

***Interactive comment on “Technical note:  
Single-shell  $\delta^{11}\text{B}$  analysis of *Cibicidoides  
wuellerstorfi* using femtosecond laser ablation  
MC-ICPMS and secondary ion mass  
spectrometry” by Markus Raitzsch et al.***

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AC: We appreciate the interactive comment of Kaoru Kubota and his careful reading of our manuscript, and will address his comments below:

Very nice work! It will be a great contribution to the community.

AC: Thank you.

Line 109: Should be 11B/10B?

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AC: Well spotted! Will be corrected.

Line: 184 Delete "large-scale"

AC: Thanks, will be deleted.

Lines: 235-243: The readers may want to know more detail on the simulation.

Figure 7: It is interesting attempt, but I could not understand how it is simulated. If  $n = 4$ , count should be 52? ( $13 \cdot 4$ ) Why so much count is obtained in this simulation?

AC: Yes, it is an interesting approach, but it is not the most appropriate one, as also Dennis Mayk suggested, because it results in an underestimation of the uncertainties. We will thus apply a Monte Carlo approach in the revised manuscript, which is similar, but with correct uncertainty estimations.

However, just for information on the `combn()` function. It uses an input population (e.g., A, B, C, D) and calculates the averages for all possible combinations among this population ( $k$ ), for a given number of subsamples ( $n$ ). For instance, for  $n=2$  it calculates the averages AB, AC, AD, BC, BD, CD, so we get 6 possible combinations. To calculate the number of possible combinations ( $N$ ) for any  $k$  and  $n$ , the binomial coefficient is used:  $N = k! / (n! \cdot (k-n)!)$ . The possible combinations of 4 samples out of a total of 18, as in Kaoru's example, thus amount to 3060.

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