Diagnostic evaluation of land surface models from decision space – the hydrologic genome approach

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Abstract: Land surface models provide a crucial capability for estimating water and energy fluxes in the terrestrial environment. The models employ mathematical formulations together with a set of internal values to provide an estimate of the land surface response to meteorological forcings and changes in the land surface. The major components of a land surface model include model parameters, initial states, input forcing data, and the model structure. These internal components make up the decision space of the model, with each internal setting providing a specific model response/output. An assessment of model decision space is crucial to the identification of model weakness and the ultimate improvement in model forecasts. However, diagnostic evaluation of land surface models is challenging, mainly because of the uncertainties associated with the internal model components and their interactions, which make it difficult to determine the inaccurate parts of the model that need improvement. Until the land surface model for subsequent adjustment will remain questionable.

In this presentation, a hydrologic genome approach is employed to quantify the uncertainty for internal components of the land surface model, in terms of its soil moisture estimation. The hydrologic genome approach was inspired by biological genome mapping, which has the capability to determine how the structure of the human body functions and the location of genes that battle disease-causing virus and bacteria. The hydro genomic method uses an evolutionary strategy together with a data assimilation framework to generate a genomic-like data set. The evolutionary strategy is able to provide the genomic-like data set to encompass the model decision space, while the data assimilation approach affords a model state updating and temporal monitoring of the changes in model decision space. The resulting genomic data set is a series of model footprints in time, with each footprint comprising an ensemble of optimal internal model settings in decision space. The genomic-like data set was examined using multi-dimensional clustering to map the model decision space, where the land surface model was evaluated on the basis of its temporal stability in decision space.

The hydro genomic approach is demonstrated for the Community Atmosphere Biosphere Land Exchange (CABLE) model for soil moisture estimation in the Yanco area in south-east Australia. Data assimilation was undertaken to assimilate retrieved soil moisture from the Advanced Microwave Scanning Radiometer for the Earth Observing System (AMSR-E) into CABLE. To evaluate the hydro genomic method, open loop and calibration estimates were used. The calibration output was generated by independently calibrating CABLE to the retrieved AMSR-E soil moisture content across the same assimilation time period, whereas the open loop was based on randomly generated values for model parameters, initial states, and input forcing data uncertainty.

The modeling results show that the updated soil moisture is superior to outputs from both the open loop and the calibration. The generated hydro genomic map was found to provide a minimum uncertainty for model components, reducing the original and updated bounds to about 70% and 60% respectively. In terms of soil moisture estimation, the hydro genome map was found to be about 60% as accurate as the updated output based on AMSR-E data, and superior to outputs from both calibration and assimilation when evaluated using in-situ OzNet (www.oznet.org.au/) soil moisture. It is noted that the hydro genomic approach is part of a broader conversation towards the diagnosis and refinement of land surface models for improved water and energy estimates. The key finding is the provision of a model diagnostic framework to better identify model weaknesses and refine land surface models on the basis of their temporal stability in decision space.

Keywords: Soil moisture, Model weakness, Diagnostic model evaluation, Data assimilation, Evolutionary strategy.