Hydrol. Earth Syst. Sci. Discuss., https://doi.org/10.5194/hess-2020-243-RC1, 2020 © Author(s) 2020. This work is distributed under the Creative Commons Attribution 4.0 License.



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Interactive comment

Interactive comment on "Targets-specified grids-tailored sub-model approach for fast large-scale high-resolution 2D urban flood modelling" by Guohan Zhao et al.

Anonymous Referee #1

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The manuscript is proposing a methodology to accelerate flood modelling.

The VRSS aggregates the depression into parameters of modelling and mass balance is used to distribute water volume within the surface runoff network. The overflow from selected sinks are therefore used as the inflow for 2D MIKE FLOOD modelling.

However, the approach is based on a lot of flawed assumptions: 1. There is no that time variable used in the VRSS calculation. How much time for the rainfall to reach the sinks, and how long will the flow take from one sink to another are unclear.

2. The sub-model is eliminating the areas out of interest and only run the 2D model in the small sub-catchment within a large basin. The same exercise has been used in

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extensive previous work. There novelty of the approach is unclear.

3. The flood maps in Figure 10 show the water accumulating along modelling boundaries, indicates the modelling boundaries do not reflect the catchment boundaries correctly. The comparison between Figure 10(c) and 10(d) shows that there are significant flooding in the north area that is modellined in sub-model and not modelled in municipality model. How are the modelling results compared in Table 2 when the information is missing in one model? The south boundary in municipality model has significant flooding, which is not seen in the sub-model. Is the flooding caused by the rainfall within the narrow strip between two boundaries?

4. The comparison in Table 3 is misleading. The sub-model and municipality model only produce the information in 263k and 148k cells, respectively, while the full basin model produced information for 27m cells. If the performance is normalised by cell number, the full basin model actually performance much faster per cell. The authors must present that all models are using the same input condition, and same or similar modelling domain.

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