

Biogeosciences Discuss., author comment AC2
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Reply on RC2

Masihullah Hasanyar et al.

Author comment on "How much do bacterial growth properties and biodegradable dissolved organic matter control water quality at low flow?" by Masihullah Hasanyar et al., Biogeosciences Discuss., <https://doi.org/10.5194/bg-2021-333-AC2>, 2022

Dear sir, madam,

First of all, I would like to thank the reviewer for their positive comments on our paper and valuable propositions for improvement. Here are our subsequent responses, clarifications and the modifications that we would add in the original manuscript in case of acceptance for publication :

In response to their comment:

"What is the novelty this manuscript brings to the field?"

[R1] Our article provides the following novelties compared to the previous works:

- In the previous works, Wang et al., (2018) have focused on both high & low flow under different conditions of bloom, non-bloom and post-bloom, whereas here we have explored further the summer post-bloom low flow condition where significant discrepancies are observed between water quality model results and dissolved oxygen (DO) observations (Wang et al., 2022). We already knew that bacterial physiological parameters control DO evolution during low flow and that was already quantified in Wang et al., (2018). However, what we didn't know is the extent to which the characteristics of the organic matter (OM), particularly its dissolved biodegradable fraction, control the oxygen dynamics at low water levels, and whether these characteristics are important with respect to the physiological properties of heterotrophic bacteria;
- To explore this question through a sensitivity analysis, we had to explicitly add the parameters of OM model inside the software CRIVE itself, and especially in the boundary conditions of the model, where CRIVE was used to read the six pools of OM (DOM1, DOM2, DOM3, POM1, POM2, POM3) as state variables defined by the user. We therefore added an OM repartition model inside CRIVE so that the DOM_i and POM_i state variables are now calculated by the model based on only one value provided by the user, i.e. the total organic carbon (TOC), and 5 new model parameters (t, b1, b2, s1, s2). This repartition model not only distributes TOC among the six CRIVE pools using the 5 parameters whose variation ranges were found using a bibliography review (Table 1) , but it also gives us the possibility to do a sensitivity analysis for evaluating their role and influence on DO variation. The main difference is that instead of reading the 6 pools (not varying) directly, now it reads TOC and uses the 5 parameters to convert it

into the 6 pools (now varying because the 5 parameters have a range).

- Compared to the previous work (Wang et al., 2018) that has studied only the direct impact of each parameter, we went further and looked into intra-parameter interactions (higher order Sobol indices) and we found that certain parameters hide the influence of other parameters due to their interactions. Thanks to that, we designed the 2nd and 3rd Sobol' sensitivity analysis which allowed us to better quantify how the share of OM influences DO in river systems with regards to the physiological parameters of heterotrophic bacteria. We believe that this methodology may also be of interest for future sensitivity analysis where parameter interactions may hide the effect of other parameters.
- In the previous study, the sensitivity analysis was conducted under a constant OM load of TOC = 3.2 mgC/L whereas in this work, we evaluated the evolution of sensitivity indices for various TOC loadings ranging from 1 up to 10 mgC/L which represents the OM load from river, treatment plants and combined sewage overflows (Fig. 7b and Fig 8).
- Conducting long-term sensitivity analysis: In the previous work, the influence of model parameters are usually studied over a short period of time, for instance a 4 day period in Wang et al. (2018). Here we looked deeper inside the system dynamics by extending the period up to 45 days. Such strategy led to a better understanding of the mid-term effect of slowly biodegradable OM. Even though those effects appear rather negligible, this result is important for improving and simplifying water quality models.

The reviewer advises to make those findings clearer in the paper. We agree with this comment and propose to add a first section to the discussion to wrap up those findings as stated here before.

In response to their comment:

"The importance of heterotrophic bacteria activity and properties of the dissolved organic matter pool are pinpointed as important parameters to explain uncertainties of water quality models in the introduction (lines 49 to 60). Then, what is this manuscript offering new (or different) from previous studies? "

[R2] The reviewer was misled by a flawed formulation of this section of the introduction. We propose to rephrase it following those clarifications : Formerly, Wang et al., (2022) simply assumed from their study that the OM degradation and OM repartition are playing a role in the model discrepancies during low flow, without explicitly quantifying their relative influences. In our paper we tested those hypotheses and therefore extended the parameters of interest to include 3 parameters representing OM kinetics and 5 representing OM repartition to quantify the sensitivity of DO variation with respect to those with a Sobol sensitivity analysis. We found that b_1 , the share of BDOM, has a significant influence on DO variations in certain circumstances, such as the presence of fast growing heterotrophic bacteria. In that case, a low b_1 value may lead to a depletion of BDOM by heterotrophic bacteria, while high b_1 allows the micro-organism to grow without limit, leading to significant oxygen depletions.

In response to their comment:

"Please, specify better what are the research questions or objectives of this work?"

[R3] We will add the following main research questions in the introduction of the article:

- What are the influential parameters controlling DO during a post-bloom summer low flow period where discrepancies are observed in different water quality models? Is a model that includes bacteria physiological parameters only sufficient to describe DO variation ?
- To what extent is the knowledge of the quantity of OM share, especially that of BDOM influential for water quality modeling?
- What is the hierarchy among the influential parameters ?

In response to their proposal on the discussion part:

[R4] We will restructure the discussion section by first answering the research questions merging our **R1** reply with the current section 3.4. This new section will be called "Hierarchy of the most influential parameters during low flow period".

The second subsection of the discussion will be dedicated to data assimilation, as is in the current version of the paper.

Finally, we will restructure the sub section "Consequences of the results on water quality monitoring in urban areas" by reformulating how important are our results in the context of water quality monitoring and what information or experimental data is required to be supplied to the water quality models in order to provide better estimates of the river water quality. Indeed, we will first show how important it is to have better identification of bacterial parameters in any water quality monitoring network and second what we can do to get more information on b1 or BDOM.

In addition, we will also discuss the limitations and assumptions of this study as indicated in the response to the comments of the first reviewer. We will provide recommendations for future studies in order to incorporate these limitations.

In response to their second question regarding the incorporation of new parameters:

[R5] We will restructure the material and method section 2.2 to display how we have incorporated the organic matter repartition model consisting of 5 new parameters inside CRIVE instead of using the 6 forced user inputs that are not model parameters.

[R6] Finally, regarding the use of repetitive and introductory paragraphs, we think that it is a good habit to brief the reader regarding what they are going to expect in different sections of an article. This will give them the chance to fast access to their intended sections or subsections. However, we will find the annoying ones and will remove them from the article.

[R7] We reply hereafter to technical questions of the reviewer. Considering the short timeline before the closure of the discussion, we preferred to reply as exhaustively as possible to the reviewer and therefore may introduce some redundancy with our former answers [R1-6]. In case of acceptance of our paper, we would pay attention to avoid any repetition in our arguments.

In response to their specific questions on the addition of new parameter like:

What do authors mean with new parameters? New regarding what exactly? C-RIVE?

[RS7.1] Here, we have two types of new parameters. First, OM degradation kinetic parameters that already exist in CRIVE but whose influence was not studied in any other research. Secondly, OM repartitioning parameters (section 2.2.2) that as I have explained in the point #2 of **R1**. This is a novelty that did not exist in CRIVE before. Indeed, CRIVE used to read the share of each one of the 6 OM pools directly as an input (that was not variable, they were created in a form of database by multiplying TOC with certain assumed values), however, what we did as a novelty was that we gave CRIVE the possibility to read directly TOC (which comes from experimental data) and convert it into the above 6 OM pools using 5 parameters for which we did an extensive bibliography to find their variation range (t, b_1, b_2, s_1, s_2). Thereby, we created these 5 new parameters whose influence on DO could be studied and thanks to which we can now have varying 6 OM pools. This is something which was not possible before.

In response to the question: Another change is that authors pooled DOM1 and DOM2 fractions to create a new fraction called BDOM. Am I missing something? What is really new/different in this approach regarding to previous work in C-RIVE?

[RS7.2] If we look at equations 12 & 13, the variation range of BDOM is found using the variation range of b_1 , therefore it is not pooled by addition of DOM1 and DOM2. On the contrary, DOM1 and DOM2 are now derived from BDOM using the parameter s_1 . But why did we do this? In the first sensitivity analysis, we found b_1 as an influential parameter, however for the second and third Sobol and in order to decrease the computation cost, we used BDOM as a parameter to get rid of the 5 initial parameters (as shown in Table 4, we went from 17 parameters to 12 parameters). BDOM is the equivalent of b_1 ($b_1 = \text{BDOM}/\text{DOM}$). DOM is constant ($\text{DOM} = t \times \text{TOC}$) because t was found to be non-influential in the first experiment and fixed here, therefore, having b_1 or BDOM does not make any difference technically.

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