Teeth!

Nastaran Ghorbani   NGHORBANILUC.EDU
Department of Mathematics and Statistics
Loyola University Chicago
Chicago, IL

Gregory J. Matthews   GMATTHEWS1LUC.EDU
Department of Mathematics and Statistics
Loyola University Chicago
Chicago, IL

Editor:

Abstract

This study presents a comprehensive analysis of morphological variations in the teeth of Tragelaphus scriptus and Tragelaphus pricei. Utilizing a combination of image processing techniques and advanced statistical analyses, we aimed to quantify and compare the morphological shapes of teeth from these two species.

Keywords: statistical Shape Analysis

1 Introduction

Understanding the morphological variation in teeth among mammalian species provides critical insights into their evolutionary history and adaptation strategies. This research focuses on the comparative analysis of Tragelaphus scriptus and Tragelaphus pricei, aiming to identify significant morphological differences through a novel combination of image processing and statistical analysis. These species, chosen for their evolutionary significance and distinct habitats, offer an opportunity to explore the relationship between morphology and environmental adaptation.

2 Methods

2.1 Data Collection and Preprocessing

The study focused on analyzing dental morphology in two species of tragelaphine antelopes: *Tragelaphus scriptus* and *Tragelaphus pricei*. High-resolution black-and-white images of six different tooth types (LM1, LM2, LM3, UM1, UM2, and UM3) were obtained for each species. The images were processed to import and preprocess the data.

Each tooth image was imported, and the contours of the teeth were extracted. The contours were then resampled to have the same number of points ($N = 500$) to ensure consistency in the representation of the shapes for subsequent analysis. This preprocessing step is crucial for standardizing the data and eliminating variations that could introduce bias in the shape analysis.

2.2 Shape Analysis

The shape analysis conducted in this study focused on quantifying the morphological differences in teeth between the two species, *Tragelaphus scriptus* and *Tragelaphus pricei*. This analysis was based on the framework of elastic shape analysis, which provides a comprehensive approach to comparing shapes by considering both the geometry and the topology of the objects.

Each tooth outline was represented as a continuous curve in a two-dimensional space. This curve, denoted as $\beta(t)$, was parameterized by a variable t ranging from 0 to 1, where $\beta(t) = (x(t), y(t))$ represents the coordinates of the points along the outline. The parameterization was chosen such that the points were uniformly distributed along the curve, ensuring a consistent representation of the shape.

To facilitate the comparison of shapes, each curve was transformed into its Square-Root Velocity Function (SRVF) representation. The SRVF of a curve $\beta(t)$ is defined as:

$$q(t) = \frac{\dot{\beta}(t)}{\sqrt{\|\dot{\beta}(t)\|}}$$

where $\dot{\beta}(t) = (\dot{x}(t), \dot{y}(t))$ is the derivative of $\beta(t)$ with respect to t, and $\|\cdot\|$ denotes the Euclidean norm. The SRVF representation has the property of being invariant under reparameterizations of the curve, making it an ideal tool for shape analysis.

The core of the shape analysis was the elastic shape analysis framework, which aims to align and compare shapes by finding an optimal warping function. Given two curves $\beta_1(t)$ and $\beta_2(t)$, their SRVFs $q_1(t)$ and $q_2(t)$ are aligned by finding a warping function $\gamma(t)$ that minimizes the geodesic distance between them:

$$d(q_1, q_2) = \inf_{\gamma \in \Gamma} \|q_1(t) - q_2(\gamma(t))\sqrt{\dot{\gamma}(t)}\|$$

where Γ is the set of all orientation-preserving diffeomorphisms of $[0, 1]$. The optimal warping function $\gamma(t)$ aligns the shapes in such a way that corresponding points on the curves are matched, allowing for a meaningful comparison of their geometries.

After aligning the shapes of all teeth within each species and tooth type, the mean shape was calculated as the average of the aligned shapes. This mean shape serves as a representative outline that captures the average geometric features of the teeth, providing a basis for comparing the shape characteristics between the two species.

By employing these techniques, the shape analysis conducted in this study offers a detailed and mathematically rigorous examination of the morphological differences in teeth between *Tragelaphus scriptus* and *Tragelaphus pricei*.

2.3 Statistical Analysis

The statistical significance of the observed morphological differences between *Tragelaphus scriptus* and *Tragelaphus pricei* was determined using multivariate and non-parametric methods.

2

2.4 Multivariate Testing

2.4.1 HOTELLING'S T-SQUARE TEST

Principal component analysis (PCA) scores for each tooth type were compiled into a combined dataset, separating samples into two groups based on their species. Hotelling's T-square test was then applied to these groups, aiming to identify significant multivariate differences in tooth shape. This test offered a comprehensive statistical assessment, taking into account the multidimensional nature of the shape data. The results from Hotelling's T-square test provided initial evidence of the morphological divergence between the two species.

The Hotelling's T-square statistic is calculated as follows:

$$t^2 = \frac{n_{scriptus}n_{pricei}}{n_{scriptus} + n_{pricei}}(\overline{\mathbf{x}} - \overline{\mathbf{y}})'\hat{\mathbf{\Sigma}}^{-1}(\overline{\mathbf{x}} - \overline{\mathbf{y}})$$

2.4.2 PERMUTATION TESTING

To complement the Hotelling's T-square test, permutation testing was conducted. This non-parametric approach involved randomly shuffling the group labels (species assignments) of the combined PCA scores dataset thousands of times (1,000 for Hotelling's T-square significance and 100,000 for distance-based permutation testing), each time recalculating the test statistic under the null hypothesis that there is no difference between species.

2.4.3 DISTANCE-BASED PERMUTATION TESTING

The distance-based permutation testing extended the analysis by focusing on the pairwise distances between teeth shapes, encapsulating both size and shape variations. The distances were calculated using the following formula:

$$d_{ij} = \sqrt{\sum_{k=1}^{p}(x_{ik} - x_{jk})^2}$$

where d_{ij} is the distance between the i-th and j-th tooth shape, and x_{ik} and x_{jk} are the k-th coordinates of the i-th and j-th shapes, respectively. For each tooth type, the average within-species distances ($\overline{D}_{within}$) and the average between-species distances ($\overline{D}_{between}$) were calculated. The test statistic, S, was derived from these distances to quantify the morphological disparity between species and is given by:

$$S = \frac{n_{scriptus}n_{pricei}}{n_{scriptus} + n_{pricei}}\left(2\overline{D}_{between} - \overline{D}_{within(scriptus)} - \overline{D}_{within(pricei)}\right)$$

Permuting the species labels and recalculating S for numerous simulations provided a distribution of S under the null hypothesis. This approach offered a robust mechanism to assess the likelihood of observing the empirical value of S by chance, thereby estimating a p-value for the test.

2.5 Conclusion

Combining Hotelling's T-square test with permutation testing has offered a rigorous statistical framework to assess the morphological differences between Tragelaphus scriptus and Tragelaphus pricei. These methods not only confirmed the initial evidence of divergence but also provided a solid foundation for claiming statistically significant shape and size variations between the two species.