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# Examining sexual dimorphism in Laticauda skull shape
# PeerJ review manuscript by Bartosz

# Code by Emma Sherratt (emma.sherratt@gmail.com)
# R version 4.2.2 (2022-10-31) -- "Innocent and Trusting"
library(geomorph) #v.4.0.5
# working directory is supplemental folder
mydata <- read.csv("peerj-80737-Raw_data.csv", header = TRUE, row.names = 1)
mydata$sex <- factor(mydata$sex)

# Calculate log-shape ratios to remove scale variation
Geomean <- apply(mydata[,(5:33)], 1, prod) ^ (1 / ncol(mydata[,(5:33)])) #
calculate geometric mean of all variables
LSR <- log(mydata[,(5:33)] / Geomean) # calculate log-shape ratio
LSR <- data.frame(mydata[,(1:4)], Geomean, LSR) # add back metadata columns

LSR <- LSR[complete.cases(LSR[,(6:34)]) ,] # remove the specimens with missing
data

# PCA of log-shape ratio data - shape variables without scale information, but
do contain allometric shape variation
PCA <- prcomp(LSR[,(6:34)], retx = TRUE, center = TRUE, scale. = FALSE)
summary(PCA)
# Importance of components:
#                          PC1    PC2    PC3
# Proportion of Variance 0.3368 0.1021 0.0788
plot(PCA$x, pch=21, bg=LSR$sex, cex=LSR$Geomean/2, asp = TRUE) @ size of points
relates to size of skull
# Not as useful as plotting shape against size, using a multivariate regression:

# Multivariate Regression, examining allometry,
csize.allom <- procD.lm(f1= as.matrix(LSR[,(6:34)]) ~ log(LSR$Geomean) *
LSR$sex)
# ANCOVA model with size and sex
summary(csize.allom)
#                            Df      SS      MS     Rsq       F      Z Pr(>F)
#   log(LSR$Geomean)          1  2.9718 2.97179 0.28554 22.9184 4.3797  0.001 **
#   LSR$sex                   1  0.3299 0.32987 0.03169  2.5440 2.9079  0.003 **
#   log(LSR$Geomean):LSR$sex  1  0.2336 0.23360 0.02245  1.8016 1.8897  0.026 *
#   Residuals                53  6.8724 0.12967 0.66032
#   Total                    56 10.4077
# Interaction term is sex, meaning that the slopes are different
# 28.6% due to allometry, 3.2% due to sex, and 2.2% due to diff in allometric
slope

# Plot & visualise
# Using the regression score, a univariate summary of the shape variation
pp <- plot(csize.allom, type = "regression",
     predictor = log(LSR$Geomean), reg.type = "RegScore",
     pch=21, bg=LSR$sex)
# Use fitted values from the model to make prediction lines
plot(csize.allom, type = "regression",
     predictor = log(LSR$Geomean), reg.type = "PredLine",
     pch=21, bg=LSR$sex)

#overlay the two
plot(x=log(LSR$Geomean), y= pp$RegScore, pch=21, bg=LSR$sex, cex=2, xlab="log-
head size", ylab="skull shape")
points(x=log(LSR$Geomean), y= pp$PredLine, pch=19, col=LSR$sex, cex=0.8)
lines(x=log(LSR$Geomean)[which(LSR$sex == "m")], y= pp$PredLine[which(LSR$sex ==
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"m")], col="red")
lines(x=log(LSR$Geomean)[which(LSR$sex == "f")], y= pp$PredLine[which(LSR$sex ==
"f")])
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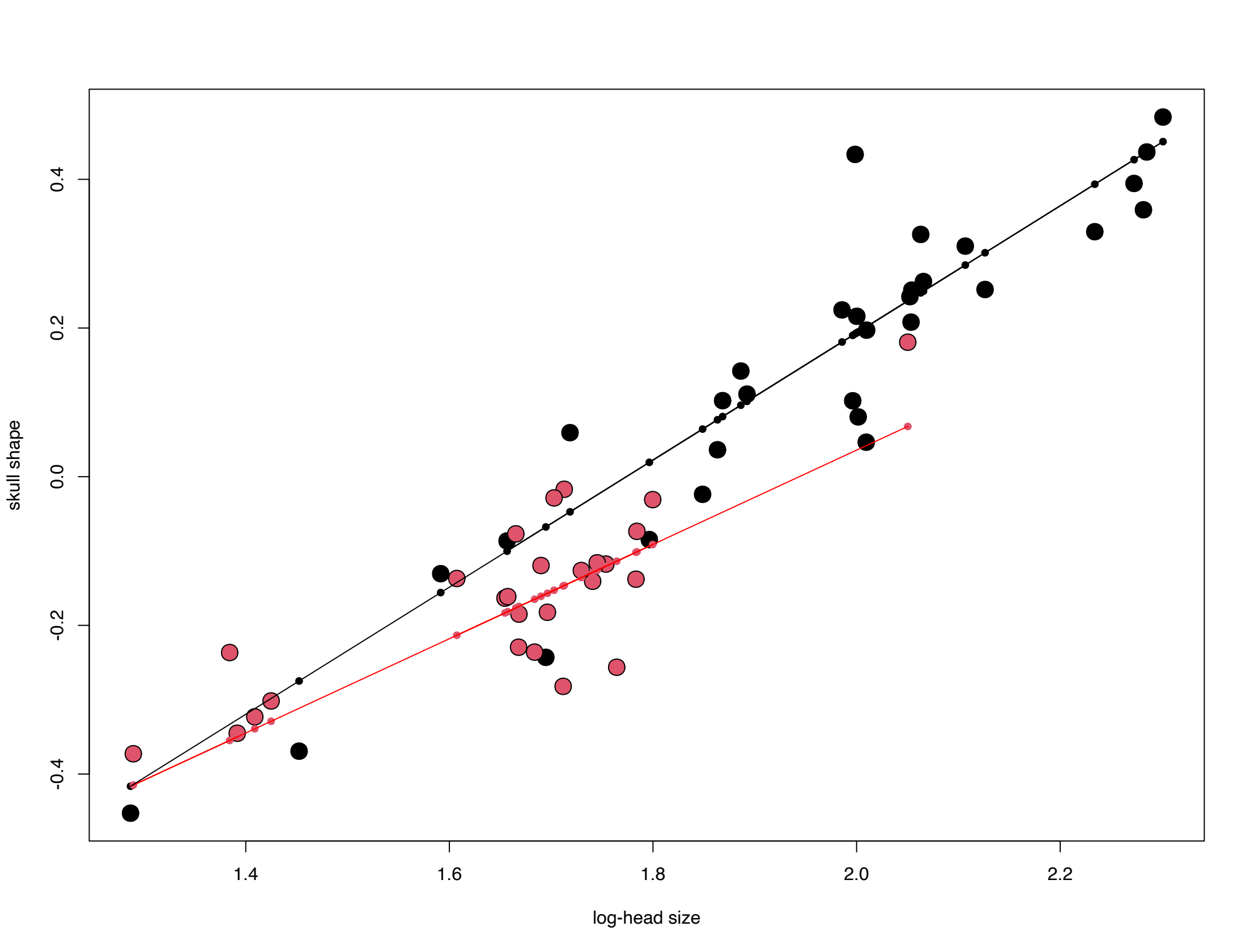
skull shape
0.4
0.2
0.0
-0.2
-0.4
1.4
1.6
1.8
2.0
2.2
log-head size