



Analysis of the Effectiveness of G3PARM Algorithm

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Outline

- Introduction
- Model description
- Experiments
- Results
- Conclusions
- Future research lines

Introduction

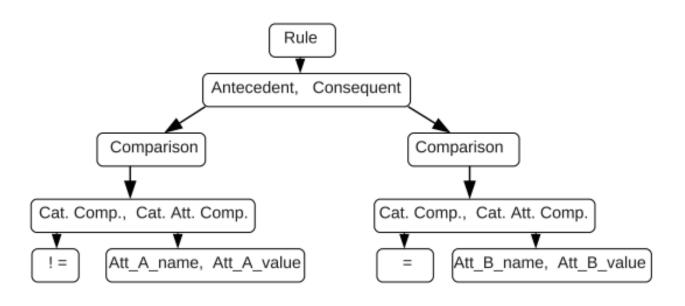
- Association rules mining (ARM): a Data Mining technique
- Classical algorithms for mining association rules:
 - Apriori
 - > FP-Growth
- Genetic Programming: computer programs
- Grammar Guided Genetic Programming (G3P)
- Our proposal is a G3P-based approach for ARM

- G3PARM = G3P Association Rules Mining
- Designed for the extraction of association rules
- Based on the use of a context-free grammar
- Each individual represents a rule
- An auxiliary population:
 - Exceed a minimum threshold for two different measures
 - Maximum auxiliary population size

Context-free grammar

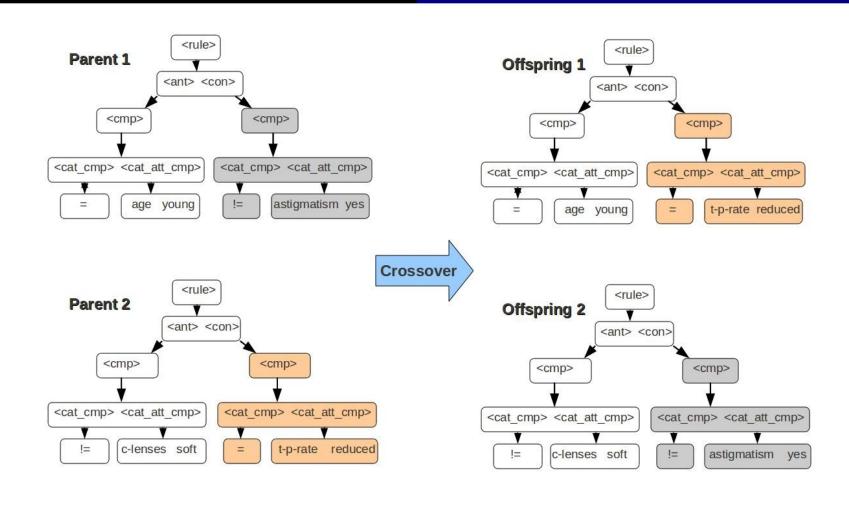
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G = (\Sigma_N, \Sigma_T, P, Rule) with: \Sigma_N = \{ \text{Rule, Antecedent, Consequent, Comparison, Categorical Comparator, }  Categorical Attribute Comparison \} \Sigma_T = \{ \text{AND, "! =" , "=" , "name", "value"} \}  P = \{ \text{Rule } = \text{Antecedent, Consequent ; }  Antecedent = \text{Comparison } | \text{AND, Comparison, Antecedent ; }  Consequent = \text{Comparison } ;  Comparison = \text{Categorical Comparator, Categorical Attribute Comparison ; }  Categorical Comparator = \text{"! =" | "=" ; }  Categorical Attribute Comparison = \text{"name", "value" ; } \}
```

Syntax-tree structure

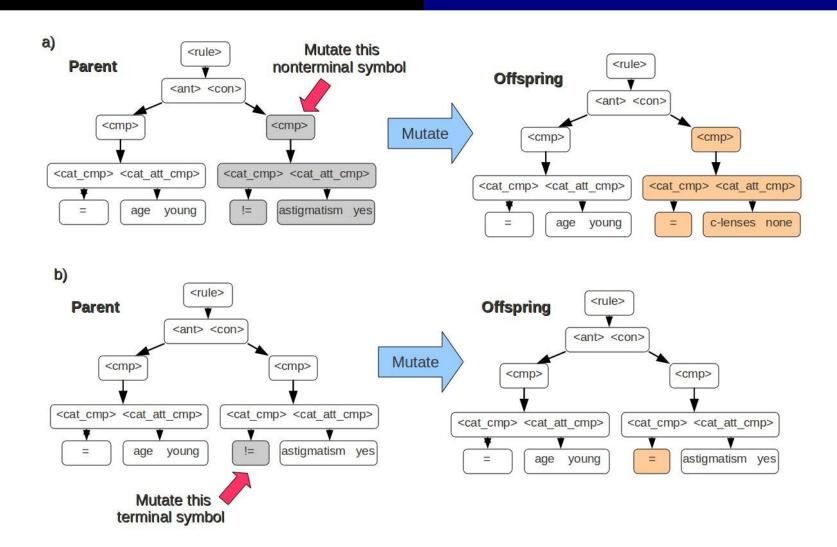


Phenotype: (!= Att_A_name Att_A_value) → (= Att_B_name Att_B_value)

Crossover



Mutation



Measures and fitness function

- G3PARM uses two measures:
 - Support measure: proportion of the number of transactions T including the antecedent A and the consequent C in a dataset D.

$$supp(A \to C) = \frac{|\{A \cup C \subseteq T, T \in D\}|}{|D|}$$

Confidence measure: proportion of the number of transactions which include A and C in transaction which include A.

$$conf(A \to C) = \frac{|\{A \cup C \subseteq T, T \in D\}|}{|\{A \subseteq T, T \in D\}|}$$

Fitness function = support measure

G3PARM algorithm

Algorithm 1 G3PARM algorithm

Require: $max_generations, N$

Ensure: A

- 1: $P \leftarrow random(N)$
- $2: A \leftarrow \emptyset$
- 3: $num_generations \leftarrow 0$
- 4: while num_generations < max_generations do
- 5: $Parents \leftarrow Select parents (P \cup A)$
- 6: Crossover (Parents)
- 7: Mutation (Parents)
- 8: Update auxiliary population (A, P)
- 9: $num_qenerations + +$
- 10: end while
- 11: return A

Algorithm 2 Update auxiliary population

Require: A, P

Ensure: A

- 1: $A' \leftarrow P \cup A$
- 2: Order (A')
- 3: Eliminate duplicate (A')
- 4: $A \leftarrow \text{Threshold}(A')$
- 5: return A

G3PARM algorithm

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Rules comprised by the same attributes are considered equals:

- 1 AND 2 -> 3
- 2 AND 1 -> 3

Algorithm 2 Update auxiliary population

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Minimum threshold for support and confidence measures

Algorithm 2 Update auxiliary population

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Experiments

Datasets

- To evaluate the usefulness of G3PARM, several experiments have been carried out on differents datasets:
 - Credit-g: 1000 instances and 21 attributes
 - HH: 22784 instances and 17 attributes.
 - Mushroom: 8124 instances and 23 attributes
 - Segment: 1500 instances and 20 attributes
 - Sonar: 208 instances and 36 attributes
 - Soybean: 683 instances and 36 attributes
 - Wisconsin Breast Cancer: 683 instances and 11 attributes
- Discretization of datasets with numerical attributes.

Experiments

Experimental set-up

G3PARM:

- Population size: 50
- Crossover probability: 70%
- Mutation probability: 10%
- Maximum derivation numbers: 24
- External population size: 20
- Support threshold: 70%
- Confidence threshold: 90%

Apriori and FP-Growth:

- Support threshold: 70%
- Confidence threshold: 90%

	$\parallel Average_support \mid$			$ Average_confidence $			% Instances		
Dataset	(1)	(2)	(3)	(1)	(2)	(3)	(1)	(2)	(3)
$\overline{CreditEqFre10}$	0.780	0.709	0.850	0.941	0.855	0.939	0.987	0.987	1.000
Credit Eq Fre 5	0.780	0.709	0.850	0.941	0.855	0.953	0.987	0.987	1.000
Credit EqWid10	0.780	0.709	0.892	0.941	0.855	0.965	0.987	0.987	1.000
Credit EqWid5	0.773	0.709	0.858	0.942	0.863	0.961	0.989	0.989	1.000
HHEqFre10	None	None	0.803	None	None	0.913	None	None	1.000
HHEqFreq5	None	None	0.740	None	None	0 .909	None	None	0.997
HHEqWid10	0.761	0.761	0.922	0.950	0.950	0.986	1.000	1.000	1.000
HHEqWid5	0.765	0.765	0.902	0.955	0.955	0.979	1.000	1.000	1.000
Mushroom	0.824	0.817	0.890	0.968	0.960	0.978	1.000	1.000	1.000
SegmentEqFre10	0.876	0.876	0.813	0.975	0.975	0.926	0.996	0.996	1.000
SegmentEqFre5	0.876	0.876	0.817	0.975	0.975	0.974	0.996	0.996	1.000
SegmentEqWid10	0.815	0.815	0.884	0.968	0.968	0.979	1.000	1.000	1.000
SegmentEqWid5	0.860	0.860	0.882	0.964	0.964	0.969	1.000	1.000	1.000
Sonar EqFre 10	None	None	0.782	None	None	0.909	None	None	1.000
Sonar EqFre 5	None	None	0.583	None	None	0.731	None	None	0.626
Sonar EqWid 10	None	None	0.958	None	None	0.887	None	None	1.000
Sonar EqWid5	0.747	None	0.835	0.942	None	0.947	0.846	None	1.000
Soybean	0.778	0.722	0.822	0.950	0.953	0.957	1.000	1.000	1.000
WBCEqFre10	None	None	0.875	None	None	0.958	None	None	1.000
WBCEqFre5	None	None	0.806	None	None	0.928	None	None	1.000
WBCEqWid10	0.821	0.821	0.900	0.996	0.996	0.971	0.821	0.821	1.000
WBCEqWid5	0.872	0.872	0.864	0.996	0.996	0.956	0.872	0.872	1.000
Ranking	2.204	2.522	1.272	2.159	2.431	1.409	2.340	2.386	1.272

- (1) Apriori
- (2) FP-Growth
- (3) G3PARM

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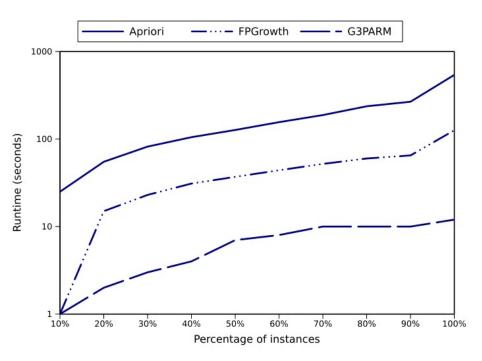
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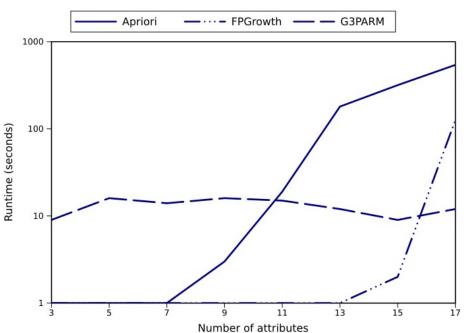
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Scalability

Different number of instances



Different number of attributes



Conclusions

- Novel G3P-based algorithm for mining association rules
- G3PARM obtains rules with:
 - High support
 - High confidence
 - High representative rules
- G3PARM scales quite linearly as we increase up the dataset size and the number of attributes

Future research lines

- Use of numerical attributes
- Modify our approach to work with infrequent pattern
- Multiobjective version using support and confidence as objectives to be optimized



Thanks!



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