Supplementary material

This appendix contains supplementary methods and results for the paper *Filtration artefacts in bacterial community composition can affect the outcome of dissolved organic matter biolability assays.*

Negative exponential fits for DOC data

In the analyses of DOC concentration as a function of incubation time in the main article, we used Generalized Additive Modeling, to allow flexible curve-fitting to the data (see Figure 1 and Table 1 in main text.)

It is more common when studying decomposition processes, to use negative exponential models of the form:

$$y = A_0 e^{-kt}$$

Where y is the amount of material observed at time t, A_0 is a parameter reflecting the initial quantity of the material, and k is a decomposition rate constant.

To allow comparison with other studies that analyze DOC biolability assay data with this model, we present here the corresponding model fits (Figure S1). The corresponding AIC for this model (where each treatment has its own values of A_0 and k) was -13, indicating a much worse fit than the GAM models presented in the main article.

Figure S1: DOC concentration dynamics over the course of the incubations for the three filtration treatments. The lines represent the best-fit negative exponential models for each treatment group, n = 5 for each time x treatment combination.

Cell counts with flow cytometry

At each sampling occasion 10 mL subsamples were taken from each replicate for determination of cell counts using flow cytometry. These subsamples were filtered with 20 μm filters and stored at 4°C as 2 mL aliqots for maximum 2 hours prior to measurement.

Measurements were made using a BD Accuri C6 Flow Cytometer on samples stained with SYTO-13 stain (Invitrogen, Carlsbad, CA, USA) at 2.5 μM final concentration following the protocol of del Giorgio et al. (1996) and using the following software settings: flowrate 14 μL / min, volume limit 20 μL, threshold, 20000 on FSC-H.

Figure S2 shows the cell count results, separated by sampling date and filtering treatment.

Figure S2: Estimates (mean +/- s.e., n=4) of cell abundance by flow cytometry using samples incubated with nucleic acid stain SYTO-13, note log10 scale on y-axis

Time series plots of bacterial taxa

Figure S3 and S4 show time series plots of relative abundances of the 12 most abundant bacterial (sub-) phyla, based on 16S rRNA gene amplicon sequencing. These are the same data used to produce Figure 4 in the main text. See main text methods for details on bioninformatic procedures.

Figure S3: Time series of relative abundances of selected bacterial (sub) phyla measured by 16S amplicon sequencing. Points represent individual replicates. Lines and grey shaded areas are loess smoothers and associated 95% confidence intervals

Figure S4: Time series of relative abundances of selected bacterial (sub) phyla measured by 16S amplicon sequencing. Points represent individual replicates. Lines and grey shaded areas are loess smoothers and associated 95% confidence intervals

References

del Giorgio, P., D. F. Bird, Y. T. Prairie, and D. Planas. 1996. Flow cytometric determination of bacterial abundance in lake plankton with the green nucleic acid stain SYTO 13. *Limnology and Oceanography* 41:783-789.