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Appendix A: Likelihood function derivations and further details regarding statistical tests, microzooplankton data and hunter gatherer data

Details regarding K, b and goodness-of-fit tests

Microzooplankton data

Determination of bin breaks knowing only that progressive bins double in size and geometric midpoints are equally spaced on a log scale

Likelihood functions for PLB and ExpB models

Likelihood function for a power-law distribution for prebinned data where bin widths progressively double in size

Likelihood function for an exponential distribution for prebinned data where bin widths progressively double in size

Previous test of the exponential distribution for the Dobe Ju/'hoansi hunter gatherer data

Details regarding K, b and goodness-of-fit tests

The number of parameters being estimated for the unbounded models is given by K (denoted K_i in Box 1 of Edwards et al. 2007), and for the bounded models the number is $K + 1$. If the lowest bin(s) had been excluded from the previously-published study, such that the start of the tail, a, was being determined by the author, then $K = 1$ because just μ or λ was being estimated here from the data. However, if the full data set was used in the previous analysis, then a was set to the minimum value of the data, and since it was specified by the data, there were two parameters being estimated from the data for the unbounded models, $K = 2$.

However, for the jackals, the value of $a = 2$ was determined by the sampling protocol – the presumed accuracy of the radio tracking devices was ± 100 m (Atkinson et al. 2002), such that movements < 200 m could not be reliably measured. Units of a are 100 m, such that $a = 2$. Thus $K = 1$ for the jackals, because a was determined by the sampling protocol rather than the data.

Whether or not a is counted towards the values of K for a particular data set does not actually affect the MLEs or the evidence ratios (because of cancellation when calculating the differences in Akaike Information Criteria), but would change the results of goodness-of-fit tests. Values of K are given in Table A2.

As mentioned in the main text, b was set to the maximum value of the data, rounded up to the nearest integer. We repeated all analyses with b set to be exactly the largest data value (unless the data were only available pre-binned, in which case b was set to the maximum value of the highest bin). This did not significantly affect the results, though for

2

the hunter gatherers data the evidence ratios changed slightly (but not enough to change the conclusions). Sensitivity to larger values of b was not tested, because increasing b would just reduce support for the PLB model over the exponential models (see Supplementary Information of Edwards et al. 2007).

For goodness-of-fit tests, we used the G-test with Williams's correction (Sokal and Rohlf 1995), as in Edwards et al. (2007). This requires binning of data (unless the data were only available in binned form). The consistent approach taken here was to start binning data from the smallest value using a bin width of 1. The G-test requires each bin to have ≥ 5 data points. Thus once a bin was reached that had < 5 data points, the bin width was doubled to 2. Bin widths of 2 were used until a bin had < 5 data points, and then the bin width doubled to 4. This doubling of bin widths was continued until all data were included. If the final bin had < 5 data points, then the penultimate bin was expanded to include the final bin.

Our main interest is in questioning support for power-law distributions. For the eight data sets for which a bounded power-law distribution was the most supported model, only one passed the goodness-of-fit test (grey seal 6124, Table 3). To see whether the choice of bin width affected the rejection of the bounded power law, we performed an additional goodness-of-fit test on all eight data sets. Instead of the procedure described above, we defined bins as follows: start the first bin from the smallest value using a bin width of one, then double the width of each successive bin. Thus the bin widths were 1, 2, 4, 8, ... If a bin had < 5 data points then its width was doubled. The doubling of bin widths was continued until all data were included. As above, if the final bin had < 5 data points, then the penultimate bin was expanded to include the final bin.

The results are shown in Table A3, with P values to be compared with those in Tables 3 or A2. The P values generally get slightly lower (so even less support for the PLB model), and the conclusions are unaffected. The PLB model is still suitable for the grey seal 6124 data, but not for any other data sets (no P values come close to crossing the 0.05 value due to the new binning procedure).

Regarding the significance level of 0.05, we explored further analyses to potentially account for the fact that multiple data sets were being tested. This was done using the sequential Bonferroni correction (e.g. Moran 2003) for the aforementioned eight data sets for which the PLB model was the most supported model, to see if more than just the grey seal 6124 data set might pass the goodness-of-fit test (and hence a bounded power-law distribution may be suitable for other data sets). The sequential Bonferroni correction works by first comparing the lowest P value, which is 0 for Peru boat 1d, with 0.05/8 (the 8 comes from there being 8 data sets). Since $0 < 0.05/8$, the null hypothesis that the data are consistent with the tested distribution is rejected (as it was for the original comparison with 0.05). The next lowest P value, 0 for Peru boat 1e, is then compared to 0.05/7, the next to 0.05/6 and so on. Continuing this sequential procedure rejects all null hypotheses until we reach $P = 0.84 > 0.05/1$ for grey seal 6124, for which the correction process would consider the data to be consistent with the PLB model (in agreement with the original conclusion reached when comparing all P values to 0.05). Thus, use of the correction does not change the conclusion that the PLB model is only suitable for one data set.

An alternative question that we asked using the sequential Bonferroni correction is whether the most suitable model for each data set is consistent with the data (i.e. apply the correction for all 17 data sets). The original conclusions are unchanged except for grey

seal 6118 and jackal F4, for which the procedure would consider the data to be consistent with the PLB distribution. This is in contrast to the conclusion reached above when the question concerned only the data sets for which the PLB model was the most suitable. This is an example of the many problems and difficulties with using such a correction; thus the main reported results do not use it. Many other problems are discussed by Perneger (1998), Peres-Neto (1999), Moran (2003) and Nakagawa (2004).

An alternative goodness-of-fit test would be the Kolmogorov-Smirnov test, but this should not be used when estimating parameters from the data (Conover, 1980, p357) – the parameters should be specified independently of the data. The R help for `ks.test` mentions that more refined theory exists for the Kolmogorov-Smirnov test with parameters estimated from the data, but this is not currently implemented.

Microzooplankton data

The approach taken for each data set was to re-analyse the particular data plotted in the original paper. For the microzooplankton data, the raw data were no longer available. The values plotted in Fig. 4 of Bartumeus et al. (2003) were obtained from F. Bartumeus (personal communication). The data for the four experimental scenarios for which power laws were concluded were analysed. These data are the $\log_{10}$ of the frequency density in each bin plotted against the $\log_{10}$ of the geometric mid-point of each bin.

Knowing that bins progressively doubled in size and that the geometric mid-points were equally spaced on a $\log_{10}$ scale, we calculated what the original bin breaks must have been (see below).

5

A second complication was that the values in Fig. 4 of Bartumeus et al. (2003) were already normalised by sample size, and the original sample sizes were not available. To calculate what the sample sizes must have been, the following piece of information was used – the final (highest) bin most likely only refers to a few flight times, and the absolute count in the bin must, by definition, be an integer.

For the final bin, we know the relative proportion, R, of total flight times in that bin. We also know that the absolute number, A, of flight times must be an integer and is most likely small. And we want to determine the sample size, n, which is the total number of flights analysed, and must be an integer.

These three quantities are, by definition, related by

$$R = \frac{A}{n} \tag{A.1}$$

such that

$$n = \frac{A}{R}. \tag{A.2}$$

Given we know R from the data, we can try small integer values for A, to see if n comes out as an integer. For example, for Experiment A under the medium-resource scenario, R = 0.003119922. Testing $A = 1$ gives

$$n = \frac{1}{0.003119922} = 320.5208 \tag{A.3}$$

which is clearly not an integer. So trying $A = 2$ gives

$$n = \frac{2}{0.003119922} = 641.0417 \tag{A.4}$$

which is close to being an integer (we expect some rounding errors to have crept in through all the various calculations), suggesting that $A = 2$ is the correct count for the final bin, and $n = 641$.

To verify this, multiplying the relative counts from all seven bins by 641 should also produce integers. This calculation gives the seven values

```
236.00532, 192.99754, 120.99900, 57.99783, 21.00109, 9.99935, 1.99987.
```

Thus, we do indeed have an integer number of counts in each bin.

A final complication is that although $n = 641$ works, so will any multiple of 641. For example, $n = 6410$ will also give integer counts in every bin. However, Fig. 3 of Bartumeus et al. (2003) shows histograms of tumbling angles, with absolute counts given. Tumbling angles $> 100°$ were used to compute flight times. So adding up the counts in the appropriate bins, 641 is indeed consistent with being the sample size (rather than a larger multiple of 641).

This method also works with the other three experiments (though for the Experiment B low-resource scenario, two of the counts came out as 90.66 and 29.33, which may be an artefact of the original binning process). All other values were accurate, and so this approach gave the sample sizes reported in Table A2.

Determination of bin breaks knowing only that progressive bins double in

size and geometric midpoints are equally spaced on a log scale

The following is needed to determined the breakpoints of the bins for the microzooplankton data. Consider the first bin to start at a, and bins to progressively double in size, so that the bins have widths $w, 2w, 4w, 8w, \ldots$. The bin breaks are then at $a, a+w, a+3w, a+7w, a+15w, \ldots$. Bin number j, where $j = 1$ represents the first bin, is the range $[a + (2^{j-1} - 1)w, a + (2^j - 1)w)$. Let x_j be the geometric midpoint on a $\log_{10}$ scale for bin j (which are the data values we have). The geometric midpoint on a $\log_{10}$ scale is the $\log_{10}$ of the square root of the product of the endpoints of bin j, such that

$$x_j \ = \ \frac{1}{2} \log_{10} \left[\left(a + (2^{j-1} - 1)w \right) \left(a + (2^j - 1)w \right) \right]. \tag{A.5}$$

For $j + 1$ we have

$$x_{j+1} \ = \ \frac{1}{2} \log_{10} \left[\left(a + (2^j - 1)w \right) \left(a + (2^{j+1} - 1)w \right) \right]. \tag{A.6}$$

For the four microzooplankton data sets, we know that

$$x_{j+1} \ = \ x_j + 0.301 \tag{A.7}$$

$$= \ x_j + \log_{10} 2. \tag{A.8}$$

Rearranging (A.8) and substituting (A.5) and (A.6) gives

$$x_{j+1} - x_j \ = \ \log_{10} 2 \tag{A.9}$$

8

$$\frac{1}{2} \log_{10} \frac{\left(a + (2^j - 1)w\right)\left(a + (2^{j+1} - 1)w\right)}{\left(a + (2^{j-1} - 1)w\right)\left(a + (2^j - 1)w\right)} = \log_{10} 2 \tag{A.10}$$

$$\log_{10} \frac{a + (2^{j+1} - 1)w}{a + (2^{j-1} - 1)w} = \log_{10} 4 \tag{A.11}$$

$$a + (2^{j+1} - 1)w = 4a + 4(2^{j-1} - 1)w \tag{A.12}$$

$$(2^{j+1} - 1)w = 3a + (2^{j+1} - 4)w \tag{A.13}$$

$$3w = 3a \tag{A.14}$$

$$w = a. \tag{A.15}$$

So, for bin widths that progressively double in size resulting in geometric midpoints of bins that are equally spaced $\log_{10} 2$ apart on a $\log_{10}$ scale, the width of the first bin, w, must equal the starting value of the first bin, a.

Substituting $a = w$ into (A.5) gives

$$x_j = \frac{1}{2} \log_{10} \left[\left(w + (2^{j-1} - 1)w\right)\left(w + (2^j - 1)w\right)\right] \tag{A.16}$$

$$= \frac{1}{2} \log_{10} \left[2^{j-1}w \cdot 2^j w\right] \tag{A.17}$$

$$= \frac{1}{2} \log_{10} \left[2^{2j-1} w^2\right] \tag{A.18}$$

$$= \log_{10} \left[2^{j-1/2} w\right] \tag{A.19}$$

$$10^{x_j} = 2^{j-1/2} w \tag{A.20}$$

$$w = \frac{\sqrt{2} \, 10^{x_j}}{2^j}. \tag{A.21}$$

We know the x_j values, so can obtain w just from using $j = 1$. Then $a = w$ and so we then know the bin breaks for all the bins. As stated earlier, bin j, with $j = 1, 2, 3, ...$ covers the range $[a + (2^{j-1} - 1)w, a + (2^j - 1)w)$, which with $a = w$, becomes the range $[2^{j-1}a, 2^j a)$. Bin breaks are therefore at $a, 2a, 4a, 8a, 16a, ...$.

Likelihood functions for PLB and ExpB models

Edwards et al. (2007, Box 1) gave likelihood functions for the PL and Exp distributions, and in their Supplementary Information calculated likelihood functions for all four distributions (PL, Exp, PLB and ExpB) for pre-binned data, where the bins have equal widths. For this work, we also require standard likelihood functions for the bounded distributions (for when we have the raw data available), and, for the microzooplankton data, likelihood functions for when we only have prebinned data and the bin widths progressively double size.

For the bounded power-law model, PLB, the probability density function (3) is

$$f(x) = Cx^{-\mu}, \quad x \in [a, b], \tag{A.22}$$

where $C = (\mu - 1)/(a^{1-\mu} - b^{1-\mu})$ for $\mu \neq 1$. Given a data set $\mathbf{x} = \{x_1, x_2, x_3, ..., x_n\}$, the log-likelihood function for μ is

$$\log[\mathrm{L}(\mu|\text{data } \mathbf{x})] = n \log(\mu - 1) - n \log(a^{1-\mu} - b^{1-\mu}) - \mu \sum_{j=1}^{n} \log x_j, \tag{A.23}$$

where $\mathrm{L}(\mu|\text{data } \mathbf{x})$ is the likelihood of a particular value of the unknown parameter μ given the known data $\mathbf{x}$ (and log is natural log). The maximum likelihood estimate for μ is analytically intractable – see equation (11) of Page (1968), shown in Table 1 of White et al. (2008), for how far the analytical approach can be taken.

Unlike the unbounded power-law model PL, the PLB model does not require the restriction $\mu > 1$ to be normalisable. For $\mu = 1$, the probability density function for the

10

PLB model is

$$f(x) = Cx^{-1}, \quad x \in [a, b], \tag{A.24}$$

where $C = 1/(\log b - \log a)$. The log-likelihood function for the PLB model at $\mu = 1$ is then

$$\log[\mathrm{L}(\mu = 1 | \text{data } \mathbf{x})] = -n \log(\log b - \log a) - \sum_{j=1}^{n} \log x_j. \tag{A.25}$$

For the bounded exponential model, ExpB, the probability density function (4) is

$$f(x) = A\mathrm{e}^{-\lambda x}, \quad x \in [a, b], \tag{A.26}$$

where $A = \lambda/(\mathrm{e}^{-\lambda a} - \mathrm{e}^{-\lambda b})$. The log-likelihood function for λ is

$$\log[\mathrm{L}(\lambda | \text{data } \mathbf{x})] = n \log \lambda - n \log(\mathrm{e}^{-\lambda a} - \mathrm{e}^{-\lambda b}) - \lambda \sum_{j=1}^{n} x_j. \tag{A.27}$$

Setting $b \to \infty$, both log-likelihood functions (A.23) and (A.27) correctly reduce to the log-likelihood functions for the unbounded distributions given in (5) and (6) of Edwards et al. (2007).

For each data set, bounds a and b are given in Table A2.

11

Likelihood function for a power-law distribution for prebinned data where

bin widths progressively double in size

The microzooplankton data were only available as the points shown in Fig. 4 of

Bartumeus et al. (2003), rather than the full raw data. These points are $\log_{10}$ of the

frequency density in each bin on the y-axis, plotted against $\log_{10}$ of the geometric

mid-point of each bin on the x-axis. The original bin breaks are determined above, and are

then needed for the likelihood calculations.

Note that care must be taken in determining the counts, as the LBN method requires the

counts in each bin to be divided by the bin width. Sims et al. (2007) noted that this

division is not always done, though it was done for the microzooplankton data, as

confirmed by F. Bartumeus (personal communication).

The following calculations closely follow those on pages 22-26 of the Supplementary

Information of Edwards et al. (2007). Those calculations were for data that were also only

available in binned form, but which had been plotted using bin widths of equal size (the

LT method), rather than using bins which progressively double in size (the LBN method).

These new calculations, together with the previous ones, therefore allow a likelihood

approach to be used for any data for which the data are only available on log-log plots for

which μ was calculated using either the LT or LBN method. One can digitize the plotted

points if the actual values are no longer available.

We now determine the likelihood functions for data that have been binned using the LBN

approach. We want to test whether a power law occurs over a given range $[a, b]$. Thus, the

probability density function (pdf) is

$$f(x) = Cx^{-\mu}, \quad x \in [a, b], \tag{A.28}$$

where C is the normalisation constant given by $C = (\mu - 1)/(a^{1-\mu} - b^{1-\mu})$, which is obtained by solving $\int_a^b f(x)\mathrm{d}x = 1$. We are only considering the distribution of data that lie in the range $[a, b]$. For now we assume that $\mu \neq 1$.

Consider the data to be counts d_j in bins indexed by $j = 1, 2, 3, ..., J$, defining J to be the index of the final bin. The right-hand side of the final bin is therefore $2^J a$. The maximum value that we consider attainable by the data, namely b, thus satisfies $b \geq 2^J a$. Simply taking $b = 2^J a$ assumes that the bin that contains the maximum data point recorded is the bin that contains the maximum possible value attainable. This is unlikely to occur in practice, particularly for small data sets, and especially in a power-law situation.

We define $b = 2^{J'} a$, where integer $J' \geq J$. Therefore new bins $J + 1, J + 2, ..., J'$ have counts of 0, and so $d_{J+1} = d_{J+2} = ... = d_{J'} = 0$. This allows the possibility that measurements could attain values higher than those that happen to be sampled in the particular data set being studied.

For a single data value, the probability of being in bin j given the parameter μ (with $\mu \neq 1$) is

$$\begin{align}
\mathrm{P}(\text{being in bin } j|\mu) &= \int_{2^{j-1}a}^{2^j a} Cx^{-\mu}\mathrm{d}x \tag{A.29} \\
&= \frac{C}{1 - \mu} \left[x^{1-\mu}\right]_{2^{j-1}a}^{2^j a} \tag{A.30} \\
&= \frac{C}{1 - \mu} \left[2^{j(1-\mu)}a^{1-\mu} - 2^{(j-1)(1-\mu)}a^{1-\mu}\right] \tag{A.31}
\end{align}$$

13

$$= \frac{2^{j(1-\mu)}a^{1-\mu}\left(2^{\mu-1}-1\right)}{a^{1-\mu}-b^{1-\mu}}, \tag{A.32}$$

substituting C to obtain (A.32). Note that $\sum_{j=1}^{J'} \mathrm{P}(\text{being in bin } j|\mu) = 1$, as required.

The log-likelihood function is

$$
\begin{aligned}
l(\mu|\text{data}) &= \sum_{j=1}^{J} d_j \log\left[\mathrm{P}(\text{being in bin } j|\mu)\right] \tag{A.33} \\
&= -n \log\left|a^{1-\mu}-b^{1-\mu}\right| + n \log\left|2^{\mu-1}-1\right| + n(1-\mu)\log a \\
&\quad + (1-\mu)\log 2 \sum_{j=1}^{J} d_j j, \tag{A.34}
\end{aligned}
$$

which can be used to find MLEs and confidence intervals. The summation is taken to J instead of J' because $d_{J+1} = d_{J+2} = \ldots = d_{J'} = 0$. Therefore, an increase in b does not change the summation term in (A.34), but only changes the first term; the first term is related to the normalisation constant C. The two terms inside the absolute symbols $|\cdot|$, i.e. $a^{1-\mu} - b^{1-\mu}$ and $2^{\mu-1} - 1$, are both positive for $\mu > 1$, and both negative for $\mu < 1$, such that taking their absolute values gives the correct answer.

For the case where $\mu = 1$, which can happen for the bounded power law, we have $C = 1/(\log b - \log a)$, and

$$\mathrm{P}(\text{being in bin } j|\mu = 1) = \frac{\log 2}{\log b - \log a}, \tag{A.35}$$

which, interestingly, is the same for all bins (i.e. there's an equal probability of being in

14

any bin). The log-likelihood function is then just

$$l(\mu = 1|\text{data}) = \sum_{j=1}^{J} d_j \log\left[\text{P}(\text{being in bin } j|\mu)\right] \tag{A.36}$$

$$= n \log\left(\frac{\log 2}{\log b - \log a}\right).$$

The likelihood function for the idealized infinite power-law tail can be derived using the same approach as above, and the resulting function is equivalent to taking the limit $b \to \infty$ in (A.34).

Likelihood function for an exponential distribution for prebinned data where bin widths progressively double in size

The pdf for an exponential distribution over the range $[a, b]$ is

$$f(x) = Ae^{-\lambda x}, \quad x \in [a, b], \tag{A.37}$$

where A is the normalisation constant given by $A = \lambda/(e^{-\lambda a} - e^{-\lambda b})$, as obtained by solving $\int_a^b f(x)\mathrm{d}x = 1$.

For a single data value, the probability of being in bin j given the parameter λ is

$$\text{P}(\text{being in bin } j|\lambda) = \int_{2^{j-1}a}^{2^j a} Ae^{-\lambda x}\mathrm{d}x \tag{A.38}$$

$$= -\frac{A}{\lambda}\left[e^{-\lambda x}\right]_{2^{j-1}a}^{2^j a} \tag{A.39}$$

$$= -\frac{1}{(e^{-\lambda a} - e^{-\lambda b})}\left[e^{-\lambda 2^j a} - e^{-\lambda 2^{j-1} a}\right] \tag{A.40}$$

$$= -\frac{e^{-\lambda 2^{j-1}a}}{\left(e^{-\lambda a} - e^{-\lambda b}\right)}\left[e^{-\lambda 2^{j-1}a} - 1\right] \tag{A.41}$$

$$= \frac{e^{-2^{j-1}\lambda a}}{\left(e^{-\lambda a} - e^{-\lambda b}\right)}\left[1 - e^{-2^{j-1}\lambda a}\right]. \tag{A.42}$$

The log-likelihood function is then

$$l(\lambda|\text{data}) = \sum_{j=1}^{J} d_j \log\left[P(\text{being in bin } j|\lambda)\right] \tag{A.43}$$

$$= -n\log\left(e^{-\lambda a} - e^{-\lambda b}\right) + \sum_{j=1}^{J} d_j \left(-2^{j-1}\lambda a + \log\left(1 - e^{-2^{j-1}\lambda a}\right)\right). \tag{A.44}$$

The likelihood function for the idealized infinite tail (so testing a standard exponential distribution that has been shifted by a) can be derived using the same approach. The resulting function is equivalent to taking the limit $b \to \infty$ in (A.44).

Previous test of the exponential distribution for the Dobe Ju/'hoansi data

In addition to the power law, Brown et al. (2007) did also test the normal, uniform and exponential distributions. In their Table IV they presented the results of a Kolmogorov-Smirnov test in SPSS, comparing the data to an exponential distribution. The resulting P value is 0.018, hence the exponential distribution was rejected. However, the analysis was incorrect for three reasons:

i) the exponential model was the default distribution that assumes data can go down to zero; i.e. $a = 0$ in the terminology used here. The parameter λ was taken to be the inverse of the mean of the data. This was verified here by doing the command

```
ks.test(x, pexp, rate = 1/mean(x))
```

in the statistical software R (R Development Core Team, 2009), where x is the data –

results are identical to those in Table IV of Brown et al. (2007).

For the power law model, the data were implicitly assumed not to reach zero (a power law

is undefined at 0). So what is more appropriate for the exponential is to test the shifted

exponential. With parameter a set to the minimum value of the data, the R command is

```
ks.test(x - a, pexp, rate = 1/(meanx - a)).
```

This gives a P value of 0.88, so the exponential model would in fact not be rejected.

ii) However, the P values as just computed are incorrect, because there are tied values in

the data. R gives a warning about this, but SPSS (as used by Brown et al. 2007) does not.

iii) Furthermore, and of greater importance, the Kolmogorov-Smirnov test should not be

used when estimating parameters from the data (Conover, 1980, p357). The parameters

should be specified independently of the data. As noted above, the R help for ks.test

mentions that more refined theory exists for the Kolmogorov-Smirnov test with parameters

estimated from the data, but this is not currently implemented. Given the results

presented from SPSS by Brown et al. (2007)) for the unshifted exponential are identical to

those computed in R, SPSS presumably does not include such advanced theory either.

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Table A1: **Full re-analysis of movement length data for 17 data sets.**

Data set	Reported μ	PL: MLE for μ (95% CI)	Exp: MLE for λ (95% CI)	PLB: MLE for μ (95% CI)	ExpB: MLE for λ (95% CI)
Peru boat 1d	1.43	1.72 (1.68, 1.76)	0.014 (0.013, 0.014)	**1.60** **(1.56, 1.65)**	0.014 (0.013, 0.014)
Peru boat 1e	2.00	1.59 (1.58, 1.61)	0.088 (0.085, 0.091)	**1.45** **(1.43, 1.48)**	0.088 (0.085, 0.091)
Peru boat 1f	2.43	1.79 (1.74, 1.85)	**0.28** **(0.27, 0.30)**	1.46 (1.38, 1.53)	0.28 (0.26, 0.30)
Dutch boats May 2001	1.60	1.41 (1.37, 1.45)	**0.24** **(0.21, 0.26)**	1.07 (1.00, 1.13)	0.24 (0.21, 0.26)
Dutch boats July 2003	1.65	1.53 (1.48, 1.59)	**0.41** **(0.37, 0.45)**	1.15 (1.06, 1.24)	0.40 (0.36, 0.45)
Microzooplankton Am	2.1	1.89 (1.82, 1.96)	2.15 (1.98, 2.33)	**1.82** **(1.74, 1.90)**	2.15 (1.98, 2.33)
Microzooplankton Al	2.1	1.74 (1.70, 1.77)	**1.72** **(1.63, 1.80)**	1.62 (1.58, 1.66)	1.72 (1.63, 1.80)
Microzooplankton Bm	2.2	2.03 (1.93, 2.14)	**2.53** **(2.26, 2.81)**	1.86 (1.74, 1.99)	2.52 (2.26, 2.81)
Microzooplankton Bl	2.2	2.03 (1.94, 2.13)	**2.56** **(2.32, 2.81)**	1.86 (1.75, 1.97)	2.56 (2.32, 2.81)

Notes: As for Table 2 in main text, but also giving the MLEs and 95% confidence intervals for the two exponential models Exp and ExpB. Units of λ are the reciprocal of the units given in Table 1. The MLEs of λ are very similar for the Exp and ExpB models, because the exponential tail of the Exp model can decay away quickly in the region $> b$, and so there might only be inconsequential differences between the Exp and ExpB models. Bold represents the model with the most support of the four tested (see Table 3).

Table A1 continued.

Data set	Reported μ	PL: MLE for μ (95% CI)	Exp: MLE for λ (95% CI)	PLB: MLE for μ (95% CI)	ExpB: MLE for λ (95% CI)
Grey seal 6118	1.26	1.60 (1.49, 1.73)	0.090 (0.073, 0.109)	**1.25** **(1.07, 1.43)**	0.089 (0.072, 0.108)
Grey seal 6124	1.12	1.93 (1.73, 2.16)	0.049 (0.038, 0.061)	**1.21** **(0.86, 1.56)**	0.040 (0.027, 0.054)
Grey seal 6125	1.30	2.04 (1.80, 2.32)	**0.045** **(0.035, 0.057)**	1.55 (1.20, 1.92)	0.043 (0.032, 0.056)
Reindeer A	2.0	1.91 (1.81, 2.02)	0.29 (0.26, 0.33)	**1.73** **(1.61, 1.86)**	0.29 (0.26, 0.33)
Reindeer BC	1.8	1.95 (1.82, 2.09)	0.15 (0.13, 0.18)	**1.64** **(1.47, 1.82)**	0.15 (0.13, 0.18)
Reindeer E	1.8	2.68 (2.36, 3.05)	**0.085** **(0.069, 0.104)**	2.41 (2.01, 2.84)	0.085 (0.068, 0.104)
Jackal F4	2.02	2.79 (2.60, 3.00)	0.41 (0.37, 0.45)	**2.71** **(2.51, 2.93)**	0.41 (0.37, 0.45)
Hunter gatherers	1.97	1.93 (1.66, 2.26)	0.22 (0.16, 0.30)	1.20 (0.73, 1.69)	**0.19** **(0.11, 0.28)**

Table A2: **Values of a, b and K (number of parameters being estimated from the data for the PL and Exp models), plus full results of goodness-of-fit tests for the most supported model.**

Data set				Goodness-of-fit for best model			
	a	b	K	n	df	G	P
Peru boat 1d	7.71	1051	1	1224	64	437	0
Peru boat 1e	1.18	234	1	3498	57	766	0
Peru boat 1f	1.00	28	1	824	14	84.0	10^{-11}
Dutch boats May 2001	0.25	45	2	364	11	8.8	0.64
Dutch boats July 2003	0.25	17	2	329	6	33.6	10^{-5}
Microzooplankton Am	0.12	15.36	2	641	2	36.0	10^{-8}
Microzooplankton Al	0.12	15.36	2	1743	3	205	0
Microzooplankton Bm	0.16	5.12	1	374	3	19.7	10^{-4}
Microzooplankton Bl	0.16	5.12	1	471	3	16.3	0.001
Grey seal 6118	1.5	77	1	96	9	19.7	0.016
Grey seal 6124	7.5	78	1	71	8	4.2	0.84
Grey seal 6125	10	118	1	63	6	3.5	0.74
Reindeer A	1.00	41	1	284	10	72.1	10^{-10}
Reindeer BC	2.2	46	1	193	10	42.7	10^{-5}
Reindeer E	12.1	99	1	89	9	3.8	0.93
Jackal F4	2	38	1	414	1	7.0	0.0081
Hunter gatherers	1.72	18	2	37	1	2.1	0.15

Notes: Values of a are given here to 2 d.p.s, but the precise value (if applicable) of the minimum data value was used in the calculations. The number of parameters being estimated from the data for the bounded PLB and ExpB models is $K + 1$, because the upper bound is also estimated from the data. The degrees of freedom and G values are given here, along with the sample sizes n and P values that were shown in Table 3.

Table A3: **For the data sets for which the bounded power-law model had the most support, the goodness-of-fit tests were repeated using the alternative binning algorithm.**

Data set	n	df	G	P
Peru boat 1d	1224	7	191	0
Peru boat 1e	3498	5	454	0
Microzooplankton Am	641	-	-	-
Grey seal 6118	96	3	12.2	0.007
Grey seal 6124	71	3	1.4	0.71
Reindeer A	284	2	47.5	10^{-10}
Reindeer BC	193	3	37.1	10^{-7}
Jackal F4	414	-	-	-

Notes: The resulting degrees of freedom, G values and p-values P are given here, along with the (unchanged) sample sizes n. The alternative binning algorithm does not change the conclusions (compare results with those in Tables 3 or A2). The microzooplankton were only available in binned form where the bins already progressively doubled in size (so that binning was used in our original goodness-of-fit test). For the jackals, the data are also only available binned, but the few number of bins precludes any further lumping of bins than in our original goodness-of-fit test, for which there was only one degree of freedom.
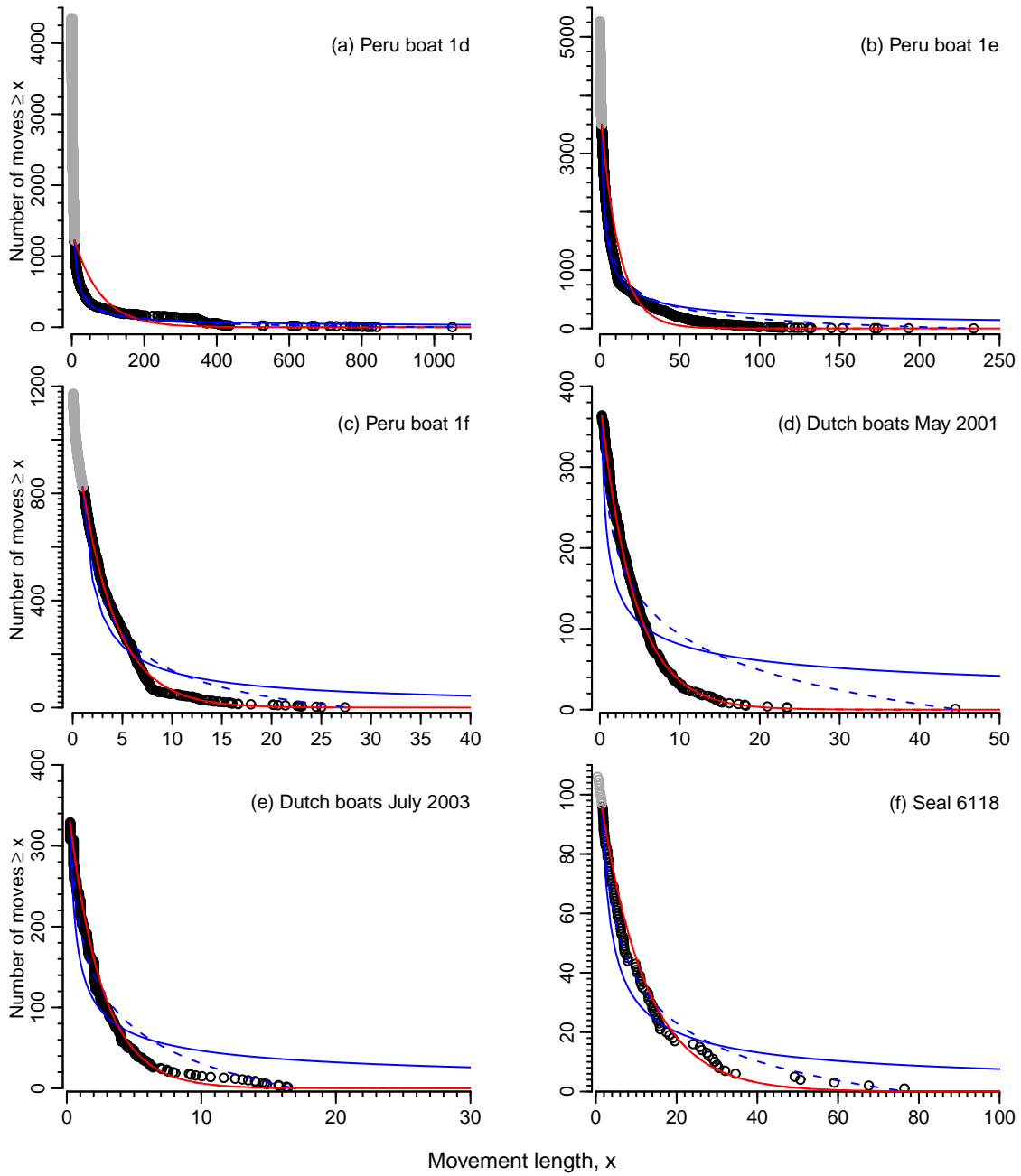
Fig. A1: **As for Fig. 2 but on unlogged axes.** The lack of support for a power-law tail can be seen in every case (solid blue line); continued overleaf.

(g) Seal 6124

(h) Seal 6125

(i) Reindeer A

(j) Reindeer BC

(k) Reindeer E

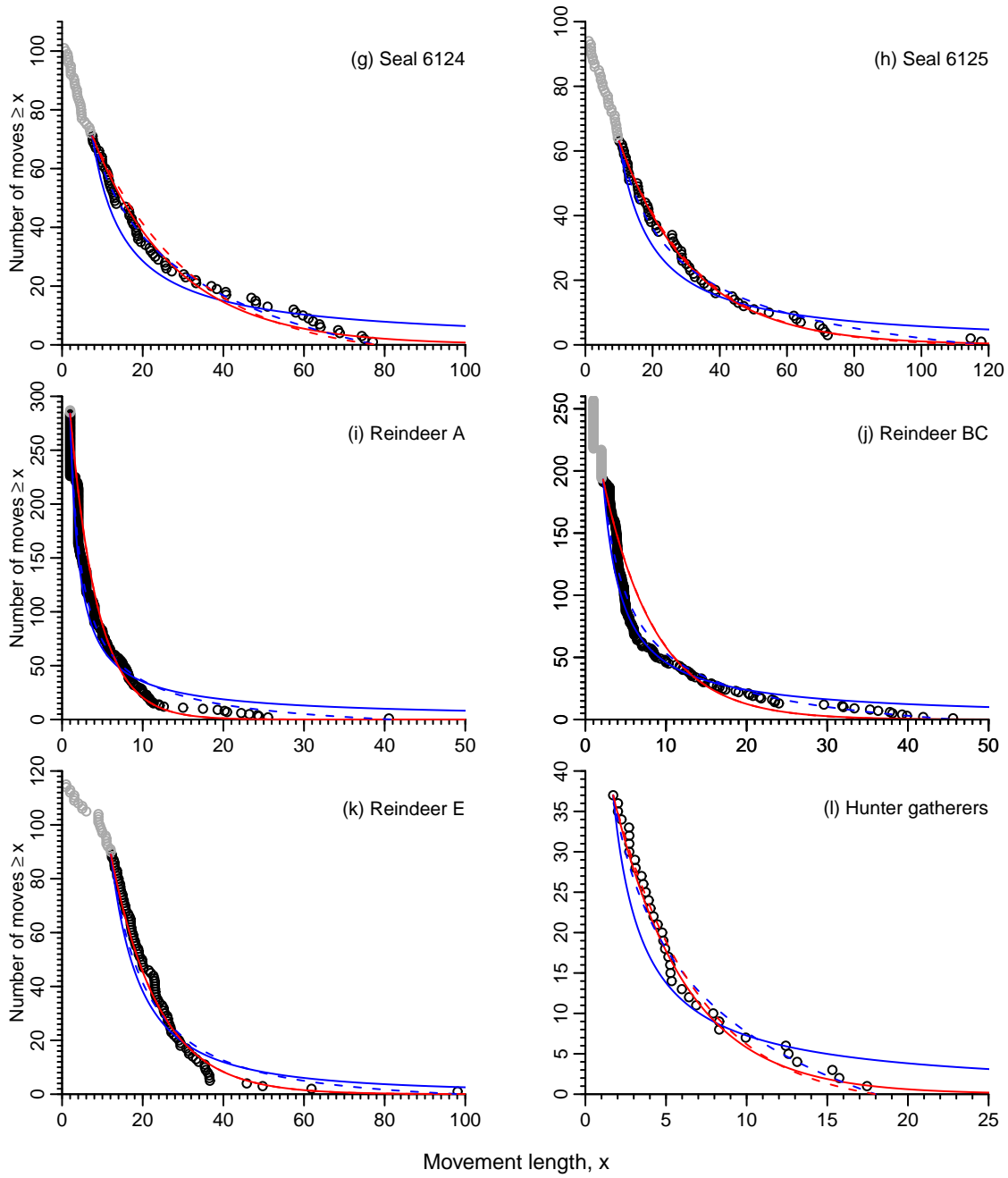(l) Hunter gatherers

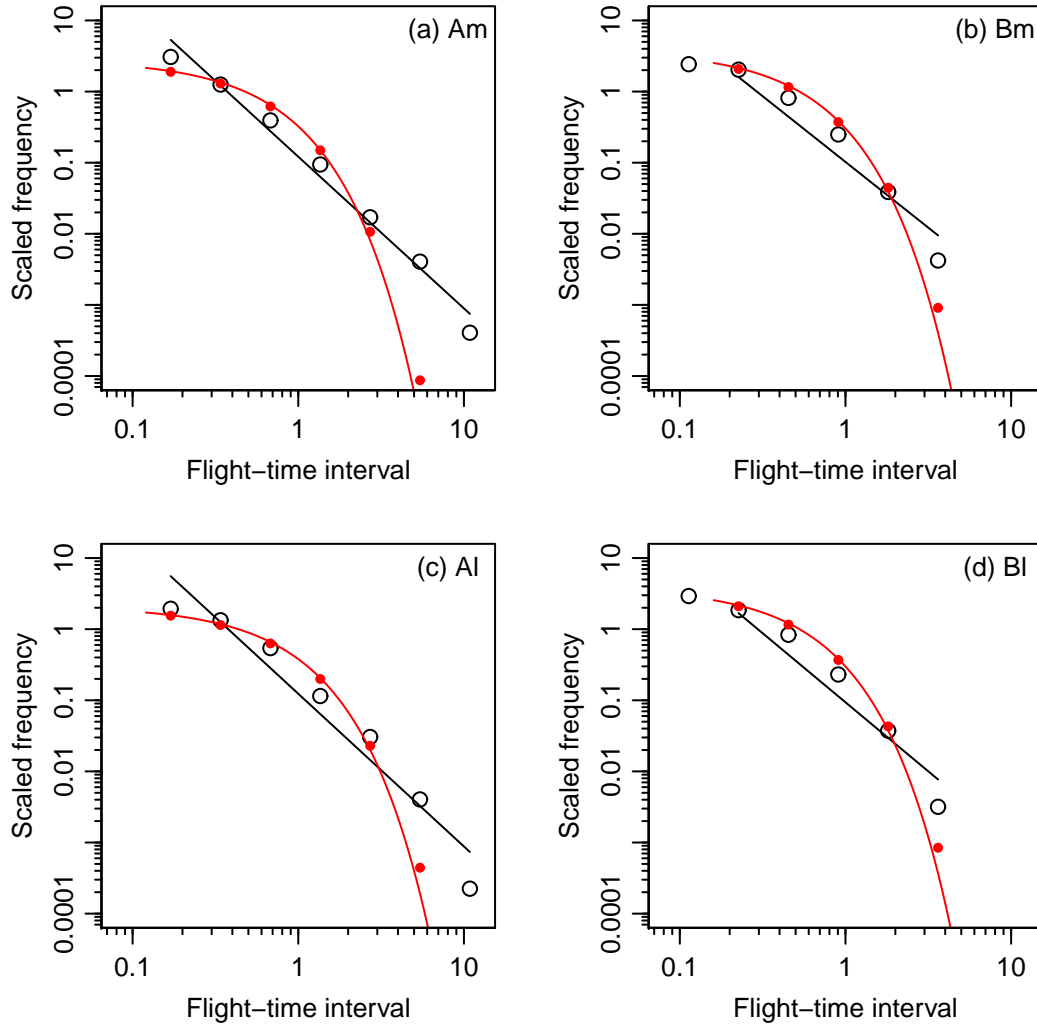Movement length, x

Fig. A1 continued.

Fig. A2: **Re-analysis of microzooplankton data.** (a) Experiment A, medium food, (b) experiment B, medium food, (c) experiment A, low food, (d) experiment B, low food. Bin widths progressively double in size, and open circles are the scaled frequencies in each bin (count in bin divided by bin width divided by total sample size), reproducing the respective plots in Fig. 4 of Bartumeus et al. (2003). Bin breaks for Am and Al are 0.12, 0.24, 0.48, 0.96, 1.92, 3.84, 7.68 and 15.36. Bin breaks for Bm and Bl are 0.08, 0.16, 0.32, 0.64, 1.28, 2.56 and 5.12, with $a = 0.16$ because the first bin was not fitted. Points are plotted at geometric mid-points of bins. Straight lines are the regression fits, yielding the original values of μ for the PL model. Red curved lines are the Exp model fitted by maximum likelihood. The solid red circles are the expected counts in each bin from the exponential model, which are what should really be compared with the open circles that represent the data (rather than comparing the curved line to the data). The re-analysis here finds that for (a), the PLB model has most support, whereas for (b)-(d) the Exp model has overwhelmingly more support than the power-law models, but none of the models are suitable models for any of the data sets. (see Table 3).