

Supporting Information

Raichlen et al. 10.1073/pnas.1318616111

SI Methods

1.1 Sample. The Hadza group is a group of hunter–gatherers living in northern Tanzania near Lake Eyasi. In the areas where we worked, Hadza individuals hunted and gathered nearly 95% of their food from wild sources (they traded for small amounts of corn) (1). The Hadza hunt and gather without mechanized transportation or guns. They travel only by foot and hunt with bows and arrows (arrows are sometimes tipped with poison). Thus, our data represent movement data for true human foraging. We recruited 44 subjects ($n_{\text{male}} = 20$; $n_{\text{female}} = 24$) from two Hadza camps in northern Tanzania (Setako and Sengeli). Data collection took place over four 2-wk periods in September of 2009, August of 2010, and January of 2011 (1). Subjects wore Garmin Forerunner 205 global positioning system (GPS) units from dawn until dusk. Table S1 provides basic data for our subjects.

1.2 Data Analysis. GPS analysis. Data collection took place over four 2-wk periods in September of 2009, August of 2010, and January of 2011. Subjects wore Garmin Forerunner 205 GPS units from dawn until dusk. GPS points were recorded using the smart recording setting on the device. This feature records points where the device changes position, elevation, heart rate, or any other parameter that denotes movement. Individual subject GPS data were downloaded and processed to determine the longest foraging bout for each day. A GPS trace was considered a foraging bout if the individual moved at least 500 m from camp and the foraging bout was greater than 500 m in length. Camp was defined as the centroid of housing structures, and positions were considered out of camp if they were beyond a perimeter defined by structure locations. After identifying the longest foraging bout for each day, GPS data were passed through custom written scripts (R) (2) to calculate step lengths and model fits.

Step length calculations. For each individual, on each day with GPS data, we first determined the longest foraging bout for a given day. We removed all foraging bouts less than 500 m from camp and bouts shorter than 500 m (total n using these methods = 342). Step lengths were calculated using GIS functions in R. To determine the effects of turning angle, θ , on model fits, we calculated step length distributions for all of our subjects' foraging bouts using turning angle definitions that varied in 10° increments from 0° to 180° .

We calculated the distance between two points (x_0 and x_1) and considered this distance a step if the following conditions were met: (i) the distance was larger than 5 m (accounts for error in GPS signal), and (ii) the angle formed by x_0 , x_1 , and the next point (x_2) is greater than the characteristic angle defining a step (θ). If these conditions were not met, we calculated the distance between x_0 and x_2 and determined whether these points met our criteria. This process was continued until a step length was found that met the criteria described above.

Model fitting. Our model fitting methods followed Clauset et al. (3) and Edwards et al. (4) with only minor deviations. We used 5 m as our minimum step length rather than the iterative procedure to determine minimum step lengths described in the work by Clauset et al. (3). This procedure is more conservative and less likely to force data into a power law distribution (5).

We used the maximum likelihood estimation (MLE) procedures described in detail in the work by Edwards et al. (4) to

determine whether a given step length distribution was best fit by a power law, a truncated power law, an exponential distribution, or a composite exponential model with two, three, or four exponential functions. Using MLE equations from the works by Edwards et al. (4) for the power law and exponential models, White et al. (6) for the truncated power law, and Jansen et al. (7) for composite exponential models, we calculated exponents for best fit power law models, truncated power law models, and exponential models.

We then used the method by Clauset et al. (3) for testing goodness of fit for the six models. Briefly, for a given model fit, a Kolmogorov–Smirnov (KS) statistic was calculated. Next, an iterative procedure was used, where 1,000 simulated datasets are generated using the calculated exponent from the sample for the power law, truncated power law, and exponential models. Each of these simulated datasets was then fit using MLE procedures. A KS statistic was calculated for each of these datasets. The proportion of datasets with larger KS statistics than the empirical dataset was the P value, and small P values indicate that the model is not a plausible fit. This method is a different use of the P value (to rule out hypothesized model fits) than most cases; however, we follow the work by Clauset et al. (3) in this interpretation of the KS statistic. When selecting the best fit model for a set of steps, we only considered those models that had a P value greater than 0.05 using the methods described above (3).

We then used the Akaike Information Criterion (AIC) as a model selection tool to choose the best fit from among the remaining models. AIC values were calculated from log likelihoods, and the model with the lowest AIC value was considered the best fit for a given step length distribution. Examples of fits for all models are shown for a representative foraging bout for each subject (Fig. S1). All data are provided in Dataset S1.

Squared displacement. We also calculated squared displacements of the outbound leg of foraging bouts [from camp to the farthest distance away from camp using information in the work by Ramos-Fernandez et al. (8)] to determine diffusive characteristics of Hadza foraging. In normal diffusion, squared displacement should be proportional to time. However, if movements are superdiffusive, such as in Lévy walks, squared displacement is proportional to time^γ , where $\gamma > 1$ [if $\gamma < 1$, movements are described as subdiffusive (9)]. Previous work has shown that truncated power laws have nonlinear diffusion patterns, with superdiffusion followed by subdiffusion (9). To determine the inflection point, where diffusive regimes change, we fit a two-segment piecewise regression to logarithmically transformed squared displacement vs. time plots for each outbound foraging leg. We iteratively split each dataset of n GPS coordinates into two subsets: the first i points in time and the last $n - i$ points, where i was allowed to iterate from 3 to $n - 3$. Ordinary least squares regressions for $\log[\text{squared displacement}]$ regressed against $\log[\text{elapsed time}]$ were then fit to the two subsets in each iteration. Goodness of fit was calculated as the sum of squared residuals from the two segments of the piecewise regression, and the value of i that minimized sum of squared residuals was used to identify the best fit model. Representative examples of these fits are shown for each subject in Fig. S2.

1. Pontzer H, et al. (2012) Hunter-gatherer energetics and human obesity. *PLoS One* 7(7): e40503.

2. Team RC (2013) *R: A Language and Environment for Statistical Computing* (R Foundation for Statistical Computing, Vienna), Version 2.15.

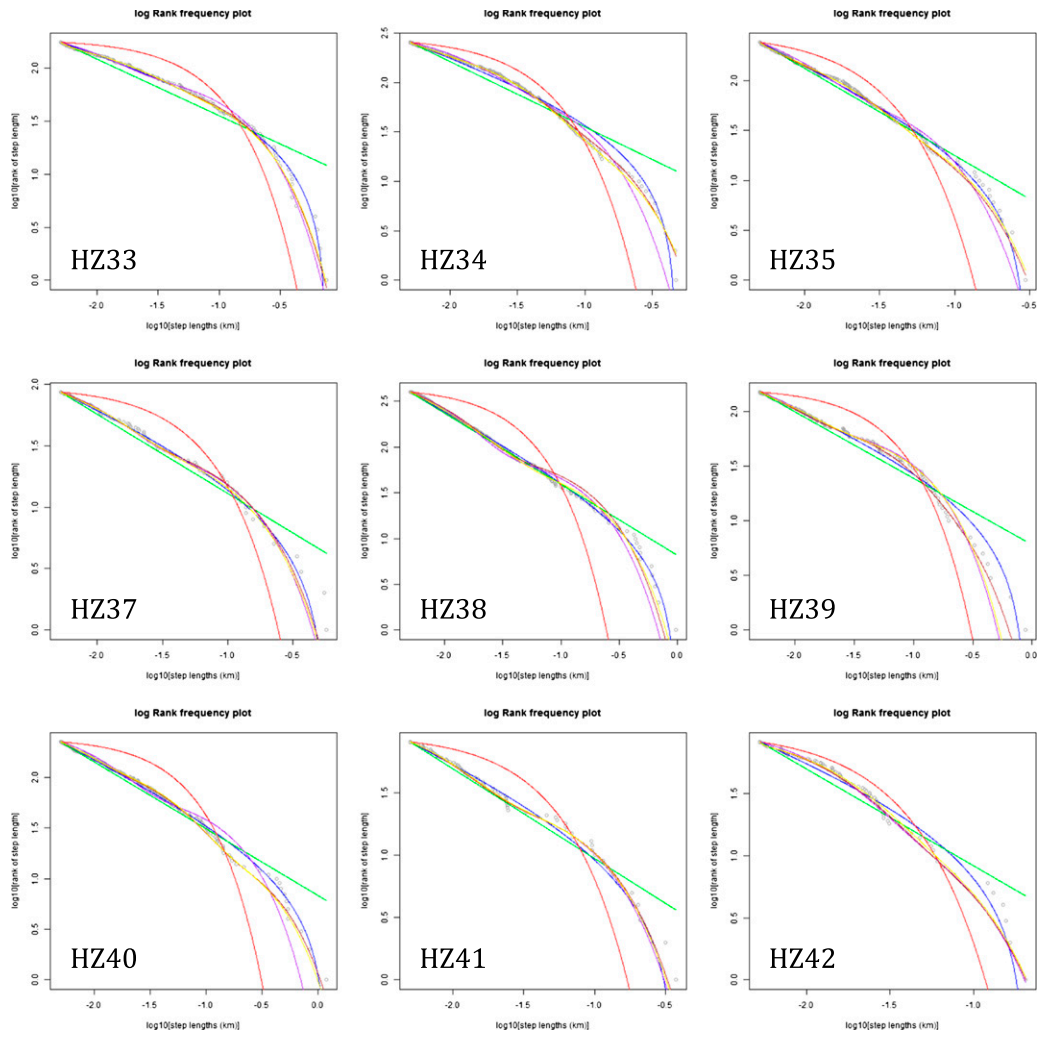


Fig. S1. (Continued)

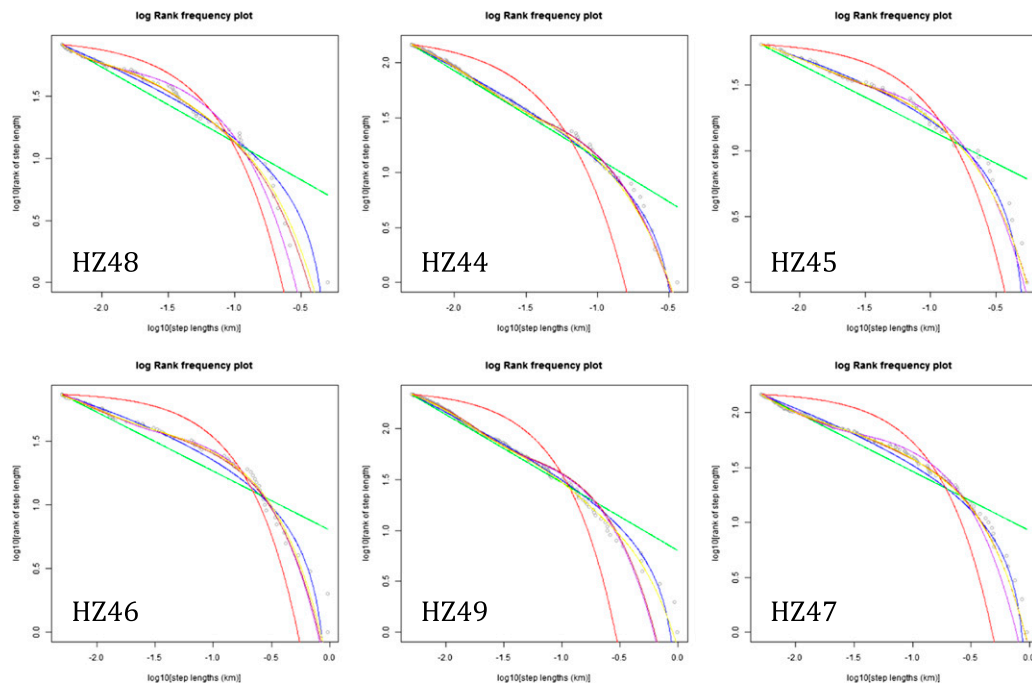


Fig. S1. Representative rank frequency plots for each Hadza subject included in the analysis. Green lines are power law, blue lines are truncated power law, red lines are exponential, purple lines are composite exponential (two exponentials), brown lines are composite exponential (three exponentials), and yellow lines are composite exponential (four exponentials) model fits to step length data (blue circles).

Representative squared displacement figures

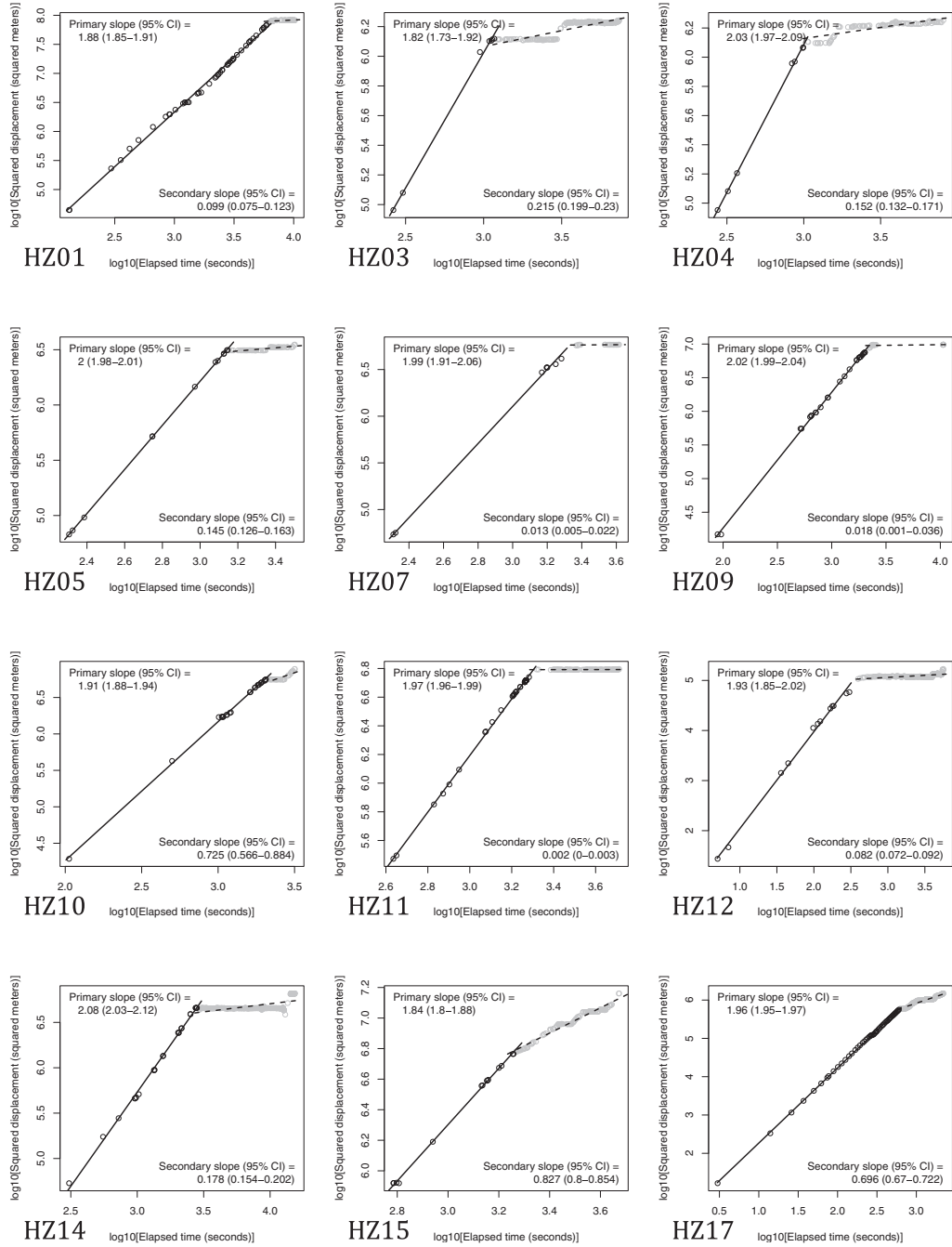


Fig. S2. (Continued)

Table S1. Subject information

Hadza ID	Sex	<i>n</i>
HZ01	Male	6
HZ03	Female	5
HZ04	Female	6
HZ05	Female	8
HZ07	Male	6
HZ08	Female	2
HZ09	Male	12
HZ10	Female	6
HZ11	Female	10
HZ12	Female	7
HZ13	Male	1
HZ14	Male	6
HZ15	Male	7
HZ17	Female	19
HZ18	Female	3
HZ19	Male	5
HZ20	Male	13
HZ21	Male	6
HZ22	Female	1
HZ23	Male	11
HZ25	Female	12
HZ26	Female	5
HZ27	Female	7
HZ28	Male	1
HZ29	Female	8
HZ30	Female	3
HZ31	Female	7
HZ32	Female	10
HZ33	Female	14
HZ34	Male	7
HZ35	Male	17
HZ37	Female	17
HZ38	Male	13
HZ39	Male	5
HZ40	Male	11
HZ41	Female	7
HZ42	Female	9
HZ43	Male	3
HZ44	Female	6
HZ45	Female	11
HZ46	Female	9
HZ47	Male	10
HZ48	Male	4
HZ49	Male	6

Other Supporting Information Files

[Dataset S1 \(XLSX\)](#)