The mass, metabolism and length explanation can simultaneously calculate an animal's mass and metabolic rate from its characteristic length

Charles C. Frasier

Organizationally unaffiliated in San Diego, California, United States of America

Abstract. It is shown that the mass, metabolism and length explanation (MMLE) can simultaneously compute an animal's body mass and BMR given its characteristic length using data for humans.

MMLE was advanced in 1984 to explain the relationship between metabolic rate and body mass for birds and mammals. It was modernized in 2015 by explicitly treating dynamic similarity of mammals' skeletal musculature and revising the treatment of BMR. Using two primary equations MMLE deterministically computes the absolute value of Basal Metabolic Rate (BMR) and body mass for individual animals as functions of an individual animal's characteristic length and sturdiness factor. The characteristic length is a measureable skeletal length associated with an animal's means of propulsion. The sturdiness factor expresses how sturdy or gracile an animal is. Eight other parameters occur in the equations that vary little among animals in the same phylogenetic group. A mass and length data set with 575 entries from the orders Rodentia, Chiroptera, Artiodactyla, Carnivora, Perissodactyla and Proboscidea and a BMR and mass data set with 436 entries from the orders Rodentia, Chiroptera, Artiodactyla and Carnivora were used to estimate values for the parameters occurring in the equations. With the estimated values MMLE can exactly compute every BMR and mass datum from the BMR and mass data set. Furthermore, MMLE can exactly compute every body mass datum from the mass and length data set. Since there is not a data set that simultaneously reports body mass, BMR and characteristic length for individual animals from the mammal orders that were analyzed it could not be determined whether or not MMLE could simultaneously compute both an animal's BMR and body mass given its characteristic length.

There are large data sets that report body mass, BMR and height for humans. A human's characteristic length can be estimated from height. In this paper human data categorized by sex, age and body mass index (BMI) are used to show that MMLE can indeed simultaneously compute a human's body mass and BMR given his or her characteristic length.

The MMLE body mass equation is modified to explicitly address body fat because it appears that humans are fatter than other running/walking placental mammals. Differences in body fat seem to account for body mass and BMR sexual dimorphism among humans. The impact on BMR of the large and metabolically expensive human brain is addressed. Also mitochondria capability decline with age is addressed.

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Introduction. The Mass, Metabolism and Length Explanation (MMLE) was advanced to explain the relationship between metabolic rate and body mass for birds and mammals (Frasier, 1984). It was modernized (Frasier, 2015) by explicitly treating Froude and Strouhal dynamic similarity of mammals' skeletal musculature, revising the treatment of BMR and using new data to estimate numerical values for the parameters that occur in the equations. MMLE deterministically computes the absolute value of Basal Metabolic Rate (BMR) and body mass for individual animals. It is thus distinct from other examinations of these topics that use species-averaged data to estimate the parameters in a statistically best fit power law relationship such as BMR = a(body mass)^b. Beginning with the proposition that BMR is proportional to the number of mitochondria in an animal and other first principles of physics and physiology, MMLE derives two primary equations that compute BMR and body mass as functions of an individual animal's characteristic length and sturdiness factor. The characteristic length is a measureable skeletal length associated with an animal's means of propulsion. The sturdiness factor expresses how sturdy or gracile an animal is. Eight other parameters occur in the equations that vary little among animals in the same phylogenetic group. A mass and length data set with 575 entries from the orders Rodentia, Chiroptera, Artiodactyla, Carnivora, Perissodactyla and Proboscidea (Nowak, 1999) and a BMR and mass data set with 436 entries from the orders Rodentia, Chiroptera, Artiodactyla and Carnivora (Kolokotrones et al, 2010) were used to estimate parameter values. With the estimated values MMLE can exactly compute every BMR and mass datum from the BMR and mass data set. Furthermore, MMLE can exactly compute every body mass datum from the mass and length data set. The animals addressed represent over two thirds of recent mammal species. But, since there was not a data set that simultaneously reported mass, BMR and characteristic length for animals from the mammal orders that were analyzed it could not be determined whether or not MMLE could simultaneously compute an animal's BMR and body mass given its characteristic length.

(Ramirez-Zea 2005) examined 261 groups of humans (*Homo sapiens*) from 175 studies that totaled over 11,000 subjects. Table 3 from that paper reports body mass, height and BMR for the subjects categorized by sex in three age groups and two body mass index (BMI) ranges. Mean values and ranges are given.

A human's characteristic length can be estimated from height. The purpose of this paper is to show that MMLE can simultaneously compute a human's body mass and BMR given his or her characteristic length using the (Ramirez-Zea, 2005) data.

Methods and materials. For the purposes of this paper the MMLE equations are (Frasier, 2015):

$$W = h[(sl)^2G_m/kfe + ((sl)^2mG_o/e)^{1/y}] \qquad (1)$$

$$BMR = G_r(sl)^2 \qquad (2)$$

W is body mass. BMR is basal metabolic rate. G_m/k is the skeletal muscle mass constant. G_o is the non-skeletal muscle constant. G_r is the resting metabolic rate constant. y is the non-skeletal muscle mass exponent. m is a dimensionality factor that adjusts the physical dimensions of this expression to mass. m is determined by y. y and m should have the same value for all animals in a phylogenetic group. k is the locomotion constant. k is a function of the type of dynamic similarity that applies to the type of propulsion used by an animal. k should be similar for all vertebrates that are dynamically similar. The fundamental propulsion frequency, f, should be the same function of the characteristic length, l, for all vertebrates that are dynamically similar. The mitochondrion capability quotient, e, is a constant whose value should be approximately identical for all vertebrates in the same phylogenetic group with the same body temperature. The characteristic length, l, and the sturdiness factor, s, have unique values for each individual animal.

h is the body fat factor. It is newly added in this paper to the MMLE equation for body mass because, with respect to other mammals, humans are fat. If equation (1) computed fat-free mass (FFM) then using the data from (Pontzer et al, 2016) Table 1 for men $h_M = 1.23$ and for women $h_F = 1.41$ whereas for gorillas $h_M = 1.12$, $h_F = 1.16$ and for chimpanzees $h_M = 1.08$, $h_F = 1.07$. Using data for young adults from (Muller et al, 2013) Table 1 gives similar results with $h_M = 1.23$ and $h_F = 1.44$.

The data for the animals considered by (Frasier, 1984; Frasier 2015) did not specify sex or body fat. The animals were wild. It is likely that their body fat is more like that of gorillas and chimpanzees than humans with little difference between males and females and h about 1.1 with respect to FFM. Adjusting the (Muller et al, 2013; Pontzeret et al, 2016) human body fat factors to work with the numerical values for the other equation (1) parameters determined by (Frasier, 2015) for mammals results with h_M about 1.12 and h_F about 1.3 and h = 1.0 for non-human running/walking mammals.

G_o is defined so that m is dimensionless with a value of 1.0 for geometrically similar non-skeletal musculature for which $y = 2/3$. G_m and k are defined so that k is non-dimensional with a value of 1.0 for running/walking placental mammals.

A general formulation for the fundamental propulsion frequency is $f = c/l^r$ where c is the propulsion frequency proportionality constant and r is the propulsion frequency exponent with a value between 0.5 and 1.0. Animals that are dynamically similar have similar values for the exponent, r and the constant c.

When gravitational force dominates the dynamics of animals' movement, two animals are dynamically similar when the ratio of gravitational force to inertial force is the same at corresponding stages of their motions. The animals are Froude similar and they have equal Froude numbers (Alexander & Jayes, 1983; Alexander, 2005). Running/walking mammals are Froude similar (Alexander et al, 1979; Alexander, 2005; Raichlen, Pontzer & Shapiro, 2013).

Strouhal similarity obtains when inertial forces are proportional to oscillatory forces. Similarity implies equal Strouhal numbers (Taylor, Nudds & Thomas, 2003).

Two animals are geometrically similar if one can be made identical to the other by multiplying all its linear dimensions by the same factor (Alexander, 2005). Body mass, W, is proportional to l^3. From equation (1) geometric similarity of the skeletal musculature means that the fundamental propulsion frequency exponent $r = 1.0$. The fundamental frequency constant, c, in equation (3) has the dimension of speed. If the non-skeletal musculature is also geometrically similar with $y = 2/3$, then the entire animal will be geometrically similar.

Froude and Strouhal dynamic similarity are separately compatible with geometric similarity.

If both Froude and Strouhal similarity simultaneously apply then the frequency, f, is proportional to the pendulum frequency, $(a/l)^{0.5}$, where a is the acceleration of gravity (Frasier, 2015). Substituting this expression for f in equation (1) shows that mass, W, is not proportional to l^3 and thus geometric similarity does not apply.

Humans are bipedal running/walking mammals. The methods used in the analysis of tetrapod running/walking mammals should also work for humans. Froude-Strouhal similarity applies to running/walking mammals from the orders Artiodactyla and Carnivora less Mustelidae while proboscideans, perissodactyls and mustelids seem to conform to geometric similarity (Frasier, 2015). For geometric similarity the parameter y in equation (1) has the value $y=2/3$ and the fundamental frequency is $f = (1.4 m/sec)/l$ where l is the characteristic length in meters (m). For Froude-Srrouhal similarity $f = [(9.81 m/sec^2)/l]^{0.5}$. To establish numerical values for other parameters occurring in equations (1) and (2) two regression analysis methods were used: Phylogenetically Informed (PI) regression employing Bayes Traits (Pagel, Meade & Barker, 2004) and AVG regression (Frasier, 1984; Frasier 2015). By the AVG method $y= 2/3$ and $m = 1.0$. By the PI method $y = 0.8$ and $m = 4.425\ g^{0.133}$. These similarity regimes are respectively called Froude-Strouhal AVG similarity and Froude-Strouhal PI similarity herein.

The sturdiness factor is best understood by looking at Fig.1. Figure 1 plots 348 samples of log body mass versus log shoulder height for running/walking mammals from the orders Artiocactyla, Carnivora, Perissodactyla and Proboscidea obtained from (Nowak, 1999). Shoulder height is a good surrogate for characteristic length for running/walking mammals. The data in Fig. 1 spread over an area in the two dimensional log shoulder height, log body mass space. Most of the area over which the data spreads is bounded by an upper line computed using equation (1) with the sturdiness factor set to the square root of 3, $(3)^{0.5}$, and a lower line computed with the sturdiness factor set to $(3)^{-0.5}$ (Frasier, 1984). These boundaries are plotted as the upper and lower slanting lines in Fig.1. Excluding the hippopotamus (*Hippopotamus amphibius*) and domestic cattle, over 97% of the data plotted in Fig.1 are contained between these boundary lines. The body masses of animals with the same characteristic length are distributed between the boundaries because they have different sturdiness factors. The mean of the body masses of animals with the same characteristic length occurs with sturdiness factor s = 1.0.

The surrogate for characteristic length for humans is leg length defined as standing height minus sitting body height. (Bogin & Varela-Silva, 2008) investigated the ratio of sitting height to standing height for men and women of white, black and Mexican American ethnicities. One minus this ratio is the leg length to standing height ratio. The mean for men is 0.479. The mean for women is 0.478. These means were calculated using the lowest body fat quartile data as gluteo-femoral fat can bias sitting height upwards.

Using the leg length to standing height ratio to convert height to characteristic length, Fig. 1 shows that the range of human body mass and characteristic length values from (Ramirez-Zea, 2005) fall within the sturdiness factor boundaries that are applicable to other running/walking mammals for geometric similarity, Froude-Strouhal AVG similarity and Froude-Strouhal PI similarity. MMLE cannot distinguish into which of the three similarity regimes humans fall. The human data must be evaluated with respect to all three possibilities.

For the remaining constants in equation (1), the value for the skeletal muscle mass constant is $G_m/k = 274000\ g/m^2$ and the value for the non-skeletal muscle constant is $G_o = 900\ g^{0.667}/m^2$ (Frasier, 2015).

For carnivores the value for the resting metabolic rate constant in equation (2) is $G_r = 95$ watts/m^2. For ruminant artiodactyls it is $G_{rR} = 138$ watts/m^2. The difference between G_{rR} and G_r is likely the result of sustained digestive activity by ruminants (McNab, 1997; White & Seymour, 2003). Mustelids also have an elevated BMR with respect to other carnivores. They do not have the digestive features that likely cause ruminants to have an elevated BMR. The MMLE parameters that could be adjusted to account for the mustelid BMR deviation are the fundamental propulsion frequency constant, c, the mitochondrion capability quotient, e and the dynamic similarity constant, k. Mustelids are geometrically similar in contrast to the other carnivores that are Froude-Strouhal similar (Frasier, 2015).

Figure 2 shows the MMLE BMR as a function of body mass sturdiness factor boundaries evaluated with these values for G_r and G_{rR} for Froude-Strouhal AVG and PI similarity. The boundaries for geometrically similar mustelids with modified c, e and/or k values are also shown. The BMR and body mass data for species in these orders from (Kolokotrones et al, 2010) are shown. The range of human BMR and body mass from (Ramirez-Zea, 2005) is shown. The human data does not entirely fit within either the ruminant or carnivore less mustelid boundaries.

Human BMR is from 1.17 to 1.5 times greater than that of chimpanzees, bonobos and orangutans with similar FFM. The elevated human BMR is attributable to greater brain size (Pontzer et al, 2016). Using (Leonard, Snodgrass & Robertson, 2007) data, human brains are from 3 to 3.5 times more massive than apes with similar body masses. Also, using (Benson-Amram et al, 2016) data, human brains are from 10 to 12 times larger than non-mustelid carnivores with similar body masses. Humans do not have the digestive features that likely cause ruminant artiodactyls to have BMRs that are greater than non-mustelid carnivores, but their metabolically expensive larger brains should cause the human resting metabolic rate constant G_{rH} to be greater than that of non-mustelid carnivores.

The (Ramirez-Zea, 2005) data are for adult men and women with BMI greater than 18.5 kg/m^2 and a subset of this group with BMI between 18.5 kg/m^2 and 25.0 kg/m^2. In each BMI-sex group data is given for ages 18 to 29.9 years, 30 to 59.9 years and 60 years and over which are respectively called the younger, middle aged and older groups herein. Data is also given for all men and for all women. A species averaged human for both of the BMI groups was constructed from the data by averaging body mass, height and BMR values for all men with the values for all women. This is the human correspondent to the species averages for the other mammals in the (Frasier, 2015) analysis.

The means for each of the BMI-sex-age groups is used. Including the species averaged humans, there are 18 different human samples in the (Ramiresz-Zea, 2005) data. To demonstrate that MMLE can simultaneously compute body mass W and BMR given characteristic length l, values for the parameters occurring in equations (1) and (2) must be determined for each of the 18 samples so that equation (1) exactly computes a sample's body mass given its characteristic length and simultaneously equation (2) exactly computes the sample's BMR given its characteristic length. In addition, values must be determined for each of the three similarity regimes: geometric, Froude-Strouhal AVG and Froude-Strouhal PI similarity.

Figure 1 shows that humans fall within the running/walking mammal MMLE boundaries for body mass and characteristic length for all three similarity regimes. Of the parameters occurring in equation (1) it is reasonable to use the values for running/walking mammals determined in (Frasier, 2015) for G_m/k, f, m, G_o, and y. Values for the mitochondria capability quotient, e, should be determined for each of the sex-age groups since mitochondria function declines with age (Shigenaga, Hagen & Ames, 1994; Navarro & Boveris, 2007). Finally, values for the sturdiness factor, s, and the body fat factor, h, need to be determined for each sample.

Figure 2 shows that humans do not entirely fall within the running/walking mammal MMLE boundaries for BMR and body mass for any of the similarity regimes. Consequently, a value for G_{rH} in equation (2) needs to be determined for each of the similarity regimes. The value should apply to all 18 samples within each of the similarity regimes.

When BMR is known, equation (2) can be solved for sl as a function of G_r. If l is also known an estimate for W as a function of G_r is obtained by substituting the values of sl and l into equation (1). Using the (Ramirez-Zea, 2005) BMR and l data the result is an estimate of W for each sample. Comparing the estimated W with the (Ramirez-Zea, 2005) W datum allows h to be estimated. Assuming e = 1.0 for men and women in the younger groups with BMI ≥ 18.5 and iterating this process with different G_{rH} values until h_M for the men is about 1.12 and, simultaneously, h_F for the women is about 1.3 establishes the G_{rH} for these sex-age-BMI groups. Using this value of G_{rH} and assuming the values of h are the same for the middle aged, the older, the all women and the all men groups allows values of e to be calculated for these groups. An e value for the species averaged human is estimated by averaging the all women and all men e values.

The G_{rH} was then used for the BMI between 18.5 and 25 and the younger groups to get values for h_M and h_F assuming e = 1.0. Then assuming the values of h are the same for the middle aged, the older, the all women and the all men groups, values for e were calculated for these groups. A species averaged human was constructed for the BMI between 18.5 and 25 group in the same way as for the BMI ≥ 18.5 group.

Finally, equation 2 was solved for s for each sample using the computed G_{rH} and the l datum for the sample.

This process was repeated for the three similarity regimes.

Results and discussion. Tables 1, 2 and 3 show the results. Each table is for a separate similarity regime. Ages, body masses, BMRs and BMIs shown in each table are from (Ramirez-Zea, 2005) except for the species averages. BMRs were converted from MJ/day to watts. Characteristic lengths were calculated from (Ramirez-Zea, 2005) standing heights using the sex appropriate leg length to standing height ratios calculated from (Bogin & Varela-Silva, 2008). The species averages were constructed by averaging the body mass, BMR, characteristic length and mitochondria capability quotient data for all men with that for all women.

The body masses shown in each table are exactly calculated with equation (1) for each sex-age-BMI category using its characteristic length l, mitochondria capability quotient e, body fat factor h, sturdiness factor s shown in the table and the parameter values determined for running/walking mammals in (Frasier, 2015): skeletal muscle mass constant $G_m/k = 274000$ g/m^2 and non-skeletal muscle constant $G_o = 900$ g$^{0.667}$/m^2 together with additional parameter values determined for running/walking mammals for each similarity regime.

Table 1 is for Froude-Strouhal AVG similarity with non-skeletal muscle mass exponent y = 2/3 and dimensionality factor m = 1.0. The fundamental propulsion frequency $f = (9.81(\text{m/sec}^2)/l)^{0.5}$. Table 2 is for Froude-Strouhal PI similarity with y = 0.8 and m = 4.425 g$^{0.133}$ and the same f. Table 3 is for geometric similarity with y=2/3, m = 1.0 and f = (1.4m/sec)/l.

The BMRs shown in each table are exactly computed with equation (2) for each sex-age-BMI category using its characteristic length l, sturdiness factor s shown in the table and its resting metabolic rate constant G_{rH}. For Table 1 G_{rH} = 131 watts/m^2. For Table 2 G_{rH} = 140 watts/m^2. For Table 3 G_{rH} = 230 watts/m^2.

Numeric values shown in the tables have been rounded to three significant digits. For this reason the BMR and body mass values computed with the values shown are only accurate to within 0.5%.

Although the methodology was to find, for each similarity regime, a G_{rH} so that the body fat factor for men $h_M = 1.12$ and for women $h_F = 1.3$ simultaneously for the BMI ≥ 18.5 group, this could only be achieved for the geometric similarity regime. For the Froude-Strouhal AVG regime the best compromise was to get the h values within 2% of their targets. For the Froude-Strouhal PI regime the best compromise was to get the h values within 3% of their targets. These compromises were 'best' in the sense that they yielded the most accurate simultaneous computations of BMR and body mass given characteristic length.

It was not a purpose of this paper to attempt to determine which similarity regime is most applicable to humans. Figure 1 shows that humans fall in the running/walking mammals body mass – characteristic length area where all three regimes intersect. Thus it was necessary to consider each regime to determine a G_{rH} value to use in equation (2). (Wang et al, 2012) found that fat-free mass scales close to height cubed irrespective of gender or ancestry. This supports geometric similarity. (Heymsfield et al, 2011) found that it scales closer to height squared. Within a species variability of the body fat factor h, the sturdiness factor s and the mitochondria capability quotient e could obscure the relationship of body mass to height.

The parameter values shown in the tables were determined using the (Ramirez-Zea, 2005) data for BMI ≥ 18.5 to find a G_{rH} for each regime so that for the younger groups the body fat factor for men h_M was about 1.12 and for women h_F was about 1.3. Had the BMI between 18.5 and 25.0 data been used instead of the BMI ≥ 18.5 data, the resulting G_{rH} values would be larger: 135 watts/m^2 instead of 131 watts/m^2 for Froude-Strouhal AVG similarity; 144 watts/m^2 instead of 140 watts /m^2 for Froude-Strouhal PI similarity; and 236 watts/m^2 instead of 230 watts/m^2 for geometric similarity. The difference in each similarity regime is 3% or less.

$G_r = 95$ watts/m^2 for carnivores less mustelids and $G_{rR} = 138$ watts/m^2 for ruminant artiodactyls (Frasier, 2015). Based on figure 2 it could be expected that G_{rH} should fall between G_r and G_{rR}. It is greater than G_r for all three similarity regimes. With respect to G_{rR} it is less for one regime, about the same for the second and much greater for the third. Both carnivores and ruminants have body fat factor $h \approx 1.0$ whereas the species averaged human in tables 1, 2 and 3 has $h = 1.2$. Thus an average human of the same body mass as another running/walking mammal only has 1/1.2 = 83% as much metabolically active tissue. Additionally the tables show that humans are more gracile than the average running/walking mammal as humans have sturdiness factors less than 1.0. The result is that comparing the average human to an average non-mustelid carnivore of the same body mass, the human's BMR is only 1.17 to 1.73 times greater than the carnivore's BMR even though the human's resting metabolic rate constant G_{rH} is from 1.38 to 2.42 times greater. Comparing the average human to an average ruminant of the same body mass, the human's BMR is only 0.805 to 1.19 as great as the ruminant's BMR. Figure 2 plots BMR with respect to body mass. It correctly shows that a human's BMR falls between the BMR of non-mustelid carnivores and ruminants with the same body mass.

Mitochondria function declines with age (Shigenaga, Hagen & Ames, 1994; Navarro & Boveris, 2007). Tables 1, 2 and 3 show a substantial decrease of mitochondria capability quotient with age. For the BMI ≥ 18.5 group it decreases by about 7% from men aged 18 to 29.9 years to men aged 30 to 59.9 years. It further decreases another 9% to the 60 years and older group. For women it decreases about 4% from the younger group to the middle aged group and another 12% from the middle aged group to the older group. For the BMI between 18.5 and 25 group it decreases only about 2% or less from the younger group to the middle aged group for both sexes; but it catches up with the BMI ≥ 18.5 group for the older groups with further decreases of up to 14% for both sexes. (Muller et al, 2013) found decreases in specific organ and tissue metabolic rates with age and obesity although it is difficult to quantitatively compare that data with the (Ramirez-Zea, 2005) data because, except for the youngest, the age groupings for the later are older.

The parameter values shown in the tables were determined by finding a G_{rH} for each similarity regime so that for the BMI ≥ 18.5 groups of 18 to 29.9 years olds the body fat factor for men h_M was about 1.12 and for women h_F was about 1.3. The mitochondria capability quotient for the other BMI ≥ 18.5 age groups were determined by using the found G_{rH} and the same body fat factors. The found G_{rH} was used to determine h_M and h_F for the BMI between 18.5 and 25 groups of 18 to 29.9 year olds and these body fat factors were used to determine the mitochondria capability quotients for the older BMI between 18.5 and 25 groups. Allowing the older age groups to have greater body fat factors would reduce the decline of the mitochondria capability quotient with age. The (Muller et al, 2013) data shows a less than 2% increase of body fat factor with age. Increasing body fat factor with age may be an unnecessary refinement.

Conclusion. MMLE can simultaneously compute a human’s body mass and BMR given his or her characteristic length using the (Ramirez-Zea, 2005) data.

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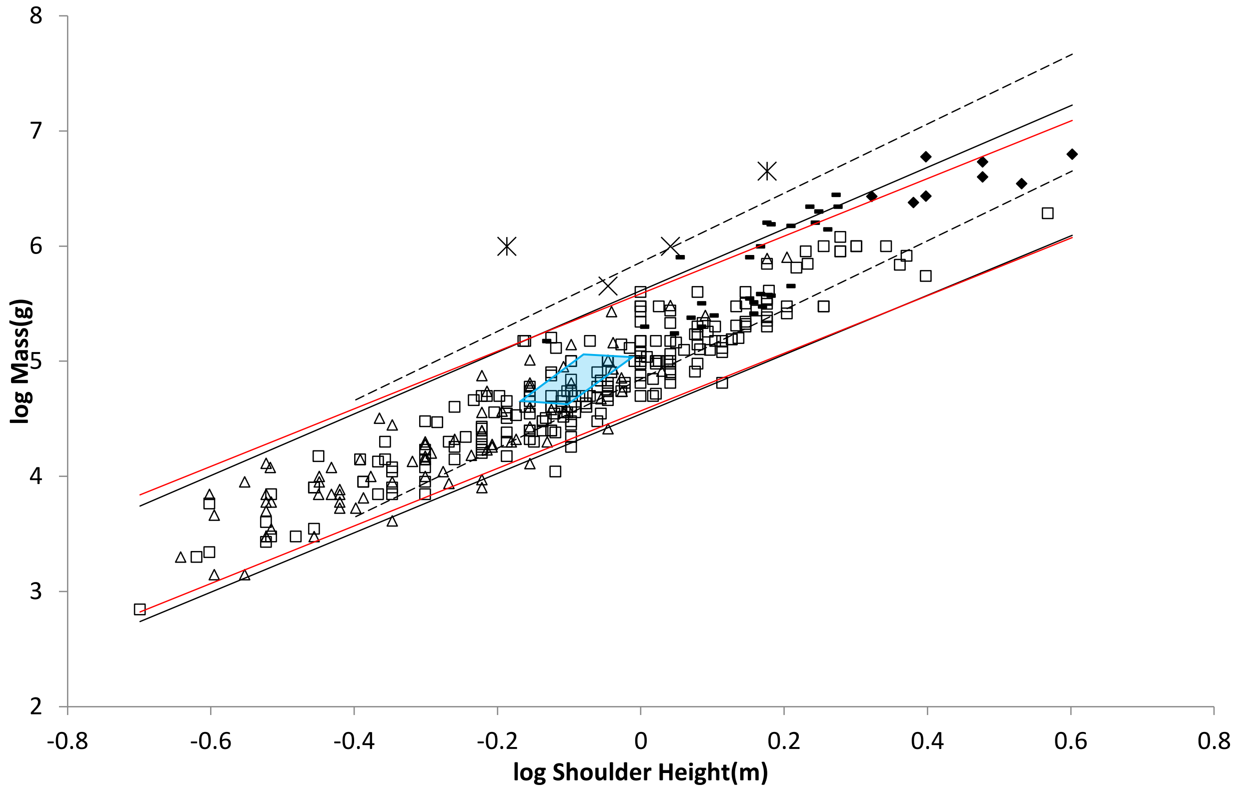

Figure 1. Log body mass as a function of log shoulder height for running/walking placental mammals. Data are from (Nowak, 1999). The solid and dashed lines are MMLE sturdiness factor boundaries. The upper boundaries were generated with a sturdiness factor s = $(3)^{0.5}$. The lower boundaries were generated with s = $(3)^{-0.5}$. The black solid lines are for Froude-Strouhal AVG dynamic similarity. The colored solid lines are for Froude-Strouhal PI dynamic similarity. The dashed boundary lines are for geometric similarity. Perissodactyls are marked with solid rectangles. Proboscideans are marked with solid diamonds. Artiodactyls are marked with open squares. Carnivores are marked with open triangles. Crossed Xes mark hippopotamus (*Hippopotamus amphibious*). Xes mark domestic cattle. The colored polygon embraces the range of human data from (Ramirez-Zea, 2005).

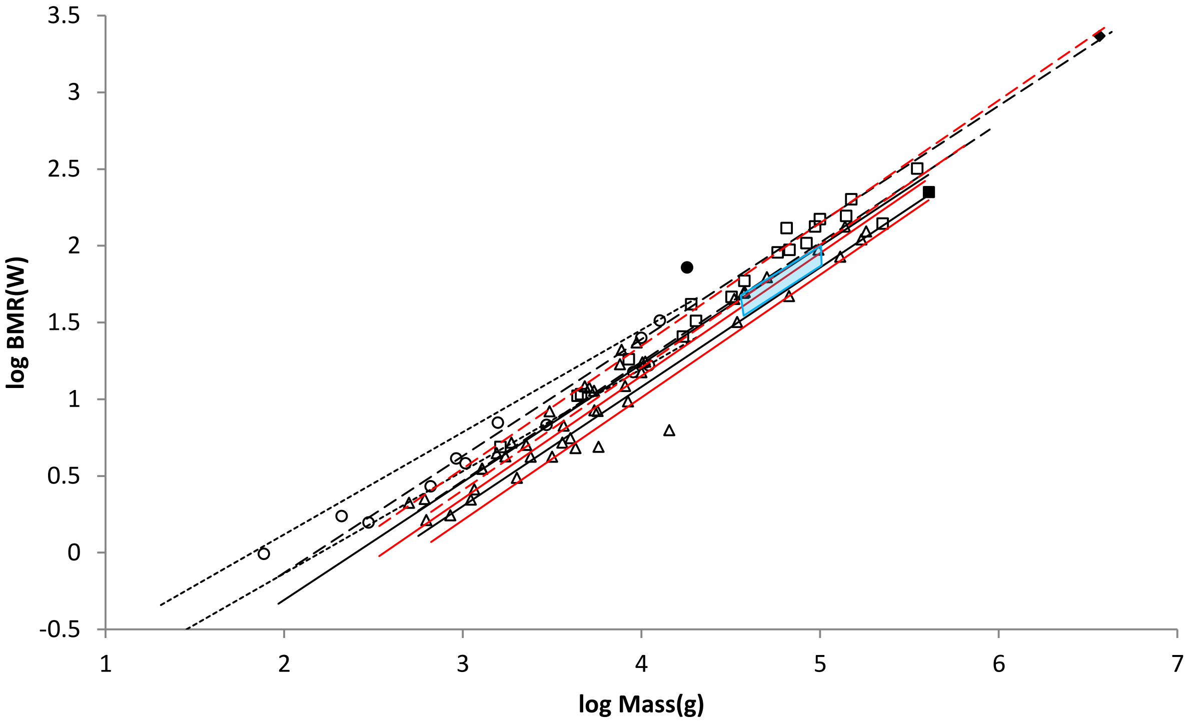

Figure 2. Log BMR as a function of log body mass for running/walking placental mammals. The Asian elephant (*Elephas maximus*) datum marked by a solid diamond is from (Savage et al, 2004). All other data are species-averages from (Kolokotrones et al, 2010). The solid, dashed and dotted lines are MMLE sturdiness factor boundaries. The upper boundaries were generated with a sturdiness factor s = $(3)^{0.5}$. The lower boundaries were generated with s = $(3)^{-0.5}$. Solid lines are for carnivores. Dashed lines are for ruminant artiodactyls. The dotted line is for mustelids less sea otters. The steeper sloping black lines are for Froude-Strouhal AVG dynamic similarity. The shallower sloping black lines are for geometric similarity. The colored lines are for Froude-Strouhal PI dynamic similarity. Ruminant are marked by open squares. The Dromedary camel (*Camelius dromedarius*) is a non-ruminant artiodactyl marked by a solid square. Carnivores less mustelids are marked with open triangles. Mustelids except the sea otter are marked with open circles The sea otter (*Enhydra lutris*) is an ocean going swimming mustelid marked by a solid circle. The colored polygon embraces the range of human data from (Ramirez-Zea, 2005).

Sex	Age (years)	Mass (kg), W	Characteristic length(m), l	BMR (watts)	BMI (kg/m^2)	Mitochondria capability quotient, e	Body fat factor, h	Sturdiness factor, s
BMI ≥ 18.5 kg/m^2:								
M	18-29.9	72.8	0.843	82.4	23.4	1.0	1.14	0.941
M	30-59.9	80.2	0.834	84.4	26.4	0.935	1.14	0.963
M	≥ 60	75.3	0.824	73.2	25.4	0.855	1.14	0.907
F	18-29.9	61.0	0.774	65.2	23.0	1.0	1.28	0.911
F	30-59.9	67.1	0.774	68.0	25.7	0.958	1.28	0.931
F	≥ 60	67.7	0.765	60.5	26.3	0.841	1.28	0.889
All M	37.5	75.8	0.838	81.3	24.8	0.949	1.14	0.94
All F	36.9	64.5	0.774	65.9	24.5	0.962	1.28	0.916
Species average		70.2	0.806	73.6	24.7	0.956	1.17	0.93
BMI between 18.5 and 25.0 kg/m^2:								
M	18-29.9	69.8	0.843	81.0	22.5	1.0	1.11	0.933
M	30-59.9	69.3	0.862	79.0	23.3	0.99	1.11	0.901
M	≥ 60	70.1	0.824	69.6	23.6	0.849	1.011	0.885
F	18-29.9	56.7	0.774	63.0	21.5	1.0	1.23	0.896
F	30-59.9	60.4	0.774	65.3	22.9	0.979	1.23	0.912
F	≥ 60	61.0	0.755	58.4	23.6	0.859	1.23	0.884
All M	32.1	69.7	0.843	79.3	22.8	0.981	1.11	0.923
All F	34.4	58.5	0.774	63.6	22.2	0.981	1.23	0.9
Species average		64.1	0.809	71.5	22.4	0.981	1.17	0.913

Table 1. Parameter values for simultaneously computing body mass and BMR given characteristic length for humans for Froude-Strouhal AVG similarity.

The resting metabolic rate constant G_{rH} = 131 watts/m^2 for all sex-age-BMI categories. The body mass W is exactly calculated with equation (1) for each sex-age-BMI category using the values shown in the table for characteristic length l, mitochondria capability quotient e, body fat factor h, sturdiness factor s and other parameter values determined for running/walking mammals in (Frasier, 2015). The BMR is exactly computed with equation (2) for each sex-age-BMI category using the l and s values shown in the table and G_{rH}. With the exception of the species averages, ages, body masses, BMRs and BMIs are from (Ramirez-Zea, 2005). BMRs were converted from MJ/day to watts. Characteristic lengths were calculated from (Ramirez-Zea, 2005) standing heights using the sex appropriate leg length to standing height ratios calculated from (Bogin &Varela-Silva, 2008). The species averages were constructed by averaging the all men with the all women body mass, BMR, l, and e data.

Sex	Age (years)	Mass (kg), W	Characteristic length(m), l	BMR (watts)	BMI (kg/m^2)	Mitochondria capability quotient, e	Body fat factor, h	Sturdiness factor, s
BMI ≥ 18.5 kg/m^2:								
M	18-29.9	72.8	0.843	82.4	23.4	1.0	1.15	0.909
M	30-59.9	80.2	0.834	84.4	26.4	0.932	1.15	0.931
M	≥ 60	75.3	0.824	73.2	25.4	0.854	1.15	0.876
F	18-29.9	61.0	0.774	65.2	23.0	1.0	1.27	0.88
F	30-59.9	67.1	0.774	68.0	25.7	0.955	1.27	0.899
F	≥ 60	67.7	0.765	60.5	26.3	0.838	1.27	0.859
All M	37.5	75.8	0.838	81.3	24.8	0.948	1.15	0.908
All F	36.9	64.5	0.774	65.9	24.5	0.96	1.27	0.855
Species average		61.8	0.806	73.6	21.76	0.954	1.21	0.898
BMI between 18.5 and 25.0 kg/m^2:								
M	18-29.9	69.8	0.843	81.0	22.5	1.0	1.12	0.901
M	30-59.9	69.3	0.862	79.0	23.3	0.99	1.12	0.87
M	≥ 60	70.1	0.824	69.6	23.6	0.849	1.12	0.855
F	18-29.9	56.7	0.774	63.0	21.5	1.0	1.23	0.865
F	30-59.9	60.4	0.774	65.3	22.9	0.977	1.23	0.881
F	≥ 60	61.0	0.755	58.4	23.6	0.857	1.23	0.854
All M	32.1	69.7	0.843	79.3	22.8	0.981	1.12	0.892
All F	34.4	58.5	0.774	63.6	22.2	0.98	1.23	0.87
Species average		64.1	0.809	71.5	22.4	0.981	1.17	0.883

Table 2. Parameter values for simultaneously computing body mass and BMR given characteristic length for humans for Froude-Strouhal PI similarity.

The resting metabolic rate constant G_{rH} = 140 watts/m^2 for all sex-age-BMI categories. The body mass W is exactly calculated with equation (1) for each sex-age-BMI category using the values shown in the table for characteristic length l, mitochondria capability quotient e, body fat factor h, sturdiness factor s and other parameter values determined for running/walking mammals in (Frasier, 2015). The BMR is exactly computed with equation (2) for each sex-age-BMI category using the l and s values shown in the table and G_{rH}. With the exception of the species averages, ages, body masses, BMRs and BMIs are from (Ramirez-Zea, 2005). BMRs were converted from MJ/day to watts. Characteristic lengths were calculated from (Ramirez-Zea, 2005) standing heights using the sex appropriate leg length to standing height ratios calculated from (Bogin and Varela-Silva, 2008). The species averages were constructed by averaging the all men with the all women body mass, BMR, l, and e data.

Sex	Age (years)	Mass (kg), W	Characteristic length(m), l	BMR (watts)	BMI (kg/m^2)	Mitochondria capability quotient, e	Body fat factor, h	Sturdiness factor, s
BMI ≥ 18.5 kg/m^2:								
M	18-29.9	72.8	0.843	82.4	23.4	1.0	1.12	0.71
M	30-59.9	80.2	0.834	84.4	26.4	0.925	1.12	0.727
M	≥ 60	75.3	0.824	73.2	25.4	0.843	1.12	0.685
F	18-29.9	61.0	0.774	65.2	23.0	1.0	1.3	0.687
F	30-59.9	67.1	0.774	68.0	25.7	0.953	1.3	0.702
F	≥ 60	67.7	0.765	60.5	26.3	0.831	1.3	0.671
All M	37.5	75.8	0.838	81.3	24.8	0.945	1.12	0.709
All F	36.9	64.5	0.774	65.9	24.5	0.959	1.3	0.691
Species average		61.8	0.806	73.6	21.76	0.952	1.2	0.702
BMI between 18.5 and 25.0 kg/m^2:								
M	18-29.9	69.8	0.843	81.0	22.5	1.0	1.1	0.704
M	30-59.9	69.3	0.862	79.0	23.3	1.0	1.09	0.68
M	≥ 60	70.1	0.824	69.6	23.6	0.839	1.1	0.668
F	18-29.9	56.7	0.774	63.0	21.5	1.0	1.25	0.676
F	30-59.9	60.4	0.774	65.3	22.9	0.976	1.25	0.688
F	≥ 60	61.0	0.755	58.4	23.6	0.845	1.25	0.667
All M	32.1	69.7	0.843	79.3	22.8	0.973	1.09	0.697
All F	34.4	58.5	0.774	63.6	22.2	0.985	1.25	0.679
Species average		64.1	0.809	71.5	22.4	0.979	1.16	0.689

Table 3. Parameter values for simultaneously computing body mass and BMR given characteristic length for humans for geometric similarity.

The resting metabolic rate constant G_{rH} = 230 watts/m^2 for all sex-age-BMI categories. The body mass W is exactly calculated with equation (1) for each sex-age-BMI category using the values shown in the table for characteristic length l, mitochondria capability quotient e, body fat factor h, sturdiness factor s and other parameter values determined for running/walking mammals in (Frasier, 2015). The BMR is exactly computed with equation (2) for each sex-age-BMI category using the l and s values shown in the table and G_{rH}. With the exception of the species averages, ages, body masses, BMRs and BMIs are from (Ramirez-Zea, 2005). BMRs were converted from MJ/day to watts. Characteristic lengths were calculated from (Ramirez-Zea, 2005) standing heights using the sex appropriate leg length to standing height ratios calculated from (Bogin and Varela-Silva, 2008). The species averages were constructed by averaging the all men with the all women body mass, BMR, l, and e data.