## Model-Fitting with Linear Regression: Power Functions

In the biological sciences it has long been recognized that body size scales predictably with various life history parameters. These scaling relationships are known as *invariant* relationships as no matter what the body size (from ants to elephants) it is possible to predict certain life history parameters from a single equation. Recently members of the biology department at UNM have proposed a hypothesis that states these invariant relationships are caused by the fundamental metabolic constraints that all organisms face. The invariance is a by-product of the fact that most organisms have similar metabolic pathways (e.g. blood-carrying capillaries) that simply scale with body size. Through some relatively complex math involving the space-filling fractal branching networks of three-dimensional animals, they predict that the scaling relationship of metabolic rate to body size should be a power function with a scaling exponent of 0.75. We can look at this hypothesis as a regression analysis.

For now let's not worry about power functions, but notice that the scaling exponent they are referring to is nothing more than β. That is they hypothesize that when we run a linear regression between the metabolic rate and body size of *any* animal, or class of animals, the slope should be 0.75 ($\pm$ error). Therefore, let's test the hypothesis that $\beta = 0.75$ by looking at a sample of data collected on a wide variety of primate species. The following data ($n = 25$) come from Leonard and Robinson (1997, AJPA):

Species	Weight (kg)	RMR
A. palliata	8.5	363
A. palliata	6.4	293
A. trivirgatus	0.85	46
A. geoffroyi	8.41	346
C. molloch	0.7	54
C. apella	2.6	143
C. albifrons	2.4	135
S. imperator	0.4	35
S. fusicollis	0.3	28
S. sciureus	0.8	66
C. albigena	7.9	327
C. guereza	7	265
M. fascicularis	5.5	331
P. anubis	29.3	956
P. anubis	13	520
H. lar	6	292
P. troglodytes	39.5	1036
P. troglodytes	29.8	839
P. pygmaeus	83.6	1948
P. pygmaeus	37.8	1074
S. syndactylus	10.5	408
!Kung	46	1383
!Kung	41	1099
Ache	59.6	1591
Ache	51.8	1394

RMR is the resting metabolic rate, which is the energy required to run the body when the body is doing nothing. Notice that primate species in this data set range from the smallest Ceboidea to largest Hominioidea.

The first thing is to plot out the data in graphical form:
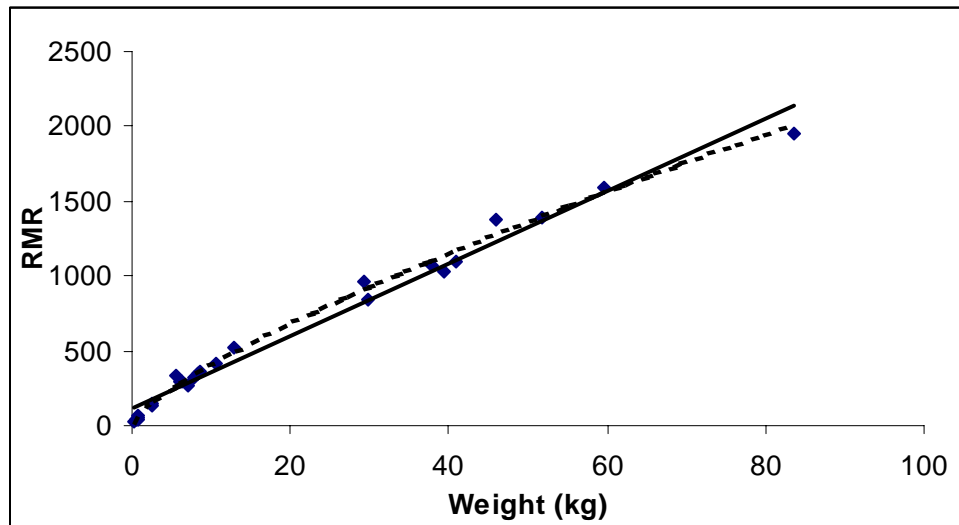
Now, from this output we can see there is a very strong relationship between weight and RMR, therefore our r^2 value will be very close to 1. But our job is to accurately describe this relationship and test our hypothesis of interest. Although the above relationship is very close, notice that it is not necessarily linear. The straight line is a fitted linear equation, and even though the data points fall close to the line, most are above it suggesting that the actual function is concave-up (the dashed line). Such relationships are often *power functions*. Like the exponential function, a power function can be calculated from a linear equation using some simple algebra once we have linearized our data.

In this example we will not go through all the hand calculations but straight to the computation in EXCEL and MINITAB, as they are the standard calculations simply run on log-transformed data.

First we take the base of the natural logarithms for both the *X* and the *Y* data, and plot them out to see if we have successfully linearized the relationship:
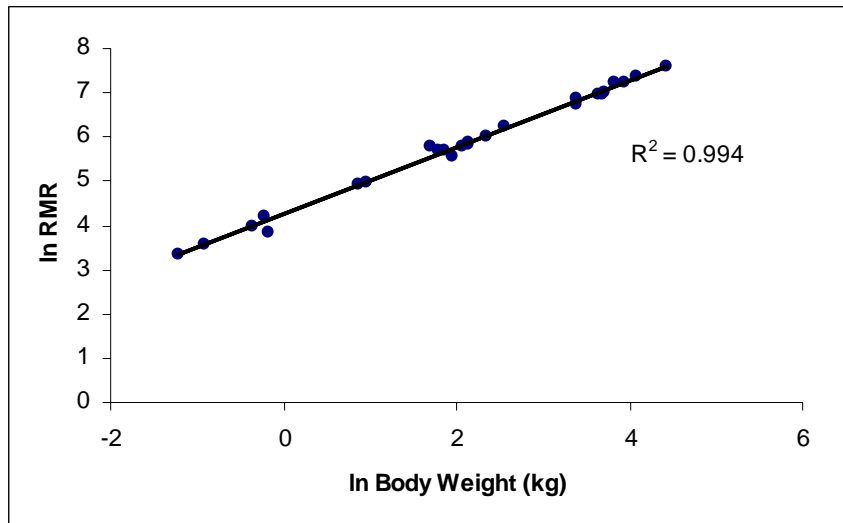
The fitted line is a linear equation, and the r^2 value is almost perfect (a very rare outcome!). Straight away, the strength of the r^2 value suggests there must be some very powerful constraints behind this relationship, a common feature of scale invariance.

To calculate our initial hypothesis test, we run the regression in MINITAB at the $a = 0.05$ (95%) confidence level to test the hypothesis:

H_O: $\beta_{H*A} = 0$
H_A : not H_O

Regression Analysis

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The regression equation is
logRMR = 4.24 + 0.760 logKg

Predictor        Coef        StDev              T          P
Constant      4.24089      0.03238         130.95      0.000
logKg         0.75989      0.01231          61.72      0.000

S = 0.1004      R-Sq = 99.4%       R-Sq(adj) = 99.4%

Analysis of Variance

Source        DF             SS            MS            F          P
Regression     1         38.380        38.380      3809.81      0.000
Error         23          0.232         0.010
Total         24         38.612
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In the ANOVA table notice that the unexplained sum of squares is extremely small, suggesting that nearly all the variation between RMR and body size can be explained by the linear function logRMR = 4.24 + 0.760 logKg. The important value we are interested in here is $\beta = 0.76$, a value very close to the hypothesized value of 0.75.

Before we test the value of our β let's convert the equation from the linearized log transform into raw values. Again, we use a little algebra.

$$\log Y = \log a + \beta \log X$$

$$e^{\log Y} = e^a + \beta e^{\log X}$$

$$Y = AX^{\beta}$$

So, our regression equation is now a power function $RMR = 69.47(Weight^{0.76})$, that is resting metabolic rate increases as a power function of weight with a scaling exponent of 0.76.

To test whether $\beta = 0.76$ is statistically significant from a predicted value of 0.75 we'll put confidence limits around our β.

To calculate our standard error of the regression coefficient:

$$S_{\beta} = \sqrt{\frac{S_{Y*X}^2}{\sum x^2}} = \sqrt{\frac{0.01}{66.467}} = 0.0123 \text{ (calculation for the denominator not shown)}$$

And the $T_{CRIT}\{0.05, 23\} = 2.069$,

Therefore the confidence limits are:

$CL_L = 0.76 - 0.0123*2.069 = 0.735$
$CL_U = 0.76 + 0.0123*2.069 = 0.785$

As the hypothesized value of $\beta = 0.75$ falls within the 95% confidence limits set around our calculated β, we conclude that the predictions of the metabolic scaling hypothesis are met by our sample of primate data. That is to say that across a wide sample of primate body sizes (representing a good estimate of the population range) the resting metabolic rate is scale invariant and determined by the scale invariance of the mammalian fractal branching network of blood-carrying capillaries.