Supplementary Information for

The Global Body Size Biomass Spectrum is Multimodal

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Statistical Evaluation of Allometric Trends and Multimodality. Statistical evaluations of the size-biomass relationship were performed among different classifications of organisms depending on ecological realms (marine, terrestrial, subterranean) and trophic levels (producer, consumer). The six classes are: all, terrestrial, marine, terrestrial and marine, producers, and consumers.

To fit statistical relationships between size and biomass, we did not perform simple hypothesis tests directly on the best estimated spectra because 1) biomass datapoints are not independent across sizes within groups, and 2) the cross-taxa biomass at any size depends on all groups, making the error structure correlated across the size range. To obtain confidence bounds, we rely on a parametric bootstrapped ensemble of possible spectra. For each bootstrap, the possible continuous spectrum is sampled once per log size bin from -18 to 11, for a sample size of 30. This is a lower resolution than used for graphical purposes; here, 30 is likely a conservative estimate of the number of independent datapoints that contribute to the cross-taxa spectrum in any trophic or habitat class. We then performed statistical regressions on 200 bootstrap sampled sets, each obtained by independently sampling from the biomass error distribution of each group and summing by size. We then found the 2.5th and 97.5th percentiles of the outputs as each regression model's 95% confidence bounds. Size bins with biomass lower than 10^{-5} Gt (1000 t) were not included as datapoints for the regression. A cutoff is necessary to avoid infinitely negative values after log transformation and to avoid size ranges that are unlikely to have been empirically observed.

We fit two kinds of regression models. For allometric relationships, ordinary least-squares regressions were performed to obtain power exponents that explain the discrete sampled log size-log biomass relationships. For Gaussian mixture models, up to four modes (components) were fit using an expectation maximization algorithm to minimize nonlinear least squares ('gauss1', 'gauss2', etc. in Matlab R2017a, MathWork, Natick, MA). During fitting for the Gaussian mixture, we added $\log_{10}(10^{-5})+1$ to log biomasses to ensure that the minimum value was 1; smaller values were already removed previously. For plotting, we subtracted $\log_{10}(10^{-5})+1$ from the solutions. Our selection among the Gaussian Mixture models was based on the minimum corrected Akaike Information Criterion (AICc, or AIC for short subsequently)[1]. We also considered whether the model with the lowest AIC was much better than a simpler model by checking whether their pairwise ΔAICs were sufficiently large. As a rule of thumb, a ΔAIC of more than 10 would indicate that the alternative model is much worse given a correct tally of the number of datapoints[1]. However, in our case the true number of datapoints is unclear, making ΔAIC sensitive to the resolution at which we sample the continuous spectra and the biomass cutoff at each bin. Our main concern is that an over-inflation of datapoints would cause AIC to not penalize complexity enough, which would inflate ΔAIC between models. We therefore did not rely solely on an ΔAIC>10 to reject a simpler model. Alternatively, we may also have underestimated the true sample size, and therefore ΔAIC>10 may have been too stringent. Instead, for each of the 200 bootstrap regressions, we checked whether each model had a lower AIC than the next simplest model. The frequency at which a model was worse (had a higher AIC) than the next across bootstraps was denoted *P.*ΔAIC. The model with the lowest average AIC was the default best model candidate, but the model was rejected if *P*.ΔAIC>0.05. The next simplest model was then examined in a similar and iterative manner until the best model with *P*.ΔAIC>0.05 was found. This bootstrapped selection procedure incorporates uncertainty in the selection process itself beyond what the default AIC score measures[2].

We also recorded the frequency at which a model, including the linear and Gaussian models, was selected based on minimum AIC within a bootstrap. This selection frequency is expressed as *P.*minAIC, or the portion of resamples that a model had the minimum AIC. These results agreed with the minimum average AIC criterion, which almost always selected more modes than when we accounted for *P*.ΔAIC (except for consumers where all AIC criteria agreed). For producers, *P*.minAIC selected three modes, while *P*.ΔAIC selected only one mode (Table S7). This was the only class in which the two methods selected models that were more than one mode apart.

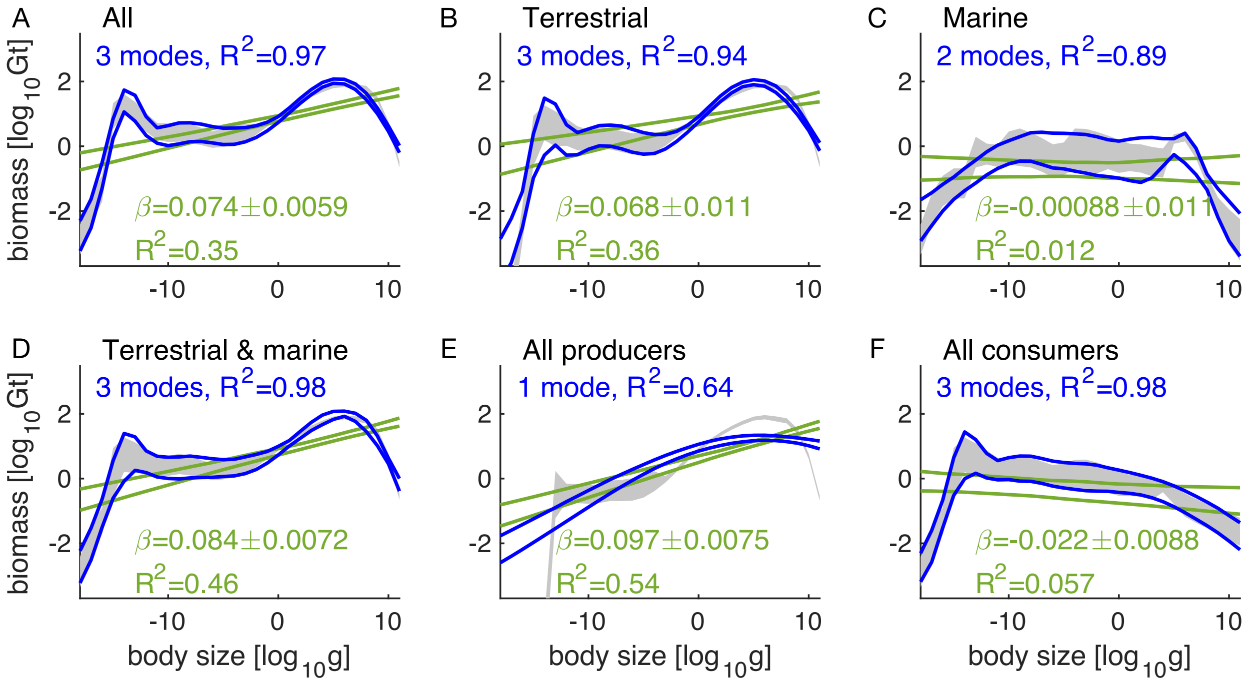

Fig. S1. Statistical descriptions of body size biomass spectra across realms and trophic levels. The empirical distributions with 95% confidence bounds (grey) are described using log-linear (green confidence bounds) and Gaussian mixture models (blue confidence bounds) from 200 bootstrap regressions over within-group biomass error distributions. The data sampling resolution was one per log size, with a cutoff biomass of 10^{-5} Gt. Linear regressions produced β estimates (± standard deviation) and mean R^2 for different habitat and trophic levels (in green). The number of components in the Gaussian models are selected according to AIC (mean R^2 in blue). “All” includes terrestrial, marine, and subterranean groups.

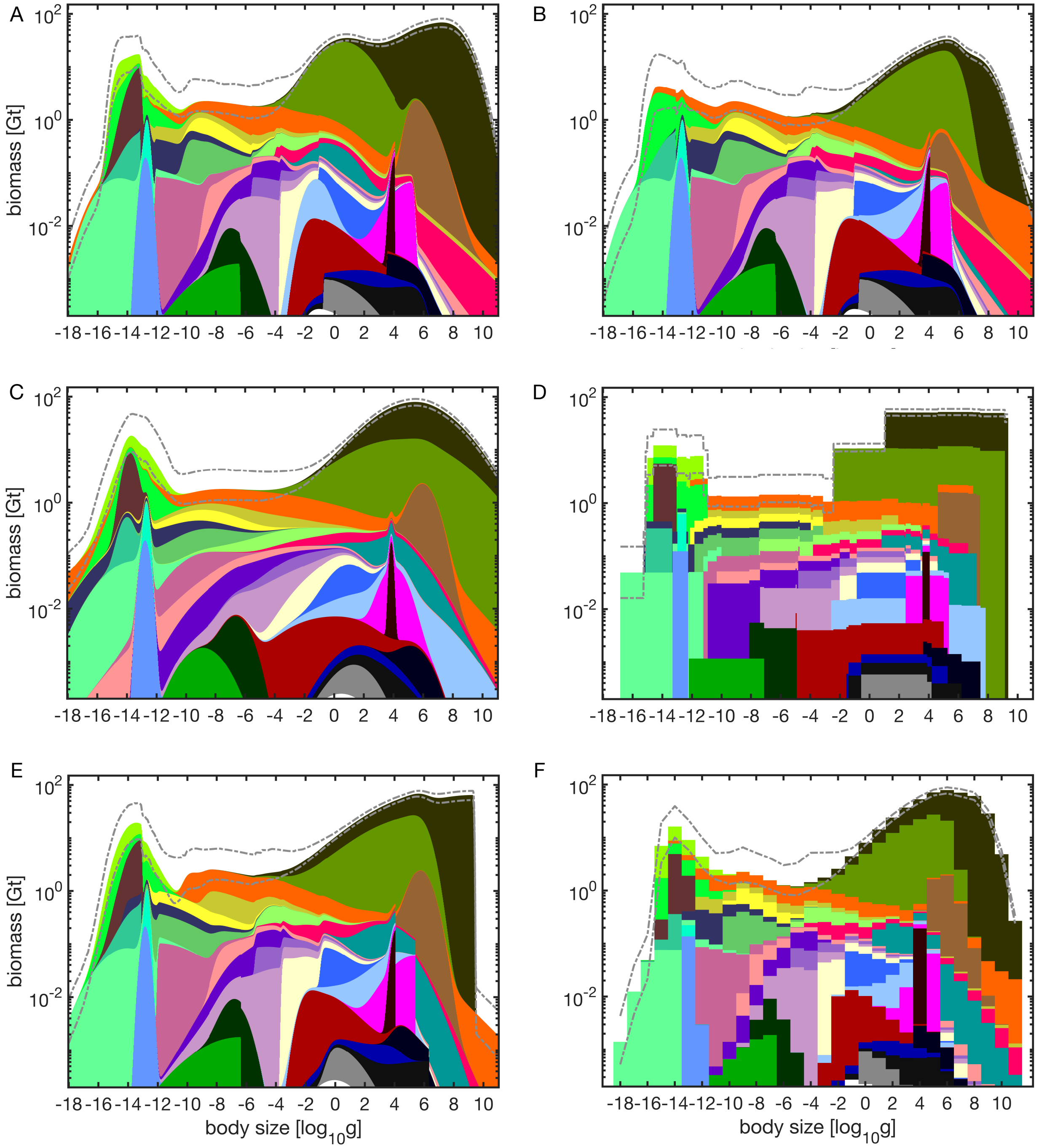

Fig. S2. Sensitivity of the global body size biomass spectrum to different assumptions. Groups with biomass above 2x10^{-4} GtC are shown. Grey dotted curves are 95% confidence bounds from 200 resamples from within-group uncertainties. See Fig. 2 for color reference and default assumptions. **A.** Sizes are defined for ramets or clones instead of genets. **B.** Mass with low metabolism is omitted from body size and biomass estimates (plant woody material, hard coral skeleton, and subterranean microbes). **C.** Normal biomass distribution within groups. **D.** Uniform biomass distribution within groups. **E.** Skew-normal biomass distribution within groups, with the minimum and maximum reported sizes corresponding to the 4.5th and 99.5th percentiles (instead of the 2.5th and 97.5th percentiles). **F.** Spectrum is plotted at one per log unit resolution (instead of 40 per log unit).

Table S1. Terrestrial body sizes and biomasses. o indicates spherical bodies formula ([3] for microbes), and ^ indicates tubular bodies formula ([4] for microbes). Biomass and uncertainty are from [5] unless indicated.

Group	**Smallest**	**Largest**	**Min. body size (g C)**	**Mean body size (g C)**	**Max. body size (g C)**	**Biomass (Gt C)**	**Uncertainty (fold)**
Producers							
Forest plants	*Salix herbacea*[o]	*Sequoiadendron giganteum*	1.08E+01[6,7]	1.13E+06	2.24E+09[8]	337.5[6]	1.2
Grassland plants	*Mibora minima*	*Holcus mollis*	3.75E-03[9]	4.32E+06	1.34E+09[6]	112.5[6]	1.2
Cryptogamic phototrophs	*Nostoc punctiforme*	*Dawsonia superba*^	1.15E-11[10]	2.72E-10[*]	8.75E+0[12]	2.5[†]	2
Consumers							
Soil bacteria	*Actinobacteria spp.* [o]	*Proteobacteria spp.* [o]	7.37E-16[15]	2.86E-14	1.15E-11[15]	7.352	6
Soil archaea	*Crenarchaeota spp.* [o]	*Crenarchaeota spp.* [o]	7.37E-16[15]	2.91E-14	4.72E-14[15]	0.516	4
Soil protists	*Myamoeba spp.* [o]	*Dictyamoeba spp.* [o]	3.19E+25[16]	7.37E-13	5.03E-11[17]	1.605	4
Soil fungi	*Batrachochytrium dendrohabditis*[o]	*Armillaria ostoyae*	7.37E-13[18]	1.53E-11	9.70E+06[19]	11.802	3
Terrestrial arthropods	*Archegozetes longisetosus*	*Birgus latro*	1.50 E-5[20]	2.00E-04	6.00E+02[21]	0.212	15
Humans	*Homo sapiens*	*Homo sapiens*	3.75E+3[22]	8.13E+03	1.13E+04[22]	0.055	1.1
Livestock	*Gallus gallus domesticus*	*Bos taurus*	270[5]	2.08E+04	2.25E+05[5]	0.107	1.1
Wild land mammals	*Craseonycteris thonglongyai*	*Loxodonta africana*	0.038[23]	2.53E+03	1.65E+06[24]	0.003	4
Terrestrial nematodes	*Protohabditis hortulana*^	*Unspecified species*^	6.02E-13[25]	5.00E-08	7.74E-08[26]	0.002	10
Wild birds	*Mellisuga helenae*	*Struthio camelus*	0.27[27]	6.67E+00	1.50E+04[28]	0.199	10
Annelids	*Dendrobaena mammalis*^	*Microchaetus rappi*	4.16E-08[29]	2.59E-04	2.25E+02[30]	0.006	10
Reptiles	*Brookseia spp.*	*Crocodylus porosus*	0.027[31]	1.05E+02	1.80E+05[32]	0.003	100
Amphibians	*Paedophryne amauensis*	*Andrias davidianus*	0.003[33]	1.00E+00	7.50E+03[34]	0.001[‡]	100

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[*] Among lichens, likely the most abundant among cryptogams, we estimate that 87% contain phycobionts (*Trebouxia* 8-21 μm)[11] and 13% contain cyanobionts (*Nostoc punctiforme* 5 μm)[10]. This composition was used to estimate the mean body size.

[†] The total lichen biomass and uncertainty were obtained from Ref.[13]; to obtain cryptogamic phototrophs' biomass, the fungal portion of lichen was subtracted out. Twenty percent of fungi species occur in lichens[14], so 20% of the total fungal biomass was subtracted from the lichen biomass to get the cryptogamic phototrophs' biomass.

[‡] Assumes amphibian habitat area is mainly rainforest, $5.5011347x10^{12}$ m^2 [6], and 0.1 individual per m^2 (lower than [5]'s likely overestimate). Uncertainty is unknown, so copied from reptiles which is the taxon with the highest uncertainty.

Table S2. Marine body sizes. o indicates spherical bodies formula ([3] for microbes). Biomass and uncertainty are from [5] unless indicated.

Group	Smallest	Largest	Min. body size (g C)	Mean body size (g C)	Max. body size (g C)	Biomass (Gt C)	Uncertainty (fold)
Producers							
Mangroves	*Rhizophora mangle*^{o} *(dwarf)*	*Rhizophora mangle*^{o} *(canopy)*	4.06E+04[35]	6.49E+05[*]	2.88E+07[35]	3.5[37]	1.4
Seagrass	*Halophila decipiens*^{o}	*Posidonia oceanica*^{o}	2.63E-03[38]	7.53E+04[†]	6.91E+07[40,41]	0.11	10
Macroalgae	*Phaeophyceae spp.*	*Macrocystis pyrifera*	1.35E-01[42,43]	2.00[‡]	2.70E+03[42,43]	0.14	10
Bacterial picophytoplankton	*Prochlorococcus spp.*	-	5.00E-14[44,45]	9.13E-14[§]	1.67E-13[**]	0.13	10
Green algae / protist picophyto-plankton	*Ostreococcus tauri*	-	1.05E-13[44,46]	1.49E-13[††]	2.10E-13[‡‡]	0.30	10
Diatoms	*Thalassiosira pseudonana*	*Ethmodiscus spp.*	4.6E-11[47,48]	9.08E-09[§§]	4.09E+04[49,50]	0.31	10
Phaeocystis	*Phaeocystis globosa cell*^{o}	*Phaeocystis globosa colony*^{o}	1.15E-11[51]	5.24E-04[***]	0.047[51]	0.28	10
Consumers							
Marine bacteria	*Pelagibacter ubique*^{o}	*Thiomargarita namibiensis*^{o}	5.50 E-16[52]	1.32E-14	1.10E-04[53]	1.327	1.8
Marine archaea	*Nanoarchaeum equitans*	*Staphylothermus marinus*^{o}	1.47E-17[54]	1.22E-14	9.90E-11[55]	0.332	3
Marine protists	*Picomonas judraskeda*^{o}	*Rhizarian spp.*^{o}	1.44E-12[56]	2.26E-12	7.37E-04[57]	1.058	10
Marine arthropods	*Stygotantulus Stocki*	*Homarus americanus*	3.537E-08[20,21]	7.08E-06	3.00E+03[58]	0.940	10
Fish	*Paedocypris progenetica*	*Rhincodon typus*	1.50E-04[59]	6.27E-01	4.63E+06[60]	0.668	8
Molluscs	*Ammonicera minortalis*	*Mesonychoteuthis hamiltoni*	0.01[61,62]	4.02E-04	3.98E+04[63–65]	0.182	10
Cnidaria	*Psammohydra nanna*	*Cyanea capillata*	1.00E-05[66,67]	5.09E-03	1.00E+05[66,68]	0.040	10
Hard corals	*Leptopsammia pruvoti*[†††]	*Porites lutea*	6.41[70,71]	1.54E+03[‡‡‡]	1.68E+07[73]	0.653[§§§]	4
Wild marine mammals	*Arctocephalus townsendi*	*Balaenoptera musculus*	4.05E+3[74]	7.42E+04	2.99E+07[60]	0.004	1.4
Marine nematodes	*Thalassomonhystera spp.*	*Platycomopsis spp.*	7.50E-09[75]	1.80E-7[75]	1.20E-5[75]	0.014	10
Marine fungi	*Malassezia restricta*	*Penicillium chrysogenum*	5.89E-12[76,77]	1.39E-11	1.89E-05[78]	0.325	10

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[*] *Rhizophora mangle*, similar to estimates for other typical species[36]

[†] Based on genet size of *Zostera marina*, a widespread species[39] and carbon density[40].

[‡] Based on *Laminaria saccharina*, a widespread species[43].

[§] Diameter corresponds to definition of picophytoplanktons (2 µm), and corresponding carbon content is based on conversion formulae from the smallest species.

[**] Maximum sizes are estimated to correspond to the same deviation from the mean size as minimum sizes are (on log scale).

[††] Same method as for bacterial picophytoplankton.

[‡‡] Same method as for bacterial picophytoplankton.

[§§] Based on *Dactyliosolen fragilissimus*[47].

[***] Mean size of colonies of *P. globosa* (2 mm) and *P. pouchetii* (1.5 mm), which are globally distributed and associated with bloom formation[51].

[†††] Classified as “generalist coral” for size estimate[69].

[‡‡‡] Mean colony size was estimated as the geometric mean of corallite or maximum colony sizes. Only maximum colony sizes were found across species and may contain several genets, hence the geometric mean. For each estimate, measures for four coral types were converted first to cubic volumes using 3D morphologies, assuming branching morphotype for "competitive" and "weedy" corals, and massive morphotype for "generalist" and "stress-tolerant" corals[69]. Each volume estimates were then converted to mass using type-specific skeletal densities[72], C per CaCO3, and weighted by global coral cover contributions[70].

[§§§] Mean skeleton biomass was the geometric mean of two biomass estimates based on global coral cover having heights corresponding to either corallites or maximum colony sizes. Mean tissue biomass was 0.05 Gt with a 10 fold uncertainty[5]. Overall mean biomass was the sum of mean skeleton and tissue biomass, and overall uncertainty was obtained from assuming that the overall min/max correspond to the sum of min/max skeleton and tissue estimates.

Table S3. Subterranean consumer body sizes.

Group	Smallest body size	Largest body size	Min. body size (g C)	Mean body size (g C)	Max. body size (g C)	Biomass (Gt C)	Uncertainty (fold)
Subterranean bacteria	*Proteobacteria spp.*	*Desulforudis audaxviator*	9.81E-16[79]	2.1E-14[80]	5.90E-12[81]	18.9*	3†
Subterranean archaea	*Thermoproteus spp.*	*Miscellaneous Crenarchaeotal Group spp.*	2.49E-15[83]	2.1E-14[80]	9.22E-14[84]	8.1‡	3§

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[*] Total subterranean microbial biomass was assumed to be the geometric mean of 23 to 31 PgC (which is 27 PgC) from [80]. 70% of microbial abundance is expected to be bacteria [82].

[†] Range of total subterranean microbial cell count from four models in [80] was 1.6 to 11.2 x 10^{29}, with a geometric mean of 4.2 x 10^{29}. This range corresponds to a three-fold uncertainty, which is similar to bacteria and archaea groups in other habitat realms.

[‡] 30% of microbial abundance is expected to be archaea [82]. See note for bacterial biomass.

[§] Same as uncertainty for subterranean bacteria.

Table S4. Body sizes measured for ramets instead of genets.

Group	Smallest body size	Largest body size	Min. body size (g C)	Mean body size (g C)[*]	Max. body size (g C)	Biomass (Gt C)	Uncertainty (fold)
Grassland plants	no change	*Phyllostachys pubesces*	no change	3.76	3.78E3[85]	no change	no change
Seagrass	no change	*Posidonia oceanica*	no change	5.95E-02	1.35[41]	no change	no change
Soil fungi	no change	*Phlebopus marginatus*	no change	1.88E-05	4.80E+02[86]	no change	no change
Hard corals	*Madracis mirabilis*	*Mussa angulosa*	3.24E-03[87][†]	1.03E+00	2.77E+02[87][‡]	no change	no change

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[*] The mean sizes for these affected groups were estimated as the geometric means of the new minimum and maximum sizes (resulting in a normal distribution on log size scale).

[†] Estimated as the skeleton density of weedy corals [70], multiplied by 0.653/0.603 (ratio of total coral biomass versus skeleton biomass) for size including tissue.

[‡] Estimated as the skeleton density of stress-tolerant corals [70], multiplied by 0.653/0.603 (ratio of total coral biomass versus skeleton biomass) for size including tissue.

Table S5. Body sizes excluding parts with low metabolism.

Group	Smallest body size	Largest body size	Min. body size (g C)	Mean body size (g C)	Max. body size (g C)	Biomass (Gt C)	Uncertainty (fold)
Forest plants	no change	no change	2.56E+00	2.67E+05	5.30E+08	80[*]	no change
Grassland plants	no change	no change	2.67E-03	3.07E+06	9.52E+08	80[†]	no change
Mangroves	no change	no change	8.21E+03	1.31E+05	5.84E+06	0.8[‡]	no change
Hard corals	no change	no change	4.91E-01	1.18E+02	1.28E+06	0.05[§]	no change
Subterranean bacteria	no change	no change	no change	no change	no change	0	no change
Subterranean archaea	no change	no change	no change	no change	no change	0	no change

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[*] Mean allocation of plant materials to leaves and roots[88]. All sizes were scaled down by 80/337.5 (ratio of non-woody biomass versus total biomass).

[†] Mean allocation of plant materials to leaves and roots[88]. All sizes were scaled down by 80/112.5 (ratio of non-woody biomass versus total biomass).

[‡] Estimated based on mangroves allocating a similar amount of material to leaves and roots as tropical plants [88]. All sizes were scaled down by 0.8/3.95 (ratio of non-woody biomass versus total biomass).

[§] Coral tissue biomass [5]. All sizes were scaled down by 0.05/0.653 (ratio of tissue biomass versus total biomass).

Table S6. Icon sources. All icons are in the public domain and are free to use.

Group	Icon source
Amphibians	Keynote
Wild birds	Keynote
Wild land mammals	Keynote
Reptiles	Keynote
Wild marine mammals	Keynote
Terrestrial nematodes	Custom
Marine nematodes	Custom
Cnidaria	Integration and Application Network, University of Maryland
Humans	Keynote
Livestock	Keynote
Seagrass	Integration and Application Network, University of Maryland
Bacterial picophytoplankton	Custom
Macroalgae	Integration and Application Network, University of Maryland
Molluscs	Keynote
Annelids	Pixabay.com
Terrestrial arthropods	Keynote
Phaeocystis	Custom
Green algae/protist picophytoplankton	Sally Bensusen, NASA EOS Project Science Office
Diatoms	Sally Bensusen, NASA EOS Project Science Office
Marine fungi	Custom
Marine archaea	Custom
Soil archaea	Custom
Hard coral	Custom
Fish	Keynote
Marine arthropods	Keynote
Marine protists	Sally Bensusen, NASA EOS Project Science Office
Marine bacteria	Custom
Soil protists	Custom
Cryptogamic phototrophs	Kisscc0.com
Mangroves	Integration and Application Network, University of Maryland
Subterranean archaea	Custom
Soil bacteria	Custom
Soil fungi	Pixabay.com
Subterranean bacteria	Custom
Grassland plants	Keynote
Forest plants	Keynote

Table S7. Regression statistics from 200 resamples for Fig. 3. Gauss-*n* stands for *n*-component mixture. The spectra were sampled once every log size bin (for 30 points total) and bins with biomass <10^{-5} GtC were excluded. Bold refers to the model selected according to each metric. *P*.ΔAIC>0 is the portion of bootstraps where the model had a lower AIC than the next simplest model. *P*.minAIC is the portion of bootstraps where the model had the lowest AIC overall. The selected model is the minimum (mean AIC) or maximum (mean R^2 and *P*.minAIC) of each column, or in the case of *P*.ΔAIC>0, the model closest to the lowest mean AIC that also has *P*.ΔAIC>0 smaller than 0.05.

Class	**Model**	**Mean R^2**	**Mean AIC**	***P*.ΔAIC>0**	***P*.minAIC**
All	**Linear**	0.35	100	0	0
	Gauss1	0.47	97	0.02	0
	Gauss2	0.87	64	0	0
	Gauss3	0.97	33	**0**	0.21
	Gauss4	**0.98**	**27**	0.21	**0.79**
Terrestrial	**Linear**	0.36	87	0	0
	Gauss1	0.43	87	0.53	0
	Gauss2	0.82	62	0	0
	Gauss3	0.94	42	**0.03**	0.33
	Gauss4	**0.97**	**39**	0.33	**0.68**
Marine	**Linear**	0.01	99	0	0
	Gauss1	0.63	72	0	0
	Gauss2	0.89	44	**0.02**	0.16
	Gauss3	0.95	**34**	0.18	**0.80**
	Gauss4	**0.96**	46	0.95	0.04
Terrestrial & Marine	**Linear**	0.46	94	0	0
	Gauss1	0.60	88	0	0
	Gauss2	0.92	49	0	0
	Gauss3	0.98	25	**0.01**	0.14
	Gauss4	**0.99**	**7**	0.14	**0.86**
Producers	**Linear**	0.54	76	0	0
	Gauss1	0.64	72	**0**	0
	Gauss2	0.92	21	0.15	0.03
	Gauss3	0.99	**-23**	0.15	**0.71**
	Gauss4	**0.99**	-17	0.73	0.27
Consumers	**Linear**	0.06	96	0	0
	Gauss1	0.64	70	0	0
	Gauss2	0.92	33	0.02	0.01
	Gauss3	0.98	**-1**	**0.03**	**0.73**
	Gauss4	**0.99**	4	0.74	0.26

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