

Roman Barták, Charles University

A NOVEL APPROACH TO INDUCTIVE LOGIC PROGRAMMING

What is ILP?

[b(no), b(n1), r(n2), b(n3), r(n4), r(n5), b(n6), r(n7), r(n8), r(n9), r(n10), r(n11), r(n12), r(n13), r(n14), r(n25), r(n16), b(n27), r(n18), r(n12), a(n10, n5), a(n19, n1), a(n5, n3), a(n7, n11), a(n5, n19), a(n0, n11), a(n0, n12), a(n4, n0), a(n3, n0), a(n8, n3), a(n0, n6), a(n2, n14), a(n7), n0), a(n0, n10), a(n0, n13), a(n17, n10), a(n0, n15), a(n3, n9), a(n5, n12), a(n0, n18), a(n1, n1), a(n1, n17), a(n1, n4), a(n11, n6), a(n6, n12), a(n6, n1), a(n5, n16), a(n7, n16), a(n4, n9), a(n13, n11), a(n5, n14), a(n1, n10), a(n56, n12), a(n5, n13), a(n8, n4), a(n12, n8), a(n2, n4), a(n2, n3), a(n1, n10), a(n6, n14), a(n15, n3), a(n8, n4), a(n19, n8), a(n2, n4), a(n2, n3), a(n18, n1), a(n9, n11), a(n7, n5)]

<



positive examples

([r(no), b(n1), b(n2), b(n3), b(n4), r(n5), b(n6), b(n7), b(n8), r(n9), b(n10), r(n11), r(n12), b(n13), r(n14), r(n15), b(n16), b(n17), b(n18), r(n19), a(n10, n2), a(n2, n9), a(n6, n3), a(n2, n13), a(n2, n11), a(n0, n1), a(n2, n12), a(n2, n0), a(n0, n4), a(n5, n2), a(n3, n0), a(n9, n6), a(n5, n0), a(n6, n0), a(n0, n7), a(n0, n10), a(n5, n11), a(n0, n12), a(n2, n18), a(n6, n4), a(n0, n14), a(n0, n13), a(n2, n13), a(n5, n13), a(n2, n1), a(n4, n1), a(n3, n16), a(13, n13), a(100, n15), a(119, n13), a(n2, n13), a(n1, n8), a(n7, n1), a(n16, n14), a(n16, n14), a(n1, n13), a(n1, n11), a(n10, n19), a(n14, n13), a(n7, n18), a(n6, n14), a(n1, n13), a(n1, n16), a(n9, n7), a(n12, n4), a(n14, n18), a(n7, n2), a(n7, n3), a(15), 1

b(No), b(N1), b(N2), b(N3), r(N4), a(N4, N2), a(N1, N4), a(No, N3), a(N1, N3), a(N1, No), a(N2, N1)

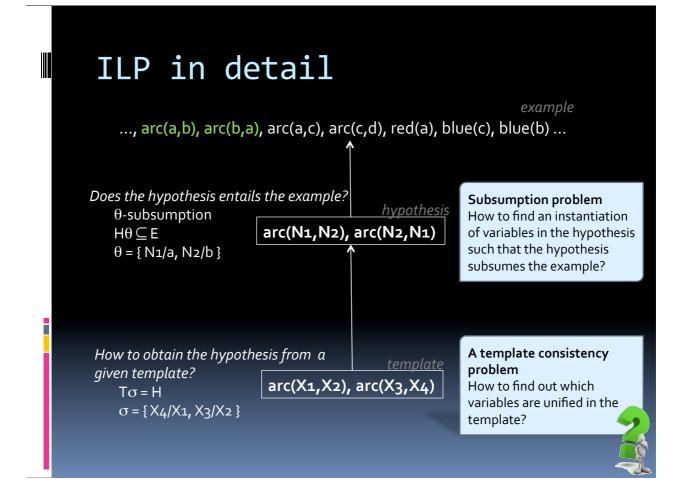
hypothesis

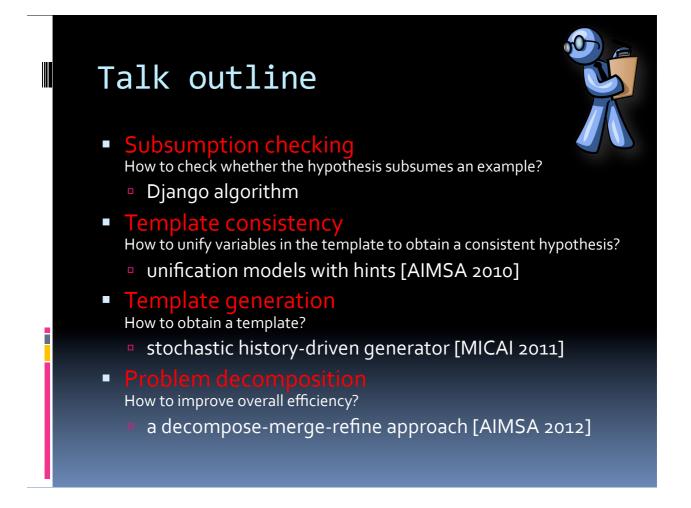
[r(no), b(n1), b(n2), b(n3), r(n4), r(n5), b(n6), r(n7), r(n8), b(n9), b(n10), b(n11), b(n12), b(n3), r(n14), b(n15), b(n16), r(n17), b(n18), r(n19), a(n13, n12), a(n7, n12), a(n12, n14), a(n6, n3), a(n13, n2), a(n9, n8), a(n5, n3), a(n1, n0), a(n0, n2), a(n4, n0), a(n0, n3), a(n7, n19), a(n5, n0), a (ns, ny), a (ns, ns), a (no, ns), a (ns, ns), a (ns, ns), a (ns, ns), a (ns), ns), a (ns, ny), a (ns, ns), a (ns, no, no), a (ns, ns, ns), a (ns, ns), a (ns, ns), a (ns, n6), a (ns, ns), a (ns), ns), a (ns, ns), a (ns, ns), a (ns, ns), a (nsi ns), a (ns), ns), a (ns), nsi), a (ns, ny), a (ns, ns), a (nsi ns), a (nsi n, rs), a (ns), ns), a (n6, nsi), a (nsi nsi), a (nsi ns), a (nsi n, rs), a (nsi nsi), a (ns k a(n9, n17), a(n1, n18), a(n4, n11), a(n7, n2)]

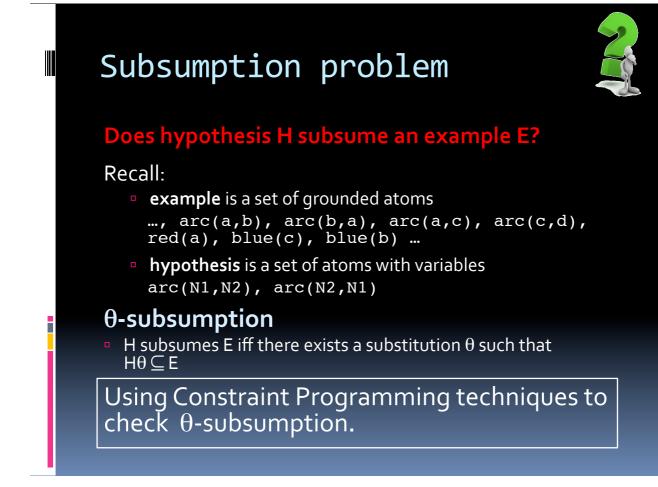
> [b(no), b(n1), b(n2), b(n3), b(n4), r(n5), b(n6), r(n7), b(n8), r(n9), b(n10), r(n11), r(n12), b(n13), r(n14), r(n15), r(n16), r(n17), b(n18), b(TEO, h(TEI), (TTEI), n5), a(n12, n15), a(n9, n7), a(n15, n17), a(n15, n14), a(n7, n2), a n5)]

[b(no), r(n1), r(n2), b(n3), r(n4), b(n5), r(n6), r(n7), b(n8), r(n9), r(n10), r(n11), r(n12), r(n13), r(n14), r(n15), r(n16), r(n17), r(n18), b(n19), a(n10, n18), a(n8, n10), a(r(n, n12), a(n16, n19), a(n6, n3), a(n3, n19), a(n2, n13), a(n11, n16), a(n15, n9), a(n5, n3), a(n0, n1), a(n2, n0), a(n2, n12), a(n9, cn=j, n(n, r, r, r, s), n(r, r, r, s), n(r, r, r, s), n(r, s), n(r, n, r, r, s), n(r, s), n(r, n, r, s), n(r, s), n(r, r, r, s), n(r, r, s), n(r, r, s), n(r, r, s), n(r, r, r), n(r), n(r a(n2, n4), a(n2, n3), a(n3, n16), a(n19, n10), a(n14, n1), a(n2, n6), a(n11, n17), a(n6, n13), a(n5, n17), a(n4, n11), a(n17, n3)]

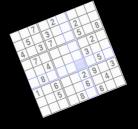
ī







What is CP?



Constraint Programming is a technology for solving combinatorial optimization problems modeled as constraint satisfaction problems:

- a finite set of decision variables
- each variable has a finite set of possible values (domain)
- combinations of allowed values are restricted by constraints (relations between variables)

Mainstream solving approach combines

inference (removing values violating constraints) with **search** (trying combinations of values)

Django algorithm

- The subsumption problem is formulated as a constraint satisfaction problem.
- Example defines the domains of constraints
 atoms with the same name → constraint domain
 - " ..., arc(a,b), arc(b,a), arc(a,c), arc(c,d), red(a), blue(c), blue(b) ...
 - binary constraint arc = {(a,b), (b,a), (a,c), (c,d)}
 - unary constraint blue = {(c), (b)}

Hypothesis formulates the CSP

- atom with variables
 constraint
- o CSP: arc(N1,N2), arc(N2,N1)

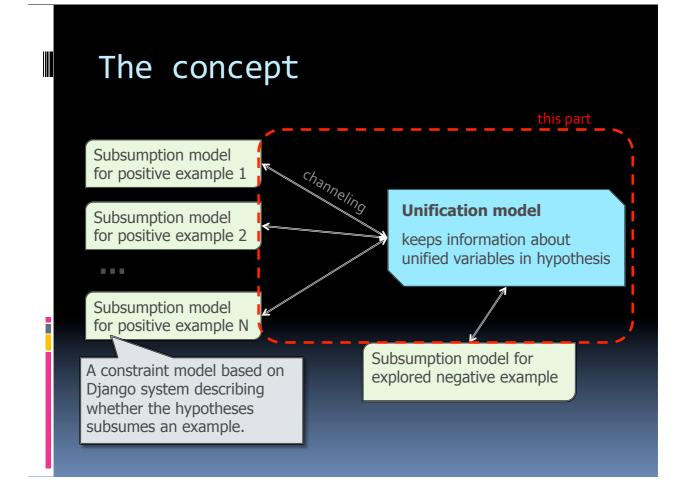
Template consistency

How to obtain a hypothesis (from a given template) consistent with examples?

Recall:

- hypothesis is a set of atoms with shared variables arc(N1,N2), arc(N2,N1)
 - hypothesis H is consistent with examples iff H subsumes all positive examples and H does not subsume any negative example
- template is a set of atoms with unique variables arc(X1,X2), arc(X3,X4)
- $T\theta = H$, where θ is a unification of variables

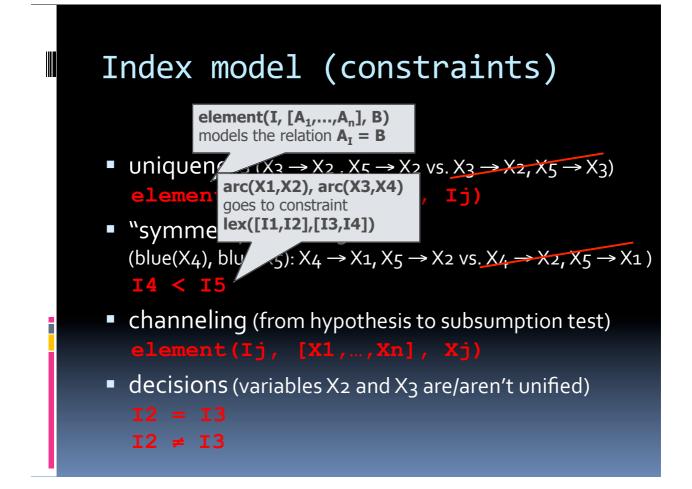
Using Constraint Programming techniques to solve the template consistency problem.



Index model (variables)

How to model which ILP variables are unified in the template? template: $arc(X_1, X_2)$, $arc(X_3, X_4)$, $blue(X_5)$ hypothesis: $arc(N_1, N_2)$, $arc(N_2, N_1)$, $blue(N_2)$

- unification can be seen as a mapping
 - $\overline{X_3 \rightarrow X_2, X_4 \rightarrow X_1, X_5 \rightarrow X_2}$
 - always map the variable with the larger index to the variable with the smaller index
- mapping is modeled using index CP variables
 - Ij with domain {1,..., j}
 ILP variable Xj maps to ILP variable X₁₁
 - I1=1, I2=2, I3=2, I4=1, I5=2



Search framework

How to decide about the unified variables?

 Unification of variables in the template is necessary only to break subsumption of negative examples!

Do for all negative examples

While the example is subsumed by current hypothesis Find subsumption θ (solution to a corresponding CSP with variables X1,..., Xn)

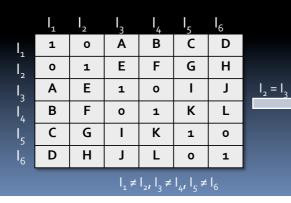
Select a pair Xi, Xj such that Xi $\theta \neq$ Xj θ

Post constraint Ii = Ij (alternatively Ii ≠ Ij)

Find subsumption for all positive examples

Boolean model

Problem: conflict I1=I2, I1≠I2 is not discovered by local (arc) consistency!
We can strengthen inference by explicitly keeping information about unified/non-unified variables in a "Boolean matrix".



1	0	0	В	C	D	
0	1	1	0	G	Н	
0	1	1	0	G	н	
В	0	0	1	К	L	
С	G	G	К	1	0	
D	Н	Н	L	0	1	
	o o B C	0 1 0 1 B 0 C G	0 1 1 0 1 1 B 0 0 C G G	0 1 1 0 0 1 1 0 B 0 0 1 C G G K	0 1 1 0 G 0 1 1 0 G B 0 0 1 K C G G K 1	

Hints

- Assume that the example contains the following atoms for predicate arc:
 - arc(a,b), arc(b,a), arc(a,c), arc(c,a)
- Clearly X1 can not unify to X2 in arc(X1,X2).
- But constraints arc(X1,X2), X1=X2 are (arc) consistent!
- By exploring atoms with the same predicate symbol in positive examples, it is possible to deduce that some variables (of this atom in the hypothesis) cannot unify (hint).

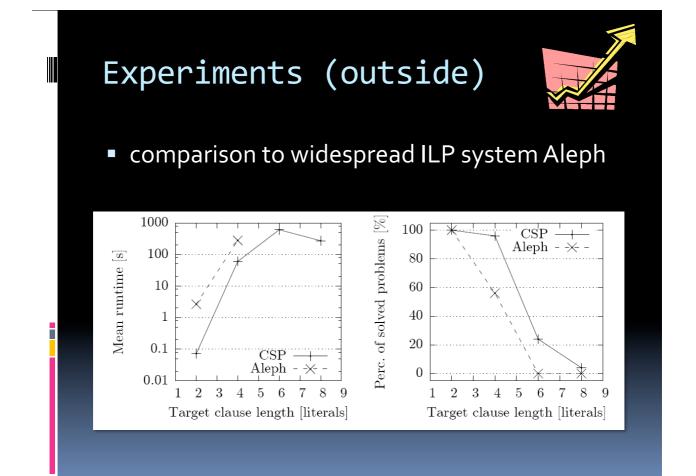
I1≠I2

Experiments (inside)



 Comparison of runtimes (milliseconds) for identifying common structures in randomly generated structured graphs (Erdős-Rényi).

#atoms	#vars	Index	Boolean	Combined	Decoupled				
#acoms		macx	Doolcall	combined	full	no SB	no hints		
7	9	0	15	16	0	16	0		
8	11	0	16	15	0	15	0		
8	11	31	281	31	21	343	32		
8	11	94	343	109	78	421	78		
9	13	94	1046	125	93	1373	94		
9	13	328	1810	436	312	2309	312		
9	13	1232	9626	1606	1170	12324	1185		
10	15	>600000	86425	>600000	236514	110981	>600000		
10	5	>0000000	00425	>000000	2305-4	110901	20000		



Obtaining a template



How to obtain a template?

Recall:

 template consists of atoms with fresh variables (each variable appears exactly once)

The task:

How many copies of each atom will appear in the template?

Searching the space of templates and learning the most promising atoms in the template.

Existing approach

Iterative deepening search

- generate all templates of given length
- if no consistent hypothesis found then increase the length

Features:

- guarantees finding the shortest hypothesis
- too slow (generate and test)

First idea

Incremental probabilistic search

- start with template containing one atom of each predicate symbol
- add new atoms randomly with uniform distribution
- if consistent hypothesis found then remove isolated atoms (do not share variables with other atoms)

Features:

- no guarantee of finding the shortest hypothesis
- faster convergence
- ready for tuning via the probability distribution for selecting added atoms

Second idea

Stochastic history-driven tabu search

- if the added atom is successful (increased the number of broken negative examples) then add it again
- if the added atom is not successful then put it to tabu list and select another atom (outside the tabu list) randomly
 - tabu list is emptied if all atoms are tabu, or added atom was successful
- stochastic version
 - probability of successful atom is set to a high value
 - probability of atoms returned from the tabu list is set to a low value

Experimental results



- looking for common sub-structure in random graphs (Barabási-Réka model)
- time limit 600 seconds

• 5 runs of stochastic algorithms

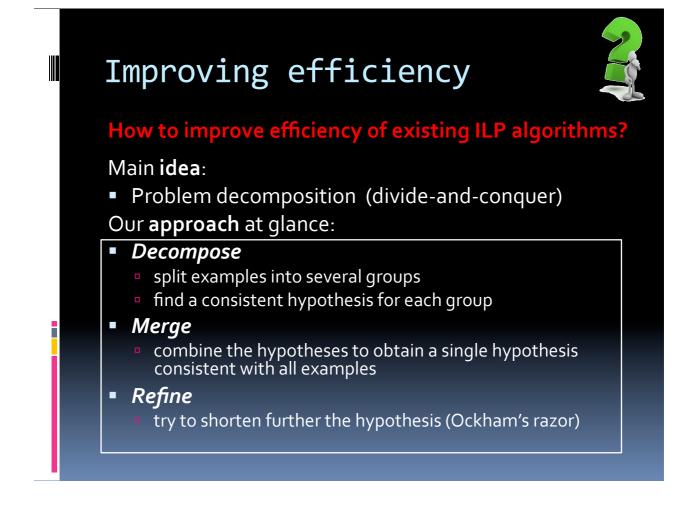
ID	S		IPS		SHDTS			
time[s]	length	time[s]	length	#unfinished	time[s]	length	#unfinished	
1.75	6	0.33	6		0.37	6		
13.97	7	2.34	7	1	1.85	7		
13.92	7	1.31	7	1	0.62	7		
0.27	5	0.11	5	1	1.17	7		
455.43	8	334.51	8		273.75	8		
10.93	7	1.16	7	1	1.02	7		
>600	-	6.13	8	1	2.11	8		
411.60	7	28.07	8		0.46	10		
11.88	7	16.41	7	1	67.70	8		
13.52	7	1.41	7	1	0.55	7	-	

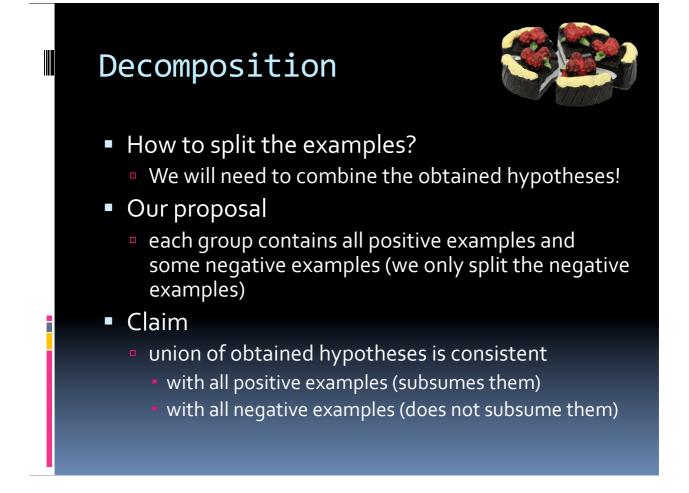
Experimental results (2)

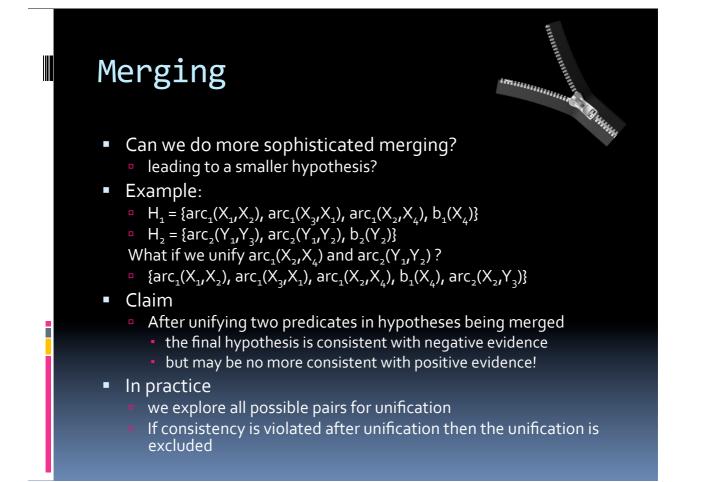


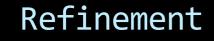
- looking for common sub-structure in random graphs (Erdös-Rényi model)
- time limit 1200 seconds

	ID	S	IP	S	SHDTS		
nodes	time[s]	length	time[s]	length	time[s]	length	
5	1.41	6	0.74	6	0.74	6	
5	>1200		204.11	9	59.65	9	
5	>1200		5.23	9	17.7	9	
5	>1200		518.47	10	448.72	10	
6	>1200		533.25	9	241.57	9	
6	>1200		313.25	9	211.78	9	
6	>1200		426.70	10	366.41	10	
6	>1200		181.28	9	215.01	9	
7	>1200		716.15	10	950.04	10	
7	27.71	7	>1200	-	3.98	7	
7	>1200		>1200	-	>1200		
7	>1200	-	201.28	10	164.61	10	





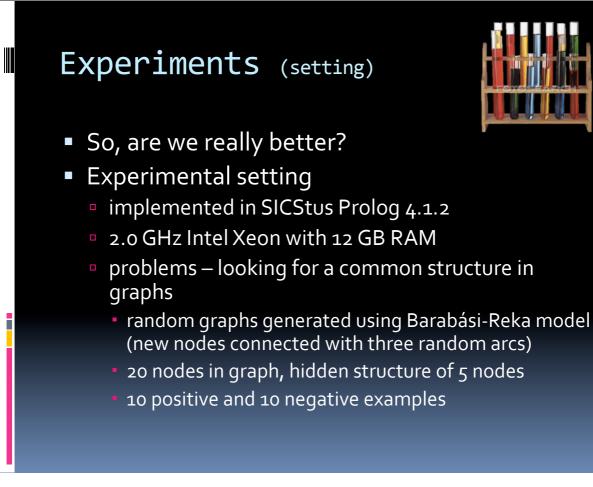


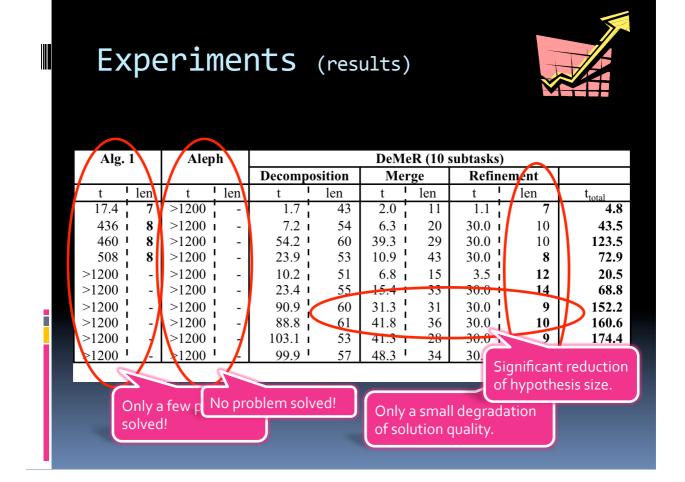




- Can we further shorten the hypothesis?
 we can remove some predicate(s)
- Claim

- After removing a predicate from the hypothesis
 - the final hypothesis is consistent with positive evidence
 - but may be no more consistent with negative evidence!
- In practice
 - we try to remove the largest subset of predicates
 - after each removal, we try to restore consistency by adding extra unifications of variables (the original template consistency algorithm)
 - if consistency is violated then the predicate is returned back





Experiments (looking inside)



DeMeR (5 subtasks)							DeMeR (3 subtasks)						
Decon	ıp.	Merge		Refin.			Decon	np.	Merge		Refin.		
t I	len	t	len	t	len	t _{total}	t	len	t	len	t	len	t _{total}
21.4	28	2.1	7	0.1	7	23.6	21.5	19	1.1	7	0.1	7	22.7
396.8	31	2.6	8	0.2	8	399.6	394.0	21	1.7	i 8	0.2	i 8	395.9
170.9	33	7.4	19	30.0	9	208.3	519.8	22	2.1	14	6.8	8	528.7
623.7	33	3.8	27	30.0	8	657.5	892.5	23	1.0	15	25.8	8	919.3
41.2	30	1.7	12	0.3	12	43.2	29.7	18	0.8	12	0.3	12	30.8
124.5 I	34	5.2	21	30.0	14	159.7	624.7	21	0.7	1 21	30.0	1 5	655.4
539.1	34	11.5	22	30.0	9	580.6	>1200	-	-		-		-
>1200	-	- 1	-	-	-	-	>1200	-	-	, -	-	, -	-
786.6	32	5.4	28	30.0	9	822.0	>1200	- 1	-	I -	-	i -	-
179.4	32	4.7	31	30.0	11	214.1	147.0	20	2.4	1 5	30.0	I 8	179.4
smaller decomposition gives worse results													

