Novel Application of Mutual Information in Transfer Learning for Genetic Programming





Yilin Liu, Gareth Taylor, Zhengwen Huang Department of Electrical and Electronic Engineering, Brunel University of London

Introduction

How to find Building Blocks early?

Identifying building blocks early can help guide evolution efficiently toward the optimum.

Transfer learning is effective:

Source Problem Knowledge

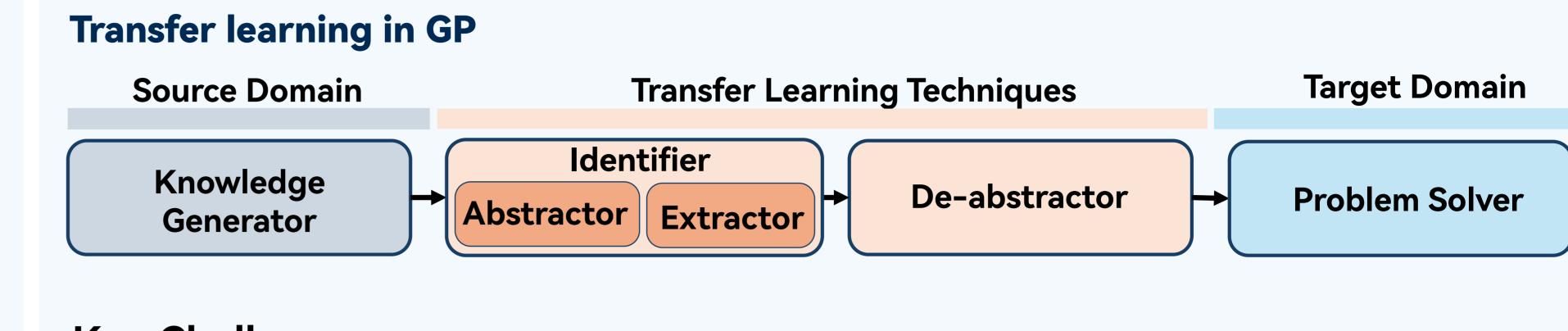
Similar, unsolved problems

Target Problem

Knowledge from solved problems directs evolution in similar tasks.

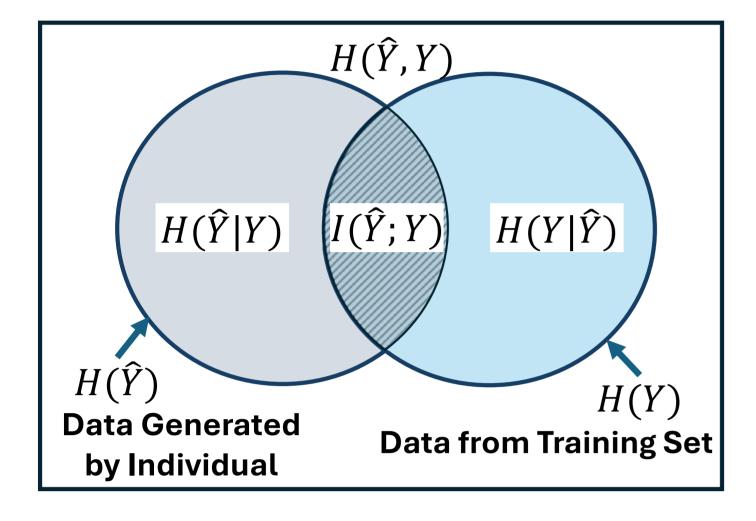
Methodology

Mutual Information – Indicator of Useful Knowledge



Key Challenge Identifying valuable knowledge for the target domain.

Existing methods often struggle with low significance, local optima, and strong dependence on specific source problems.



$$I(\hat{Y};Y) = \sum_{\hat{y} \in \hat{Y}} \sum_{y \in Y} p(\hat{y},y) \log \left(\frac{p(\hat{y},y)}{p(\hat{y})p(y)} \right)$$

Normalization Methodology target-norm MI: By H(Y) - Emphasize redundancy

 $I_N(\widehat{Y};Y) = \frac{I(\widehat{Y};Y)}{H(\widehat{Y};Y)}$

joint-norm MI: By $H(Y, \hat{Y})$ – Emphasize both

$$I_N(\widehat{Y};Y) = \frac{I(\widehat{Y};Y)}{H(Y)}$$

Two important characteristics

- No assumption on the distribution of data before measuring.
- Remains unchanged after a smooth invertible operation.

Proposed Method Target Domain Mutual Information-based Transfer Learning GP Start (Target Domain Process) Initial **Source Domain Proposed Population** Randomly Generate Method Start Biasing Individuals (Source Domain Process) (1-k)%Screen Subtrees with **k**% Population Population Satisfied Height Initialization Initialization Calculate the Mutual Updated **Updated Population** Information with Data in Population **Target Domain** Yes **Stop Condition** Yes Satisfied? **Stop Condition** Select Subtrees with Highest Satisfied? No **Mutual Information** No **Evolution Process** End **Evolution Process** (Source Domain Process) End (Target Domain Process) **Experiment and Results**

What to Transfer?

Subtrees with High Mutual Information

- These subtrees approximate the global optimum and can evolve into it via smooth and investable structural changes.
- High overlap with target data makes them more relevant and reduces error.

How to Transfer? & When to Transfer? Initial Population Biasing

- Avoids disrupting the search space.
- Guides evolution to focus on small, highinformation subspaces.
- Flexibility to further self-adaptation.

Trial Problems

10 symbolic regression problems from existing work*[1]

Baseline

Standard GP and SubTree50*[1]

Problems	Poly-1	Poly-2	Poly-3	Poly-4	Poly-5	Trig-1	Trig-2	Trig-3	Trig-4	Trig-5
Mean of Best Fitness										
Standard GP	0.0180	0.0204	0.0379	0.0506	0.0622	0.0365	0.0088	0.0159	0.0156	0.0947
SubTree50	0.0139	0.0138	0.0258	0.0419	0.0563	0.0230	0.0057	0.0177	0.0105	0.0933
no-norm MI	0.0139	0.0129	0.0238	0.0418	0.0516	0.0141	0.0052	0.0103	0.0043	0.0470
	(+,=)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)
target-norm MI	0.0127	0.0128	0.0254	0.0377	0.0449	0.0172	0.0066	0.0126	0.0075	0.0485
	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)	(+,-)	(+,+)	(+,+)	(+,+)
joint norm MI	<u>0.0117</u>	0.0129	0.0222	0.0488	0.0540	0.0129	0.0057	0.0089	0.0070	0.0627
	(+,+)	(+,+)	(+,+)	(+,-)	(+,+)	(+,+)	(+,=)	(+,+)	(+,+)	(+,+)
Median of Test Error										
Standard GP	126.965	47.900	91.983	156.348	5955826.581	2.892	4.973	6.426	8.910E-17	1.200
SubTree50	<u>116.750</u>	38.099	90.793	155.527	5169346.282	2.854	7.912	6.172	8.351E-17	1.286
no-norm MI	125.207	<u>26.601</u>	82.773	<u>132.057</u>	23010016.817	2.614	2.766	4.077	8.042E-17	1.137
	(+,-)	(+,+)	(+,+)	(+,+)	(-,-)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)
target-norm MI	126.428	<u>43.425</u>	<u>67.320</u>	<u>139.002</u>	23010016.840	2.732	3.175	4.796	8.188E-17	<u>1.000</u>
	(+,-)	(+,-)	(+,+)	(+,+)	(-,-)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)
joint norm MI	126.529	34.971	<u>76.556</u>	157.080	23010016.801	2.662	2.746	4.062	8.243E-17	1.080
	(+,-)	(+,+)	(+,+)	(-,-)	(-,-)	(+,+)	(+,+)	(+,+)	(+,+)	(+,+)

Observations

For MI-based Methods:

- Improve training fitness and reduce test error in most tasks.
- More often passes significance tests, better preserves initial subtree advantages.

Insights and Future Works

- Mutual information is key for selecting transferable subtrees and boosting GP performance.
- It helps identify relevant parts of past models for current tasks.
- Future work will explore its use in complex systems like power systems to guide model reuse.





[1] T. T. Huong Dinh, T. H. Chu and Q. U. Nguyen, "Transfer learning in genetic programming," 2015 IEEE Congress on Evolutionary Computation (CEC), Sendai, Japan, 2015.
[2] S. W. Card and C. K. Mohan, "Information theoretic indicators of fitness, relevant diversity & pairing potential in genetic programming," 2005 IEEE Congress on", Applied Soft Computing, Evolutionary Computation, Edinburgh, UK, 2005.

[2] S. W. Card and C. K. Mohan, "Information theoretic indicators of fitness, relevant diversity & pairing potential in genetic programming," 2005 IEEE Congress on", Applied Soft Computing, Evolutionary Computation, Edinburg [3] Zahra Zojaji, Mohammad Mehdi Ebadzadeh, Hamid Nasiri, "Semantic schema based genetic programming for symbolic regression", Volume 122,2022.

[&]quot;+" Outperforming | "-" Outperformed | "=" Similar Performance
Underlined: Passed Wilcoxon Significance Test Compared with Standard GP
Bolded: The Best in One Test Problem

Smaller figure indicates better results.