EvobiR (evolutionary biology in R) is an R package with a collection of functions for research and pedagogical tasks. The open source scientific computing language R offers a modular package based system that eases the development of new analyses by allowing users to easily build on existing functionality available in other packages (R Development Core Team 2013). Here we describe a novel comparative method developed to determine if the derived state of a discrete binary character originates when a continuous character has extreme values. We evaluate the performance of this method with simulated datasets and show that it is a conservative test. We also briefly discuss other functions included in the EvobiR package.

*Ancestral Condition Test*