**Aerodynamic reconstruction of the primitive fossil bat *Onychonycteris finneyi* (Mammalia: Chiroptera)**

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**Appendix 2.**

**R-language script written to calculate and simulate species distance in WL-AR space.**

Data used in this study are provided in the variables wl and ar (*n* = 366, no missing data). Data representing *Onychonycteris* are given in the first element of each variable vector. Bootstrap replicates (resampling with replacement) are set by the user (default 10,000). To run this script, just copy it to the R-interface of choice (Rterm or Rgui). The script calculates:

h: the distance of *Onychonycteris* to the all-bats centroid in WL-AR space.

hh: the vector of distances of each bat species to the bat centroid in WL-AR space.

p: the proportion of bat species that equate or exceed h

xp: bootstrap probability of h to be obtained by chance alone

Confidence interval: lower and upper limit of a 95% (default) confidence interval for mean distance to centroid across all bat species obtained by means of bootstrap resampling of hh.

#==BEGIN OF SCRIPT ============================================================

rm(list=ls())

#==ALL DATA: WING LOADING (WL) AND ASPECT RATIO (AR)============================

wl=c(22.7, 9.0, 10.9, 11.7, 21.3, 15.4, 8.0, 8.9, 7.1, 5.7, 5.2, 8.1, 5.8, 5.7, 5.9, 4.3, 14.5, 18.4, 5.9, 17.8, 13.3, 25.9, 22.4, 13.0, 9.0, 4.9, 3.8, 4.3, 12.2, 6.3, 6.1, 6.6, 6.6, 4.9, 15.7, 6.2, 11.5, 10.8, 6.1, 5.6, 8.9, 12.1, 5.4, 5.8, 8.0, 8.9, 15.5, 13.4, 12.0, 16.8, 11.8, 6.2, 6.4, 12.6, 7.8, 10.2, 10.3, 18.6, 9.6, 21.8, 11.8, 34.6, 14.2, 15.1, 25.1, 9.0, 22.1, 14.1, 17.6, 18.0, 14.2, 11.4, 21.7, 20.5, 13.4, 9.3, 10.2, 8.8, 8.8, 12.7, 12.9, 14.9, 21.6, 10.8, 12.0, 19.6, 11.5, 20.2, 19.2, 5.0, 11.2, 8.0, 7.3, 4.6, 7.9, 6.5, 5.9, 20.2, 12.3, 2.9, 3.9, 13.9, 15.2, 5.9, 11.4, 5.4, 7.1, 6.3, 7.7, 5.0, 12.5, 8.4, 14.9, 17.7, 16.8, 13.6, 13.8, 12.4, 9.6, 11.4, 14.0, 9.4, 10.4, 13.7, 14.9, 9.6, 15.9, 14.0, 17.2, 16.5, 9.6, 13.1, 8.1, 9.3, 10.5, 12.8, 10.6, 8.4, 15.0, 10.2, 6.9, 7.3, 11.5, 9.6, 15.6, 13.7, 10.9, 15.8, 25.2, 11.4, 18.2, 11.6, 12.2, 12.9, 11.6, 15.3, 10.1, 14.5, 18.4, 11.4, 11.1, 13.1, 17.2, 15.6, 34.9, 26.4, 19.8, 30.6, 19.3, 27.0, 27.4, 19.4, 19.3, 36.3, 12.3, 11.4, 12.6, 17.7, 16.3, 18.5, 13.1, 14.7, 16.0, 11.4, 28.6, 32.8, 39.0, 57.8, 24.6, 17.8, 17.1, 23.1, 12.5, 21.8, 23.2, 13.3, 17.6, 7.3, 7.5, 7.3, 8.9, 7.8, 4.7, 7.9, 12.2, 8.4, 7.7, 9.8, 7.1, 6.7, 5.7, 9.1, 4.8, 7.4, 9.3, 5.1, 5.5, 7.1, 4.7, 6.0, 5.8, 8.4, 6.0, 6.3, 6.8, 7.1, 6.2, 9.2, 14.0, 20.5, 4.1, 4.1, 16.5, 8.1, 9.1, 6.6, 10.7, 8.9, 10.5, 7.1, 5.9, 7.2, 7.2, 7.0, 7.3, 9.4, 14.0, 8.1, 12.2, 14.8, 8.6, 7.5, 7.1, 7.2, 6.8, 9.0, 5.7, 8.0, 15.4, 6.6, 6.6, 4.3, 3.9, 5.8, 5.1, 4.0, 3.4, 7.0, 7.5, 8.2, 14.0, 14.4, 10.8, 18.0, 6.1, 5.2, 4.8, 7.9, 7.5, 4.2, 9.0, 6.4, 4.8, 6.8, 9.5, 6.7, 10.4, 7.0, 5.1, 7.1, 6.1, 8.2, 5.3, 6.8, 6.7, 7.5, 7.7, 7.5, 6.1, 11.2, 7.1, 6.1, 6.1, 7.3, 10.1, 5.6, 6.8, 5.0, 6.5, 6.2, 8.2, 6.3, 9.0, 8.3, 7.5, 7.8, 7.1, 8.4, 9.9, 5.7, 19.7, 19.3, 16.1, 6.7, 10.7, 6.2, 7.2, 7.8, 6.7, 6.9, 5.6, 4.3, 9.6, 8.5, 6.4, 8.5, 9.8, 8.1, 6.8, 7.0, 7.1, 7.9, 5.3, 6.1, 6.8, 13.0, 12.8, 11.5, 9.6, 10.4, 12.4, 15.0, 16.8, 5.2, 13.7, 10.9, 7.9, 11.1, 9.1, 5.7, 7.7, 7.3, 6.6, 6.4, 6.4, 10.2)

ar=c(5.0, 6.1, 6.0, 5.5, 7.6, 7.1, 6.5, 6.4, 6.2, 6.8, 7.1, 6.5, 7.7, 7.1, 7.6, 6.5, 7.9, 8.6, 6.1, 9.8, 8.2, 10.0, 9.5, 7.5, 7.0, 5.7, 4.3, 5.3, 5.6, 5.8, 6.2, 6.3, 6.1, 4.5, 7.7, 6.3, 5.5, 5.8, 6.3, 6.1, 5.3, 5.1, 4.8, 5.8, 6.6, 6.5, 6.3, 5.7, 5.4, 6.1, 6.2, 6.8, 6.3, 8.7, 6.4, 7.0, 8.4, 9.1, 8.1, 11.1, 8.6, 10.7, 8.9, 8.9, 9.5, 7.3, 10.4, 9.2, 9.1, 9.1, 8.3, 8.9, 7.7, 8.7, 7.9, 9.2, 8.6, 8.2, 7.5, 10.1, 8.3, 9.3, 9.4, 7.6, 9.7, 11.1, 8.2, 14.3, 9.8, 6.6, 7.1, 8.3, 8.0, 7.6, 6.7, 6.7, 7.5, 9.2, 7.0, 5.9, 5.8, 7.8, 9.0, 4.8, 5.2, 4.8, 5.2, 5.5, 4.7, 5.4, 7.2, 6.7, 6.1, 6.1, 6.2, 6.4, 7.0, 5.5, 6.5, 6.1, 6.4, 6.4, 6.2, 6.9, 5.5, 6.3, 6.6, 6.7, 8.5, 6.7, 6.2, 6.1, 8.3, 6.4, 6.4, 6.6, 5.9, 6.6, 6.4, 6.4, 6.2, 5.6, 6.5, 7.4, 6.3, 7.5, 6.6, 6.6, 7.6, 6.4, 5.9, 6.0, 6.5, 6.6, 6.3, 6.3, 6.3, 6.5, 5.4, 8.1, 6.0, 7.7, 7.9, 6.7, 6.8, 6.7, 6.2, 6.9, 8.6, 5.9, 6.2, 6.5, 6.1, 6.7, 6.5, 6.1, 8.7, 5.9, 6.1, 6.2, 6.3, 6.2, 5.6, 5.8, 6.9, 7.3, 7.1, 8.4, 5.9, 6.3, 6.0, 6.0, 5.6, 5.6, 6.7, 6.2, 6.7, 6.9, 5.6, 5.6, 5.6, 6.3, 6.0, 6.2, 6.1, 4.5, 6.7, 6.8, 5.7, 6.1, 5.6, 5.5, 5.0, 6.1, 6.7, 4.8, 5.4, 6.6, 5.1, 5.4, 5.5, 5.3, 5.9, 6.6, 5.3, 4.8, 5.2, 7.4, 6.9, 8.0, 5.9, 6.0, 8.1, 6.1, 6.0, 6.0, 7.8, 7.4, 7.8, 6.0, 5.9, 5.9, 7.6, 7.0, 6.2, 6.4, 7.2, 6.6, 6.5, 9.0, 6.2, 5.2, 6.8, 6.6, 5.4, 5.7, 5.7, 5.8, 6.9, 5.8, 6.1, 6.9, 5.6, 4.6, 5.6, 4.9, 4.8, 5.7, 5.6, 6.6, 6.7, 7.7, 7.2, 6.7, 5.1, 4.7, 5.4, 6.7, 6.9, 5.5, 6.0, 8.5, 5.6, 5.8, 5.5, 6.1, 6.8, 6.3, 6.2, 5.9, 6.0, 6.4, 6.4, 5.8, 6.1, 6.0, 6.4, 6.1, 7.5, 6.3, 6.0, 6.4, 6.5, 6.0, 6.7, 5.7, 5.8, 5.5, 5.4, 6.1, 6.2, 6.2, 7.4, 5.8, 5.7, 6.3, 6.4, 7.3, 5.5, 6.4, 7.2, 7.9, 7.4, 6.9, 6.8, 5.2, 7.0, 6.9, 6.2, 5.7, 6.1, 5.3, 7.9, 5.5, 5.5, 6.3, 7.2, 7.5, 6.3, 6.8, 5.7, 6.1, 6.1, 6.3, 6.2, 6.3, 5.3, 6.7, 5.9, 7.5, 7.3, 8.0, 7.0, 6.7, 5.5, 7.2, 6.2, 7.2, 6.9, 6.2, 6.5, 7.4, 6.8, 6.5, 7.5, 7.0)

#==WING LOADING AND ASPECT RATIO OF ONYCHONYCTERIS =============================

wlonyc=wl[1]

aronyc=ar[1]

#==SET BOOTSTRAP REPLICATIONS ==================================================

boot=c(10000)

#==PITAGOREAN DISTANCE OF ONYCHONYCTERIS TO ALL-BATS CENTROID: h ===============

armed=median(AR)

wlmed=median(WL)

a=(wlmed-wlonyc)

b=(armed-aronyc)

h=sqrt((a^2) + (b^2))

#==VECTOR OF DISTANCES OF EACH BAT SPECIES TO CENTROID: hh =====================

armedvec=c(seq(armed, armed, length.out=length(ar)))

wlmedvec=c(seq(wlmed, wlmed, length.out=length(wl)))

aa=(WL - wlmedvec)

bb=(AR - armedvec)

hh=sqrt((aa^2) + (bb^2))

#==PROPORTION p OF BAT SPECIES THAT EQUAL OR EXCEED h ==========================

hhs=sort(hh)

exceed=(hhs[hhs>=h])

p=(length(exceed))/(length(hhs))

#==BOOTSTRAP: xp IS THE PROBABILITY OF h BEING OBTAINED BY CHANCE ==============

hhsam=sample(hh, replace=TRUE)

app=numeric()

for (i in 1:boot)

{ hhsam=sample(hh, replace=TRUE)

b=c(hhsam[1])

app=c(app, b)

rm(hhsam)

rm(b)

}

sapp=sort(app)

xexceed=(app[app>=h])

xp=(length(xexceed))/(length(app))

#==CONFIDENCE INTERVAL calculation DEFAULT 95% =================================

CI=c(95)

{if (CI == 99)

{(lownum=1)

(highnum=99)}

else

{(lownum=5)

(highnum=95)

}}

low=round(((lownum\*boot)/100))

high=round(((highnum\*boot)/100))

CIlow=(sapp[low])

meanhh=mean(hh)

CIhig=(sapp[high])

#==REPORT=======================================================================

cat("distance h of ONYCHONYCTERIS to bat centroid in WL-AR space = ", h, "\n")

cat("proportion of bat species that equal or exceeding h = ", p, "\n")

cat("bootstrapped probability of h being obtained by chance alone = ", xp, "\n")

cat("lower limit of bootstrap CI = ", CIlow, "\n")

cat("mean of bootstrap CI = ", meanhh, "\n")

cat("upper limit of bootstrap CI = ", CIhig, "\n")

#==CLEANING=====================================================================

rm(list=ls())

#==END OF SCRIPT================================================================