

# **Ontogenetic Shape Variation in the Facebase 3D Facial Norm Data**

The 3D Facial Norms project "spoke" of Facebase has two major goals; 1) create a large, publicly available data and 2) use the data contained therein to identify specific genes and pathways that influence midfacial phenotypic variation. This poster displays a preliminary, non-exhaustive geometric morphometric examination of the facial norm phenotypes as the sample approaches 1,000 subjects. The left column presents a series of descriptive statistics about the current make up of the sample including the gross size and shape variation within the sample. The middle column describes the landmarks used for rest of the analyses and what kinds of shape variation separates the different age groups in the sample after a correction for allometry. The last column takes the a closer look at the age groups and each box tests whether or not sexual dimorphism is present in the three age groups even after allometry is removed.

### Summary Statistics

Sample Size: 931 (Female n = 563; Male n = 368) Youngest Age: 3.1 Oldest Age: 40.7 Mean Age: 23.2 Median Age: 24.1 Number of Landmarks Collected: 24 three dimensional landmarks Total Number of Shape Data Variables Analyzed: 67,032



These two principal component (PC) scatter plots paint the picture of the nature of the shape variation in the sample. Each dot on the graph represents the shape of one individual in the sample; the shape variables have not been corrected for any covariate. The life stage of the subjects in the left plot have been identified by color; the first PC somewhat teases the groups apart with mature subjects on the right, juveniles on the left and adolescents in between (though largely overlapping with both). The 90% frequency ellipses show the general pattern of overlap between the groups. The scatter plot on the right is color-coded by sex; the sexes only show mild separation tendencies on PCs 3 and 7. The ellipses in the center represent the 85% confidence interval of the means for each sex.

#### Does size explain these trends in the overall variation?



Centroid size (CS) predicts a significant amount of the variation captured by the first PC, 41.6% (p-value < 0.0001, pooled w/in group by sex, plot on left). While significant, it shows that are other factors causing facial shape differences between age groups. CS also only predicts 5.56% of the shape variation that separates the sexes (p-value < 0.0001, pooled w/in \group by age, plot on the right).

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#### Landmarks



## The Shape, Whole Shape and Nothing but the Shape...



## Ch-ch-ch-changes...



This plot shows the 2 canonical variates (CV) from a comparison of shape variation between age groups. The adult subjects are separated from the younger groups along the CV1 and the juveniles and adolescents separate along the CV2. The shapes corresponding to each CV are displayed on the sides of the plot and Procrustes distances between group means and corresponding p-values are in the upper right hand corner.

The figure on the left displays the 24 landmarks used in the geometric morphometric analyses presented on this poster. These landmarks include: nasion, pronasale, subnasale, labiale superius, stomion, labiale inferius, sublabiale, gnathion, left/right (l/r) endocanthion, I/r exocanthion, I/r alare, I/r alar curvature point, l/r subalare, l/r crista philtri, l/r chelion and l/r tragion. These same landmarks were also used to create the 'morphs' in the ensuing analyses. All analyses were performed using MorphoJ 1.04a and morphs were created in Landmark 3.0.0.6.

From the previous regression of the first PC on CS, we know that the size differences in the sample are very large and are likely overwhelming other types of shape variation. In order to be able to look beyond the variation differences that are due to size-related shape (aka allometry - a whole field os study unto itself) we need to remove that variation. One way to do that is use a multivariate regression of total shape on CS. The scatter plot to the left shows this variation. CS predicts 11.53% of the total variation in the sample (which consists of individuals ages 3 - 40) with a pvalue < 0.0001 after a X10000 permutation tests. The rest of the analyses presented below and to the right of this column will use the residuals of this regression and so are testing shape not related to size.

**Procrustes Distances:** Juvenile-Adult: 0.018, p<0.0001 Adolescent-Adult: 0.02, p<0.0001 Juvenile-Adolescent: 0.013, p=0.0017





