Genetic Improvement in the Shackleton Framework for Optimizing LLVM Pass Sequences

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https://arxiv.org/abs/2204.13261
Key Points

- Using genetic improvement to find optimized LLVM Pass sequences
- Automatic way to find a problem-specific optimization sequence
  - Without expert domain knowledge
- 3.7% runtime improvement (good in compiler world)
Overview

I. Shackleton Framework

II. Target Application: LLVM
   A. Experiments & Results

III. Edit Representations

IV. Experiments & Results

V. Conclusion
I. The Shackleton Framework
Osaka List Structure

Generalized linear representation of objects that unifies:

- Initialization
- Selection
- Crossover
- Mutation
- Customized fitness
II. LLVM Optimization Passes

• New target application, mostly unrelated to GA
• Variety of possible injection points for GA
  • Common Optimizer
  • Transitions from frontend to middle, middle to backend
• Open source
  • Easily accessible, popular
A bit more about LLVM - default optimization levels

- **-O0**: compiles the fastest and generates the most debuggable code
- **-O1**: in between -O0 and -O2
- **-O2**: moderate level of optimization which enables most optimizations
- **-O3**: -O2 plus optimizations that take longer to perform or that may generate larger code (in an attempt to make the program run faster)
- **-O4**: adds link-time optimization
- **-Os**: -O2 with extra optimizations to reduce code size
- **-Oz**: -Os (and thus -O2) but reduces code size further
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-O0: compiles the fastest and generates the most debuggable code

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-O2: moderate level of optimization which enables most optimizations

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III. Genetic “Edit” Rules

1. Deletion
2. Insertion
3. Replacement

Inside an “Edit”:

1. Edit type
2. Position
3. New Pass (null for deletion)

“Edit” Representations in Osaka List Structure

Edit ↔ Gene
Example Walk-through

**Edit 1**
- type: replace
- position: 0.8
- pass: -gvn

**Edit 2**
- type: deletion
- position: 0.21
- pass: N/A

**Edit 3**
- type: insertion
- position: 0.001
- pass: -licm
Experimental Outline

a. **Target program**: Backtracker Algorithm for the Subset Sum Problem (SSP)

b. **Hyperparameters**:

<table>
<thead>
<tr>
<th>Hyperparameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>num_generations</td>
<td>50</td>
</tr>
<tr>
<td>population_size</td>
<td>40</td>
</tr>
<tr>
<td>percent_crossover</td>
<td>60</td>
</tr>
<tr>
<td>percent_mutation</td>
<td>80</td>
</tr>
<tr>
<td>percent_elite</td>
<td>10</td>
</tr>
<tr>
<td>tournament_size</td>
<td>4</td>
</tr>
<tr>
<td>nest_size</td>
<td>6</td>
</tr>
<tr>
<td>individual_size</td>
<td>0 (this means random length)</td>
</tr>
</tbody>
</table>

c. **8 repeated runs**
Results

Runtime Improvement: 3.7% (±0.8768)

Hoste, Kenneth and Eeckhout, Lieven (2008): 3.1%
Ashouri, Amir Hossein et. al. (2016): 4%, 2%
Ashouri, Amir Hossein et. al. (2017): 5%
Wang, Zheng and O’Boyle, Michael (2018): 5%
Efficiency Analysis

Entire search space: $10^{167}$ → would take decades!

Genetic Improvement: start from known solution (-O3) → a few hours
Conclusions

- Don’t need domain expertise
- Problem-specific
- Efficient search process
- 3.7% runtime improvement

Future Directions

- Hyperparameter tuning specific for GI
- More test cases & standard benchmarks
thanks for listening!

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