Paleobiology

Supporting Information for

Small but mighty: how overlooked small species maintain community structure through middle Eocene climate change

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Contents

1 Introduction to Supplementary Material

This supplement is intended to provide reproducible code for the results presented in the manuscript. All analyses were performed in the freely distributed R environment (R Core Team (2020)). This supporting information was written using knitr (Xie (2020)) and kableExtra (Zhu (2019)). The code uses the tidyverse (Wickham (2019)) , readxl (Wickham and Bryan (2019)) and mgcv (Wood (2017)) and packages within as well as dependencies (Aze et al. (2011)). Here we provide the sample information for all samples included in our analysis as well as morphological and ecological classification of identified genera which are all referenced within the manuscript. For ease of use Tables 1, 3-8 and 11-12 are also uploaded as Comma separated values (CSV) files.

```
library(readxl)
library(tidyverse)
library(knitr)
library(kableExtra)
library(mgcv)
library(FSA)
library(broom)
library(itsadug)
library(xtable)
library(formatR)
library(MuMIn)
library(rstatix)
library(ggpubr)
```

Supplementary Figure 1: Expedition 342 Site locations used in this study (colored circles) on a plate reconstruction from 36 Ma from www.odsn.de. Site U1406 (black circle; 40°21.0 N, 51°39.0 W), U1408 (green circle; 41°26.3 N, 49°47.1 W) and U1410 (red circle; 41°19.6993 N, 49°10.1847 W) (Norris et al (2012)).

Supplementary Table 1: IODP Expedition 342 samples used in this study. Lab ID= Study specific sample ID, Expedition = IODP expedition number, Top Depth = Top interval (m), Bottom Depth = Bottom interval (m), Sample ages were calculated based on an age depth model constructed using available biostratigraphic and magnetostratigraphic data for Sites U1408 and U1410 (Norris et al (2012), Yamamoto et al (2018) and Cappelli et al (2019)). Age calibrations from the 2012 geologic timescale were used for middle Eocene geomagnetic polarity reversals (GTS2012; Gradstein et al (2012), Ogg et al (2012))

LAB ID	**EXPEDITION**	**SITE**	**HOLE**	**CORE**	**SECTION**	**TOP__DEPTH**	**BOTTOM__DEPTH**	**Depth (CCSF-A, m)**	**U1408 Mapped Depth (CCSF-M, m)**	**Inter-site Mapped Depth (CCSF-X)**	**Age (GTS__2012)**
67	342	1406	A	27	3	88	90				38.00
7	342	1406	A	27	4	137.5	139				38.16
68	342	1406	A	27	5	100	102				38.25
80	342	1408	B	5	2	60	62				38.50
8	342	1406	A	27	6	62	63.5				38.72
74	342	1408	A	5	2	38	40				39.00
75	342	1408	A	5	5	30	32				39.25
82	342	1408	B	7	1	98	100	49.08	49.08	49.76	39.56
96	342	1408	C	7	2	58	60	54.19	54.26	54.94	39.68
34	342	1408	B	8	1	120	121.5	60.11	60.13	60.81	39.85
20	342	1406	B	28	5	1.5	3				39.92
83	342	1408	B	8	4	28	30	63.69	63.69	64.32	39.95
35	342	1408	B	8	4	106.5	108	64.47	64.47	64.89	39.97
59	342	1410	B	10	5	117	118.5	90.04	90.04	70.64	40.14
76	342	1408	A	8	2	117	118	71.57	71.57	78.89	40.38
30	342	1408	A	8	3	69	71	72.59	72.59	79.91	40.41
98	342	1408	C	9	2	98	100	75.28	75.46	82.78	40.49
51	342	1410	A	11	1	97	98.5	102.20	101.93	102.98	41.09
53	342	1410	A	11	5	129.5	131	108.53	108.53	109.79	41.31
48	342	1408	C	11	5	137	139	99.33	99.33	113.51	41.45
54	342	1410	A	12	2	64	65.5	115.07	115.07	116.66	41.58
61	342	1410	B	14	2	79	80.5	121.82	121.56	122.99	41.83
62	342	1410	B	14	3	92.5	94	123.46	124.05	125.48	41.94
49	342	1408	C	13	1	142	144	114.37	114.37	129.48	42.10
78	342	1408	A	13	1	140	142				43.00
114	342	1410	A	15	7	49.5	51				43.25
115	342	1410	A	16	4	120	121.5				43.50
116	342	1410	A	17	1	2	3.5				43.75
117	342	1410	A	17	4	56	57.5				44.00
118	342	1410	A	18	1	67	68.5				44.25
119	342	1410	A	18	4	122	123.5				44.50
120	342	1410	A	19	1	114	115.5				44.75
121	342	1410	A	19	5	18	19.5				45.00

Supplementary Table 2: Genera found in this study and there morphogroup and depth habitat based on Table S9 and Table S10 below, which are updated from those published by Aze et al. (2011)

Genera	**Morphogroup**	**Depth Habitat**
Acarinina	7	Mixed layer
Catapsydrax	2	Subthermocline
Chiloguembelina	9	Mixed layer
Dentoglobigerina	2	Thermocline
Globigerina	2	Mixed layer
Globigerinatheka	3	Mixed layer
Globorotaloides	2	Subthermocline
Globoturborotalita	2	Mixed layer
Hantkinena	5	Thermocline
Jenkinsina	10	Subthermocline
Morozovelloides	8	Mixed layer
Orbulinoides	11	Mixed layer
Parasubbotina	2	Subthermocline
Planorotalites	8	Mixed layer
Pseudohastigerina	4	Mixed layer
Subbotina	2	Thermocline
Turborotalita	1	Mixed layer
Turborotalia	6	Mixed layer

Supplementary Table 3: Raw counts of genera in the >63μm size fraction

Age (Ma)	**Turborotalita**	**Subbotina**	**Globigerina**	**Catapsydrax**	**Globoturborotalita**	**Parasubbotina**	**Dentoglobigerina**	**Globorotaloides**	**Globigerinatheka**	**Pseudohastigerina**	**Hantkinena**	**Turborotalia**	**Acarinina**	**Morozovelloides**	**Chiloguembelina**	**Jenkinsina**	**Planorotalites**	**Orbulinoides**	**Total**
38.00	0	73	0	5	0	0	0	15	0	41	0	0	48	0	8	0	184	0	374
38.16	0	30	0	22	0	180	3	0	4	0	0	0	15	0	9	0	13	0	276
38.25	0	152	0	7	0	0	0	13	3	8	0	0	8	0	16	0	63	0	270
38.50	0	64	0	13	0	0	2	20	3	25	1	6	22	0	44	0	134	0	334
38.72	1	35	0	10	0	122	0	9	1	29	0	1	26	2	0	30	56	0	322
39.00	0	64	0	4	0	0	2	31	5	36	0	0	11	0	51	0	111	0	315
39.25	0	89	0	17	0	0	0	50	0	43	0	2	31	0	43	0	235	0	510
39.56	0	37	0	22	0	19	0	40	0	52	0	0	8	1	53	4	83	0	319
39.75	0	41	4	6	12	11	0	49	2	53	0	2	9	0	56	0	94	0	339
39.85	0	8	0	0	6	35	0	24	2	32	0	0	14	0	160	1	88	0	370
39.92	0	56	0	27	0	77	0	0	16	0	0	0	9	0	2	0	36	0	223
39.95	0	51	0	5	0	7	0	23	0	41	0	1	6	0	50	0	69	0	253
39.97	0	53	0	1	0	20	0	35	7	36	0	1	25	0	57	19	105	0	359
40.14	0	37	4	0	0	47	0	3	3	3	0	1	27	4	4	0	182	0	315
40.38	0	128	0	41	4	19	0	8	38	22	0	6	15	3	11	1	38	1	335
40.41	0	43	0	0	1	44	0	17	9	16	1	1	12	1	5	73	17	0	240
40.49	0	109	0	42	4	44	2	70	9	57	0	4	48	24	58	1	150	0	622
41.09	0	20	4	0	4	32	0	27	2	13	0	2	20	1	65	0	98	0	288
41.31	0	18	0	0	18	87	0	23	1	32	1	0	28	35	28	1	20	0	292
41.45	0	19	0	0	0	41	0	38	2	51	0	1	13	15	404	155	34	0	773
41.58	0	23	0	0	2	49	0	33	0	59	0	2	26	2	65	8	45	0	314
41.83	0	74	11	9	12	32	0	0	15	39	1	1	111	12	6	5	32	0	360
41.94	0	34	0	0	0	40	0	33	1	48	0	1	31	13	76	18	84	0	379
42.10	0	21	0	0	7	26	0	23	2	67	0	0	62	15	14	8	40	0	285
43.00	0	74	0	2	0	26	0	10	4	59	1	6	99	20	59	36	116	0	512
43.25	0	74	0	5	0	39	0	28	0	32	0	3	75	2	41	10	83	0	392
43.50	0	90	1	3	0	17	0	30	10	5	0	4	81	5	2	4	58	0	310
43.75	0	84	0	0	0	28	0	7	0	26	0	2	50	19	12	6	88	0	322
44.00	0	56	4	5	0	26	0	30	1	59	0	18	129	17	60	45	135	0	585
44.25	0	59	0	3	0	10	0	21	0	55	0	25	104	1	3	4	96	0	381
44.50	0	47	0	3	0	0	0	19	3	38	0	15	106	1	1	1	43	0	277
44.75	0	67	0	0	0	0	0	84	0	35	0	0	89	1	5	4	47	0	332
45.00	0	99	0	1	0	0	0	27	0	55	0	0	104	2	10	5	62	0	365

Supplementary Table 4: Raw counts of genera in the >180μm size fraction

Age (Ma)	**Turborotalita**	**Subbotina**	**Globigerina**	**Catapsydrax**	**Parasubbotina**	**Dentoglobigerina**	**Globoturborotalita**	**Globorotaloides**	**Globigerinatheka**	**Pseudohastigerina**	**Hantkinena**	**Turborotalia**	**Acarinina**	**Morozovelloides**	**Chiloguembelina**	**Jenkinsina**	**Planorotalites**	**Orbulinoides**	**Total**
38.00	0	238	0	21	0	3	0	0	5	0	0	0	22	2	0	0	0	0	291
38.16	0	285	0	12	0	12	21	0	24	0	0	2	5	0	0	0	0	0	361
38.25	0	298	0	10	0	0	0	0	2	0	0	0	3	0	6	0	0	0	319
38.50	0	291	0	9	3	5	0	0	29	3	0	12	13	4	0	0	0	0	369
38.72	0	220	2	15	14	3	2	0	29	0	0	1	16	4	0	0	0	0	306
39.00	0	220	0	18	5	5	12	0	15	2	2	14	15	1	0	0	0	0	309
39.25	0	192	0	10	4	1	2	1	0	2	0	9	11	0	0	0	0	0	232
39.56	0	209	0	34	37	0	7	1	10	15	0	0	6	0	6	0	0	0	325
39.75	0	157	0	22	3	0	6	2	16	9	0	18	31	1	2	0	6	0	273
39.85	0	94	0	7	43	15	38	0	24	11	0	0	28	17	0	0	0	3	280
39.92	0	209	0	24	4	0	3	0	76	1	0	0	0	0	0	0	0	0	317
39.95	0	159	0	9	38	0	0	0	34	8	0	4	9	4	0	0	0	0	265
39.97	0	281	0	40	3	0	0	0	50	0	1	2	0	1	0	0	0	0	378
40.14	0	192	7	0	43	0	8	0	21	0	0	2	16	14	0	0	0	0	303
40.38	0	145	0	27	0	5	1	0	102	1	1	12	11	1	0	0	1	0	307
40.41	0	139	0	27	12	0	3	0	100	0	0	2	2	5	0	0	0	0	290
40.49	0	257	0	31	18	0	1	3	18	0	0	1	30	20	0	0	0	0	379
41.09	0	81	4	12	25	0	19	0	10	2	3	20	95	10	0	0	0	0	281
41.31	0	152	0	10	15	0	39	0	24	6	3	8	39	73	0	0	0	0	369
41.45	0	99	9	11	16	0	16	2	11	17	2	15	36	47	0	0	0	0	281
41.58	0	131	8	3	30	1	20	5	25	15	0	22	84	32	0	1	1	0	378
41.83	0	207	0	0	15	0	5	0	54	3	2	0	100	32	0	0	0	0	418
41.94	0	125	3	11	15	0	6	0	9	0	1	10	35	35	0	0	0	0	250
42.10	0	167	0	5	43	0	24	0	27	3	0	12	47	43	0	0	0	0	371
43.00	0	148	0	9	9	0	0	0	21	1	1	21	121	46	0	0	0	0	377
43.25	0	174	1	13	18	0	7	0	19	4	1	15	45	18	0	0	4	0	319
43.50	0	124	0	9	7	0	4	0	72	0	0	6	114	18	0	0	0	0	354
43.75	0	167	0	10	7	0	0	0	16	0	0	3	37	19	0	0	0	0	259
44.00	0	191	0	23	0	0	0	0	10	2	0	8	27	37	0	0	3	0	301
44.25	0	244	0	7	2	0	0	0	0	1	0	26	146	2	0	0	2	0	430
44.50	0	147	0	9	3	0	16	0	0	0	0	24	148	7	0	0	0	0	354
44.75	0	198	0	0	0	0	0	0	0	4	0	4	209	3	0	0	0	0	418
45.00	0	154	0	6	0	0	9	18	0	22	0	7	148	0	57	2	0	0	423

Supplementary Table 5: Raw counts of morphogroups in the >63μm size fraction

Age (Ma)	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
38.00	0	93	0	41	0	0	48	184	8	0	0	374
38.16	0	235	4	0	0	0	15	13	9	0	0	276
38.25	0	172	3	8	0	0	8	63	16	0	0	270
38.50	0	99	3	25	1	6	22	134	44	0	0	334
38.72	1	176	1	29	0	1	26	58	0	30	0	322
39.00	0	101	5	36	0	0	11	111	51	0	0	315
39.25	0	156	0	43	0	2	31	235	43	0	0	510
39.56	0	118	0	52	0	0	8	84	53	4	0	319
39.75	0	123	2	53	0	2	9	94	56	0	0	339
39.85	0	73	2	32	0	0	14	88	160	1	0	370
39.92	0	160	16	0	0	0	9	36	2	0	0	223
39.95	0	86	0	41	0	1	6	69	50	0	0	253
39.97	0	109	7	36	0	1	25	105	57	19	0	359
40.14	0	91	3	3	0	1	27	186	4	0	0	315
40.38	0	200	38	22	0	6	15	41	11	1	1	335
40.41	0	105	9	16	1	1	12	18	5	73	0	240
40.49	0	271	9	57	0	4	48	174	58	1	0	622
41.09	0	87	2	13	0	2	20	99	65	0	0	288
41.31	0	146	1	32	1	0	28	55	28	1	0	292
41.45	0	98	2	51	0	1	13	49	404	155	0	773
41.58	0	107	0	59	0	2	26	47	65	8	0	314
41.83	0	138	15	39	1	1	111	44	6	5	0	360
41.94	0	107	1	48	0	1	31	97	76	18	0	379
42.10	0	77	2	67	0	0	62	55	14	8	0	285
43.00	0	112	4	59	1	6	99	136	59	36	0	512
43.25	0	146	0	32	0	3	75	85	41	10	0	392
43.50	0	141	10	5	0	4	81	63	2	4	0	310
43.75	0	119	0	26	0	2	50	107	12	6	0	322
44.00	0	121	1	59	0	18	129	152	60	45	0	585
44.25	0	93	0	55	0	25	104	97	3	4	0	381
44.50	0	69	3	38	0	15	106	44	1	1	0	277
44.75	0	151	0	35	0	0	89	48	5	4	0	332
45.00	0	127	0	55	0	0	104	64	10	5	0	365

Supplementary Table 6: Raw counts of morphogroups in the >180μm size fraction

Age (Ma)	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**Total**
38.00	0	262	5	0	0	0	22	2	0	0	0	291
38.16	0	330	24	0	0	2	5	0	0	0	0	361
38.25	0	308	2	0	0	0	3	0	6	0	0	319
38.50	0	308	29	3	0	12	13	4	0	0	0	369
38.72	0	256	29	0	0	1	16	4	0	0	0	306
39.00	0	260	15	2	2	14	15	1	0	0	0	309
39.25	0	210	0	2	0	9	11	0	0	0	0	232
39.56	0	288	10	15	0	0	6	0	6	0	0	325
39.75	0	190	16	9	0	18	31	7	2	0	0	273
39.85	0	197	24	11	0	0	28	17	0	0	3	280
39.92	0	240	76	1	0	0	0	0	0	0	0	317
39.95	0	206	34	8	0	4	9	4	0	0	0	265
39.97	0	324	50	0	1	2	0	1	0	0	0	378
40.14	0	250	21	0	0	2	16	14	0	0	0	303
40.38	0	178	102	1	1	12	11	2	0	0	0	307
40.41	0	181	100	0	0	2	2	5	0	0	0	290
40.49	0	310	18	0	0	1	30	20	0	0	0	379
41.09	0	141	10	2	3	20	95	10	0	0	0	281
41.31	0	216	24	6	3	8	39	73	0	0	0	369
41.45	0	153	11	17	2	15	36	47	0	0	0	281
41.58	0	198	25	15	0	22	84	33	0	1	0	378
41.83	0	227	54	3	2	0	100	32	0	0	0	418
41.94	0	160	9	0	1	10	35	35	0	0	0	250
42.10	0	239	27	3	0	12	47	43	0	0	0	371
43.00	0	166	21	1	1	21	121	46	0	0	0	377
43.25	0	213	19	4	1	15	45	22	0	0	0	319
43.50	0	144	72	0	0	6	114	18	0	0	0	354
43.75	0	184	16	0	0	3	37	19	0	0	0	259
44.00	0	214	10	2	0	8	27	40	0	0	0	301
44.25	0	253	0	1	0	26	146	4	0	0	0	430
44.50	0	175	0	0	0	24	148	7	0	0	0	354
44.75	0	198	0	4	0	4	209	3	0	0	0	418
45.00	0	187	0	22	0	7	148	0	57	2	0	423

Supplementary Table 7: Raw counts of depth habitats in the >63μm size fraction

Age (Ma)	**Mixed_Layer**	**Thermocline**	**Subthermocline**	**Total**
38.00	281	73	20	374
38.16	41	33	202	276
38.25	98	152	20	270
38.50	234	67	33	334
38.72	116	35	171	322
39.00	214	66	35	315
39.25	354	89	67	510
39.56	197	37	85	319
39.75	232	41	66	339
39.85	302	8	60	370
39.92	63	56	104	223
39.95	167	51	35	253
39.97	231	53	75	359
40.14	228	37	50	315
40.38	138	128	69	335
40.41	62	44	134	240
40.49	354	111	157	622
41.09	209	20	59	288
41.31	162	19	111	292
41.45	520	19	234	773
41.58	201	23	90	314
41.83	239	75	46	360
41.94	254	34	91	379
42.10	207	21	57	285
43.00	363	75	74	512
43.25	236	74	82	392
43.50	166	90	54	310
43.75	197	84	41	322
44.00	423	56	106	585
44.25	284	59	38	381
44.50	207	47	23	277
44.75	177	67	88	332
45.00	233	99	33	365

Supplementary Table 8: Raw counts of depth habitats in the >180μm size fraction

Age (Ma)	**Mixed_Layer**	**Thermocline**	**Subthermocline**	**Total**
38.00	29	241	21	291
38.16	52	297	12	361
38.25	11	298	10	319
38.50	61	296	12	369
38.72	54	223	29	306
39.00	59	227	23	309
39.25	24	193	15	232
39.56	44	209	72	325
39.75	89	157	27	273
39.85	121	109	50	280
39.92	80	209	28	317
39.95	59	159	47	265
39.97	53	282	43	378
40.14	68	192	43	303
40.38	129	151	27	307
40.41	112	139	39	290
40.49	70	257	52	379
41.09	160	84	37	281
41.31	189	155	25	369
41.45	151	101	29	281
41.58	207	132	39	378
41.83	194	209	15	418
41.94	98	126	26	250
42.10	156	167	48	371
43.00	210	149	18	377
43.25	113	175	31	319
43.50	214	124	16	354
43.75	75	167	17	259
44.00	87	191	23	301
44.25	177	244	9	430
44.50	195	147	12	354
44.75	220	198	0	418
45.00	243	154	26	423

Supplementary Table 9: Descriptions of morphological classification applied to genera of this study updated from previous work (Aze et al (2011)) to include microperforate genera

Morphogroup	**Description**
1	Spinose, flat
2	Spinose, globular
3	Spinose globular with supplementary apertures
4	Non-spinose, planispiral
5	Non-spinose, tubilospinate
6	Non-spinose, turborotaliform, keeled
7	Non-spinose, muricate, acariniform
8	Non-spinose, muriconate, keeled
9	Microperforate, non-spinose, biserial
10	Microperforate, non-spinose,triserial
11	Spinose, spherical, flat

Supplementary Table 10: Descriptions of depth habitat classifications applied to genera found in this study updated from previous research (Aze et al (2011)) to include microperforate genera

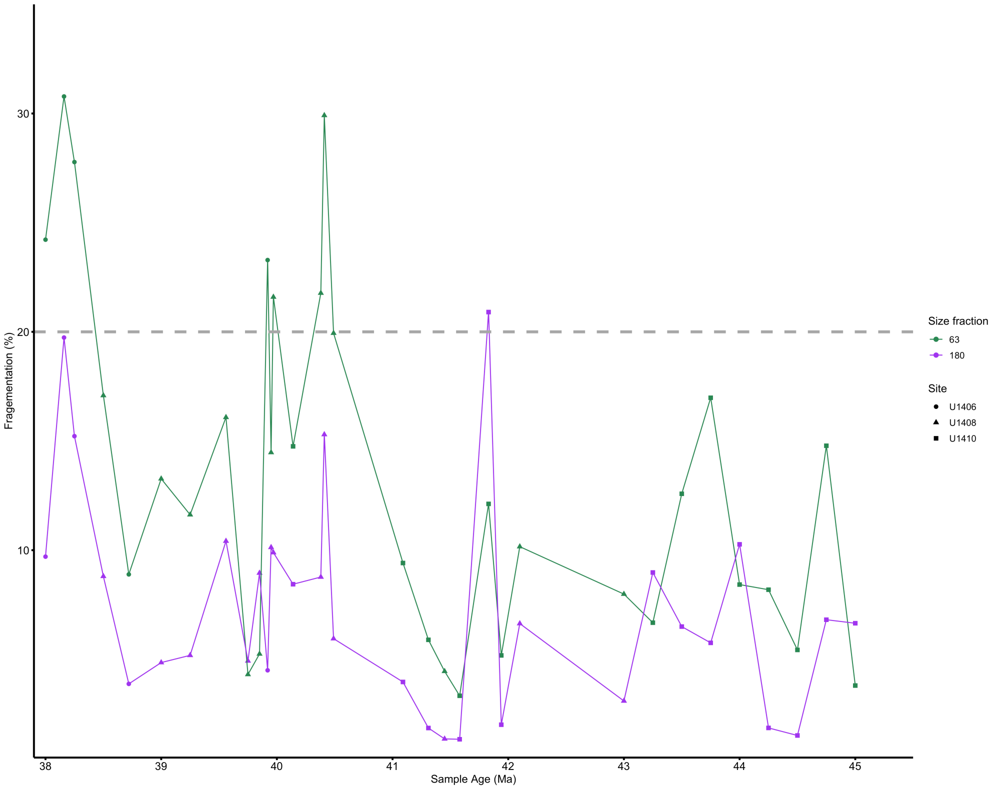
Depth Habitat	**Description**
Mixed layer	Heavy 13C, light 18O
Thermocline	Light 13C, relativley heavy 18O
Subthermocline	Very light 13C, very heavy 18O

Supplementary Table 11: Calculated hill numbers for genera, morphogroup and depth habitat. Columns relating to different measured diversity are as follows: genera begin with Genus, morphogroup begin with Morph, and depth habitat begin with Eco. Hill refers to calculated hill numbers, UCI is the upper confidence interval, LCI is the lower confidence interval and SD is the standard deviation. Size fraction relates to the size fraction measured whilst Q is the order of q effective diversity was calculated. This table is too large in its entirety so only the first 11 lines are presented here with the .csv available as a supplement .

Size Fraction	**Age**	**Fragmentation %**	**Q**	**Genus_Hill**	**Genus_UCI**	**Genus_LCI**	**Genus_SD**	**Morph_Hill**	**Morph_UCI**	**Morph_LCI**	**Morph_SD**	**Eco_Hill**	**Eco_UCI**	**Eco_LCI**	**Eco_SD**
180	38	9.7	0.0	6.00	6.19	5.19	0.41	4.00	4.15	3.15	0.36	3.00	3.00	3.00	0.00
180	38	9.7	0.1	5.22	5.51	4.49	0.33	3.43	3.66	2.77	0.28	2.82	2.86	2.78	0.02
180	38	9.7	0.2	4.55	4.89	3.90	0.28	2.97	3.23	2.45	0.22	2.66	2.73	2.58	0.04
180	38	9.7	0.3	3.98	4.35	3.41	0.25	2.60	2.86	2.19	0.18	2.50	2.60	2.40	0.06
180	38	9.7	0.4	3.50	3.87	3.00	0.22	2.30	2.56	1.98	0.15	2.36	2.48	2.23	0.07
180	38	9.7	0.5	3.11	3.47	2.68	0.20	2.07	2.32	1.81	0.13	2.23	2.37	2.09	0.08
180	38	9.7	0.6	2.79	3.13	2.42	0.18	1.89	2.12	1.67	0.11	2.12	2.26	1.96	0.08
180	38	9.7	0.7	2.53	2.85	2.20	0.17	1.75	1.96	1.55	0.10	2.02	2.17	1.86	0.09
180	38	9.7	0.8	2.32	2.62	2.02	0.15	1.64	1.83	1.47	0.09	1.93	2.09	1.76	0.09
180	38	9.7	0.9	2.15	2.43	1.87	0.14	1.55	1.72	1.40	0.08	1.85	2.01	1.68	0.09
180	38	9.7	1.0	2.01	2.28	1.76	0.13	1.48	1.64	1.34	0.08	1.78	1.94	1.62	0.09

Supplementary Table 12: Fragmentation of samples at both size fractions including recounts. Lab ID= Study specific sample ID, Expedition = IODP expedition number, Top Depth = Top interval (m), Bottom Depth = Bottom interval (m)

LAB ID	**EXPEDITION**	**SITE**	**HOLE**	**CORE**	**CORE__TYPE**	**SECTION**	**CC**	**TOP__DEPTH**	**BOTTOM__DEPTH**	**Age__2021(Ma)**	**180__Fragmentation (%)**	**180__Recount__Fragmentation (%)**	**63__Fragmentation (%)**	**63__Recount__Fragmentation (%)**
67	342	1406	A	27	X	3	no	88	90	38.00	9.70	9.79	24.22	
7	342	1406	A	27	X	4	no	137.5	139	38.16	19.74		30.78	25.38
68	342	1406	A	27	X	5	no	100	102	38.25	15.22	15.12	27.78	31.02
80	342	1408	B	5	H	2	no	60	62	38.50	8.80		17.08	
8	342	1406	A	27	X	6	no	62	63.5	38.72	3.88		8.89	
74	342	1408	A	5	H	2	no	38	40	39.00	4.85		13.27	
75	342	1408	A	5	H	5	no	30	32	39.25	5.18	4.97	11.62	11.09
82	342	1408	B	7	H	1	no	98	100	39.56	10.42	12.35	16.08	17.14
96	342	1408	C	7	H	2	no	58	60	39.75	4.93		4.31	
20	342	1406	B	28	X	5	no	1.5	3	39.92	4.50	4.67	23.29	
34	342	1408	B	8	H	1	no	120	121.5	39.85	8.95		5.25	
83	342	1408	B	8	H	4	no	28	30	39.95	10.13		14.47	
35	342	1408	B	8	H	4	no	106.5	108	39.97	9.89		21.59	
59	342	1410	B	10	H	5	no	117	118.5	40.14	8.44		14.76	
98	342	1408	C	9	H	2	no	98	100	40.49	5.95		19.94	
76+77	342	1408	A	8	H	2	no	117	118	40.38	8.77		21.77	
30	342	1408	A	8	H	3	no	69	71	40.41	15.30	16.05	29.91	
51	342	1410	A	11	H	1	no	97	98.5	41.09	3.96	2.92	9.41	
53	342	1410	A	11	H	5	no	129.5	131	41.31	1.85		5.89	6.20
54	342	1410	A	12	H	2	no	64	65.5	41.58	1.34		3.33	3.66
48	342	1408	C	11	H	5	no	137	139	41.45	1.36		4.45	3.21
61	342	1410	B	14	H	2	no	79	80.5	41.83	20.91		12.12	
62	342	1410	B	14	H	3	no	92.5	94	41.94	2.01		5.18	
49	342	1408	C	13	H	1	no	142	144	42.10	6.64		10.16	
78	342	1408	A	13	H	1	no	140	142	43.00	3.09		7.99	
114	342	1410	A	15	H	7	no	49.5	51	43.25	8.98		6.68	
115	342	1410	A	16	H	4	no	120	121.5	43.50	6.50	5.26	12.58	
116	342	1410	A	17	X	1	no	2	3.5	43.75	5.76		16.98	
117	342	1410	A	17	X	4	no	56	57.5	44.00	10.27		8.42	
118	342	1410	A	18	X	1	no	67	68.5	44.25	1.86		8.19	8.58
119	342	1410	A	18	X	4	no	122	123.5	44.50	1.51		5.43	
120	342	1410	A	19	X	1	no	114	115.5	44.75	6.81		14.78	14.20
121	342	1410	A	19	X	5	no	18	19.5	45.00	6.65		3.80	



Supplementary Figure 2: Fragmentation across samples from Expedition 342 at both size fractions. Symbols indicate site, whilst color indicates size fraction.

1.1 Data preparation and processing

Here we will show how we processed our data from raw abundance plots to data sets suitable for Hill number analysis. We only present the process for genera here for simplicity but morphogroup and ecogroup data sets were prepared in the same manner. Firstly, we import the data selecting only one sheet from the data set provided, the first two lines are skipped to remove surplus information then only the column containing abundance counts:*Turborotalita* to *Orbulinoides.* We then select only rows 1 to 33 so that any blank space in the datasheet is removed.

We then create a function so that all abundance data is transformed into the structure needed to Hill number analysis with the code provided in Chao and Jost (2015) (Appendix S8 of Chao and Jost (2015)). The data we import is structured so that each column is a genera whilst each row is a sample. The function transforms this in the following steps:

STEP 1. Transposes the data so that each column is now sample and each row is the genera STEP 2. Removes all row names STEP 3. Reorders each column into ascending order. For this analysis the name of genera does not matter, the analysis is based purely on counts STEP 4. Creates a dataframe fo easy export

We then run the function on the data frame and we recommend saving the restructured data as a separate .csv file for future reference.

```
genus_63 <- read_excel("Data/Final_Abundance.xlsx", sheet = "Genus_>63_abs", skip = 2) %>%
  select(Turborotalita:Orbulinoides) %>%
  slice(1:33) # 18 Columns
```

```
structure_chao <- function(x) {
  x1 <- t(x)
  rownames(x1) <- c()
  ordered <- apply(x1, 2, sort)
  data.frame(ordered)
}

genus_63_chao <- structure_chao(genus_63)
write_csv(genus_63_chao, "Data/genus_180_chao.csv") # This is for illustration only.
```

Using this data we can then calculate Hill numbers using the code of Chao and Jost (2015) (as shown Appendix S8 Chao and Jost (2015)). You will need to download the code and run it once for the following code to work, without it the following lines of code will not work. If you are not interested in the process of calculating Hill numbers and are instead looking for the statistical analysis presented in the manuscript we recommend you skip to Section 2. As before we only show the process for genera but all data can be processing in the same manner. The data we provide (Supplementary Data 1) contains the combined calculated hill numbers generated following these steps, you do not need to do the following steps if you want replicate our statistical analysis, this is shown for transparency.

- STEP 1 - Read in data and source and the analysis script
- STEP 2 - Create a variable of sample ages
- STEP 3 - Transform the restructured data set into a matrix
- STEP 4 - Create a variable of n which should equal the number of columns in your matrix (i.e the number of samples)
- STEP 5 - Create empty matrix's to put the calculated hill numbers into. The number of rows assumes you're outputting the default Hill numbers from 0 to 3 in steps of 0.1.

```
# STEP 1
source("Scripts/Chao_2014_Script.R")


# Create a variable of age
age <- read_excel("Data/Final_Abundance.xlsx", sheet = "Genus_>63_abs", skip = 2) %>%
  select(Age_2021) %>%
  slice(1:33)

# STEP 2
Age <- signif(age$Age_2021, digits = 4)

# STEP 3
genus_63_chao <- as.matrix(genus_63_chao)

# STEP 4
## Set the number of columns - this will be the number of samples you want to analyse
### (Should be the same as the number of rows in imported data set)
n <- 33 # Number of columns

# STEP5
# Create matrix for the output
# 31 assumes you're outputting the default Hill numbers from 0 to 3 in steps of 0.1
# est = hill number calculated EMPERICAL
# lci = lower confidence interval
# uci = upper confidence interval
# sd = standard deviation ?
# With P e.g estP this is the proposed data using the Chao Estimator
est <- matrix(0, nrow = 31, ncol = n)
lci <- matrix(0, nrow = 31, ncol = n)
uci <- matrix(0, nrow = 31, ncol = n)
sd <- matrix(0, nrow = 31, ncol = n)
estP <- matrix(0, nrow = 31, ncol = n)
lciP <- matrix(0, nrow = 31, ncol = n)
uciP <- matrix(0, nrow = 31, ncol = n)
sdP <- matrix(0, nrow = 31, ncol = n)
```

- STEP 6 - Calculate Hill numbers. **WARNING** this calculation will take a long time !

```
# STEP 6 - WARNING this calculation will take a long time !
## Time code
ptm <- proc.time()
# Loop to calculate the above for each sample and extract the calculated values
for (i in 1:n)
{
  cat(i, "\n")
  tmp <- genus_63_chao[, i]
  mych <- ChaoHill(tmp, "abundance")
  est[, i] <- as.numeric(mych$EST[1, ])
  lci[, i] <- as.numeric(mych$LCI[1, ])
  uci[, i] <- as.numeric(mych$UCI[1, ])
  sd[, i] <- as.numeric(mych$SD[1, ])
  estP[, i] <- as.numeric(mych$EST[2, ])
```

```r
  lciP[, i] <- as.numeric(mych$LCI[2, ])
  uciP[, i] <- as.numeric(mych$UCI[2, ])
  sdP[, i] <- as.numeric(mych$SD[2, ])
}
## Stop the Clock
proc.time() - ptm
```

- STEP 7 - Extract information from the matrix's and create a dataframe including sample age, this extracts empirical and predicted values. For the manuscript we only use empirical values.
- STEP 8 - Save your data frames as a .csv.

```r
# STEP 7
## EXTRACTING VALUES##
# Reformat empirical values into a data frame
chaolist <- list(est, uci, lci, sd)

df_reform <- lapply(chaolist, function(x) {
  x1 <- data.frame(x)
  names(x1) <- Age
  x1$Q <- seq(0, 3, 0.1)
  x1 %>% gather(Age, Hill, "38":"45", factor_key = TRUE)
})

emp_est <- df_reform[[1]]
emp_uci <- df_reform[[2]] %>% rename(UCI = Hill)
emp_lci <- df_reform[[3]] %>% rename(LCI = Hill)
emp_sd <- df_reform[[4]] %>% rename(SD = Hill)


emp_full <- list(emp_est, emp_uci, emp_lci, emp_sd) %>% reduce(left_join, by = c("Q", "Age"))


## PROPOSED##
chaolistP <- list(estP, uciP, lciP, sdP)

df_reformP <- lapply(chaolistP, function(x) {
  x1 <- data.frame(x)
  names(x1) <- Age
  x1$Q <- seq(0, 3, 0.1)
  x1 %>% gather(Age, Hill, "38":"45", factor_key = TRUE)
})

pred_est <- df_reform[[1]]
pred_uci <- df_reform[[2]] %>% rename(UCI = Hill)
pred_lci <- df_reform[[3]] %>% rename(LCI = Hill)
pred_sd <- df_reform[[4]] %>% rename(SD = Hill)


pred_full <- list(pred_est, pred_uci, pred_lci, pred_sd) %>%
  reduce(left_join, by = c("Q", "Age"))

# STEP 8
```

```
write_csv(pred_full, "Data/genus_63_Hill_predicted.csv")
write_csv(emp_full, "Data/genus_63_Hill_emperical.csv")
```

2 Generalized additive models (GAMs)

```r
full <- read_csv("Data/Hill_Emperical_All_Frag_2021.csv") %>%
  rename(frag = `Fragmentation %`)
Age <- full$Age
full$size <- as.factor(full$size)
```

```r
shan <- function(x) {
  conv <- log(x)
  return(conv)
}
```

```r
simps <- function(x) {
  conv <- (x - 1) / x
  return(conv)
}
```

Supplementary Table 13: AICc Comparison between models of genera richness

		df	AIC	ΔAIC	AICweight	ΔAICc
Genera	s(Age, by = size) + size + Frag	15.00	260.22	269.81	9.988117e-01	0.00
Genera	s(Age)	4.52	283.18	284.00	8.276721e-04	14.19
Genera	s(Age) + Frag	5.56	284.74	285.97	3.101523e-04	16.15
Genera	s(Age, by = size) + Frag	7.57	287.34	289.60	5.044274e-05	19.79

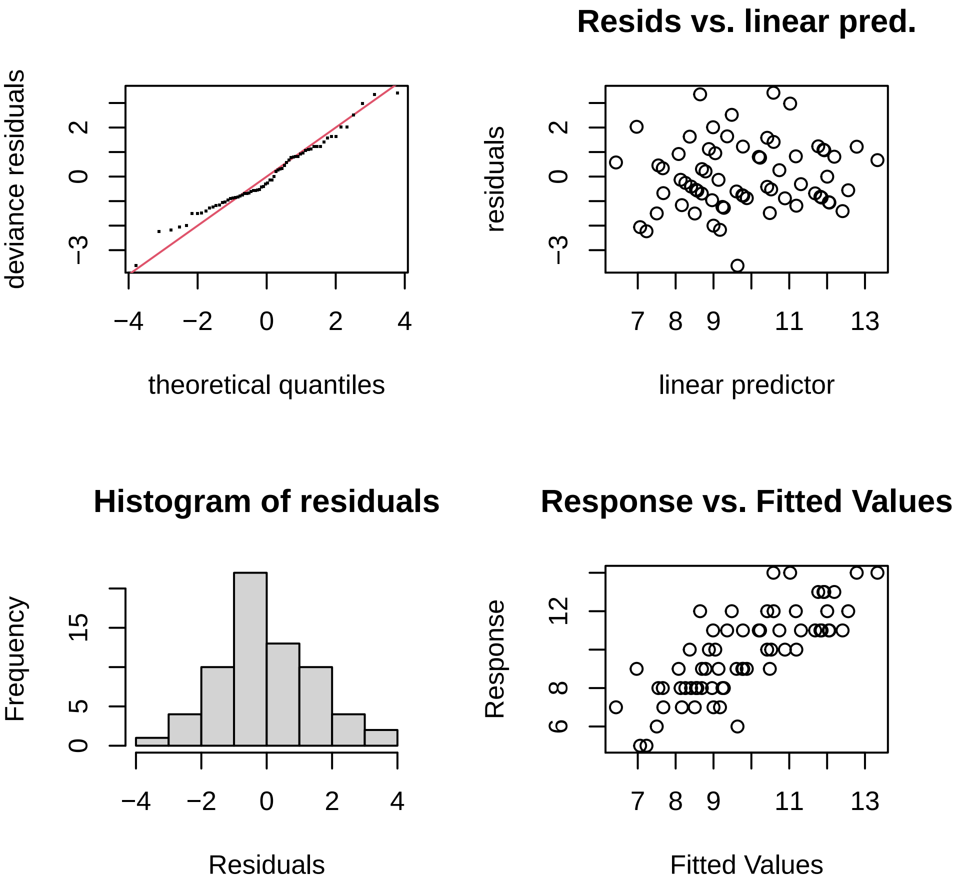
2.1 Genera

2.1.1 Richness

```
gh_0null <- gam(Genus_Hill ~ s(Age, k = 11), data = full %>% filter(Q == 0))
gh0_0 <- gam(Genus_Hill ~ s(Age, k = 11) + frag, data = full %>% filter(Q == 0))
gh1_0 <- update(gh0_0, Genus_Hill ~ s(Age, k = 11, by = size) + size + frag)
gh2_0 <- update(gh0_0, Genus_Hill ~ s(Age, k = 11, by = size) + frag)
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 6 iterations.
## The RMS GCV score gradient at convergence was 2.165044e-05 .
## The Hessian was positive definite.
## Model rank =  23 / 23
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                  k'  edf k-index p-value
## s(Age):size63  10.0  8.6    0.88    0.13
## s(Age):size180 10.0  2.4    0.88    0.14
```

```
## null device
##           1
```



Supplementary Figure 3: Diagnostic plots for best fitting GAM for genera richness

Supplementary Table 14: AICc Comparison between models of genera Shannon’s index

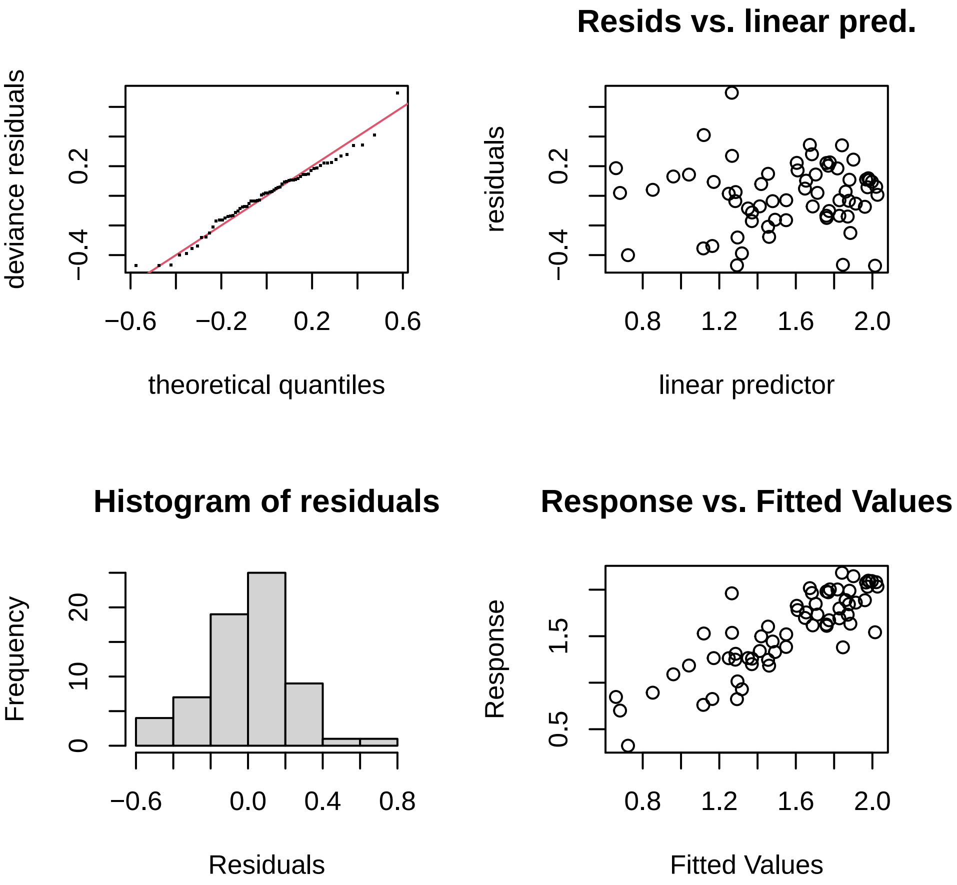
		df	AIC	ΔAIC	AICweight	ΔAICc
Genera	s(Age, by = size) + size + Frag	9.20	7.00	10.36	1.000000e+00	0.00
Genera	s(Age) + Frag	5.65	56.53	57.80	5.005720e-11	47.44
Genera	s(Age, by = size) + Frag	7.56	59.49	61.74	6.970436e-12	51.38
Genera	s(Age)	4.44	262.97	263.77	9.384318e-56	253.41

2.1.2 Shannon’s index

```r
gh_1null <- gam(Genus_Hill ~ s(Age, k = 7), data = full %>% filter(Q == 1))
gh0_1 <- update(gh0_0, shan(Genus_Hill) ~ s(Age, k = 7) + frag, data = full %>% filter(Q == 1))
gh1_1 <- update(gh0_1, shan(Genus_Hill) ~ s(Age, k = 7, by = size) + size + frag)
gh2_1 <- update(gh0_1, shan(Genus_Hill) ~ s(Age, k = 7, by = size) + frag)
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 6 iterations.
## The RMS GCV score gradient at convergence was 9.868576e-07 .
## The Hessian was positive definite.
## Model rank =  15 / 15
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(Age):size63   6.00 2.18    1.07    0.77
## s(Age):size180 6.00 3.02    1.07    0.68
```

```
## null device
##           1
```



Supplementary Figure 4: Diagnostoc plots for best fitting GAM for genera Shannon's index

Supplementary Table 15: AICc Comparison between models of genera Simpson's index

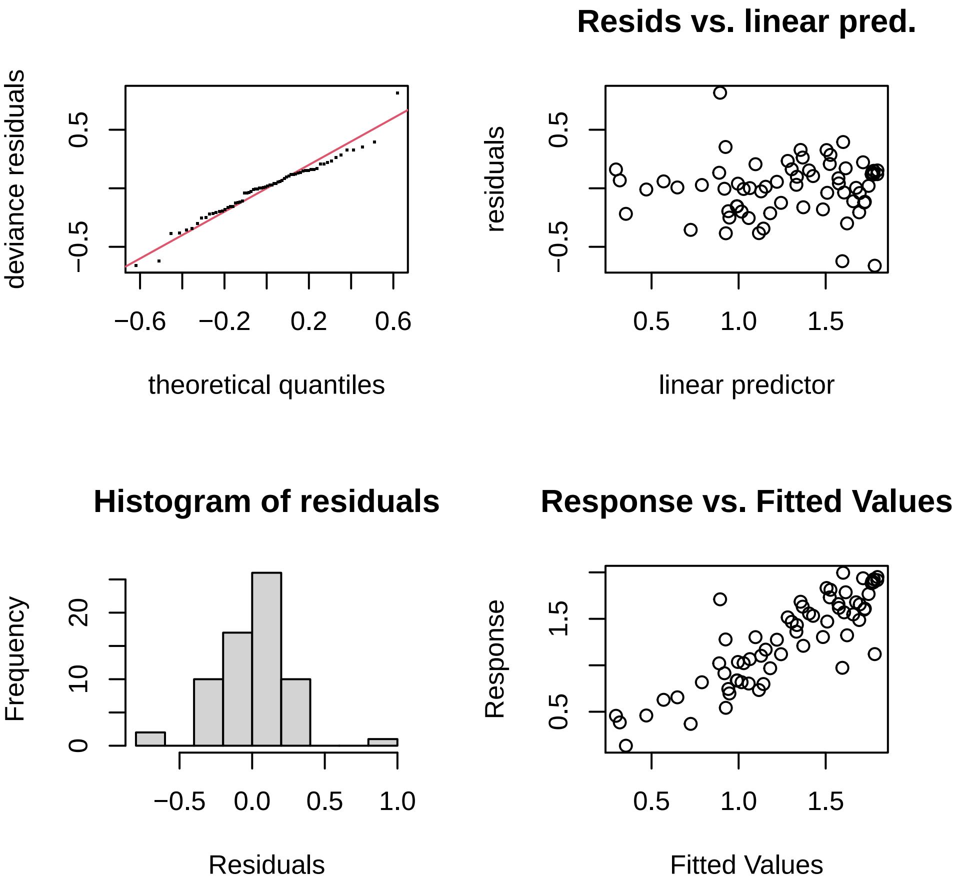
		df	AIC	ΔAIC	AICweight	ΔAICc
Genera	s(Age, by = size) + size + Frag	9.55	16.88	20.51	1.000000e+00	0.00
Genera	s(Age) + Frag	5.53	71.57	72.78	4.469471e-12	52.27
Genera	s(Age, by = size) + Frag	7.46	75.10	77.29	4.687029e-13	56.78
Genera	s(Age)	4.27	249.66	250.40	1.202466e-50	229.89

2.1.3 Simpson's index

```
gh_2null <- gam(Genus_Hill ~ s(Age, k = 7), data = full %>% filter(Q == 2))
gh0_2 <- update(gh0_0, shan(Genus_Hill) ~ s(Age, k = 7) + frag, data = full %>% filter(Q == 2))
gh1_2 <- update(gh0_2, shan(Genus_Hill) ~ s(Age, k = 7, by = size) + size + frag)
gh2_2 <- update(gh0_2, shan(Genus_Hill) ~ s(Age, k = 7, by = size) + frag)
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 5 iterations.
## The RMS GCV score gradient at convergence was 5.013104e-06 .
## The Hessian was positive definite.
## Model rank =  15 / 15
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(Age):size63  6.00 2.20    1.15    0.84
## s(Age):size180 6.00 3.35    1.15    0.84
```

```
## null device
##           1
```



Supplementary Figure 5: Diagnostoc plots for best fitting GAM for genera Simpson's index

```
gh1_0_para <- summary(gh1_0)$p.table
gh1_1_para <- summary(gh1_1)$p.table
gh1_2_para <- summary(gh1_2)$p.table
genera_para <- rbind(gh1_0_para, gh1_1_para, gh1_2_para)
genera_para <- data.frame(genera_para)
genera_para$q <- c("0", "0", "0", "1", "1", "1", "2", "2", "2")
genera_para$model <- c("Genera ~ s(Age, by = size) + size + Frag")
genera_para$Parametric_Coefficient <- rep(c("Intercept", "Size:180", "Fragmentation"),
  times = 3
)
genera_para <- genera_para[, c(6, 5, 7, 1, 2, 3, 4)]
row.names(genera_para) <- NULL
genera_para$Pr...t.. <- round(genera_para$Pr...t.., digits = 2)
genera_para$Estimate <- round(genera_para$Estimate, digits = 2)
genera_para$Std..Error <- round(genera_para$Std..Error, digits = 2)
genera_para$t.value <- round(genera_para$t.value, digits = 2)
```

```
gh1_0_smooth <- summary(gh1_0)$s.table
gh1_1_smooth <- summary(gh1_1)$s.table
gh1_2_smooth <- summary(gh1_2)$s.table
genera_smooth <- rbind(gh1_0_smooth, gh1_1_smooth, gh1_2_smooth)
genera_smooth <- data.frame(genera_smooth)
genera_smooth$q <- c("0", "0", "1", "1", "2", "2")
```

```
genera_smooth$model <- c("Genera ~ s(Age, by =size) +size + Frag")
genera_smooth$Smooth_term <- rep(c("s(Age):Size=63", "s(Age):Size=180"), times = 3)
genera_smooth <- genera_smooth[, c(6, 5, 7, 1, 3, 4)]
row.names(genera_smooth) <- NULL
genera_smooth$p.value <- round(genera_smooth$p.value, digits = 2)
genera_smooth$edf <- round(genera_smooth$edf, digits = 2)
genera_smooth$F <- round(genera_smooth$F, digits = 2)
```

Supplementary Table 16: AICc Comparison between models of morphogroup richness

		df	AIC	ΔAIC	AICweight	ΔAICc
Morphogroup	s(Age, by = size) + size + Frag	14.64	194.25	203.35	9.999427e-01	0.00
Morphogroup	s(Age) + Frag	9.73	220.21	223.98	3.298426e-05	20.64
Morphogroup	s(Age)	4.38	224.30	225.07	1.912761e-05	21.73
Morphogroup	s(Age, by = size) + Frag	7.36	225.56	227.70	5.153883e-06	24.35

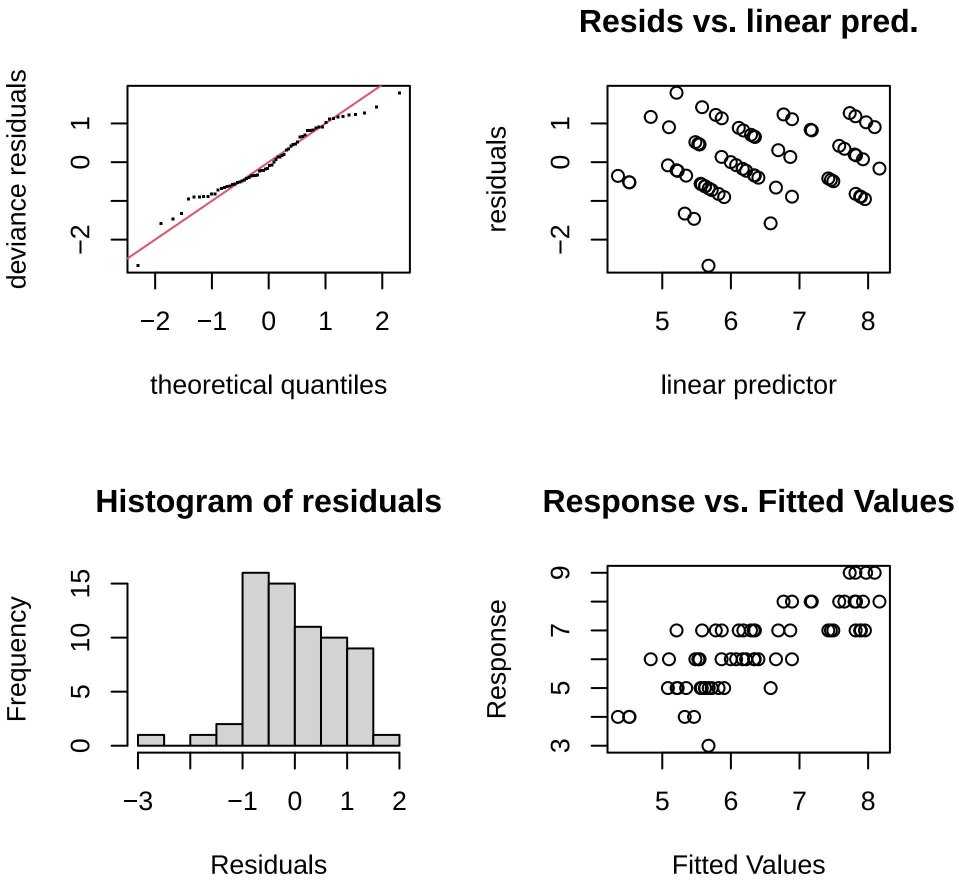
2.2 Morphogroup

2.2.1 Richness

```
mh_0null <- gam(Morph_Hill ~ s(Age, k = 20), data = full %>% filter(Q == 0))
mh0_0 <- gam(Morph_Hill ~ s(Age, k = 20) + frag, data = full %>% filter(Q == 0))
mh1_0 <- update(mh0_0, Morph_Hill ~ s(Age, k = 20, by = size) + size + frag)
mh2_0 <- update(mh0_0, Morph_Hill ~ s(Age, k = 20, by = size) + frag)
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 7 iterations.
## The RMS GCV score gradient at convergence was 5.71158e-05 .
## The Hessian was positive definite.
## Model rank =  41 / 41
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                    k'   edf k-index p-value
## s(Age):size63  19.00  8.26    0.97    0.34
## s(Age):size180 19.00  2.38    0.97    0.35
```

```
## null device
##           1
```



Supplementary Figure 6: Diagnostoc plots for best fitting GAM for morphological richness

Supplementary Table 17: AICc Comparison between models of morphogroup Shannon's index

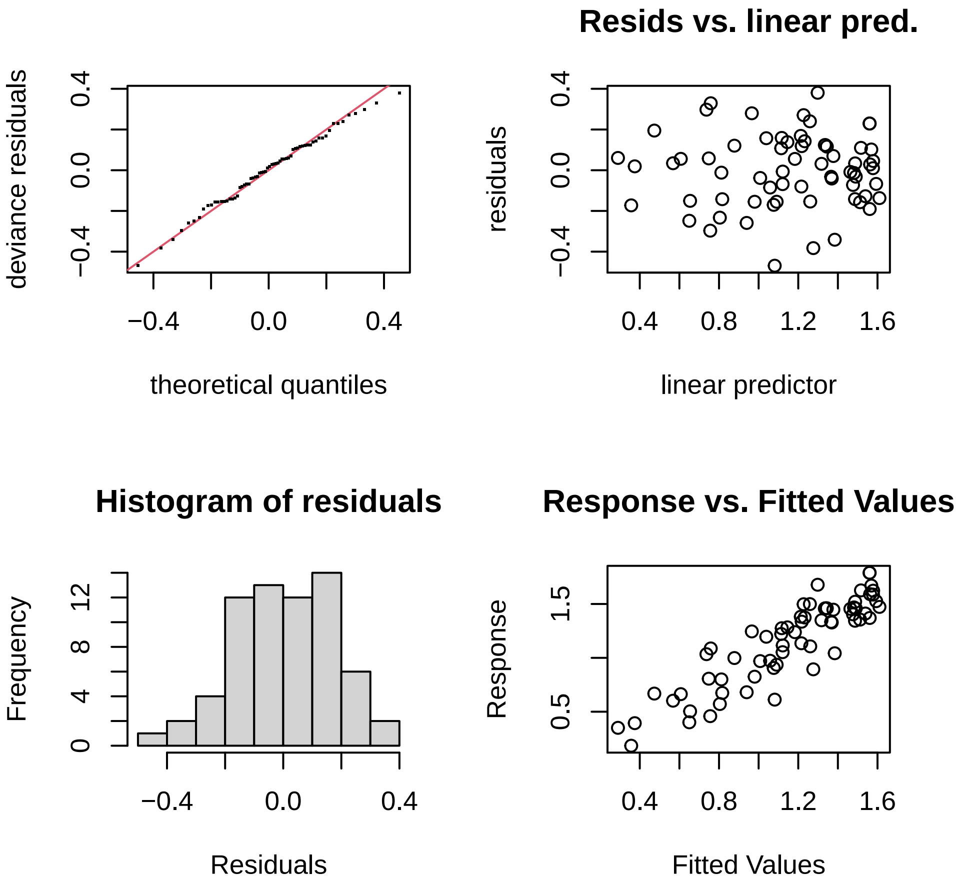
		df	AIC	ΔAIC	AICweight	ΔAICc
Morphogroup	s(Age, by = size) + size + Frag	9.09	-24.63	-21.35	1.000000e+00	0.00
Morphogroup	s(Age) + Frag	5.40	48.84	50.00	3.222099e-16	71.34
Morphogroup	s(Age, by = size) + Frag	6.87	51.18	53.03	7.050141e-17	74.38
Morphogroup	s(Age)	4.16	201.85	202.56	2.395645e-49	223.91

2.2.2 Shannon's index

```
mh_1null <- gam(Morph_Hill ~ s(Age, k = 8), data = full %>% filter(Q == 1))
mh0_1 <- update(mh0_0, shan(Morph_Hill) ~ s(Age, k = 8) + frag, data = full %>%
  filter(Q == 1))
mh1_1 <- update(mh1_0, shan(Morph_Hill) ~ s(Age, k = 8, by = size) + size + frag, data = full %>%
  filter(Q == 1))
mh2_1 <- update(mh2_0, shan(Morph_Hill) ~ s(Age, k = 8, by = size) + frag, data = full %>%
  filter(Q == 1))
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 5 iterations.
## The RMS GCV score gradient at convergence was 1.076856e-06 .
## The Hessian was positive definite.
## Model rank =  17 / 17
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(Age):size63  7.00 1.62    1.13    0.83
## s(Age):size180 7.00 3.47    1.13    0.82
```

```
## null device
##           1
```



Supplementary Figure 7: Diagnostoc plots for best fitting GAM for morphogroup Shannon's index

Supplementary Table 18: AICc Comparison between models of morphogroup Simpson's index

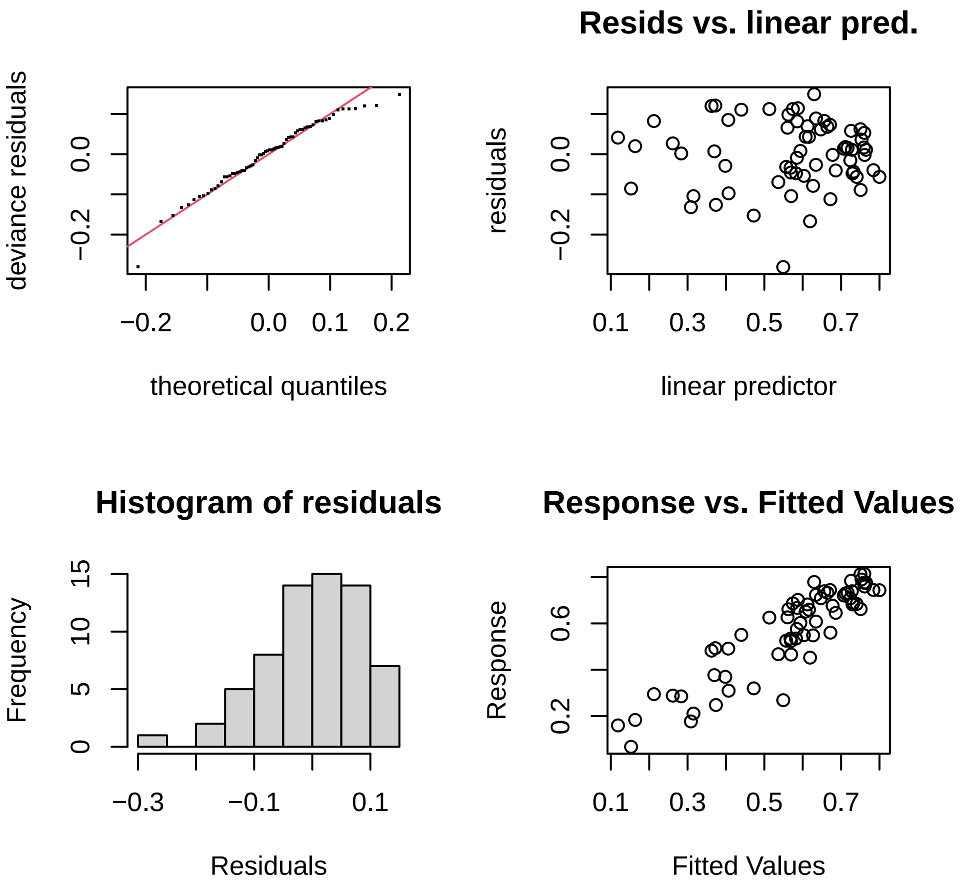
		df	AIC	ΔAIC	AICweight	ΔAICc
Morphogroup	s(Age, by = size) + size + Frag	8.70	-124.93	-121.93	1.000000e+00	0.00
Morphogroup	s(Age) + Frag	5.22	-49.04	-47.96	8.653347e-17	73.97
Morphogroup	s(Age, by = size) + Frag	6.60	-49.44	-47.73	7.709662e-17	74.20
Morphogroup	s(Age)	3.77	192.83	193.42	3.342410e-69	315.34

2.2.3 Simpson's index

```
mh_2null <- gam(Morph_Hill ~ s(Age, k = 10), data = full %>% filter(Q == 2))
mh0_2 <- update(mh0_0, simps(Morph_Hill) ~ s(Age, k = 10) + frag, data = full %>%
  filter(Q == 2))
mh1_2 <- update(mh1_0, simps(Morph_Hill) ~ s(Age, k = 10, by = size) + size + frag, data = full %>%
  filter(Q == 2))
mh2_2 <- update(mh2_0, simps(Morph_Hill) ~ s(Age, k = 10, by = size) + frag, data = full %>%
  filter(Q == 2))
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 4 iterations.
## The RMS GCV score gradient at convergence was 2.679448e-06 .
## The Hessian was not positive definite.
## Model rank =  21 / 21
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(Age):size63  9.00 1.06    1.15    0.86
## s(Age):size180 9.00 3.64    1.15    0.89
```

```
## null device
##           1
```



Supplementary Figure 8: Diagnostoc plots for best fitting GAM for morphogroup Shannon's index

```
mh1_0_para <- summary(mh1_0)$p.table
mh1_1_para <- summary(mh1_1)$p.table
mh1_2_para <- summary(mh1_2)$p.table
morph_para <- rbind(mh1_0_para, mh1_1_para, mh1_2_para)
morph_para <- data.frame(morph_para)
morph_para$q <- c("0", "0", "0", "1", "1", "1", "2", "2", "2")
morph_para$model <- c("Morphogroup ~ s(Age, by = size) + size + Frag")
morph_para$Parametric_Coefficient <- rep(c("Intercept", "Size:180", "Fragmentation"),
  times = 3
)
morph_para <- morph_para[, c(6, 5, 7, 1, 2, 3, 4)]
row.names(morph_para) <- NULL
morph_para$Pr...t.. <- round(morph_para$Pr...t.., digits = 2)
morph_para$Estimate <- round(morph_para$Estimate, digits = 2)
morph_para$Std..Error <- round(morph_para$Std..Error, digits = 2)
morph_para$t.value <- round(morph_para$t.value, digits = 2)
```

```
mh1_0_smooth <- summary(mh1_0)$s.table
mh1_1_smooth <- summary(mh1_1)$s.table
mh1_2_smooth <- summary(mh1_2)$s.table
morph_smooth <- rbind(mh1_0_smooth, mh1_1_smooth, mh1_2_smooth)
morph_smooth <- data.frame(morph_smooth)
morph_smooth$q <- c("0", "0", "1", "1", "2", "2")
```

Supplementary Table 19: Parametric coefficients for best fitting GAM models based on AIC difference compared to next best fitting model being more than 2

Model	*q*	Parametric Coefficient	Estimate	Std. Error	t.value	*p*
Genera s(Age, by = size) + size + Frag	0	Intercept	12.40	0.63	19.80	0.00
Genera s(Age, by = size) + size + Frag	0	Size:180	-2.64	0.46	-5.75	0.00
Genera s(Age, by = size) + size + Frag	0	Fragmentation	-0.12	0.04	-2.91	0.01
Genera s(Age, by = size) + size + Frag	1	Intercept	1.93	0.08	23.56	0.00
Genera s(Age, by = size) + size + Frag	1	Size:180	-0.58	0.07	-8.75	0.00
Genera s(Age, by = size) + size + Frag	1	Fragmentation	-0.01	0.01	-1.40	0.17
Genera s(Age, by = size) + size + Frag	2	Intercept	1.68	0.09	19.09	0.00
Genera s(Age, by = size) + size + Frag	2	Size:180	-0.67	0.07	-9.42	0.00
Genera s(Age, by = size) + size + Frag	2	Fragmentation	-0.01	0.01	-1.20	0.23
Morphogroup s(Age, by = size) + size + Frag	0	Intercept	7.49	0.37	20.04	0.00
Morphogroup s(Age, by = size) + size + Frag	0	Size:180	-1.73	0.28	-6.23	0.00
Morphogroup s(Age, by = size) + size + Frag	0	Fragmentation	-0.03	0.03	-1.02	0.31
Morphogroup s(Age, by = size) + size + Frag	1	Intercept	1.57	0.06	24.56	0.00
Morphogroup s(Age, by = size) + size + Frag	1	Size:180	-0.61	0.05	-11.61	0.00
Morphogroup s(Age, by = size) + size + Frag	1	Fragmentation	-0.01	0.00	-2.74	0.01
Morphogroup s(Age, by = size) + size + Frag	2	Intercept	0.77	0.03	25.96	0.00
Morphogroup s(Age, by = size) + size + Frag	2	Size:180	-0.28	0.02	-11.62	0.00
Morphogroup s(Age, by = size) + size + Frag	2	Fragmentation	-0.01	0.00	-3.07	0.00

```r
morph_smooth$model <- c("Morphogroup ~ s(Age, by = size) + size + Frag")
morph_smooth$Smooth_term <- rep(c("s(Age):Size = 63", "s(Age):Size = 180"), times = 3)
morph_smooth <- morph_smooth[, c(6, 5, 7, 1, 3, 4)]
row.names(morph_smooth) <- NULL
morph_smooth$p.value <- round(morph_smooth$p.value, digits = 2)
morph_smooth$edf <- round(morph_smooth$edf, digits = 2)
morph_smooth$F <- round(morph_smooth$F, digits = 2)
```

```r
para_tab <- rbind(genera_para, morph_para)
kbl(para_tab,
  col.names = c(
    "Model", "\\textit{q}", "Parametric Coefficient",
    "Estimate", "Std. Error", "t.value",
    "\\textit{p}"
  ),
  escape = FALSE, caption = "Parametric coefficients for best fitting GAM models based on
    AIC difference compared to next best fitting model being more than 2"
) %>%
  kable_styling(latex_options = "scale_down")
```

```r
smooth_tab <- rbind(genera_smooth, morph_smooth)
kbl(smooth_tab,
  col.names = c(
    "Model", "\\textit{q}", "Smooth Term", "Estimated d.f",
    "F statistics", "\\textit{p}"
  ),
  escape = FALSE,
  caption = "Smooth terms for best fitting GAM models"
)
```

Supplementary Table 20: Smooth terms for best fitting GAM models

Model	q	Smooth Term	Estimated d.f	F statistics	p
Genera s(Age, by =size) +size + Frag	0	s(Age):Size=63	8.60	3.18	0.00
Genera s(Age, by =size) +size + Frag	0	s(Age):Size=180	2.40	3.80	0.01
Genera s(Age, by =size) +size + Frag	1	s(Age):Size=63	2.18	2.78	0.05
Genera s(Age, by =size) +size + Frag	1	s(Age):Size=180	3.02	11.68	0.00
Genera s(Age, by =size) +size + Frag	2	s(Age):Size=63	2.20	3.73	0.02
Genera s(Age, by =size) +size + Frag	2	s(Age):Size=180	3.35	10.34	0.00
Morphogroup s(Age, by = size) + size + Frag	0	s(Age):Size = 63	8.26	2.16	0.03
Morphogroup s(Age, by = size) + size + Frag	0	s(Age):Size = 180	2.38	3.08	0.03
Morphogroup s(Age, by = size) + size + Frag	1	s(Age):Size = 63	1.62	2.28	0.11
Morphogroup s(Age, by = size) + size + Frag	1	s(Age):Size = 180	3.47	13.68	0.00
Morphogroup s(Age, by = size) + size + Frag	2	s(Age):Size = 63	1.06	2.23	0.12
Morphogroup s(Age, by = size) + size + Frag	2	s(Age):Size = 180	3.64	17.96	0.00

Supplementary Table 21: AICc Comparison between models of depth habitat richness

	df	AIC	ΔAIC	AICweight	ΔAICc
Depth Habitat s(Age, by = size) + Frag	7.40	-93.38	-91.22	0.5645456	0.00
Depth Habitat s(Age, by = size) + size + Frag	8.42	-92.76	-89.96	0.2993750	1.27
Depth Habitat s(Age)	3.97	-88.48	-87.83	0.1034386	3.39
Depth Habitat s(Age) + Frag	4.94	-86.50	-85.52	0.0326408	5.70

2.3 Depth Habitat

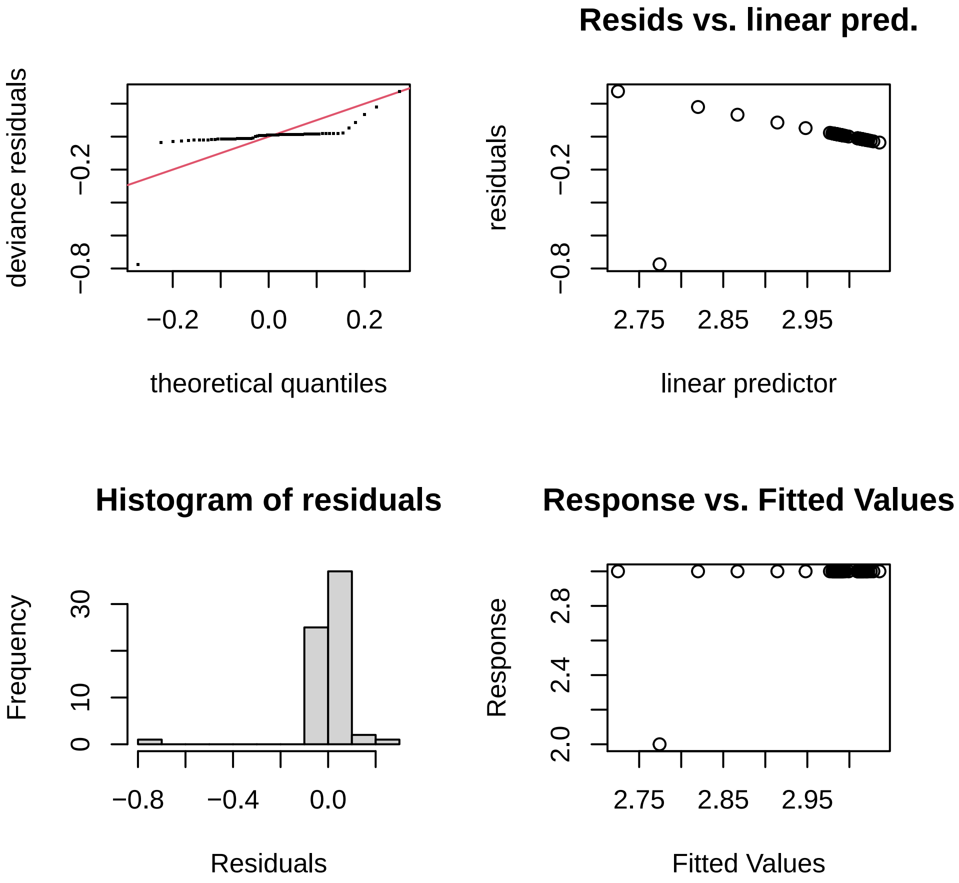
These results are not discussed in the manuscript but are included here for completeness.

2.3.1 Richness

```
eh_0null <- gam(Eco_Hill ~ s(Age), data = full %>% filter(Q == 0))
eh0_0 <- gam(Eco_Hill ~ s(Age) + frag, data = full %>% filter(Q == 0))
eh1_0 <- update(eh0_0, Eco_Hill ~ s(Age, by = size) + size + frag)
eh2_0 <- update(eh0_0, Eco_Hill ~ s(Age, by = size) + frag)
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 9 iterations.
## The RMS GCV score gradient at convergence was 8.004899e-08 .
## The Hessian was positive definite.
## Model rank =  20 / 20
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k' edf k-index p-value
## s(Age):size63  9.0 1.0    1.03    0.73
## s(Age):size180 9.0 3.4    1.03    0.68
```

```
## null device
##           1
```



Supplementary Figure 9: Diagnostoc plots for best fitting GAM for depth habitat richness

Supplementary Table 22: AICc Comparison between models of depth habitat Shannon's index

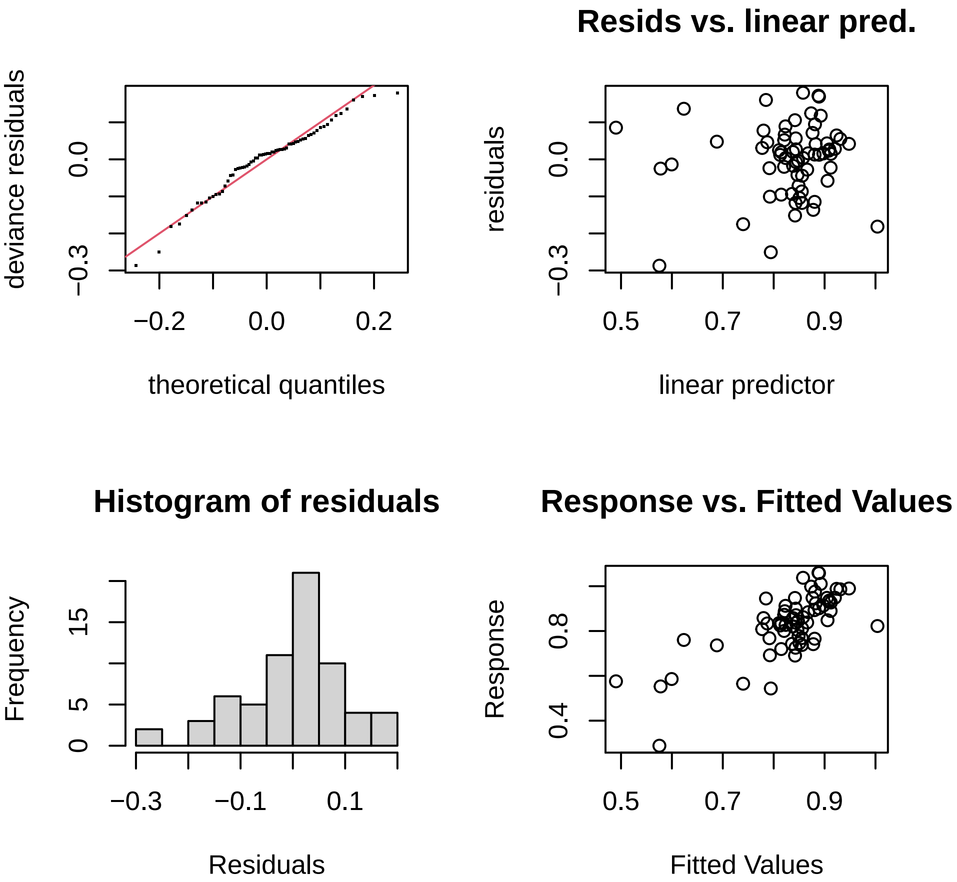
		df	AIC	ΔAIC	AICweight	ΔAICc
Depth Habitat	s(Age, by = size) + Frag	7.59	-108.01	-105.74	7.843871e-01	0.00
Depth Habitat	s(Age, by = size) + size + Frag	8.54	-106.01	-103.12	2.118117e-01	2.62
Depth Habitat	s(Age) + Frag	6.21	-96.60	-95.08	3.801111e-03	10.66
Depth Habitat	s(Age)	5.05	13.93	14.95	4.859187e-27	120.69

2.3.2 Shannon's index

```
eh_1null <- gam(Eco_Hill ~ s(Age), data = full %>% filter(Q == 1))
eh0_1 <- update(eh0_0, shan(Eco_Hill) ~ s(Age) + frag, data = full %>%
  filter(Q == 1))
eh1_1 <- update(eh1_0, shan(Eco_Hill) ~ s(Age, by = size) + size + frag, data = full %>%
  filter(Q == 1))
eh2_1 <- update(eh2_0, shan(Eco_Hill) ~ s(Age, by = size) + frag, data = full %>%
  filter(Q == 1))
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 4 iterations.
## The RMS GCV score gradient at convergence was 5.380348e-07 .
## The Hessian was positive definite.
## Model rank =  20 / 20
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(Age):size63   9.00 1.51    0.97     0.4
## s(Age):size180 9.00 3.08    0.97     0.3
```

```
## null device
##           1
```



Supplementary Figure 10: Diagnostoc plots for best fitting GAM for Depth habitat Shannon's index

Supplementary Table 23: AICc Comparison between models of depth habitat Simpson's index

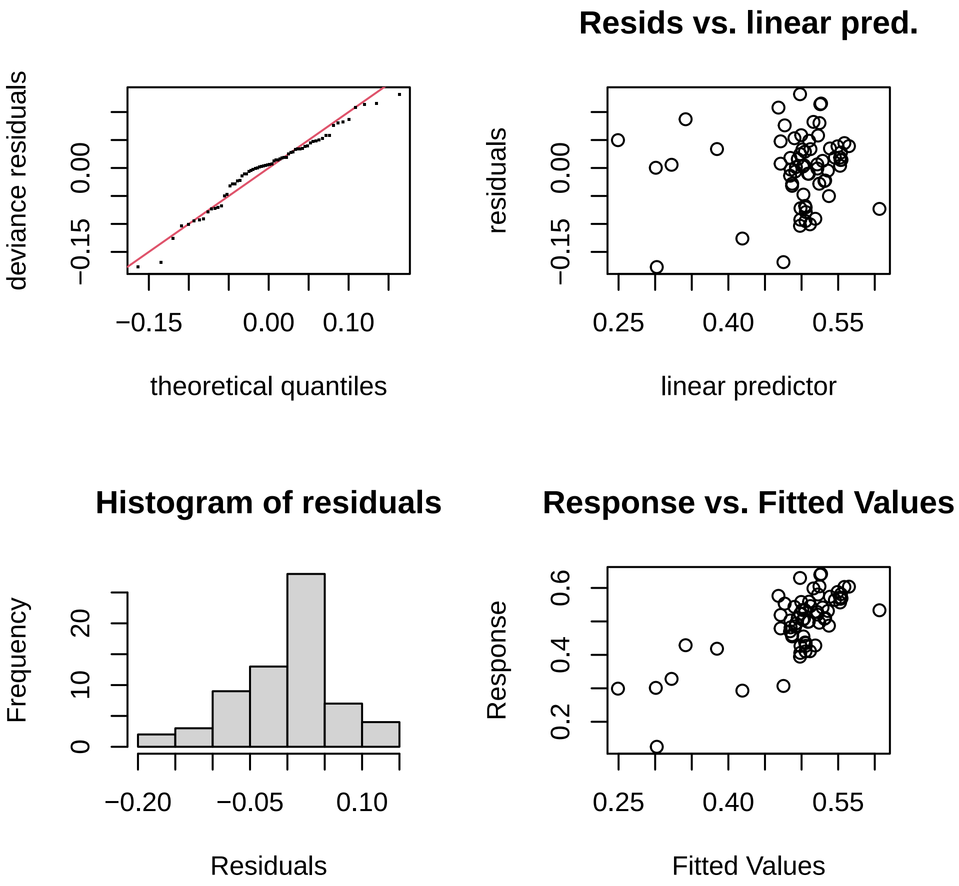
		df	AIC	ΔAIC	AICweight	ΔAICc
Depth Habitat	s(Age, by = size) + Frag	7.52	-160.60	-158.37	7.441301e-01	0.00
Depth Habitat	s(Age, by = size) + size + Frag	8.61	-159.17	-156.23	2.550421e-01	2.14
Depth Habitat	s(Age) + Frag	6.00	-146.19	-144.77	8.277223e-04	13.60
Depth Habitat	s(Age)	4.79	33.54	34.46	9.965258e-43	192.83

2.3.3 Simpson's index

```
eh_2null <- gam(Eco_Hill ~ s(Age), data = full %>% filter(Q == 2))
eh0_2 <- update(eh0_0, simps(Eco_Hill) ~ s(Age) + frag, data = full %>%
  filter(Q == 2))
eh1_2 <- update(eh1_0, simps(Eco_Hill) ~ s(Age, by = size) + size + frag, data = full %>%
  filter(Q == 2))
eh2_2 <- update(eh2_0, simps(Eco_Hill) ~ s(Age, by = size) + frag, data = full %>%
  filter(Q == 2))
```

```
##
## Method: GCV   Optimizer: magic
## Smoothing parameter selection converged after 4 iterations.
## The RMS GCV score gradient at convergence was 2.928622e-06 .
## The Hessian was positive definite.
## Model rank =  20 / 20
##
## Basis dimension (k) checking results. Low p-value (k-index<1) may
## indicate that k is too low, especially if edf is close to k'.
##
##                   k'  edf k-index p-value
## s(Age):size63  9.00 1.50    1.02    0.58
## s(Age):size180 9.00 3.03    1.02    0.46
```

```
## null device
##           1
```



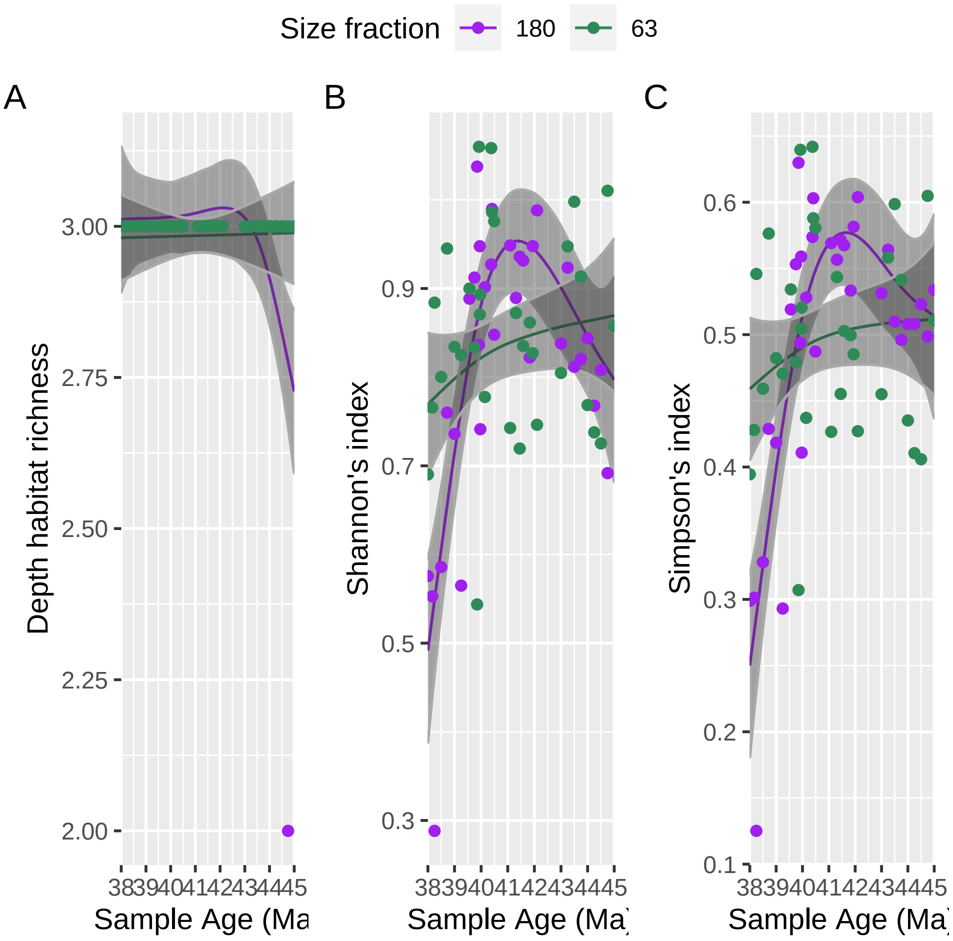
Supplementary Figure 11: Diagnostoc plots for best fitting GAM for Depth habitat Simpson's

2.4 Predicting GAMs

```r
e_0_plot <- ggplot(predicted_eh2_0, aes(Age, fit, group = size)) +
  geom_line(aes(col = size)) +
  geom_ribbon(aes(ymax = upper, ymin = lower), col = "darkgrey", alpha = 0.4) +
  geom_point(data = full %>% filter(Q == 0), aes(Age, Eco_Hill, col = size)) +
  scale_colour_manual(values = c("purple", "seagreen")) +
  scale_x_continuous(expand = c(0, 0), breaks = seq(from = 38, to = 45, by = 1)) +
  labs(x = "Sample Age (Ma)", y = "Depth habitat richness", col = "Size fraction", tag = "A")

e_1_plot <- ggplot(predicted_eh2_1, aes(Age, fit, group = size)) +
  geom_line(aes(col = size)) +
  geom_ribbon(aes(ymax = upper, ymin = lower), col = "darkgrey", alpha = 0.4) +
  geom_point(data = full %>% filter(Q == 1), aes(Age, shan(Eco_Hill), col = size)) +
  scale_colour_manual(values = c("purple", "seagreen")) +
  scale_x_continuous(expand = c(0, 0), breaks = seq(from = 38, to = 45, by = 1)) +
  labs(x = "Sample Age (Ma)", y = "Shannon's index", col = "Size fraction", tag = "B")

e_2_plot <- ggplot(predicted_eh2_2, aes(Age, fit, group = size)) +
  geom_line(aes(col = size)) +
  geom_ribbon(aes(ymax = upper, ymin = lower), col = "darkgrey", alpha = 0.4) +
  geom_point(data = full %>% filter(Q == 2), aes(Age, simps(Eco_Hill), col = size)) +
  scale_colour_manual(values = c("purple", "seagreen")) +
  scale_x_continuous(expand = c(0, 0), breaks = seq(from = 38, to = 45, by = 1)) +
  labs(x = "Sample Age (Ma)", y = "Simpson's index", col = "Size fraction", tag = "C")
```



Supplementary Figure 12: Depth habitat diversity at integers of q. A - Richness, B - Shannon's index, C - Simpsons index

3 Hill Numbers

3.1 Kruskal Test

```r
full <- read_csv("Data/Hill_Emperical_All_Frag_2021.csv")
full$interval <- rep(
  c("postMECO", "MECO", "preMECO", "postMECO", "MECO", "preMECO"),
  c(403, 155, 465, 403, 155, 465)
)
full$interval <- as.factor(full$interval)
```

```r
k1 <- tidy(kruskal.test(Genus_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 63)
))
k2 <- tidy(kruskal.test(Genus_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63)
))
k3 <- tidy(kruskal.test(Genus_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 180)
))
k4 <- tidy(kruskal.test(Genus_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180)
))
k5 <- tidy(kruskal.test(Morph_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 63)
))
k6 <- tidy(kruskal.test(Morph_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63)
))
k7 <- tidy(kruskal.test(Morph_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 180)
))
k8 <- tidy(kruskal.test(Morph_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180)
))
k9 <- tidy(kruskal.test(Eco_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 63)
))
k10 <- tidy(kruskal.test(Eco_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63)
))
k11 <- tidy(kruskal.test(Eco_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 180)
))
k12 <- tidy(kruskal.test(Eco_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180)
))
```

```r
e1 <- kruskal_effsize(
  data = full %>% filter(Q < 1) %>%
    filter(size == 63), Genus_Hill ~ interval, ci = FALSE,
  conf.level = 0.95, ci.type =
```

```
    "perc", nboot = 1000
)

e2 <- kruskal_effsize(
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63),
  Genus_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e3 <- kruskal_effsize(
  data = full %>% filter(Q < 1) %>% filter(size == 180),
  Genus_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e4 <- kruskal_effsize(
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180),
  Genus_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e5 <- kruskal_effsize(
  data = full %>% filter(Q < 1) %>% filter(size == 63),
  Morph_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e6 <- kruskal_effsize(
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63),
  Morph_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e7 <- kruskal_effsize(
  data = full %>% filter(Q < 1) %>% filter(size == 180),
  Morph_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e8 <- kruskal_effsize(
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180),
```

```r
  Morph_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e9 <- kruskal_effsize(
  data = full %>% filter(Q < 1) %>% filter(size == 63),
  Eco_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e10 <- kruskal_effsize(
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63),
  Eco_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e11 <- kruskal_effsize(
  data = full %>% filter(Q < 1) %>% filter(size == 180),
  Eco_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
e12 <- kruskal_effsize(
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180),
  Eco_Hill ~ interval,
  ci = FALSE,
  conf.level = 0.95,
  ci.type = "perc",
  nboot = 1000
)
```

Supplementary Table 24: Results from Kruskal test, bold and italic p values show those models that indicate significant differences between intervals. Effect size was calculated using the eta squared based on the H-statistic (eta2[H]), A large effect size is classified as a value > 0.14, whilst a small effect size is a value < 0.06, with a moderate effect size values in between 0.06 and 0.14

Model formula	Size fraction	q	Z-score	p	Effect Size	Magnitude
Genera Interval	63	<1	55.783	***0.000***	0.1644754	large
Genera Interval	63	1-2	10.647	***0.005***	0.1372551	moderate
Genera Interval	180	<1	21.303	***0.000***	0.0590297	small
Genera Interval	180	1-2	16.472	***0.000***	0.2297179	large
Morphogroup Interval	63	<1	44.825	***0.000***	0.1309620	moderate
Morphogroup Interval	63	1-2	14.146	***0.001***	0.1927881	large
Morphogroup Interval	180	<1	62.655	***0.000***	0.1854895	large
Morphogroup Interval	180	1-2	34.307	***0.000***	0.5128037	large
Depth Habitat Interval	63	<1	6.753	0.034	0.0145352	small
Depth Habitat Interval	63	1-2	2.375	0.305	0.0059556	small
Depth Habitat Interval	180	<1	15.845	***0.000***	0.0423392	small
Depth Habitat Interval	180	1-2	13.611	***0.001***	0.1842991	large

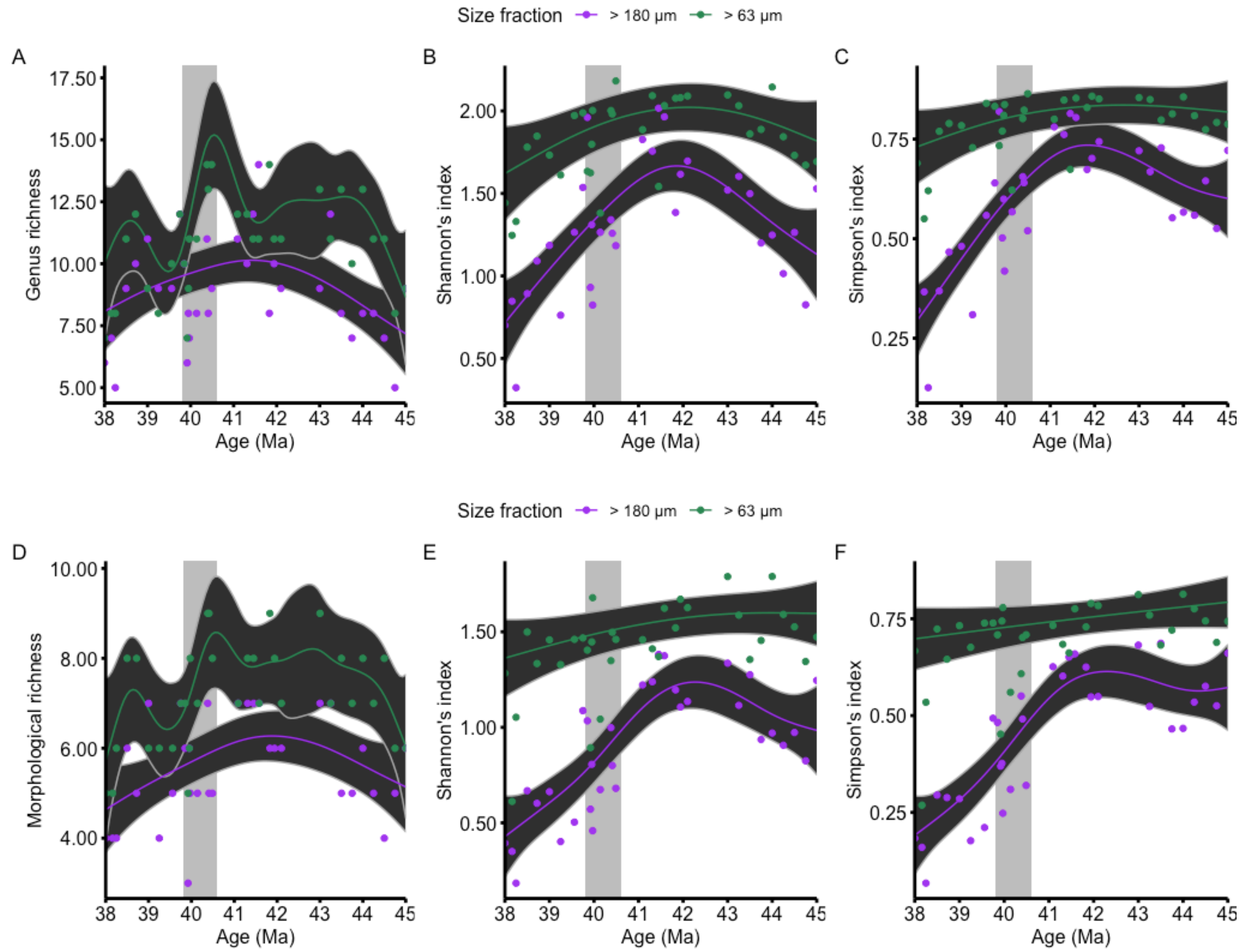
3.2 *Post-hoc* Dunn Test

```r
d1 <- dunnTest(Genus_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 63),
  method = "none"
)
d2 <- dunnTest(Genus_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63),
  method = "none"
)
d3 <- dunnTest(Genus_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 180),
  method = "none"
)
d4 <- dunnTest(Genus_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180),
  method = "none"
)
d5 <- dunnTest(Morph_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 63),
  method = "none"
)
d6 <- dunnTest(Morph_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 63),
  method = "none"
)
d7 <- dunnTest(Morph_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 180),
  method = "none"
)
d8 <- dunnTest(Morph_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180),
```

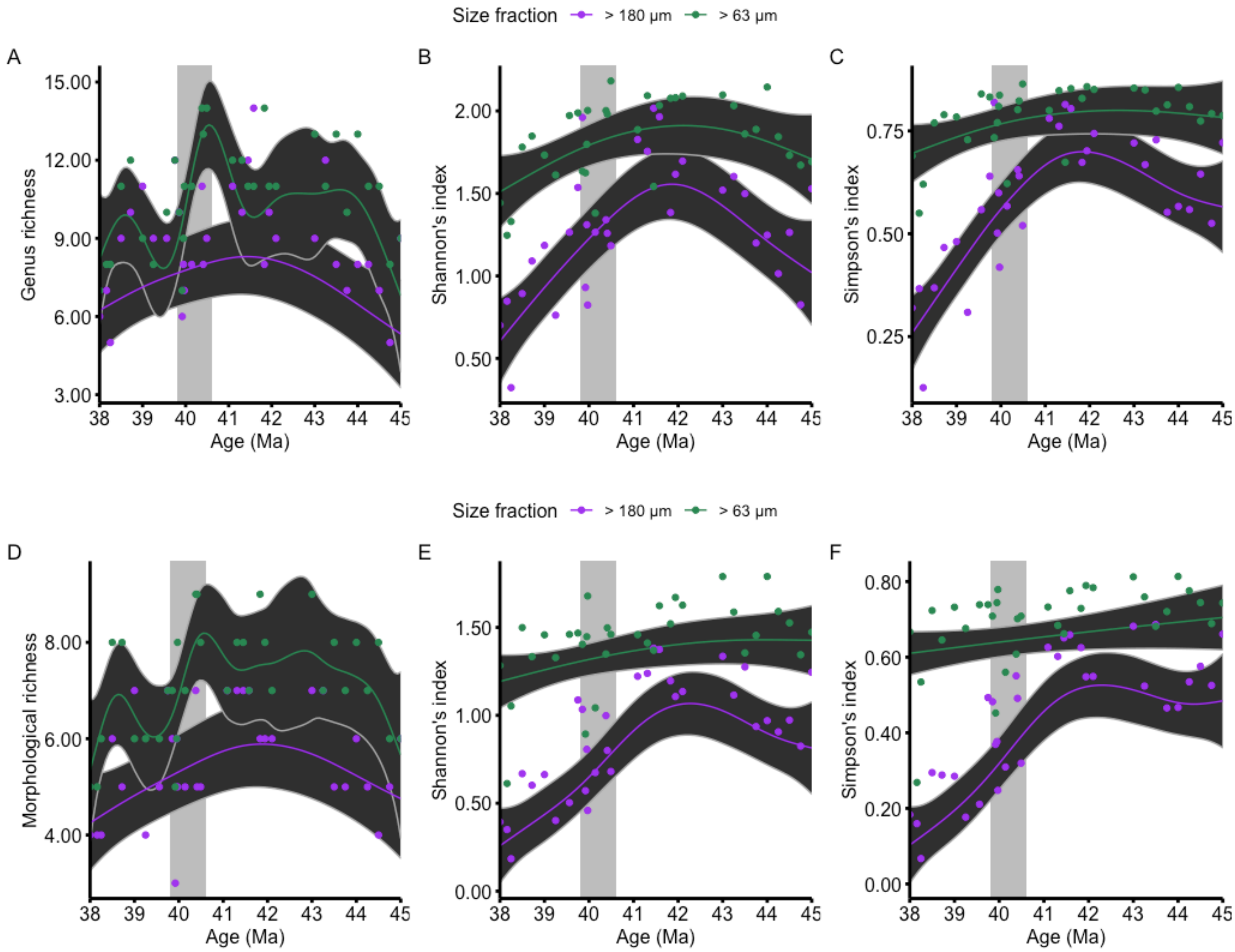
Supplementary Table 25: Results from *post-hoc* Dunn test showing differences between paleoclimatic intervals, bold and italic p values show significantly different intervals

Model		Size fraction	*q*	Interval Comparison	Z-score	*p*
Genera	Interval	63	<1	MECO - postMECO	6.01	***0.00***
Genera	Interval	63	<1	MECO - preMECO	1.43	***0.15***
Genera	Interval	63	<1	postMECO - preMECO	-6.41	***0.00***
Genera	Interval	63	1-2	MECO - postMECO	1.71	***0.09***
Genera	Interval	63	1-2	MECO - preMECO	-0.63	0.53
Genera	Interval	63	1-2	postMECO - preMECO	-3.22	***0.00***
Genera	Interval	180	<1	MECO - postMECO	2.76	***0.01***
Genera	Interval	180	<1	MECO - preMECO	-0.48	***0.63***
Genera	Interval	180	<1	postMECO - preMECO	-4.48	0.00
Genera	Interval	180	1-2	MECO - postMECO	2.09	***0.04***
Genera	Interval	180	1-2	MECO - preMECO	-0.81	0.42
Genera	Interval	180	1-2	postMECO - preMECO	-4.02	***0.00***
Morphogroup	Interval	63	<1	MECO - postMECO	3.25	***0.00***
Morphogroup	Interval	63	<1	MECO - preMECO	-1.57	0.12
Morphogroup	Interval	63	<1	postMECO - preMECO	-6.65	***0.00***
Morphogroup	Interval	63	1-2	MECO - postMECO	-0.08	0.94
Morphogroup	Interval	63	1-2	MECO - preMECO	-2.60	***0.01***
Morphogroup	Interval	63	1-2	postMECO - preMECO	-3.44	***0.00***
Morphogroup	Interval	180	<1	MECO - postMECO	2.92	***0.00***
Morphogroup	Interval	180	<1	MECO - preMECO	-2.84	0.00
Morphogroup	Interval	180	<1	postMECO - preMECO	-7.91	***0.00***
Morphogroup	Interval	180	1-2	MECO - postMECO	2.31	***0.02***
Morphogroup	Interval	180	1-2	MECO - preMECO	-1.94	0.05
Morphogroup	Interval	180	1-2	postMECO - preMECO	-5.86	***0.00***
Depth Habitat	Interval	180	<1	MECO - postMECO	3.98	***0.00***
Depth Habitat	Interval	180	<1	MECO - preMECO	2.98	***0.00***
Depth Habitat	Interval	180	<1	postMECO - preMECO	-1.47	***0.14***
Depth Habitat	Interval	180	1-2	MECO - postMECO	3.26	***0.00***
Depth Habitat	Interval	180	1-2	MECO - preMECO	1.23	0.22
Depth Habitat	Interval	180	1-2	postMECO - preMECO	-2.85	***0.00***

```r
  method = "none"
)
d11 <- dunnTest(Eco_Hill ~ interval,
  data = full %>% filter(Q < 1) %>% filter(size == 180),
  method = "none"
)
d12 <- dunnTest(Eco_Hill ~ interval,
  data = full %>% filter(Q %in% (1:2)) %>% filter(size == 180),
  method = "none"
)
```



Supplementary Figure 13: Best fitting GAM model as shown in main text in Figure 2 with fragmentation at 5% instead of the mean fragmentation we observed at 10%. A-C show genus diversity indices; D-F show morphological diversity indices. Raw data is shown in filled circles. Black shaded area represents 95% confidence intervals around the central predicted response. The light grey box represents the MECO interval.



Supplementary Figure 14: Best fitting GAM model as shown in main text in Figure 2 with fragmentation at 20% instead of the mean fragmentation we observed at 10%. A-C show genus diversity indices; D-F show morphological diversity indices. Raw data is shown in filled circles. Black shaded area represents 95% confidence intervals around the central predicted response. The light grey box represents the MECO interval.

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