Supplement 1.

Comparison of the DBA and BEnergetix methods for estimating behavioural time budgets and associated metabolic rate of (a) scallops *Pecten maximus* each placed individually into a respirometry chamber and (b) free-ranging aquatic biologists *Homo sapiens* sitting, drinking and tracking invasive crayfish around Danebridge, UK. Animal acceleration data recorded at 25 Hz using an AXY-2 data logger (TechnoSmArt, Italy). All means are ± the 95% confidence interval (CI).
<table>
<thead>
<tr>
<th>Scallops</th>
<th>Actual time moving per h (s)</th>
<th>Difference between estimated time moving using BENERGETIX and actual time moving (%)</th>
<th>Difference between estimated time moving using the DBA method and actual time moving (%)</th>
<th>Mean VeDBA during movement within a 1 h period calculated using BENERGETIX (g)</th>
<th>Mean VeDBA during movement within a 1 h period calculated using the DBA method (g)</th>
<th>Actual activity metabolic rate⁴ (mg O₂ h⁻¹)</th>
<th>Difference between estimated activity metabolic rate using the DBA method and actual activity metabolic rate (%)</th>
<th>Actual overall metabolic rate⁴ (mg O₂ h⁻¹)</th>
<th>Difference between estimated overall metabolic rate using BENERGETIX and actual overall metabolic rate (%)</th>
<th>Difference between estimated overall metabolic rate using the DBA method and actual overall metabolic rate (%)</th>
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<td>Difference between estimated time moving using BEnergetix and actual time moving (%)</td>
<td>Difference between estimated time moving using the DBA method and actual time moving (%)</td>
<td>Mean VeDBA during movement within a 1 h period calculated using BEnergetix (g)</td>
<td>Mean VeDBA during movement within a 1 h period calculated using the DBA method (g)</td>
<td>Activity metabolic rate $^{d,f}$ (l O$_2$ h$^{-1}$)</td>
<td>Activity metabolic rate using the DBA method and activity metabolic rate (%)</td>
<td>Overall metabolic rate $^{g}$ (l O$_2$ h$^{-1}$)</td>
<td>Overall metabolic rate using BEnergetix and overall metabolic rate (%)</td>
<td>Difference between estimated overall metabolic rate using the DBA method and overall metabolic rate (%)</td>
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<td>Mean ± 95% CI</td>
<td>23.63 ± 1.79</td>
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<td>19.3 ± 1.1</td>
<td>0.449 ± 0.033</td>
<td>0.394 ± 0.029</td>
<td>28.98 ± 2.84</td>
<td>6.12 ± 0.34</td>
<td>43.07 ± 3.19</td>
<td>-0.08 ± 0.16</td>
<td>4.18 ± 0.20</td>
</tr>
</tbody>
</table>

$^a$ Each raw x, y, z acceleration and associated VeDBA data set was plotted against time and signatures within the traces indicating active behaviours were selected manually. VeDBA was selected only where a corresponding change in raw x,y,z acceleration was recorded. From the manually selected VeDBA trace for each behaviour, the duration of the behaviour was calculated, along with mean VeDBA to estimate energy cost.

$^b$ See main text and Supplement 2 for details on how to use BEnergetix to accurately determine the behaviour duration of scallops and humans.

$^c$ See main text for details on the DBA method (Shepard et al. 2008). Using the DBA method within BEnergetix scallop and human VeDBA were calculated by smoothing acceleration data using running means of 3 (Robson et al. 2012) and 1 s (Wilson et al. 2006), respectively. Thus, using the packages FullDBA and BehFeatures within BEnergetix to estimate behaviour duration and VeDBA of scallops from their raw tri-axial acceleration data recorded at 25 Hz, DBAbehav running mean = 75 data points, minimum DBAbehav = 0.05 g, rest period = 0 data points, minimum movement length = 4 data points and VeDBA running mean = 75 data points. To estimate behaviour duration and VeDBA of adult humans from their raw tri-axial acceleration data recorded at 25 Hz: DBAbehav running mean = 25 data points, DBAbehav minimum g = 0.05, rest period = 0 data points, minimum movement length = 10 data points and DBA running mean = 25 data points.
Activity metabolic rate = overall metabolic rate – resting metabolic rate (Halsey et al. unpubl.).

The time moving and mean VeDBA values estimated using the DBA and BEnergetix methods were used to estimate the activity metabolic rate of each scallop individually, by applying the individual-specific regressions of activity metabolic rate against mean VeDBA. Estimated overall metabolic rate = estimated activity metabolic rate + measured resting metabolic rate.

Human activity metabolic rate was estimated using the actual time moving, the actual mean VeDBA and the appropriate common activity metabolic rate against overall dynamic body acceleration (ODBA, \(g\)) prediction equation (included human resting metabolic rate and thus, resting metabolic rate (3.5 ml min\(^{-1}\) kg\(^{-1}\)) was subsequently removed to calculate true activity metabolic rate) for use with any adult human (Halsey et al. 2008). To use the metabolic rate equation VeDBA values were converted to ODBA values using the equation: ODBA = (1.5881 x VeDBA) – 0.0218.

Human overall metabolic rate was estimated: estimated routine metabolic rate (3.5 ml min\(^{-1}\) kg\(^{-1}\)) + estimated activity metabolic rate.

**LITERATURE CITED**


Supplement 2.

Using the packages FullDBA and BehFeatures within BEnergetix to accurately determine the behaviour duration and DBA of scallops *P. maximus* from their raw tri-axial acceleration data recorded at 25 Hz, we recommend inputting a DBAbehav running mean of ca. 9 data points, a minimum DBAbehav of ca. 0.05 g, a rest period of ca. 1 data point, a minimum movement length of ca. 4 data points and a DBA running mean of ca. 75 data points. These input values vary between different animals e.g for shore crab data recorded at 25 Hz: DBAbehav running mean = ca. 15 data points, DBAbehav minimum g = ca. 0.05, rest period = ca. 9 data points, minimum movement length = ca. 10 data points and DBA running mean = ca. 249 data points. For adult human data recorded at 25 Hz: DBAbehav running mean = ca. 5–7 data points, DBAbehav minimum g = ca. 0.05, rest period = ca. 5 data points, minimum movement length = ca. 10 data points and DBA running mean = ca. 25 data points.

How to use BEnergetix:

```r
### read in the demonstration dataset, data can take a number of forms but must consist of a timestamp and acceleration in two or three axes.

# load library and data
library(BEnergetix)
data(dba.data)
# view data
head(dba.data)

### the package includes the ability to work with pressure data to calculate height and depth of an organism, useful for detecting flight or dives
pressure.data<-dba.data[,c("DataPoints","press.mBar","SurfPress.mBar","degreesLat")]
### note extra columns indicating latitiude (30) and surface pressure measurements (1008 mBar)
# correct for surface pressure
pressure.data$press.mBar<-pressure.data$press.mBar-1008
### run function
Depth<-depth(pressure.data$DataPoints,pressure.data$press.mBar,30)
# view result
head(Depth)
```
#Now various DBA equations

dbaDat<-FullDBA(dba.data$surge
dba.data$sway
dba.data$heave
9 # running mean to calculate DBAbehav
c("VeDBA2"
,"VeDBAbehav"
,"pitchsurge"
,"roll"
,"pitchheave")
0.05 #min g
1 #rest period
4 #movement length
B.var="VeDBAbehav"
MoveAve2=75) #running mean to calculate actual VeDBA
dba.data$DataPoints
extras=data.frame(Depth=Depth$Meters.Depth))

#Use
dbaDat<-dbaDat[!is.na(dbaDat$VeDBA2),] #to remove NAs
dbaDat[dbaDat$Behaviours==0,"VeDBA2"]<-0 #no behaviour VeDBA=0

#view result
head(dbaDat)

#we can plot this because it is a short dataset. There are limitations to how many points you can plot in R but there are functions to help, see package vignette
plot(DBA~Time,type="l",data=dbaDat)
# we can also deal with respirometry data (rate of O₂ consumption/CO₂ production), here we have used random data.

```r
dba.data<-data.frame(Time=dba.data$DataPoint,
                      data=abs(rnorm(4884)))
```

# When dealing with respirometry plots we require the resting metabolic rate which is often taken to be the lowest mean value calculated over 5 consecutive minutes within a dataset. This function will calculate that for you.

```r
minRange(resp.data$data
         ,resp.data$Time
         ,15
         ,SumData=dbaDat)
```

# Make subsets of the data (e.g. DBA and metabolic rate) and average them.

```r
aveRange(resp.data$data
         ,resp.data$Time
         ,7500 #7500 data points = 5 min when data are recorded at 25 Hz
         ,SumData=dbaDat[,1:5])
```

# Alternatively, by feeding in the results of FullDBA and adding respirometry data, the function MetRate will work out the activity metabolic rate (V O₂) for each detected scallop (non-steady-state, often partially anaerobic) behaviour using the equation: the estimated activity V O₂ of a scallop during a period of movement = (((V O₂ during rapid scallop movement - routine V O₂) x rapid movement duration) + ((V O₂ during period of raised V O₂ before and after rapid movement - routine V O₂) x (duration of raised V O₂ - rapid movement duration))) / rapid movement duration. Thus, automating the methods in Robson et al. (2012).

```r
MetRate(dbaDat,dba.data[,c("O2.Time","O2.use")])
```

# Determine the types of behaviour occurring using BehFeatures. You can input data such as body angle(s), pressure, depth and metabolic rate and BehFeatures will provide summary statistics for each behaviour.

```r
feat<-BehFeatures(dbaDat$Time
```
#view data
head(feat)

#Once names have been assigned to each kind of behaviour a labelling matrix can be constructed
Bmat<-BehMatrix(feat)

#which can then be used to assign names to each detected behaviour across the whole dataset
Groups<-BehLabel(feat,Bmat)

#view data
head(Groups)

LITERATURE CITED