

Visualizing the Evolution of Horned Lizards Using 3D Morphing Techniques

Reuben Reyes¹, Wendy Hodges², Kelly Gaither¹

Introduction

Reconstructing the evolutionary history of diverse species is a basic goal of systematic biology and is essential to comparative biology. Phylogenies representing this history are constructed from the analyses of molecular or morphological data and used as tools for understanding the evolution of complex traits. Objectives of this research are to create visualization tools that dynamically reconstruct horn morphology in three-dimensions (3D) for horned lizards and show how changes occur along a phylogeny via metamorphosis (morphing). These objectives will be met by incorporating results from phylogenetic analyses with ancestral trait reconstructions applied to 3-D images generated from a high-resolution x-ray computed tomography (CT) scanner. Ancestral reconstruction algorithms are incorporated with nonlinear morphing to accommodate different rates of change along and between lineages. The application of 3-D morphing to systematics and ancestral reconstruction is a novel approach in visualization methods and opens a new realm of collaborative learning and discovery. We believe these tools will provide a greater understanding of how complex traits have evolved by allowing scientists to peer into the past, to see what ancestral states look like, and to visualize changes through time.

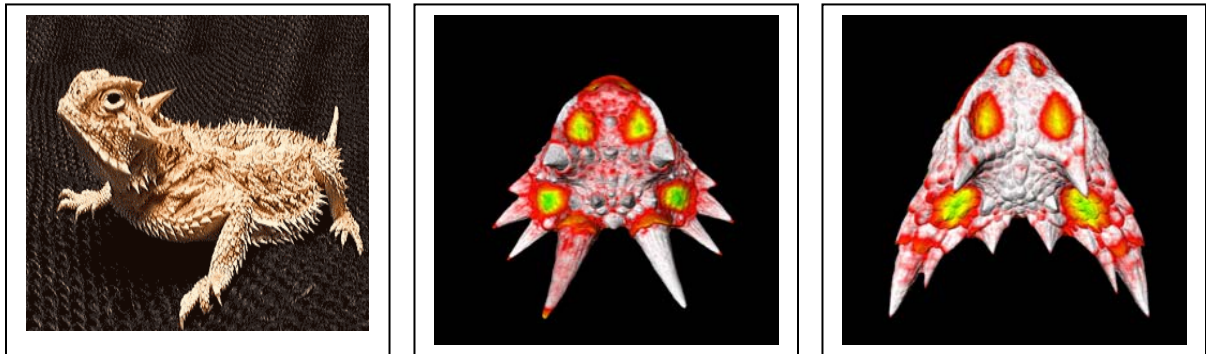


Figure 1: The Texas Horned Lizard and rendered images of the CT scans of the Texas and Mexican Horned Lizards.

3D Morphing

Morphing is a dynamic process that allows the visualization of the transformational changes from one form to another in real time. The morphing for this project was applied to 3D CT data to visualize the morphological changes in two lizard species. Figure 1 shows rendered images of the Texas Horned Lizard in the middle and the Mexican Horned Lizard on the right. In order to accommodate different evolutionary rates, a table of time curves was used to morph sets of traits between two end-state forms. This table

¹ Texas Advanced Computing Center, The University of Texas at Austin

² University of California at Riverside

ties control points on the morphology of different species corresponding to homologous traits and allows the research to set different time functions obtained from phylogenetic information to produce nonlinear morphing across the model. The morphing modules in 3D Studio Max are used to accomplish the morph between the Texas Horned Lizard and the Mexican Horned Lizard. The result of the morph (a possible common ancestor) is shown in the middle image in Figure 2.

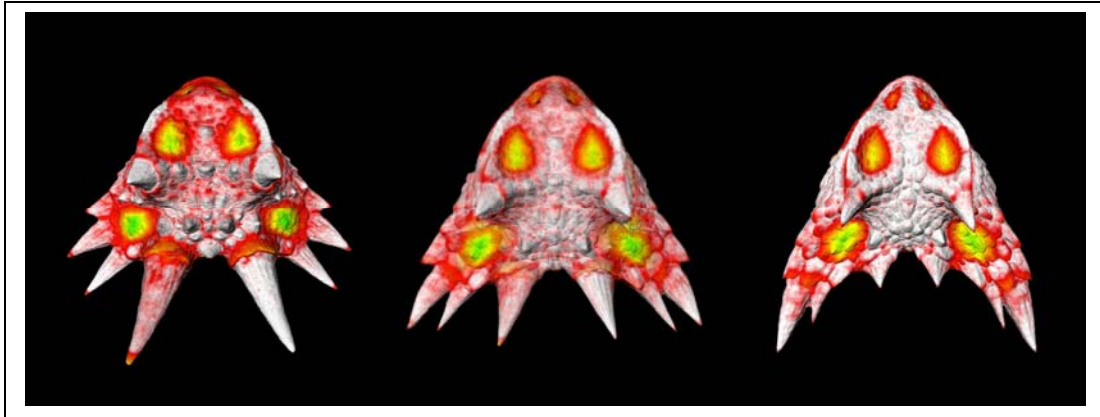


Figure 2: The Texas Horned Lizard on the left, the Mexican Horned Lizard on the right, and a possible common ancestor shown in the middle.

The image below displays the range of techniques that are used to accomplish this morphing and visualization. This research integrates visualization, 3D morphing, and CT reconstruction methods to produce novel analysis tools in systematic and comparative biology. These tools are important for understanding the evolution of complex traits and will enable scientists to investigate changes in existing structures arising from mathematically modeled phenomena.

