**Appendix S1. R-package ‘MASSTIMATE’, for estimating body mass in terrestrial tetrapods.**

In an effort to make the equations derived in Campione and Evans (2012) and in this study accessible to all for estimating body mass in terrestrial bipeds and quadrupeds, this study presents a software package based on the statistical language R (<http://www.r-project.org/>), which is now uploaded to the CRAN website. The package, MASSTIMATE, provides all equations generated in this study and in Campione and Evans (2012) under the functions: QE, cQE, and MR; all incorporate the option of using the raw or phylogenetically corrected equations. The results of these functions provide both the log10 and non-log results as well as the mean percent prediction error on the non-log estimates. MASSTIMATE provides the option to estimate a single specimen or a large dataset of specimens rapidly with clear utility for large-scale studies of body size evolution in the fossil record. The intention is to eventually expand the models available for use within MASSTIMATE to make all equations in the literature easily available for future studies. In addition, various other estimation equations based on stylopodial circumferences were included: CF2004, Christiansen & Fariña (2004); MCF2004, Mazzetta, Christiansen & Fariña (2004); CM1992, Campbell and Marcus (1992); and AHR1985, Anderson, Hall-Martin and Russell (1985). Finally, the functions quadrupeds and bipeds provide mass estimates based on all functions.

SOURCE CODE (for functions ‘QE’, ‘MR’, and ‘cQE’)

QE <-

function(HC,FC,equation=c("raw","phylocor"),data=NULL) {

if(equation=="raw") {

log.QE<-2.749\*log10(HC+FC)-1.104

QE<-round(10^log.QE,1)

ppe.err<-QE\*0.2563

upper.QE<-round(QE+ppe.err,1)

lower.QE<-round(QE-ppe.err,1)

}

if(equation=="phylocor") {

log.QE<-2.754\*log10(HC+FC)-1.097

QE<-round(10^log.QE,1)

ppe.err<-QE\*0.2503

upper.QE<-round(QE+ppe.err,1)

lower.QE<-round(QE-ppe.err,1)

}

return(cbind(data,log.QE,QE,upper.QE,lower.QE))

}

MR <-

function(HC,FC,equation=c("raw","phylocor"),data=NULL) {

if(equation=="raw") {

log.MR<-1.78\*log10(HC)+0.939\*log10(FC)-0.215

MR<-round(10^log.MR,1)

ppe.err<-MR\*0.24932

upper.MR<-round(MR+ppe.err,1)

lower.MR<-round(MR-ppe.err,1)

}

if(equation=="phylocor") {

log.MR<-1.54\*log10(HC)+1.195\*log10(FC)-0.234

MR<-round(10^log.MR,1)

ppe.err<-MR\*0.24624

upper.MR<-round(MR+ppe.err,1)

lower.MR<-round(MR-ppe.err,1)

}

return(cbind(data,log.MR,MR,upper.MR,lower.MR))

}

cQE <-

function(FC,equation=c("raw","phylocor"),cor=2,data=NULL) {

if(equation=="raw") {

log.cQE<-2.749\*log10(FC\*sqrt(cor))-1.104

cQE<-round(10^log.cQE,1)

ppe.err<-cQE\*0.2563

upper.cQE<-round(cQE+ppe.err,1)

lower.cQE<-round(cQE-ppe.err,1)

}

if(equation=="phylocor") {

log.cQE<-2.754\*log10(FC\*sqrt(cor))-1.097

cQE<-round(10^log.cQE,1)

ppe.err<-cQE\*0.2503

upper.cQE<-round(cQE+ppe.err,1)

lower.cQE<-round(cQE-ppe.err,1)

}

return(cbind(data,log.cQE,cQE,upper.cQE,lower.cQE))

}

See associated package information for more details and functions:

http://cran.r-project.org/web/packages/MASSTIMATE/index.html