# 3D quantification of mandibular asymmetry using the SPHARMPDM tool box 

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#### Abstract

Purpose-Pretreatment diagnosis of mandibular asymmetry in orthognathic surgery patients can be improved by quantitative shape modeling and analysis. The UNC SPHARM-PDM (University of North Carolina Spherical Harmonics-Point Distribution Model) toolbox was applied to a cohort of patients and the results were evaluated.

Methods-Three-dimensional (3D) virtual surface models are constructed from CBCT scans of each patient in the cohort by segmentation. Mirroring on a sagittal arbitrary plane is used to flip the left and right sides of each image. An automatic voxel-based registration on the cranial base is used to align the volume and its mirror for comparison. SPHARM-PDM is used to compute correspondent models for each hemimandible and the mirror of the contralateral side. Procrustes analysis was used to evaluate discrepancies between each pair of models to assess asymmetry. Mandibular asymmetry was also located and quantified by computing corresponding surface distances between each hemimandible (left and right sides) and the mirror of the contralateral side.

Results-There were no statistically significant differences in surrogates for mandibular asymmetry assessment based on right or the left side mirroring. Those surrogates are the rotational and translational differences between each hemimandible and the mirror of the contralateral side in 3 planes of space (the absolute values of Procrustes registration output in 6 degrees of freedom). Absolute and signed distance maps between each hemimandible and the mirror of the contralateral


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side located and quantified areas of asymmetry diagnosis for each patient. Even though mandibular condyle asymmetry was observed in $8 \%$ of the cases and mandibular asymmetry along areas of the ramus and mandibular corpus was noted in $17.8 \%$ of the cases, the remaining $74.2 \%$ showed generalized morphological and positional asymmetry at the condyle, the ramus and mandibular corpus.

Conclusion-Three-dimensional diagnosis of mandibular asymmetry revealed the complex involvement of morphological components of the mandible and the heterogeneous nature of this clinical condition. SPHARM-PDM has a promising role in the individual diagnosis and quantification of mandibular asymmetry.

## Keywords

Mandibular asymmetry; Shape correspondence; SPHARM-PDM; Statistical shape analysis

## Introduction

Treatment planning and assessment of the surgical correction of asymmetrical deformities are limited by reliance on 2D radiographs in the current clinical setting. The 2D radiographs conventionally used in orthodontic practice are particularly problematic when rotational or asymmetrical correction is required since surgical jaw displacements are inherently three dimensional. Clinical examination and frontal radiographs detect gross asymmetries; however, for treatment planning purposes, localization and quantification of the asymmetry are required. In 2D frontal head radiographs, the anatomic structures are overlapped.
Additionally, frontal X-rays are very dependent on geometry and can give false measurements of the location, extent, and severity of mandibular asymmetry.

The use of cone-beam computed tomography (CBCT) or spiral computer tomography (CT) provides the 3D imaging data necessary to generate precise knowledge of the location and the magnitude of facial asymmetry features, which are essential for the diagnosis of facial deformities and for the planning of corrective procedures. An increasing number of studies have demonstrated that computer-aided surgical simulation (CASS) can predict possible surgical complications and lowers material costs while decreasing surgery duration, with comparable or better surgical outcomes [1-3]. However, the ability to visualize the facial asymmetry in 3D surface models does not imply the ability to quantify and precisely locate areas of asymmetry. Detailed analysis of positional as well as morphological discrepancy between the affected side and the normal side in an asymmetric patient is a prerequisite for ideal treatment planning.

Shape analysis has become of increasing interest to the medical image analysis community due to its potential to precisely locate and quantify morphological changes between healthy and pathological structures. As part of the National Alliance for Medical Image Computing (http://www.na-mic.org), the Neuro-Image Research and Analysis Lab (NIRAL) at the University of North Carolina developed a comprehensive set of tools for the computation of 3D structural statistical shape analysis that have been mostly used for brain morphometry studies.

The shape correspondence framework selected for this study is SPHARM-PDM toolbox, which presents a comprehensive set of tools for the computation of 3D structural statistical shape analysis [4]. In summary, the SPHARM description is a hierarchical, global, multiscale boundary description that can only represent objects of spherical topology, proposed initially by Brechbuhler et al. [5]. This SPHARM shape analysis approach was further developed (SPHARM-PDM, PDM stands for Point Distribution Models) and extensively used for applications in neuroimaging [6,7].

In previous work we established the accuracy of SPHARM-PDM to quantify the direction and degree of simulated known amounts of mandibular asymmetry [8]. The objective of the work presented in this manuscript is the clinical application of this technology to assess mandibular asymmetry in a cohort of patients with a previous clinical diagnosis of mandibular asymmetry.

## Materials and methods

The cohort consisted on 45 pretreatment CBCT scans from patients that sought care at our Dentofacial Deformities Program and consented to participate in the project. This project was approved by a university committee for research on human subjects. These scans are part of a bigger sample of consecutive prospectively collected images, collected in the grant "Improving Treatment Outcomes for Patients with Facial Deformity using 3D Imaging". Inclusion criteria for our study were patients with clinically detectable asymmetry, defined as more than 2 mm of chin deviation or cant of the occlusal plan before the start of their orthodontic treatment. Exclusion criteria were history of previous jaw surgery and patients who required reconstructive surgery, as graft planning. Figure 1 shows an overview of the methodological framework.

## Image acquisition

New Tom 3G Cone-beam CTs (AFP Imaging, Elmsford, NY) with the patient in supine position were obtained prior to orthodontic treatment.

## Construction of virtual 3D models from the CBCT dataset

Segmentation involved outlining of the shape of structures visible in the cross-sections of a volumetric dataset in the CBCT-3D images. Segmentation of anatomic structures was performed using ITK-SNAP (open-source software, http://www.itksnap.org) [9]. 3D virtual models were built for each patient from a set of $\sim 300$ axial cross-sectional slices for each image with the image voxels reformatted for an isotropic resolution of $0.5 \mathrm{~mm} \times 0.5 \mathrm{~mm} \times 0.5 \mathrm{~mm}$. This resolution was used because higher spatial resolution with smaller slice thickness would have increased image file size and required greater computational power and user interaction time. After segmentation with ITK-SNAP tool, a 3D graphic rendering of the volumetric object allowed navigation between voxels in the volumetric image and the 3D graphic representation with zooming, rotating, and panning.

## Mirroring and cranial base registration

Each model was mirrored on an arbitrary sagittal plane. The mirroring is done by arbitrarily converting the image orientation from (Right-Left, Antero-Posterior, and Infero-Superior) to (Left-Right, Antero-Posterior, and Infero-Superior). The original and the arbitrarily mirrored images were then registered on the cranial base. The registration was accomplished using IMAGINE software (National Institutes of Health, Bethesda, MD; Open-source, http:// www.ia.unc.edu/dev/download/imagine/index.htm) consisting on a voxel-based registration method. This method utilizes maximization of mutual information to avoid the problems associated with observer-dependent techniques. After the software masks the maxillary and mandibular structures, it compares the gray-level intensity of each voxel in the cranial base to register the two CBCT images. The rotation and translation parameters that are used to register the two gray scale images are also applied to register the 3D surface models (Fig. 2).

Cranial base registration is important since it provides information of the mandibular asymmetry relative to the face. Asymmetry was defined as the difference between each hemimandible and the mirror of the contralateral side.

Before computing correspondent point-based models using SPHARM-PDM, spherical topology of the models must be assured, which is achieved with the following preprocessing steps. In order to simplify the ridges and waves of the hemimandibular segments, a Laplacian smoothing procedure was applied to each hemimandible. Then, a binary segmentation volume is created again from the surfaces. This was done via finding the enclosing bounding box of the shape and binarizing the cross-sections. These binary segmentation volumes are the input of the SPHARM-PDM framework.

## SPHARM-PDM shape correspondence and Procrustes alignment

The UNC SPHARM-PDM shape analysis toolbox was employed to compute unique correspondent point-based models of all the hemimandibular surfaces per patient.

The segmented 3D surface models of the hemimandibles are first converted into surface meshes, and mapped into the unit sphere using an area-preserving and distortion-minimizing spherical mapping. The SPHARM description is computed from the mesh and its spherical parameterization. Using the first-order ellipsoid from the spherical harmonic coefficients, the spherical parameterizations are aligned to establish correspondence across all surfaces. The SPHARM description is then sampled into triangulated surfaces (SPHARM-PDM). Alignment of all surfaces was performed using rigid Procrustes alignment. This rigid Procrustes alignment procedure computes an optimal linear, geometric transformation $\phi(n)$ that best maps the shape changes between the affected hemimandible and the mirror of the opposite healthy side based on the established correspondence [10].

A preliminary analysis is computed by subtracting the models of each hemimandible and the mirror of the contralateral side and displayed via color-coded distance magnitude and vector maps. Vector maps provide visualization and quantification of distances between paired correspondent point-based models, indicating the direction and magnitude of each side and the mirrored side discrepancies. Figure 3 shows an example of this analysis. Procrustes was
used to capture translational and rotational differences between each hemimandible and the mirror of the contralateral side in the three planes of space.

Results
The average and standard deviation of translational differences in mm and the rotational differences in degrees between original hemimandible and the hemimandible mirrored in the contralateral side calculated with Procrustes alignment are displayed in Table 1. No statistically significant difference was observed in the absolute values of Procrustes output based on whether the right or the left side of the mandible is being mirrored. This demonstrates the consistency of Procrustes in evaluating mandibular asymmetry.

Location of mandibular asymmetry was heterogenous in this sample; however, $8 \%$ of the cases showed characteristic larger asymmetry surface distances at the condyles, while $17.8 \%$ presented more marked mandibular body and ramus asymmetry. Most patients ( $74.2 \%$ ) exhibited generalized asymmetric mandibular morphology with the involvement of both condyle ramus and corpus (Fig. 4).

Most detected asymmetries in this cohort had translational component in the medio-lateral followed by the cranio-caudal direction. These differences ranged from 0.03 to 9.05 mm with a mean of $(1.76 \pm 1.99) \mathrm{mm}$, and $0.05-6.86 \mathrm{~mm}$ with a mean of $(0.80 \pm 1.36) \mathrm{mm}$, respectively. As for the rotational component,bigger changes were detected in the yaw followed by the roll then the pitch of those hemimandible. Differences in the yaw ranged from 2.54 to 10.37 degrees with a mean of $(2.54 \pm 2.14)$ degrees while those of the roll and pitch ranged from 0.17 to 10.19 degrees with a mean of ( $2.57 \pm 2.11$ ) degrees, and 0.08-6.2 degrees with a mean of $(2.38 \pm 1.72)$ degrees.

## Discussion

Most commercially available and academic software that are able to compute color-coded surface maps use closest point algorithm to obtain surface distances. Closest point is a brute force algorithm that calculates a vertex-to-vertex Euclidean closest point distance [11,12]. This method does not map corresponding surfaces based in anatomical geometry, and thus, it usually underestimates rotational and large translational movements.

The application of conventional closest point distances for mirror images in mandibles of patients with rudimentary condyles, severe cants, or a rotated mandible does not represent the difference between corresponding anatomical locations, but rather differences based in the minimal distances between any point in the original and mirrored models. These clinical situations mandate the use of a more "anatomy sensitive" shape analysis technique.

Shape correspondence is a promising alternative to overcome the shortcomings of the commonly used closest point algorithm. It is one of the currently used statistical shape analysis techniques that allows measuring the surface distance between an area on one model to the corresponding anatomical area in the other model regardless the alignment of those models. The main shape correspondence challenges involve the representation of a population by means of correspondent point-based models. Surface representation could be accomplished by several different options including, matching of template surface geometry (curvature and location) [13], entropy-based Particle Systems [14], or by Spherical harmonic representation (SPHARM) [6]. In SPHARM the surface model gets mapped in a sphere, and correspondence point-based models are computed after finding the spherical harmonic basis that best fits the model. After surface mapping is achieved, correspondence could be based on different frameworks depending on the clinical problem on hand.

SPHARM-PDM allows for comprehensive statistical evaluations to be computed for the correspondent models as a whole or for specific regions of interest within these models. For asymmetry assessment and future treatment planning, an individual-based analysis was chosen in this project when compared to group analysis. Group analysis is usually used to examine general trends and cross-sectional tendencies, both those will be of limited utility to a "patient per patient" treatment planning approach.

To maximize the usefulness of the extensive data that SPHARM-PDM can provide, regions of interest that correspond to surgical segments could be analyzed separately (Fig. 5). This quantitative asymmetry measure could either be communicated to the surgeon or used as an input for surgical simulation software.

The translational and rotational differences between mandibular halves as measured by Procrustes are an accurate representation of the location component of mandibular asymmetry; however, in patients with marked morphological differences between both hemimandibles, grafting andlor reshaping procedures might be needed. In these cases, pure shape analysis after accounting for positional differences is a better approach.

While this study applied shape analysis to a pretreatment assessment of mandibular asymmetry, future investigations are needed to apply the preliminary findings in this study to presurgical treatment planning and surgical simulation of corrective surgeries of patients with complex asymmetries.

## Conclusion

SPHARM-PDM has a promising role in individual diagnosis and quantification of mandibular asymmetry. Three-dimensional diagnosis of mandibular asymmetry revealed the complex involvement of morphological components of the mandible and heterogeneous nature of this clinical condition.

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Fig. 1.
After segmenting hard tissue (a), the image volume and segmentation models were mirrored by flipping left and right sides and then registering the mirrored image onto the cranial base (b). Quantification of mandibular asymmetry for a patient is done using SPHARMPDM shape analysis (c). Original model white and left hemi-mandible arbitrary mirror matching on the cranial base yellow. Shape analysis is used to quantify right and left differences by computing vector maps, absolute surface distance maps and signed surface distance maps of the differences between the original and arbitrary mirrored models (both registered in the cranial base). Signed distances color maps show the directionality of the differences


Fig. 2.
Arbitrary plane mirroring followed by cranial base registration: cranial base virtual surface model for a patient white and arbitrarily mirrored image model purple before registration in (a); the original model and arbitrary mirror matching on the cranial base as a result of a voxel- based registration (b); in cacor map of the surface distance between the registered original and arbitrary mirror models shown at 0 mm surface distances green


Fig. 3.
An example of 3D analysis for a patient in the cohort: clinical photographs are shown in $\mathbf{A}$. Note the maxillary cant in $A .1$, the discrepancy in dental midline $A .2$, the deviation of the chine to the left in A. 3 and A.4; Group $\mathbf{B}$ represents hard tissue surface models of the same patient. $B .1$ is a frontal view, $B .2$ is a SMV view, $B .3$ and $B .4$ are the same views, respectively also showing the mirror of the mandible registered on the cranial base (Mirror model in maroon); In $\mathbf{C}$ is 3D analysis color maps of the right side of the mandible in relation to the mirror of the left half of the mandible, Vector maps are shown in C.l and signed distance maps shown in C. 2


Fig. 4.
Examples of patients from the cohort with mandibular asymmetry mostly localized to the condyle (row $\mathbf{a}$ ), or in the ramus body of the mandible (row $\mathbf{b}$ ), examples of generalized mandibular asymmetry are shown in (row c)


Fig. 5.
ROI analysis: a hard tissue surface model for a patient showing the mirror of the left mandible registered on the cranial base (Mirror model in maroon), in $\mathbf{b}$ vector and surface distance maps of the right side of the mandible in relation to the mirror of the left half of the mandible. Vector maps computed for specific regions of interest (lateral pole of the condyle and lateral surface of the ramus) are shown in (c)

Table 1
The average and standard deviation of translational differences in mm and rotational differences in degrees between the left heminadible and the mirror of the right side (_Left) and between the right side and the mirror of the left (_Right)

|  | Tx_Left | Tx_Right | Tz_Left | Tz_Right | Rx_Left | Rx_Right | Rz_Left | Rz_Right |
| :--- | ---: | ---: | ---: | ---: | :--- | :--- | :--- | :--- |
| Average | -0.89 | -0.91 | -0.33 | -0.01 | 2.28 | 2.33 | 2.36 | 2.54 |
| SD | 2.47 | 2.51 | 1.94 | 1.80 | 1.79 | 1.73 | 2.03 | 2.14 |
| $P$ value |  | 0.72 |  | 0.55 | 0.62 |  | 0.11 |  |

Notice the non-significant $P$ value between the 2 sides. $X$ is in medio-lateral and $Z$ is in cranio-caudal direction. Readings from the anterioposterior are not included since this plane is irrelevant for asymmetry assessment


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