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Interactive comment on "Changes in the composition of marine and sea-ice diatoms derived from sedimentary ancient DNA of the eastern Fram Strait over the past 30,000 years" *by* Heike H. Zimmermann et al.

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Note to all: This is my first foray into the open review process, and my first non-anonymous review. I hope that my review meets expectations.

Summary This paper expounds on recent advances in the use of marine sedimentary ancient DNA (sedaDNA(as a proxy for sea ice reconstructions by investigating diatom assemblages in an Eastern Fram Strait downcore extending back to the Late Weichselian period (approx 30 kya). The authors contribute this novel diatom sedaDNA rela-

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tive abundance data to existing biomarker (IP25 and brassicasterol) proxy data from the same core. The three research objectives of the study are to assess diatom sedaDNA quality and reproducibility, to assess diatom assemblage dynamics over time, and to explore diatom sedaDNA as a new sea-ice proxy.

General comments I would first like to congratulate the authors on an extremely well-written manuscript. The structure is both logical and well-rounded, the language is accessible yet precise, the literature cited is appropriate and well-updated, and the inclusion of the comprehensive dataset (Table S1) bespeaks a desire to promote science through the sharing of raw data.

Specific questions/comments l.127 - Less than 50% of 3 replicates?

l.147 - What was the constraining factor used for CONISS analyis? Please include.

l.201 - What are the rare ASVs? A quick perusal of the Table S1 indicates many zeros. Would it be possible or useful to include a supplementary figure showing rank-abundance curves, either for the entire dataset or for the individual samples?

l.205 - Interesting theory, but why would inhibition only appear in some samples? I think this might be easy to test by a dilution PCR of a few representative samples. Also, if there are differences in the relative amount of diatom DNA in each sedaDNA sample, would it be possible to do a quick qPCR check of rbcL target abundance using the same primer set?

l.209 (Section 5) - My first impression from reading the results is that the authors have some difficulty in interpreting diatom community assemblage differences according to the results of the CONISS analysis, i.e. division into five aggregate "zones". In particular because trends in the relative abundance of specific sympagic diatom taxa between different CONISS "zones" are mentioned but not statistically tested. This leads me to question whether CONISS analysis is useful given the present dataset. Were any other analyses attempted to identify discriminant ASVs/taxa? And how did the authors con-

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clude that there are two diatom assemblage reorganizations (l.340) when the CONISS analysis identifies four?

l.223 - Could you please elaborate on what is meant by "richness of taxonomic names". According to l.184 different ASVs can be assigned to the same name, so how might this affect the apparent richness? And why use "taxonomic names" for richness calculations when taxonomic rank assignment is not uniform across all ASVs?

l.224 - I am not quite comfortable with the use of "turnover" in the context it is used, since the samples are discrete and therefore a discontinuous representation of time. In my opinion, "turnover" suggests a biological/ecological linkage from one sample to the next, while in this study the samples compared are isolated snapshots in time. Can the authors comment on the choice to use this term?

Fig.5 - I wonder if the reader might find this figure somewhat difficult to interpret given that relative taxon abundance at multiple taxonomic ranks are presented for each sample. Could the authors please the reasoning for presenting the data in this way?

Table 1 - The Paleoenvironmental conditions descriptions seem somewhat arbitrary. For example, how is "sea-ice retreat" (3.1 m depth) different from "Reduced sea-ice cover allowing spring sea-ice algal and summer phytoplankton productivity" (7.85 m depth).

l.239 - foraminifer

Fig.6 - Family-level taxonomy is presented but l.170-174 states that this collation may mask functional differences.

Fig.6 - The double top axes (depth and age) are very helpful, but identify very clear differences in sedimentation rates in the downcore. For example, zone II has higher temporal resolution than zone I. Might not differences in sedimentation rates also affect sedaDNA signal?

l.247 - Again, ambiguous results from CONISS analysis?

l.336 - "highly detailed taxonomic resolution" depends on what is meant by highly detailed, and what fraction of the data is being referred to. I suggest moderating this statement.

l.320 - Very interesting that N. cf. frigida sticks out as a possible new sea-ice proxy. However, according to Fig.6, this taxon as highest relative abundance in the most recent sample (0.4 kya BP) when sea-ice cover is low. What about Cylindrotheca closterium? Or Haslea avium? Again, I think it would be very helpful if taxon relative abundances were statistically tested in order to identify ASVs/taxa that contribute significantly the observed diatom diversity in different samples.

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