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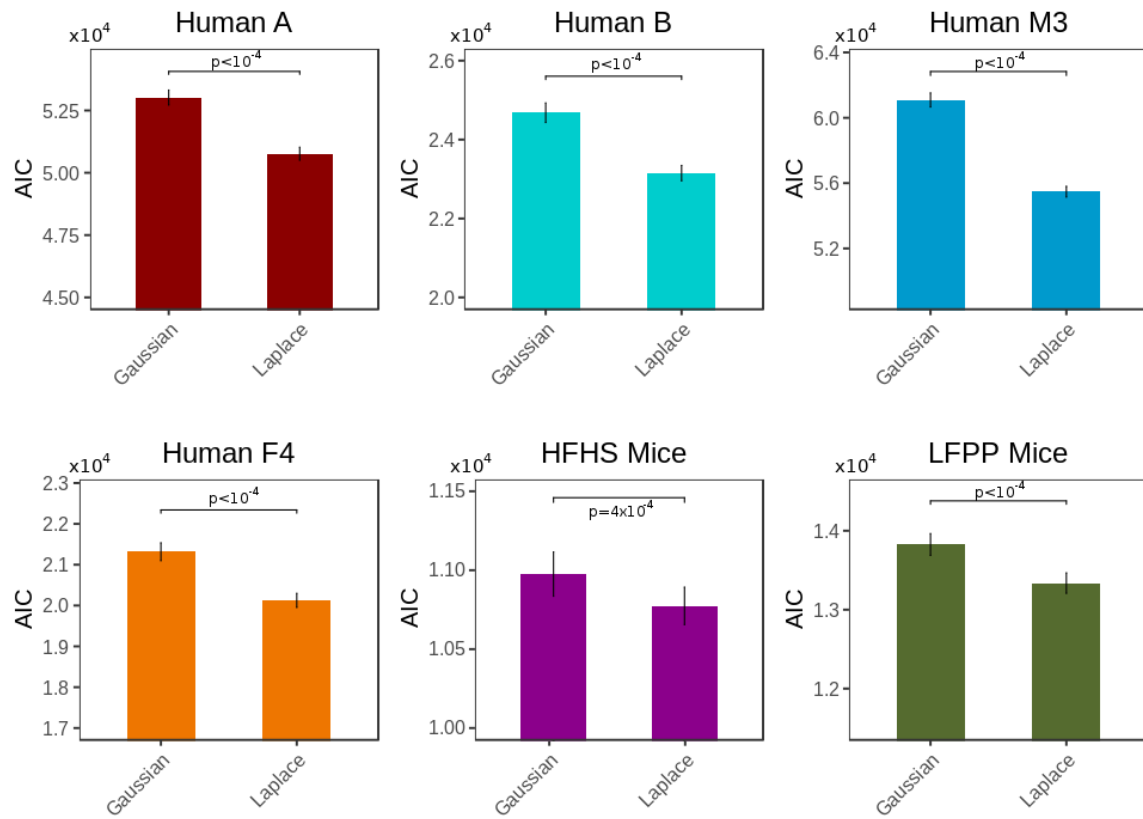
Macroecological dynamics of gut microbiota

Brian W. Ji^{1,4}, Ravi U. Sheth ^{1,4}, Purushottam D. Dixit^{1,2}, Konstantine Tchourine¹ and
Dennis Vitkup ^{1,3} 

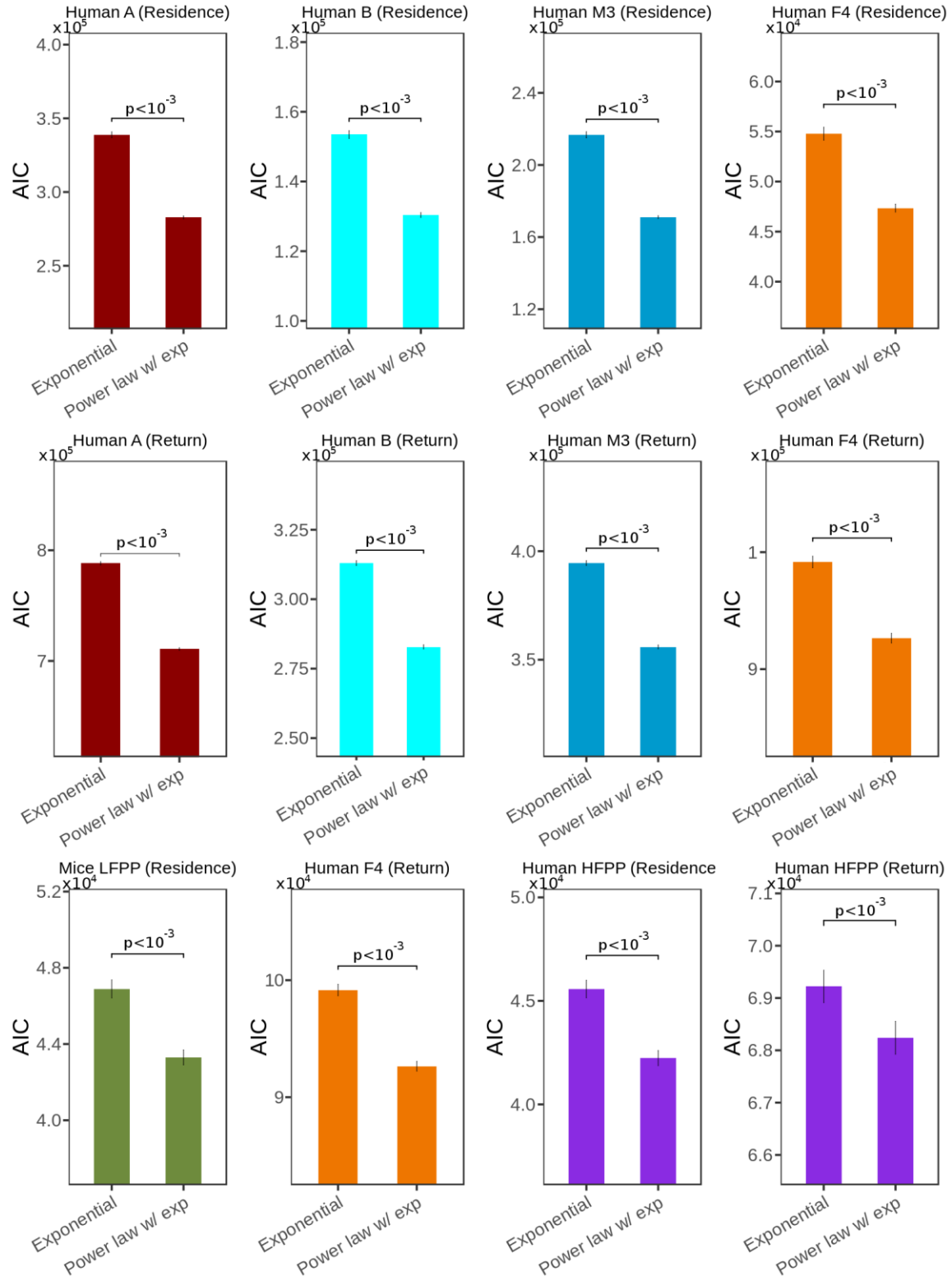
¹Department of Systems Biology, Columbia University, New York, NY, USA. ²Department of Physics, University of Florida, Gainesville, FL, USA.

³Department of Biomedical Informatics, Columbia University, New York, NY, USA. ⁴These authors contributed equally: Brian W. Ji and Ravi U. Sheth.

e-mail: dv2121@cumc.columbia.edu



Supplementary Figure 1. Quality of fits to the daily abundance changes distributions of gut microbiota. Quality of fits were assessed using Akaike Information Criterion (AIC) comparing the Laplace distribution to the Gaussian distribution. Height of the bar denotes the mean AIC across 10,000 bootstrap samples of the abundance changes data, error bars denote the standard deviation, and p-value denotes the fraction of bootstrap samples for which the AIC was lower for the Gaussian fit; $p < 10^{-4}$ indicates that AIC was never lower for the Gaussian fit in 10^4 bootstrap samples.



Supplementary Figure 2. Quality of fits to the residence and return times of gut microbiota. Quality of fits were assessed using Akaike Information Criterion (AIC) comparing the power law with exponential tail to the exponential distribution. Height of the bar denotes the mean AIC across $n = 1000$ bootstrap samples of the residence and return times

data, error bars denote the standard deviation, and p denotes the fraction of bootstrap samples for which the AIC was lower for the Exponential distribution fit; $p < 10^{-3}$ indicates that the AIC was never lower for the Exponential distribution in 10^3 bootstrap samples.

Supplementary Table 1. OTUs in humans with a single day abundance exceeding the average abundance (calculated across all others days in a dataset) by over 25-fold.

Human	OTU	Phylum	Class	Order	Family	Genus
A	13	Proteobacteria (100%)	Gammaproteobacteria (97%)	Enterobacteriales (85%)	Enterobacteriaceae (85%)	Escherichia/Shigella (37%)
A	25	Firmicutes (98%)	Clostridia (98%)	Clostridiales (98%)	Peptostreptococcaceae (93%)	Clostridium XI (71%)
A	29	Proteobacteria (100%)	Gammaproteobacteria (100%)	Pasteurellales (100%)	Pasteurellaceae (100%)	Haemophilus (76%)
A	36	Firmicutes (100%)	Negativicutes (100%)	Selenomonadales (100%)	Veillonellaceae (100%)	Veillonella (100%)
A	42	Firmicutes (100%)	Clostridia (99%)	Clostridiales (99%)	Clostridiaceae 1 (99%)	Clostridium sensu stricto (99%)
A	5771	Proteobacteria (100%)	Gammaproteobacteria (100%)	Enterobacteriales (95%)	Enterobacteriaceae (95%)	Salmonella (91%)
B	13	Proteobacteria (100%)	Gammaproteobacteria (97%)	Enterobacteriales (85%)	Enterobacteriaceae (85%)	Escherichia/Shigella (37%)
B	59	Actinobacteria (100%)	Actinobacteria (100%)	Coriobacteriales (100%)	Coriobacteriaceae (100%)	Eggerthella (100%)
B	95	Firmicutes (71%)	Clostridia (59%)	Clostridiales (55%)	Ruminococcaceae (23%)	Gemmiger (12%)
B	110	Firmicutes (67%)	Clostridia (60%)	Clostridiales (53%)	Ruminococcaceae (20%)	Butyrivibrio (11%)
B	5928	Firmicutes (99%)	Clostridia (99%)	Clostridiales (99%)	Lachnospiraceae (99%)	Oribacterium (60%)
M3	10	Verrucomicrobia (100%)	Verrucomicrobiae (100%)	Verrucomicrobiales (100%)	Verrucomicrobiaceae (100%)	Akkermansia (100%)
M3	11	Bacteroidetes (100%)	Bacteroidia (100%)	Bacteroidales (100%)	Bacteroidaceae (100%)	Bacteroides (100%)
M3	12	Proteobacteria (100%)	Gammaproteobacteria (98%)	Enterobacteriales (85%)	Enterobacteriaceae (85%)	Cronobacter (30%)
M3	31	Bacteroidetes (100%)	Bacteroidia (100%)	Bacteroidales (100%)	Porphyromonadaceae (100%)	Porphyromonas (99%)
M3	41	Firmicutes (53%)	Clostridia (45%)	Clostridiales (41%)	Clostridiales_Incertae_Sedis XIII (7%)	Anaerovorax (7%)
M3	44	Firmicutes (86%)	Clostridia (86%)	Clostridiales (86%)	Ruminococcaceae (85%)	Oscillibacter (77%)
M3	71	Firmicutes (100%)	Bacilli (100%)	Lactobacillales (100%)	Streptococcaceae (100%)	Streptococcus (100%)
M3	75	Firmicutes (94%)	Clostridia (94%)	Clostridiales (94%)	Ruminococcaceae (93%)	Subdoligranulum (78%)
M3	346	Firmicutes (100%)	Clostridia (93%)	Clostridiales (93%)	Lachnospiraceae (92%)	Roseburia (86%)
F4	14	Bacteroidetes (100%)	Bacteroidia (99%)	Bacteroidales (99%)	Prevotellaceae (99%)	Prevotella (99%)
F4	2643	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Lachnospiraceae (100%)	Ruminococcus2 (94%)

Supplementary Table 2. OTUs for mice on the LFPP and HFHS diets with either significantly higher or significantly lower variability than expected based on Taylor's power law.

Mouse	OTU	Direction	Phylum	Class	Order	Family	Genus
HFHS1	4	High	Firmicutes (51%)	Clostridia (49%)	Clostridiales (45%)	Ruminococcaceae (16%)	Butyricoccus (9%)
HFHS1	33	High	Firmicutes (61%)	Clostridia (58%)	Clostridiales (51%)	Ruminococcaceae (19%)	Butyricoccus (8%)
HFHS1	36	High	Firmicutes (28%)	Erysipelotrichia (8%)	Erysipelotrichales (8%)	Erysipelotrichaceae (8%)	Allobaculum (3%)
HFHS1	55	High	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Lachnospiraceae (100%)	Robinsoniella (32%)
HFHS2	67	High	Firmicutes (38%)	Clostridia (27%)	Clostridiales (26%)	Clostridiaceae 3 (7%)	Brassicibacter (6%)
HFHS2	264	High	Firmicutes (53%)	Clostridia (49%)	Clostridiales (43%)	Lachnospiraceae (28%)	Robinsoniella (2%)
HFHS2	183	Low	Bacteroidetes (67%)	Sphingobacteriia (16%)	Sphingobacteriales (16%)	Cyclobacteriaceae (15%)	Indibacter (4%)
HFHS3	5	High	Firmicutes (95%)	Clostridia (92%)	Clostridiales (92%)	Lachnospiraceae (91%)	Clostridium XIVa (59%)
HFHS3	21	High	Firmicutes (98%)	Clostridia (98%)	Clostridiales (98%)	Lachnospiraceae (96%)	Ruminococcus2 (15%)
HFHS3	33	High	Firmicutes (61%)	Clostridia (58%)	Clostridiales (51%)	Ruminococcaceae (19%)	Butyricoccus (8%)
HFHS3	2431	High	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Ruminococcaceae (98%)	Pseudoflavonifractor (71%)
LFPP1	237	Low	Bacteroidetes (84%)	Bacteroidia (61%)	Bacteroidales (61%)	Porphyromonadaceae (38%)	Barnesiella (2%)
LFPP1	364	Low	Bacteroidetes (86%)	Bacteroidia (77%)	Bacteroidales (77%)	Porphyromonadaceae (63%)	Barnesiella (5%)
LFPP2	93	High	Firmicutes (100%)	Clostridia (100%)	Clostridiales (100%)	Clostridiaceae 1 (23%)	Anaerosporebacter (23%)
LFPP2	99	High	Firmicutes (83%)	Clostridia (73%)	Clostridiales (73%)	Ruminococcaceae (50%)	Clostridium IV (26%)
LFPP2	276	High	Firmicutes (99%)	Clostridia (98%)	Clostridiales (98%)	Lachnospiraceae (97%)	Dorea (30%)
LFPP2	237	Low	Bacteroidetes (84%)	Bacteroidia (61%)	Bacteroidales (61%)	Porphyromonadaceae (38%)	Barnesiella (2%)
LFPP3	16	High	Firmicutes (90%)	Clostridia (90%)	Clostridiales (90%)	Lachnospiraceae (86%)	Butyrivibrio (16%)
LFPP3	22	Low	Firmicutes (82%)	Clostridia (82%)	Clostridiales (82%)	Ruminococcaceae (55%)	Saccharofermentans (20%)
LFPP3	118	Low	Bacteroidetes (83%)	Bacteroidia (73%)	Bacteroidales (73%)	Porphyromonadaceae (46%)	Butyricimonas (19%)
LFPP3	237	Low	Bacteroidetes (84%)	Bacteroidia (61%)	Bacteroidales (61%)	Porphyromonadaceae (38%)	Barnesiella (2%)
LFPP3	364	Low	Bacteroidetes (86%)	Bacteroidia (77%)	Bacteroidales (77%)	Porphyromonadaceae (63%)	Barnesiella (5%)