Abstract

Traditionally, 3D biological shapes are studied via geometric morphometrics, which uses landmarks for geometric comparisons and statistical analyses. Although this targeted approach has many advantages, it necessarily leads to a massive loss of information contained within the original 3D object. Meanwhile, the proliferation of deep learning techniques has produced new methods which directly process 3D meshes, paving the way for landmark-free morphological analysis. The aim of this PhD is to move beyond 3D geometric morphometrics via novel deep learning techniques. To accomplish this, we will study three fully landmarked 3D datasets of extant vertebrates. These datasets are already well-studied and will serve as a litmus test for validating our new methods. They consist of humeri and ulnae from three species of mole (genus Talpa), cervical vertebrae from 16 species of bird, and heads from 83 species of snake. First, since deep learning algorithms require substantial datasets for training, we will elaborate new data augmentation techniques using 3D diffusion models for complex and realistic mesh generation. Next, we will perform phenotypical classification on our datasets using 3D graph neural networks (GNNs). Then, we will use deep saliency mapping with attention mechanisms to highlight discriminatory classification regions, allowing us to interpret network decisions. Finally, similarly to geometric morphometrics, we will quantify geometric differences between samples using neural flow deformation. Once our models have been refined on extant datasets, as a challenging first real-world application we will apply them to a 3D dataset of ornithomimosaur (Dinosauria, Theropoda) tibiae from the Angeac-Charente Lagerstätte in southwestern France. We will seek to find morphological evidence for allometry in this exceptionally large (at least 70 individuals), coeval population of Cretaceous theropods. This work would lay the foundation for new ways of studying shape evolution in (paleo)biology and open the door for streamlined, landmark-free morphological analysis.

Word count: 300