

Talk: Automated Shape Alignment and Registration

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Abstract:

A primary way that phenotypic evolution of body form is assessed is through comparisons of geometric differences in homologous regions of the body. However, translating geometric measurements of difference among anatomies into perspectives on biodiversity, disparity and evolutionary rates is typically complicated by the incomplete and/or subjective nature of correspondences used to measure geometric differences.

We present computational methods that register samples of 3D digital models of bones to a common template. The use of a common template means that discrete landmarks can be distilled and analyzed according to any method used with conventional landmarks. We demonstrate two different approaches to registering digital models, one in which correspondences are determined among evenly spread surface landmarks, and another in which correspondences are determined from pre-populated landmark samples emulating traditional type II and III landmarks. Which of these two approaches is more appropriate for a given study and sample depends on a number of kinds of logistical and theoretical considerations. Finally, we present a non-landmark-based approach to shape comparison enabled by these methods.

All of the methods discussed here use an alignment method called 'auto3dgm' as their foundation. Though auto3dgm has existed since 2015, computational bottlenecks to its use on full-size research samples have hindered its utility and adoption. As part of this work, we refactored auto3dgm in Python and parallelized its computations achieving reductions in computation time by 30-100 fold. The Python application of auto3dgm is publicly available for use. Some of the downstream techniques are available as matlab routines that can be provided upon request. We hope these methods can help facilitate larger scale, more data driven investigations into phenotypic diversity.

Bio:

Doug is an associate professor in the Department of Evolutionary Anthropology at Duke University in Durham, North Carolina where he has been employed since 2012. His research focus is on evolutionary origins and diversification of primate mammals. These studies draw on evidence from comparative skeletal morphology of extant and fossil species. He has a long history working for museums and with museum collections. Before and while pursuing a BS in Geology at the University of Michigan (1997-2003), he worked as a fossil preparator and paleo artist in the University of Michigan Museum of Paleontology. He earned a PhD in Evolutionary Anatomy at Stony Brook University (2003-2009), learning key principles of specimen collection management by working with his advisor's extensive Crazy Mountain Basin Collection of Paleocene mammal fossils, while continuing to develop fossil preparation and documentation techniques. He also began to learn techniques for CT scanning and laser scanning at this time. As a bioinformatics postdoc under Jukka Jernvall of the University of Helsinki (2009-2010) he was charged with developing initial designs for what would ultimately become [MorphoSource](#) in 2013. Boyer connected with Dr. Ingrid Daubechies (Duke Dept of Mathematics) and Dr. Julie Winchester (lead developer and Technical

Director of MorphoSource) through Jernvall. Upon arriving at Duke in 2012, he set up a multi-user microCT facility that is widely used today and founded MorphoSource. In 2016, Julie Winchester joined the team at Duke. Together, Boyer and Winchester develop and run MorphoSource and pursue research into methods for morphometric shape comparison with Daubechies.