

1 **Determinants of inter-specific variation in basal metabolic rate: a review**

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13 **Running head:** Variation in Basal Metabolic Rate

14

15 **Abstract**

16 Basal metabolic rate (BMR) is the rate of metabolism of a resting, postabsorptive, non-  
17 reproductive, adult bird or mammal, measured during the inactive circadian phase at a thermoneutral  
18 temperature. BMR is one of the most widely measured physiological traits, and data are available for  
19 over 1200 species. With data available for such a wide range of species, BMR is a benchmark  
20 measurement in ecological and evolutionary physiology, and is often used as a reference against  
21 which other levels of metabolism are compared. Implicit in such comparisons is the assumption that  
22 BMR is invariant for a given species, and that it therefore represents a stable point of comparison.  
23 However, BMR shows substantial variation between individuals, populations, and species.  
24 Investigation of the ultimate (evolutionary) explanations for these differences remains an active area  
25 of inquiry, and explanation of size-related trends remains a contentious area. Whereas explanations  
26 for the scaling of BMR are generally mechanistic and claim ties to the first principles of chemistry  
27 and physics, investigations of mass-independent variation typically take an evolutionary perspective  
28 and have demonstrated that BMR is ultimately linked with a range of extrinsic variables including  
29 diet, habitat temperature, and net primary productivity. Here we review explanations for size-related  
30 and mass-independent variation in the BMR of animals, and suggest ways that the various  
31 explanations can be evaluated and integrated.

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33

## 34 **Introduction**

35 Basal metabolic rate (BMR) is perhaps the most widely reported physiological metric.  
36 ‘Basal’ has long been recognised as a poorly chosen term (Krogh, 1916) because metabolic rate can  
37 fall below BMR under a range of conditions (Geiser, 2004; Green et al., 2007; Halsey et al., 2008;  
38 Green et al., 2009). The term nevertheless remains in widespread use and has come to refer not to  
39 the lowest metabolic rate that an endotherm can achieve, but instead to metabolic rate measured  
40 under precisely defined conditions. BMR is the rate of metabolism of a resting, normothermic,  
41 postabsorptive, non-reproductive, adult bird or mammal, measured during the inactive circadian  
42 phase at a thermoneutral temperature (McNab, 1997; Frappell and Butler, 2004). BMR is usually  
43 measured by indirect calorimetry as rate of oxygen consumption, using well described techniques  
44 and commercially available equipment (Withers, 2001; Lighton, 2008). Being relatively easy to  
45 measure in the laboratory, the number of species for which data are available has grown steadily  
46 since the 1930s (Figure 1), and data are presently available for nearly 700 species of mammal (Sieg  
47 et al., 2009), and more than 500 species of bird (McNab, 2009). The highest reported BMR (of  
48 *Elephas maximus*: Benedict, 1938) is almost five orders of magnitude greater than the lowest (of  
49 *Myotis nigricans*: McNab, 1989), and size is well known to account for much of the inter-specific  
50 variation in BMR (Peters, 1983; Calder, 1984; Schmidt-Nielsen, 1984). However, the strong  
51 relationship between mass and BMR conceals a great deal of variation, and species of the same size  
52 can differ by up to several fold (White and Seymour, 2004). Even within a species, BMR varies  
53 seasonally (Lovegrove, 2005; Smit and McKechnie, 2010) as well as between populations (Wikelski  
54 et al., 2003; Broggi et al., 2007; Tieleman et al., 2009b) and individuals (Nespolo and Franco, 2007).  
55 That differences between individuals and species can be significant, substantial, and repeatable, has  
56 led to the speculation that this variation must be important. The present review examines the causes  
57 and consequences of this variation, approaching the topic from both ultimate (evolutionary) and  
58 proximate (mechanistic) perspectives. We focus on inter-specific variation in BMR, though we do

59 use some examples from intra-specific studies; a more in-depth coverage of intra-specific variation is  
60 provided by Konarzewski and Książek (2012). We begin by discussing the profound influence of  
61 body mass on metabolism, and follow this with a discussion of the causes and consequences of the  
62 variation in BMR that is not explained by body mass. We conclude with the suggestion that  
63 integrative examinations of mass-dependent and mass-independent variation are likely to yield  
64 valuable insights into the evolutionary causes of the allometric scaling of metabolic rate with body  
65 mass.

## 66 **Non-isometric scaling and the influence of body mass**

67 Body mass alone explains most (generally > 90%) of the variation in BMR between species,  
68 and a great deal of ink has been spilled debating the exact form of the scaling relationship between  
69 body mass and metabolism. Like many physiological variables, BMR does not increase in direct  
70 proportion to body mass (isometrically). Instead, the relationship between body mass (M) and BMR  
71 is allometric and often well described by a power function of the form:

$$72 \quad \text{BMR} = a M^b$$

73 where a is the scaling constant, and b is the scaling exponent (see White, 2011; White and Kearney,  
74 2012 for discussion of statistical analyses of metabolic scaling). The value of the scaling exponent  
75 has been the subject of interest since at least the 19<sup>th</sup> century, when Sarrus and Rameaux (1838, cited  
76 by Brody, 1945) suggested that metabolic rate should scale in proportion to body surface area rather  
77 than body mass. Sarrus and Rameaux's hypothesis found empirical support when Rubner (1883)  
78 reported that the metabolic rates of dogs were proportional not to their body mass, but to their body  
79 surface area. This finding came to be known as the surface law of metabolism (e.g. Brody, 1945;  
80 Kleiber, 1961). Although some subsequent studies have supported the exponent of  $\frac{2}{3}$  implied by  
81 these early analyses (e.g. Heusner, 1991; White and Seymour, 2003), the heat loss hypothesis is  
82 unlikely to be correct, since animals with relatively high body surface areas do not have relatively  
83 high BMRs (White and Seymour, 2004). Moreover, in the decades following publication of Rubner's

84 (1883) work, the exponent of  $\frac{2}{3}$  was supplanted by a value of  $\frac{3}{4}$  (Kleiber, 1932). Later analyses  
85 expanded the data set to include a wider range of species (Benedict, 1938; Brody, 1945;  
86 Hemmingsen, 1960) and the  $\frac{3}{4}$ -power scaling relationship came to be known as Kleiber's law (e.g.  
87 Smil, 2000; Wang et al., 2001). Notably, however, recent analyses reject any single value of the  
88 exponent for mammals (e.g. Duncan et al., 2007; Sieg et al., 2009; White et al., 2009; Capellini et al.,  
89 2010) and demonstrate that the scaling exponent of BMR increases with body size (e.g. Clarke et al.,  
90 2010; Kolokotronis et al., 2010). These analyses further refute the idea that heat loss dictates the  
91 scaling of BMR, because the exponent of BMR for large animals with low surface area: volume  
92 ratios is significantly different from the scaling exponent of body surface area ( $\frac{2}{3}$ : Reynolds, 1997).  
93 Among birds, the most recent phylogenetically-informed (PI) analyses demonstrate a difference  
94 between wild-caught and captive species (McKechnie et al., 2006). Wild-caught birds scale with an  
95 exponent close to  $\frac{3}{4}$ , whereas captive species scale with an exponent close to  $\frac{2}{3}$  (McKechnie et al.,  
96 2006), although other studies favour different values (White et al., 2007a). Clearly, there is no  
97 consensus on a single value for the scaling exponent of BMR, and recent meta-analyses have  
98 generally stressed the lack of a single universal value (Savage et al., 2004; Glazier, 2005; White et  
99 al., 2007b). The *causes* of the non-isometric scaling of metabolism remain a lively subject of  
100 ongoing debate (e.g. Krogh, 1916; Kleiber, 1961; McMahon, 1973; Heusner, 1982; Kooijman, 1986;  
101 Heusner, 1991; Patterson, 1992; West et al., 1997; Banavar et al., 1999; West et al., 1999; Dodds et  
102 al., 2001; Banavar et al., 2002b; Darveau et al., 2002; Kozłowski et al., 2003b, a; Agutter and  
103 Wheatley, 2004; Kozłowski and Konarzewski, 2004; Weibel et al., 2004; Brown et al., 2005;  
104 Glazier, 2005; Kozłowski and Konarzewski, 2005; Weibel and Hoppeler, 2005; Demetrius, 2006;  
105 Chown et al., 2007; Gillooly and Allen, 2007; White et al., 2007b; Ginzburg and Damuth, 2008;  
106 White et al., 2008; Banavar et al., 2010; Demetrius and Tuszynski, 2010; Glazier, 2010; Roberts et  
107 al., 2010; Agutter and Tuszynski, 2011; Riveros and Enquist, 2011; Roberts et al., 2011; Seymour  
108 and White, 2011; White et al., 2011c).

109 Hypotheses for the scaling of metabolic rate have been reviewed in detail by a number of  
110 authors (e.g. Dodds et al., 2001; Agutter and Wheatley, 2004; Glazier, 2005; da Silva et al., 2006;  
111 O'Connor et al., 2007), and many hypotheses will not be discussed further here (e.g. Patterson, 1992;  
112 Witting, 1995; Kozłowski and Weiner, 1997; Bejan, 2000; Demetrius, 2003; Makarieva et al., 2003;  
113 Bejan, 2005; Demetrius, 2006; Ginzburg and Damuth, 2008; Demetrius and Tuszynski, 2010).  
114 Instead, we focus on those hypotheses that we view as most prominent, emphasising those that are  
115 the subject of ongoing empirical scrutiny.

### 116 **Resource Distribution**

117 The most prominent recent explanations for the scaling of metabolic rate are the resource distribution  
118 theories of West, Brown, and Enquist (West et al., 1997, 1999) and Banavar and co-workers  
119 (Banavar et al., 1999; Banavar et al., 2002b). These theories predict the scaling of metabolic rate  
120 with body size on the basis of models of resource transport. The two theories have influenced a  
121 general model for quarter-power scaling in animals, which incorporates a minimum of specific detail  
122 and requires only a few simplifying assumptions (reproduced from Banavar et al., 2010 p 15816,  
123 with minor modifications for clarity):

- 124 1. Definition of metabolic rate: Metabolic rate,  $B$ , can be measured as the rate of flow of discrete  
125 particles through a supply network. In mammals, for example, metabolic rate is routinely measured  
126 as the rate of oxygen consumption, and the oxygen molecules are transported in the blood vessels  
127 from a central source, the heart, to terminal units, the mitochondria.
- 128 2. Steady-state postulate: The flux of resources is at steady state, so supply matches demand, the rate  
129  $B$  of particles being consumed by the terminal units matches the rate  $B$  of particles leaving the  
130 source, and the number of particles in transit does not change over time.
- 131 3. Geometric similarity: Animals, especially those in the same taxonomic or functional group, are  
132 geometrically similar, so their geometry can be characterized by length,  $L$ , surface area,  $A$ , and  
133 volume,  $V$ , and simple Euclidean geometrical scaling gives  $V \sim L^3$  and  $A \sim L^2$ .
- 134 4. Directed transport: The average distance ( $d$ ) from the source to each terminal unit is proportional to  
135 the length,  $L$ , of the animal.
- 136 5. Velocity,  $v$ , is assumed to be uniform within an animal. The average transit time,  $\tau$ , scales as  $\tau \sim d/v$ .

- 137 6. Mass is proportional to volume: The density of protoplasm is approximately constant across animals,  
138 so mass,  $M$ , is proportional to volume,  $V$ .
- 139 7. Particles in transit are contained within animal volume: The number of resource particles in transit,  
140  $N$ , scales linearly with  $M$  and  $V$ .
- 141 8. Definition of service volume: a service volume is defined as a unit of tissue that has a fixed metabolic  
142 rate independent of animal mass. Thus the number of service volumes is proportional to  $B$ . In an  
143 animal with volume  $V$ , each service volume is proportional to  $V/B$  and radius or length  $l_s \sim (V/B)^{1/3}$ .  
144 The service volume does not necessarily correspond to any biological structure, although in  
145 mammals the service volume can be thought of as the volume of tissue supplied by a capillary, the  
146 terminal unit of the vascular network.

147 The theory assumes only that resources are distributed from a point source through a distribution  
148 network with no particular branching pattern, and therefore applies equally to hierarchically  
149 branched and explosion networks. It also assumes the transported resources are not stored near the  
150 service volume, and hence the ideas relate strongly to those metabolites that cannot be stored in the  
151 body (e.g.  $O_2$ ). The model predicts that the scaling exponent of metabolic rate is  $2/3$  if velocity of  
152 flow is independent of mass (consistent with an alternative model: Dodds, 2010), but can attain a  
153 maximum value of  $3/4$  if velocity scales with its maximum exponent,  $1/12$  (Banavar et al., 2010). It  
154 is worth noting, however, that real animals clearly violate some assumptions of the model. Not all  
155 animals have outward directed transport systems that distribute resources from a single point and,  
156 even for those that do, flow velocity is not uniform throughout the animal (Banavar et al., 2010).

157 Although the central tendency of  $3/4$ -power scaling is supported by some studies (Savage et al., 2004;  
158 Moses et al., 2008), other studies emphasise the many deviations from quarter-power scaling and the  
159 resource distribution model has yet to adequately explain differences in the scaling exponent  
160 between endotherms and ectotherms (Phillipson, 1981; Glazier, 2005; White et al., 2006; White et  
161 al., 2007b; Glazier, 2010), and between rest and activity (White and Seymour, 2005a; Glazier, 2008;  
162 White et al., 2008; Glazier, 2010), although attempts to do so have been made (Gillooly and Allen,  
163 2007). Debate regarding resource distribution models has been vociferous, focussing on issues of  
164 mathematical validity and empirical support (Banavar et al., 2000; Dodds et al., 2001; Banavar et al.,

165 2002a; West et al., 2002a; Banavar et al., 2003; Darveau et al., 2003; West et al., 2003; Kozłowski  
166 and Konarzewski, 2004; Suarez et al., 2004; West et al., 2004; Brown et al., 2005; Kozłowski and  
167 Konarzewski, 2005; Painter, 2005a; Suarez and Darveau, 2005; Chaui-Berlinck, 2006, 2007; Savage  
168 et al., 2007; Agutter and Tuszynski, 2011).

169         Interestingly, much of the empirical evaluation of the predictions of the resource distribution  
170 models has focussed on the scaling of metabolic rate with body mass (e.g. Bokma, 2004; Savage et  
171 al., 2004; Glazier, 2005; Duncan et al., 2007; White et al., 2007b), and the range of other scaling  
172 exponents predicted by these models has rarely been examined (Table 1). Examining the congruence  
173 between predicted and observed values for circulatory variables, in particular, seems to be a valuable  
174 step in evaluating the core of these models, which are grounded in principles of hydrodynamics.  
175 West et al.'s (1997, 1999) models for  $\frac{3}{4}$  power scaling, for example, assume that natural selection  
176 has optimized the resource distribution network to minimize transport costs. This seems reasonable  
177 because the heart contributes a significant fraction of whole-animal metabolic rate (2.4-10.4%:  
178 Loisel and Gibbs, 1979) and individuals with low metabolic rates are favoured in at least some  
179 situations (e.g. Blackmer et al., 2005; Artacho and Nespolo, 2009). Some of the predictions of the  
180 models are supported by empirical data, suggesting that they are plausible models of resource  
181 transport (Table 1). In birds and mammals, for example, heart rate scales with an exponent close to  
182 the predicted value of -0.25 (Table 1). For fish, on the other hand, heart rate is independent of body  
183 mass (Clark and Farrell, 2011; White and Seymour, 2011).

184         A significant product of the resource distribution model has been its use as a foundation for a  
185 Metabolic Theory of Ecology (MTE), which aims to use metabolism as a basis for applying first  
186 principles of physics and chemistry to link the biology of individual organisms to the ecology of  
187 populations, communities, and ecosystems (Brown et al., 2004b). The fundamental equation of MTE  
188 describes variation in MR in terms of an empirically determined normalisation constant independent



189 of body size and temperature ( $i_0$ ), body mass (M), activation energy (E), Boltzmann's constant (k),  
190 and absolute temperature (T) (Gillooly et al., 2001; Brown et al., 2004b):

$$191 \quad MR = i_0 M^{3/4} e^{-E/kT}$$

192 While early work on the MTE applied only a narrow range of parameters to describe the  
193 temperature- and mass-dependence of metabolic rate, recent work by the original proponents of MTE  
194 has acknowledged a wider range of variation in the parameters of the fundamental equation (Wang et  
195 al., 2009; DeLong et al., 2010; Dell et al., 2011). The strength of MTE lies in its ability to predict a  
196 wide range of ecological patterns (Allen et al., 2002; Brown et al., 2004b; Meehan et al., 2004;  
197 Meehan, 2006; Buckley et al., 2008; Munch and Salinas, 2009), its grounding in first principles  
198 (although some contention exists about the extent to which this holds for the temperature term:  
199 Clarke, 2006; Irlich et al., 2009), and its deliberate simplicity (Brown et al., 2004a). Not all tests of  
200 MTE support the theory (e.g. Algar et al., 2007; Duncan et al., 2007; Hawkins et al., 2007a;  
201 O'Connor et al., 2007; Downs et al., 2008), however, and it is worth noting that other theories also  
202 predict the scaling of metabolic rate with body mass with similar accuracy (see below), and  
203 application of these alternative explanations to explaining size-dependent ecological patterns is likely  
204 to be similarly successful.

### 205 ***Dynamic Energy Budget***

206 In the framework of the Dynamic Energy Budget (DEB) theory (Kooijman, 2010), metabolic rate is  
207 considered to comprise a weighted sum of four processes: assimilation, maintenance, growth, and  
208 maturation. DEB theory decomposes body mass into two indirectly measurable state variables, the  
209 'reserve' and the 'structure', and is based on generalized surface area (source) and volume (sink)  
210 relationships. It makes the key assumptions that the composition of reserve and structure each  
211 remains constant but may differ from each other ('strong homeostasis') and that, under constant  
212 food, the relative amount of reserve and structure stays constant and hence so does the entire body  
213 composition ('weak homeostasis'). Energy and matter are assimilated in proportion to structural

214 surface area (because food enters the body across surfaces), and directed first to the reserve pool of  
 215 the organism. The reserve is not necessarily metabolites ‘set aside for later’, but rather is defined by  
 216 its turnover rate. It reflects the part of the dry mass of an organism that fluctuates with resource  
 217 supply, and is constantly used and replenished. DEB theory assumes that no costs are paid for the  
 218 maintenance of reserves, but costs are paid for their turnover and are included in the overheads of  
 219 assimilation and utilization. The structure is the “permanent” biomass and does require energy for its  
 220 maintenance (protein turnover and the maintenance of concentration gradients and ionic potentials,  
 221 etc.) in direct proportion to structural volume.

222 Under DEB theory, the allometric scaling of metabolic rate arises because the contribution of  
 223 non-respiring reserves to body mass increases with body size. For example, body fat (which can be  
 224 considered as part of the reserve, but is by no means all of it) scales as  $M^{1.19}$  in mammals (Pitts and  
 225 Bullard, 1968; Calder, 1984) and has a very low mass-specific metabolic rate (Elia, 1992). For  
 226 interspecific comparisons, DEB theory predicts the scaling of mass-specific standard or basal  
 227 metabolic rate for fully grown animals as (Kooijman et al., 2007; Kooijman, 2010):

$$\propto \frac{L_h L^2 + L^3}{d_V L^3 + d_E L^4}$$

228 where respiration has contributions from growth and maintenance (assimilation is excluded because  
 229 animals are postabsorptive). The parameters  $d_E$  and  $d_V$  represent the specific density ( $\text{g cm}^{-3}$ ) of  
 230 reserve ( $E$ ) and structure ( $V$ ) and the amount of structure is proportional to the cubed volumetric  
 231 length  $L^3$ , so  $d_V$  is independent of mass. The ratio of reserve to structure is proportional to  $L$ , so  
 232 metabolic rate scales allometrically with an exponent less than 1. Inclusion of a “heating length”  
 233 multiplier  $L_h$  (a positive constant for endotherms, and zero for ectotherms) for a surface area term  
 234 ( $L^2$ ) in the numerator means that the scaling exponent of metabolic rate is predicted to be lower for  
 235 endotherms than ectotherms, a pattern that is supported by empirical data (Phillipson, 1981; White et  
 236 al., 2006; White et al., 2007b). However, the appropriateness of including a surface-specific heating  
 237 term  $L_h L^2$  requires further scrutiny since body surface area and basal metabolic rate are not related in  
 238

239 mammals (White and Seymour, 2004), and it is not clear that heat loss determines basal metabolism  
240 in a mechanistic sense (da Silva et al., 2006; Seymour and White, 2011).

241 The mechanisms invoked by DEB theory to explain intraspecific scaling relationships are  
242 different from those that explain interspecific scaling. Interspecifically, the allometric scaling of  
243 metabolic rate arises because of the increase in reserve with mass, and differences between  
244 endotherms and ectotherms arise because of differences in the heating constant. Although the idea  
245 has not yet been formally explored, it seems likely that at least some of the variation in the  
246 interspecific scaling exponent of metabolic rate could be explained by DEB theory on the basis of  
247 size- and activity-dependent variation between species in the energy turnover of structure, and  
248 thereby the relative contributions of reserve and structure to whole-body metabolism. It is not yet  
249 clear, however, if DEB theory can explain the frequently observed covariation between metabolic  
250 level and the scaling exponent of metabolic rate (Glazier, 2005, 2008, 2009a, b, c, 2010).

### 251 ***Metabolic Level Boundaries***

252 The metabolic level boundaries (MLB) hypothesis (Glazier, 2005, 2010) predicts that scaling  
253 exponents for MR will vary between two boundary constraints: surface-area limits on fluxes of  
254 metabolic resources, wastes and (or) heat that scale allometrically as  $M^{2/3}$ , and volume limits on  
255 energy use or power production that scale isometrically as  $M^1$ . Thus, metabolic rate is predicted to  
256 scale isometrically at low levels of sustained metabolic intensity, and the scaling exponent of  
257 metabolic rate is predicted to decrease toward 2/3 as sustained metabolic intensity increases. During  
258 intense activity, volume limits on power production by the locomotory musculature dominate, and  
259 metabolic rate is predicted to scale isometrically. The pattern of variation predicted by the metabolic  
260 level boundaries hypothesis is supported by variation in the scaling exponent for birds and mammals  
261 (Glazier, 2008, 2009a), unicellular organisms (Glazier, 2009b), and ectothermic animals (Glazier,  
262 2009c; Killen et al., 2010). In support of the hypothesis, the body temperature of large animals has  
263 been shown to rise continually during intense aerobic exercise (e.g. Jones et al., 1989; Nagano et al.,

264 1990b), which demonstrates the metabolic rate during intense exercise is not constrained by heat  
265 flux.

### 266 **Allometric cascade**

267 The allometric cascade (AC) theory (Darveau et al., 2002; Hochachka et al., 2003) regards the  
268 scaling of metabolic rate as a consequence of multiple causes, where the exponent  $b$  is the sum of the  
269 influences of multiple contributors to metabolism and control, and where the relative strength of each  
270 contributor, with its own characteristic exponent value, is determined by its control contribution.

271 The original mathematical model derived from the allometric cascade theory has been criticised  
272 (Banavar et al., 2003; West et al., 2003), and a revised model subsequently appeared (Darveau et al.,  
273 2003; Hochachka et al., 2003):

$$274 \quad MR = MR_0 \sum c_i (M/M_0)^{b_i}$$

275 where  $MR_0$  is the ‘characteristic metabolic rate’ of an animal with a ‘characteristic body mass’,  $M_0$ .  
276 With  $M_0$  of 1 unit mass (usually kg),  $MR_0$  takes the place of the value  $a$ , found in the standard scaling  
277 equation,  $b_i$  is the scaling exponent of the process  $i$ , and  $c_i$  is its control contribution to overall flux,  
278 or the control coefficient of the process  $i$ .

279 For animals working at  $\dot{V}O_2\text{max}$  (i.e. their maximal sustainable work rates, equivalent to  
280 maximum sustainable ATP turnover rates), major contributors to control include the lung, heart and  
281 circulation (Wagner, 1993; Jones, 1998), as well as cellular-level energy-supply and ATP-demand  
282 pathways (Thomas and Fell, 1998; Jeneson et al., 2000; Cloutier and Wellstead, 2010). Based on the  
283 control coefficients for these processes, the predicted global  $b$  value is 0.82 – 0.92 (Darveau et al.,  
284 2002), in good agreement with empirical data (Bishop, 1999; Weibel et al., 2004; White and  
285 Seymour, 2005a; White et al., 2007b; White et al., 2008). For animals under BMR conditions, on the  
286 other hand, all of the oxygen delivery steps have an excess capacity of at least several-fold, which  
287 allows animals to increase the metabolic rate from BMR to  $\dot{V}O_2\text{max}$ . Thus, the control contributions  
288 of these steps are considered to be zero under basal conditions, and the global scaling of BMR is

289 driven by energy demand processes. Under basal conditions, major energy sinks are  $\text{Na}^+$ - $\text{K}^+$ -  
290 ATPase, protein turnover, substrate cycles, and mitochondrial proton leak (Rolfe and Brand, 1997),  
291 and the control coefficients for these processes contribute to the global  $b$  value for BMR, which is  
292 predicted to be within the range 0.76 – 0.79 (Darveau et al., 2002), which is somewhat higher than  
293 observed for mammals over most of their mass range (Kolokotronis et al., 2010). The principles of  
294 allometric cascade theory also appear to be valid for resting and exercising humans (Batterham and  
295 Jackson, 2003, 2005; but see Nevill and Bate, 2005 for an alternative viewpoint).

### 296 **Cell Size**

297 The cell size (CS) model proposes that the mass scaling of metabolism is shaped by the evolutionary  
298 coupling of cell size and body size, since, with increasing cell size, the cell surface area:volume ratio  
299 decreases (Davison, 1955; Kozłowski et al., 2003a; Kozłowski et al., 2010). All other things being  
300 equal, the model predicts that metabolic rate should scale isometrically when evolutionary increases  
301 in body size are achieved entirely through increases in cell number (i.e. cell size scales as  $M^0$ ), or as  
302  $M^{2/3}$  when increases in size are achieved through increases in cell volume (i.e. cell size increases  
303 with  $M$ ). Experimental studies have supported the link between cell size and metabolic rate (Maciak  
304 et al., 2011), and the cell size model for metabolic scaling has been supported in studies of  
305 endotherms (Vinogradov, 1995; Kozłowski et al., 2003a; Opazo et al., 2005), reptiles (Starostová et  
306 al., 2009), tetrapods (Vinogradov and Anatskaya, 2006), and insects (Chown et al., 2007). Recent  
307 work, however, has demonstrated that patterns of mass-dependence of cell sizes in different animal  
308 groups are inconsistent with the assumptions of the model, and has called for revision of the model  
309 (Glazier, 2005; Kozłowski et al., 2010). Cell volume scales with exponents between 0 and 0.3 in  
310 birds and mammals (Kozłowski et al., 2010). The cell size model predicts that a cell volume scaling  
311 exponent of 0.3 should be associated with a metabolic rate scaling exponent of 0.9 (Kozłowski et al.,  
312 2003a; Kozłowski et al., 2010), which is greater than the exponents observed for these groups  
313 (McKechnie and Wolf, 2004; White and Seymour, 2005a; McKechnie et al., 2006; White et al.,

314 2007b; White et al., 2009). The cell size model is also difficult to reconcile with the observation that  
315 the metabolism of individual cells in culture does not scale with the 2/3-power of cell volume (West  
316 et al., 2002b), though the relevance of cell preparations to the *in vivo* metabolism of cells remains an  
317 open question. Similarly, the ratio of mitochondrial volume to cell volume is a more important  
318 predictor of the respiration of isolated hepatocytes than cell volume itself (Porter and Brand, 1995).

### 319 **Heat dissipation limits**

320 The heat dissipation limit (HDL) theory (Speakman and Król, 2010) proposes that an upper  
321 boundary on sustained energy expenditure is imposed by the maximal capacity to dissipate body heat  
322 and therefore avoid the detrimental consequences of hyperthermia. In contrast to other theories, HDL  
323 seeks to explain the scaling of average daily energy expenditure (field metabolic rate), which it  
324 estimates on the basis of the exponent of maximal capacity to dissipate heat ( $\propto M^{0.47-0.50}$ , all other  
325 things being equal). Interestingly, the value of  $\sim 0.5$  is similar to that predicted for the scaling  
326 exponent of metabolic rate at a constant temperature by an analytical model of the thermal niche of  
327 an ellipsoid furred endotherm (Porter and Kearney, 2009), as well as to the empirically-determined  
328 scaling exponent of minimum wet thermal conductance ( $b = 0.42$  to  $0.62$ : Schleucher and Withers,  
329 2001; Withers et al., 2006), and the scaling exponent of daily energy expenditure (DEE) measured at  
330 any given temperature (Calder, 1984). Incorporating empirical data for the scaling of plumage/fur  
331 mass ( $\propto M^{0.95-0.98}$ ), skin mass ( $\propto M^{0.94}$ ), and body temperature ( $\propto M^{0.05}$ ), the predicted scaling  
332 exponent of maximum heat dissipation capacity is about  $0.63$ , a value close to the measured scaling  
333 exponents (shown  $\pm$  SE) of FMR of  $0.647 \pm 0.013$  in mammals and  $0.658 \pm 0.017$  in birds  
334 (Speakman and Król, 2010). When analysed using phylogenetic independent contrasts (Felsenstein,  
335 1985) the exponent of FMR for birds and mammals are  $0.679 \pm 0.032$  and  $0.576 \pm 0.036$ ,  
336 respectively (Speakman and Król, 2010).

337 The HDL theory is also supported by the observation that the daily energy turnover of  
338 lactating animals is increased by manipulating heat dissipation capacity through pelage removal or

339 cold exposure (Johnson and Speakman, 2001; Król and Speakman, 2003; Król et al., 2007; Wu et al.,  
340 2009; Simons et al., 2011), but not by increases in litter size, by forced exercise, or by simultaneous  
341 pregnancy (Hammond and Diamond, 1994; Johnson et al., 2001a, b; Laurien-Kehnen and Trillmich,  
342 2003). Similarly, lactating red squirrels *Tamiasciurus hudsonicus* raising large litters occupy poorly  
343 insulated nests in warm years (Guillemette et al., 2009). Support for the predictions of the theory is  
344 not universal, however, and other studies of small mammals report mixed results (Zhao and Cao,  
345 2009; Speakman and Król, 2011; Zhao, 2011). The generality of the HDL theory also remains to be  
346 verified on animals performing other energetically-demanding activities, such as locomotion, and the  
347 theory explains the scaling of metabolic rate only in free-living endotherms, and does not apply to  
348 ectotherms. Nonetheless, for endotherms, the theory is relevant to BMR because it represents an  
349 upper limit to DEE. Given that BMR contributes a substantial component of DEE, an upper limit to  
350 DEE with a scaling exponent of  $\sim 0.63$  will constrain BMR to a similarly low exponent to ensure that  
351 there is scope for activity ( $= DEE - BMR$ ) across the size range of endotherms.

### 352 ***Evaluating explanations for metabolic scaling***

353 It is a truism that all biological models are wrong because they are simplifications of complex  
354 systems and rarely, if ever, fully account for the variation they aim to explain. Ideally, models  
355 should maximise generality, realism, and precision, but this is not always possible and one of these is  
356 often sacrificed in favour of the others (Levins, 1966). Nevertheless, these three goals offer criteria  
357 by which competing models can be evaluated. With respect to metabolic scaling, distinguishing  
358 among competing models on the grounds of how well they predict empirical data is difficult because  
359 many models predict similar values. Metabolic rate may scale allometrically because of the  
360 geometry of resource distribution networks, leading to predictions of metabolic scaling exponents of  
361  $0.67 - 0.75$  (Banavar et al., 2010) or  $0.5 - 1$  (Price et al., 2007). A definitive test of the resource  
362 distribution model has proven elusive, however, because like several other models it predicts a  
363 central tendency of 0.75-power scaling (West et al., 1997, 1999). Thus, while this prediction shows

364 good general agreement with the mean scaling exponent observed in both intra-specific (Moses et al.,  
365 2008) and inter-specific (Savage et al., 2004) studies, other models make similar predictions: the Cell  
366 Size (Kozłowski et al., 2003a), Metabolic Level Boundaries (Glazier, 2010), and Dynamic Energy  
367 Budget models all predict  $b$  to vary between 0.67 and 1, the mid-point of which is close to 0.75.  
368 Similarly, the metabolic level boundaries (Glazier, 2010) and dynamic energy budget (Kooijman,  
369 2010) models both predict that scaling exponents for resting endotherms will be lower than those for  
370 resting ectotherms. Given that the predictions from the models overlap so strongly, it is important  
371 that the presentation of models include clear descriptions of their unique predictions to facilitate tests  
372 that distinguish between alternatives (Shipley, 2000; Currie et al., 2004; Hawkins et al., 2007b;  
373 Glazier, 2010; White et al., 2011b; Kearney and White, 2012).

374 An alternative criterion by which competing explanations for metabolic scaling can be  
375 compared is their relative complexity. Simple explanations that incorporate a minimum of detail are  
376 sometimes regarded as more parsimonious than more complicated ones (Zuo et al., 2009). Implicit in  
377 such a judgement is the idea that a model should be evaluated not only on how well it fits available  
378 data, but that comparisons of alternative models should incorporate information about how many  
379 parameters are required to describe the data. Thus, of two models that describe variation in metabolic  
380 rate equally well, the ‘best’ model is the one that includes the fewest parameters. Such ideas form the  
381 basis of information theoretic approaches to model comparison (Burnham and Anderson, 2002;  
382 Johnson and Omland, 2004; Hobbs and Hilborn, 2006); in the case of metabolic scaling, such tests  
383 generally favour complex models over simple ones (Isaac and Carbone, 2010), because the  
384 additional predictive power of complex models outweighs their need to estimate extra parameters. It  
385 should be borne in mind, however, that some models are more connected to formal theories (e.g.  
386 DEB) than others (e.g. MLB); theory-based models must also be evaluated on the legitimacy of the  
387 theoretical assumptions in addition to model complexity (Kearney and White, 2012).



388           The two most common problems associated with tests of explanations for metabolic scaling  
389 have been a failure to account for phylogenetic non-independence in comparative data, and a reliance  
390 on correlational approaches to understand the scaling of physiological traits with body mass. While  
391 the former is rarely a problem in recent analyses (e.g. Sieg et al., 2009; White et al., 2009; Capellini  
392 et al., 2010; Kolokotronis et al., 2010), the latter is almost unavoidable because the metabolic rate  
393 and body mass are necessarily measured in intact individuals. The resultant correlation between these  
394 traits is then assessed; this approach precludes examination of the causal effect of mass on the trait of  
395 interest. Correlational approaches to distinguishing between competing explanations are problematic  
396 because many variables in addition to metabolic rate co-vary with body mass. For example, body  
397 mass is correlated with climate, diet, and life-history traits including litter size and maximum  
398 longevity (McNab, 2008; Jones et al., 2009), all of which have been shown to have confounding  
399 effects on metabolic rate (e.g. White and Seymour, 2004; McNab, 2008). A potential solution to this  
400 problem is the examination of scaling relationships for colonial organisms. The size of colonies can  
401 be manipulated experimentally and the consequences of the manipulation for scaling relationships  
402 can be examined (e.g. Nakaya et al., 2005; White et al., 2011b). An additional alternative approach  
403 is the manipulation of biotic and abiotic variables, and examination of the size-dependence of the  
404 resultant effect (Glazier, 2005). Such an approach is most commonly applied to intraspecific studies  
405 (e.g. Table 2) but could also be applied to interspecific ones, and represents a potentially powerful  
406 tool to understand the factors that constrain and influence the allometry of metabolic rate.

#### 407 ***Integrating explanations for metabolic scaling***

408 The various explanations for metabolic scaling are not necessarily exclusive, and integration of  
409 various aspects of the associated theories and models may lead to a greater understanding of why  
410 metabolic rate scales allometrically with body mass (Ginzburg and Damuth, 2008; Glazier, 2010).  
411 For example, Clarke et al. (2010) suggest that the reason why the relationship between  $\log(M)$  and  
412  $\log(MR)$  for mammals is not linear (e.g. Hayssen and Lacy, 1985; Dodds et al., 2001; Glazier, 2005;

413 Makarieva et al., 2008; Kolokotronis et al., 2010; White, 2011) is because at large sizes the scaling  
414 is dominated by factors that dictate 0.75-power scaling (e.g. resource distribution: West et al., 1997),  
415 whereas at small sizes this factor is overridden by considerations of heat flow and hence the  
416 exponent is closer to 0.67. They note that the pattern of variation in the scaling exponent arising from  
417 this prediction is analogous to the metabolic level boundaries hypothesis of Glazier (2005, 2010).  
418 Similar arguments could be made using several of the other theories discussed above, since they also  
419 invoke fluxes that scale allometrically (e.g. of heat across body surfaces or metabolites across cell  
420 surfaces). Indeed, since the sum of two non-isometric scaling relationships will not be a strict power  
421 function of mass (Figure 2) (see also Garland, 1983; Calder, 1984), any theory that includes additive  
422 combinations of isometric ( $\propto M^1$ ) and allometric (e.g.  $\propto M^{0.67}$ ) components that vary with metabolic  
423 level will match a number of observed scaling patterns, at least qualitatively. Examples of such  
424 patterns include the curvature in BMR scaling for mammals (Hayssen and Lacy, 1985; Painter,  
425 2005b; Kolokotronis et al., 2010), differences between the scaling exponent of basal and standard  
426 metabolic rate of endotherms and ectotherms (White et al., 2007b; White et al., 2008), the high  
427 scaling exponent of hibernating endotherms compared to daily heterotherms and euthermic  
428 endotherms (Geiser, 1988; White and Seymour, 2005a), and the high scaling exponent of field  
429 metabolic rate in reptiles compared to birds and mammals (Nagy et al., 1999; Nagy, 2005; Speakman  
430 and Król, 2010). This prediction is made explicit by the MLB hypothesis, which includes fluxes of  
431 metabolic resources, wastes and (or) heat that scale allometrically (Glazier, 2005, 2008, 2010), but  
432 the principle of summed allometric and isometric components (or summed components that each  
433 scale allometrically with different exponents) of metabolic rate applies equally to combinations of  
434 organ-tissue compartments that differ in their association with body mass (see e.g. Wang et al., 2001;  
435 Glazier, 2005; Painter, 2005b; Glazier, 2010; Killen et al., 2010).

436 Differences in the scaling of BMR and  $\dot{V}O_2\text{max}$ , for example, can be explained by  
437 considering differences in the metabolic scaling exponents between tissues that contribute to energy

438 turnover during rest and exercise (Glazier, 2005). Most metabolic activity during basal metabolism  
439 is associated with the internal organs including liver, kidney, gastrointestinal tract, heart, and brain  
440 (Krebs, 1950; Rolfe and Brown, 1997), and variation in BMR between species and individuals has  
441 therefore been attributed to variation in organ mass (Daan et al., 1990; Konarzewski and Diamond,  
442 1995; Meerlo et al., 1997; Książek et al., 2004; Song and Wang, 2006; Brzęk et al., 2007; Raichlen  
443 et al., 2009; Williams et al., 2010) and tissue metabolism (Krebs, 1950; Wang et al., 2001). During  
444 exercise-induced maximal metabolism, on the other hand, most (>90%) metabolic activity is  
445 associated with work done by the locomotor muscles and delivery of substrates and oxygen to these  
446 (Weibel et al., 2004). There is therefore a hierarchy of contributions to organismal metabolism  
447 depending on demand (see Darveau et al., 2002; Suarez and Darveau, 2005): whole-animal  
448 metabolism is a function of organ mass and metabolism, which in turn is a function of tissue and  
449 mitochondrial metabolism, which is governed by the activity of metabolic enzymes. At rest,  
450 allometric scaling of visceral organism metabolism dominates (see e.g. Porter, 2001; Wang et al.,  
451 2001; Glazier, 2005), whereas during exercise isometric scaling of muscle metabolism dominates  
452 (see e.g. Weibel et al., 2004; Glazier, 2005). Evidence for the validity of such an approach comes  
453 from the human literature, which includes examples where specific body compartments have been  
454 shown to be more appropriate than whole body mass for standardising inter-individual differences in  
455  $\dot{V}O_2\text{max}$  (Eliakim et al., 1996; Nevill et al., 2004; Nevill et al., 2006; Tolfrey et al., 2006). Similarly,  
456 muscular parameters better explain inter-specific variation in mammalian  $\dot{V}O_2\text{max}$  than does body  
457 mass (Weibel et al., 2004; Weibel and Hoppeler, 2005).

458         Decomposition of whole-animal metabolism into organ-tissue compartments that scale with  
459 different exponents can also explain the higher scaling exponent of ectotherm SMR compared to  
460 endotherm BMR (White et al., 2006; White et al., 2007b). The organs that contribute to resting  
461 metabolism are smaller in ectotherms than in endotherms (Crile and Quiring, 1940; Martin, 1981;  
462 Karasov, 1987; Franz et al., 2009) and the tissue-mass-specific metabolic intensity is lower (Hulbert

463 and Else, 1981; Hulbert et al., 2002). Thus, if whole-animal metabolism is assumed, for simplicity,  
464 to have two compartments (e.g. muscle + bone compartment that scales as  $M^{-1}$ , and a visceral organ  
465 + brain compartment that scales as  $M^{-0.67}$ ) and the mass-specific intensity of both compartments is  
466 higher for endotherms than ectotherms, then the scaling exponent of SMR is predicted to be lower for  
467 endotherms than ectotherms (Figure 3). This approach also predicts that the curvature in MR will be  
468 less pronounced or absent in ectotherms than endotherms, as is also apparently the case (Ehnes et al.,  
469 2011; Müller et al., 2011a). The exact values of the exponents predicted by this approach will  
470 depend on the scaling exponent of organ masses and tissue-mass-specific metabolic intensities.  
471 However, while this ‘multi-compartment’ approach can explain variation in the scaling exponent of  
472 whole-animal metabolic rate, it does not offer an explanation for *why* the compartments scale as they  
473 do. First principles explanations for these organ-specific scaling patterns might come from the  
474 mechanistic models discussed above, and further understanding of the ultimate (evolutionary) causes  
475 of the allometric relationship between metabolic rate and body size could be gleaned from  
476 examination of the genetic associations between traits that contribute to metabolic rate (Glazier,  
477 2005). For example, examination of how the genetic correlation between brain size and body size  
478 varies during development has been beneficial in understanding why the scaling exponent of brain  
479 size is lower during development than for interspecific comparisons (Lande, 1979; Riska and  
480 Atchley, 1985; Lynch and Walsh, 1998).

## 481 **Causes of mass-independent variation in BMR**

### 482 ***Climate and habitat productivity***

483 Perhaps the most prominent and well-supported abiotic correlate of mass-independent variation in  
484 BMR is environmental temperature, which is negatively related to BMR in both birds (Jetz et al.,  
485 2007; White et al., 2007a) and mammals (Lovegrove, 2003; Careau et al., 2007), including humans  
486 (Froehle, 2008). This relationship probably arises as a consequence of the need to limit endogenous

487 heat production in hot environments (McNab and Morrison, 1963), and to maximise heat production  
488 in cold environments (BMR is positively correlated with maximum cold-induced metabolic rate in  
489 both birds and mammals: Dutenhoffer and Swanson, 1996; Rezende et al., 2002; Rezende et al.,  
490 2004). The low BMR of species from hot environments may also arise because lower differential  
491 between body and ambient temperatures means that the contribution of endogenous heat production  
492 to thermoregulation can be reduced, thereby saving energy and/or water, or because high temperature  
493 limits the sustained metabolism of endotherms (Speakman and Król, 2010). If energy expenditure  
494 attributable to maintenance (BMR) and activity ( $AMR = FMR - BMR$ ) are considered independent  
495 (i.e. the 'partitioned pathways' model of Ricklefs et al., 1996), as is the case in at least free-ranging  
496 great cormorants *Phalacrocorax carbo* (White et al., 2011a), then, in an environment where daily  
497 energy expenditure is restricted by heat dissipation, a reduction in BMR increases the scope for  
498 activity. Support for the idea that scope for activity (=FMR divided by BMR) is restricted by the  
499 difference between maximum rates of heat dissipation and BMR arises from the observation that  
500 scope for activity decreases from up to 8-fold for small mammals to less than 3-fold for large ones  
501 (Westerterp and Speakman, 2008), though it is not currently clear if scope for activity also with  
502 climate. While the relationship between environmental temperature and BMR is likely to have a  
503 genetic component, as has been shown for stonechats (Wikelski et al., 2003), the extent to which  
504 phenotypic plasticity contributes to the observed relationship between environmental temperature  
505 and BMR remains unclear, as cold acclimation causes an increase in metabolic rate for birds and  
506 mammals (Williams and Tieleman, 2000; Song and Wang, 2006; McKechnie et al., 2007;  
507 McKechnie, 2008). Recent comparative analysis suggest that the magnitude and direction of seasonal  
508 acclimatization in free-living birds depends upon their thermal environment: species that experience  
509 cold winters at high latitude have higher BMR in winter than summer, whereas species that inhabit  
510 warmer subtropical latitudes have lower BMR in winter (Smit and McKechnie, 2010). These  
511 acclimation and acclimatization responses act on timescales of weeks, suggesting that ambient

512 temperature has a proximate role in influencing BMR (Swanson and Olmstead, 1999; McKechnie et  
513 al., 2007), though changes associated with environmental triggers for reproduction are also  
514 implicated as drivers of seasonal variation (Smit and McKechnie, 2010). However, there is evidence  
515 that inter-specific and inter-population differences are maintained for multiple generations in  
516 captivity, and that populations from more seasonal environments show a greater capacity for thermal  
517 acclimation than populations from stable environments (Tieleman et al., 2003; Cavieres and Sabat,  
518 2008). These findings suggest a genetic component to climate-associated variation in BMR. Thus,  
519 there remains a clear need for common-garden experiments comparing differences in BMR between  
520 animals from warm and cold environments to separate the genetic and phenotypic components of the  
521 negative relationship between environmental temperature and BMR.

522         Related to the effect of temperature, BMR is often thought to be associated with  
523 environmental productivity, such that animals from highly productive environments have higher  
524 BMRs than those from less productive environments. This conclusion stems from the observation  
525 that the BMRs of arid species are generally lower than those of mesic species (e.g. Tieleman and  
526 Williams, 2000; Withers et al., 2006). However, the BMR of birds is not related to net primary  
527 productivity (White et al., 2007a). This contrasts with the situation in mammals, where  
528 environmental productivity has been shown to be positively correlated with BMR in a range of  
529 studies (Mueller and Diamond, 2001; Bozinovic et al., 2007; Bozinovic et al., 2009). BMR is  
530 similarly correlated with rainfall parameters associated with environmental productivity for  
531 marsupials (Withers et al., 2006) and small (< 1 kg) eutherians (Lovegrove, 2003). Birds and  
532 mammals also differ in the relationship between BMR and rainfall variability: the relationship is  
533 negative in mammals (Lovegrove, 2003; Withers et al., 2006), but positive (White et al., 2007a) or  
534 absent (Jetz et al., 2007) in birds. The reason for this difference between birds and mammals is  
535 unclear, but it could be genuine, reflecting perhaps a difference in mobility, or it could arise as a  
536 consequence of methodological differences between the avian and mammalian analyses. Future

537 analyses applying uniform phylogenetically-informed methods (see e.g. Rezende and Diniz-Filho,  
538 2012) and drawing on environmental data from a single database could resolve the issue, and could  
539 be extended to other groups for which latitudinal and climate effects on metabolic rate have been  
540 identified, such as insects (Addo-Bediako et al., 2002) and fish (White et al., 2012). The ongoing  
541 accumulation of readily available climate data (e.g. [www.worldclim.org](http://www.worldclim.org)), large compilations of  
542 metabolic data (e.g. McNab, 2009; Sieg et al., 2009) and complete species-level supertrees (e.g.  
543 Bininda-Emonds et al., 2007) will facilitate such work.

544         Probably the most controversial correlate of BMR is diet. Early work tended to report  
545 significant associations between diet and BMR (e.g. McNab, 1969, 1986). These were, however, not  
546 supported by subsequent PI analyses (e.g. Cruz-Neto et al., 2001; Rezende et al., 2004), though  
547 problems in correctly assigning dietary categories could contribute to this discrepancy (McNab,  
548 2003). More recent PI analyses have supported an association between diet and BMR for Carnivora  
549 (Muñoz-Garcia and Williams, 2005), and between diet and FMR for birds (Anderson and Jetz,  
550 2005), but no association is observed between BMR and diet for birds (Table 3) or mammals in  
551 general (White, 2011; see also Clarke et al. 2010 for a discussion of covariation between diet and  
552 body temperature in mammals).

### 553 ***Organ-tissue contributions to mass-independent BMR***

554 The internal organs contribute substantially to BMR, and variation in BMR between species has  
555 therefore been attributed to variation in organ mass (Daan et al., 1990; Raichlen et al., 2009) and  
556 tissue metabolism (Krebs, 1950; Wang et al., 2001). Within species, 71% of the variation in BMR of  
557 Chilean mouse opossums is explained by variation in the mass of digestive organs (Nespolo et al.,  
558 2002), strains of mice with high BMR tend to have relatively large metabolically active organs  
559 (heart, kidney, liver, and small intestine) (Konarzewski and Diamond, 1995), and mice artificially  
560 selected for high BMR have larger small intestine, liver, kidneys, and heart than mice selected for  
561 low BMR (Książek et al., 2004; Brzęk et al., 2007). Similarly, cold-acclimated Brandt's voles

562 *Lasiopodomys brandtii* have higher BMR and heavier liver, kidneys and gastrointestinal segments  
563 than warm-acclimated ones (Song and Wang, 2006). In field voles *Microtus agrestis*, BMR is  
564 positively correlated with heart mass (Meerlo et al., 1997). However, the relationship between organ  
565 mass and BMR differs between sexes in red junglefowl *Gallus gallus* (Hammond et al., 2000), BMR  
566 is associated with only the mass of reproductive tissue in adult house sparrows *Passer domesticus*  
567 (Chappell et al., 1999), and diet-induced changes in the mass of the gastrointestinal tracts, gizzards,  
568 and livers of starlings are not associated with increases in BMR (Geluso and Hayes, 1999). Thus,  
569 while comparative studies of birds have revealed a clear effect of inter-specific variation in organ  
570 masses on BMR (Daan et al., 1990), the results of intraspecific studies are more equivocal.

571 A controversial correlate of metabolic rate is brain size (Imamura and Clowes, 1975; Martin,  
572 1981; Harvey and Bennett, 1983; McNab, 1989; Nagano et al., 1990a; Pastor, 2000; Isler and van  
573 Schaik, 2006; Weisbecker and Goswami, 2010). Recent comparative analyses are generally in favour  
574 of an association between brain size and metabolism for at least eutherian mammals; the presence or  
575 absence of an association for marsupials is more equivocal and depends upon the method of analysis  
576 (Imamura and Clowes, 1975; Weisbecker and Goswami, 2010). A potential problem with  
577 comparative analyses of the association between brain size and BMR, however, is that brain size is  
578 correlated with a range of other ecological and life-history traits (e.g. Burrin et al., 1989; Eisemann  
579 and Nienaber, 1990; Huntington et al., 1990; Guerino et al., 1991; Sol et al., 2002; Sol et al., 2005),  
580 and disentangling the associations between these traits, BMR, and brain size is difficult. Intra-  
581 specific studies have also demonstrated an association between brain size and BMR for humans  
582 (Javed et al., 2010; Müller et al., 2011b) and inbred strains of mice (Konarzewski and Diamond,  
583 1995), and artificial selection studies offer an alternative experimental approach to examining the  
584 association. Brain weight has been shown to respond to artificial selection in mice in only 6-10  
585 generations (Roderick et al., 1976), and comparison of BMR in lines divergently selected for low and  
586 high brain size should help resolve the issue.



587 ***Mitochondrial contributions to mass-independent BMR***

588 Approximately 90% of oxygen consumption is associated with ATP production by mitochondria,  
589 with ~19-28% used by Na<sup>+</sup>-K<sup>+</sup>-ATPase and ~20% associated with mitochondrial proton leak (Rolfe  
590 and Brand, 1997). Variation in BMR between populations and individuals within a species have been  
591 attributed to variation in mitochondrial function (Speakman et al., 2004; Tieleman et al., 2009a), and  
592 individual mice with high metabolic rates have more uncoupled mitochondria than those with low  
593 metabolic rates (Speakman et al., 2004). However, differences in BMR between eutherians and  
594 marsupials are not explained by differences in mitochondrial proton leak (Polymeropoulos et al.,  
595 2011), nor are differences in BMR between individual humans (Larsen et al., 2011). Differences in  
596 BMR between individual humans are explained instead by differences in mitochondrial oxygen  
597 affinity (Larsen et al., 2011). Inter-individual and inter-population differences in mitochondrial  
598 function have been linked to fitness-enhancing traits in ectotherms (e.g. Ellison and Burton, 2006;  
599 Seebacher and Wilson, 2006), and similar links between BMR, mitochondrial function, and  
600 Darwinian fitness surely await discovery in endotherms. In addition to measurement of  
601 mitochondrial activity, attention should also be given to variation in the density of mitochondria, as  
602 variation in total mitochondrial volume accounts for significant variation in aerobic capacity (Weibel  
603 et al., 2004). Since aerobic capacity is often correlated with BMR (e.g. Hayes and Garland, 1995; see  
604 also Table 4) and mitochondrial processes contribute significantly to BMR, it seems likely that BMR  
605 will be correlated with the metabolic intensity and abundance of mitochondria, as well as  
606 mitochondrial morphology, which is related to proton leak across the inner mitochondrial membrane  
607 (Porter et al., 1996).

608 ***Approaches to understanding mass-independent variation***

609 Quantitative genetic analyses and artificial selection experiments are a promising approach for  
610 elucidating the evolutionary factors that influence BMR. Several of these are ongoing, including  
611 divergent selection on BMR directly in laboratory mice (Książek et al., 2004); divergent selection on

612 locomotor activity, predatory behaviour, and ability to cope with herbivorous diet in bank voles  
613 *Myodes (Clethrionomys) glareolus* (Sadowska et al., 2008); and selection on maximum rate of  
614 oxygen consumption ( $\dot{V}O_{2\max}$ ) during treadmill exercise, as well as selection to generate a negative  
615 correlation between  $\dot{V}O_{2\max}$  and BMR (see Swallow et al., 2009; Wone et al., 2011). Results available  
616 to date have demonstrated support for an association between diet and BMR, although the ability to  
617 cope with a low-quality herbivorous diet shows a positive additive genetic correlation with BMR  
618 (Sadowska et al., 2009), rather than the negative association expected from studies of the effect of  
619 dietary manipulation on BMR (Veloso and Bozinovic, 1993; Koteja, 1996; Perissinotti et al., 2009;  
620 Zhao and Wang, 2009). Seven generations of selection for high  $\dot{V}O_{2\max}$  has so far yielded a 12.3%  
621 increase in  $\dot{V}O_{2\max}$  in selected lines compared to control lines, and a non-significant 3.5% increase in  
622 BMR (Wone et al., 2011).

623         Selection on BMR directly has generated lines of mice that differ significantly in BMR and  
624  $\dot{V}O_{2\max}$  elicited by forced swimming (Książek et al., 2004). The body-mass-corrected masses of four  
625 visceral organs (small intestine, liver, kidneys, and heart) are also consistently and substantially  
626 higher in mice selected for high BMR than those selected for low BMR (Książek et al., 2004); these  
627 differences are considered large enough to claim the existence of positive genetic correlations  
628 between BMR and the masses of examined viscera (Książek et al., 2004). It will be interesting to  
629 examine the outcomes of the suite of selection experiments not only for BMR, but also on the traits  
630 that are believed to underlie variation in BMR including the sizes of visceral organs and  
631 mitochondrial characteristics. Brain and liver mass are heritable in mice (Jones et al., 1992), as are  
632 the masses of brain, heart, liver, and kidney in baboons *Papio hamadryas* (Mahaney et al., 1993),  
633 and the liver in wild mice *Phyllotis darwini* (Bacigalupe et al., 2004). Baboons show additive  
634 genetic correlations between the masses of brain and liver, as well as between liver and kidneys  
635 (Mahaney et al., 1993), but no additive genetic correlations were detected between liver, heart, lungs,  
636 small intestine, and caecum in *Phyllotis darwini* (Bacigalupe et al., 2004). Given the phenotypic

637 associations observed between visceral organs and BMR as well as between mitochondrial  
638 characteristics and BMR, the likely heritability of these traits, and the genetic associations among  
639 visceral organs, it seems plausible that genetic associations between BMR and these traits will also  
640 be revealed. Such analyses will yield valuable information regarding the mechanistic bases of  
641 variation in BMR that arises as a consequence of direct selection on BMR, or as a consequence of  
642 correlated responses in BMR associated with selection on other traits.

### 643 **Consequences of variation in BMR for animal performance**

644         Mass-independent variation in BMR amounts to up to several-fold between individuals,  
645 populations, and species, and understanding the consequences of this variation for organismal  
646 performance is essential to understanding the selection pressures that act on energy expenditure in  
647 the wild. In this regard, the most strident criticism of the BMR concept is that while the strict  
648 conditions prescribed for its measurement facilitate comparison by ensuring that all animals are in a  
649 similar physiological state, these conditions potentially come with the sacrifice of biological  
650 relevance. Basal conditions can be paraphrased as the measurement of a starving, stationary, sleeping  
651 animal, suggesting that the measurement is likely to have little practical utility in understanding the  
652 evolution of energy expenditure. Nevertheless, the observation that BMR varies significantly has led  
653 to the idea that the variation is important and might therefore be the subject of natural selection,  
654 either directly on BMR itself, or indirectly on a trait related to BMR. Indeed, BMR is repeatable  
655 (Nespolo and Franco, 2007), has low to moderate heritability (Table 5; see also Table 6 for  
656 heritabilities of metabolic rate for ectotherms), varies between individuals, responds to artificial  
657 selection (Książek et al., 2004), and is correlated with a wide range of other traits (Table 4, see also  
658 Biro and Stamps, 2010; Burton et al., 2011). This suggests that BMR could be the subject of  
659 selection, but studies demonstrating this in wild populations are rare.

660         Measurements of the association between juvenile survival and SMR in snails *Helix aspersa*  
661 suggest that maintenance metabolism is under a combination of directional and stabilising selection

662 (Artacho and Nespolo, 2009), such that individuals with low and intermediate metabolic rates are  
663 favoured over those with high metabolic rates. Natural selection therefore eliminates individuals  
664 with high metabolic rates but does not necessarily favour individuals with the absolute lowest  
665 metabolic rates. Similarly, inbreeding results in an increase in resting metabolic rate in crickets  
666 *Gryllobates sigillatus*, suggesting that low quality individuals have higher metabolic rates than high  
667 quality individuals (Ketola and Kotiaho, 2009). This contrasts with the finding that BMR is  
668 positively related to over-winter survival in short-tailed field voles *Microtus agrestis* (Jackson et al.,  
669 2001) and reproductive success in bank voles *Myodes (Clethrionomys) glareolus* (Boratyński and  
670 Koteja, 2010), although BMR is not related to over-winter survival in bank voles (Boratyński and  
671 Koteja, 2009). This discrepancy presumably arises for the same reason that stabilising selection was  
672 observed by Artacho and Nespolo (2009): high BMR may be an advantage in some situations, but a  
673 liability in others, and *vice versa*. Thus, high BMR and maximum rates of thermogenesis increase  
674 over-winter survival by improving cold tolerance (Hayes and O'Conner, 1999; Jackson et al., 2001),  
675 but low BMR improves starvation resistance (Rixon and Stevenson, 1957). Male Leach's storm-  
676 petrels *Oceanodroma leucorhoa* with low BMR breed earlier and produce chicks that grow faster  
677 than males with relatively high BMR (Blackmer et al., 2005), but mice with low BMR die sooner  
678 than those with high BMR (Speakman et al., 2004). Other studies have found no link between BMR  
679 and reproductive traits in mice (Hayes et al., 1992; Johnson et al., 2001a; Johnston et al., 2007), a  
680 positive correlation between energy expenditure during lactation and BMR in *Peromyscus* mice  
681 (Glazier, 1985), no link between interspecific differences in age at first reproduction and BMR  
682 (Lovegrove, 2009), and a positive relationship between BMR and maximum running speed  
683 (Lovegrove, 2004).

684         The level of BMR therefore appears to be maintained as a consequence of a series of trade-  
685 offs such that low BMR is an advantage during food deprivation or reproduction, but high BMR is an  
686 advantage during cold exposure or predation events. This list is very unlikely to be exhaustive and

687 other relationships presumably await discovery. However, an unanswered and intriguing question  
688 concerns the extent to which the “file drawer problem” (Csada et al., 1996) influences our current  
689 understanding of the consequences of variation in BMR, and it is presently unclear how many non-  
690 significant relationships between BMR and other traits remain unpublished.

## 691 **Looking forward: the evolution of BMR and allometric scaling**

692 BMR is ultimately linked with a range of extrinsic variables including habitat temperature,  
693 net primary productivity, and diet, and BMR is correlated with variation in survival, reproduction,  
694 and lifespan. An enduring area of interest that remains active, despite decades of research, concerns  
695 understanding the mechanistic basis of the allometric scaling of metabolic rate with body mass (e.g.  
696 Agutter and Wheatley, 2004; Savage et al., 2008; White and Kearney, 2012). However, if the non-  
697 isometric scaling of metabolic rate is ever to be understood, it is first necessary to know exactly what  
698 the relationship is. Recent meta-analyses (Glazier, 2005; White et al., 2007b), and PI analyses of  
699 hundreds of species of birds (McKechnie and Wolf, 2004; McKechnie et al., 2006; Kabat et al.,  
700 2008) and mammals (Duncan et al., 2007; Sieg et al., 2009; White et al., 2009; Capellini et al., 2010)  
701 have failed to support any single value of the allometric scaling exponents relating BMR to body  
702 mass. Without very substantial increases in the size of the data set, these conclusions are unlikely to  
703 change (White and Seymour, 2005b). Thus, an emerging challenge is to understand, for example, the  
704 differences in metabolic scaling between endotherms and ectotherms (Farrell-Gray and Gotelli,  
705 2005; White et al., 2007b), and between metabolic levels (White and Seymour, 2005a; Glazier, 2008,  
706 2009a). One promising area for understanding the allometry of metabolic rate is the use of  
707 experimental manipulation of intra-specific scaling exponents in species that span a wide range of  
708 body masses during development. During development, many species of ectotherm grow over  
709 several orders of magnitude in body size (e.g. Soling and Kleineke, 1976; Killen et al., 2007; Moran  
710 and Wells, 2007), and the scaling of metabolic rate in ectotherms has proven amenable to  
711 experimental manipulation (e.g. Table 2) (Glazier, 2005). Such experimental studies, which might

712 involve manipulation of any of the factors known to influence metabolism, potentially represent  
713 powerful tools to understand the factors that constrain and influence the allometric scaling exponent  
714 relating metabolic rate to body mass.

715 Further progress toward understanding why metabolic rate scales allometrically is also likely  
716 to be made by complimenting the ongoing emphasis on mechanistic explanations with an approach  
717 that views metabolic scaling as an evolutionary outcome of trait associations, and explicitly  
718 incorporates the factors associated with mass-independent variation in metabolic rate between  
719 species (e.g. temperature, productivity, reproductive output) (see e.g. Glazier, 2005; Killen et al.,  
720 2010). Quantitative genetic tools have previously been applied to other problems of allometric  
721 scaling (e.g. Lande, 1979; Riska and Atchley, 1985; Lynch and Walsh, 1998), and are increasingly  
722 being applied to understanding other aspects of metabolic evolution (Artacho et al., 2005; Hayes,  
723 2010; Nespolo et al., 2011, see also Konarzewski and Książek, 2012). The application of this tool  
724 set also has the potential to yield substantial benefits not only to the understanding of mass-  
725 independent variation, but also to the scaling of metabolic rate with body mass. As an example,  
726 because the genetic correlation between body mass and metabolic rate is positive and often less than  
727 1 (Table 7), allometric scaling of metabolic rate with body mass can arise in a simple evolutionary  
728 model that includes random variation in body mass and correlated changes in metabolic rate (Figure  
729 4; see Appendix B for modelling procedures). The scaling exponent of metabolic rate in such a  
730 model can take a wide range of values, depending on the strength of the association between  
731 metabolic rate and body mass (Figure 4). While this example is obviously simplistic, it nonetheless  
732 demonstrates that the evolution of allometric scaling might be explained without the need to invoke  
733 first principles mechanistic hypotheses grounded in chemistry or physics (see also Witting, 1995;  
734 Kozłowski and Weiner, 1997; Glazier, 2005 for other examples). Taking the resource distribution  
735 hypotheses as an example, this evolutionary approach based on trait associations assumes not that the  
736 geometry of the resource distribution network dictates metabolic scaling, but that the geometry of the

737 resource distribution network has evolved to support the pattern of metabolic scaling (see also  
738 Weibel and Hoppeler, 2005). For evolutionary models of allometric scaling to be of any value,  
739 however, it is essential that plausible models of evolution and trait association are specified, and,  
740 critically, that appropriate tests are either presented in conjunction with the models, or that clear  
741 descriptions of the unique predictions of the models are presented, so that appropriate tests can be  
742 designed (Shipley, 2000; Currie et al., 2004; Hawkins et al., 2007b; Glazier, 2010; White et al.,  
743 2011b; Kearney and White, 2012).

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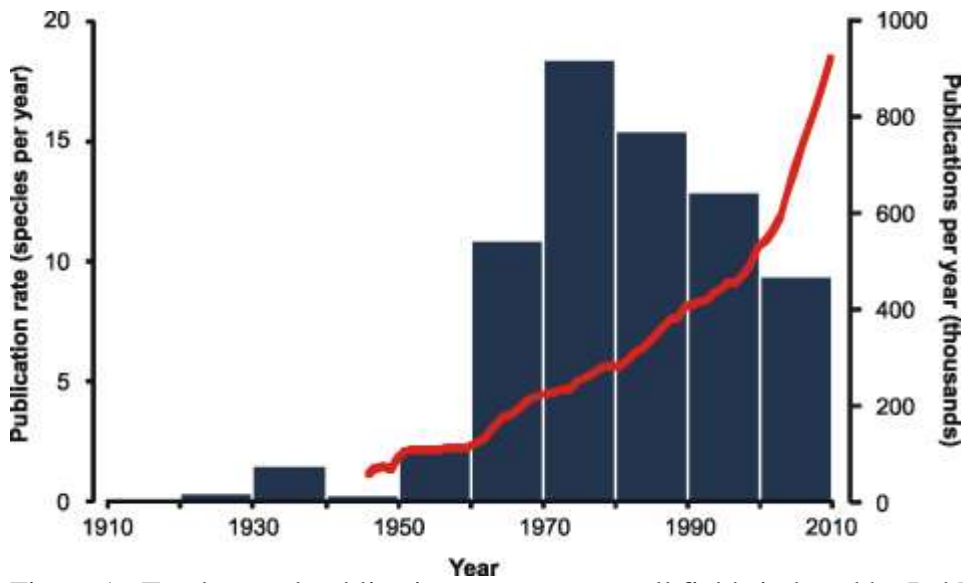
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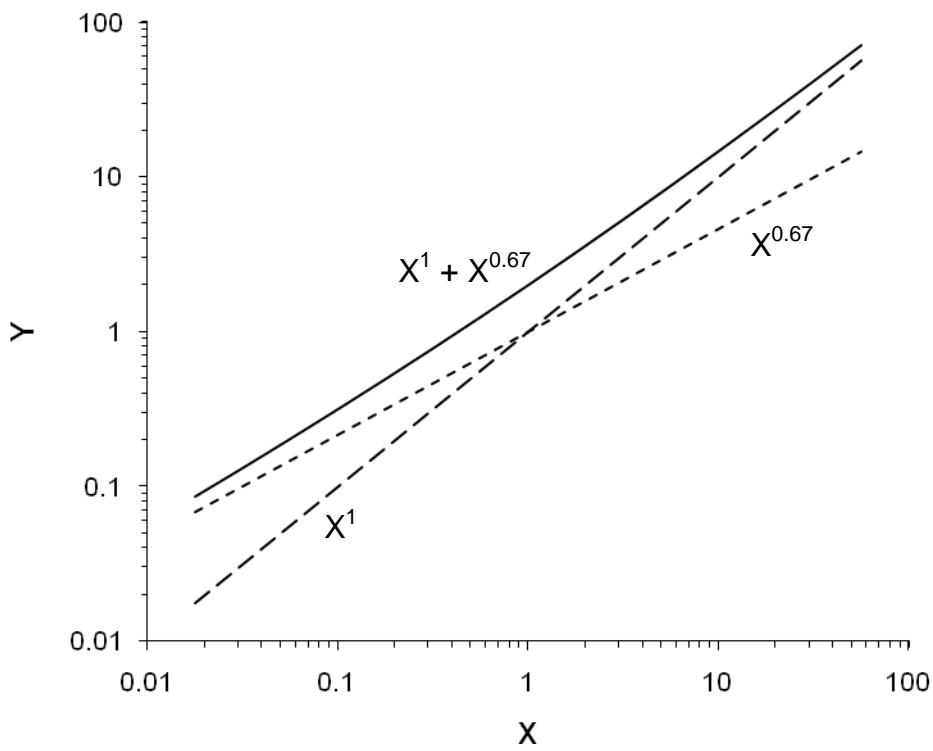




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Figure 1. Total annual publication output across all fields indexed by PubMed (Publications per year, red line) and publication rate of data for mammalian basal metabolic rate (BMR, filled bars). BMR data are from a recent compilation (Sieg et al., 2009). Where BMR data for a species have been published multiple times, only the first instance is included.

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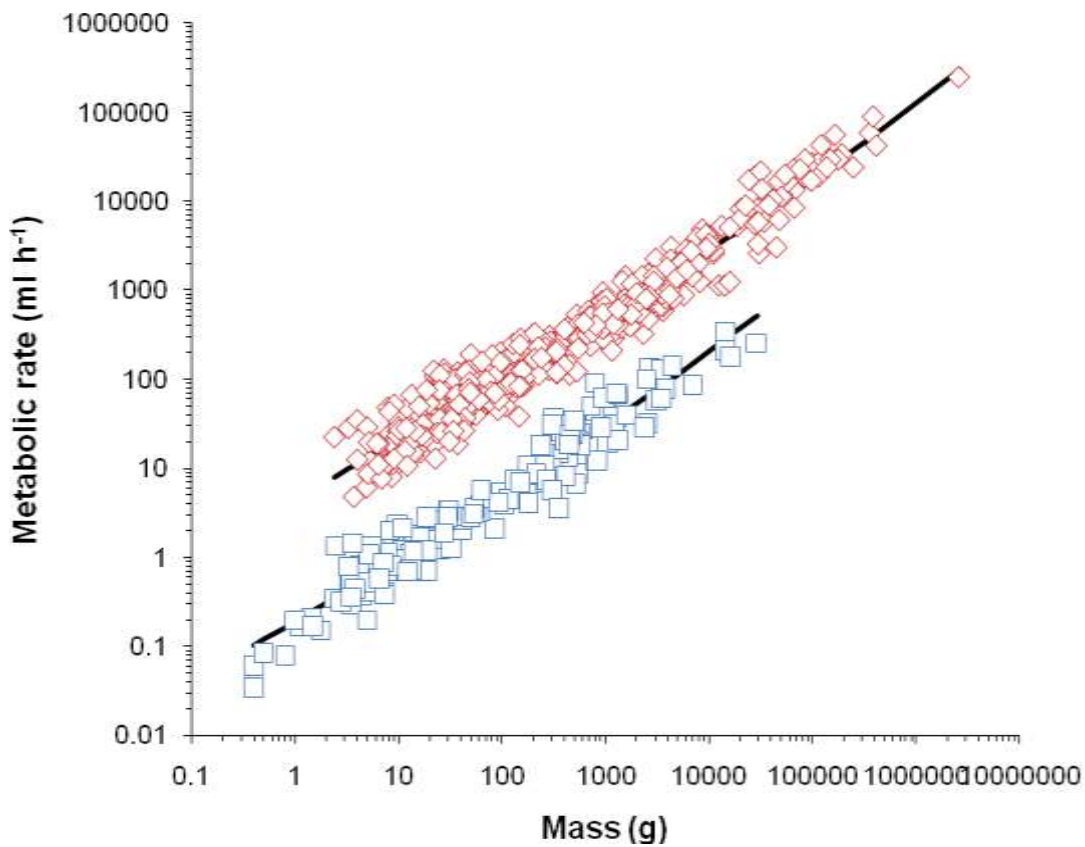
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1617 Figure 2. Summing isometric and allometric relationships introduces curvature into the relationship  
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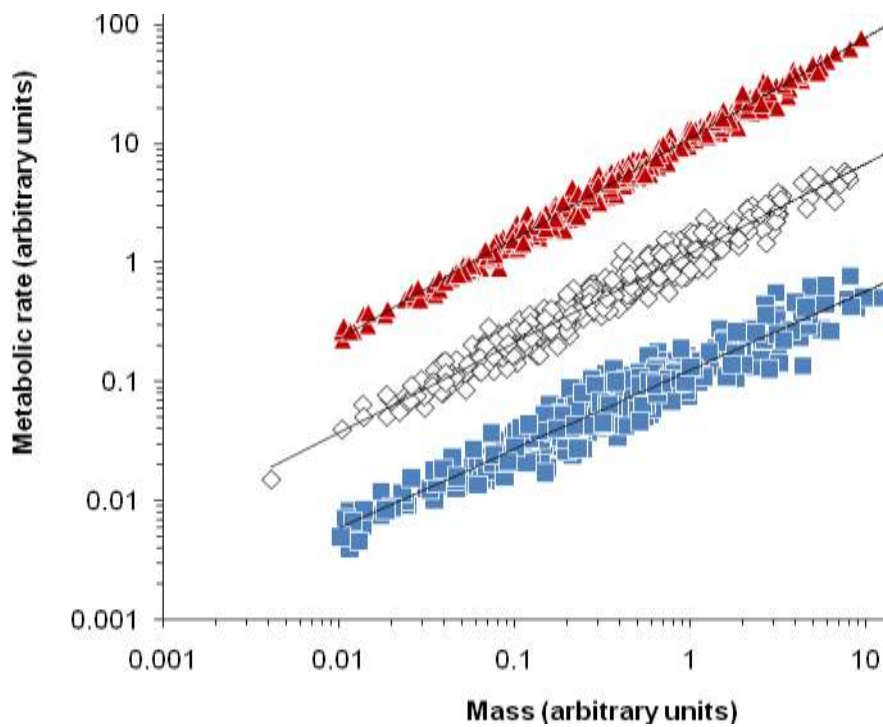
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Figure 3. Relationships between mammalian BMR (unfilled diamonds: Sieg et al., 2009) and reptile SMR (unfilled squares: White et al., 2006) and mass ( $M$ , g) estimated by fitting summed allometric ( $\propto M^{0.67}$ ) and isometric ( $\propto M^1$ ) components by iteration (Gauss-Newton algorithm) using JMP v8.0.1 (SAS Institute, Cary, NC, USA). Mammal BMR =  $4.30 M^{0.67} + 0.084 \text{ mass}^1$ ; Reptile SMR =  $0.18 M^{0.67} + 0.012 M^1$ . Data for reptiles were normalised to a body temperature of 25 °C using a  $Q_{10}$  value of 2.44 (White et al., 2006).



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Figure 4. Simulated associations between metabolic rate (MR) and mass (M) generated according to the methods in Appendix B. The scaling exponent ( $b$ ) and strength of the association is dependent on the relationship between changes in MR and changes in M (filled triangles: the change in MR at each time step is equal to 0.7 to 1 times the change in M,  $b = 0.84$ ; unfilled diamonds: change in MR is 0.5 to 1 times the change in M,  $b = 0.75$ ; filled squares: change in MR is 0.33 to 1 times the change in M,  $b = 0.66$ ). The model does not predict the elevation of the relationship; filled triangles and filled squares are offset by for clarity by +1 and -1 orders of magnitude, respectively.

1639 Table 1. Selected scaling exponents (b) for the cardiovascular system predicted by the fractal  
 1640 resource distribution model of West, Brown, and Enquist (WBE: West et al., 1997) and the Resource  
 1641 Distribution Network model of Banavar et al. (RDN: Banavar et al., 2010).  
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<b>Variable</b>	<b>WBE</b>	<b>RDN</b>	<b>Observed</b>
Cardiac frequency	-0.25		Mammals: -0.23 (Seymour and Blaylock, 2000) Birds: -0.28 (Seymour and Blaylock, 2000) Fish: ~0 (White and Seymour, 2011)
Aorta radius	0.375	0.33	0.33 (Peters, 1983)
Aorta length	0.25	0.33	0.32 (Günther and León de la Barra, 1966)
Aorta pressure	0		0.05 (Seymour and Blaylock, 2000)
Blood velocity	0	0 to 0.083	0.07 (Peters, 1983)
Respiratory frequency	-0.25		-0.56 to -0.25 (Stahl, 1967; Frappell et al., 2001; Mortola and Limoges, 2006; Terblanche et al., 2008; Mortola and Seguin, 2009)

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1644 Table 2. Examples of manipulative studies of the scaling of metabolic rate (see Glazier, 2005 for an  
 1645 extensive compilation of further examples).  
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<b>Treatment</b>	<b>Species</b>	<b>Reference</b>
Diet	<i>Daphnia</i>	(Jeyasingh, 2007)
Light intensity	<i>Daphnia pulex</i>	(Buikema, 1972)
	Atlantic cod <i>Gadus morhua</i>	(Finn et al., 2002)
Oxygen availability	Marine nematode <i>Enoplus brevis</i>	(Atkinson, 1973)
pH	Ornate rainbowfish <i>Rhadinoventrus ornatus</i>	(Vaca and White, 2010)
Salinity	Crab <i>Hemigrapsus oregonensis</i>	(Dehnel, 1960)
	Crab <i>Hemigrapsus nudus</i>	(Dehnel, 1960)
	Rainbow trout <i>Salmo gardneri</i>	(Rao, 1971)
Starvation	Shore crab <i>Carcinus maenus</i>	(Marsden et al., 1973)
	Sand Dollar <i>Mellita quinquesperforata</i>	(Lane and Lawrence, 1979)
Temperature	American cockroach <i>Periplaneta americana</i>	(Dehnel and Segal, 1956)
	Freshwater snail <i>Marisa cornuarietis</i>	(Åkerlund, 1969)
	Shore crab <i>Carcinus maenus</i>	(Marsden et al., 1973)
	Sea anemone <i>Metridium senile</i>	(Walsh and Somero, 1981)
	Wood louse <i>Porcellio laevis</i>	(Lardies et al., 2004)
	Vendace <i>Coregonus albula</i>	(Ohlberger et al., 2007)
Water availability	Manchurian ash <i>Fraxinus mandshurica</i>	(Chen and Li, 2003)
	Amur cork tree <i>Phellodendron amurense</i>	(Chen and Li, 2003)
Colony size	<i>Botrylloides simodensis</i> (colonial ascidian)	(Nakaya et al., 2005)
	<i>Hippoporina indica</i> (Colonial marine bryozoan)	(White et al., 2011b)
Inbreeding	Cricket <i>Gryllodes sigillatus</i>	(Ketola and Kotiaho, 2012)

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1648 Table 3. Parameter estimates for a model for avian basal metabolic rate (BMR, ml h<sup>-1</sup>) as assessed by  
 1649 phylogenetic generalised least squares ( $\lambda = 0.83$  and AIC = -395.2; AIC for an equivalent non-  
 1650 phylogenetic model is 247.0). Significant ( $p < 0.05$ ) parameters are indicated with \*; n.s. is non-  
 1651 significant. See Appendix A for a description of the analysis.  
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<b>Parameter</b>	<b>Estimate</b>	<b>s.e.</b>
Intercept	-1.11 *	0.06
logM	0.72 *	0.02
Diet		
Aquatic vegetation	0.03 n.s.	0.07
Aquatic invertebrates	0.06 n.s.	0.05
Fruit	-0.04 n.s.	0.03
Flying insects	-0.06 n.s.	0.05
Grass	0.07 n.s.	0.08
Leaves	0.04 n.s.	0.04
Insects	0.01 n.s.	0.02
Omnivore	0.07 n.s.	0.04
Pollen	0.08 n.s.	0.04
Seeds	-0.01 n.s.	0.03
Vertebrates	-0.01 n.s.	0.04

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Table 4. A selection of significant correlates of metabolic rate in animals (values in parentheses are additive genetic correlations).

Species	MR level	Correlate	Direction	Reference
Laboratory rat <i>Rattus norvegicus</i>	RMR	Starvation resistance	-	(Rixon and Stevenson, 1957)
Great tit <i>Parus major</i>	RMR	Social dominance	+	(Røskaft et al., 1986)
Pied flycatchers <i>Ficedula hypoleuca</i>	RMR	Social dominance	+	(Røskaft et al., 1986)
Willow tit <i>Parus montanus</i>	RMR	Social dominance	+	(Hogstad, 1987)
Deer mouse <i>Peromyscus maniculatus</i>	BMR	$\dot{V}O_2\text{max}$	+	(Hayes, 1989)
Belding's ground squirrel <i>Spermophilus beldingi</i>	RMR	$\dot{V}O_2\text{max}$	+	(Chappell and Bachman, 1995)
Masu salmon <i>Oncorhynchus masou</i>	RMR	Social dominance	+	(Yamamoto et al., 1998)
House sparrows <i>Passer domesticus</i>	BMR <sub>juvenile</sub>	Juvenile $\dot{V}O_2\text{max}$	+	(Chappell et al., 1999)
Short-tailed field vole <i>Microtus agrestis</i>	RMR	Over-winter survival	+	(Jackson et al., 2001)
Nine-banded armadillos <i>Dasypus novemcinctus</i>	BMR	MMR <sub>cold</sub>	+	(Boily, 2002)
Short-tailed field vole <i>Microtus agrestis</i>	RMR	Daily energy expenditure*	+	(Speakman et al., 2003)
Laboratory mice <i>Mus musculus</i>	RMR	Longevity	+	(Speakman et al., 2004)
Leach's storm-petrel <i>Oceanodroma leucorhoa</i>	BMR ♂	Offspring growth	-	(Blackmer et al., 2005)
Leach's storm-petrel <i>Oceanodroma leucorhoa</i>	BMR ♂	Hatch date	+	(Blackmer et al., 2005)
Bank vole <i>Myodes glareolus</i>	BMR	MMR <sub>swim</sub>	(+)	(Sadowska et al., 2005)
Laboratory mouse <i>Mus musculus</i>	BMR	Gestational weight loss	+	(Johnston et al., 2007)
Garden snail <i>Helix aspersa</i>	SMR	Juvenile survival	- and stabilising	(Artacho and Nespolo, 2009)
Laboratory mice <i>Mus musculus</i>	BMR	MMR <sub>exercise</sub>	(+)	(Wone et al., 2009)
Bank vole <i>Myodes glareolus</i>	BMR	Postweaning growth rate	(+)	(Sadowska et al., 2009)
Bank vole <i>Myodes glareolus</i>	BMR	Ability to cope with poor diet	(+)	(Sadowska et al., 2009)
Bank vole <i>Myodes glareolus</i>	BMR ♂	Reproductive success	+	(Boratyński and Koteja, 2010)
Bank voles <i>Myodes glareolus</i>	BMR ♀	Over-winter survival	+	(Boratyński et al., 2010)



Red squirrels <i>Tamiasciurus hudsonicus</i>	RMR	Over-winter survival	-	(Larivée et al., 2010)
Root vole <i>Microtus oeconomus</i>	RMR	Proactive behaviour	+	(Lantová et al., 2011)
Deer mouse <i>Peromyscus maniculatus</i>	RMR	Exploratory behaviour	(+)	(Careau et al., 2011)
Atlantic salmon <i>Salmo salar</i>	SMR	Social dominance	+	(Reid et al., 2011)
Atlantic salmon <i>Salmo salar</i>	SMR	Feeding rate	+	(Reid et al., 2011)
Atlantic salmon <i>Salmo salar</i>	SMR	Growth rate	-	(Reid et al., 2011)

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1659 \*Extrinsic association caused by environmental differences between habitats, rather than an intrinsic  
1660 one. Note that a number of other studies have found no association between metabolic rate and a  
1661 range of traits (Hayes et al., 1992; Chappell et al., 1999; Hammond et al., 2000; Dohm et al., 2001;  
1662 Johnson et al., 2001a; Nespolo et al., 2005; Sadowska et al., 2005; Vézina et al., 2006; Chappell et  
1663 al., 2007; Boratyński and Koteja, 2009; Bouwhuis et al., 2011; Timonin et al., 2011; Schimpf et al.,  
1664 2012). See also Biro and Stamps (2010) and Burton et al. (2011) for compilations of associations  
1665 between metabolic rate and other traits.

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Table 5. Narrow-sense heritability ( $h^2$ ) of basal metabolic rate (BMR), standard metabolic rate (SMR), sustained metabolic rate (susMR), cold-induced maximum metabolic rate (MMR), and exercise-induced maximum metabolic rate ( $\dot{V}O_{2max}$ ) of birds and mammals. \* indicates  $p < 0.05$ .

Species	Measurement	$h^2 \pm SE$	Reference
Laboratory mouse <i>Mus musculus</i>	BMR	$0.08 \pm 0.06$	(Lacy and Lynch, 1979)
Laboratory mouse <i>Mus musculus</i>	RMR	$0.21 \pm 0.04^*$	(Lynch and Sulzbach, 1984)
Hsd:ICR strain, <i>Mus domesticus</i>	BMR	0.09	(Dohm et al., 2001)
	$\dot{V}O_{2max}$	$0.64^*$	(Dohm et al., 2001)
Leaf-eared mouse <i>Phyllotis darwini</i>	BMR	0.15	(Nespolo et al., 2003)
Leaf-eared mouse <i>Phyllotis darwini</i>	BMR	$0.21 \pm 0.21$	(Bacigalupe et al., 2004)
	susMR	$0.20 \pm 0.38$	(Bacigalupe et al., 2004)
Laboratory mouse <i>Mus musculus</i>	BMR	$0.38 \pm 0.21^*$	(Konarzewski et al., 2005)
	Swim $\dot{V}O_{2max}$	$0.40 \pm 0.21^*$	(Konarzewski et al., 2005)
Leaf-eared mouse <i>Phyllotis darwini</i>	BMR	$0.11 \pm 0.18$	(Nespolo et al., 2005)
	MMR	$0.69 \pm 0.35^*$	(Nespolo et al., 2005)
Bank vole <i>Clethrionomys glareolus</i>	BMR	$0.40^*$	(Sadowska et al., 2005)
	Swim $\dot{V}O_{2max}$	$0.40^*$	(Sadowska et al., 2005)
	MMR	$0.43^*$	(Sadowska et al., 2005)
Zebra finch <i>Taeniopygia guttata</i>	BMR	$0.25 \pm 0.04^*$	(Rønning et al., 2007)
Blue tit <i>Cyanistes caeruleus</i>	RMR	$0.59 \pm 0.25$	(Nilsson et al., 2009)
Stonechat <i>Saxicola torquate rubicola</i>	BMR <sub>residual</sub>	$0.48 \pm 0.16$	(Tieleman et al., 2009b)
Stonechat <i>Saxicola torquata axillaris</i>	BMR <sub>residual</sub>	$0.20 \pm 0.35$	(Tieleman et al., 2009b)
Stonechat <i>Saxicola torquate maura</i>	BMR ( $g^{-1}$ )	$0.37 \pm 0.47$	(Tieleman et al., 2009b)
Laboratory mouse <i>Mus musculus</i>	BMR <sub>residual</sub>	$0.19 \pm 0.07^*$	(Wone et al., 2009)
	$\dot{V}O_{2max}$ <sub>residual</sub>	$0.16 \pm 0.06^*$	(Wone et al., 2009)
Pied Flycatcher <i>Ficedula hypoleuca</i>	RMR	$0.43 \pm 0.17^*$	(Bushuev et al., 2011)
Deer mouse <i>Peromyscus maniculatus</i>	RMR <sub>residual</sub>	$0.39 \pm 0.20$	(Careau et al., 2011)

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1673 Table 6. Broad-sense ( $H^2$ ) and narrow sense ( $h^2$ ) heritability of metabolic rate in ectothermic animals  
 1674 (\*  $p < 0.05$ , \*\*\*  $p < 0.001$ ).  
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Species	Measurement	Heritability $\pm$ SE	Reference
Garter snake <i>Thamnophis sirtalis</i>	Maximum	$H^2 = 0.88^{***}$	(Garland and Bennett, 1990)
<i>Drosophila melanogaster</i>			
5 d post-eclosion	Routine MR	$H^2 = 0.07^{***}$	(Khazaeli et al., 2005)
	Routine MR	$H^2 = 0.14^{***}$	(Khazaeli et al., 2005)
16 d post-eclosion	Routine MR	$H^2 = 0.48^{***}$	(Khazaeli et al., 2005)
	Routine MR	$H^2 = 0.45^{***}$	(Khazaeli et al., 2005)
29 d post-eclosion	Routine MR	$H^2 = 0.43^{***}$	(Khazaeli et al., 2005)
	Routine MR	$H^2 = 0.26^{***}$	(Khazaeli et al., 2005)
47 d post-eclosion	Routine MR	$H^2 = 0.30^{***}$	(Khazaeli et al., 2005)
	Routine MR	$H^2 = 0.29^{***}$	(Khazaeli et al., 2005)
Sand cricket <i>Gryllus firmus</i>	Resting	$H^2 = 0.045 \pm 0.04$	(Nespolo et al., 2007)
	Average	$H^2 = 0.052 \pm 0.06$	(Nespolo et al., 2007)
	Minimum	$H^2 = 0.10 \pm 0.06$	(Nespolo et al., 2007)
	Maximum	$H^2 = 0.085 \pm 0.05$	(Nespolo et al., 2007)
Cricket <i>Gryllodes sigillatus</i>	Resting	$h^2 = 0.142 \pm 0.187$	(Ketola and Kotiaho, 2009)
	Exercise	$h^2 = 0.718^* \pm 0.313$	(Ketola and Kotiaho, 2009)

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1678 Table 7. Additive genetic correlations between metabolic rate and body mass in animals, shown  $\pm$   
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Species	MR level	Correlation	Reference
Zebra finch <i>Taeniopygia guttata</i>	BMR	$0.914 \pm 0.081$	(Rønning et al., 2007)
Blue tit <i>Cyanistes caeruleus</i>	RMR	$1.178 \pm 0.456$	(Nilsson et al., 2009)
Stonechat <i>Saxicola torquata rubicola</i>	BMR	$0.400 \pm 0.349$	(Tieleman et al., 2009b)
Stonechat <i>Saxicola torquata axillaris</i>	BMR	$0.780 \pm 0.360$	(Tieleman et al., 2009b)
Deer mouse <i>Peromyscus maniculatus</i>	BMR	$0.72 \pm 0.23$	(Careau et al., 2011)

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## Appendix A. Phylogenetic methods for the analysis of the effect of diet on avian basal metabolic rate.

The relationship between log transformed basal metabolic rate (BMR), log transformed body mass (M) and dietary categories was analysed using phylogenetic generalised least squares (PGLS) (Grafen, 1989; Martins and Hansen, 1997; Garland and Ives, 2000) in the APE (Analysis of Phylogenetics and Evolution) package (Paradis et al., 2004) within R (Ihaka and Gentleman, 1996) according to established procedures (Halsey et al., 2006; Duncan et al., 2007; White et al., 2009). Data for avian BMR matched to a phylogenetic hypothesis were obtained from a published analysis of the scaling of BMR (Kabat et al., 2008), and were matched to dietary categories provided by McNab (2009). Matched BMR and diet data were available for a total of 287 species. Since the true branch lengths in the phylogeny are unknown, two branch length assumptions were compared: all branches set equal to 1, and an alternative assumption that branch lengths were proportional in length to the number of taxa descended from the node to which the branch leads (Grafen, 1989). A measure of phylogenetic correlation,  $\lambda$  (Pagel, 1999; Freckleton et al., 2002), was estimated by fitting PGLS models with different values of  $\lambda$  and finding the value that maximizes the log likelihood. The degree to which trait evolution deviates from Brownian motion ( $\lambda = 1$ ) was accommodated by modifying the covariance matrix using the maximum likelihood value of  $\lambda$ , which is a multiplier of the off-diagonal elements of the covariance matrix (i.e., those quantifying the degree of relatedness between species). All models were compared on the basis of Akaike's Information Criterion (AIC) as a measure of model fit (Burnham and Anderson, 2001, 2002). The relative support of alternative models was compared on the basis of  $\Delta_i$  ( $= \text{AIC} - \text{minimum AIC}$ ); models having  $\Delta_i \leq 2$  have substantial support, those where  $4 \leq \Delta_i \leq 7$  have considerably less support, while models having  $\Delta_i > 10$  have essentially no support (Burnham and Anderson, 2001).

1708 **Appendix B. Methods for the generation of an allometric**  
1709 **association between metabolic rate and body mass.**

1710 The model for allometric scaling is based on Monte Carlo simulations developed to understand the  
1711 causes of the observed right-skewed lognormal distribution of mammalian body masses (Maurer et  
1712 al., 1992; Blackburn and Gaston, 1994, 1998, 1999). Initially, 400 ‘species’ with a mass (M) of 1 and  
1713 a metabolic rate (MR) of 1 were generated. For each species, a random change in M was then  
1714 generated by multiplying M by a normal deviate with a mean of 0 and standard deviation of 0.02 and  
1715 then adding M. This was then repeated a total of 5000 times for each ‘species’. Thus, for each of the  
1716 5000 time steps, mass varied randomly with a standard deviation of 2% of the value of M at the  
1717 previous time step. Because the genetic correlation between MR and M is positive and often less  
1718 than 1 (Table 7), factorial changes in MR at each time step were randomly smaller than the changes  
1719 in MR (see e.g. Figure 4). This procedure generates lognormal distributions of M and MR,  
1720 consistent with the idea that body size evolves multiplicatively, and could be made more realistic by  
1721 the introduction of size-biased selection and extinction, and anagenetic size change within species  
1722 between speciation and extinction events (e.g. Stanley, 1973; Maurer et al., 1992; Kingsolver and  
1723 Pfennig, 2004; Clauset and Erwin, 2008; Mattila and Bokma, 2008; Clauset et al., 2009). The  
1724 consequences of variation in MR for allometric scaling could be examined by including selections  
1725 against low (e.g. Jackson et al., 2001) or high (e.g. Artacho and Nespolo, 2009) MR.

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