Reply on RC1
Aditi Sengupta et al.

The authors present work of good quality, and I especially commend them for making the data available already. My biggest concern is the presentation of the experiment's hypotheses as a conceptual framework, as the notion that microbial community assembly influences and is influenced by microbial functions is not novel. Rather, the authors present what seems to be the basis for a very interesting SEM in their final figure. They might consider pursuing this! Additional comments are listed below in order of decreasing importance.

- Thanks for your constructive feedback. We will work to present the hypotheses as directing readers attention to the need for this relationship to be tested. We would also like to note that while relationships between microbial community assembly and function may not be novel, integrating the concepts by tying in various pieces of our conceptual understanding of microbial structure, function, assembly, and environment interactions into one coherent framework we feel is novel, and in our opinion has value.
- Unfortunately we do not have enough data to develop a SEM. We would need at least a 100 data points as pointed out in the book "A Beginners Guide to Structural Equation Modeling" by Randall E. Schumacker. In addition, the relationship between dry days and the response variables is a step function. SEM needs linear relationships, which can sometimes be achieved through transformation, but in the case of a step function it is not clear how to make this linear through transformation. While it would be fantastic to formally test the conceptual model as an SEM, that will need to wait for future studies due to technical limitations.

The authors should be careful with their description and interpretation of deterministic forces throughout the manuscript. Deterministic forces are caused both by biotic interactions and abiotic forces, and the research presented cannot disentangle these two. I therefore think it is important that the authors temper their discussion of determinism as an informative emergent property. In L85, they state "a stronger influence of determinism over community assembly is hypothesized to cause higher respiration rates (a microbial processes) due to a larger contribution of well-adapted taxa (Graham and Stegen, 2017).", however this is entirely dependent on the identity of the deterministic force and the community it is exerted upon. A stronger influence of determinism on microbial community assembly can be caused by an infinitiy of factors, but it is these
factors that determine how the community is shaped. Thus the expected effect on the community cannot be linked directly to the change in the relative influence of determinism.

- We agree that our work cannot disentangle biotic vs abiotic forces of deterministic assembly. We will rephrase the hypothesis to indicate that this may be one possible outcome but may be dependent on the existing community composition and the deterministic force that is exerted.

While I think that the sequencing of both gDNA and cDNA is a strong feature of this manuscript, I don't think that the authors discuss it in sufficient depth. Why might the disturbances change the relative strength of deterministic forces according to cDNA but not gDNA?

- We hypothesize that the duration of imposed experimental treatments (2 weeks) was not a sufficient amount of time for birth and death events to restructure the composition of the community. The data suggest that instead there were physiological responses in terms of decreases and increases in activity level without strong changes in composition itself. If we would have imposed a stronger disturbance and/or imposed the treatments for a longer period of time, we may have observed clearer impacts of disturbance on the whole community (i.e., via gDNA analyses). We will elaborate on this idea in the Discussion.

In figure 2, the authors present the treatments in a different order than what is used throughout the rest of the manuscript (i.e., dry days). I think this is a great description of a complex experiment, and I would suggest the treatments are reordered to reflect the order in the analyses.

- We will reorder the panels to reflect that in the analyses.

In figures 3 and 5, I would like to see the points colored by treatment. In 5B, the positive correlation is driven (almost?) entirely by the differences between the two treatments with most dry days and the rest. I would be curious to see whether that is the case in the rest of the figures.

- We will do this and provide discussion on any new inferences that emerge.