Description of GADEL

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Abstract

This article describes the first implementation of the GADEL system : a Genetic Algorithm for Default Logic. The goal of GADEL is to compute extensions in Reiter's default logic. It accepts every kind of finite propositional default theories and is based on evolutionary principles of Genetic Algorithms. Its first experimental results on certain instances of the problem show that this new approach of the problem can be successful.

General Info

The system works on SUN/Solaris or PC/Linux with Sicstus Prolog3.7.x and C. It is written in Prolog and it generates a Sicstus library in C. The current version is about 3000 lines of Prolog.

Description of the System

Default Logic and Genetic Algorithms

Default Logic has been introduced by Reiter (Reiter 1980) in order to formalize common sense reasoning from incomplete information, and is now recognized as one of the most appropriate framework for *non monotonic reasoning*. In this formalism, knowledge is represented by a default theory (W, D) where W is a set of first order formulas representing the sure knowledge, and D a set of *default rules* (or defaults). A *default* $\delta = \frac{\alpha : \beta_1,...,\beta_n}{\gamma}$ is an inference rule providing conclusions relying upon given, as well as absent information meaning "if the *prerequisite* α is proved, and if for all $i = 1, ..., n$ each *justification* β_i is individually consistent (in other words if nothing proves its negation) then one concludes the *consequent* γ". From a default theory (W, D) one tries to build some extensions, that are maximal sets of plausible conclusions. Reiter has given the following pseudo iterative characterization of an extension E: we define

- $E_0 = W$
- and for all $k \geq 0$,

$$
\begin{aligned}
E_{k+1} = \; & Th(E_k) \cup \{\gamma \mid \frac{\alpha : \beta_1,...,\beta_n}{\gamma} \in D, \\
& \alpha \in E_k, \neg\beta_i \notin E, \forall i = 1, ..., n\}
\end{aligned}
$$

then, E is an extension of (W, D) iff $E = \bigcup_{k=0}^{\infty} E_k$. The computation of an extension is known to be $\Sigma_2^p - complete$ (Gottlob 1992). Even if the system DeRes (Cholewiński *et al.* 1999) has very good performance on certain classes of default theories, there is no efficient system for general extension calculus. The aim of the present work is to describe the first implementation of the GADEL system (*Genetic Algorithms for DEfault Logic*) which applies *Genetic Algorithms* principles to propositional default reasoning (Nicolas, Saubion, & Stéphan 2000).

Based on the principle of natural selection, Genetic Algorithms have been quite successfully applied to combinatorial problems such as scheduling or transportation problems. The key principle of this approach states that, species evolve through adaptations to a changing environment and that the gained knowledge is embedded in the structure of the *population* and its members, encoded in their *chromosomes*. If individuals are considered as potential solutions to a given problem, applying a genetic algorithm consists in generating better and better individuals. A genetic algorithm consists of the following components:

- a representation of the potential solutions in a chromosome, in most cases, a string of bits representing its *genes*,

- an initial population,

- an *evaluation function* which rates each potential solution w.r.t. the given problem,

- genetic operators that define the composition of the offsprings : two different operators will be considered : *crossover* allows to generate two new chromosomes (the offsprings) by crossing two chromosomes of the current population (the parents), *mutation* arbitrarily alters one or more genes of a selected chromosome,

- parameters : population size p_{size} and probabilities of crossover p_c and mutation p_m.

and an iteration process:

- evaluate each chromosomes,
- order the population according to evaluation rates and select the bests chromosomes,
- perform crossover and mutation on pairs of randomly selected chromosomes,
- repeat this full process until a user-defined number of populations has been explored.

The best chromosome of each population w.r.t. the evaluation function represents the current best solution to the problem.

Before a detail description of the GADEL system, it is necessary to give some arguments about the choice of the implementation language:

- In the previous section we have presented the most common version of GA but in fact each part of the system can take various forms. To develop easily a GA system the implementation language must be very flexible and modular.
- A GA system is an iterative system. The implementation language must be efficient.
- Default Logic is based on classical logic. To develop easily a GA system about Default Logic, the implementation language must be logic and symbolic.

From above, the choice of the implementation language is obvious: the most popular and efficient of the logic programming language, Prolog. We assume in the rest of the paper a minimal knowledge of Prolog. The article is organized as follows: section 2 presents the genetic algorithms aspects of GADEL, section 3 provides the process of compilation of a default theory to a prolog program, section 4 focuses on the evaluation function of GADEL and section 5 describes our experiments w.r.t. other existing systems.

GADEL: a GA system

Representation and semantics. Our purpose is to construct an extension of a given default theory (W, D). For each default $\frac{\alpha : \beta_1, ..., \beta_n}{\gamma}$ we encode in the chromosome the prerequisite α and all justifications $\beta_1, ..., \beta_n$ conjointly. Given a set of defaults of size n the chromosome will be of size $2n$. A *candidate extension* $CE(G)$ associated to a chromosome G is :

$$CE(G) = Th(W \cup \left\{ \begin{array}{l} \gamma_i \mid \frac{\alpha_i : \beta_i^1, ..., \beta_i^{k_i}}{\gamma_i} \in D \\ and \ G|_{2i-1} = 1 \ and \ G|_{2i} = 0 \end{array} \right\})$$

Population tree. According to the principles of Genetic Algorithms, we now consider a population of individuals representing candidate extensions. Usually chromosomes are strings of bits and population are sets of chromosomes. We have chosen a new representation for the population: binary trees. A population is defined inductively on the set of constructors Λ, *zero*, *one* and *zero − one* of arity, respectively, 0, 1, 1, and 2. The
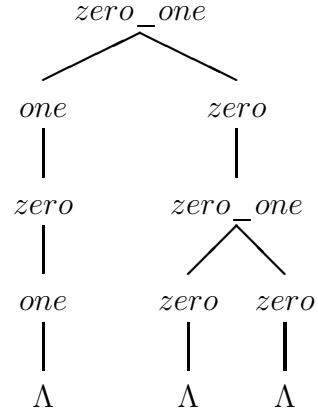

Figure 1: Population $\{0101, 1000, 1010\}$

two advantages of this representation are its compactness and unicity of each chromosome.

For example, the population $\{0101, 1000, 1010\}$ is represented by the tree in Figure 1.

Compilation of default theory

A default theory is the given of a set of (propositional) formulas W and a set of defaults D. Prerequisite, conclusion and justifications of a default are all (propositional) formulas. So the GADEL system needs a classical theorem prover. It must be efficient because it is applied on each chromosome at each new population. The obvious choice is to compile all these sets of formulas into a set of clauses. We have chosen the compilation to a disjunctive Prolog program.

Small introduction to disjunctive logic programming. The theoretical basis of Prolog is the SLD-resolution for Horn clauses[1]. It is not possible to directly insert disjunctive clauses in a Prolog program[2]. Disjunctive logic programming (resp. disjunctive Prolog) is an "extension" of Horn logic programming (resp. Prolog) which allows disjunctions in the heads of definite[3] clauses (resp. Prolog clauses). A way to handle disjunctive clauses is the *case-analysis principle*: a set of clauses $\{C \vee C', C_1, \ldots, C_m\}$ is unsatisfiable if and only if the two sets of clauses $\{C, C_1, \ldots, C_m\}$ and $\{C', C_1, \ldots, C_m\}$ are also unsatisfiable. Disjunctive clauses $(h_1 \vee \ldots \vee h_p \vee \neg b_1 \vee \ldots \vee \neg b_n)$ $(h_k, 1 \leq k \leq p$ and $b_k, 1 \leq k \leq n$ atoms) are then written $(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n)$. We have chosen the SLOU-resolution approach (Stéphan 1998) (case-analysis and SLD-reduction) as the theoretical basis of SLOU Prolog, our implementation of disjunctive Pro-

[1] A Horn clause is a clause with at most one positive literal

[2] A clause is disjunctive if it contains at least two positive literals

[3] A clause is definite if it contains one and only one positive literal

log.

The strategy of SLOU Prolog applies case-analysis by necessity: the case-analysis is used only when a head h_i of a disjunctive clause $(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n)$ is useful in the proof. This strategy needs that a negative clause[4] $\neg b_1 \vee \ldots \vee \neg b_n$ is written $false \leftarrow b_1 \wedge \ldots \wedge b_n$ and $false$ becomes the goal. This choice assumes that almost all the clauses are definite (Prolog) clauses.

From set of defaults to disjunctive Prolog program. Let us give a default $\frac{\alpha_i : \beta_i^1, \ldots, \beta_i^{k_i}}{\gamma_i}$, the ith of the default theory and a chromosome G. If $G|_{2i-1} = 1$ and $G|_{2i} = 0$ then the default is supposed to be applied and γ must be added to the candidate extension. Hence G has to be a parameter of the theorem prover. In order to calculate $(CE(G) \vdash \alpha_i)$ or $(\exists j (CE(G) \vdash \neg \beta_i^j))$, i and (i, j) also have to be parameters of the theorem prover. So a propositional variable h is compiled in a disjunctive Prolog atom $h(I, G)$. We can now describe the compilation of the three parts of a default rule.

- Compilation of a conclusion: In order to calculate $CE(G)$, we must add γ_i to the candidate extension if $G|_{2i-1} = 1$ and $G|_{2i} = 0$. We first normalize γ_i in a set of disjunctive clauses $\{h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n\}$ and compile it in a disjunctive Prolog definition:

$$\{h_1(I, G); \ldots ; h_p(I, G) : -$$
$$G|_{2I-1} = 1, G|_{2I} = 0, b_1(I, G), \ldots, b_n(I, G)\}$$

- Compilation of a prerequisite: The function f of the GADEL evaluation function compares $G|_{2i-1}$ with $CE(G) \vdash \alpha_i$ (see section 4). To prove it with a disjunctive logic program we prove $CE(G), \neg \alpha_i \vdash false$. We first normalize $\neg \alpha_i$ in a set of clauses $\{h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n\}$ and compile it in a disjunctive Prolog definition:

$$\{h_1(I, G); \ldots ; h_p(I, G) : -$$
$$I = i, b_1(I, G), \ldots, b_n(I, G)\}$$

- Compilation of justifications: The function f of the GADEL evaluation function compares $G|_{2i}$ with $\exists j (CE(G) \vdash \neg \beta_i^j)$. To prove it with a disjunctive logic programs we prove $(\exists j (CE(G), \beta_i^j \vdash false))$. We first normalize β_i^j in a set of clauses $\{h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n\}, \forall j$, and compile it in a disjunctive Prolog definition:

$$\{h_1(I, G); \ldots ; h_p(I, G) : -$$
$$I = (i, j), b_1(I, G), \ldots, b_n(I, G)\}$$

- Compilation of a formula $\omega \in W$: We first normalize ω in a set of clauses $\{h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n\}$ and compile it in a disjunctive Prolog definition:

$$\{h_1(I, G); \ldots ; h_p(I, G) : -$$
$$b_1(I, G), \ldots, b_n(I, G)\}$$

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[4] A clause is negative if it contains only negative literals

From disjunctive Prolog to Prolog. During the execution of a disjunctive Prolog program, some clauses are dynamic: case-analysis creates from a disjunctive clause $(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n)$ p new clauses $(h_1 \leftarrow b_1 \wedge \ldots \wedge b_n)$ and $\{h_k\}_{1 < k \leq p}$. A disjunctive clause is called *usable* if it has not been splitted in this set of clauses otherwise it is called *unusable*. A new clause is usable if it is the result of a case-analysis. To realize the case-analysis principle in Prolog, one needs to extend each predicate with a *program continuation P* (a difference list) that handles those dynamic clauses. A disjunctive Prolog clause $(h_1(I, G); \ldots ; h_p(I, G) : - b_1(I, G), \ldots, b_n(I, G))$ is then compiled in a set of Prolog clauses as follows:

$$h_1(I, G, P) : -$$
$$\quad usable\_?(h_1 \leftarrow b_1 \wedge \ldots \wedge b_n, P),$$
$$\quad b_1(I, G, P), \ldots, b_n(I, G, P)$$
$$;$$
$$\quad usable\_?(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n, P),$$
$$\quad unusable\_!(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n, P),$$
$$\{ \quad same\_assumptions(P, P_l),$$
$$\quad usable\_!(h_l, P_l), false(I, G, P_l),\}_{1 < l \leq p}$$
$$\quad usable\_!(h_1 \leftarrow b_1 \wedge \ldots \wedge b_n, P),$$
$$\quad b_1(I, G, P), \ldots, b_n(I, G, P).$$
$$\{h_k(I, G, P) : -$$
$$\quad usable\_?(h_k, P)$$
$$;$$
$$\quad usable\_?(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n, P),$$
$$\quad unusable\_!(h_1 \vee \ldots \vee h_p \leftarrow b_1 \wedge \ldots \wedge b_n, P),$$
$$\{ \quad same\_assumptions(P, P_l),$$
$$\quad usable\_!(h_l, P_l), false(I, G, P_l),\}_{1 \leq l \leq p, l \neq k}$$
$$\quad usable\_!(h_k \leftarrow b_1 \wedge \ldots \wedge b_n, P).\}_{1 < k \leq p}$$

Evaluation function of GADEL

The evaluation function is the heart of the GADEL system. It rates each chromosome given a default theory compiled in a disjunctive prolog program.

Evaluation of pair of genes. For a default $\delta_i = \frac{\alpha_i : \beta_i^1, \ldots, \beta_i^{k_i}}{\gamma_i}$, an intermediate evaluation function f is defined in Table 1. Given the two positions $G|_{2i-1}$ and $G|_{2i}$ in the chromosome associated to the default δ_i, the first point is to determine w.r.t. these values if this default is supposed to be involved in the construction of the candidate extension and then to check if this application is relevant.

We only illustrate f on the case $G|_{2i-1} = 1$ and $G|_{2i} = 0$ of the Table 1 (with penalty p_2 and a default

$G|_{2i-1}$	$G|_{2i}$	$CE(G) \vdash \alpha_i$	$\exists j, CE(G) \vdash \neg\beta_i^j$	penality
1	0	*true*	*false*	0
1	0	*true*	*true*	p_2
1	0	*false*	*true*	p_3
1	0	*false*	*false*	p_4
1	1	*true*	*false*	p_5
1	1	*true*	*true*	0
1	1	*false*	*true*	0
1	1	*false*	*false*	0
0	1	*true*	*false*	p_9
0	1	*true*	*true*	0
0	1	*false*	*true*	0
0	1	*false*	*false*	0
0	0	*true*	*false*	p_{13}
0	0	*true*	*true*	0
0	0	*false*	*true*	0
0	0	*false*	*false*	0

Table 1: Evaluation

with only one justification):

$$f(I, (G, Eval\_G_{>I}), (G, Eval\_G_{\geq I})) : -$$
$$G|_{2I-1} = 1, G|_{2I} = 0,$$
$$false(I, G, \_P), \qquad \%\%(CE(G) \vdash \alpha_i) = true$$
$$false((I, 1), G, \_P), \quad \%\%(CE(G) \vdash \neg\beta_i) = true$$
$$Eval\_G_{\geq I} \ is \ Eval\_G_{>I} + p_2.$$

Evaluation of chromosome and population. The evaluation of a chromosome is the total sum of the evaluations for each pair of genes. Our evaluation function is calculated directly over the population tree by a depth-first traversal. The result is a set of pairs of a chromosome and its evaluation. During the traversal, the construction of the current evaluated chromosome is prefixed and the evaluation of the genes is postfixed.

$$evaluation(Current\_Pop, Evaluated\_Pop) : -$$
$$eval\_alpha(0, \emptyset, Current\_Pop, Evaluated\_Pop).$$

$$eval\_alpha(I, G, one(Subtree), Evaluations) : -$$
$$G|_{2I-1} = 1,$$
$$eval\_beta(I, G, Subtree, Evaluations).$$

$$eval\_beta(I, G, zero(Subtree), Evaluations') : -$$
$$G|_{2I} = 0,$$
$$I' \ is \ I + 1,$$
$$eval\_alpha(I', G, Subtree, Evaluations),$$
$$map(f, I, Evaluations, Evaluations').$$

Applying the System

Methodology

Methodology for using GADEL is the same as using default logic as a framework for knowldege representation.

Specifics

The semantics of our system is the Reiter's propositional default logic.

Users and Useability

The GADEL system takes default theory as Prolog facts in an input file. Classical formulas of default theory are arbitrary formulas with conjunctions, disjunctions and negations (noted resp. &&, || and !). A default is a triplet composed of a prerequisite, a list of justifications and a conclusion. GADEL is a framework for non monotonic reasoning systems. To extend GADEL to an other system, one needs to redefine the evaluation function.

Evaluating the System

Benchmarks

We define two kinds of benchmarks: a taxonomic default theory "*people*" described in Table 2 and the well known Hamiltonian cycle problem in Table 5 as it has been described and encoded in (Cholewiński *et al.* 1999).

Comparison

DeRes and GADEL are compared on our two kinds of benchmarks. CPU times given are in seconds on a SUN E3000 ($2 \times 250Mhz$). The parameters of the genetic algorithm are $p_c = 0.8$ and $p_m = 0.1$.

GADEL:1/DeRes:0. Table 3 gives results about the people default theory. Each line corresponds to the common part of W_{people} augmented with one of the specified formula of the first column. The second column gives p_{size} the initial number of chromosomes in the population, the third one is the average number of populations needed to find an extension. The last two columns give CPU times. (Cholewiński *et al.* 1999) describes the very good performances of DeRes on some kind of default theories: the stratified ones. But it is also noticed that for a non stratified default theory the performance of DeRes are not enough to deal with a non very few number of defaults. Results given in this table shows that DeRes has a lot of difficulties with our taxonomic people example (even if the local prover is used). Conversely the number of populations are quite small for GADEL (even if the time is not so good: all the implementation is written in Prolog).

Table 4 gives results about $W_{people} \cup \{man\}$ with different sizes of populations (200 tests for each size of population). The second line gives p_{size} the initial number of chromosomes in the population. The third one gives the time spent for one complete computation of a new population. The fourth one gives the average number of populations needed to find an extension. The last one gives the average time to find an extension. These results demonstrate that the size of the population must be balanced by the time spent for one complete computation of a new population. The increase of the population size does not necessarily increase the efficiency

$W_{people} =$
$$\left\{\begin{array}{ll} \neg boy \vee \neg girl, & \neg boy \vee kid, \\ \neg girl \vee kid, & \neg human \vee male \vee female, \\ \neg kid \vee human, & \neg student \vee human, \\ \neg adult \vee human, & \neg adult \vee \neg kid, \\ \neg adult \vee \neg male \vee man, & \neg adult \vee \neg female \vee woman, \\ \neg academic \vee adult, & \neg academic \vee diploma, \\ \neg doctor \vee academic, & \neg priest \vee academic, \\ \neg prof \vee academic, & \neg bishop \vee priest, \\ \neg cardinal \vee bishop, & \neg redsuit \vee suit, \\ \neg whitesuit \vee suit, & \neg blacksuit \vee suit, \\ \neg redsuit \vee \neg whitesuit, & \neg whitesuit \vee \neg blacksuit, \\ \neg redsuit \vee \neg blacksuit \end{array}\right\}$$
$\cup \{boy\} or \cup \{girl\} or \cup \{man\} or \cup \{woman\} \cup \{man, student\}$
$or \cup \{woman, student\}$

$D_{people} =$
$$\left\{\begin{array}{ll} \dfrac{human : name}{name} & \dfrac{kid : toys}{toys} \\[4pt] \dfrac{student : adult}{adult} & \dfrac{student : \neg employed}{\neg employed} \\[4pt] \dfrac{student : \neg married}{\neg married} & \dfrac{student : sports}{sports} \\[4pt] \dfrac{adult : \neg student}{employed} & \dfrac{adult : \neg student, \neg priest}{married} \\[4pt] \dfrac{adult : car}{car} & \dfrac{adult : \neg academic}{\neg toys} \\[4pt] \dfrac{man : \neg prof}{beer} & \dfrac{man : \neg vegetarian}{steak} \\[4pt] \dfrac{man : coffee}{coffee} & \dfrac{man \vee woman : wine}{wine} \\[4pt] \dfrac{woman : tea}{tea} & \dfrac{academic : \neg prof}{\neg employed} \\[4pt] \dfrac{academic : \neg priest}{toys} & \dfrac{academic : books}{books} \\[4pt] \dfrac{academic : glasses}{glasses} & \dfrac{academic : \neg priest}{late} \\[4pt] \dfrac{doctor : medicine}{medicine} & \dfrac{doctor : whitesuit}{whitesuit} \\[4pt] \dfrac{prof : employed}{employed} & \dfrac{prof : grey}{grey} \\[4pt] \dfrac{prof : tie}{tie} & \dfrac{prof : water}{water} \\[4pt] \dfrac{prof : conservative}{conservative} & \dfrac{priest : male}{male} \\[4pt] \dfrac{priest : conservative}{conservative} & \dfrac{priest : \neg cardinal}{blacksuit} \\[4pt] \dfrac{cardinal : redsuit}{redsuit} & \dfrac{car : mobile}{mobile} \\[4pt] \dfrac{tie : suit}{suit} & \dfrac{wine \wedge steak \wedge coffee : \neg sports}{heartdisease} \\[4pt] \dfrac{sports : man}{football \vee rugby \vee tennis} & \dfrac{sports : woman}{swim \vee jogging \vee tennis} \\[4pt] \dfrac{toys \wedge (football \vee rugby) : ball}{ball} & \dfrac{toys : boy}{weapon} \\[4pt] \dfrac{toys : girl}{doll} \end{array}\right\}$$

Table 2: The taxonomic problem : "people"

		GADEL		DeRes
Problem	p_{size}	Number of populations	CPU time	CPU time
boy	325	3.3	15.4	>7200
girl	325	3.4	15.6	>7200
man	325	3.5	25.3	>7200
woman	325	3.0	14.6	>7200
$man \wedge student$	325	186.7	467.5	>7200
$woman \wedge student$	325	271.6	704.4	>7200

Table 3: GADEL:1/DeRes:0

N	$p_{size} = \frac{N(N+1)}{2}$	CPU time	Number of populations	CPU time
15	120	2.6	6.6	17.2
16	136	2.8	6.9	19.7
17	153	3.4	4.9	17.0
18	171	3.8	5.0	19.0
19	190	4.2	5.0	21.2
20	210	4.7	4.5	21.3
21	231	4.9	4.8	23.8
22	253	5.6	3.9	22.1
23	276	5.8	4.7	27.1
24	300	6.0	5.0	30.3
25	325	7.2	3.5	25.3

Table 4: $W_{people} \cup \{man\}$

		GADEL		DeRes
Problem	p_{size}	Number of pop	CPU time	CPU time
$ham.b\_3, 2, 0, 0, 1, 0, 0\_$	465	1.8	5.6	0.5
$ham.b\_4, 2, 0, 0, 1, 0, 0\_$	465	-	>7200	19.4
$ham.b\_5, 2, 0, 0, 1, 0, 0\_$	465	-	>7200	566.4
$ham.b\_6, 2, 0, 0, 1, 0, 0\_$	465	-	>7200	>7200

Table 5: GADEL:1/DeRes:1

of the genetic algorithm. Finally, Figure 2 presents for $W_{people} \cup \{man\}$ with $N = 17$ the number of tests w.r.t. the number of populations needed to obtain an extension. This figure suggests to stop computation after 6 populations and to restart with a brand new one since 80% of tests end after 6 populations at most.
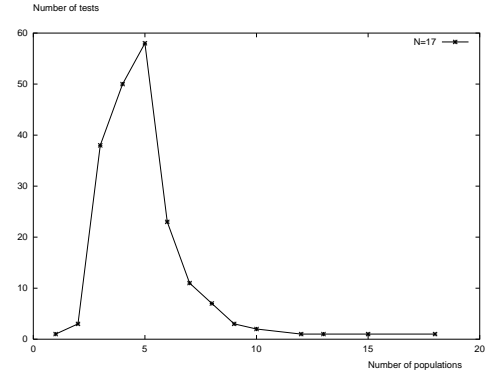

Figure 2: $W_{people} \cup \{man\}$ with $N = 17$ ($p_{size} = 153$)

GADEL:1/Deres:1. GADEL has poor performances on Hamiltonian problems. We think that it is because we do not take into account the groundedness (Schwind 1990) into our evaluation function. As a matter of fact, in the Hamiltonian problem, a solution is exactly one "chain"[5] of defaults, but, there is a lot of potential solutions (whose evaluation is null) based on two, or more, chains of defaults. The only criterion to

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[5] We say that δ is chained to δ' if the prerequisite of δ' is deducible from W and the consequent of δ.

discard these candidate extensions is the groundedness property that they do not satisfy. Conversely, in people example, a solution is a set of non conflicting defaults, but at most four defaults are chained together, and so the groundedness property is less important to reach a solution. We are now testing some new evaluation functions in order to take into account this criterion.

Other systems. We have also in mind that in the area of logic programming and non monotonic reasoning there exist others systems (Smodels (Niemelä & Simons 1997), DLV (Eiter *et al.* 1998)) able to compute stable models of extended logic program. Since this task is equivalent to compute an extension of a default theory it seems interesting to compare GADEL to these systems. But, even if DLV has the advantage to accept formulas with variables which are instantiated before computation, this system does not accept theories like our people example. On its part, Smodels does not deal with this default theory because it can not be represented by a normal logic program without disjunction. Because we have the objective to deal with every kind of propositional formulas, GADEL spends a lot of time in theorem proving and it seems not realistic to compare it with those two systems. But it will be very inter-resting to work on GADEL's architecture in order to improve its performances on particular subclasses of default theories.

Problem Size

The system is a prototype which can handle non stratified theories with about one hundred defaults.

Conclusion

In this paper, we have described the first implementation of our system GADEL whose goal is to compute extensions of every kind of finite propositional Reiter's default theories. Our new approach, using principles of genetic algorithms, seems to be relevant as it is illustrated by our experimental results. But this present work is a first approach and we have in mind many improvements as : more accurate definition of the evaluation function, using reparation techniques, local search heuristics.

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