



Toward essential union between evolutionary strategy and data assimilation for model diagnostics: An application for reducing the search space of optimization problems using hydrologic genome map[☆]



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ABSTRACT

Multi-objective evolutionary algorithms (EAs) and data assimilation (DA) methods are usually employed independently in water resources modeling. EAs are widely recognized to possess stochastic and adaptive capabilities but they lack temporal evolution of model behavior when applied in hydrology. However, DA methods have gained credibility to account for observation and model uncertainties, and to temporally update model states. While these independent capabilities are naturally needed in hydrology, there are limited methodologies to combine EAs with DA methods. Consequently, this study demonstrates the evolutionary data assimilation (EDA) approach as a unified framework to combine the capabilities of multi-objective EAs and DA. A unique feature of the EDA is its provision of biological genome-like data leading to further development of a hydrologic genome map with diagnostic and predictive descriptions of the model. The developed genomic map is shown to be temporally persistent connecting distinct landmarks in initial model states, parameters, and input forcing variables. The approach is demonstrated for the assimilation of daily streamflow into the Sacramento Soil Moisture Accounting (SAC-SMA) model in Fairchild Creek catchment in southern Ontario, Canada. The findings show that the genomic map reduced the original search space by 75% and the updated bound by 63%. The diagnostic capability of the genome map is supported by its identification of robust and sensitive model parameters/variables leading to a better description of the model behavior to changes in decision space. In terms of streamflow estimation, the genome map was found to be 84% as accurate as the updated streamflow estimate, 36% more accurate than the calibration output, and 54% more accurate than the open loop estimate. When evaluated for streamflow forecasts for up to 30 days ahead, the genomic map was found to be 99% accurate as the updated estimate and 16% more accurate than the calibrated forecasts. These demonstrated diagnostic and predictive capabilities of the genome map provide an appealing framework towards a better understanding of water resource modeling to improve planning and management outcomes.

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1. Introduction and background

As noted by Maier et al. (2014), most real world problems are represented on a large decision space, making it difficult for evolutionary algorithms (EAs) to identify near-global optimal solutions in acceptable time frames. Consequently, to adapt EAs for practical and operational purposes, the decision space needs to be reduced into a smaller and a manageable search space. Accordingly,

this paper presents a method based on the union between evolutionary strategy and data assimilation to reduce the search space for a hydrologic model in a streamflow forecasting procedure.

EAs are widely known for their population based approach, together with stochastic and adaptive capabilities to addressing complex and indeterminate problems. EAs employ biological evolution and natural selection to evolve a population of members through several evolutionary cycles usually referred to as a generation (Eiben and Smith, 2003; Coello Coello et al., 2002; Deb, 2001). The candidate members (or solutions) of the problem compete among themselves under environment conditions (or objectives), with the high performing members naturally selected to reproduce

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new members for evaluation. Typically, the members are represented in two important spaces: i) the genotype (or decision space), representing the internal properties (e.g., input values) of the problem, and ii) the phenotype, representing the expressed behavior of the problem. In water resources modeling, the genotype represents a vector string of values for model parameters, initial states and input forcing data, whereas the simulated output (e.g., discharge) from the model represents the phenotype. The members in the population undergo competition and selection in phenotype space, whereas in genotype space, the members undergo variation and reproduction of new members.

The population members are usually evaluated under multiple but independent objectives using the concept of Pareto-optimality (Deb, 2001; Coello Coello et al., 2002; Goldberg, 1989), which is, an advanced multi-objective procedure with the capability to assess members under multiple objectives simultaneously. The high performing members adapt to changing environment conditions, due to continual improvement in the quality of population members for each cycle of evolution. The continued competition and selection of high performing members, together with the evolution of the population through several cycles of evolution, produces the non-dominated (or the Pareto-optimal) set of members with each providing a unique compromise between the evaluation objectives.

In hydrology, EA was first employed by Wang (1991) for single objective model calibration, then followed by a justification for multi-objective parameter estimation by others including Gupta et al. (1998); Yapo et al. (1998); Duan et al. (1993, 1992). The multi-objective evolutionary strategy has now been widely applied in water resources primarily for model calibration studies (Dumedah et al., 2012a; Efstratiadis and Koutsoyiannis, 2010; Dumedah et al., 2010; van Werkhoven et al., 2009; Wohling et al., 2008; Bekele and Nicklow, 2007; Nazemi et al., 2006; Tang et al., 2006; Khu and Madsen, 2005; Madsen, 2003). The multi-objective EA applications have mainly focused on model prediction accuracy, with its related emphasis on phenotype space. Studies have examined numerous methods of choosing members from the Pareto-optimal set defined in phenotype space (Dumedah et al., 2012b; Crispim and de Sousa, 2009; Wohling et al., 2008; Bekele and Nicklow, 2007; Taboada and Coit, 2006; Khu and Madsen, 2005; Madsen, 2003). However, very few studies have actually focused on the properties of population members and their evaluation in genotype space (Dumedah et al., 2012a, b; 2010; Wagener et al., 2009; Nazemi et al., 2006; Wagener et al., 2003, 2002). Wagener et al. (2003) underscored a dynamic identification of parameter sets through the assessment of model decision variables using clustering analysis. It is noteworthy that the Dynamic Identifiability Analysis (DYNIA) Analysis by (Wagener et al., 2002) examined parameter identifiability over time without considering parameter interactions. Nazemi et al. (2006) identified robust parameter sets through the assessment of Pareto-optimal members in genotype space. The assessment of members in genotype space is crucial because the genotype connects to the internal dynamics of the model, which is made up of parameters, initial states, and input forcing variables. That is, the assessment of members in genotype space is appealing and it holds a huge potential for evolutionary strategy in water resources. This integrated evaluation in model decision space is relevant because the indeterminate nature of water resources modeling is typically associated with numerous sources of uncertainty.

While the assessment of members in genotype space is not straight-forward, it has the potential to reduce the search space, provide a better description about the underlying hydrologic processes, and the prediction model. In fact, the evaluation in genotype space has the potential to provide a framework for mapping the hydrologic genome – that is, an ensemble string of values

describing the internal dynamics of a hydrologic model under varied landscape properties, initial states, and weather conditions. To achieve this objective, analytical approaches are needed to provide formalized procedures towards efficient evaluation of population members in genotype space.

To address these issues, the current state of application of multi-objective EAs needs to be refined to specifically account for temporal challenges in water resource modeling. EA applications in water resources have been temporally static, in a way that models are usually examined for a fixed time period. The temporally static applications are partly due to the nature of evolution in EAs, where population members are evaluated, usually against temporally static observations over several cycles of evolution. It has been widely recognized that the performance of calibrated hydrologic models usually decline when applied to out-of-sample or validation time periods (Vrugt and Sadegh, 2013; Dumedah et al., 2012b,a; Efstratiadis and Koutsoyiannis, 2010; van Werkhoven et al., 2009; Gupta et al., 2008; Nazemi et al., 2006; Beven, 2000). The accuracy decline in model performance for out-of-sample applications illustrate the inability of the estimated parameter values and initial states to adapt to changing environment (or evaluation) conditions.

In water resources modeling, time (aside from spatial variability) is one major cause of the changes in environment conditions (Gupta et al., 2012; Kling and Gupta, 2009; Pappenberger and Beven, 2006; Beven, 2000). Temporal changes in landscape properties (e.g., vegetation cover) and fluctuations in weather conditions play a significant role to cause changes in model behavior, thereby introducing changes in the environment conditions (Gupta et al., 2012, 2008; Beven, 2000). But the unique property of population based membership in multi-objective EAs is appealing, with each member providing a distinct function to adapt to changing environmental conditions. A procedure to refine this unique property is needed to address temporal dynamics in water resources modeling.

However, the indeterminate (and related temporal) nature of modeling the water cycle has ratified data assimilation (DA) as a popular and a promising approach to account for several sources of uncertainty in hydrologic modeling. Primarily, data assimilation improves upon model predictions by updating the model state trajectories through time (Houtekamer and Mitchell, 1998; Evensen, 2003). The temporal component of data assimilation is vital, because it offers the opportunity to monitor the dynamics of the model behavior through time. That is, the prediction model can be monitored for its response to temporal changes in landscape properties and weather conditions. Consequently, a union between multi-objective EAs and data assimilation offers a unique capability to diagnose the model dynamics, with the potential to map out the hydrologic genome in concert with landscape properties and weather conditions.

This study outlines the research prospects, provides a demonstration framework to combine the multi-objective evolutionary strategy with data assimilation, and presents an assessment framework for evaluating members in genotype space. The evolutionary strategy and data assimilation are complementary, with the potential to synthesize the stochastic and adaptive capabilities of EA, and the ability of temporal state updating from DA into a unified framework. That is, when put together, the combined EA and DA approach offer a unique procedure to simultaneously explore the internal dynamics of a hydrologic model, update its initial states through time, with the potential to improve upon model predictions, provide a diagnostic description about the model and its weaknesses, thereby leading to better understanding of hydrologic processes.

As a contribution to the special issue in Maier et al. (2014), this study: i) outlines the research prospects of combining evolutionary strategy with data assimilation approach; ii) uses a case study to

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