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A solute and water flux library for catchment models

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MOTIVATION

Simple coupling of models can be inhibited by overlapping process descriptions and differing spatial and temporal scales. However the process of bringing together multiple models can be enhanced if at least one of the models provides capabilities to adjust itself to the more specific requirements of other models.

Key design considerations in the development of such models include successive layers of abstraction in the process description, and efforts to preserve generality of process description in deep layers of specialization. Object orientated design of model code, using generalized interfaces, is one way to create such functionality. The advantages of an object oriented code structure for hydrological models, even without the utilization of inheritance, were outlined by Wang et al. [2005].

This paper focuses on the development of a coupled model system designed to evaluate landscape level nitrogen fluxes across multi-use watersheds. The goal is to outline the general steps and decision-making processes that are required in the development of coupled systems, with particular attention on the development of model code to facilitate coupling. This case study focuses on the coupling a hydrologic catchment modeling framework, CMF (see Vaché and McDonnell [2006]), with a plot scale biogeochemical nitrogen flux model MOBILE, and extension of the DNDC model (Li et al. 1992).

The MOBILE (MOdular BIOSphere SimuLation Environment) model is a plot scale model framework describing biomass production, decomposition, mineralization, nitrification and denitrification. CMF is a DHSVM (Wigmosta et al. [1994]) style catchment model, primarily designed for the calculation of catchment runoff generation, mean residence times, and of travel paths of conservative tracer.

THE MODEL FRAMEWORK

As a fully distributed simulation model, CMF is the natural framework for the coupled model, where the coupling invokes a number of instances of the lumped MOBILE model, each allocated to represent a different location within the CMF landscape. Despite the simplicity of the concept, a wide variety of details are involved, beginning with the fact that although the original CMF software was designed to operate in different modes of process description depth, its internal structure was not explicitly designed to facilitate the modular use of the different components. The initial step was therefore a redesign of the CMF code base to transform the solitary CMF model, including a GUI, into a solute and water flux library for catchment models, considering different kinds of application modes. The previous CMF version was implemented in C++ using the Microsoft Foundation Classes, and therefore only able to run on Windows PC. The library is implemented in ANSI C++ which allows compilation on any platform providing a standard conform C++ compiler.

SPATIAL RESOLUTION

The simulations are spatially-distributed with the catchment domain divided into model cells defined by location, center elevation, area, and adjacent neighbors. Under this definition the model is not restricted to square raster approaches, allowing to run the model in finer resolution in areas of greater spatial heterogeneity. A similar approach was taken by Band et al. [2001] in an application of the RHESSys model, where a fine resolution was used to capture the highly variable riparian dynamics, and was coarsened in less variable upslope regions. This type of flexibility is designed to balance the need to capture spatial dynamics with the pragmatic need to maintain acceptable computational times. Nonetheless, within the CMF framework, the use of a regular squared raster is still supported.

The cell class, called "UpslopeCell", is an abstract class. It implements the neighborhood relation to other cells, though, as an abstract class, the actual transport of water and solutes is not included. Interfaces are provided as pure virtual functions to access information about the cell state, for example depth of the saturated zone, amount of ponded water, or average saturation. A complete subbasin is described as a collection of interconnected UpslopeCells. Inheritance is used to support different implementations of the UpslopeCell class. The current version of the framework currently supports two implementation of UpslopeCell: the vertical homogenous cell and the layered cell. **Figure 1** outlines the this approach

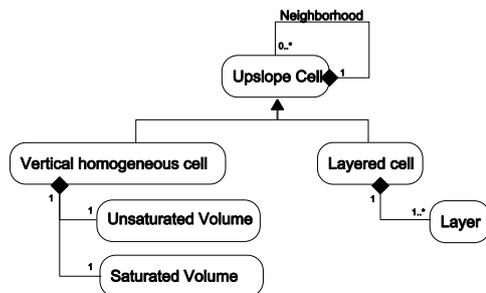


Figure 1: UML 2.0 diagram of the UpslopeCell class.

VERTICAL RESOLUTION

The key assumption of the vertical homogenous cell is that the shallow soil can be described using two layers, each with constant soil properties. The upper layer corresponds to the unsaturated zone, and the lower layer to the saturated zone. Vertical flow is assumed in the unsaturated zone, horizontal flow in the saturated zone. The size of the storages is variable according to the saturated depth. The mass balance equations of the two storages are based on DHSVM and described in detail in Vaché and McDonnel [2006]. The layered cell is tailored for application with biogeochemical models, like MOBILE, that require a detailed description of soil layer heterogeneity and concentration profiles. The vertical resolution of the soil layers is constant, and each layer is either unsaturated (with vertical flow only) or partially or fully saturated (with lateral flow). Each water store derives from the abstract class "StateVariable", and implements a function "Derive". This function calculates the storage change rate and includes a get/set function pair to interact with the current state of the storage variable. **Figure 2** shows the inheritance graph of "StateVariable".

The class "Concentration" also inherits from StateVariable and represents the concentration of an arbitrary conservative tracer. Derivates of "Concentration" can implement concentrations of species reacting with the environment, via simple time dependent decay functions, or via more complex transformation functions. Each water storage maintains a collection of concentrations.

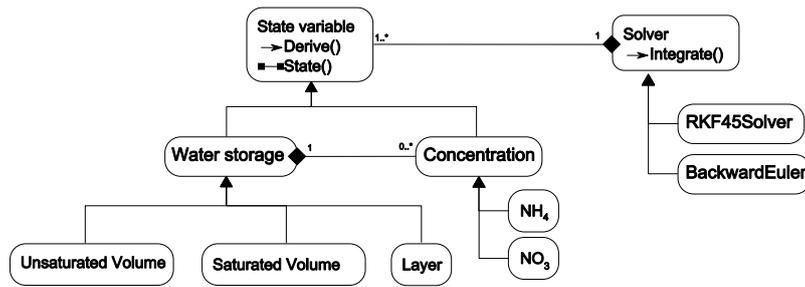


Figure 2: Inheritance diagram of "StateVariable"

The existence of a "StateVariable" abstract class allows the model to be solved by a central ODE-solver, which can be selected from a list of available solvers. Hillyer et al. [2003] built a COM-based general purpose modelling system, with a comparable structure.

MODEL COUPLING

To give the user the full power to combine these different features, a wrapper for scripting languages is provided, using a Simplified Wrapper and Interface Generator (SWIG, www.swig.org). Application is made more generic in that the user is not required to provide input files in a specific format, but rather writes a configuration script in Python or another SWIG supported language, and merges the environments. Any data source accessible through the scripting language, like (spatial) databases, plain text files, or XML files and web services can be incorporated. Many script programs are written with the purpose to build input files required by environmental models, with unit conversions and insertion of default values, where the direct use of a script language for model setup can spare the step of writing the specific model input files.

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