



Reimplementation and reuse of the Canegro model: From sugarcane to giant reed



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ABSTRACT

Model reuse can be limited by software design, which often forces third parties to completely rewrite new versions of existing models before adapting them to new needs. This tendency removes resources from the improvement of models and from the extension of their domain, leading to the proliferation of software tools representing a variety of different implementations of the same algorithms. The component-oriented paradigm allows these limitations to be overcome, facilitating model reuse and extension. This study presents the application of component-oriented principles to the reimplementation of the sugarcane (*Saccharum officinarum* L.) model Canegro (DSSAT v4.5) in a framework-independent component following the BioMA architecture. The potential for reuse and extension of the component (UNIMI.Cassandra.CaneML.Canegro) is here demonstrated by its straightforward adaptation to the simulation of giant reed (*Arundo donax* L.), a promising energy crop that shares several morphological and physiological features with sugarcane. The new component, named UNIMI.Cassandra.CaneML.Arungro, extends UNIMI.Cassandra.CaneML.Canegro, and was effectively developed by inheriting about 70% of the sugarcane model code. The development, calibration and evaluation of the giant reed model were performed using field data collected in two experimental sites in Northern Italy between 2009 and 2012. Model performances were satisfactory, with average relative root mean square error and modelling efficiency for aboveground biomass simulation of 34.33% and 0.57, respectively. The Canegro component is distributed via a Software Development Kit that includes documentation of code and algorithms, and the source code of sample applications illustrating how to use it.

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1. Introduction

Although the advantages of model reuse and extension are well known and widely recognized within the international modelling community (Holzworth et al., 2010), these activities are – to a large extent – prevented by the design of agro-environmental models, that often forces third parties interested in modifying an existing model to re-implement it from the beginning (Donatelli et al., 2012). This time-consuming process often removes resources that could otherwise be available for model improvement; moreover, it often leads to solutions again characterized by a low level of extensibility. In other cases, reimplementation leads to new versions of a model that are extensible but tightly coupled to specific frameworks, and this generates dependencies that, in turn, limit the model reusability in other simulation environments (Donatelli

et al., 2012). Resources needed for reimplementation increase with model complexity and this, coupled with the difficulties in improving or extending the way processes are formalized, often restricts the opportunity to revise and improve agro-ecological models only to their original developers.

The component-oriented paradigm allows these limitations to be overcome, favouring model reuse by limiting dependencies, specifying interfaces, and encapsulating the algorithms in discrete units (Szyperski, 2002). As a consequence, models implemented in framework-independent libraries can be effectively used, composed and improved by third parties (Argent, 2005; Stella et al., 2014) by implementing the Adapter design pattern (Gamma et al., 1994), i.e., by developing adapters to specific frameworks. An example of the application of these principles to agro-environmental models is given by the BioMA (Biophysical Model Applications; Donatelli et al., 2012) platform, where the focus is shifted from the framework to the development of independent software components for the simulation of processes

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within different sub-domains (e.g., crop growth and development, soil hydrology, plant-pathogen interactions).

This paper presents a component-based reimplementation of the sugarcane model Canegro (Inman-Bamber, 1991; Singels and Bezuidenhout, 2002; Singels et al., 2005); in particular, the version of the model we started from is the one implemented in the DSSAT suite (Jones et al., 2003; Singels et al., 2008). Canegro was re-built as a framework-independent .NET 4 software library (i.e., UNIMI.Cassandra.CaneML.Canegro), characterized by a fine level of granularity. Each simulated process (e.g., photosynthesis) is made up of independent basic units (e.g., light interception, carbon fixation, maintenance and growth respirations) which can be easily substituted by alternative approaches. The main advantages of this kind of re-implementation lie (i) in the possibility of sharing knowledge via ready-to-use software units, because of the fine granularity and of the absence of dependencies, and (ii) in the ease of reuse and extension of the component algorithms. The latter is here demonstrated with the extension of the component to the simulation of giant reed (*Arundo donax* L.), a promising energy crop (Pilu et al., 2014) that shares several morphological and physiological traits with sugarcane. Giant reed is a perennial grass with a pronounced tolerance to a broad spectrum of soil types (Perdue, 1958) and high productivity levels even with low agronomic inputs (Christou et al., 2000; Williams et al., 2009). These features make the cultivation of giant reed advantageous from both an economic and energetic point of view even in marginal areas, where competition for land surfaces between food (or feed) and energy crops is not a critical issue. However, the interest in giant reed as an energy crop has increased only recently and this is probably the reason why process-based crop models for simulating this species are still not available, although a structural model (Thornby et al., 2007) and some phenological (Spencer and Ksander, 2006; Graziani and Steinmaus, 2009) and biometric (Pompeiano et al., 2013) relationships were proposed. Some peculiar features of giant reed (e.g., the presence of a rhizome and its role in determining the rate of stalk emission) make generic crop simulators (e.g., CropSyst, WOFOST, STICS) unsuitable, and attempts to target their calibration would likely lead to poor performance or to inconsistent parameterizations, potentially undermining model robustness (Confalonieri et al., 2010). However, giant reed is an ideal crop for the development of an explanatory simulation model, since its low genetic variability (Mariani et al., 2010) (i) minimizes the risk of losing generality because of processes modulated in different ways for different cultivars, and (ii) allows to identify a single set of parameters to adequately represent the ecophysiology of the species.

2. Materials and methods

2.1. Software architecture

The software design follows the guidelines outlined by Donatelli and Rizzoli (2008), thus promoting component reusability by limiting dependencies and providing a semantically rich, public interface (i.e., *IStrategyCanegro*). According to the design pattern façade, this interface is implemented by simple and composite model units included in the UNIMI.Cassandra.CaneML.Canegro component (i.e., the strategies). More specifically, a simple strategy is an indivisible unit of algorithm coherently representing a sub-process, i.e., the smallest piece of an algorithm for which alternate approaches exist or could exist in the future (Fig. 1). Simple strategies are composed into objects of increasing complexity, that – according to the composite pattern – are in turn subject to composition, leading to a hierarchical structure

culminating with a composite strategy that represents the whole model (Fig. 1). This architecture allows both model developers and third parties to extend the component by simply adding new strategies implementing original or existing modelling approaches to reproduce the processes of interest. The implementation of the bridge pattern implies the separation of model algorithms from data-types structures in two different components (Donatelli and Rizzoli, 2008). This pattern allows the substitution of modelling approaches, that are non-unique by definition, without changing the interfacing with I/O services and the description of the biophysical domain, that does not vary in case different modelling approaches are used. The domain classes describe the biophysical domain by including inputs and outputs of the model with their attributes, whereas the ontology of the parameters, related to the specific modelling representation and not to the domain, is made available via the related strategies. The coherence of input, output and parameter values with their ontology can be verified through the test of pre- and post-conditions, according to the design-by-contract approach (Meyer, 1997). UNIMI.Cassandra.CaneML.Canegro – currently used for sugarcane simulations within the BioMA platform – is distributed in a Software Development Kit including hypertext files documenting the component code, the implemented approaches and the software design; it also includes the code (C#, Visual Studio 2010) of a sample application illustrating how to use the component. Strategies, domain classes and interfaces can be inspected via an external application named Model Component Explorer (<http://agsys.cra-cin.it/Tools/MCE/help/>). UNIMI.Cassandra.CaneML.Canegro can be coupled to other available .NET framework-independent components for the simulation of, e.g., soil water balance (<http://agsys.cra-cin.it/tools/soilw/help/>) or plant-pathogen interactions (<http://agsys.cra-cin.it/tools/diseases/help/>).

The component version of Canegro was tested by comparing its outputs with those produced using DSSAT v4.5 (<http://dssat.net/downloads/dssat-v45>). In order to isolate the differences due to the implementation of the plant growth algorithms from those generated by the simulation of water balance, (i) a fully irrigated treatment was chosen among those available from the DSSAT setup (Pongola site, 1968–1971; parameters were set to the default values for the variety NCo376; Singels et al., 2008), whereas (ii) UNIMI.Cassandra.CaneML.Canegro was run under potential conditions, i.e., with solar radiation and air temperature as the only factors driving crop growth and development.

2.2. Component reuse

The Canegro model – in its component version – was used as a starting point for the definition of a new, explanatory giant reed model (Arungro, hereafter). This choice is suggested by the affinity of giant reed to sugarcane, since the two species share many morphological and physiological traits. Canegro has a high level of detail in describing key processes for sugarcane, like the dynamics of leaf area index (LAI) expansion at leaf and tiller level, while accounting for leaf size heterogeneity within the same tiller and among different tiller cohorts. In most cases, the representation of processes was modulated via parameter calibration to adapt it to giant reed. For the processes where the differences between the two species required the formalization of new algorithms, the extensibility of UNIMI.Cassandra.CaneML.Canegro simplified the modification of specific modelling approaches via the development and addition of alternative strategies (Fig. 1). The extension of Canegro to the simulation of giant reed was based on an actual reuse of the UNIMI.Cassandra.CaneML.Canegro code for about 70% of the strategies.

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