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teethR: a new R package to reconstruct crown heights and estimate perikymata counts on worn teeth

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Dental studies are key to understanding the evolution of the growth and developmental processes of extinct hominins. Central to these studies is the intrinsic nature of dental tissues (enamel and dentin), as they record periodicity lines in their histological structure, enabling us to calculate very accurately their formation times. In this regard, the total number of long growth markers present in the tooth crown surface (known as perikymata) is an essential variable for assessing enamel formation times [1].

Many teeth in the fossil record are naturally worn due to masticatory forces during the life of the individual, and the part of the crown preserving the perikymata lines on the surface of the crown are lost. This wear complicates studies of dental development in two ways: 1) the crown height that disappeared due to wear is unknown, and 2) the existing perikymata of that missing enamel is unknown. These two hurdles significantly reduce the available sample sizes of teeth in dental anthropological analyses and the inferences about paleobiology that can be extracted.

In order to address these two hurdles, we developed a new package in R named *teethR*. Its name means *teeth aRe wonderful*, and it is released under GPL v3.0 license and hosted in GitHub (<https://github.com/paleomariomm/teethR>). *teethR* contains, to date, two functions that address the two potential problems abovementioned.

The first function is named as *crown_height_recons_2d()*. The aim of this function is to reconstruct the cusp areas to locate the cusp tips of the different tooth types. With these cusp tips, crown height is now able to be estimated, and therefore, we can calculate the percentage of crown height that has been worn. This function significantly improves the method to reconstruct this part of the enamel based on polynomial regressions [2-3] with an easy straightforward two-step process.

The second function is named *predict_perikymata()*. The aim of this function is to predict the number of perikymata in the first three deciles of the crown height (crown heights can be divided in ten equal segments named as deciles) by using already-trained artificial neural networks.

The combination of the two functions allows the estimation either of the percentage of crown height lost or the estimation of the perikymata that existed in that part of the enamel that is no longer present. This user-friendly R package provides future studies with a statistically validated high level of accuracy, enabling the use of increased sample sizes, and, consequently, more robust insight to the paleobiology of our ancestors.

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References: [1] FitzGerald, C.M., Rose, J.C., 2008. Reading between the lines: dental development and subadult age assessment using the microstructural growth markers of teeth. In: Katzenberg, M.A., Saunders, S.R., (Eds.), *Biological Anthropology of the Human Skeleton* (2nd ed.), pp. 237–263. Wiley Liss. [2] Modesto-Mata, M., Dean, M.C., Lacruz, R.S., Bromage, T.G., García-Campos, C., Martínez de Pinillos, M., Martín-Francés, L., Martín-Torres, M., Carbonell, E., Arsuaga, J.L., Bermúdez de Castro, J.M., 2020. Short and long period growth markers of enamel formation distinguish European Pleistocene hominins. *Scientific Reports* 10(1), 1–12. [3] Modesto-Mata, M., García-Campos, C., Martín-Francés, L., Martínez de Pinillos, M., García-González, R., Quintino, Y., Canals, A., Lozano, M., Dean, M.C., Martín-Torres, M., Bermúdez de Castro, J.M., 2017. New methodology to reconstruct in 2-D the cuspal enamel of modern human lower molars. *American Journal of Physical Anthropology* 163(4), 824–834.