

## ***Interactive comment on “A global viral oceanography database (gVOD)” by Le Xie et al.***

**Le Xie et al.**

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We thank both reviewers for their very constructive comments and suggestions that greatly helped us improve our manuscript. We have responded (in blue fonts) to the comments point by point and revised the manuscript accordingly.

### **To Reviewer 2:**

#### **Summary:**

The authors have gathered an extensive dataset describing global oceanographic virus abundance and productivity, along with other oceanographic and environmental data (salinity, temperature, etc.). Virus abundance data using three different methods (transmission electron microscopy, flow cytometry, and epifluorescence microscopy) are included in the dataset. Furthermore, data describing lytic virus production using five complementary methods, and lysogenic production using Mitomycin C treatments, are

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included. The authors provide a summary of the geographic patterns evident in their data and use two complementary statistical models to infer global virus abundance and biomass, the latter utilizing a model relating virus carbon content to capsid size. Their global estimates are consistent with, and complementary to, prior estimates of global ocean virus abundance. The authors also leverage their new dataset to assess whether complementary methods to infer abundance produce consistent results in similar environments. They find, reassuringly, that different methods to measure virus abundance produce similar results.

#### **Main comments**

This manuscript has been extremely carefully put-together. I really appreciated the concise explanation of different techniques used, and the clarity with which the results are reported. Clearly, a lot of effort has gone into this work. I enjoyed seeing the methodology used to infer global virus abundance (I always see the  $10^{30}$  number banded around, without knowing how those estimates are reached). I also appreciate that effort has been made to quantify uncertainty in all of their estimates, and to evaluate the consistency of different techniques. Overall, this manuscript is a timely and necessary contribution.

**Response:** We thank the reviewer for her/his support and very useful comments to our manuscript. We have revised the manuscript accordingly. The detailed responses are listed below.

#### **Specific comments:**

Overall, the language is very clear, there are only very minor English language issues. I pointed out a couple, but it could be useful to have one final sweep through to look for language edits.

Line 8: “Viriplankton are a key component of the marine biosphere” (suggested change)

Line 9: “They also contribute greatly to nutrient cycles/cycling” (suggested edit)

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**Response:** Thanks for your reminding. We checked the language thoroughly and numerous edits, including the two pointed out by the reviewer, were made in the revised manuscript.

Line 21: The link to the database is no longer valid, I understand it was temporary and wouldn't have been an issue if I had done my review earlier. Noting it will need to be updated nevertheless.

**Response:** Thanks for your reminding. The data repository, PANGAEA, has granted a persistent DOI link to the database <https://doi.org/10.1594/PANGAEA.915758>, although it takes up to 30 days to become valid once the DOI registration process is completed. The link has been updated (**Line 21**).

Line 88: "For notational simplicity," (suggested edit). Also, maybe clarify what FPB stands for? Is it Fraction-Prokaryote-Burst?

**Response:** Yes, the FPB stands for Fraction-Prokaryote-Burst. We changed "For simplifying reason" to "For notational simplicity" and added the explanation of FPB in the revised manuscript (**Line 89 and 90**).

Line 122: consider providing your code used for the modeling, either in a public repository, or as a supplement to the article.

**Response:** Thanks for your suggestion. The code (a MATLAB script) will be attached as a supplement material to the article.

Line 210: It looks like the range for lysogenic production goes negative? Is this an artefact or something real? These negative ranges sometimes happen when you take a standard deviation of data that are heavily positive-skew (often the case with biological data). Log-transforming can help (although I see you have done this elsewhere). May be worth commenting on this point to clarify if it is an artefact or something real.

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**Response:** The reviewer was correct that the standard deviation higher than the mean is an artefact because of some large positive data. We decide to use mean of the original data (i.e. mathematic mean), instead of that of log-transformed data (i.e. the geometric mean), and the associated standard deviations, to facilitate direct comparing with numbers reported by other studies.

We added the range of the data for clarifying: "The overall mean and standard deviation of lytic VP in the global ocean were  $9.87(\pm 24.16) \times 10^5$  particles ml<sup>-1</sup> h<sup>-1</sup> (ranging in  $0.00746 \times 10^5 - 350 \times 10^5$ )." (**Line 190**)

"The overall lysogenic VP in the global ocean is  $2.53(\pm 8.64) \times 10^5$  particles ml<sup>-1</sup> h<sup>-1</sup> (ranging in  $0.00132 \times 10^5 - 68.8 \times 10^5$ )." (**Line 212**)

Line 214: update link

**Response:** The link has been updated (**Line 216**).

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