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Single- and Multi-Objective Genetic Programming: New Runtime Results for SORTING

Overview

Genetic Programming (GP):

- Highly complex GP variants address challenging problems, e.g., in symbolic regression
- Currently, it seems to be impossible to analyse these complex variants on complex problems.

Our key questions

- Which optimisation problems can provably be solved by (simple) GPs in polynomial time?
- Can we provide design support to a practitioner?

Current Status "EA Theory"

- Computational Complexity Analysis of Evolutionary Computing
- EAs for discrete combinatorial optimisation (lots of results)
- Evolutionary Multi-Objective Optimisation (many results)
- Ant Colony Optimisation (some results)
- EAs for continuous optimisation (initial results)
- Particle Swarm Optimisation (initial results)
- Our Goal: Rigorous insights into the working principles of GP using existing approaches!

Current Status "GP Theory"

Initial article [Durrett/Neumann/O'Reilly 2011] "GP Computational Complexity on ORDER/MAJORITY" Properties of the functions:

- Separable (subproblems can be optimised independently)
- Admit multiple solutions
- Additional works by Kötzing, Neumann, Nguyen, O'Reilly, Sutton, Urli, and Wagner (2011-2014):
- MAX problem, generalised ORDER/MAJORITY
- Different mutation strategies
- Different multi-objective GPs

In summary:

- Techniques: fitness-based partitions, random walks, coupon collector arguments, drift analysis, failure events, ...
- many bounds known

SORTING



- One of the basic problems in computer science.
- Optimisation problem: maximise the sortedness in a given permutation of elements.
- First combinatorial optimisation problem analysed for EAs.
- Many measures of sortedness work provably well for permutation based EAs (Scharnow/Tinnefeld/Wegener 2002).

Measures of Sortedness

Given a permutation s (e.g. 1 3 2 4 5)

- INV(s) pairs in order in s
- HAM(s) Hamming distance to *optimum*
- RUN(s) number of ascending (sorted) subsequences
- LAS(s) longest ascending sequence length
- EXC(s) number of pairwise exchanges

Scharnow/Tinnefeld/Wegener 2002: Polynomial upper bounds for all functions, except RUN.

GP and SORTING

Four Algorithms

- Tree-based approaches
- Inorder parse leads to (incomplete) permutation**
- Consider different sortedness (fitness) measures



Algorithms (summary)

(1+1)-GP*, F(X)

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(1+1)-GP, F(X)
requires:
noteworthy:
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not worse no bloat control

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(1+1)-GP, MO-F(X)
requires:
noteworthy:
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at least not longer parsimony pressure towards shorter solutions

SMO-GP, MO-F(X) requires: noteworthy:

weak dominance number of different sortedness values limits population size

Variation Operator: HVL-mutate

With equal probability, do...



Choice of parameter k:

- k=1
 do a single operation
- k=1+Poisson(1) do multiple operations

Results (before this paper)

F(X)	(1+1)-G	(1+1)-GP, F(X)	
	single	multi	single/multi
INV			
LAS			
HAM			
EXC			
RUN			

F(X)	(1+1)-GP, MO-F(X)		SMO-GP, MO-F(X)
	single	multi	single/multi
INV			
LAS			
HAM	∞		$O(nT_{init} + n^4)$
EXC	∞		$O(nT_{init} + n^3 \log n)$
RUN	∞		$O(nT_{init} + n^3 \log n)$

Results (*this paper)

F(X)	(1+1)-G	(1+1)-GP, F(X)	
	single	multi	single/multi
INV	$O(n^3T_{max})$ *	$O(n^3T_{max})$ *	
LAS	∞ *	$\Omega\left(\left(\frac{n}{e}\right)^n\right)^\star$	
HAM	∞ *	$\Omega\left(\left(\frac{n}{e}\right)^n\right)^{\star}$?
EXC	∞ *	$\Omega\left(\left(\frac{n}{e}\right)^n\right)^\star$	
RUN	∞ *	$\Omega\left(\left(\frac{\tilde{n}}{e}\right)^n\right)^\star$	

F(X)	(1+1)-GP, MO-F(X)		SMO-GP, MO-F(X)
	single	multi	single/multi
INV	$O(T_{init} + n^5)^*$?	$(-2\pi + 5) \star$
	- (- 1/10)		Advertisement
LAS	$O(T_{i-i} + n^2 \log n)^*$	$O(I_{init}+$	Approximation-Guided
LAS	$O(I_{init} + n \log n)$	$n^2 \log n$ †*	Approximation duraca
TTAM		2	Evolution (AGE)
HAM	∞	4	
EXC	∞	?	- Theory-motivated
DUN	~	2	many dimension (2 20D)
KUN		· ·	- many atmension (2-200)





Algorithms (summary)

(1+1)-GP*, F(X)

number of sortedness improving steps limits solution size

(1+1)-GP, F(X) no bloat control

(1+1)-GP, MO-F(X) parsimony pressure

SMO-GP, MO-F(X) number of different sortedness values limits population size

Results SMO-GP

Proof idea:

- 1. Introduce the empty solution in $O(kT_{init})$
- 2. Build up the Pareto front step by step.



Polynomial bounds for SMO-GP–single/-multi using INV & LAS

Algorithm (1/4) (1+1)-GP*-single for maximisation

- 1 Choose an initial solution X;
- 2 repeat
- $3 \quad | \quad \text{Set } Y := X;$
- 4 Apply the mutation operator HVL mutate with k = 1 to Y;
- 5 if f(Y) > f(X) then set X := Y;

Algorithm (1/4) (1+1)-GP*-single for maximisation

- 1 Choose an initial solution X;
- 2 repeat
- $3 \quad | \quad \text{Set } Y := X;$
- 4 Apply the mutation operator with k = 1 to Y;
- 5 if f(Y) > f(X) then set X := Y;

Algorithm (2/4) (1+1)-GP -single for maximisation

- 1 Choose an initial solution X;
- 2 repeat
- $3 \quad | \quad \text{Set } Y := X;$
- 4 Apply the mutation operator with k = 1 to Y;
- 5 | if $f(Y) \ge f(X)$ then set X := Y;

Algorithm (3/4) (1+1)-GP -single for maximisation

- 1 Choose an initial solution X;
- 2 repeat
- $3 \quad | \quad \text{Set } Y := X;$
- 4 Apply the mutation operator with k = 1 to Y;
- 5 | if $f(Y) \ge f(X)$ then set X := Y;

Parsimony pressure to favour short solutions: use MO-F(X) instead of F(X)

 $MO-F(Y) \ge MO-F(X)$ holds iff F(Y) > F(X) or (F(Y) = F(X) and $C(Y) \le C(X))$

Algorithm (4/4) SMO-GP

- 1 Choose an initial solution X;
- 2 Set $P := \{X\};$
- 3 repeat
- 4 Choose $X \in P$ uniformly at random;
- 5 Set Y := X;
- 6 Apply mutation to Y;
- 7 **if** $\{Z \in P \mid Z \succeq Y\} = \emptyset$ then set
 - $P := (P \setminus \{Z \in P \mid Z \succ Y\}) \cup \{Y\};$

A proper MO algorithm for the sortedness F(X) and the solution quality C(X).

Results (1+1)-GP*

→ The expected optimisation time is $O(n^3T_{max})$ using INV.

Proof based on fitness-based partition:

- n(n-1)/2+1 different sortedness values possible
- Probability to make an improving mutation
- Overall optimisation time bounded by

$$\frac{1}{3} \cdot \frac{1}{2} \cdot \frac{1}{n} \cdot \frac{1}{T_{max}} = \Omega\left(\frac{1}{nT_{max}}\right)$$
$$\sum_{k=0}^{n \cdot (n-1)/2} O\left(nT_{max}\right) = O(n^3 T_{max})$$

For HAM, LAS, RUN & EXC: local optima exist that can only be left in expected exponential time with n mutations.

Results (1+1)-GP

→ No results for the (1+1)-GP, F(X).

→ The expected optimisation time of (1+1)-GP-single on MO-LAS is O(T_{init}+n²log n).

Proof idea:

- Deleting all blocking and surplus leaves takes O(T_{init}+n log n)
- Correctly inserting the missing leaves then takes O(n²log n)
- "Multi" case: a sortedness improvement may be accompanied by the insertion of many elements...

Results (1+1)-GP

Bound the solution size $[t=poly(n) \text{ steps and } C(T_{init})=poly(n)]$

- Failure probability for inserting at most n^ε in a single HVL operation is e^{-Ω(nε)}.
- For LAS and EXC, at most n sortnedness improving steps are possible.
- Thus, the failure probability for adding at most nn^{ϵ} in t time steps is $te^{-\Omega(n\epsilon)} = e^{-\Omega(n\epsilon)}$.
- Thus, the size does not exceed T_{init}+nn^ε within poly(t) time steps, with high probability.
- ➔ The optimisation time of (1+1)-GP-multi on MO-LAS is O(T_{init}+n²log n), with probability 1-o(1).

Proof idea:

- As before
- Use Chernoff bounds and multiplicative drift with tail bounds to consider multiple mutations.

Methods

Huge set of methods for the analysis is available:

- Fitness-based partitions
- Expected distance decrease
- Coupon Collector's Theorem
- Markov, Chebyshev, Chernoff, Hoeffding bounds
- Markov chain theory: waiting times, first hitting times
- Rapidly mixing Markov chains
- Random walks: gambler's ruin, drift analysis, martingale theory
- Identifying typical events and failure events
- Potential functions

Computational Complexity Analysis

Black Box Scenario

- Measure the runtime T by the number of fitness evaluations.
- Consider time to reach
 - an optimal solution
 - a good approximation

Alternative: Analyse

- expected number of fitness evaluations
- success probability after a fixed number of t steps.

Introduction

There are many

- successful applications and
- experimental studies
- of Genetic Programming.

We want to

- argue in a rigorous way about GP algorithms and
- contribute to their theoretical understanding.

This is also important for the acceptance of GP outside the EC community.

Classical Algorithm Analysis

• Classical algorithm analysis has a large focus on runtime and approximation behavior of algorithms.

Our key questions

- Which optimization problems can provably be solved by (simple) GPs in polynomial time?
- (Which functions can provably be learned by (simple) GP systems in polynomial time?)