



World spatial phylogenetics of the angiosperms.

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Spatial phylogenetic analyses combine phylogenies and spatial data at any taxonomic and geographic level. All studies to date have concentrated on either a particular taxonomic group, for example Australian *Acacia*, or the flora of a particular geographic region, for example the analyses on the flora of Australia, California and Chile. The PAFTOL angiosperm phylogeny created the opportunity to make a spatial phylogenetic world analysis at the genus level. We cleaned institutional plant records stored in the Global Biodiversity Information Facility (GBIF) so that they reflected the worldwide native range of each species (over 200000 species). The final spatial dataset contained over 23 million records and projected using World Mollweide at 50 ×50 km grid cells. The PAFTOL tree and spatial data were combined using Biodiverse to make diversity analyses and randomisations for the CANAPE, Relative Phylogenetic Diversity and Phylogenetic Diversity Randomisation tests. The results of two spatial phylogenetic analyses will be presented, one using a raw branched PAFTOL phylogram and one using a PAFTOL chronogram. We will also present comparisons of results against climatic variables and the biodiversity hotspots of the world.

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