

Tag-accessed memory data analyses

Contents

Overview	1
Package Setup	1
Data Loading	1
Preliminary Results	2
Successful Runs after 300 Generations	2
Experimental Results	3
Successful Runs after 500 Generations	3
Statistical Analysis	4
Problem: Number IO	4
Problem: Smallest	4
Problem: Median	5
Problem: Grade	5
Problem: For Loop Ind.	5
References	6

Overview

Here, we analyze our experimental results comparing tag-accessed memory to more traditional, direct-indexed memory. Specifically, we conducted a series of experiments using simple linear-GP representations on program synthesis problems. In all experiments, we evolved genetic programs that used tag-accessed memory and programs that used direct-indexed memory. Aside from how programs were allowed to access memory, both genetic programming systems/representations were identical (*e.g.*, had identical sets of instructions).

First, we present data from our preliminary experiments, which used a range of numeric argument and tag-based argument mutation rates. Based on these preliminary data, we decided to remove our two most extreme mutation rates and run a higher-replicate-count experiment with new random number seeds.

This document was generated using R markdown with R version 3.3.2 (2016-10-31) (R Core Team, 2016).

Package Setup

```
library(tidyr)      # (Wickham & Henry, 2018)
library(ggplot2)    # (Wickham, 2009)
library(plyr)       # (Wickham, 2011)
library(dplyr)      # (Wickham et al., 2018)
library(cowplot)    # (Wilke, 2018)
```

Data Loading

Set path information (for both preliminary data and for final experiment data).

```
prelim_u300_summary_loc <-
  "../data/prelim/min_programs__update_300__solutions_summary.csv"

u500_summary_loc <-
  "../data/sweep/min_programs__update_500__solutions_summary.csv"
```

Load data in from file(s). Pretty it up (for our graphs).

```
# Load preliminary data.
prelim_u300_summary <- read.csv(prelim_u300_summary_loc, na.strings = "NONE")
prelim_u300_summary$arg_mut_rate <- as.factor(prelim_u300_summary$arg_mut_rate)

prelim_u300_summary$problem <- factor(prelim_u300_summary$problem,
  levels = c("number-io", "smallest", "median", "grade", "for-loop-index"))
levels(prelim_u300_summary$problem) <- c("Number IO", "Smallest",
  "Median", "Grade", "For Loop Ind.")

# Load experiment data.
u500_summary <- read.csv(u500_summary_loc, na.strings = "NONE")
u500_summary$arg_mut_rate <- as.factor(u500_summary$arg_mut_rate)

u500_summary$problem <- factor(u500_summary$problem, levels = c("number-io",
  "smallest", "median", "grade", "for-loop-index"))
levels(u500_summary$problem) <- c("Number IO", "Smallest", "Median",
  "Grade", "For Loop Ind.")
```

Preliminary Results

We ran a set of preliminary experiments, applying our simple linear GP representation (with tag-based memory *and* direct-indexed memory) to 5 problems from the general program synthesis benchmark suite (Helmuth & Spector, 2015): for loop index, grade, median, small or large, and smallest.

We tried several tag-argument and numeric-argument mutation rates in our preliminary runs. For runs that used tag-based arguments, we tried the following per-bit tag-argument mutation rates: 0.00001, 0.0001, 0.001, 0.0025, 0.005, 0.0075, 0.01, 0.025, 0.05, 0.075, 0.1, 0.5. For runs that used numeric arguments, we tried the following per-argument mutation rates: 0.00001, 0.0001, 0.001, 0.0025, 0.005, 0.0075, 0.01, 0.025, 0.05, 0.075, 0.1, 0.5.

We ran the number io problem for 100 generations and 300 generations for all other problems. For each problem, we looked at the proportion of runs (30 replicates per condition) that produced solutions.

Successful Runs after 300 Generations

Saving 6.5 x 4.5 in image



Experimental Results

In our second (final) set of runs, we applied our two linear GP representations (one with tag-accessed memory and one with direct-indexed memory) to five problems: number IO, for loop index, grade, median, and smallest.

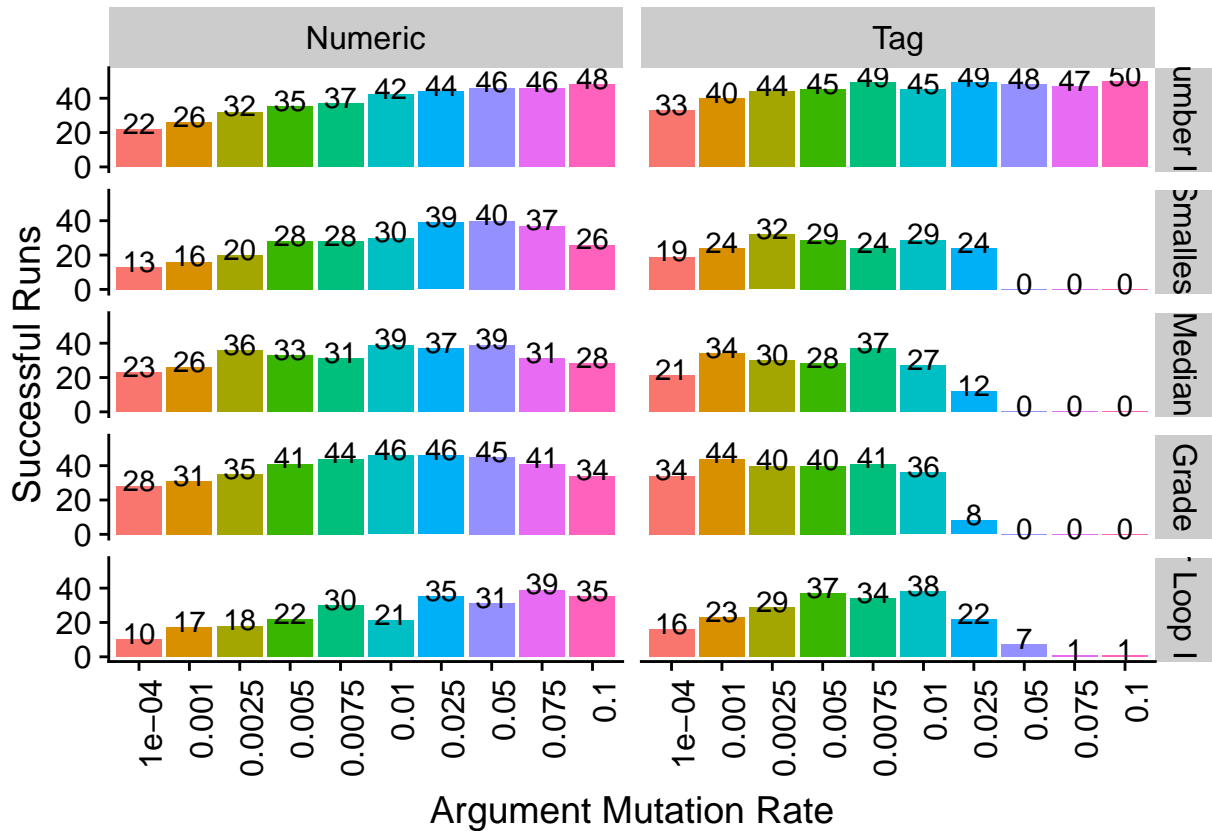
We ran number IO for 100 generations. To increase the solve rates of the other problems, we increased the number of generations we ran for loop index, grade, median, and smallest runs from 300 to 500 generations.

Because the most extreme mutation rates (0.00001 and 0.5) were never the best mutation rate for finding solutions, we dropped them from this experiment to dedicate more computational resources toward running more replicates.

As before, for each problem we looked at the proportion of runs (**50 replicates per condition**) that produced solutions.

Successful Runs after 500 Generations

Saving 6.5 x 4.5 in image



Statistical Analysis

For each problem, we compared the success rates of the best-performing mutation rate conditions for tag-based memory and direct-indexed memory using a Fisher's exact test.

Problem: Number IO

	Successful Runs	Failed Runs
Numeric Args	48	2
Tag Args	50	0

Fisher's Exact Test for Count Data

```
data: contingency_table
p-value = 0.4949
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.000000 5.307419
sample estimates:
odds ratio
0
```

Problem: Smallest

	Successful Runs	Failed Runs
--	-----------------	-------------

Numeric Args	40	10
Tag Args	32	18

Fisher's Exact Test for Count Data

```
data: contingency_table
p-value = 0.1182
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.8394778 6.2269207
sample estimates:
odds ratio
 2.231652
```

Problem: Median

	Successful Runs	Failed Runs
Numeric Args	39	11
Tag Args	37	13

Fisher's Exact Test for Count Data

```
data: contingency_table
p-value = 0.8153
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.4494643 3.4916226
sample estimates:
odds ratio
 1.24296
```

Problem: Grade

	Successful Runs	Failed Runs
Numeric Args	46	4
Tag Args	44	6

Fisher's Exact Test for Count Data

```
data: contingency_table
p-value = 0.7407
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.3434417 8.0502248
sample estimates:
odds ratio
 1.561184
```

Problem: For Loop Ind.

	Successful Runs	Failed Runs
Numeric Args	39	11

Fisher's Exact Test for Count Data

```
data: contingency_table
p-value = 1
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.3970095 3.1774697
sample estimates:
odds ratio
 1.118352
```

References

- Claus O. Wilke (2018). *cowplot: Streamlined Plot Theme and Plot Annotations for 'ggplot2'*. R package version 0.9.3. <https://CRAN.R-project.org/package=cowplot>
- Helmuth, T., & Spector, L. (2015). General Program Synthesis Benchmark Suite. In Proceedings of the 2015 on Genetic and Evolutionary Computation Conference - GECCO '15 (pp. 1039–1046). New York, New York, USA: ACM Press. <https://doi.org/10.1145/2739480.2754769>
- R Core Team (2016). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.
- H. Wickham. *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York, 2009.
- Hadley Wickham and Lionel Henry (2018). *tidyr: Easily Tidy Data with 'spread()' and 'gather()' Functions*. R package version 0.8.1. <https://CRAN.R-project.org/package=tidyr>
- Hadley Wickham (2011). The Split-Apply-Combine Strategy for Data Analysis. *Journal of Statistical Software*, 40(1), 1-29. URL <http://www.jstatsoft.org/v40/i01/>.
- Hadley Wickham, Romain François, Lionel Henry and Kirill Müller (2018). *dplyr: A Grammar of Data Manipulation*. R package version 0.7.5. <https://CRAN.R-project.org/package=dplyr>