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Coupling Hydrological models using BMI in eWaterCycle

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The eWaterCycle platform is a fully Open-Source platform built specifically to advance the state of FAIR and Open Science in hydrological Modeling. eWaterCycle builds on web technology, notebooks and containers to offer an integrated modeling experimentation environment for scientists. It allows scientists to run any supported hydrological model with ease, including setup and pre-processing of all data required. Common datasets such as ERA-Interim and ERA-5 forcing data and observations for verification of model output quality are available for usage by the models, and a Jupyter based interface is available for ease of use.

As the main API for models, we use the Basic Model Interface (BMI). This allows us to support models in a multitude of languages. Our gRPC based system allows coupling of models, and running of multiple instances of the same model. Our system was designed to work with higher level interfaces such as PyMT, and we are currently integrating PyMT into our platform. During my talk I will give an overview of the different elements of the eWaterCycle platform.

The BMI interface was specifically designed to make it easy to implement in any given model. During the FAIR Hydrological Modeling workshop a number of modelers worked on creating a BMI interface for their models, and making them available in the eWaterCycle system. To show the amount of effort required in common cases, I will show the BMI interface that was created for a number of these models, including SUMMA, HYPE, Marrmot, TopoFlex, LisFlood, WFLOW, and PCR-GLOBWB.

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