

P ρ Log: Combining Logic Programming with Conditional Transformation Systems (Tool Description)*

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Abstract

P ρ Log extends Prolog by conditional transformations that are controlled by strategies. We give a brief overview of the tool and illustrate its capabilities.

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1 Brief overview

P ρ Log is a tool that combines, on the one hand, the power of logic programming and, on the other hand, flexibility of strategy-based conditional transformation systems. Its terms are built over function symbols without fixed arity, using four different kinds of variables: for individual terms, for sequences of terms, for function symbols, and for contexts. These variables help to traverse tree forms of expressions both in horizontal and vertical directions, in one or more steps. A powerful matching algorithm helps to replace several steps of recursive computations by pattern matching, which facilitates writing short and intuitively quite clear code. By the backtracking engine, nondeterministic computations are modeled naturally. Prolog's meta-programming capabilities allowed to easily write a compiler from P ρ Log programs (that consist of a specific Prolog code, actually) into pure Prolog programs.

P ρ Log program clauses either define user-constructed strategies by transformation rules or are ordinary Prolog clauses. Prolog code can be used freely in P ρ Log programs, which is especially convenient when built-ins, arithmetics, or input-output features are needed.

P ρ Log is based on the ρ Log calculus [15], whose inference system is basically the SLDNF-resolution, with normal logic program semantics [14]. Therefore, Prolog was a natural choice to implement it. The ρ Log calculus has been influenced by the ρ -calculus [5], which, in itself, is a foundation for the rule-based programming system ELAN [2]. There are some other languages for programming by rules, such as, e.g., ASF-SDF [16], CHR [11], Claire [4], Maude [6], Stratego [17], Tom [1]. The ρ Log calculus and, consequently, P ρ Log differs from

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them, first of all, by its pattern matching capabilities. Besides, it adopts logic programming semantics (clauses are first class concepts, rules/strategies are expressed as clauses) and makes a heavy use of strategies to control transformations. We showed its applicability for XML transformation and Web reasoning [7], and in modeling rewriting strategies [9].

Here we briefly describe the current status of P ρ Log. A more detailed overview can be found in [10]. The system can be downloaded from its Web page <http://www.risc.jku.at/people/tkutsia/software/prholog/>. The current version has been tested for SWI-Prolog [18] version 7.2.3 or later.

2 How P ρ Log works

P ρ Log atoms are supposed to transform term sequences. Transformations are labeled by what we call *strategies*. Such labels (which themselves can be complex terms, not necessarily constant symbols) help to construct more complex transformations from simpler ones.

An instance of a transformation is finding duplicated elements in a sequence and removing one of them. We call this process double merging. The following strategy implements it:

$$\text{merge_doubles} :: (s_X, i_x, s_Y, i_x, s_Z) \Longrightarrow (s_X, i_x, s_Y, s_Z).$$

Here `merge_doubles` is the strategy name. It is followed by the separator `::` which separates the strategy name from the transformation. Then comes the transformation itself in the form $lhs \Longrightarrow rhs$. It says that if the sequence in lhs contains duplicates (expressed by two copies of the variable i_x , which can match individual terms and therefore, is called an *individual variable*) somewhere, then from these two copies only the first one should be kept in rhs . That “somewhere” is expressed by three sequence variables, where s_X stands for the subsequence of the sequence before the first occurrence of i_x , s_Y takes the subsequence between two occurrences of i_x , and s_Z matches the remaining part. These subsequences remain unchanged in the rhs . Note that one does not need to code the actual search process of doubles explicitly. The matching algorithm does the job instead, looking for an appropriate instantiation of the variables. There can be several such instantiations.

Now one can ask a question, e.g., to merge doubles in a sequence (1, 2, 3, 2, 1):

$$?- \text{merge_doubles} :: (1, 2, 3, 2, 1) \Longrightarrow s_Result.$$

P ρ Log returns two different substitutions: $\{s_Result \mapsto (1, 2, 3, 2)\}$ and $\{s_Result \mapsto (1, 2, 3, 1)\}$. They are computed via backtracking. Each of them is obtained from (1, 2, 3, 2, 1) by merging one pair of duplicates. A completely double-free sequence is just a normal form of this single-step transformation. P ρ Log has a built-in strategy for computing normal forms, denoted by **nf**, and we can use it to define a new strategy `merge_all_doubles` in the following clause (where `:-`, as in Prolog, stands for the inverse implication):

$$\text{merge_all_doubles} :: s_X \Longrightarrow s_Y \text{ :- } \mathbf{nf}(\text{merge_doubles}) :: s_X \Longrightarrow s_Y, !.$$

The effect of **nf** here is that it starts applying `merge_doubles` to s_X , and repeats this process iteratively as long as it is possible, i.e., as long as doubles can be merged in the obtained sequences. When `merge_doubles` is no more applicable, it means that the normal form of the transformation is reached and it is returned in s_Y . The Prolog cut at the end cuts the alternative ways of computing the same normal form. In general, Prolog primitives and clauses can be used freely in P ρ Log. Now, for the query

$$?- \text{merge_all_doubles} :: (1, 2, 3, 2, 1) \Longrightarrow s_Result.$$

we get a single answer $s_Result \mapsto (1, 2, 3)$. Instead of using the cut, we could have defined `merge_all_doubles` purely in P ρ Log terms, with the help of a built-in strategy `first_one`. It applies to a sequence of strategies (in the clause below there is only one such strategy, `nf(merge_doubles)`), finds the first one among them which successfully transforms the input sequence (s_X below), and gives back just *one result* of the transformation (in s_Y):

$$\text{merge_all_doubles} :: s_X \Longrightarrow s_Y \text{ :- } \mathbf{first_one}(\mathbf{nf}(\text{merge_doubles})) :: s_X \Longrightarrow s_Y.$$

P ρ Log is good not only in selecting arbitrarily many subexpressions in “horizontal direction” (by sequence variables), but also in working in “vertical direction”, selecting subterms at arbitrary depth. *Context variables* provide this flexibility, by matching the context above the subterm to be selected. A context is a term with a single “hole” in it. When it applies to a term, the latter is “plugged in” the hole, replacing it. There is yet another kind of variable, called *function variable*, which stands for a function symbol. With the help of these constructs and the `merge_doubles` strategy, it is pretty easy to define a transformation that merges two identical branches in a tree, represented as a term:

$$\begin{aligned} \text{merge_double_branches} :: c_Con(f_Fun(s_X)) \Longrightarrow c_Con(f_Fun(s_Y)) \text{ :-} \\ \text{merge_doubles} :: s_X \Longrightarrow s_Y. \end{aligned}$$

Here c_Con is a context variable and f_Fun is a function variable. This is a naming notation in P ρ Log, to start a variable name with the first letter of the kind of variable (individual, sequence, function, context), followed by the underscore. After the underscore, there comes the actual name. For anonymous variables, we write just $i_$, $s_$, $f_$, $c_$.

Now, we can ask to merge double branches in a given tree:

$$?- \text{merge_double_branches} :: f(g(a, b, a, h(c, c)), g(a, b, h(c))) \Longrightarrow i_Result.$$

P ρ Log returns two different substitutions via backtracking:

$$\begin{aligned} \{i_Result \mapsto f(g(a, b, h(c, c)), g(a, b, h(c)))\}, \\ \{i_Result \mapsto f(g(a, b, a, h(c)), g(a, b, h(c)))\}. \end{aligned}$$

To obtain the first one, c_Con matched to the context $f(\circ, g(a, b, h(c)))$ (where \circ is the hole), f_Fun to the symbol g , and s_X to the sequence $(a, b, a, h(c, c))$. `merge_doubles` transformed $(a, b, a, h(c, c))$ to $(a, b, h(c, c))$. The other result is obtained by matching c_Con to $f(g(a, b, a, \circ), g(a, b, h(c)))$, f_Fun to h , s_X to (c, c) , and merging the c 's in the latter.

One can have an arbitrary sequence (not necessarily a variable) in the right hand side of transformations in the queries, e.g., instead of i_Result above we could have had $c_C(h(c, c))$, asking for the context of the result that contains $h(c, c)$. Then the output would be $\{c_C \mapsto f(g(a, b, \circ), g(a, b, h(c)))\}$.

Similar to merging all doubles in a sequence above, we can also define a strategy that merges all identical branches in a tree repeatedly, as `first_one(nf(merge_double_branches))`. It would give $f(g(a, b, h(c)))$ for the input term $f(g(a, b, a, h(c, c)), g(a, b, h(c)))$.

P ρ Log execution principle is based on depth-first inference with leftmost literal selection in the goal. If the selected literal is a Prolog literal, then it is evaluated in the standard way. If it is a P ρ Log atom of the form $st :: \tilde{s}_1 \Longrightarrow \tilde{s}_2$, due to the syntactic restriction called well-modedness (formally defined in [9]), st and \tilde{s}_1 do not contain variables. Then a (renamed copy of a) program clause $st' :: \tilde{s}'_1 \Longrightarrow \tilde{s}'_2 \text{ :- } body$ is selected, such that st' matches st and \tilde{s}'_1 matches \tilde{s}_1 with a substitution σ . Next, the selected literal in the query is replaced with

the conjunction $(body)\sigma$, $\mathbf{id} :: \tilde{s}'_2\sigma \implies \tilde{s}_2$, where \mathbf{id} is the built-in strategy for identity: it succeeds iff its rhs matches the lhs. Evaluation continues further with this new query. Success and failure are defined in the standard way. Backtracking explores other alternatives that may come from matching the selected query literal to the head of the same program clause in a different way (since context/sequence matching is finitary, see, e.g., [8, 12, 13]), or to the head of another program clause. Negative literals are processed by negation-as-failure.

The P ρ Log distribution consists of the main file, parser, compiler, the library of built-in strategies, and a part responsible for matching. P ρ Log programs are written in files with the extension `.rho`. A P ρ Log session is initiated withing Prolog by consulting the main file. After that, the user can load a `.rho` file, which is parsed and compiled into a Prolog code. P ρ Log queries are also transformed into Prolog queries, which are then executed.

P ρ Log can be used in any development environment that is suitable for SWI-Prolog. We provide a special Emacs mode for P ρ Log, which extends the Prolog mode for Emacs [3]. It supports syntax highlighting, makes it easy to load P ρ Log programs and anonymize variables via the menu, etc. A tracing tool for P ρ Log is under development.

One can summarize the main advantages of P ρ Log as follows: compact and declarative code; capabilities of expression traversal without explicitly programming it; the ability to use clauses in a flexible order with the help of strategies. Besides, P ρ Log has access to the whole infrastructure of its underline Prolog system. These features make P ρ Log suitable for nondeterministic computations, manipulating XML documents, implementing rule-based algorithms and their control, etc.

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