Comment on gmd-2021-344
Anonymous Referee #2

Referee comment on "The eWaterCycle platform for Open and FAIR Hydrological collaboration" by Rolf Hut et al., Geosci. Model Dev. Discuss., https://doi.org/10.5194/gmd-2021-344-RC2, 2022

This manuscript summarizes an interesting and significant advancement in hydrologic modeling. The e-water cycle platform uses open source, modern tools to provide access to a range of hydrologic models, input datasets and observations for comparison. I have some comments below, but they are only suggestions. I recommend this manuscript be accepted as-is.

- I thought the discussion of other platforms was helpful. This puts e-water cycle in context with related efforts.

- I particularly liked the glossary and careful definition of terms. While many of these terms are not new to the readership of GMD, some of them are, and all these terms are new to someone who is just starting the process of learning to use hydrologic models. Aspects like this for the manuscript (and the platform itself) broaden the scope of this manuscript beyond simply a documentation of the work but also a how-to guide for new users.

- In the list of models to be added (line 205+), I'm curious what makes the models listed "different" from the set of models included? Is this a technical difference, or something in the way the equations solved are developed?

- While by no means a verification of the platform, I did review the website and read the docs for getting started with e-water cycle. The instructions seemed clear and complete. I did notice some platform specific language (e.g. the use of wget instead of curl) that might cause issues for more novice users.
- With respect to the explorer (line 157+ / S2.1), I could not find a link to where or how run this part of the platform? Is this hosted somewhere? Something that needs to be installed locally? The explorer concept is very interesting and I liked the automatic notebook generation concepts, but was left wanting more detail.

- I'm curious about the limitations of the BMI. Does this require access to the models as a subroutine via python, as a wrapper around the models, or something else? How are the differences in model file structure handled?