We are writing to enquire about the suitability of our article entitled “EvobiR: an R package with tools for research and teaching in evolutionary biology.” for publication in *Methods in Ecology and Evolution*. Our article describes an R package that includes a novel comparative method that allows users to test whether extreme values of a continuous trait are associated with the origins of derived state of a discrete binary trait. Using simulated data we show that this is a conservative but useful test when the number of taxa included is sufficient. We also briefly describe other functions useful in comparative and population genetic analyses. Finally we discuss three Shiny Apps that we have included for their usefulness in teaching evolutionary biology and related topics.

Sincerely,

Heath Blackmon

Richard H. Adams