Automatic generation of material laws based on rheological models using a genetic algorithm

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Developing material laws based on rheological models is an established method in the field of material modelling. Here, the identification of an appropriate rheological model fitting a given set of experimental data is often a challenging task. This contribution presents an automated method for searching such rheological models. To this end, a tree representation for rheological models is defined first. Then, a generic material law, that can implement any rheological model given by a model tree, is introduced. Based on this, a genetic algorithm is used to generate rheological models, which are subsequently evaluated by fitting to measurements. This method allows to search for a global optimum in the space of material models. Successful applications to both synthetic and actual experimental data are demonstrated.

1 Rheological models

The application of rheological models within the formulation of material laws is established [1]. The basic elements, which are elasticity, viscosity and plasticity, are combined in parallel and series connections. By nesting these connections, an infinite number of models can be constructed. Each model can be represented by a tree structure with integer nodes. The inner nodes are the parallel and serial connections (encoded by -2 and -1) with a subtree for each component in the connection. The terminal nodes are the basic elements encoded by 2 (elasticity), 3 (viscosity) and 4 (plasticity). As an example, a rheological model and its representation as a tree are shown in Fig. 1. Within a generic material subroutine, the connections relations and the basic element laws can be recursively resolved to evaluate the material law specified by an arbitrary tree structure. Currently it is implemented as a one-dimensional model, but an extension to full 3D is straightforward having the work by Kießling et al. in mind [4].

Fig. 1: Rheological model and its tree representation according to the chosen encoding.

2 Genetic Algorithm

The described generic material subroutine allows to test a large variety of different models. By augmenting it with a standard parameter identification procedure, the fitting quality with respect to a given set of measurements can be evaluated. However, the number of possible models grows exponentially with the number of involved basic elements, making manual testing tedious and unreliable. Hence, a genetic algorithm is used to search for good models automatically. Genetic algorithms are stochastic optimization procedures inspired by evolution [2]. The application demonstrated within this context is especially similar to the subclass of evolutionary programming pioneered by Koza, where the objective is the automated development of algorithms [3]. The basic idea of all types of evolutionary algorithms states that the potential solutions are considered as individuals, which compete for survival and procreation. The success of an individual is expressed by a scalar fitness value. Here, this value contains the fit quality as main component, but also complementary aspects as the number of fit parameters (fewer is better) and the depth of the model tree (flatter is better). New individuals are created by selecting from the existing individuals at random and applying genetic operators. This selection is not performed uniformly, but with an advantage for the fitter individuals. The population space is usually limited and requires removal of individuals for inserting new ones. Again, fit individuals are granted an advantage. Both mechanisms generate an selection pressure, that usually leads to an improvement of the average fitness over time. The two main classes of genetic operators applied to the selected individuals are mutation and crossover. Mutation is the exploration operator. It takes one individual and alters it slightly to create a new one. Here, a variety of different mutation operators are implemented including removing a node, inserting a node and switching the type of a base element. Crossover is the operator that exploits the fact, that models with useful building blocks should accumulate.

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in the population over time. It takes two individuals and creates a new one by recombining the two. The standard method is the so-called subtree crossover, which is cutting the model trees in half at random and exchanging the subtrees. All genetic operators often generate redundant models. For example, multiple elasticity elements in a connection can be merged into one element. Similarly, nested parallel connections can be merged into one without changing the model. Hence, each model is reduced to its smallest and unique tree representation before the evaluation and fitting is performed. The fitting process itself occasionally fails or yields useless results, usually due to overparametrization of the model. Here, the error tolerance of genetic algorithms is beneficially, as any problem cases can be just signalled by a low fitness. The algorithm terminates after a given number of model evaluations, or if no improvement was found after a given time. As a result, not just the very best, but a set of the best individuals is returned.

3 Results

Fig. 2: Models found when re-identifying the linear standard model from synthetic tension and relaxation tests. These models can fit the synthetic data exactly (except artificial noise). In addition to the original linear standard solid model (leftmost), models extended by inactive elements (rightmost) are found.

As a first test, synthetic experimental data were generated with a linear standard solid model with additive Gaussian noise. The model response to uniaxial tension tests with a different loading rate and a relaxation test were used for identification. Obviously, rediscovering the linear standard solid model would be the optimal result. The genetic algorithm was started multiple times with different random number seeds and always found a model providing a precise fit. However, the discovered model did not always match the original linear standard solid (see Fig. 2). A typical issue are models that are extended by completely ineffective components like plasticity elements with huge yield stress. Consequently, better methods for cropping back models, once a good fit was found, are required. Similar tests were conducted with more complex models, like Bingham-Hooke model, with similar results. Overall, the method works for synthetic data and is very noise-resistant as well.

Fig. 3: Rheological found for the experimental data for Polyamide 6. Here, the fit on the right side shows considerable deviations.

Next, the genetic algorithm was applied to search for a suitable rheological model for fitting real experimental data. The investigated material was Polyamide 6 and the measurements consisted of two uniaxial tension tests at two strain rates and a relaxation test. The model identified by the algorithm as well as the resulting fit to the experimental data are shown in Fig. 3. Obviously, the model fit does not match that well this time. Further investigations show, that this is due to the limited set of basic elements. Specifically, having only linear elasticity available, matching the nonlinear tension curves is difficult. In fact, a manual search did not yield a better model within the given search space. This demonstrates the potential of the developed and presented approach.

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