ANALYZING PLANKTONIC FORAMINIFERA AS A PROXY FOR PAST SEA SURFACE TEMPERATURE: A STATISTICAL ANALYSIS

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BACKGROUND AND PROCEEDING RESEARCH

Background and motivation – Base Study

Carbonate-clumped isotope thermometry (Δ47) of Planktonic Foraminifera is an important tool for paleoclimate reconstruction. However, obtaining enough material of a certain species of planktonic foraminifera limits the applicability of these abundant microfossils. The overarching objective for this research is to test weather or not it is necessary to pick out specific species in planktonic foraminifera thermometry.

Base Study Preliminary Results

Bulk planktonic foraminifera fit the carbonate clumped isotope calibration just as well as (ie, within the same error as) monospecific foraminifera results presented in previous studies (Zaarur et al., 2013) with no constraints on the used size fraction. Thus, Δ47-paleothermometry can be applied without the time intensive work of picking enough material from individual foraminifera species (Robin. R. Canavan., 2019).

Background and Motivation – Senior Project

Characterization of the analyzed sample's species composition from the base study is necessary for study replicability. Building off the base study, this senior project focuses on a statistical analysis of 13 samples (including both bulk and 'picked' samples from seven North Atlantic core-tops and six South Pacific core-tops).The question that this subproject seeks to answer is, for each sample, how much of this empirical data must be manually quantified in order to determine a sample composition breakdown for each location that is both representative of its entire core-top and replicable?

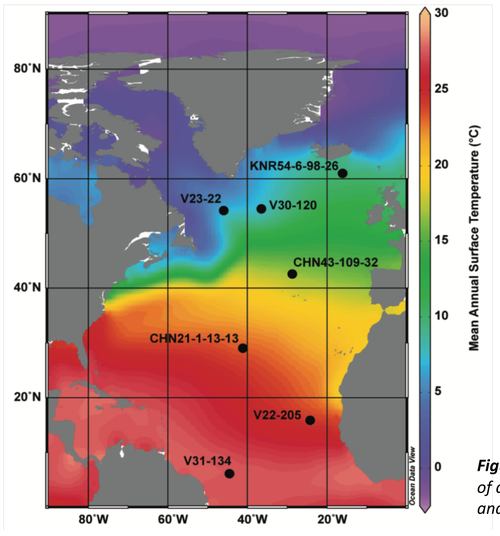


Figure 1. *Map indicating the core top locations of different foraminifera samples included in this analysis.* ***Source:*** *Robin. R. Canavan (2019).*

Base Study – Research Objective:

Evaluate the suitability of mixed species bulk planktonic foraminifera for Δ47 thermometry – can bulk analysis yield the same reliable results?

Senior Project – Research Objective:

What amount of data that must be characterized in order to determine a sample composition breakdown that is both representative and replicable?

METHODS

Methods: Base Study

Sample selection:

- (See figure 1). With the goal of increasing the applicability of these abundant microfossils in palaeothermometry and paleoclimate work, the base study analyzes modern mixed species (bulk) planktonic foraminifera samples from 19 different core tops to test whether it is necessary to pick out individual species when performing clumped isotope thermometry – as obtaining enough material of an individual species is a time-intensive limiting factor.

Sample preparation;

- Focused on juvenile planktonic foraminifera which are common in the 63-150 µm fraction *(Hermelin, 1989; Smart, 2002).*
- The modern samples were sieved at around 65-200µm. The Eocene samples were sieved into 60-150µm and 150-250µm size fractions.
- Bulk sediment was split into two subsamples: 'picked' and 'unpicked'. 'Picked' splits of each sample were handpicked under a microscope to remove any benthic foraminifera, remaining sediment, or other non-foraminiferal material to leave only the remaining planktonic foraminifera to compare against the results of running the bulk ('unpicked') splits

Sample imaging:

- Slides representing each core-top location and size fraction were imaged to quantify the relative composition of microfossils, and other carbonate and non-carbonate material within the bulk size fractions, as well as to confirm that planktonic foraminifera comprised the majority of the picked samples.

Sample analysis:

- During sample running and analysis measurements were taken on ThermoMAT253 gas source isotope ratio mass spectrometer following procedures outlined in Zaarur et al. (2013).

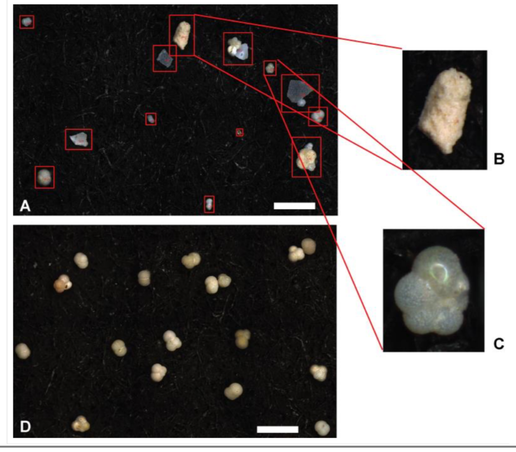


Figure 2. Example of high-resolution images. ***A.*** *CHN21-1-13-13, (63-150 µm) bulk fraction, showing objects identified by AutoMorph.* ***B.*** *Object classified as unidentified carbonate.* ***C.*** *Object classified as planktonic foraminifera.* ***D.*** *CHN21- 1-13-13, (125-150 µm) 'planktonic' split with objects other than small planktonic foraminifera removed. Scale bar in* ***A&D*** *is 1 mm.* ***Source:*** *Robin. R. Canavan. (2019).*

Methods: Statistical Sub-Analysis

- Empirical data collection: With the aid of AutoMorph image recognition software, these images were used to come up with empirical data on the relative composition of each core top. See Figure 3 below for example compositions of different samples.
- Statistical simulations: model is coded in R to re-sample progressively smaller numbers of randomized individuals to eventually form a rarefaction curve for each sample looking at the number counted against different output statistics (mainly MSE).
- Chose to measure the proportion of planktonic foraminifera in the total composition as our target, as this was the most dominant and relevant category.
- R code randomly subsamples the empirical data from each core top and then calculates the proportion of planktonic foraminifera captured in each sample. One function subsamples by sequencing the data by 10 and stores the subsampled results in a matrix with each row equal to a different step or number of data sampled. For each size step, this function is applied 500 times to generate a replicable dataset.
- For each value in each samples subsampled dataset, the error between the empirical proportion of planktonic and the proportion captured in the subsample is calculated. The mean squared error (MSE) for each size step is then calculated in order to form a graph plotting a each of the 13 samples' MSE in proportion of planktonic vs subsample size.
- A second graph is generated by forming a combined dataset of all the results for each sample to plot the median (50th percentile) error and the upper and lower confidence bounds across our combined data.

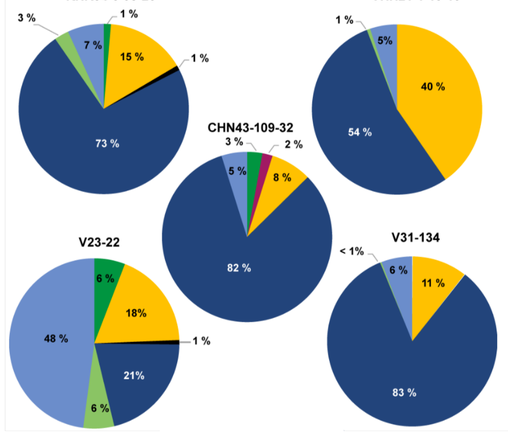


Figure 3: *Example composition breakdown for bulk core-top samples (63-125/150 µm) from North Atlantic. Demonstrates the various categories that samples may be comprised of.* ***Source:*** *Robin. R. Canavan. (2019).*

RESULTS – STATISTICAL ANALYSIS

Figure 5 shows the mean squared error (MSE) in the portion of planktonic captured against the step size for each of the 13 samples. This graph allows us to see what the variations look like across the dataset. As is expected, 'picked' samples resulted in less error for small specimen counts than the 'unpicked' because, for the picked samples, there were fewer overall categories represented.

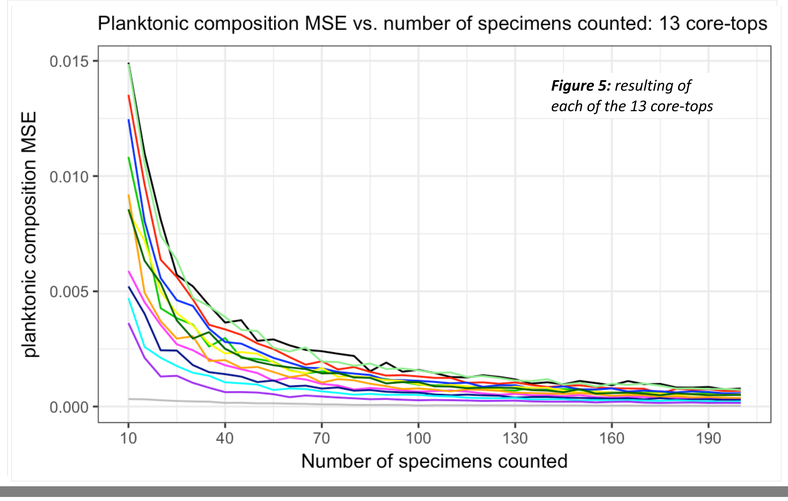


Figure 5: *resulting of each of the 13 core-tops*

Figure 6 displays the median error of the entire dataset along with the variation around the 5th and 95th percentile confidence bounds. Rather than choosing a specific cutoff error, we've displayed the different errors that result according to progressively larger count numbers so that future users can interpret this data to determine how sensitive to error their study is and thus how much data they must manually quantify .

For our purposes, given samples ranging from 19 to 99% planktonic, counting 200 specimens is in fact enough to form a representative sample that is replicable within reasonable error bounds.

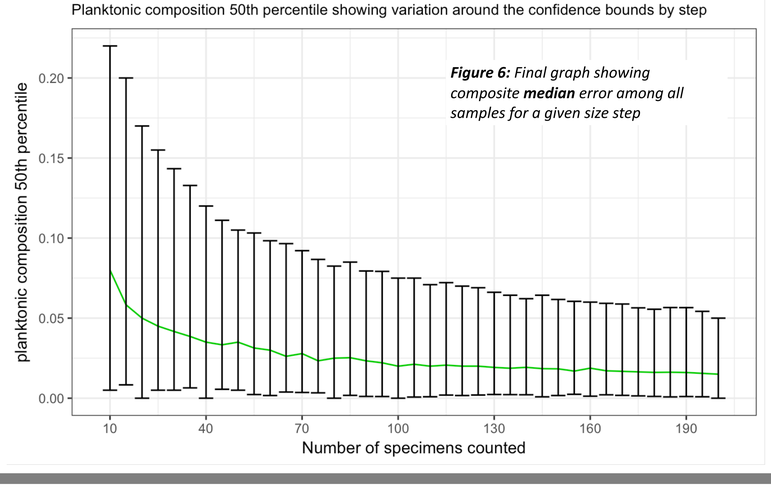


Figure 6: *Final graph showing composite* ***median*** *error among all samples for a given size step*

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