

Data quality and automatic landmarking for ~1,000 cranial CT scans from MorphoSource

Mario Modesto-Mata^{1,2}, Arthur Thiebaut¹, Marina Martínez de Pinillos^{1,3}, Ian Towle¹, Raquel Hernando¹, Kristin Krueger⁴, Chi Zhang⁵, Murat Maga⁶, James M. Cheverud⁴, Leslea J. Hlusko¹

1 - Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), Burgos, Spain · 2 - Universidad Internacional de La Rioja (UNIR), Logroño, Spain · 3 - Universidad de Burgos, Burgos, Spain · 4 - Loyola University Chicago, Chicago, USA · 5 - Texas A&M University, Dallas, USA · 6 - University of Washington, Washington, USA

In any statistical analysis there's a large investment of time, mostly unseen, dedicated to ensuring and consolidating the datasets that will be used to feed the models. In this study, we measured the distance Prosthion-Basion (PR-BA) between the real skulls and the CT models that were scanned at different slice spacing for the Southwest National Primate Research Center (SNPRC) baboon skull collection downloaded from MorphoSource (n=986). Many scans experienced unexpected problems of slice spacing identity, so we checked the automatic value when they were loaded in 3D Slicer [1], and the expected one in the header that was introduced manually. We compared the values with previously-published landmark data from the same CT models [2] and the real measurements. Our results indicate that scans for which we didn't experience problems loading their DICOM files had a high level of overlap between the real PR-BA distance and the CT-measured distance, no matter the slice spacing. Skulls for which the slice spacing was automatically calculated by the software (and not the value present in the header), the distances exhibited a high level of overlap with the real values. In the latter skulls, when the slice spacing is manually-introduced to fit the header, the CT-measured distance is significantly overestimating the real distance. Because of this mis-match, we also validated the published data to confirm that there was no error in how they calculated the distances between their landmarks.

Once we validated that the CTs are reliable for obtaining linear distances, our next step was to automatically place landmarks over the skulls. To achieve this goal for such a large sample of CT scans, we used 3D Slicer and the functions ALPACA/MALPACA [3-4] of the SlicerMorph extension [5]. We divided the sample in source/target subsamples. For the source sample, we selected 10 male and 10 female skulls based on the "Template selection" option in the software. In these samples we manually selected different landmarks to analyze prognathism and calculated a pairwise distance matrix. The target sample consisted in the remaining skulls where the landmarks were automatically placed based on the average of the source samples. The resulting pairwise distance matrices were calculated. We then randomly selected 20 male and 20 female skulls from the target samples and we manually placed the landmarks.

The comparison of landmark distances in these 40 skulls between automatic and manual landmark positioning are below 5% different. Although the automatic placement of landmarks was highly precise, a quick check of each scan is needed to confirm that the landmarks were placed accurately and the measurements can be reliably calculated. The accuracy and precision of these cranial data meet the requirements for quantitative genetic analyses, which is the next step in our research.

This research was supported with funding from the European Research Council within the European Union's Horizon Europe (ERC-2021-ADG, Tied2Teeth, project number 101054659) to Leslea J. Hlusko.

References: [1] Fedorov, A., Beichel, R., Kalpathy-Cramer, J., Finet, J., Fillion-Robin, J.-C., Pujol, S., Bauer, C., Jennings, D., Fennessy, F., Sonka, M., Buatti, J., Aylward, S., Miller, J.V., Pieper, S., Kikinis, R., 2012. 3D Slicer as an image computing platform for the Quantitative Imaging Network. *Magnetic Resonance Imaging*. 30, 1323–1341. [2] Joganic, J.L., Willmore, K.E., Richtsmeier, J.T., Weiss, K.M., Mahaney, M.C., Rogers, J., Cheverud, J.M., 2018. Additive genetic variation in the craniofacial skeleton of baboons (genus *Papio*) and its relationship to body and cranial size. *American Journal of Physical Anthropology*. 165, 269–285. [3] Porto, A., Rolfe, S., Maga, A.M., 2021. ALPACA: A fast and accurate computer vision approach for automated landmarking of three-dimensional biological structures. *Methods in Ecology and Evolution*. 12, 2129–2144. [4] Zhang, C., Porto, A., Rolfe, S., Kocatulum, A., Maga, A.M., 2022. Automated landmarking via multiple templates. *PLOS ONE*. 17, e0278035. [5] Rolfe, S., Pieper, S., Porto, A., Diamond, K., Winchester, J., Shan, S., Kirveslahti, H., Boyer, D., Summers, A., Maga, A.M., 2021. SlicerMorph: An open and extensible platform to retrieve, visualize and analyse 3D morphology. *Methods in Ecology and Evolution*. 12, 1816–1825.