An atlas of modern human cranial morphology constructed via non-rigid deformation analysis of high-resolution CT images

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Abstract

Comparative studies of skeletal morphology are only as good as the quality of the comparison sample. Comparisons made to a limited sample, or one that has unrecognized biases, can compromise the conclusions. A standardized atlas representing average morphology - and incorporating information about localized variation - is of obvious usefulness to the field. We present a method for constructing such an atlas using non-rigid deformation analysis of high-resolution CT images. The technique involves morphing CT images of crania into an arbitrarily selected target image. Distortion matrices that describe how each individual image differs from the target are then used to estimate the morphological average of all the images. The individual images are then remorphed into this average, and a new average is calculated. The process is repeated until subsequent iterations do not change. Variation at each point across the sample can be determined from this data, allowing for detailed global statistical analyses of the difference between an individual (e.g., a fossil) and the population average at each point. Beneficial qualities of this approach include: 1) additional specimens can easily be added, increasing the sample pool used to estimate the population average; 2) external and internal structures (e.g., endocranial surface) are automatically included; 3) sub-population comparisons can easily be made by appropriate subdivisions of the resulting distortion matrices. We demonstrate the technique with a pilot study of images of crania obtained from the Open Research Scan Archive at Penn, including 10 individuals from India, 10 from Africa, and 9 from Asia.

Problem

Crania represent highly complex 3D shapes. Assessing similarity or difference in shape between crania or sets of crania is important for comparative evolutionary studies.

- How might one determine the average cranial shape for a population?
- How might one determine differences in shape between populations, or between individual and a population of interest?

Goals

- Demonstrate a method for deriving a 3D volume representing the average shape of a given set of crania
- Describe differences between sub-population averages or individual crania on a voxel-by-voxel basis

Methods

Estimating global average cranial shape

Step I: determine average cranial size and shape for each geographic area:

1) create initial target image (crude overlay average of all individuals)
2) morph each individual separately into target image
3) calculate new average target image (shape distance minimizing update of the template based on the transformation matrices calculated in step 2)
4) repeat steps 2 and 3 until target image does not change (about 3 iterations)

Step II: determine global average cranial size and shape (GLOBALtemplate) from geographic area averages (apply procedures from Step I to geographic area averages derived in Step I)

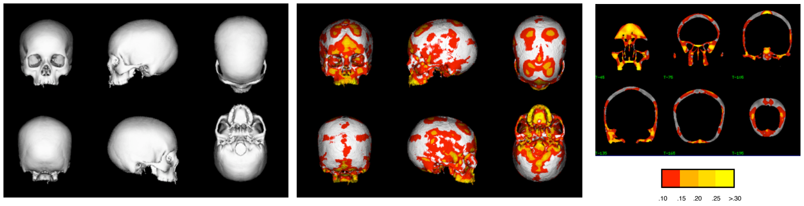
Step III: determine range of variation around the GLOBALtemplate (derived in Step II) among all individuals for each variable

1) morph each individual separately into GLOBALtemplate
2) calculate localized measures of difference between GLOBALtemplate and each individual. Specifically: Jacobians, which represent localized scaling factors at each point (voxel) in 3D space necessary to map GLOBALtemplate to an individual (log transformed so their values are symmetrical around 0)
3) calculate standard deviations of log Jacobians
4) map these measures of individual variation onto GLOBALtemplate

Once this is done, one can:

- Statistically assess population differences (voxel-by-voxel)
- Statistically assess individual differences (including fossil specimens) from GLOBALtemplate (voxel-by-voxel)
- Update and refine the GLOBALtemplate as additional scans are obtained

Derived Global Average



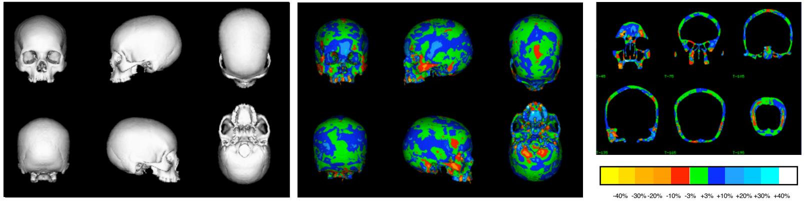
Average Shape

Jacobian Standard Deviations

Coronal Views of Jacobian Standard Deviations

Derived Geographic Population Averages

African

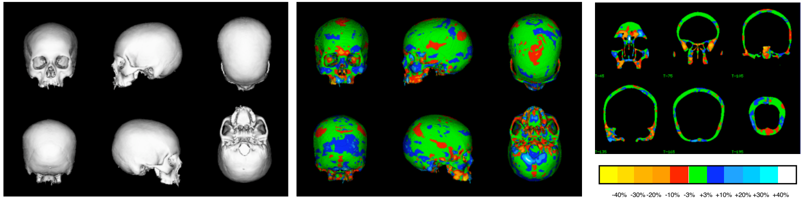


Average Shape

Jacobian Differences from Global Shape Average

Coronal Views of Jacobian Differences

Indian

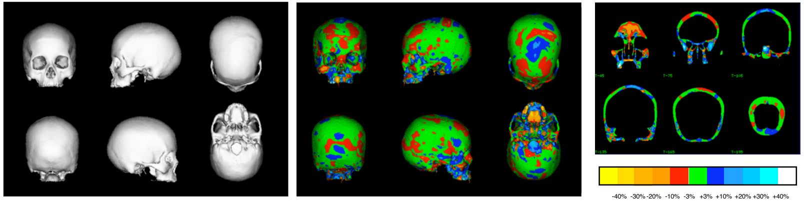


Average Shape

Jacobian Differences from Global Shape Average

Coronal Views of Jacobian Differences

Asian



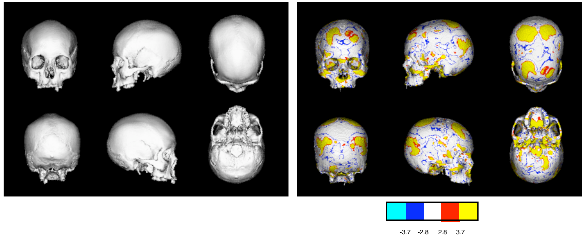
Average Shape

Jacobian Differences from Global Shape Average

Coronal Views of Jacobian Differences

Comparison of an Individual Specimen to the Global Average

Individual
Asian
Specimen



3D rendering

t-values of differences from Global Average Shape

Morphing

For each image, the following transformations were calculated:

1) rigid alignment: determine the rigid transformation needed to align the morphing image with the target atlas image in 3D space
2) affine transformation: determine the optimal compression/expansion of the along each of the X, Y and Z axes of the morphing image such that it matches as closely as possible the target atlas image
3) diffeomorphic transformation: determine the localized distortions of the morphing image needed such that it matches the target atlas image.
4) combine the transformations calculated in steps 2 and 3
5) calculate the localized scaling factors at each point (voxel) in 3D space implied by the combined transformations: specifically, determine the Jacobians of the matrix of partial derivatives of the vector functions describing the necessary transformations at each voxel of the target atlas

These steps create, for each subject crania, a new image, identical in shape to the target atlas, for which each voxel represents the localized distortion needed to map the target atlas cranium into a given individual subject's cranium.

All the algorithms used for this study are implemented in ANTS (**A**dvanced **N**ormalization **T**ool**s** - Open Source Tools for Normalization and Neuroanatomy). This software is freely available from http://www.picsl.upenn.edu/ANTS/

Benefits of this approach

- Derives an average cranium for a given set of individual crania
- Results in a 3D volume that can be shared, measured, and compared, easily and widely.
- Allows for statistical tests on a voxel-by-voxel basis, either of differences between populations or differences between an individual and a given population (e.g., a fossil specimen compared to modern humans).

Specimens Used

African
1 South African (female aged 40)
1 Liberian (female aged 30)
1 Malagasy (male aged 40)
1 West African (male aged 40)
6 African (unknown location; 3 females aged 30, 2 males aged 30-40, 1 unknown age and sex)

Indian
7 Bengal (3 female aged 25-30, 4 male aged 30-40)
3 Indian (unknown location; 2 female aged 40, 1 male aged 40)

Asian
4 Chinese (3 males aged 25-30, 1 female aged 40),
2 Japanese (females aged 30-40),
2 Siberian (Tchuktchi; females aged 40-45),
1 Thai (unknown age and sex)

All specimens obtained from ORSA (Open Research Scan Archive at Penn):
http://jmonge01.anthro.upenn.edu/~ctdatabase/pennct/

Literature Cited

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