Parent Selection and Diversification in Genetic Programming

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ABSTRACT

More things!

Keywords

lexicase selection, hyperselection, PushGP, other stuff

1. INTRODUCTION

I bet we start here!

Lexicase selection [8] is nifty, eh?

Hyperselection provided initial motivation [3], but later we became interested more generally in what lexicase and tournament do differently starting with the same population.

[TMH: I'm not sure if we want to talk about error diversity in the Intro or somewhere else. But, the following paragraph could be moved to be the first paragraph of Experimental Design if we don't need to talk about diversity earlier]

In this paper we concentrate on diversity measures related to the outputs of the programs. One such diversity measure, *behavioral diversity*, has been shown to have correlation with problem-solving performance [6]. In behavioral diversity, the output of each program is recorded on each training case input and stored as a *behavior vector*. Behavioral diversity is then the percentage of distinct behavior vectors in the population. *Error diversity*, a slight variation of behavioral diversity, considers the percentage of distinct error vectors in the population where each error vector is computed by applying the error function to each output in the behavior vector. We believe error diversity does a good job of measuring how well evolution is exploring meaningful differences between programs that might be lost with a diversity measure that only takes into account syntactic (genotypic) diversity of the population, where two wildly different programs may actually compute the same function.

2. EXPERIMENTAL DESIGN

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Previous work has shown that using lexicase selection results in higher population error diversity than tournament selection across a variety of problems [2, 5]. These papers examined the diversity of entire GP runs, each starting with a different initial population and random number seed.

Here we examine the effcts of these parent selection methods on population error diveristy starting from specific population conditions besides a random initial population. In particular, we want to see how each method changes diversity in populations that occur naturally during an evolutionary run.

In order to produce the populations on which to experiment, we started GP runs and let them continue until they met certain stopping conditions; we then stored those populations and later conducted multiple trials with different random number seeds starting with those stored populations. We used three different stopping conditions in order to generate naturally occuring populations with interesting properties:

1. In a run using lexicase selection, we stopped if the population error diversity was greater than 0.9. This results in very diverse populations, allowing us to observe whether evolution is able to maintain such high diversity in the following generations.

2. In a run using tournament selection, we stopped if the population error diversity was less than 0.15. These populations allow us to see if methods promote diversification starting from such undiverse populations. They also allow us to see if methods perform differently on a population produced by tournament selection versus one produced by lexicase selection.

3. As described above, we were initially motivated here by observations of runs using lexicase selection that underwent major drops in diversity following hyperselection events, where one or a few individuals in the population received the majority of the parent selections in a generation. We had anecdotally noticed rapid diversity recovery following these events, but not examined them systematically [3].

   In this condition, we stopped a run using lexicase selection when the error diversity reached a level at least 0.25 less than it had been at some point in the previous 10 generations. This allowed us to detect populations that had recently undergone large drops in diversity. We do not definitively know whether those drops are related to hyperselection events, but we expect that they are.

Table 1: PushGP parameters

Parameter	Value
runs per problem/parent selection combination	100
population size	1000
maximum genome size	1600
maximum initial genome size	400
Genetic Operator	**Prob**
alternation	0.2
uniform mutation	0.2
uniform close mutation	0.1
alternation followed by uniform mutation	0.5

In all three conditions, we only considered populations occuring after the first 10 generations in order to give evolution a chance to settle down after the extreme shifts that can happen at the beginning of a run.

In each trial, we continued running GP on a stored population for 20 generations and recorded the population error diversity. For each parent selection setting (lexicase and tournament selections), we conducted 100 trials with different random number seeds from each stored population.

We conducted these tests on two problems taken from a recent program synthesis benchmark suite [4]. The first problem, Replace Space With Newline (RSWN), searches for a program that takes as input a string and both prints the string after replacing all of the spaces in the input with newline characters and functionally returns the number of non-whitespace characters in the string. Previous examinations of error vector diversity on the RSWN problem indicate that lexicase selection maintains significantly higher diversity than tournament selection, which across 100 runs never achieved a median diversity higher than 0.25 [2].

The second problem, Double Letters, asks for a program that takes a string as input and prints the string after doubling every alphabetic character and tripling every exclamation point. All other characters should be printed once. As with the RSWN problem, lexicase selection consistently achieves high diversity on this problem. Differently than RSWN, runs using tournament selection show slow but steady increases in diversity, though not approaching that of lexicase selection runs [2].

For our experiments we used PushGP [11, 10], a stack-based genetic programming system.[1] PushGP supports a variety of control structures and multiple data types, making it a good choice for program synthesis tasks such as the problems we explore here. Except for parent selection, we used the exact same PushGP parameters in both the initial runs used to store interesting populations as well as the continuations of the stored populations. We give the most relevant parameters in Table 1. The parameters not listed here exactly follow those used in the experiments in [1].

These runs use the most recent version of PushGP, in which individuals are stored as linear genomes that we translate into hierarchical Push programs prior to execution [1]. These linear genomes admit a range of uniform genetic operators; we use four, listed in Table 1 with their probabilities. Alternation is a linear crossover operator modeled after the sexual portion of ULTRA [9]. Uniform mutation may replace each instruction with 1% probability. Uniform close mutation may add or remove parentheses from the program. Finally, the last operator runs alternation on two parents and then uniform mutation on that child to produce a new child.

[1]Lexicase selection has also been shown to be effective in tree-based genetic programming [5, 7].

3. RESULTS

Using the techniques presented in the previous section we obtained populations on which to perform continuation experiments. For each combination of the 2 problems and 3 stopping conditions we stored populations from 2 runs, for a total of 12 populations. In the following subsections we group the results based on the stopping conditions, since they produce the most similar populations within a single stopping condition.

Starting with each stored population we conducted 100 GP runs with lexicase selection and 100 with tournament selection. We let each run go for 20 generations, and plot the population error diversity across the runs. In particular, each figure has a standard box-and-whisker plot for each generation, with the box showing the median and quartiles. The whiskers stretch to the maximum and minimum values, ignoring outliers. In each figure we also plot the error diversity of each individual run at each generation, giving another way of visualizing the spread of diversities across runs and making it easier to trace outliers.

Note that in a few settings, one or two runs found solutions to the problem before the end of 20 generations. In these cases, we terminate the runs, and they do not contribute data past their termination generation. We do not believe this has a large effect on the plots since no plot had more than two of these early-terminating runs.

3.1 Starting with high diversity

In this subsection we use stored populations that occured in runs using lexicase selection and achieved error diversity greater than 0.9. As such, the initial populations of the runs have very high diversity, with most individuals producing distinct error vectors.

Figure 1 plots continued runs started from two populations (C and D) stored from GP evolving on the RSWN problem.

3.2 Starting with low diversity

3.3 Starting after a diversity crash

4. DISCUSSION

Why does lexicase do so much better at diversification??? Does it have to do with specialists? Probably! Does it have to do with concentrating on individual test cases or combinations thereof? Probabily!

5. CONCLUSIONS

I'm hoping we have conclusions.

Acknowledgments

Lots of cool people helped us.

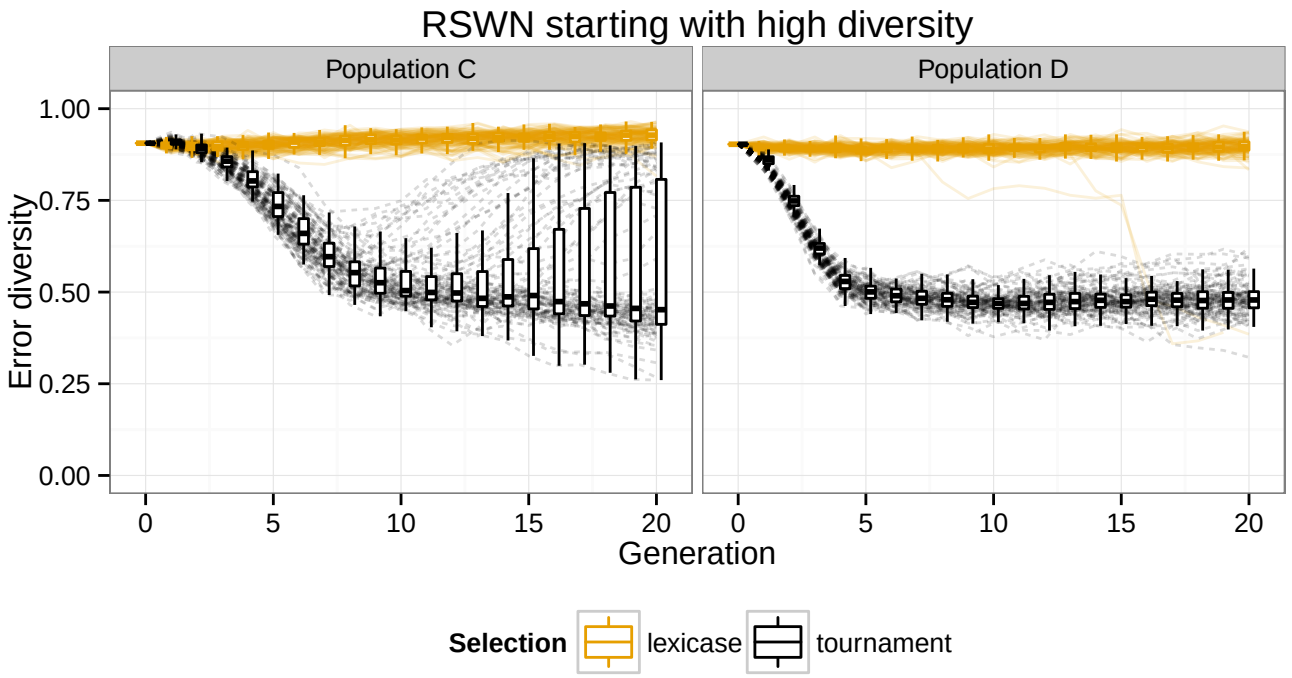

Figure 1: Error diversity over 100 "continuations" of the RSWN problem with both lexicase and tournament selections, starting from a population with high diversity naturally occuring in a run using lexicase selection.

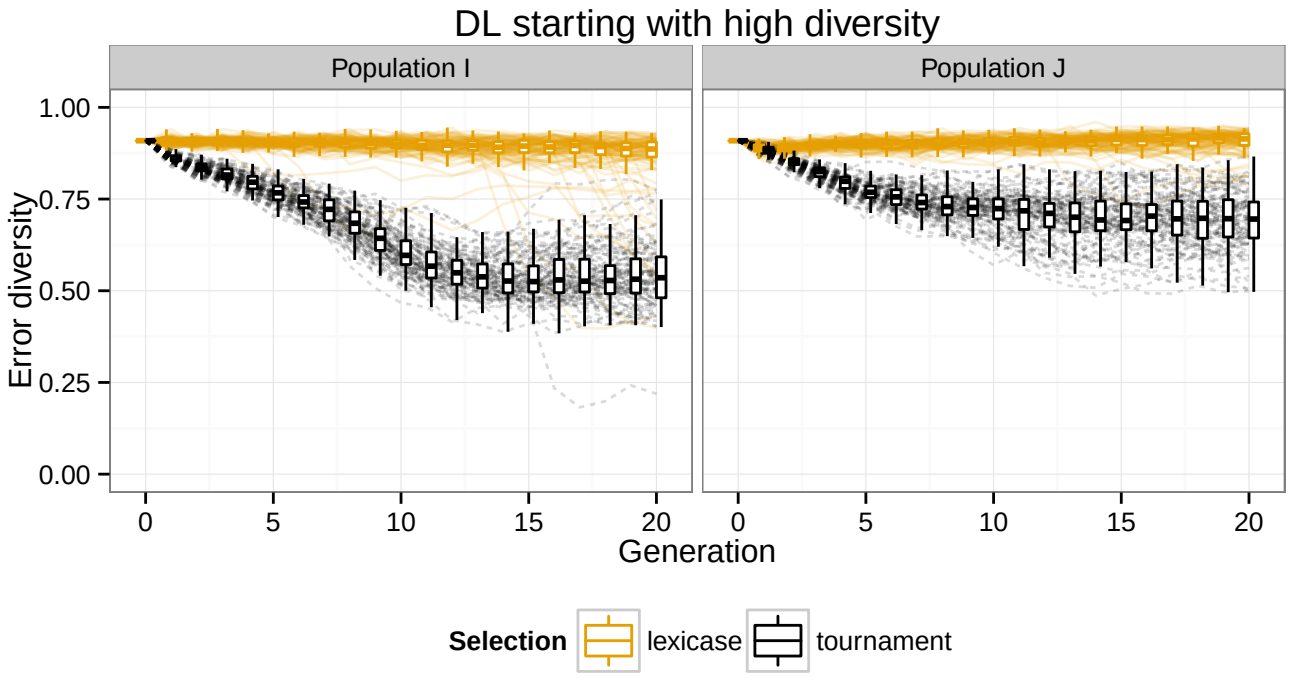

Figure 2: Error diversity over 100 "continuations" of the double-letters problem with both lexicase and tournament selections, starting from a population with high diversity naturally occuring in a run using lexicase selection.

Figure 3: Error diversity over 100 "continuations" of the RSWN problem with both lexicase and tournament selections, starting from a population with low diversity naturally occuring in a run using tournament selection.

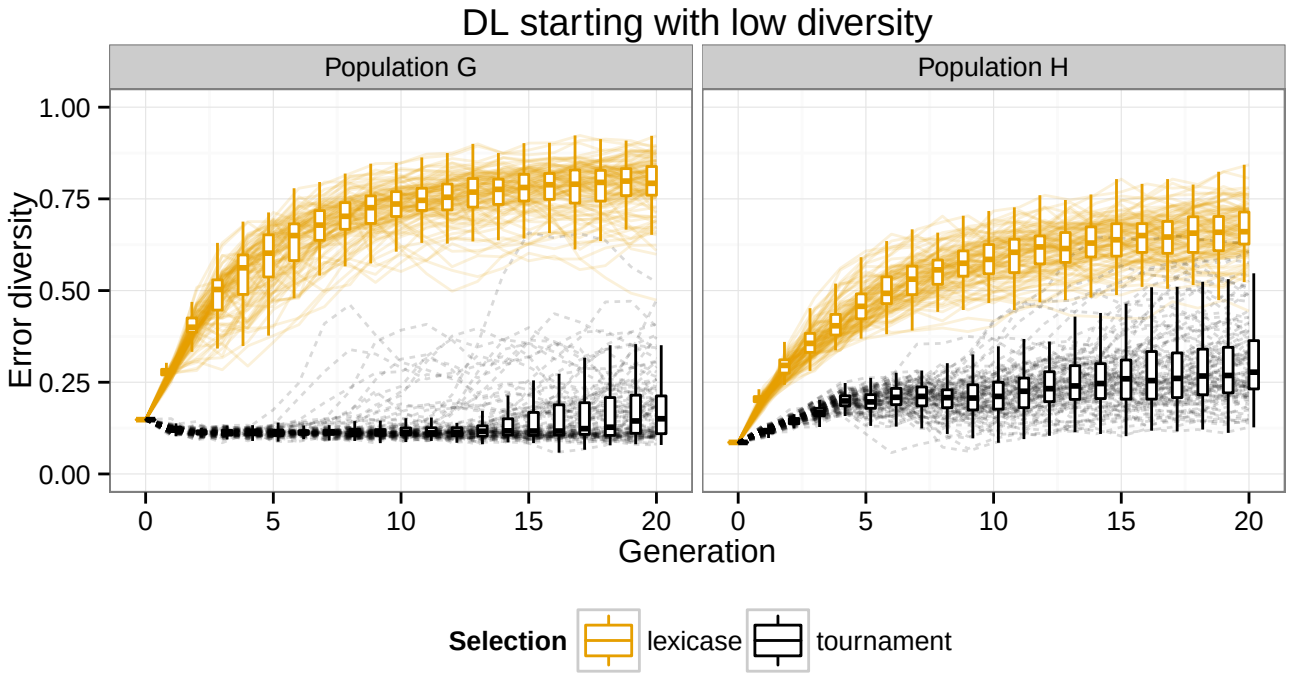

Figure 4: Error diversity over 100 "continuations" of the double-letters problem with both lexicase and tournament selections, starting from a population with low diversity naturally occuring in a run using tournament selection.

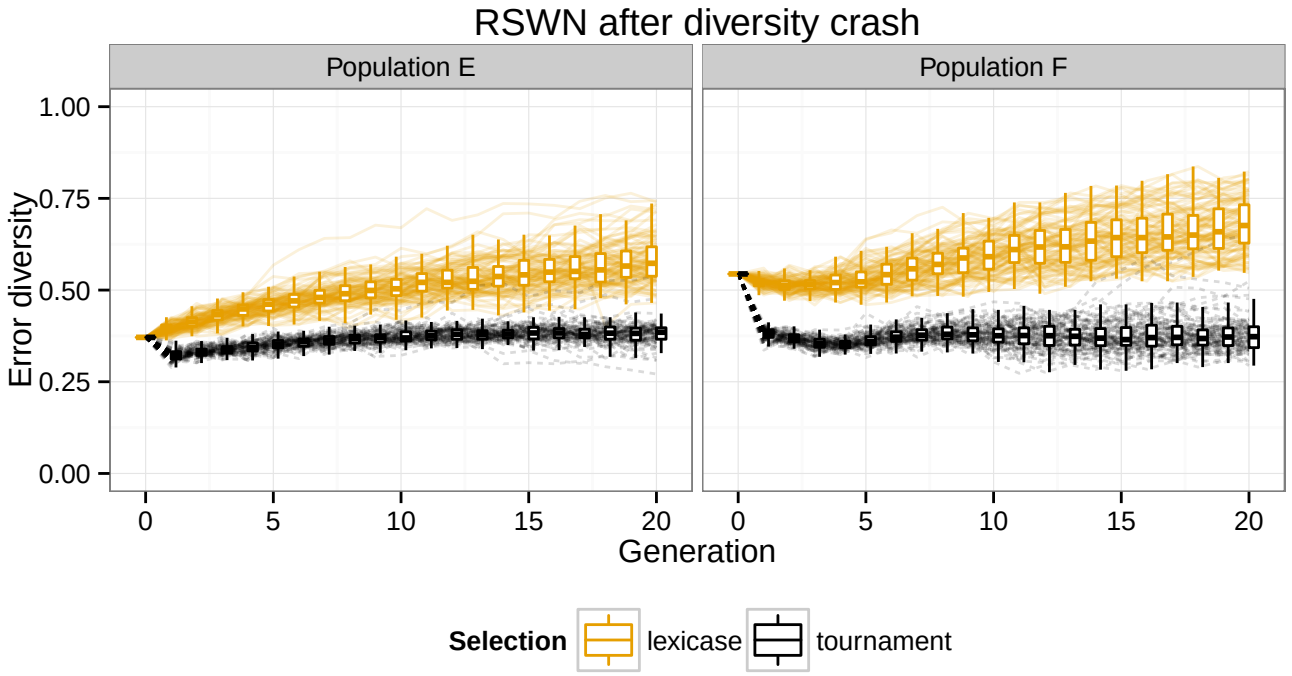

Figure 5: Error diversity over 100 "continuations" of the RSWN problem with both lexicase and tournament selections, starting from a population that had lost diversity in a diversity crash in a lexicase selection run.

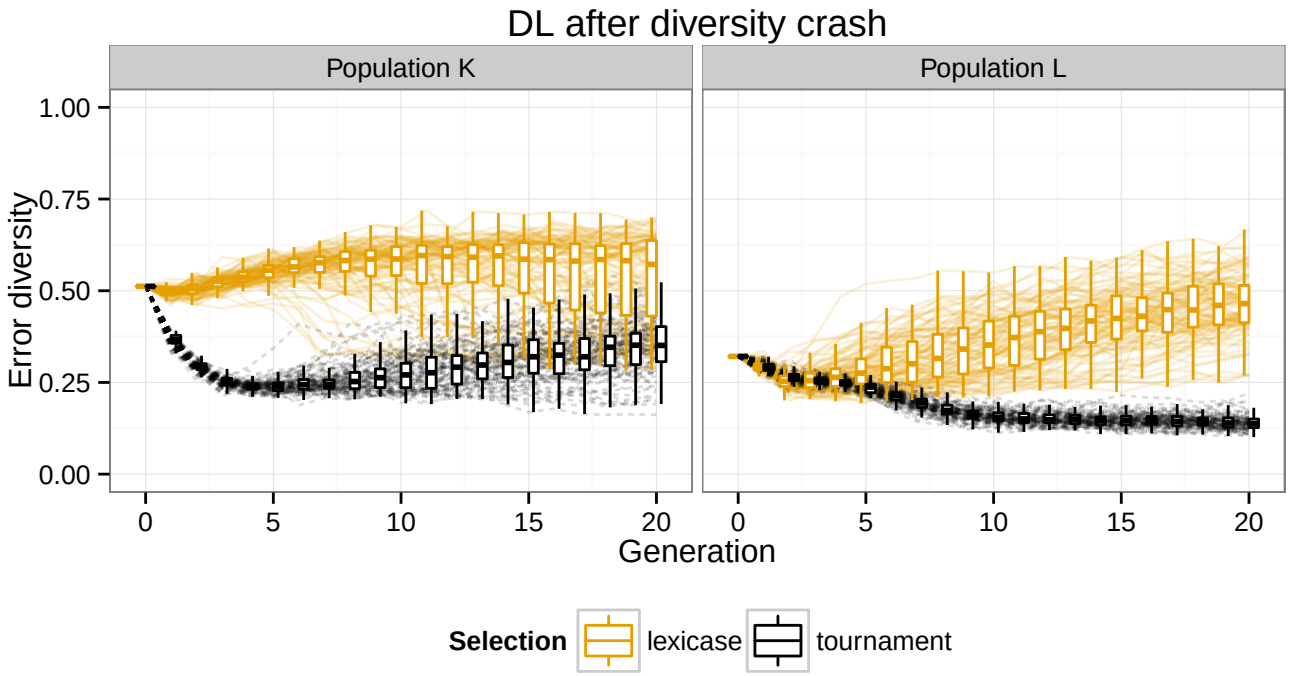

Figure 6: Error diversity over 100 "continuations" of the double-letters problem with both lexicase and tournament selections, starting from a population that had lost diversity in a diversity crash in a lexicase selection run.

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