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Design and implementation of a general software library for using NSGA-II with SWAT for multi-objective model calibration

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ABSTRACT

Calibrating watershed-scale hydrologic models remains a critical but challenging step in the modeling process. The Soil and Water Assessment Tool (SWAT) is one example of a widely used watershed-scale hydrologic model that requires calibration. The calibration algorithms currently available to SWAT modelers through freely available and open source software, however, are limited and do not include many multi-objective genetic algorithms (MOGAs). The Non-Dominated Sorting Genetic Algorithm II (NSGA-II) has been shown to be an effective and efficient MOGA calibration algorithm for a wide variety of applications including for SWAT model calibration. Therefore, the objective of this study was to create an open source software library for multi-objective calibration of SWAT models using NSGA-II. The design and implementation of the library are presented, followed by a demonstration of the library through a test case for the Upper Neuse Watershed in North Carolina, USA using six objective functions in the model calibration.

Software availability: The software is available free and open source on Github: https://github.com/mehmetbercan/NSGA-II_Python_for_SWAT_model.

1. Introduction

The Soil and Water Assessment Tool (SWAT) is a widely used watershed model with numerous applications around the world for water quantity and quality simulations (e.g., Cools et al., 2011; Gassman et al., 2007; Liu et al., 2013). It can be classified as a semi-distributed conceptual watershed model that is capable of running on a daily or sub-daily time step over long time periods. SWAT is able to simulate large watersheds with different management scenarios where the impact on water supply and non-point source pollution can be assessed (Arnold et al., 1998). For SWAT and other similar watershed models, there are often hundreds of modeling units in a model for a single watershed and dozens of model parameters used to describe properties within the model. One of the modeler's most important and difficult tasks is to calibrate these model parameters so that the model's output matches observational data such as streamflow observations collected within the watershed.

Many algorithms and tools have been developed and applied for calibrating SWAT models. SWAT-CUP represents one widely used tool in the SWAT community for applying calibration algorithms to SWAT models. SWAT-CUP includes different calibration algorithms, as well as routines for sensitivity analysis, validation, and uncertainty analysis of SWAT models (Abbaspour et al., 2007). There are other procedures and algorithms developed in the scientific community for calibration that have not yet been included in SWAT-CUP, but that would benefit SWAT modelers. For example, SWAT-CUP does not include multi-objective calibration approaches, nor does it include genetic algorithm calibration approaches (Abbaspour, 2013). SWAT modelers, however, could benefit from these calibration procedures, especially for large watersheds where multiple streamflow observations are available (Arnold et al., 1999; Bekele and Nicklow, 2007; Kirsch et al., 2002; Santhi et al., 2001; White and Chaubey, 2005).

Genetic Algorithms (GAs) offer the ability to effectively solve

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highly non-linear optimization problems and have been used for a variety of water resources challenges. Being an evolutionary algorithm, GAs use principles of genetics and natural selection for optimization (Haupt and Haupt, 2004). They are well suited for hydrologic models, which usually cannot be adequately calibrated by gradient-based calibration algorithms. The objective function for each solution in a GA can be evaluated in parallel computations, which provide computational advantages (Zhang et al., 2013, 2012). The heuristic search procedure of GAs, relying on stochastic search rules, increases the probability of finding non-unique solutions. Previous studies have shown that these properties of GAs allow them to converge to optimal solutions for a variety of problems (Winston et al., 2003) including the challenge of calibrating watershed-scale hydrologic models (Arabi et al., 2006; Nicklow and Muleta, 2001).

Multi-objective calibration algorithms have been shown to increase model performance for hydrologic models of large watersheds (Andersen et al., 2001). In contrast to the more widely used single-objective calibration algorithms available to SWAT users now in tools like SWAT-CUP, multiple-objective calibration better constrains the calibration process, resulting in a calibrated model that better matches the physical conditions within the watershed (Niraula et al., 2012). Watershed models may use multiple objective functions in a calibration procedure to account for potentially competing objectives, even for cases when only a single streamflow station is available for calibration (e.g., two objectives might be better able to match peak flows and maintain annual water volume balance between the model and observations). They can also allow modelers to take advantage of multiple observational time series (e.g., streamflow at two or more locations in the watershed or streamflow and soil moisture observations at two or more locations in the watershed).

There is a class of calibration routines that combine the benefits of both multi-objective and genetic algorithm calibration approaches: the so called multi-objective genetic algorithms (MOGAs). One of the most popular MOGAs is the Non-Dominated Sorting Genetic Algorithm II (NSGA-II). NSGA-II is a fast and efficient population-based optimization technique that can be parallelized. The algorithm has been shown to be superior to other MOGAs (Deb et al., 2002; Zitzler et al., 2000) and it has the potential to reduce calibration time through efficiency in the algorithm itself and its ability to easily be mapped to parallel computing resources (Deb et al., 2002; Tang et al., 2006; Zitzler et al., 2000). The algorithm has significant improvements over the original NSGA (Srinivas and Deb, 1994) including adding elitism, reducing the complexity of the non-dominated sorting procedure, and replacing a sharing function with a crowded-comparison function. The NSGA-II algorithm has also been shown to be an effective tool for watershed model calibration (Bekele and Nicklow, 2007; Confesor and Whittaker, 2007; Hejazi et al., 2008; Kayastha et al., 2011; Khu and Madsen, 2005; Lu et al., 2014; Shafii and Smedt, 2009; Zhang et al., 2012).

While NSGA-II has been used for calibrating watershed models, there is no known software implementation of NSGA-II for calibrating SWAT models that is freely available to the community. Some studies did report creating a multi-objective calibration tool for SWAT models using NSGA-II (Bekele and Nicklow, 2007; Kayastha et al., 2011; Lu et al., 2014). However, based on personal communication, the source code for these implementations is either no longer available or not publicly available. The goal of this work, therefore, is to create an open source and freely-available NSGA-II software library for SWAT model calibration. We designed the tool to be library that can be used alone or incorporated into other software tools. We specifically designed the software to be easily integrated into SWAT-CUP given the popularity of this tool within the SWAT community. We chose to implement the library using the Python programming language because of its growing popularity in the scientific computing community.

In the remaining sections of this paper, we first describe the algorithm for using NSGA-II with SWAT for model calibration, then describe the design and implementation of the NSGA-II/SWAT library including compatibility with SWAT-CUP, and finally present a test case application of the library for calibrating a SWAT model of the Upper Neuse watershed in North Carolina. As part of this test case application, we compare the results of the NSGA-II calibration to results from a single-objective calibration to show the improvement obtained by using the multi-objective NSGA-II algorithm. We have provided the source code for the NSGA-II/SWAT library as an open source and freely available repository through GitHub: https://github.com/mehmetbercan/NSGA-II_Python_for_SWAT_model.

2. The NSGA-II algorithm and its integration with SWAT

2.1. Overall process flow

In this section we explain the NSGA-II algorithm and how we integrated SWAT calibration into the algorithm when designing the NSGA-II/SWAT library. Our approach follows the example of past work using NSGA-II for SWAT calibration (e.g., Bekele and Nicklow, 2007; Kayastha et al., 2011; Lu et al., 2014), but extends this past work to create a general and reusable software tool. For further detail on the NSGA-II algorithm itself, readers are referred to Deb et al. (2002). For convenience, we provide a mapping between NSGA-II and SWAT calibration terminology in Table 1.

A standard NSGA-II process typically begins with a random parent population P_i (Deb et al., 2002). However, here we start with a Latin Hypercube Sampling (LHS) (See Step 1 in Fig. 1) because better results have been achieved for SWAT models using this approach (Bekele and Nicklow, 2007). The LHS operator is executed first to create an initial combined population ($R_{i=0}$). We use the subscription “i” to represent a generation (iteration) number. The initial combined population must be at least twice as large the population size for reasons that will become clearer in forthcoming steps of the algorithm.

Each solution in the initial combined population ($R_{i=0}$) is considered to be a SWAT calibration parameter set. The SWAT input files are edited to include this solution, the model is executed, and the objective functions are evaluated using observational data and the SWAT model output data (See Steps 2–4 in Fig. 1). These model runs can be performed in parallel for each solution within the population. Once this process has been completed, the solutions within the population (R_i) are ranked using the results of the objective function evaluation process and a non-dominating sorting approach (See Step 5 in Fig. 1). Details of this non-dominating sorting approach are provided in Section 2.2.1.

The best performing solutions from R_i as determined by the non-dominating sorting approach are used to form the parent population (P_i). The number of solutions in the parent population is determined by the user defined population size. In the case of ties where multiple solutions exist with the exact same ranking at the cut-off point for creating P_i, a crowded distance sorting operator is used to break the tie (See Step 6 in Fig. 1). This operator is explained in Section 2.2.2. In short, the solutions with the larger crowding distance value, which acts as a dummy fitness in the sorting operator, are chosen to fill the remaining spots in P_i. Using the parent population, a new child population ($C_{i+=1}$) is determined through a selection, crossover and mutation operator (See Step 7 in Fig. 1), which is explained in Section 2.2.3. This entire procedure is repeated until the termination criteria are met.