate, with an average Euclidean distance between the manual and automatic placements of ~1.2 mm. The process is robust to variation due to scan quality, camera systems, and ancestries. Though validated using 19 landmarks, for comparison with traditional methods, this method allows for automated dense phenotyping, freeing the researcher from the use of a limited number of landmarks and allowing for more comprehensive investigations of facial shape variation. This expansion opens up an exciting avenue of study in assessing genomic and phenomic data to better understand the genetic contributions to complex morphological traits.

# Introduction

The phenotypic complement to genomics is *phenomics*, which aims to obtain high-throughput and high-dimensional phenotyping in line with our ability to characterize genomes (Houle et al., 2010). The paradigm shift is simple and similar to the one made in the Human Genome Project: instead of ‘phenotyping as usual’ or measuring a limited set of simplified features that seem relevant, why not measure it all? In contrast to genomic technologies, which successfully measure and characterize complete genomes, the scientific development of phenomics lags behind. However, with the advent of new technologies, hardware exists for extensively and intensively collecting quantitative phenotypic data. For example, 3D image surface and/or medical scanners provide the optimal means to capture information of biological morphology and appearance at the phenomic level. Today, the challenge lies in the ability to provide semantic interpretations from large scale image data that capture the phenome in the context of genetic variations (Walter et al., 2010), which is a challenge that we address with the development of the MeshMonk software.

Of interest to anthropologists, geneticists, biologists, and medical clinicians is the ability to accurately and reproducibly characterize anatomical structures, like a femur, skull, or face, such that underlying qualities about the structure can be understood. The study of variation and covariation in anatomy can provide insights into the genetic causes and evolution of the anatomical structure. In addition, comparing the anatomy of an individual patient to a control population can indicate pathology to a medical practitioner. Traditionally, this has been achieved using visual clinical assessment or by taking measurements between manually placed anatomical ‘landmarks’, traditionally defined as precise locations on biological forms that hold some developmental, functional, structural or evolutionary significance (Richtsmeier et al., 2002) and are unambiguously defined and reliably locatable (Aldridge et al., 2005; Corner et al., 1992; Richtsmeier et al., 1995). Some examples include the endo- and exocanthi (the inner and outer corners of the eyes, respectively) and the pronasale (the tip of the nose).

However, manual landmarking is tedious to perform, difficult to standardize in practice, and prone to intra and inter-operator error (Fagertun et al., 2014; Toma et al., 2009; von Cramon-Taubadel et al., 2007; Weinberg et al., 2004; Wong et al., 2008). Furthermore, sparse landmark configurations can only quantify the form at defined landmark indications that can be reliably identified and indicated by a human and lack the resolution to fully characterize shape variation in-between landmarks. An alternative is to automatically indicate quasi-landmarks across the entire surface of the structure. This is achieved by gradually warping a generic template image (anthropometric mask) composed of thousands of points into the shape of each target image through a non-rigid registration algorithm (Andresen and Nielsen, 2001; Claes, 2007; Claes et al., 2012; Hutton et al., 2003b; Snyders et al., 2014). The coordinates of these warped templates, now in the shape of each target, can then be treated by geometric morphometric analysis. An automatic approach like this is preferable for the analysis of large datasets, avoiding the problems of manual landmarking at different sites by multiple operators. They are also more suitable for applications that require synthesis of a recognizable instance of the actual structure, such as predicting a complete shape from DNA (Claes et al., 2014a), synthetic growth and ageing of a face (Imaizumi et al., 2015; Matthews et al., 2018a), constructing 3D facial composites for forensic applications (Blanz and Vetter, 1999), and characterization of dysmorphology for clinical diagnostics (Baynam et al., 2014; Hammond et al., 2005). Here, we report the MeshMonk toolbox for fast and reproducible high-throughput phenotyping of 3D images, or quasi-landmark indication, which can be applied to 3D facial images as well as 3D scans of other complex morphological structures, such as the human brain and skeletal bones.

Surface registration, utilized in the MeshMonk software, defines a mapping of the vertices from one (template) image to their corresponding locations on another (target) and allows us to quantify and visualize both subtle and acute variation in surface form across a sample by finding the geometrical relationship (one-to-one correspondences) between 3D shapes (Andresen and Nielsen, 2001; Claes, 2007; Claes et al., 2012; Hutton et al., 2003a; Snyders et al., 2014). When the template is warped onto each target, the coordinates of any anatomical landmark, manually annotated on the template, is also defined on each target, thus the complete quasi-landmark indication can also be considered a method for automatic placement of sparse anatomical landmarks (Wei et al., 2011). As a validation of the MeshMonk toolbox, we compare manual and automatic indications of sparse landmarks.

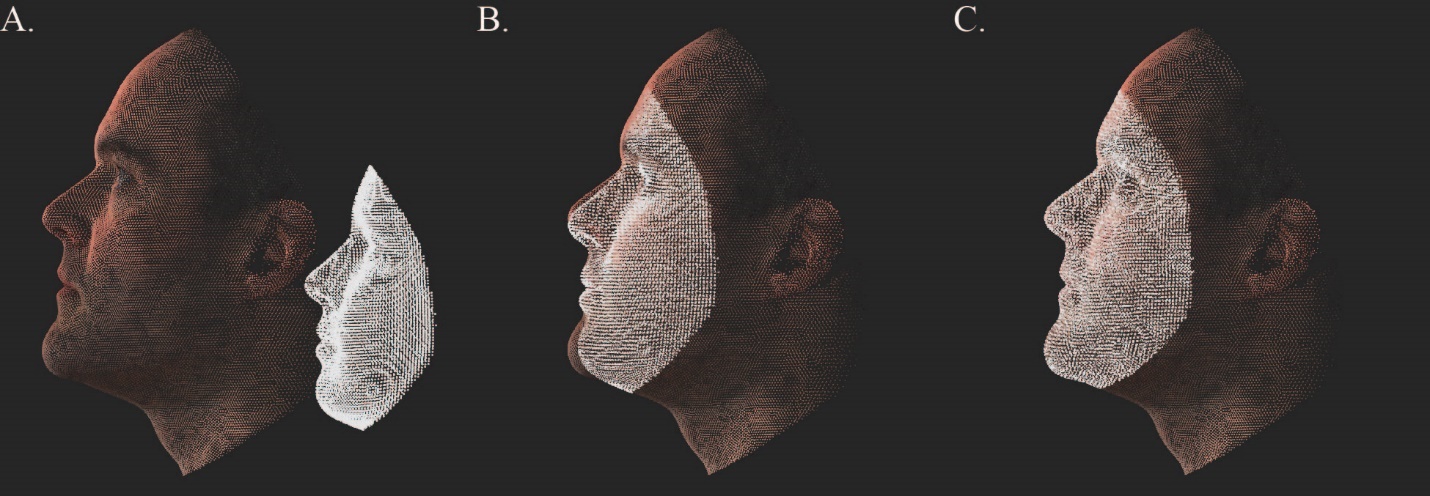
# Materials and Methods

## MeshMonk

MeshMonk is a free, open-source implementation of a modular surface registration framework developed in a partnership between researchers at the Medical Imaging Research Center (MIRC) at KU Leuven, Pennsylvania State University (PSU), and WebMonks ([www.webmonks.vision](http://www.webmonks.vision)), with MIRC and PSU delivering the research and IP behind the methods and algorithms and WebMonks being the implementation partner.

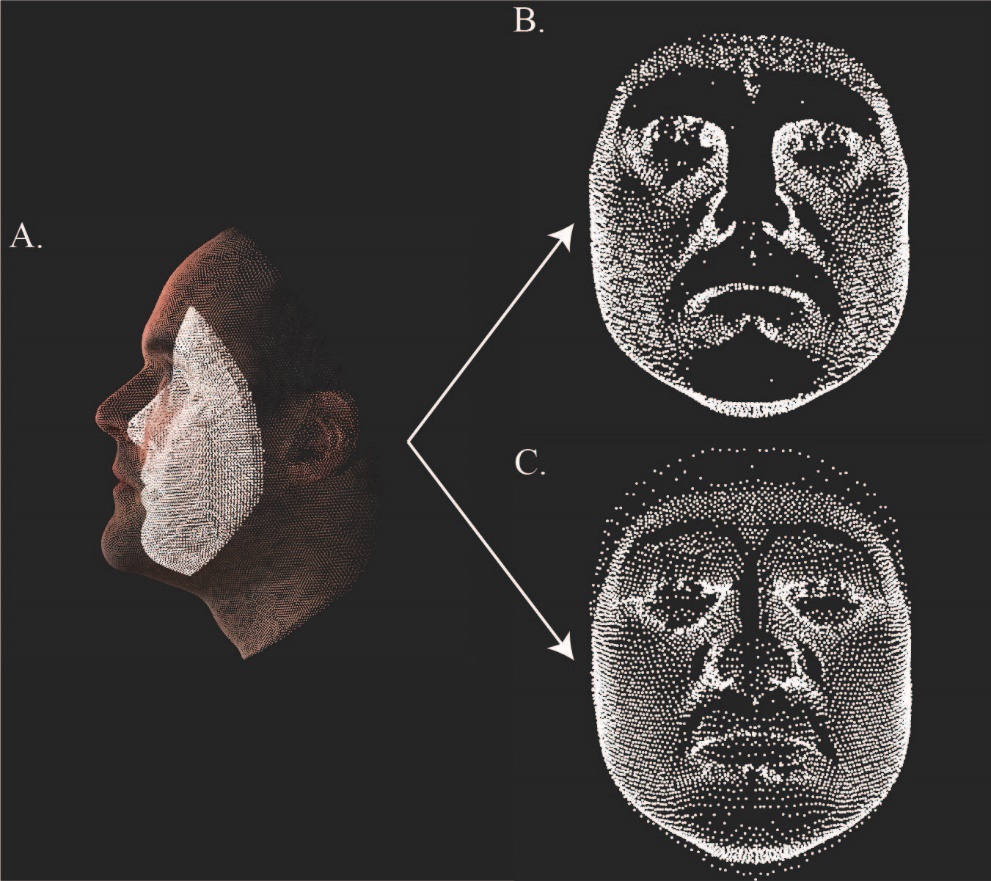
The C++ library takes a multi-scale, iterative ICP-based approach (Besl & McKay, 1992). Characteristic to its registration process are (1) a bi-directional, weighted K-Nearest Neighbor point matching algorithm, (2) an outlier classification step and (3) a Visco-Elastic transformation model (Claes et al., 2012; Snyders et al., 2014). With the library come wrappers to compile the library’s functions so that they can be used in Matlab.

## Explanation of process (Alejandra?)



**Figure X. Depiction of MeshMonk registration process.** **(A)** The target face and anthropometric mask are separated and not necessarily aligned in space or scale. **(B)** The anthropometric mask is scaled to fit the target face and is matched with the target face using a rigid registration algorithm. **(C)** The anthropometric mask is further modified to fit the target face using a nonrigid registration that allows for fine adjustment.

## Parameters and tuning (Alejandra?)



**Figure X. Nonsymmetric vs. Symmetric alignment.** **(A)** The registration of the anthropometric mask to the target face, stopped prior to the completion of the rigid registration step. **(B)** Illustration of registration using a nonsymmetric alignment. **(C)** Illustration of registration using a symmetric alignment. Dark areas in **(B)** and **(C)** represent parts of the target face that have no correspondence on the anthropometric mask.

## Validation

### Sample and data curation

Over many years, our collaborative group has recruited study participants through several studies at the Pennsylvania State University and sampled in the following locations: State College, PA (IRB 44929 and 4320); New York, NY (IRB 45727); Urbana-Champaign, IL (IRB 13103); Dublin, Ireland; Rome, Italy; Warsaw, Poland; and Porto, Portugal (IRB 32341). Stereo photogrammetry was used to capture 3D facial surfaces of N~6,000 participants using the 3dMD Face 2-pod and 3-pod systems (3dMD, Atlanta, GA). This well-established method generates a dense 3D point cloud representing the surface geometry of the face from multiple 2D images with overlapping fields of view. During photo capture, participants were asked to adopt a neutral facial expression with their mouth closed and to gaze forward, following standard facial image acquisition protocols (Heike et al., 2010). 3D surface images were visually checked to make sure that no major holes or artifacts existed.

### Manual placement of validation landmarks

Of the larger sample, N=48 surface images were chosen at random for validation. This number was then reduced by excluding surface images from participants that reported major facial injury or surgery. This resulted in N=41 surface images for validation, which were diverse with respect to sex (NFemale=29, NMale=12), age (range: 18-79, *M* = 32.78), height (range: 149.86-184.00 cm, *M* = 167.13 cm), weight (range: 43.00-103.80 kg, *M* = 67.62 kg), and 3D camera system used (SI Table 1). Most participants reported being of European descent. 3dMDpatient was used to record the 3D coordinates of 19 standard landmarks (7 midline and 12 bilateral) from each unaltered surface (i.e. still containing hair and clothing) in wavefront.obj format (Fig. X; Table X). Two independent observers placed landmarks three times each, with at least 24 hours in-between landmarking sessions, resulting in six total landmark indications for each facial scan. For each individual, we checked for gross landmark coordinate errors (e.g. mislabeling right and left side landmarks) before analysis.

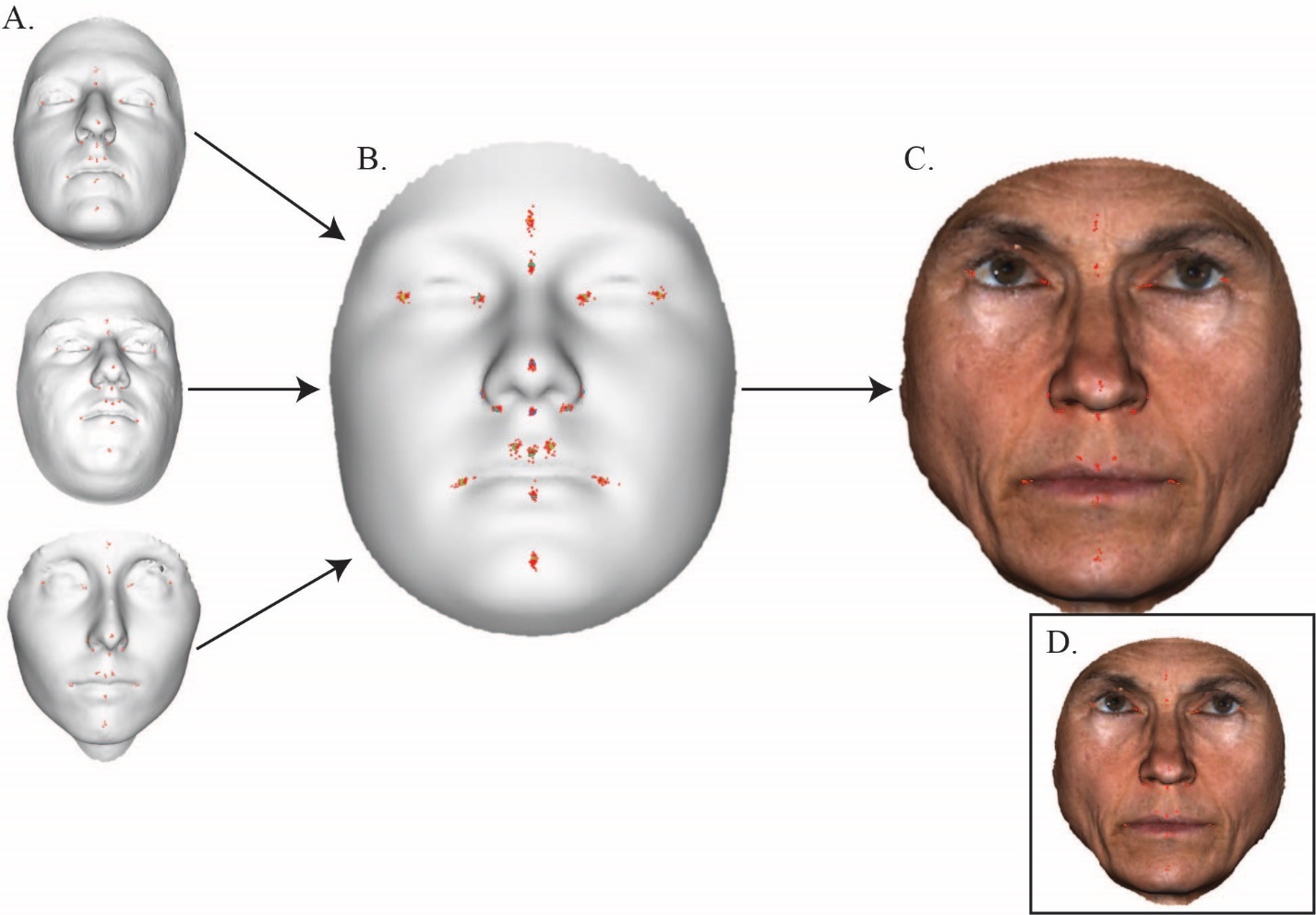
**Table X. Description of landmarks used in validation.** Landmark descriptions are those reported on the the Richtsmeier Lab website (http://www.getahead.la.psu.edu/).

|  |  |  |  |
| --- | --- | --- | --- |
| Landmark | Abbr. | Location | Definition |
| Glabella | g | Midline | The most prominent midline point between the eyebrows. |
| Nasion | n | Midline | The point in the midline of both the nasal root and the nasofrontal suture. This point is always above the line that connects the two inner canthi. |
| Pronasale | prn | Midline | The most protruded point of the apex nasi. |
| Subnasale | sn | Midline | The midpoint of the angle at the columella base where the lower border of the nasal septum and the surface of the upper lip meet. |
| Labiale superius | ls | Midline | The midpoint of the upper vermillion line. |
| Labiale inferius | li | Midline | The midpoint of the lower vermillion line. |
| Pogonion | SPg | Midline | The most anterior point of the chin. |
| Endocanthion | en | Bilateral | The point at the inner commissure of the eye fissure. |
| Exocanthion | ex | Bilateral | The point at the outer commissure of the eye fissure. |
| Alar curvature | ac | Bilateral | The most lateral point in the curved base of each ala. Indicating the facial insertion of the nasal wingbase. |
| Subalare | sbal | Bilateral | The point at the lower limit of each alar base, where the alar base disappears into the skin of the upper lip. The landmarks indicate the labial insertion of the alar base |
| Crista philtri | cph | Bilateral | The lower point on each elevated margin of the philtrum just above the vermillion line. |
| Chelion | ch | Bilateral | Point located at each labial commissure at the most lateral intersection of upper and lower lip. |

### Automatic placement of validation landmarks

To obtain automatic indications of the 19 validation landmarks, a leave-one-out approach was used to identify the placement of the validation landmark on the anthropometric mask, then indicate these landmarks on the left-out face. Specifically, for each surface image the manual landmark coordinates were averaged and aligned to the anthropometric mask using barycentric coordinates (Hille, 1982), giving a set of 41 total landmark placements on the anthropometric mask, which were then converted to cartesian coordinates. One by one, each face was left out while averaging the other 40 landmark placements to “train” the automatic landmarks. This average was then placed back onto the left-out (target) face, which resulted in the automatic placement of the validation landmarks using a “training” set that did not include the target face.

The placement of automatic landmarks was performed three times, changing the manual landmark data used as input: once using the average of observer AZ’s three manual landmark iterations, again using the average of observer JW’s three manual landmark iterations, and a final time using the average of all six manual landmark iterations from both observers. This process resulted in three placements of automatic landmarks for comparison.



**Figure X. Depiction of automatic landmark indication. (A)** Each facial scan was manually landmarked six times, three times each by two observers. These iterations were then averaged together and are placed on the anthropometric mask, except the landmark indications corresponding to the test face. **(B)** Placement of N=40 manual landmark indications on the anthropometric mask, leaving out the test face. The average of all 40 placements is shown as a colored point, which is colored based on the level of dispersion between the average and the manually placed indications for that landmark. **(C)** The average of all 40 placements of manual landmarks is indicated on the test face, serving as the automatic landmark indication. **(D)** The manual landmark indications for the shown example face, for comparison to the automatic indication in **(C)**.

### Validation

To validate the MeshMonk anthropometric mask registration, we compared the placement of manual and automatic landmarks and analyzed the variance structures captured by the two methods. In direct comparisons of landmark placements, we considered the manually placed landmarks to be the “gold standard” while calculating the root mean squared error (RMSE) between the manual and automatic *x*, *y*, and *z* coordinates. We also calculated Bland-Altman (Altman and Bland, 1983) and Intraclass Correlation Coefficient (Fisher, 1925) statistics to compare the manual and automatic landmark indications. The Bland-Altman method is preferred over correlation or regression as it is less influenced by the variance of the sample and the ICC is preferred because it tests both the degree of correlation and agreement between methods.

We additionally estimated the manual landmarking intra-observer error as the standard deviation between the x, y, and z coordinates of each observer’s manual landmarking indications. The inter- observer error of the manual landmark indications was calculated as the root mean squared error between each observer’s average *x*, *y*, and *z* coordinates. As an additional method to understand the variation present in the manual landmark indications only, we performed a multivariate analysis of variance (MANOVA) after aligning the six manual landmarking indications using a generalized Procrustes alignment (GPA). Study individual, observer, and iteration were used as predictors and landmark configuration as the response.

To determine if the automatic indication process increased the variation of landmark placements, we compared the inter-observer error calculated using only the manual landmarks (AML vs JML) to the RMSE between one observer’s manual landmarks and the automatic landmarks trained using the other observer’s manual placements (AML vs. JAuto and AAuto vs. JML), as if the automatic landmarks replaced the manual ones in a calculation of inter-observer error. A paired T-test was used to determine whether the “inter-observer errors” calculated using the automatic indications were significantly different than the error calculated using only the manual landmarks.

We utilized several methods to determine if the variance structures compared by the two methods were similar. MANOVAs were performed separately on the GPA-aligned average manual landmark indications from each observer as well as on the GPA-aligned automatic landmark indications trained using the average of each observer’s three landmark placements, with individual and observer as predictors in both tests. By comparing the results of these two tests, we can determine how the explanation of shape variance changes given a different landmarking method. To directly determine if any variance in shape was attributable to landmarking method, we combined the average manual landmark placements of each observer with the automatic placements trained using each of these averages and aligned them using GPA. We then tested the shape variation in this combined space as the response in a MANOVA, with individual, observer, method, and individual x observer as predictors.

The covariation structure between the manual and automatic landmarks was compared using a two-block partial least squares (PLS). This test was performed using each observer’s average manual landmark indications compared against the automatic landmark placements trained using each observer’s average. We also tested the degree of association between the manual landmark placements averaged across all six manual landmark indications and the automatic landmarks trained using that global average.

As a final validation that the automatic landmark indications captured the same information as the manual landmark indications, we compared centroid sizes calculated using the manual and automatic methods. We also performed an analysis of variance (ANOVA) test on the centroid size calculations, with individual, observer, method, and individual x observer as predictors to determine if variation in centroid size could be attributable to variation in landmarking method.

All analyses were performed in R using the Geomorph (Adams and Otárola-Castillo, 2013), BlandAltmanLeh (https://cran.r-project.org/web/packages/BlandAltmanLeh/BlandAltmanLeh.pdf), and ICC (https://cran.r-project.org/web/packages/ICC/ICC.pdf) packages, as well as packages for data manipulation (readxl, reshape2, plyr, car, data.table, dplyr, broom) and graphing (ggplot2, GGally, GGpubr). Centroid sizes were calculated using Geomorph and MANOVAs for shape variation were implemented using the ProcD.lm function from Geomorph (Collyer et al., 2015). The 19 manual and automatic landmark indications as well as the code used to perform this analysis are available in the following GitHub repository: https://github.com/juliedwhite/RemappingValidation/.

# Results

## Intra- and inter-observer error of manual landmarks

The quantitative study of morphology using 3D coordinates requires specific attention to measurement error and has a robust presence in the literature. For each independent observer, we calculated the intra-observer error of the manual landmarks as the standard deviation between the *x*, *y*, and *z* coordinates of each landmark iteration. Table X reports the per-landmark standard deviation, averaged across dimensions and images. Supplemental Table X reports values for each axis, averaged only across images. The average standard deviation of observer AZ across all landmarks was 0.5787 mm while the average standard deviation of observer JW across all landmarks was 0.4367 mm. The average inter-observer error, measured as the root mean squared error (RMSE) between the average *x*, *y*, and *z* coordinates of each observer’s landmark iterations was 0.5620 mm. This range of deviation is considered highly precise and is similar to previously reported measures of landmark error (Aldridge et al., 2005; von Cramon-Taubadel et al., 2007).

**Table X.** **Intra- and inter-observer error of manual landmarks.** Values have been averaged across each participant as well as *x*, *y*, and *z* axes to give an estimate of the error per landmark. Supplemental Table X reports error per *x*, *y*, and *z* axis.

|  |  |  |  |
| --- | --- | --- | --- |
| *Landmark* | *Standard deviation (mm)* | | *RMSE (mm)* |
| *Observer AZ* | *Observer JW* | *Inter-observer* |
| *Alar curvature left* | 0.6020 | 0.4339 | 0.4337 |
| *Alar curvature right* | 0.6304 | 0.3773 | 0.4648 |
| *Chelion left* | 0.6080 | 0.4472 | 0.5914 |
| *Chelion right* | 0.6002 | 0.4934 | 0.4220 |
| *Crista philtri left* | 0.5016 | 0.3041 | 0.5488 |
| *Crista philtri right* | 0.5358 | 0.2949 | 0.6699 |
| *Endocanthion left* | 0.7447 | 0.4372 | 0.6168 |
| *Endocanthion right* | 0.7697 | 0.4462 | 0.5102 |
| *Exocanthion left* | 0.5863 | 0.4380 | 0.4166 |
| *Exocanthion right* | 0.6543 | 0.3579 | 0.4038 |
| *Glabella* | 0.5761 | 0.6881 | 0.6423 |
| *Labiale inferius* | 0.5032 | 0.3175 | 0.8283 |
| *Labiale superius* | 0.4254 | 0.2666 | 0.4504 |
| *Nasion* | 0.5365 | 0.5402 | 0.6983 |
| *Pogonion* | 0.8208 | 0.7593 | 0.8466 |
| *Pronasale* | 0.4593 | 0.3157 | 0.4700 |
| *Subalare left* | 0.5018 | 0.4262 | 0.5664 |
| *Subalare right* | 0.4883 | 0.4848 | 0.6057 |
| *Subnasale* | 0.4504 | 0.4695 | 0.4921 |
| ***Mean*** | ***0.5787*** | ***0.4367*** | ***0.5620*** |

The analysis of measurement and observer error for the manual landmarks alone, assessed using a MANOVA for shape, with individual, observer, observer x individual, and nested observer x iteration as factors showed that non-individual factors contributed significantly to variation in shape (Table X). Individual variation contributed to most of the variation in shape (85%), as expected. Simple measurement error accounted for 3.5% of the total variation in shape. Additional to this, differences in observer accounted for 1.8% of shape variation, and drift in landmark iteration contributed an additional 1.5% of the total variation in shape. In total, non-individual effects contributed to 15% of the total shape variation, with 8.3% of this variation unexplained by our model.

**Table X.** MANOVA on all manual landmark indications to assess manual landmarking error.

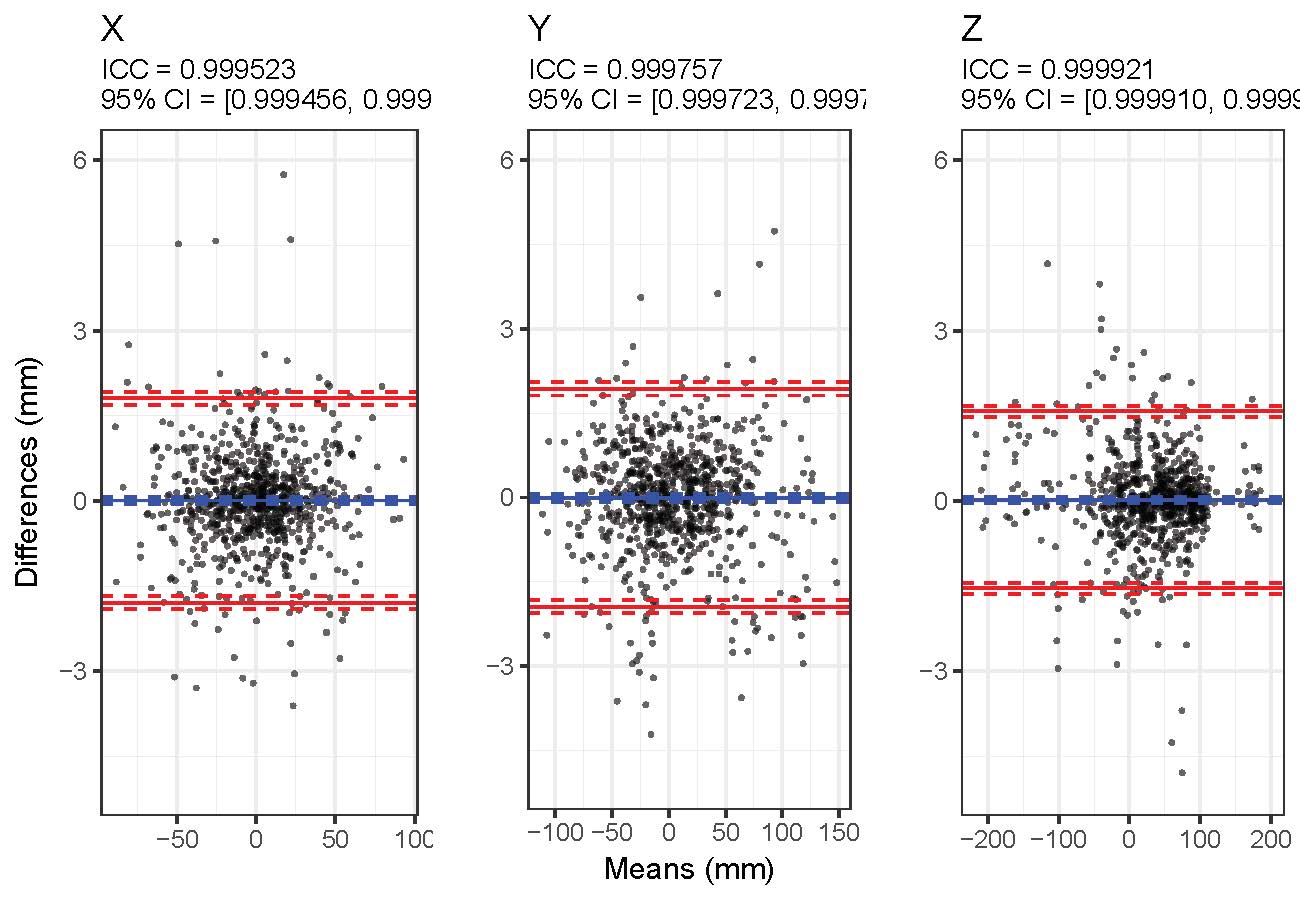
|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Variable | DF | SS | MS | R2 | F | Z | Pr(>F) |
| Individual | 40 | 1.1803 | 0.0295 | 0.8491 | 40.7135 | 26.620 | 0.001 |
| Observer | 1 | 0.0244 | 0.0244 | 0.0176 | 33.6563 | 14.568 | 0.001 |
| Individual x Observer | 40 | 0.0492 | 0.0012 | 0.0354 | 1.6963 | 26.292 | 0.001 |
| Observer x Iteration | 4 | 0.0203 | 0.0051 | 0.0146 | 6.9974 | 19.485 | 0.001 |
| Residuals | 160 | 0.1160 | 0.0007 | 0.0834 |  |  |  |
| Total | 245 | 1.3901 |  |  |  |  |  |

## Direct comparison of manual and automatic landmark placements

As one measure of validation of the automatic landmark indications, we compared the raw coordinate values of the manual landmark indications with the raw coordinate values of the automatic landmark indications. Because of the leave-one-out nature of our approach, we can compare the manual and automatic landmark coordinates directly without fear of training bias. To compare landmark indications, we calculated the root mean squared error between the x, y, and z manual and automatic coordinates, as well as the intraclass correlation coefficient between the x, y, and z coordinates produced by the two methods.

**Table X. Root mean squared error between manual and automatic landmarks**. Root mean squared error between the manual and automatic landmarks for the *x*, *y*, and *z* coordinates was calculated using the mean of all manual landmark indications and the automatic data trained using this mean. Values are presented for each axis, averaged across all faces, as well as averaged across the axes (mean).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| *Landmark* | *Root mean squared error (mm)* | | | |
| *X* | *Y* | *Z* | *Mean* |
| *Alar curvature left* | 0.1605 | 0.5233 | 0.6085 | 0.4308 |
| *Alar curvature right* | 0.1653 | 0.5221 | 0.5661 | 0.4178 |
| *Chelion left* | 1.1061 | 0.7131 | 0.6077 | 0.8089 |
| *Chelion right* | 0.9822 | 0.6600 | 0.5539 | 0.7320 |
| *Crista philtri left* | 0.7537 | 0.8927 | 0.4515 | 0.6993 |
| *Crista philtri right* | 0.7556 | 1.0005 | 0.4395 | 0.7319 |
| *Endocanthion left* | 0.7751 | 0.5437 | 0.4002 | 0.5730 |
| *Endocanthion right* | 1.0360 | 0.6517 | 0.5024 | 0.7300 |
| *Exocanthion left* | 0.9081 | 0.7362 | 0.8761 | 0.8401 |
| *Exocanthion right* | 0.9421 | 0.6537 | 0.9457 | 0.8472 |
| *Glabella* | 0.4806 | 1.3053 | 0.5583 | 0.7814 |
| *Labiale inferius* | 0.4560 | 0.7216 | 0.4756 | 0.5511 |
| *Labiale superius* | 0.5887 | 0.8055 | 0.3319 | 0.5754 |
| *Nasion* | 0.3543 | 0.9732 | 0.4748 | 0.6008 |
| *Pogonion* | 0.4313 | 1.0009 | 0.3791 | 0.6038 |
| *Pronasale* | 0.3987 | 0.5606 | 0.2827 | 0.4140 |
| *Subalare left* | 0.7271 | 0.4349 | 0.5570 | 0.5730 |
| *Subalare right* | 0.6526 | 0.4329 | 0.6008 | 0.5621 |
| *Subnasale* | 0.3239 | 0.4752 | 0.2620 | 0.3537 |
| *Mean* | 0.6315 | 0.7162 | 0.5197 | 0.6224 |



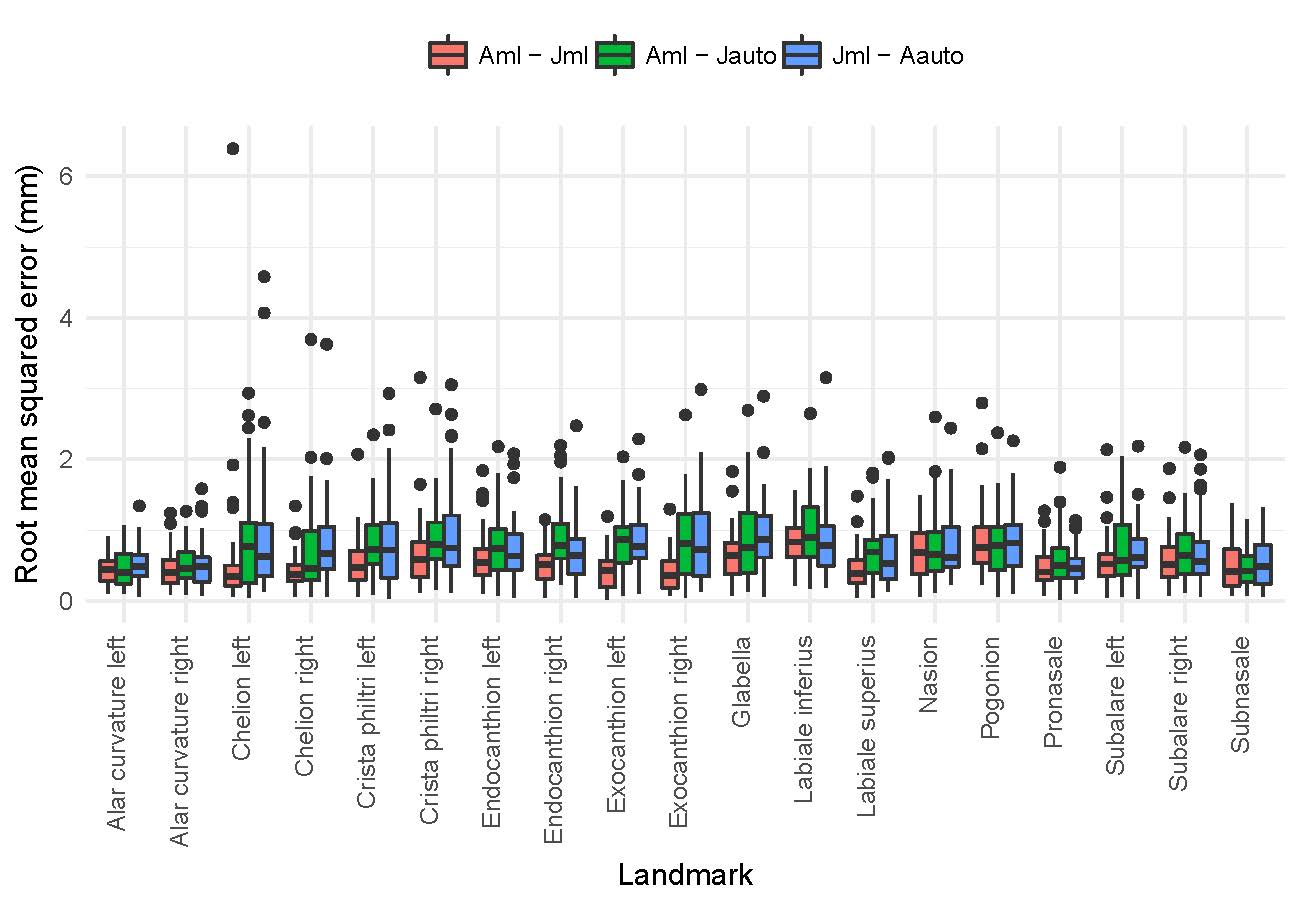
**Figure X. Bland-Altman plot for similarity between manual and automatic landmark placements.** For *x*, *y*, and *z*, Bland-Altman plot showing the differences between the manual and automatic landmark indications against the averages of the two techniques. Blue lines represent the mean difference value (solid) and 95% confidence limits (dashed). Red lines represent the upper and lower difference limits (solid) and the 95% confidence limits (dashed). Also given are the intra-class correlation coefficient with 95% confidence interval for the manual and automatic comparison.

#### Comparison of inter-observer errors

To test whether the automatic indication process increased the variation of landmark placements, we compared the inter-observer error calculated using only the manual landmarks (section 2.4.4.1) to inter-observer errors calculated by replacing one of the observer’s manual landmark indications with the automatic landmark indications trained using that average. This resulted in two extra calculations of inter-observer errors (AML vs. JAuto and AAuto vs. JML). The inter-observer error calculation was the root mean squared error between the *x*, *y*, and *z* coordinates. We used a paired T-test to determine whether the inter-observer errors calculated using the automatic indications were significantly different than those calculated using only the manual landmarks.

**Table X. Comparison of inter-observer errors.** The root mean squared error between the manual landmark placements (AML vs. JML) are compared to the root mean squared error between manual and automatic placements after replacing each observer’s manual landmark indications with their automatic landmark indications (AML vs. JAuto and AAuto vs. JML). Paired T-tests was used to determine if the new inter-observer error RMSE values were significantly different than the RMSE values for the manual landmark inter-observer error calculation (AML vs. JML). Comparisons that are significantly different at an alpha of 0.05 are in bold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | *AML-JML* | *AML – JAuto* | | | *AAuto - JML* | | |
| *Landmark* | *Mean RMSE (mm)* | *Mean RMSE (mm)* | *T*  *statistic* | *P value* | *Mean RMSE (mm)* | *T statistic* | *P value* |
| *Alar curvature left* | 0.43 | 0.44 | -0.10 | 0.9197 | 0.52 | -2.14 | **0.0382** |
| *Alar curvature right* | 0.46 | 0.52 | -0.99 | 0.3275 | 0.53 | -1.23 | 0.2266 |
| *Chelion left* | 0.59 | 0.89 | -1.89 | 0.0665 | 0.91 | -2.40 | **0.0212** |
| *Chelion right* | 0.42 | 0.72 | -2.59 | **0.0132** | 0.8 | -3.78 | **5.20x10-4** |
| *Crista philtri left* | 0.55 | 0.85 | -2.87 | **0.0066** | 0.83 | -3.11 | **0.0034** |
| *Crista philtri right* | 0.67 | 0.88 | -1.89 | 0.0661 | 0.95 | -3.53 | **0.0010** |
| *Endocanthion left* | 0.62 | 0.78 | -2.50 | **0.0167** | 0.74 | -1.46 | 0.1527 |
| *Endocanthion right* | 0.51 | 0.90 | -5.49 | **2.50 x 10-6** | 0.73 | -2.84 | **0.0071** |
| *Exocanthion left* | 0.42 | 0.88 | -6.14 | **3.00 x 10-7** | 0.87 | -5.80 | **8.93x10-7** |
| *Exocanthion right* | 0.40 | 0.85 | -5.54 | **2.09 x 10-6** | 0.88 | -5.65 | **1.49x10-6** |
| *Glabella* | 0.64 | 0.90 | -2.63 | **0.0121** | 0.93 | -3.12 | **0.0033** |
| *Labiale inferius* | 0.83 | 0.98 | -2.14 | **0.0381** | 0.88 | -0.54 | 0.5895 |
| *Labiale superius* | 0.45 | 0.70 | -3.05 | **0.0040** | 0.69 | -3.21 | **0.0026** |
| *Nasion* | 0.70 | 0.78 | -0.93 | 0.3556 | 0.81 | -1.25 | 0.2188 |
| *Pogonion* | 0.85 | 0.83 | 0.15 | 0.8835 | 0.86 | -0.22 | 0.8245 |
| *Pronasale* | 0.47 | 0.58 | -2.16 | **0.0366** | 0.51 | -0.65 | 0.5169 |
| *Subalare left* | 0.57 | 0.67 | -1.35 | 0.1842 | 0.72 | -2.24 | **0.0308** |
| *Subalare right* | 0.61 | 0.74 | -1.63 | 0.1114 | 0.67 | -0.84 | 0.4083 |
| *Subnasale* | 0.49 | 0.45 | 0.69 | 0.4939 | 0.51 | -0.26 | 0.7930 |



**Figure X. Comparison of inter-observer errors.** The root mean squared error between the manual landmark placements (AML vs. JML) are compared to the root mean squared error between manual and automatic placements after replacing each observer’s manual landmark indications with their automatic landmark indications (AML vs. JAuto and AAuto vs. JML).

#### Independent analyses of shape variance using manual and automatic landmarks

A multivariate analysis of variance (MANOVA) of shape, based on only the average of each observer’s manual landmark indications, was performed with individual, camera, and observer as covariates. We also performed a MANOVA on shapes originating from the automatic landmark indications, with individual, camera, and observer as covariates. The results of these two MANOVAs can be compared to determine if the variation in shape attributable to individual, camera, and observer is similar across manual and automatic landmarking methods.

**Table X.** **MANOVA on average manual landmark indications.** The average manual landmark placements of each observer were tested as the response in a MANOVA with individual, camera, observer, and the interaction of individual and camera as predictors.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Variable | Df | SS | MS | Rsq | F | Z | Pr(>F) |
| Individual | 1 | 0.0247 | 0.0247 | 0.0607 | 5.2368 | 4.0513 | **0.001** |
| Camera | 1 | 0.0107 | 0.0107 | 0.0263 | 2.2679 | 2.2227 | **0.009** |
| Observer | 1 | 0.0082 | 0.0082 | 0.0201 | 1.7311 | 1.6958 | 0.056 |
| Individual\*Camera | 1 | 0.0095 | 0.0095 | 0.0233 | 2.0109 | 2.1344 | **0.016** |
| Residuals | 75 | 0.3538 | 0.0047 | 0.8696 |  |  |  |
| Total | 79 | 0.4069 |  |  |  |  |  |

**Table X. MANOVA on automatic landmark indications.** The automatic landmark placements trained by the manual indications of each observer were tested as the response in a MANOVA with individual, camera, observer, and the interaction of individual and camera as predictors.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Variable | Df | SS | MS | Rsq | F | Z | Pr(>F) |
| Individual | 1 | 0.0161 | 0.0161 | 0.0511 | 4.3835 | 3.4988 | **0.001** |
| Camera | 1 | 0.0054 | 0.0054 | 0.0171 | 1.4658 | 1.1224 | 0.132 |
| Observer | 1 | 0.0084 | 0.0084 | 0.0265 | 2.2733 | 2.1167 | **0.016** |
| Individual\*Camera | 1 | 0.0098 | 0.0098 | 0.0310 | 2.6620 | 2.5293 | **0.004** |
| Residuals | 75 | 0.3755 | 0.0037 | 0.8743 |  |  |  |
| Total | 79 | 0.3151 |  |  |  |  |  |

#### Analysis of shape variance for manual and automatic indications together

The landmark placements averaged across all six manual landmark iterations were combined with the automatic indications trained using this average and then aligned by generalized procrustes alignment (GPA). A MANOVA was then performed with shape as the response and individual, camera, and method as predictors (Table X).

**Table X. MANOVA on combined manual and automatic landmarks.** The manual and automatic landmark placements corresponding to the average of all six manual landmark indications were GPA aligned and then used as the response in a MANOVA with individual, camera, method, and the interaction of individual and camera.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Variable | Df | SS | MS | Rsq | F | Z | Pr(>F) |
| Individual | 1 | 0.0182 | 0.0182 | 0.0526 | 4.3887 | 3.6134 | **0.001** |
| Camera | 1 | 0.0072 | 0.0072 | 0.0209 | 1.7402 | 1.5699 | 0.059 |
| Method | 1 | 0.0002 | 0.0002 | 0.0005 | 0.0450 | -6.5345 | 1.000 |
| Individual\*Camera | 1 | 0.0091 | 0.0091 | 0.0264 | 2.2008 | 2.2159 | **0.017** |
| Residuals | 75 | 0.3105 | 0.0041 | 0.8996 |  |  |  |
| Total | 79 | 0.3452 |  |  |  |  |  |

#### Two-block partial least squares

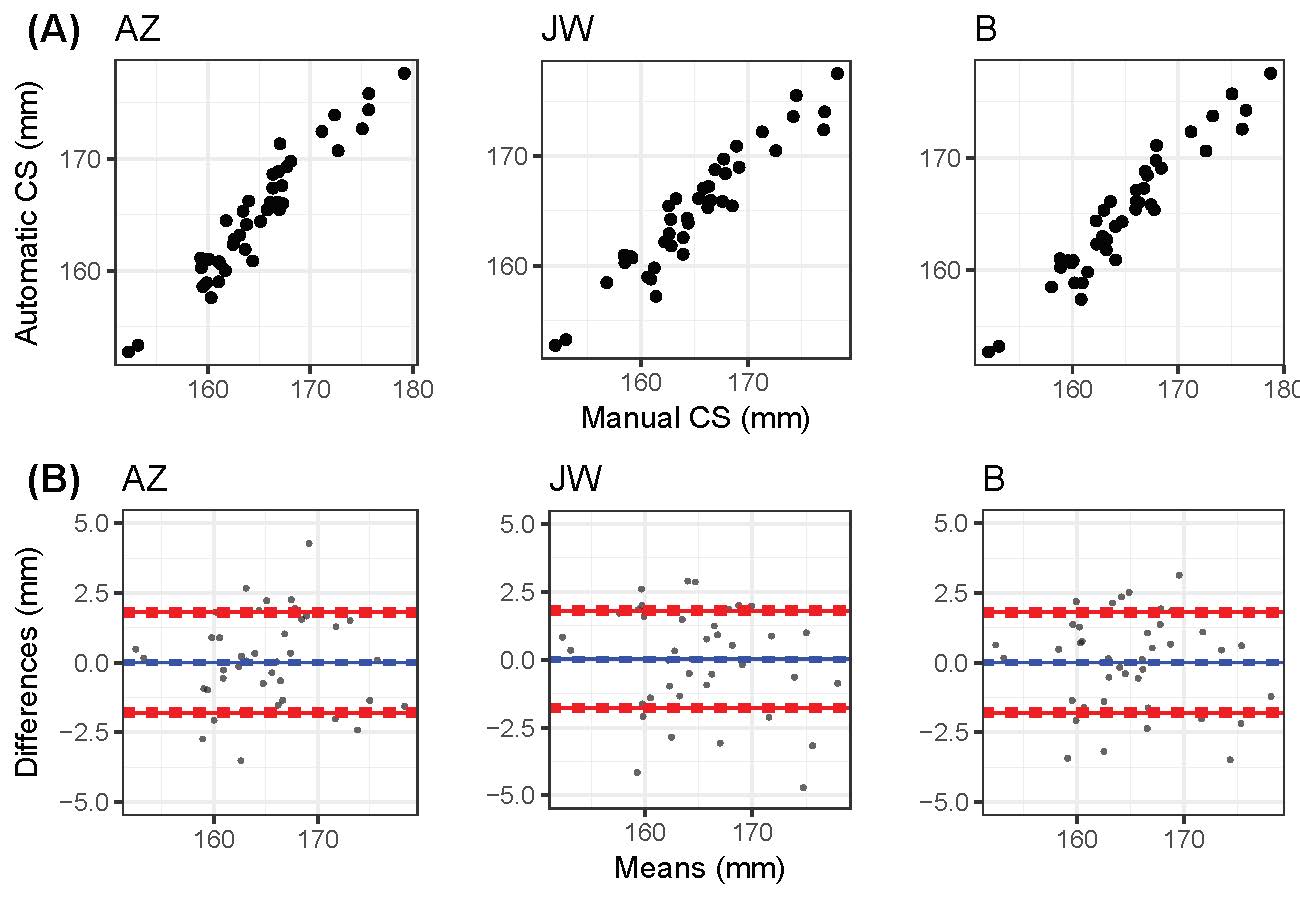
Several two-block partial least squares tests were used to test the degree of association between two blocks of Procrustes aligned coordinates. This test was performed using each observer’s manual landmark indications compared against the automatic landmark placements trained using each observer’s average. We also tested the degree of association between the manual landmark placements averaged across all six manual landmark indications and the automatic landmarks trained using this global average.

**Table X. PLS results (don’t keep this table, put in results)**

|  |  |  |
| --- | --- | --- |
|  | r-PLS | P-value |
| AML vs. AAuto | 0.975 | 0.001 |
| JML vs. JAuto | 0.973 | 0.001 |
| BML vs BAuto | 0.977 | 0.001 |

#### Centroid size comparison

As a final validation that the automatic landmark indications captured the same information as the manual landmark indications, we compared centroid sizes calculated using the manual and automatic methods. We also performed an ANOVA on the centroid size results, with individual, observer, camera, and method as predictors.



|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Variable | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| Individual | 1 | 79 | 78.56 | 2.349 | 0.127 |
| Observer | 2 | 1 | 0.28 | 0.008 | 0.992 |
| Camera | 1 | 77 | 77.42 | 2.315 | 0.129 |
| Method | 2 | 0 | 0.03 | 0.001 | 0.999 |
| Residuals | 233 | 7792 | 33.44 |  |  |

# Results (not updated)

## Direct comparison of manual and automatic landmark placements

The correlation between the manual and automatic landmarks was calculated based upon the average of all six iterations of manual landmarks and the automatic landmarking iteration based on this average. The Pearson’s correlation coefficients were high: 0.9995226 for the x-dimension, 0.9997573 for the y-dimension, and 0.9999215 for the z-dimension (Figure X). We also calculated the standard deviation between the average manual landmarks and the automatic landmarks, reported in Table X. The standard deviation averaged across dimensions and landmarks was 0.4401 (0.4465 along the x-axis, 0.5064 along the y-axis, and 0.3675 along the z-axis). Per-landmark values are given in Table X.

## Comparison of inter-observer errors (In the discussion, make sure to talk about how this is an expected result because of the averaging of many landmarks during the training process).

We calculated the inter-observer error using the automatic landmark placements trained using each observer’s manual landmark averages (i.e. AutoAZ vs. AutoJW) and compared this to the inter-observer error calculated using the manual landmark placements (i.e. MLAZ vs. MLJW) using Levene’s test, which was chosen to compare variances while being robust to departures from normality. The inter-observer errors and the Levene test statistics are provided in Table X and correspond to those in Figure X. In all but one case, the variance of the inter-observer error was significantly smaller when calculated using the automatic landmarks. The only case in which the two variances were not significantly different was the labiale superius landmark (F statistic = 2.4213, p-value = 0.1236).

## Comparison of Arslan ML – Arslan Auto, Julie ML – Julie Auto, etc. 2 way comparison to make sure that the automatic landmarking doesn’t add error

## Centroid size comparison

1. **Discussion**

Many authors have supplemented or replaced traditional analysis of inter-landmark measurements with geometric morphometric analysis (Adams et al., 2004; Rohlf and Marcus, 1993), which uses representations of the complete geometry of a configuration of landmarks, rather than simple distances. This can take the form of all pairwise distances between landmarks (Lele and Richtsmeier, 1991), but is more commonly the coordinates of the landmarks themselves. These techniques allow multivariate analysis, comparison, and prediction of the entire form (up to the resolution and density of landmark points) and have become a mainstay of taxonomic analyses (Baab, 2008; Frost et al., 2003; Havarti et al., 2004; Terhune et al., 2007), morphological evolution (Bastir et al., 2006; Klingenberg, 2010, 2013; O’Higgins, 2000), the examination of morphological ontogeny and growth (Kesterke et al., 2016; Martinez-Abadias et al., 2012; Matthews et al., 2018b; Mitteroecker et al., 2004; Smith, 2006), studies of population admixture (Martinez-Abadias et al., 2006; Quinto-Sánchez et al., 2015; Schlager and Alexandra, 2015), and genotype-phenotype mapping studies (Claes et al., 2014b, 2018; Liu et al., 2012; Paternoster et al., 2012; Shaffer et al., 2016), and studies of dysmorphology (Hammond et al., 2014; Klingenberg et al., 2010; Richtsmeier et al., 2000; Shaner et al., 2000; Starbuck et al., 2011).

Through studies utilizing manually placed sparse landmarks, we have begun to understand the biological basis and evolution of complex phenotypes, both normative and clinical. However, there is still much to be learned. One avenue for improvement is to expand and speed up the production and analysis of data using methods derived from engineering and computer vision, which allow for the description of shapes as “big data” structures instead of sparse sets of landmarks or linear distances, thus matching our ability to describe phenotypes with our ability to describe genomes.

## Validation

Manual landmarks were considered the gold standard and have long been used and validated in morphological studies (Aldridge paper).

The standard deviations are all considered highly precise, even when calculated as the difference between the ML and auto landmarks.

The correlation between the ML and auto landmarks is extremely high

The variance of the Auto landmarks is on a whole MUCH smaller than the ML landmarks. This speaks well of the repeatability of the auto landmarking.

Don’t necessarily have accuracy on the rest of the face (i.e. the cheeks), but neither do manual landmarks.

## Usefulness of MeshMonk (previous and future uses)

MeshMonk gives us much more data than the automatic landmarking methods that have the purpose of estimating a sparse set of landmarks. Cite recent successes in GWAS of facial shapes, both clinical and non-clinical (Plos Genetics 2014, Nature Genetics 2018, Karlijne’s paper in this issue).

Opportunities for using MeshMonk on other surfaces besides faces (Harry?)

### Spatially dense quasi-landmarking of 3D facial scans

One of the possible applications of MeshMonk is spatially dense landmarking of 3D facial scans. This process involves the cleaning of 3D surface image to remove hair, ears, and any dissociated polygons. Five crude positioning landmarks are then placed on the face to establish a rough facial orientation, but not to guide the eventual landmark mask to the face. An anthropometric mask (Claes et al., 2012) is non-rigidly mapped (Snyders et al., 2014) onto all 3D surface images and their reflections, constructed by changing the sign of the *x* coordinate (Claes et al., 2011), using the MeshMonk software and parameters described in the methods. This establishes homologous spatially dense (~10,000) quasi-landmark (QL) configuration for all 3D surface images and their reflections. Facial shape can be symmetrized using generalized Procrustes alignment (Rohlf and Slice, 1990) to eliminate differences in position, orientation and size of both original and reflected quasi-landmark configurations. The average of an original and its reflected quasi-landmark configuration constitutes the symmetric component, while the difference between the two configurations constitutes the asymmetric component. Mahalanobis distance for each face to the overall average face in the symmetrized shape space can be used to detect registration outliers.

### Brains

### Skulls

### Femur

## Future improvements/issues with the algorithm

# Conclusion

# Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

# Author Contributions

JW performed validation analyses and landmarked the 3D scans used for validation with AZ. JW, AOC, and HM wrote the first draft of the manuscript under supervision of PC. PC and JW conceptualized the design of the study. OE, SVD, and MS provided input throughout the analyses and writing process. JS developed the MeshMonk code.

# Funding

# Acknowledgments

We thank the many participants who have volunteered their time over the years, without which we would have never been able to develop this software or perform the various research that this software has contributed to. We are also grateful to the all members of the Shriver and Claes Labs, as well as all the members of WebMonks, for their dedication and contributions to all aspects of this software, research, and manuscript.

# Ethics statement

Institutional review board (IRB) approval was obtained at all locations and all participants signed a written consent form before participation. The Pennsylvania State University IRB board approved the collection of the participants recruited at the following locations: State College, PA (IRB 44929 and 4320); New York, NY (IRB 45727); Urbana-Champaign, IL (IRB 13103); Dublin, Ireland; Rome, Italy; Warsaw, Poland; and Porto, Portugal (IRB 32341).

# References

Adams, D. C., and Otárola-Castillo, E. (2013). Geomorph: An r package for the collection and analysis of geometric morphometric shape data. *Methods Ecol. Evol.* 4, 393–399. doi:10.1111/2041-210X.12035.

Adams, D. C., Rohlf, F. J., and Slice, D. E. (2004). Geometric morphometrics: Ten years of progress following the ‘revolution.’ *Ital. J. Zool.* 71, 5–16. doi:10.1080/11250000409356545.

Aldridge, K., Boyadjiev, S. A., Capone, G. T., DeLeon, V. B., and Richtsmeier, J. T. (2005). Precision and error of three-dimensional phenotypic measures acquired from 3dMD photogrammetric images. *Am. J. Med. Genet.* 138 A, 247–253. doi:10.1002/ajmg.a.30959.

Altman, D. G., and Bland, J. M. (1983). Measurement in Medicine: The Analysis of Method Comparison Studies. *Stat.* 32, 307–317. doi:10.2307/2987937.

Andresen, P. R., and Nielsen, M. (2001). Non-rigid registration by geometry-constrained diffusion. *Med. Image Anal.* 5, 81–88. doi:10.1016/S1361-8415(00)00036-0.

Baab, K. L. (2008). The taxonomic implications of cranial shape variation in Homo erectus. *J. Hum. Evol.* 54, 827–847. doi:10.1016/j.jhevol.2007.11.003.

Bastir, M., Rosas, A., and O’Higgins, P. (2006). Craniofacial levels and the morphological maturation of the human skull. *J. Anat.* 209, 637–654. doi:10.1111/j.1469-7580.2006.00644.x.

Baynam, G., Walters, M., Claes, P., Kung, S., LeSouef, P., Dawkins, H., et al. (2014). Phenotyping: Targeting genotype’s rich cousin for diagnosis. *J. Paediatr. Child Health* 51, 381–386. doi:10.1111/jpc.12705.

Blanz, V., and Vetter, T. (1999). A morphable model for the synthesis of 3D faces. in *Proceedings of the 26th annual conference on Computer graphics and interactive techniques - SIGGRAPH ’99* (New York, NY: ACM Press/Addison-Wesley Publishing Co), 187–194. doi:10.1145/311535.311556.

Claes, P. (2007). A robust statistical surface registration framework using implicit function representations: application in craniofacial reconstruction. Available at: http://mic.uzleuven.be/download/public/MIC/publications/2967/PHD\_ pclaes.pdf.

Claes, P., Hill, H., and Shriver, M. (2014a). Towards DNA-based facial composites: preliminary results and validation. *Forensic Sci. Int.*

Claes, P., Liberton, D., Daniels, K., Matthes Rosana, K., Quillen, E., Pearson, L., et al. (2014b). Modeling 3D Facial Shape from DNA. *PLOS Genet.* 10, 1–14.

Claes, P., Roosenboom, J., White, J. D., Swigut, T., Sero, D., Li, J., et al. (2018). Genome-wide mapping of global-to-local genetic effects on human facial shape. *Nat. Genet.* doi:10.1038/s41588-018-0057-4.

Claes, P., Walters, M., and Clement, J. (2012). Improved facial outcome assessment using a 3D anthropometric mask. *Int. J. Oral Maxillofac. Surg.* 41, 324–330. doi:10.1016/j.ijom.2011.10.019.

Claes, P., Walters, M., Vandermeulen, D., and Clement, J. G. (2011). Spatially-dense 3D facial asymmetry assessment in both typical and disordered growth. *J. Anat.* 219, 444–55. doi:10.1111/j.1469-7580.2011.01411.x.

Collyer, M. L., Sekora, D. J., and Adams, D. C. (2015). A method for analysis of phenotypic change for phenotypes described by high-dimensional data. *Heredity (Edinb).* 115, 357–365. doi:10.1038/hdy.2014.75.

Corner, B. D., Lele, S., and Richtsmeier, J. T. (1992). Measuring Precision of Three-Dimensional Landmark Data. *J. Quantative Anthropol.* 3, 347–359.

Fagertun, J., Harder, S., Rosengren, A., Moeller, C., Werge, T., Paulsen, R. R., et al. (2014). 3D facial landmarks: Inter-operator variability of manual annotation. *BMC Med. Imaging* 14, 35. doi:10.1186/1471-2342-14-35.

Fisher, R. (1925). Statistical methods for research workers. *Biol. Monogr. Manuals*. doi:10.1056/NEJMc061160.

Frost, S., Marcus, L., Bookstein, F. L., Reddy, D., and Delson, E. (2003). Cranial allometry, phylogeography, and systematics of large-bodied papionins (Primates: Cercopithecinae) inferred from geometric morphometric analysis of landmark data. *Anat. Rec. Part A* 275A, 1048–1072. doi:10.1002/ar.a.10112.

Hammond, P., Hutton, T. J., Allanson, J. E., Buxton, B. F., Campbell, L. E., Clayton-Smith, J., et al. (2005). Discriminating Power of Localized Three-Dimensional Facial Morphology. *Am. J. Hum. Genet.* 77, 999–1010.

Hammond, P., McKee, S., Suttie, M., Allanson, J. E., Cobben, J.-M., Maas, S. M., et al. (2014). Opposite effects on facial morphology due to gene dosage sensitivity. *Hum. Genet.* 133, 1117–25. doi:10.1007/s00439-014-1455-z.

Havarti, K., Frost, S., and McNulty, K. (2004). Neanderthal taxonomy reconsidered: implications of 3D primate models of intra- and interspecific differences. *Proc. Natl. Acad. Sci. USA* 101, 1147–1152. doi:10.1046/j.1469-7580.2000.19710103.x.

Heike, C. L., Upson, K., Stuhaug, E., and Weinberg, S. M. (2010). 3D digital stereophotogrammetry: a practical guide to facial image acquisition. *Head Face Med.* 6, 18. doi:10.1186/1746-160X-6-18.

Hille, E. (1982). *Analytic Function Theory, Volume I*. Second edi. New York: Chelsea Publishing Company.

Houle, D., Govindaraju, D. R., and Omholt, S. (2010). Phenomics: The next challenge. *Nat. Rev. Genet.* 11, 855–866. doi:10.1038/nrg2897.

Hutton, T., Buxton, B., Hammond, P., and Unit, B. (2003a). Automated registration of 3D faces using dense surface models. in *British Machine Vision Conference*, eds. R. Harvey and A. Bangham (Norwich: Citeseer), 1–10. doi:10.5244/C.17.45.

Hutton, T. J., Buxton, B. F., Hammond, P., and Potts, H. W. W. (2003b). Estimating Average Growth Trajectories in Shape-Space Using Kernel Smoothing. *IEEE Trans. Med. Imaging* 22, 747–753.

Imaizumi, K., Taniguchi, K., Ogawa, Y., Matsuzaki, K., Nagata, T., Mochimaru, M., et al. (2015). Three-dimensional analyses of aging-induced alterations in facial shape: a longitudinal study of 171 Japanese males. *Int. J. Legal Med.* 129, 385–393. doi:10.1007/s00414-014-1114-x.

Kesterke, M. J., Raffensperger, Z. D., Heike, C. L., Cunningham, M. L., Hecht, J. T., Kau, C. H., et al. (2016). Using the 3D Facial Norms Database to investigate craniofacial sexual dimorphism in healthy children, adolescents, and adults. *Biol. Sex Differ.* 7. doi:10.1186/s13293-016-0076-8.

Klingenberg, C. P. (2010). Evolution and development of shape: integrating quantitative approaches. *Nat. Rev. Genet.* 11, 623–635.

Klingenberg, C. P. (2013). Evolutionary Covariation in Geometric Morphometric Data: Analyzing Integration, Modularity, and Allometry in a Phylogenetic Context. *Syst. Biol.* 62, 591–610. doi:10.1093/sysbio/syt025.

Klingenberg, C. P., Wetherill, L., Rogers, J., Moore, E., Ward, R., Autti-Rämö, I., et al. (2010). Prenatal alcohol exposure alters the patterns of facial asymmetry. *Alcohol* 44, 649–657. doi:10.1016/j.alcohol.2009.10.016.

Lele, S., and Richtsmeier, J. T. (1991). Euclidean distance matrix analysis: A coordinate‐free approach for comparing biological shapes using landmark data. *Am. J. Phys. Anthropol.* 86, 415–427. doi:10.1002/ajpa.1330860307.

Liu, F., van der Lijn, F., Schurmann, C., Zhu, G., Chakravarty, M. M., Hysi, P. G., et al. (2012). A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. *PLoS Genet.* 8. doi:10.1371/journal.pgen.1002932.

Martinez-Abadias, N., Gonzalez-Jose, R., Gonzalez-Martin, A., Van der Molen, S., Talavera, A., Hernandez, P., et al. (2006). Phenotypic evolution of human craniofacial morphology after admixture: a geometric morphometrics approach. *Am. J. Phys. Anthropol.* 129, 387–98. doi:10.1002/ajpa.20291.

Martinez-Abadias, N., Mitteroecker, P., Parsons, T. E., Esparza, M., Sjovold, T., Rolian, C., et al. (2012). The Developmental Basis of Quantitative Craniofacial Variation in Humans and Mice. *Evol Biol* 39, 554–567.

Matthews, H., Penington, A., Clement, J., Kilpatrick, N., Fan, Y., and Claes, P. (2018a). Estimating age and synthesising growth in children and adolescents using 3D facial prototypes. *Forensic Sci. Int.* 286, 61–69. doi:10.1016/j.forsciint.2018.02.024.

Matthews, H. S., Penington, A. J., Hardiman, R., Fan, Y., Clement, J. G., Kilpatrick, N. M., et al. (2018b). Modelling 3D craniofacial growth trajectories for population comparison and classification illustrated using sex-differences. *Sci. Rep.* 8. doi:10.1038/s41598-018-22752-5.

Mitteroecker, P., Gunz, P., Bernhard, M., Schaefer, K., and Bookstein, F. L. (2004). Comparison of cranial ontogenetic trajectories among great apes and humans. *J. Hum. Evol.* 46, 679–698. doi:10.1016/j.jhevol.2004.03.006.

O’Higgins, P. (2000). The study of morphological variation in the hominid fossil record: biology, landmarks and geometry. *J. Anat.* 197, 103–120.

Paternoster, L., Zhurov, A. I., Toma, A. M., Kemp, J. P., St. Pourcain, B., Timpson, N. J., et al. (2012). Genome-wide association study of three-dimensional facial morphology identifies a variant in PAX3 associated with nasion position. *Am. J. Hum. Genet.* 90, 478–485. doi:10.1016/j.ajhg.2011.12.021.

Quinto-Sánchez, M., Adhikari, K., Acuña-Alonzo, V., Cintas, C., Silva de Cerqueira, C. C., Ramallo, V., et al. (2015). Facial asymmetry and genetic ancestry in Latin American admixed populations. *Am. J. Phys. Anthropol.* 157, 58–70. doi:10.1002/ajpa.22688.

Richtsmeier, J. T., Baxter, L. L., and Reeves, R. H. (2000). Parallels of craniofacial maldevelopment in Down syndrome and Ts65Dn mice. *Dev. Dyn.* 217, 137–45. doi:10.1002/(SICI)1097-0177(200002)217:2<137::AID-DVDY1>3.0.CO;2-N.

Richtsmeier, J. T., Burke Deleon, V., and Lele, S. R. (2002). The promise of geometric morphometrics. *Am. J. Phys. Anthropol.* 119, 63–91. doi:10.1002/ajpa.10174.

Richtsmeier, J. T., Paik, C. H., Elfert, P. C., Cole III, T. M., and Dahlman, H. R. (1995). Precision, Repeatibility, and Validation of the Localization of Cranial Landmarks Using Computed Tomography Scans. *Cleft Palate-Craniofacial J.* 32, 217–227.

Rohlf, F. J., and Marcus, L. F. (1993). A revolution morphometrics. *Trends Ecol. Evol.* 8, 129–132. doi:10.1016/0169-5347(93)90024-J.

Rohlf, F. J., and Slice, D. (1990). Extensions of the Procrustes Method for the Optimal Superimposition of Landmarks. *Syst. Zool.* 39, 40–50. doi:10.2307/2992207.

Schlager, S., and Alexandra, R. (2015). Analysis of the Human Osseous Nasal Shape — Population Differences and Sexual Dimorphism. *Am. J. Phys. Anthropol.* 00. doi:10.1002/ajpa.22749.

Shaffer, J. R., Orlova, E., Lee, M. K., Leslie, E. J., Raffensperger, Z. D., Heike, C. L., et al. (2016). Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. *PLoS Genet.* 12, 1–21. doi:10.1371/journal.pgen.1006149.

Shaner, D. J., Peterson, A. E., Beattie, O. B., and Bamforth, J. S. (2000). Assessment of soft tissue facial asymmetry in medically normal and syndrome-affected individuals by analysis of landmarks and measurements. *Am. J. Med. Genet.* 93, 143–154. doi:10.1002/1096-8628(20000717)93:2<143::AID-AJMG12>3.0.CO;2-Q.

Smith, K. K. (2006). Craniofacial development in marsupial mammals: developmental origins of evolutionary change. *Dev. Dyn.* 235, 1181–93. doi:10.1002/dvdy.20676.

Snyders, J., Claes, P., Vandermeulen, D., and Suetens, P. (2014). Development and comparison of non-rigid surface registraion and extensions, Technical report KUL/ESAT/PSI/1401. Leuven, Belgium.

Starbuck, J. M., Reeves, R. H., and Richtsmeier, J. T. (2011). Morphological integration of soft-tissue facial morphology in Down Syndrome and siblings. *Am. J. Phys. Anthropol.* 146, 560–8. doi:10.1002/ajpa.21583.

Terhune, C. E., Kimbel, W. H., and Lockwood, C. A. (2007). Variation and diversity in Homo erectus: a 3D geometric morphometric analysis of the temporal bone. *J. Hum. Evol.* 53, 41–60.

Toma, A. M., Zhurov, A. I., Playle, R., Ong, E., and Richmond, S. (2009). Reproducibility of facial soft tissue landmarks on 3D laser-scanned facial images. *Orthod Craniofac Res* 12, 33–42. doi:10.1111/j.1601-6343.2008.01435.x.

von Cramon-Taubadel, N., Frazier, B. C., and Mirazon-Lahr, M. (2007). The problem of assessing landmark error in geometric morphometrics: Theory, methods, and modifications. *Am. J. Phys. Anthropol.* 134, 24–35. doi:10.1002/ajpa.

Walter, T., Shattuck, D. W., Baldock, R., Bastin, M. E., Carpenter, A. E., Duce, S., et al. (2010). Visualization of image data from cells to organisms. *Nat. Methods* 7, S26–S41. doi:10.1038/nmeth.1431.

Wei, R., Claes, P., Walters, M., Wholley, C., and Clement, J. G. (2011). Augmentation of linear facial anthropometrics through modern morphometrics: A facial convexity example. *Aust. Dent. J.* 56, 141–147. doi:10.1111/j.1834-7819.2011.01315.x.

Weinberg, S. M., Scott, N. M., Neiswanger, K., Brandon, C. A., and Marazita, M. L. (2004). Digital three-dimensional photogrammetry: Evaluation of anthropometric precision and accuracy using a Genex 3D camera system. *Cleft Palate-Craniofacial J.* 41, 507–518. doi:10.1597/03-066.1.

Wong, J. Y., Oh, A. K., Ohta, E., Hunt, A. T., Rogers, G. F., Mulliken, J. B., et al. (2008). Validity and reliability of craniofacial anthropometric measurement of 3D digital photogrammetric images. *Cleft Palate-Craniofacial J.* 45, 232–239. doi:10.1597/06-175.

# Data Availability Statement

The informed consent with which the data were collected does not allow for dissemination of identifiable data to persons not listed as researchers on the IRB protocol. Thus, the full surface 3D facial images used for validation cannot be made publicly available. In the interest of reproducibility, we have provided the 19 manual and automatic landmarks used for validation as well as the code used to analyze them. These data are available in the following GitHub repository: https://github.com/juliedwhite/RemappingValidation/. The MeshMonk code and tutorials are available at https://github.com/TheWebMonks/meshmonk.