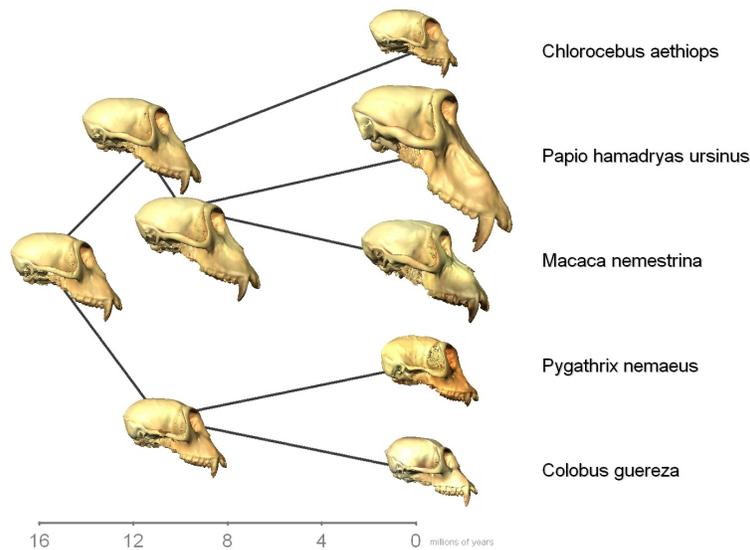# EVOLUTIONARY MORPHING:
STATISTICAL INTERPOLATION OF ANCESTRAL
MORPHOLOGY ALONG AN EVOLUTIONARY TREE

This entry is an interim report on a collaborative research project to visualize and analyze how skull shape has changed during evolutionary history. Here we use the Old World monkeys as an example. In this study, we combine research in genetics, anatomy, paleontology, biostatistics and computer science to reconstruct the shape of the skull in inferred intermediate ancestors along an evolutionary tree. Rather than simply morphing graphically between two shapes, this work uses a statistical model of evolutionary change to calculate average shape information from 3D laser scans of actual skulls.

Our work is a truly collaborative effort among researchers at eight institutions. In response to an NSF initiative to encourage computer scientists to team with other researchers to solve problems in the latter's discipline, in December we submitted a research grant application to undertake this study over three years. During the spring, we prepared a video to illustrate this planned study and then submitted it to this competition in late May. In mid-June, we were awarded a research grant for $1.1 million to carry out the full research project.

The purpose of this video is to document our approach and visualize the results we have obtained to date. This is not a demonstration of a specific event or visualization of a repeated occurrence. Instead, it is a snapshot of ongoing research, the first of its kind to use a large sample of virtual skulls as a database. We show 3D images of what may have been the intermediate ancestral conditions in morphological evolution; our next step is to test them against known fossils of the same group.

In this example, we use monkey skulls (actually crania, as we don't include the lower jaw), but our approach is equally applicable to dinosaur legs or snail shells, if an accurate evolutionary tree can be developed.

Here, we have built a tree (or cladogram) from mitochondrial (and some nuclear) DNA data on living monkey species. A molecular clock model permits the estimation of branching dates of the lineages leading to each living form. We wish to visualize (and then statistically compare and study) the intermediate forms along this tree, both at the branching points or nodes and between them. In effect, the shapes at the nodes represent an approximation of the form of the common ancestor of all the species (living and extinct) along the lineages more recent than ("descending from") these nodes.

We begin with high-resolution laser surface scans with an accuracy of under 0.5 mm. The Generalized Procrustes Analysis, which forms the heart of the statistical method, is an accurate way to retain the geometric relationships among landmarks on an object– it preserves shape information while removing the effects of differences in position and orientation (and adjusting for differences in size); our landmark editing program permits the precise location of landmarks on virtual images; the squared-change-parsimony model of evolutionary change allows all data to affect the interpolated shape but gives greatest weight to the shapes of those species temporally closest to the intermediate form being reconstructed. We realize that this is not a completely accurate model of real evolutionary change, but it is relatively easy to calculate and provides an approximation which can be tested and refined as our work progresses. Moreover, we will be combining our laser scan data (mainly of single individuals) with sets of 3D landmark points collected with a digitizer on much larger samples (many individuals) as part of prior research.

Previous modeling of ancestral morphology has almost invariably been based on interpretations of possible evolutionary pathways deduced by reconstructing how sets of anatomical characteristics have evolved. In contrast, our work is innovative in applying the tools of computer visualization to solve problems in the biostatistical analysis of evolutionary morphology, based on known anatomical shapes. No previous work has produced 3D visualizations of ancestral skeletal form, much less in a statistically rigorous manner. Moreover, our evolutionary framework incorporates the most recent DNA results on the relationships among and calculated ages of branching points between living monkey species. Finally, by incorporating the fossils themselves in the calculation of interpolates, we will further improve the reliability of our reconstructions through successive approximation. Many fossils are partially distorted by damage close to the time of death or by pressure in the ground afterwards; another aspect of this project is to virtually "undeform" such specimens so that they can be included in our analysis.

The video entry for the AAAS/NSF Scientific Visualization Competition was produced under the direction of Dr. David F. Wiley[1,2] (who also narrated). The overall project is a collaboration directed by Professors Nina Amenta[1,2] (computational graphics and visualization), Eric Delson[4,5,6,7,8] (primate morphology and evolution), and F. James Rohlf[3,4,5,6] (statistical biology), with the assistance of Professors Bernd Hamann[1,2] and Katherine St. John[5,6,9]. Additional colleagues and their areas of competence include: Mr. Dan Anthony Alcantara[1,2], Mr. Yong J. Kil[1,2] and Ms. Deboshmita Ghosh[1,2] (Graphics Software and Video Production); Drs. Will Harcourt-Smith[6,8], Steven Frost[6,10], Alfred L. Rosenberger[4,5,6,11] and

Ms. Lissa Tallman[4,5,6,7] (Primate Morphology, Evolution and Data Collection). Molecular Phylogeny courtesy of Professor Todd Disotell[5,12].

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