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#CetaceaBodyBrain.R----- Body size and relative brain size in archaeocetes
#Philip D. Gingerich: Univ. Mich. January 16, 2015
#Files read here must be in an 'R_cetacea' folder in the 'c:\' root directory
print (date())
#<ctr>-s to save, <ctr>-a to select all, <ctr>-r to run
#dim() for dimensions, summary() for summary
#----- Read reference file
#definition: mw = modern whale and pinniped body weight and vertebral size matrix
#weights are in kg; lengths are in mm
bb="c:/r_cetacea/bodybrain_ref_file.csv" #reference file name
mw<-read.csv(bb,header=TRUE) #read reference file
#mw
#----- Plot setup
win.graph(width=12, height=7, pointsize=14)
xrange <- c(0, 65) #limits for plot axes
yrange <- c(0, 7) #limits for plot axes
plot(xrange, yrange, #set up plot
      type='n', #type 'n' means no plotting
      pin=c(6, 6), #plot dimensions in inches
      col=1, #color black
      las=1, #axis labels always horizontal
      mgp=c(1.5, .3, 0), #margin for axis title/labels/tickline
      tck=-0.01, #tick-mark length
      xlab='Vertebral position',
      xaxp=c(0, 65, 13),
      ylab='Ln centrum length (mm)',
      yaxp=c(0, 7, 7), #y-axis extremes and number of ticks
      cex.lab=1.2) #label size
#----- Plot reference
sample
for (i in 1:13){
  for(j in 1:62){
    lines(c(j-1, j), c(log(mw[i, 3*(j-1)-2+9]), log(mw[i, 3*j-2+9])),
          lwd=2, col=gray(.6))
  }
  for(j in 1:62){
    points(j, log(mw[i, 3*j-2+9]), pch=20, type="o", cex=.5, lwd=3,
           col=gray(.6))
  }
}
rect(7.5, 1.5, 26.5, 6, col=NA, lty=2) #dashed rectangle showing sample area
#----- Multiple regression
rcoef <- matrix(nrow=26, ncol=7) #Regression coefficients
colnames(rcoef)<-c('Intcpt', 'X1', 'X2', 'X3', 'MultR2', 'Sigma', 'df')
for (i in 8:26){
  results=lm(log(mw[, 6])~log(mw[, 3*i-2+9])+log(mw[, 3*i-1+9])+log(mw[, 3*i-0+9]))
  rcoef[i, 1:4]=coefficients(results)
  rcoef[i, 5]=summary(results)$r.square
  rcoef[i, 6]=summary(results)$sigma
  rcoef[i, 7]=summary(results)$df[2]
}
rcoef[8:26, ]
#----- Wt. prediction (edit this block as
necessary)
Taxname='Dorudon atrox'
bi='c:/r_cetacea/Dorudon_atrox.csv' #input file name
mi<-read.csv(bi, skip=3, header=TRUE) #read measurement input file
vf=8; vl=26 #first & last verts. for prediction
#-----
#Vertebral centrum length (L); centrum width (W); and centrum height (H)
G.sp <- matrix(nrow=vl, ncol=8)
colnames(G.sp)<-c('CentL', 'CentW', 'CentH', 'EstLnWt', '2-sigma', 'EstWt',
                 'MinWt', 'MaxWt')
for (i in vf:vl){ #use only actual measurements

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    if (mi[i, 3]=="m"){G.sp[i, 1]=mi[i, 2]}else{G.sp[i, 1]=NA}
    if (mi[i, 5]=="m"){G.sp[i, 2]=mi[i, 4]}else{G.sp[i, 2]=NA}
    if (mi[i, 7]=="m"){G.sp[i, 3]=mi[i, 6]}else{G.sp[i, 3]=NA}
}
for (i in vf:vl){
    #fill rest of G.sp matrix
    G.sp[i, 4]=rcoef[i, 1]+log(G.sp[i, 1])*rcoef[i, 2]+
        log(G.sp[i, 2])*rcoef[i, 3]+log(G.sp[i, 3])*rcoef[i, 4]
    G.sp[i, 5]=qt(.975, rcoef[i, 7])*rcoef[i, 6]#t value df for 95% conf. estimate
    G.sp[i, 6]=exp(G.sp[i, 4])
    G.sp[i, 7]=exp(G.sp[i, 4]-G.sp[i, 5])
    G.sp[i, 8]=exp(G.sp[i, 4]+G.sp[i, 5])
}
G.sp
for (i in vf:vl){
    points(i, log(G.sp[i, 1]), pch=21, type="p", cex=1.5, col=1, bg="black")
    text(i+1, 1, round(exp(G.sp[i, 4])), srt=90, pos=2, cex=.8, col=1)
}
Wgt.est=median(G.sp[8:26, 6], na.rm=TRUE); Wgt.est #body weight estimate in kg
Wgt.low=median(G.sp[8:26, 7], na.rm=TRUE); Wgt.low #0.025 minimum body weight estimate
Wgt.upp=median(G.sp[8:26, 8], na.rm=TRUE); Wgt.upp #0.975 maximum body weight estimate
#-----
#brain weight in grams = endocranial volume in cc minus any rete volume in cc
#read brain weight from file
brain<-read.csv(bi, skip=2, nrow=1, header=FALSE); Brain=brain[1, 1]
Brain=0
if (Brain>0){
    Eobs=log2(Brain)

    P=1000*median(G.sp[8:26, 6], na.rm=TRUE) #body weight in grams
    Eexp=0.740*log2(P)-4.004 #Expected log2 brain weight
    ER=Eobs-Eexp
    ER #Enceph residual log2 units
    2^ER #Encephalization quotient
    text(54, 1.65, Taxname, font=4, pos=1, cex=1.2, col=1)
    text(54, 1.2, bquote(' Body wgt (kg)' ==
        .(format(Wgt.est, digits=4, nsmall=0))~' (' ~
        .(format(Wgt.low, digits=3, nsmall=0))~' -' ~
        .(format(Wgt.upp, digits=4, nsmall=0))~' )' ), pos=1, cex=1.1, col=1)
    text(54, .8, bquote(' Brain wgt (g)' == .(format(Brain, digits=4, nsmall=0))),
        pos=1, cex=1.1, col=1)
    text(54, .4, bquote(' ER' [' TC' ] == .(format(ER, digits=2, nsmall=2))),
        pos=1, cex=1.1, col=1)
}else{
    text(54, 1.1, Taxname, font=4, pos=1, cex=1.2, col=1)
    text(54, 0.6, bquote(' Body wgt (kg)' ==
        .(format(Wgt.est, digits=4, nsmall=0))~' (' ~
        .(format(Wgt.low, digits=3, nsmall=0))~' -' ~
        .(format(Wgt.upp, digits=4, nsmall=0))~' )' ), pos=1, cex=1.1, col=1)
}
#----- END -----

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