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Interactive comment on "Technical note: A time-integrated sediment trap to sample diatoms for hydrological tracing" *by* Jasper Foets et al.

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Studying fluvial processes and sediment dynamics is important to understanding key sources of environmental stress in stream and rivers. This study advances our methodological approaches to sampling suspended sediment, characterizing flood attributes, and source-tracking inputs of sediment using diatom assemblages. The latter point is vitally important in understanding when, where, and how fine sediment is mobilized and exported in stream-riparian networks. The Authors compared suspended sediment sampling methods using Phillips and ISCO automated samplers over the course of three high-flow events in the same stream. A novel aspect builds on previous research by investigating the potential for terrestrial and aquatic diatom assemblages in the captured samples to indicate event severity and trace the sources of transported

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sediment. The study is well executed and clearly written, with the discussion highlighting the state-of-the-art in sediment research and how complementary methods to the present research could be used to better quantify sediment inputs across the land-water interface. Overall, I think this study is useful and should definitely be reported as a Technical Note demonstrating the results as a proof of concept.

However, I do have some concerns about the data analysis. Over the three sampling events there is a great mismatch in the number of samples used for each sampling method. This concerns me for two reasons. Firstly, low sample replication for the method using the Phillips sampler increases the chance of a Type II error (i.e., not detecting a difference where there is one). Secondly, the analyses involve comparing samples collected over the entire duration of the event (Phillips sampler) with samples collected in three-hourly intervals (Automatic sampler). This is problematic for two reasons – the samples are not directly equivalent, and the automatic samples are non-independent (i.e., temporally auto-correlated). Below are some more points relating to these aspects and other comments I have.

1. In each sampling event, the Phillips samples seem to be at the periphery of each cluster (Fig.6), suggesting that there is some systematic bias in assemblages collected, yet the ANOSIM results suggest that in the first two events, samples were representative (i.e., not significantly different). With only two samples to compare with 38 automatic samples per sampling event it is likely that low statistical power increases the chance of a Type II error (although by not pooling the automatic samples actually inflates the replication – akin to pseudoreplication). I think the authors need to be more cautious with the inferences made (e.g., L228, L285, etc.).

2. I thought the automatic samplers might be pooled over time so that the comparison between these and the Phillips samples are equivalent, but they are not. Is it not a problem to compare the automatic samples collected every 3 hours with a couple of time-integrated samples using the different sampling method? The weighting using discharge for time-integrated samples in the Mann-Whitney U tests (L153-155,

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L173) probably helps control for differences across events but it is not clear if the same principle is applied for the cumulative discharge and automatic samples (i.e., temporal auto-correlation of samples collected progressively through the flow event).

3. L160 - Removing rare and uncommon taxa is contentious for multivariate community analysis. See Cao et al. (2001) for more regarding the potential issues. Perhaps the authors can better explain why they did this and what (if any) influence it had on their results. Cao, Y., Larsen, D., & Thorne, R. (2001). Rare species in multivariate analysis for bioassessment: Some considerations. Journal of the North American Benthological Society, 20, 144-153. doi:10.2307/1468195

4. L163-167 - The cluster analysis appears to follow practices recommended by Borcard et al. (2011), but Quinn and Keough (2002) highlight one disadvantage of agglomerative cluster analysis relating to the interpretability of the dendogram. Essentially because the hierarchical approach forms clusters that cannot be later broken, the dendogram is not a representation of all pairwise dissimilarities in objects like in multidimensional scaling. Thus, it could be useful to visualize a MDS plot of the data to determine their relative dissimilarity – also opening up the potential to use PERMANOVA ("adonis") to test differences (which has the advantage of being less susceptible to dispersion effects than ANOSIM). That approach has the advantage of using a "strata" term for event and just testing the overall difference between sampling methods. Using a SIMPER analysis could help bolster the observations made at L283-285 about why the sampling methods differ (i.e., there is some systematic bias for certain taxa). If the authors see this as useful, I would also strongly consider pooling the automatic samples (power issues notwithstanding) and using relative abundances. The removal of rare taxa is probably essential here since the much greater effort identifying diatoms for a pooled automatic sample increases the probability of detecting rare taxa. Borcard, D., et al. (2011). Numerical Ecology with R. New York, NY, Springer New York. Quinn, G. and M. Keough (2002). Experimental Design and Data Analysis for Biologists. Cambridge, UK, Cambridge University Press.

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