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Identification of dominant hydrological mechanisms for ungauged basins via bayesian approach

Cristina Prieto (1,2,3), Nataliya Le Vine (2), Dimitri Kavetski (4), Claudia Vitolo (5,6), Eduardo García (1), Raúl Medina (1), and César Álvarez (1)

(1) Fundación Instituto de Hidráulica Ambiental, Santander, Spain (prietoc@unican.es), (2) Imperial College London, United Kingdom (c.prieto13@alumi.imperial.ac.uk), (3) Bristol University (cp14186@my.bristol.ac.uk), (4) School of Civil, Environmental and Mining Engineering, University of Adelaide, SA, Australia, (5) Institute of Environment, Health and Society, Brunel University London, (6) European Centre for Medium-Range Weather Forecasts, ECMWF, Reading, UK

This work presents a Bayesian statistical methodology to identify dominant hydrological model components intended to represent a particular catchment process for ungauged catchments using an ensemble of hydrological models and the information regionalized for such catchments. From the ensemble of hydrological models, each model structure is given by a combination of model components, and each mechanism is treated as a sample from a complete (but unobservable) set of mechanisms. The hydrological behavior from donor catchments is represented using a set of orthogonal (principle) components and regionalized to ungauged catchments using a random forest technique. This regionalized information is then assimilated into the ensemble of hydrological models via a Bayesian approach.

The new methodology is demonstrated for basins in northern Spain. The results show that:

1) For some processes (routing, evaporation, lateral flow and runoff), dominant hydrological mechanisms can be identified from just a few pieces of information (the first four principal components); while for the other processes, dominant hydrological mechanisms cannot be identified even when the majority of available information is used.

2) The methodology reliably identifies dominant mechanisms when there is no model error and a large quantity of high quality information is available.

3) Large numbers of hydrological indices considered in typical regionalization applications might not be sufficient to identify the mechanisms that govern the hydrological processes in the upper soil layer and the mechanisms that govern the percolation process.

4) A successful identification of dominant processes depends on: a) presence of model error, b) information quality, c) available information content and d) hydrological process sensitivity to the available hydrological indices.

The identified dominant mechanisms are used to define a hydrological model structure of minimal complexity, and therefore, the methodology offers a path for reducing model structure uncertainty and/or help with model selection or identification.