CREST

Genetic Improvement Programming

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GISMOE: Genetic Improvement of Software for Multiple Objectives

16.10.2013

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Genetic Programming to Improve Existing Software

- Examples
  - Evolving code for a new environment (gzip)
  - Improving non-functional properties IEEE TEC
  - Faster parallel code for stereo imaging
- Discussion

GP Automatic Coding

- Target non-trivial open source system:
  - State of the art Bowtie2 DNA lookup tool
  - Six year old CUDA stereoKernel
- Tailor existing system for specific use:
  - nextGen DNA from 1000 genomes project
  - 3010 office environment image pairs
- Use existing system as test “Oracle”
- Use inputs & *answer* to train GP.
- Clean up new code

Problems with BLAST

- BLAST contains biologists heuristics and approximations for mutation rates. It is the “gold standard” answer.
  - A few minutes per look up
- “Next Gen” DNA sequencing machines generate 100s millions short noisy DNA sequences in about a day.
- BLAST originally designed for longer sequences. Expects perfect data. Human genome database too big for PC memory.

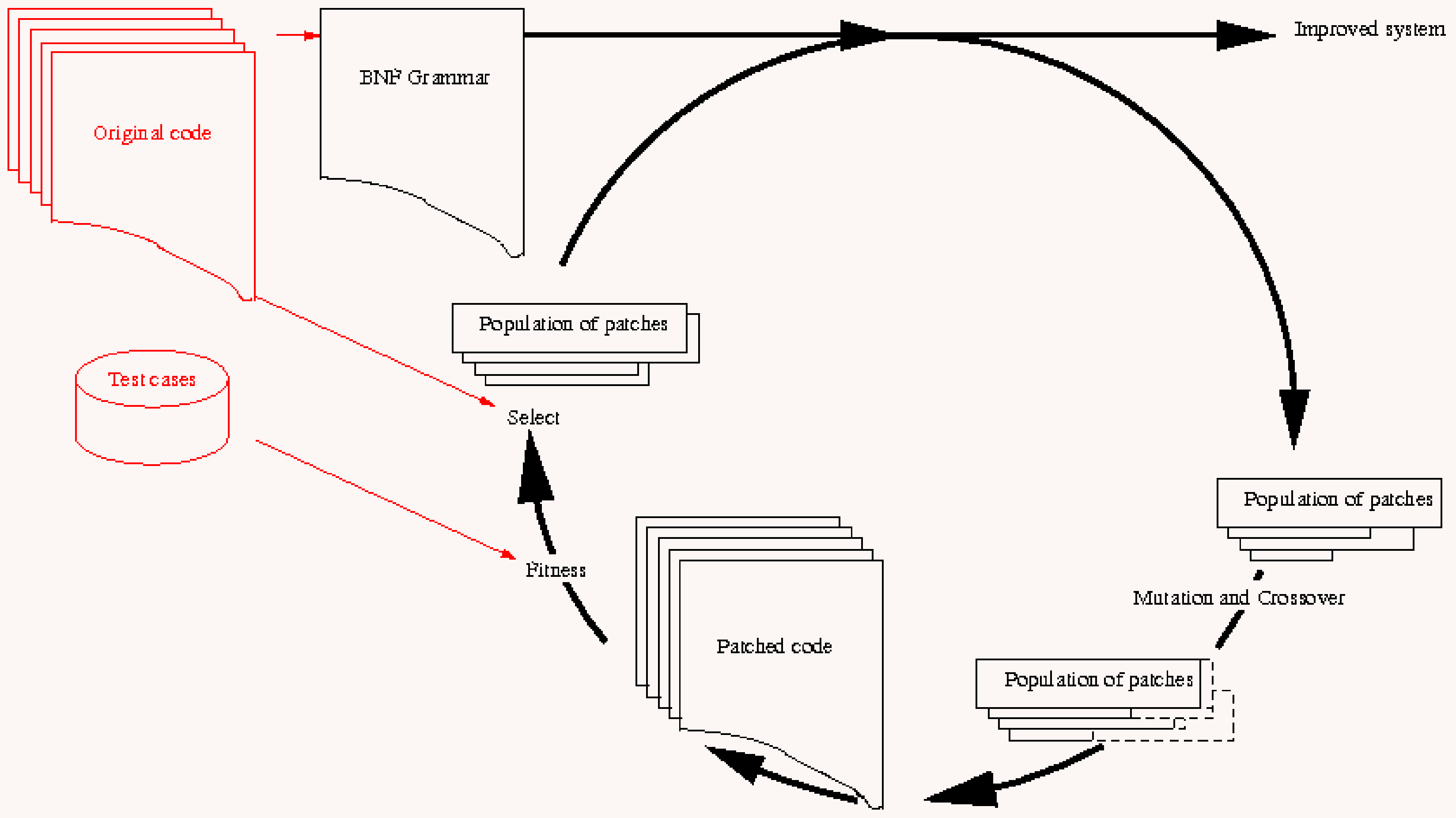
Why Bowtie 2 ?

- Bowtie2 maps short DNA sequence→ref genome
  - 50000 line C++, 50 .cpp 67 .h files, scripts, makefile, data files, examples, documentation
  - SourceForge
  - New rewrite by author of successful C Bowtie
- Aim to tailor existing system for specific (important data source)
- The 1000 Genomes Project
  – aims to map all human mutations
  – 100s millions of short human DNA sequences
  – Download raw data via FTP

Evolving Bowtie2

- Convert code to grammar
- Grammar used to both instrument code and control modifications to code
- Genetic programming manipulates patches
  - Small
  - New code is syntactically correct
  - Compilation errors mostly variable out-of-scope

GP Evolving Patches to Bowtie2



BNF Grammar

```
vhi = _mm_cmpeq_epi16(vhi, vhi); // all elts = 0xffff
vlo = _mm_xor_si128(vlo, vlo);   // all elts = 0
vmax = vlo;
```

Lines 363-365 aligner_swsse_ee_u8.cpp

```
<aligner_swsse_ee_u8_363>  ::="" <_aligner_swsse_ee_u8_363>
.                                 "{Log_count64++;/*28575*/}\n"
<_aligner_swsse_ee_u8_363> ::="vhi = _mm_cmpeq_epi16(vhi, vhi);"

<aligner_swsse_ee_u8_364>  ::="" <_aligner_swsse_ee_u8_364>
.                                 "{Log_count64++;/*28576*/}\n"
<_aligner_swsse_ee_u8_364> ::="vlo = _mm_xor_si128(vlo, vlo);"

<aligner_swsse_ee_u8_365>  ::="" <_aligner_swsse_ee_u8_365>
.                                 "{Log_count64++;/*28577*/}\n"
<_aligner_swsse_ee_u8_365> ::="vmax = vlo;"
```

Fragment of Grammar (Total 28765 rules)

7 Types of grammar rule

- Type indicated by rule name
- Replace rule only by another of same type
- 5792 statement (eg assignment, **Not** declaration)
- 2252 IF
- <pe_118> ::= "{Log_count64++;/*20254*/} if" <IF_pe_118> " {\n"
- <IF_pe_118> ::= "(!olap)"
- 272 for1, for, for3
- <sam_36> ::= "for(" <for1_sam_36> ";" <for2_sam_36> ";" <for3_sam_36> ") {\n"
- 106 WHILE
- <pat_731> ::= "while" <WHILE_pat_731> " {\n"
- <WHILE_pat_731> ::= "(true)"
- 24 ELSE
- <aln_sink_951> ::= "else {" <ELSE_aln_sink_951> " {Log_count64++;/*21439*/}};\n"
- <ELSE_aln_sink_951> ::= "met.nunp_0++;"

Representation

- GP evolves patches. Patches are lists of changes to the grammar.
- Append crossover adds one list to another
- Mutation adds one randomly chosen change
- 3 possible changes:
  - Delete   line of source code (or replace by “”, 0)
  - Replace with line of Bowtie2 (same type)
  - Insert   a copy of another Bowtie2 line

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Example Mutating Grammar

```
<_aligner_swsse_ee_u8_707> ::=    "vh = _mm_max_epu8(vh, vf);"
<_aligner_swsse_ee_u8_365> ::=    "vmax = vlo;"
```

2 lines from grammar

```
<_aligner_swsse_ee_u8_707><_aligner_swsse_ee_u8_365>
```

Fragment of list of mutations

Says replace line 707 of file aligner_swsse_ee_u8.cpp by line 365

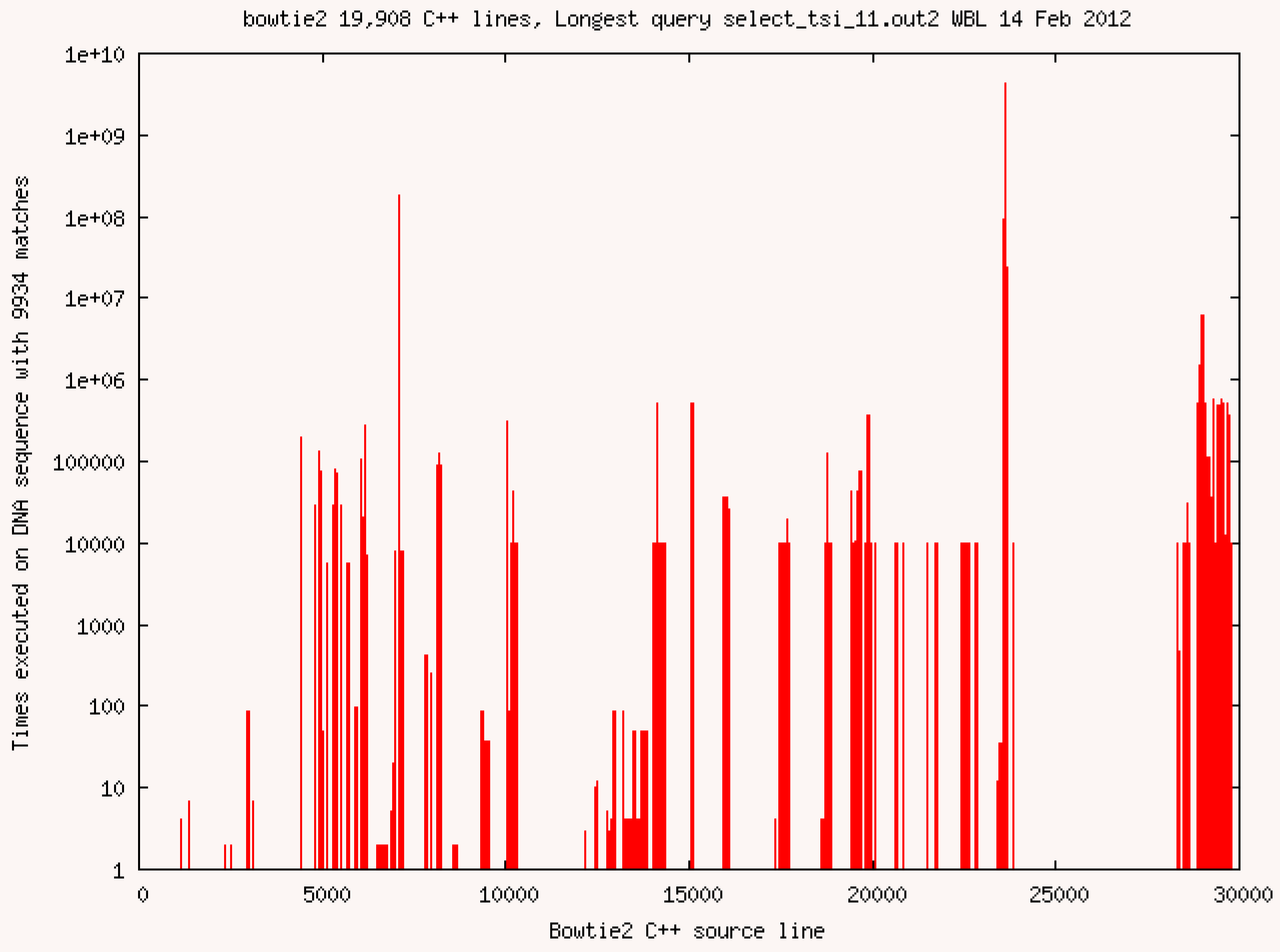
```
vh = _mm_max_epu8(vh, vf);{Log_count64++;/*28919*/}
```

Instrumented original code

```
vmax = vlo;{Log_count64++;/*28919*/}
```

New code

Which Parts of Bowtie2 are Used



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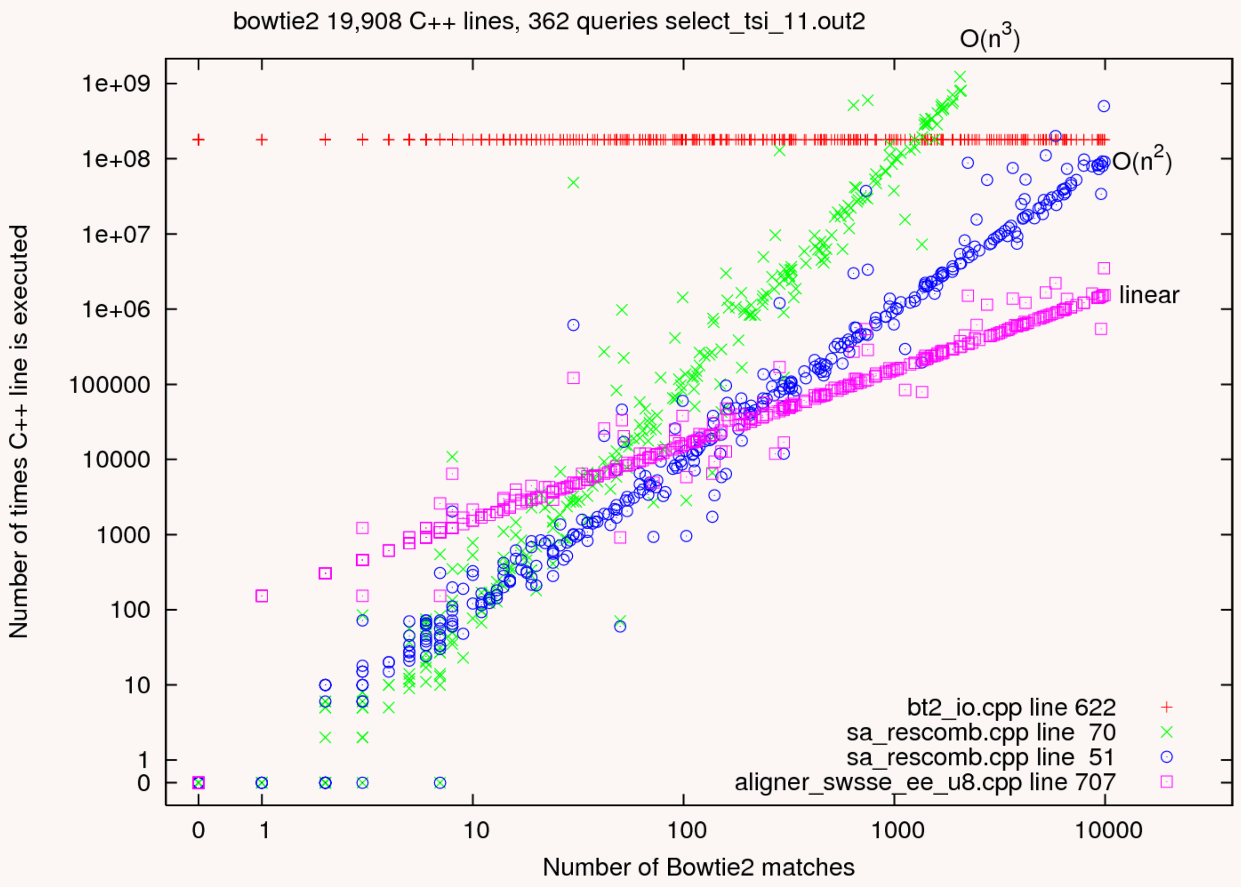
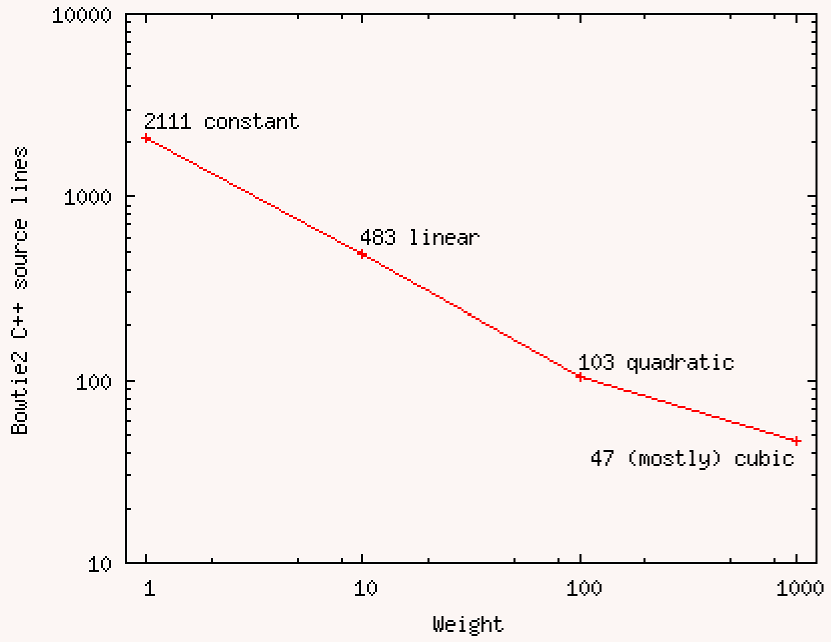
Scaling of Parts of Bowtie2



4 Heavily used Bowtie2 lines which scale differently

Focusing Search

C++ Lines	Files	Bowtie2
50745	50 .cpp, 67 .h	All C++ source files
19908	40 .cpp	no conditional compilation no header files.
2744	21 .cpp	no unused lines
		Weights target high usage
39	6 .cpp	evolve
7	3 .cpp	clean up



Fitness testing Bowtie2 variants

- Apply patch generated by GP to instrumented version of Bowtie2
- “make” only compiles patched code
  - precompile headers, no gcc optimise
- Run on small but diverse random sample of test cases from 1000 genomes project
- Calculate fitness
- Each generation select best from population of patched Bowtie2

Fitness

- Multiple objective fitness
  - Compiles? No→no children
  - Run patched Bowtie2 on 5 example DNA sequences, from The 1000 Genomes Project
  - Compare results with ideal answer (Smith-Waterman)
  - Sort population by
    - Number of DNA which don't fail or timeout
    - Average Smith-Waterman score
    - Number of instrumented C++ lines executed (minimise)
  - Select top half of population.
- Mutate, crossover to give 2 children per parent.
- Repeat 200 generations

Run time errors

- During evolution 74% compile
- 6% fail at run time
  - 3% segfault
  - 2% CPU limit expired
  - 0.6% heap corruption, floating point (e.g. divide by zero) or Bowtie2 internal checks
- 68% run ok

GP Evolution Parameters

- Pop 10, 200 generations
- 50% append crossover
- 50% mutation (3 types delete, replace, insert)
- Truncation selection
- 5 test examples, reselected every generation
- ≈25 hours

Clean up evolved patch

- Allowed GP solution to grow big
- Use fixed subset (441 DNA sequences) of training data
- Remove each part of evolved patch one at time
- If makes new bowtie2 (more than a little) worse restore it else remove it permanently
- 39 changes reduced to 7
- Took just over an hour (1:08:38)

Patch

Weight	Mutation	Source file	line	type	Original Code	New Code
999	replaced	bt2_io.cpp	622	for2	i < offsLenSampled	i < this->_nPat
1000	replaced	sa_rescomb .cpp	50	for2	i < satup_->offs.size()	0
1000	disabled		69	for2	j < satup_->offs.size()	
100	replaced	aligner_swsse_ee _u8.cpp	707		vh = _mm_max_epu8(vh, vf);	vmax = vlo;
1000	deleted		766		pvFStore += 4;	
1000	replaced		772		_mm_store_si128(pvHStore, vh);	vh = _mm_max_epu8(vh, vf);
1000	deleted		778		ve = _mm_max_epu8(ve, vh);	

- Evolved patch 39 changes in 6 .cpp files
- Cleaned up 7 changes in 3 .cpp files
- 70+ times faster

offsLenSampled=179,215,892 _nPat=84

Bowtie2 Results

- Patched code (no instrument) run on 200 DNA sequences (randomly chosen from same scanner but different people)
- Runtime 3:56:01 v 12.2 days
- Quality of output
  - 89% identical
  - 9% output better (higher mean Smith-Waterman score). Median improvement 0.1
  - 0.5% same
  - 1.5% worse (in 4th and 6th decimal place).

Results

- Wanted to trade-off performance v. speed:
  - On “1000 genomes” nextGen DNA sequences
  - 70+ faster on average
  - Very small *improvement* in Bowtie2 results

Conclusions

- Genetic programming can automatically re-engineer source code.
- create new code in a new environment (graphics card) for existing program, gzip WCCI 2010
- speed up legacy CUDA graphics code
- speed up 50000 lines of code IEEE TEC

GECCO 2014, Vancouver 12-16 July

Abstract submission:
January 15, 2014
Full papers: January 29, 2014

http://www.sigevo.org/gecco-2014

END

http://www.cs.ucl.ac.uk/staff/W.Langdon/ http://www.epsrc.ac.uk/

Discussion Points

- Scaling
- Code is not so fragile
- Build from existing code (source, assembler, binary)
- Template/source for new code
- fitness testing framework
- Grammar
- Weighting
- How to get genetic improvement programming adopted?

GECCO Vancouver July 12-16, 2014
Genetic Programming

GECCO 2014 – GP call for papers

The Genetic and Evolutionary Computation Conference will beheld on Saturday 12 July to Wednesday 16 July 2014

Important dates

Abstract submission: **January 15, 2014**
Full papers: January 29, 2014

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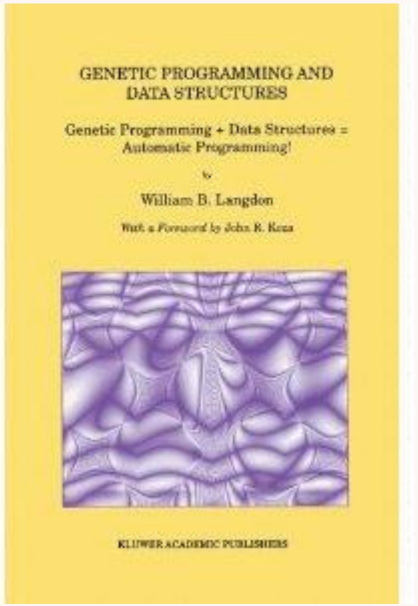
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Genetic Programming + Data Structures = Automatic Programming!

by

William B. Langdon

With a Foreword by John R. Koza

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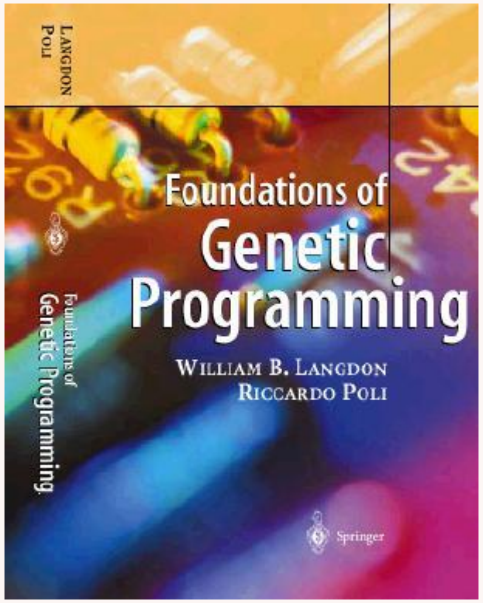
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Foundations of Genetic Programming

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Foundations of Genetic Programming

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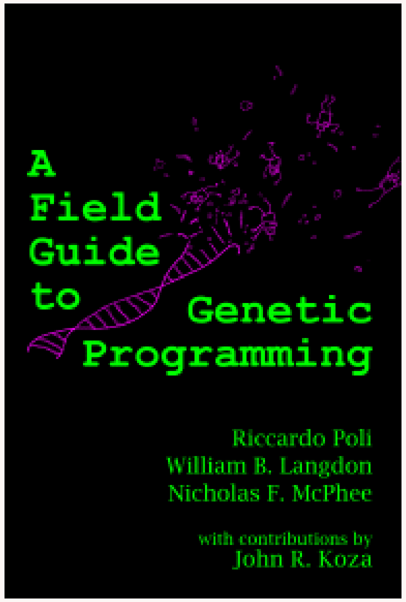
A Field Guide to Genetic Programming

Riccardo Poli
William B. Langdon
Nicholas F. McPhee

with contributions by
John R. Koza

The Genetic Programming Bibliography

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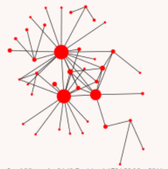

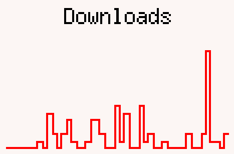

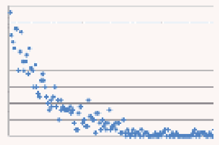

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