Evolving Differential Equations with Developmental Linear Genetic Programming and Epigenetic Hill Climbing

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Abstract

Classical genetic programming (GP) solves problems by applying the Darwinian concepts of selection, survival and reproduction to a population of computer programs. Here we extend the biological analogy to incorporate epigenetic regulation through both learning and evolution. Using inheritable Lamarckian mechanisms as inspiration, we propose a system that allows for updating of individuals in the population during their lifetime while simultaneously preserving both genotypic and phenotypic traits during reproduction.

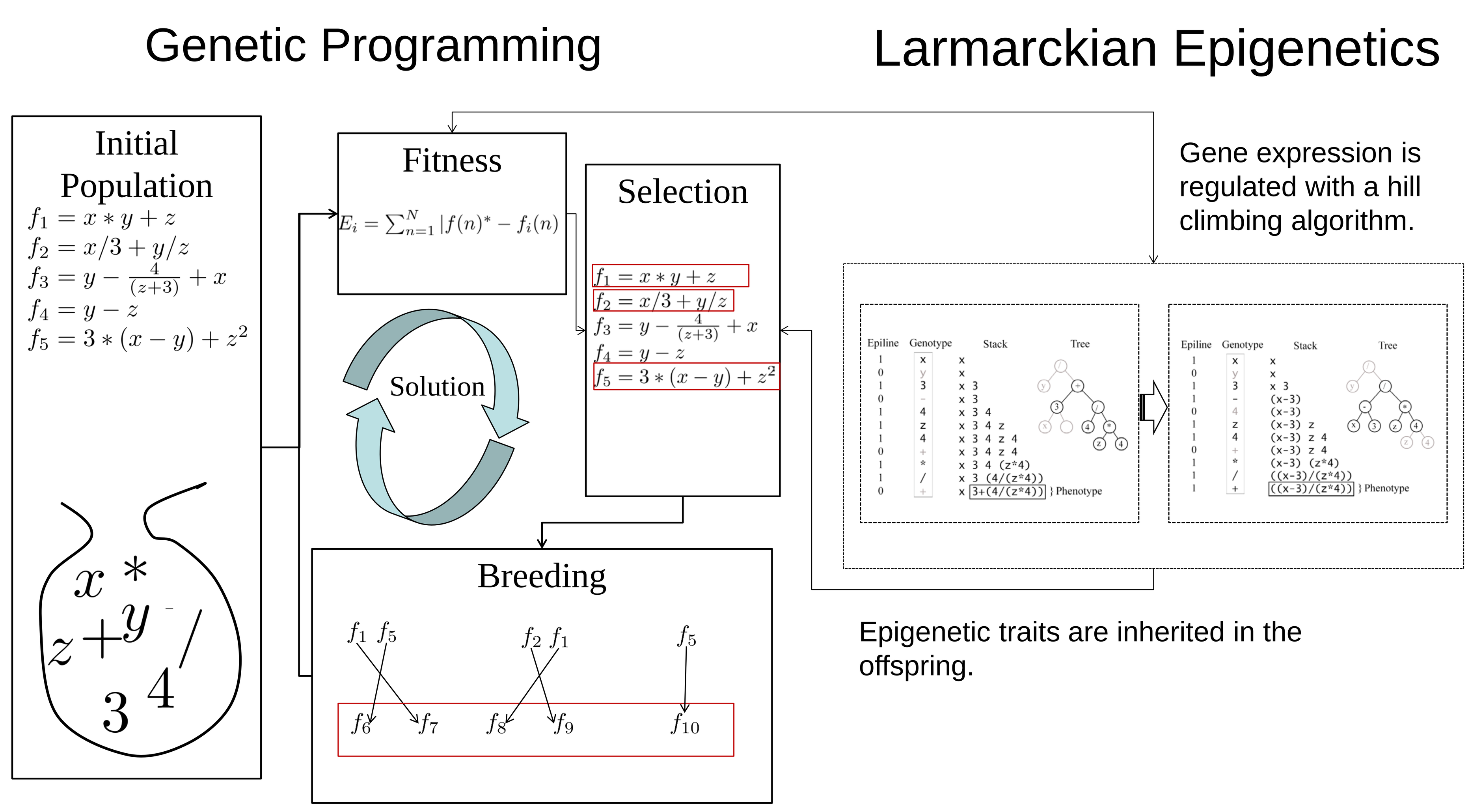
The implementation is made simple through the use of syntax-free, developmental, linear genetic programming (DLGP) [1]. The representation allows for arbitrarily-ordered genomes to be syntactically valid programs, thereby creating a genetic programming approach upon which quasi-uniform epigenetic updating and inheritance can be easily applied. Generational updates are made using an in faster convergence, less bloat, and an improved ability to find exact solutions on a number of symbolic regression problems.

Motivation

Today, Lamarckian mechanisms are known to exist in biology and have been demonstrated in many studies. The studies constitute the growing field of epigenetics, a term that refers broadly to the ways in which gene expressions are regulated and inherited [2, 3]. Recent studies have not only shown that environmental factors influence gene expression in organisms, but also that epigenetic mechanisms may be inheritable [4, 5].

We present a GP method that captures this understanding of epigenetics as a layer of environmentally influenced, evolving gene regulation that interacts with the genotype to produce the phenotype. This system captures the advantages of Lamarckian updating without changing the genotype, and yet directly preserves inheritable phenotypic improvements in offspring, unlike Baldwinian evolution.

Addition of an Epigenetic Layer to GP



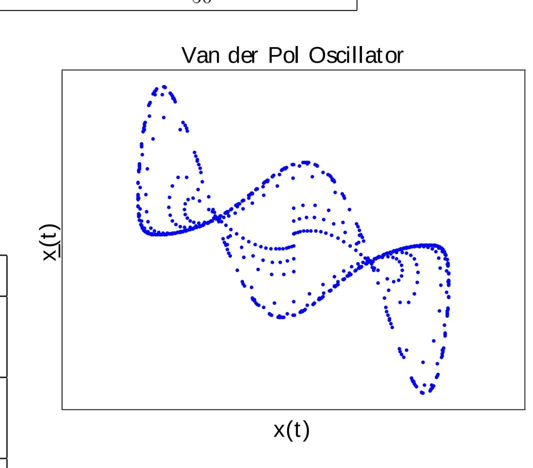
Examples

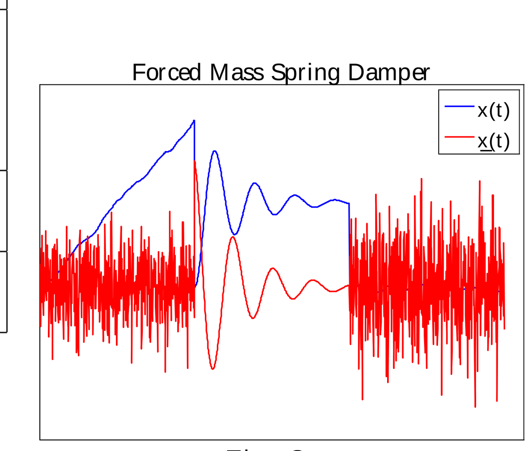
Runtime Settings. All problems used {+,-,*,/} operators. The differential equation problems used ephemeral random constants picked uniformly from [-1.0,1.0]. Pagie-1 and Nguyen-7 instead use 1.0, and Nguyen-7 includes log and exp functions. + Deterministic Crowding. *Age-Fitness Pareto Survival.

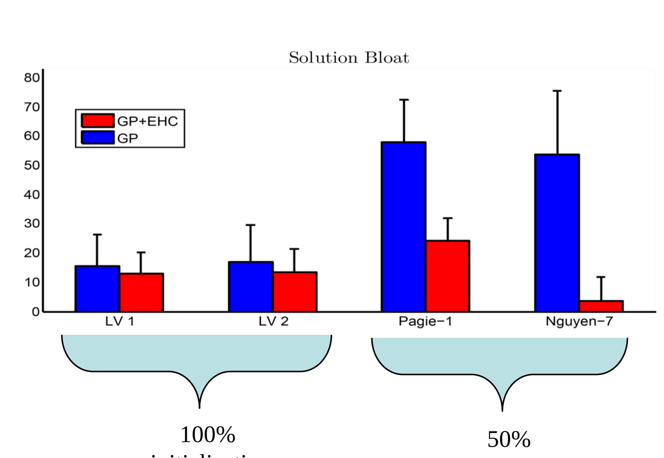
Setting	MSD	van der Pol	Lotka-Volterra	Pagie-1	Nguyen-7
Target Equation	$\ddot{x} = -1/2(0.75\dot{x} + 3x - F)$	$\ddot{x} = -1.5(x^2+1)\dot{x} - x$	$\dot{x} = 3x - 2xy - x^2, \dot{y} = 2y - xy - y^2$	$f(x,y) = \frac{1}{1+x^{-4}} + \frac{1}{1+y^{-4}}$	$f(x) = log(x+1) + log(x^2+1)$
Initial program length	[50,200]	[50,200]	[3, 50]	[10, 100]	[10, 100]
Method	DC+	DC+	DC+	AFP*	AFP*
Pop Size	1000	1000	1000	1000	1000
Max Generations	1000	1000	5000	5000	5000
Initial % Active Genes	100	100	100	50	50

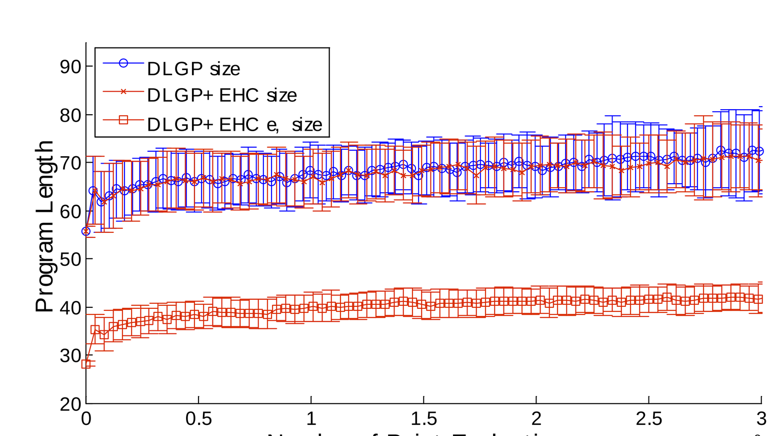
Performance Comparisons. A successful run finds a floating-point exact match to the target equation. Results in bold are significant to $p < .05$ using the non-parametric ranked t-test for mean evaluations and program lengths and Fischer's exact test for success rate.

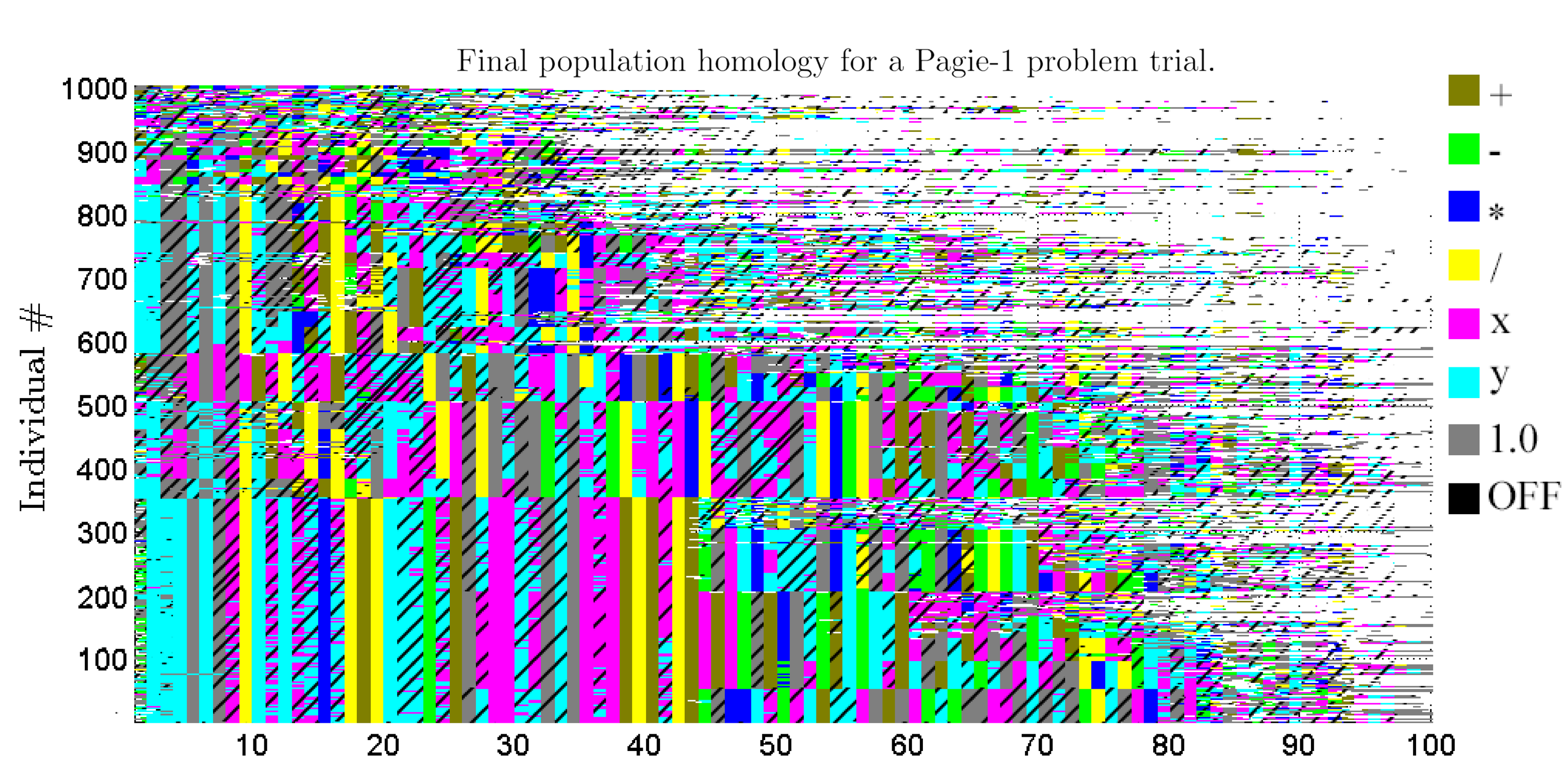
Problem	Trials	Method	Success Rate	Mean Point Evaluations	Mean Effective Size
Forced Mass Spring Damper	30	DLGP	83.33%	1.97E11	**145.11**
	30	DLGP+EHC	100%	1.60E11	**96.65**
van der Pol Oscillator	30	DLGP	83.33%	**9.91E10**	**140.06**
	30	DLGP+EHC	100%	**7.21E10**	**101.34**
Lotka-Volterra $\dot{x}$	50	DLGP	100%	**2.20E10**	**29.63**
	50	DLGP+EHC	100%	**1.66E10**	**24.69**
Lotka-Volterra $\dot{y}$	50	DLGP	100%	2.07E10	**30.36**
	50	DLGP+EHC	100%	1.81E10	**25.13**
Pagie-1	100	DLGP	**13%**	**2.61E11**	**68.73**
	100	DLGP + EHC	**27%**	**2.62E11**	**40.32**
Nguyen-7	50	DLGP	**72%**	**4.48E9**	**68.97**
	50	DLGP+EHC	**100%**	**4.56E8**	**20.25**











Impacts and Future Work

We represented two characteristics of epigenesis in this implementation: 1) dependence on environmental factors by use of the EHC, and 2) inheritability by evolution of epilines with their corresponding genotypes. Unlike previous methods, our system allows offspring to inherit both the learned phenotypic traits of their parents as well as the genotypic underpinning. With this system we demonstrate higher success rates and lower solution bloat for a number of symbolic regression problems, with equivalent or lower computational effort required. We hope this work will provide the basis for further investigation into how epigenetic learning and evolution can interact to improve genetic programming for many applications. Namely, further work should address various levels of epigenetic inheritability, as well as the contributions of environmental factors or inheritance to the improvement in success.

This system identification approach is being used to identify wind turbine dynamics of the National Renewable Energy Laboratory's CART3 turbine (pictured) and for developing bird migration models based on measured data. In the future, we hope to apply it to the design of nonlinear controllers for offshore wind turbines.

Source: nrel.gov/wind

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