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## **phyloshapeR: plotting phylogenies to look like maps**

The R package phyloshapeR aims to create visual plots of phylogenies to match any shape, including polygons, maps, or any custom shape. It can be already installed from GitHub, and includes an extended tutorial of use (<https://iramosgutierrez.github.io/phyloshapeR/>).

The workflow of 'phyloshapeR' is to modify a phylogeny's tree branch lengths in order for them to end matching a shapefile silhouette. To do so, it depends on two extensively used R packages, namely 'ape' (to work with phylogenies) and 'terra' (to calculate distances to a shapefile's silhouette). Different parameters can be edited within phyloshapeR's functions, as can be the branch elongation method, the filling depth of internal branches, the number of tips, the coordinates where the root of the phylogeny should be plotted or the plotting options (as colour or width) of the phylogeny.

As a warning to all potential users, the objective of this package is just to create aesthetic phylogenies, never to return data to be used in analyses. However, its outcomes can result visually attractive and may be used for a variety of purposes such as rendering project logos, images for conferences or book covers, combining users' phylogenies and contours for each individual situation.

### **¿Presentas la comunicación a premio?**

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