How biased is the Henry Buckley Collection of Planktonic Foraminifera?

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1 Introduction

The original deposits, from which the Buckley collection was created, are still stored at the NHMUK Ocean-Bottom Deposits (OBD) Collection. There is no record of how Buckley picked the specimens to amass his collection. However, since he personally carried out the sample processing, isolation of foraminiferal specimens and their identification, all biases in his collection are likely to be systematic. The two main potential sources of bias are taxonomic bias (systematic misidentification or incomplete representation of the assemblage) and size bias (bias towards larger specimens or larger lineages). The presence of such bias could significantly affect trait distribution and variance. Therefore, the recognition of the biases in the Buckley Collection is crucial to use it to study morphological variation. The bias information assessed in the course of my research in Bremen will be placed together with the collection dataset on the open online NHMUK Data Portal and will be valuable for other researchers that want to use this collection in the future.

2 Methods

2.1 Sampling and picking

The NHMUK Ocean-Bottom Deposits (OBD) Collection houses most of the sea-bottom samples used by Henry Buckley to amass his planktonic foraminifera collection. These samples were collected by historical marine expeditions spanning mostly from the late 1800s until mid 1900s. We re-sampled ten OBD samples used by Buckley in his collection (Table 1). We focussed on core-top samples which encompass different oceans, latitudes and marine expeditions. The final choice of the ten OBD samples, however, could not be completely randomized since it depended on the amount of sediment available for re-sampling as well as us being able to identify the bulk sample in the NHMUK off-site storage facility. Once we defined the ten samples, we took roughly half of the amount available in the OBD jars and tubes (see Table 11 for sampled masses). Each of these samples was further split into two equal parts, leaving an archive sample and a sample to be processed. The processing of the samples consisted of weighting each of them, then wet-washing over a 63μm sieve and drying in

Table 1: Sediments re-sampled for bias analysis

IRN	Vessel	Ocean	Latitude	Longitude	Depth (m)	Mass (g)	Forams
32657		Indian	-50.01667	123.06667	-3976	grams	318
38482		Indian	-40.45000	49.81667	-3780	grams	177
36053		Indian	-26.93667	111.18167	-3350	grams	279
34991		Atlantic	-21.25000	-14.03333	-3740	grams	265
34671		Indian	-19.56667	64.63333	-2708	grams	376
34993		Pacific	-15.65000	-179.06250	-2519	grams	300
37148		Indian	-7.59167	61.48333	-3507	grams	305
33668		Pacific	-0.70000	147.00000	-2213	grams	331
33286		Atlantic	24.33333	-24.46667	-5153	grams	260
14609		Arctic	85.25000	-167.90000	-1774	grams	226
							2837

the 60C oven. The samples were further dry-sieved over a 150μm sieve and the fraction bigger than 150μm was further split with a microsplitter to produce a sample containing around 300 specimens. All specimens in these final splits were picked and identified (**supp info with species table for each sample**). In total 2837 specimens were picked, identified and mounted on slides. These slides are now part of the Henry Buckley Collection at the Micropalaeotology Section NHMUK and can be used as a type-collection covering intraspecific morphological variability across each species' biogeographical range.

2.2 Size measurements

To obtain the size distribution from the bulk sediments we manually mounted specimens on slides. The shell position on the slide will correspond to the shell position Buckley established for each lineage. These slides will were imaged and the foraminiferal shell size was measured using in NOC Southampton. Brombacher et al. (in preparation) quantified the reproducibility of shell size measurements and concluded that it is highly consistent with remounting the slides.

2.3 Data Analysis

Taxonomic bias was assessed by comparing for each sample the species identified by us and the ones present in the Buckley Collection. Dissimilarity

Size bias can be detected as a bias towards larger specimens or larger lineages. The latter has the same effect as an incomplete representation of the assemblage, as it would mean that Buckley only identified a sub-sample (large lineages) of the full assemblage. Size bias towards larger individuals will be assessed by comparing the shell size distribution obtained from my re-sampling of the sediments and the one obtained from the Buckley collection. Shell size distributions were compared using statistical test.

Size distributions already have an artificial cut-off dictated by the mesh size of the sieve used when processing the bulk sediment. This artificial cut-off influences each lineage differently, because depending on the lineage's average shell size the cut-off will eliminate a different portion of its population.

3 Results

3.1 Taxonomic bias

we expected that Buckley's species richness for each sample would be a subsample (i.e. nested) of the species richness found by us. A incomplete representation of the assemblage.

3.2 Size bias

4 Discussion

- Rarefaction curve MARGO
- Similarity among neighbouring samples MARGO
- bias of rare species

5 Conclusion

Table 2: GLM Gamma (link sqrt) Results

	df	logLik	AICc	delta	weight	p value
Trilobatus sacculifer						
tmn_0m	3	-504.55	1015.79	0.00	0.66	< 0.001
rel_abund_median + tmn_0m	4	-504.40	1017.98	2.18	0.22	
rel_abund_median * tmn_0m	5	-504.02	1019.86	4.06	0.09	
rel_abund_median	3	-507.70	1022.08	6.28	0.03	< 0.01
null	2	-510.66	1025.66	9.86	0.00	-
Globigerinoides ruber						
rel_abund_median	3	-468.86	944.41	0.00	0.30	
null	2	-470.04	944.42	0.01	0.29	-
tmn_0m	3	-469.17	945.03	0.62	0.22	
rel_abund_median + tmn_0m	4	-468.30	945.77	1.36	0.15	
rel_abund_median * tmn_0m	5	-468.24	948.30	3.89	0.04	
Globigerinoides conglobatus						
null	2	-501.31	1006.95	0.00	0.29	-
tmn_0m	3	-500.42	1007.53	0.59	0.22	
rel_abund_median	3	-500.61	1007.91	0.96	0.18	
rel_abund_median + tmn_0m	4	-499.38	1007.94	0.99	0.18	
rel_abund_median * tmn_0m	5	-498.27	1008.35	1.41	0.14	
Globigerinella siphonifera						
tmn_0m	3	-464.98	936.68	0.00	0.72	< 0.001
rel_abund_median + tmn_0m	4	-464.95	939.14	2.46	0.21	
rel_abund_median * tmn_0m	5	-464.83	941.59	4.91	0.06	
rel_abund_median	3	-469.68	946.08	9.40	0.01	
null	2	-471.02	946.40	9.72	0.01	-
Neogloboquadrina pachyderma						
tmn_0m	3	-250.67	508.60	0.00	0.52	< 0.001
rel_abund_median * tmn_0m	5	-248.03	509.58	0.98	0.32	< 0.05
rel_abund_median + tmn_0m	4	-250.61	511.44	2.84	0.12	
rel_abund_median	3	-253.13	513.53	4.93	0.04	< 0.01
null	2	-258.80	522.20	13.60	0.00	-
Neogloboquadrina dutertrei						
null	2	-366.22	736.89	0.00	0.42	-
rel_abund_median	3	-365.69	738.31	1.42	0.21	
tmn_0m	3	-365.73	738.38	1.49	0.20	
rel_abund_median + tmn_0m	4	-364.95	739.50	2.60	0.11	
rel_abund_median * tmn_0m	5	-364.11	740.71	3.82	0.06	
Pulleniatina obliquiloculata						
tmn_0m	3	-393.79	794.43	0.00	0.58	< 0.01
rel_abund_median + tmn_0m	4	-393.20	795.88	1.46	0.28	
rel_abund_median * tmn_0m	5	-392.99	798.28	3.86	0.08	
rel_abund_median	3	-396.55	799.96	5.53	0.04	.
null	2	-398.31	801.04	6.61	0.02	-
Globorotalia menardii						
rel_abund_median	3	-410.14	827.21	0.00	0.31	
rel_abund_median * tmn_0m	5	-407.57	827.64	0.43	0.25	< 0.05
null	2	-411.72	827.88	0.66	0.22	-
rel_abund_median + tmn_0m	4	-409.61	828.81	1.60	0.14	
tmn_0m	3	-411.47	829.85	2.64	0.08	
Globorotalia truncatulinoides						
rel_abund_median * tmn_0m	5	-385.70	783.81	0.00	0.58	< 0.01
rel_abund_median	3	-389.70	786.28	2.48	0.17	
null	2	-391.09	786.60	2.79	0.14	-
rel_abund_median + tmn_0m	4	-389.45	788.44	4.63	0.06	
tmn_0m	3	-391.03	788.95	5.15	0.04	
Globoconella inflata						
null	2	-232.75	470.20	0.00	0.63	-
rel_abund_median	3	-232.74	472.97	2.77	0.16	
tmn_0m	3	-232.74	472.98	2.79	0.16	
rel_abund_median + tmn_0m	4	-232.73	476.13	5.93	0.03	
rel_abund_median * tmn_0m	5	-231.21	476.70	6.50	0.02	