

Finding Sufficient Mutation Operators via Variable Reduction

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Outline

- Introduction
- Related Work
- Experimental Procedure
- Statistical Analysis
- Preliminary Results
- Discussion
- Conclusion and Future Work

Introduction

- Needs faulty versions for experiments
 - Applying mutation operators to programs
- Many mutation operators have been proposed
 - Enormous number of mutants \Rightarrow Infeasible Computation
- Finding a reduced set which is sufficient
- Our approach
 - Applying variable reduction techniques

Related Work

Mutation Testing and Analysis

- Mutation Testing
 - Generating faulty versions: measuring the test suites adequacy (Offutt et al.)
- Mutants behave very similarly to real faults (Andrews et al.)
- Mutant generator tools: Mothra (Fortran), Proteum (C), and MuJava (Java)

Related Work (cont)

Sufficient Mutation Operators

- Sufficient mutation operators problem (Offutt et al.)
- Experiments to find the sufficient set for Fortran (Wong)

Variable Reduction

- Decreasing the number of variables (Jolliffe)

Experimental Procedure

Setup

- Subject programs: Siemens programs
 - Seven subject programs
- Mutant generator: Proteum, C mutant generator (Maldonado et al.)
 - 108 mutation operators
- Code coverage tool: ATAC
 - Block, Decision, Computation Use, Predicate Use

Experimental Procedure (cont)

Definitions of Sets and Measurements

- Mutation operators: $\mu_i, 1 \leq i \leq 108$
- $NMNE_i$, $\#$ of non-equivalent mutants generated using μ_i
- $TNMNE$, total $\#$ of mutants that are nonequivalent
- For each test suite S :
 - $kills_i(S)$, The set of mutants generated by μ_i and killed by S
 - $kills(S)$, The set of all mutants killed by S
 - $Am_i(S) = |kills_i(S)|/NMNE_i$, the adequacy ratio for mutants of operator μ_i
 - $AM(S) = |kills(S)|/TNMNE$, the adequacy ratio for all mutants

Experimental Procedure (cont)

Test Suite Groups

- Sufficient operators may depend on test suite construction
- Test suite construction methods studied:
 - *SING*, group of singleton test suites
 - *RAND_i*, $i = \{10, 20, 50, 100\}$, groups of randomly-selected test suites with size i
 - *BLK*, *DEC*, *CUSE*, *PUSE*, coverage-based test suites

Statistical Analysis

- All-Subset Regression (SUB)
- Elimination-Based Correlation Technique (EBC)
- Cluster Analysis (CA)

Statistical Analysis

All Subset Regression (SUB)

- Select a subset from a larger number of variables to predict another variable
- Finding subsets which fit well
- Number of variables in the prediction formula can be identified
- Constructing all regression models (Exhaustive)

Statistical Analysis

Elimination-Based Correlation Technique (EBC)

- Based on the correlation coefficients between variables
- constructing correlation matrix
- Eliminating one which has higher correlation with others
- High correlation: $cor(X, Y) \geq 0.90$

Statistical Analysis

Cluster Analysis (CA)

- Based on similarities of two variables
- Constructing proximity matrix
- Distances of variables in multi-dimensional space (Nearest Neighbor)
- Producing dendrogram

Preliminary Results

- Applied the techniques to `tcas.c` program so far.
- 300 test suites for each group
- 49 operators: no generated mutants
- Applied only to *SING*, *RAND_i*
- Applied each technique to each group of test suites
- Merged data for groups \Rightarrow Core set of operators from each technique

Preliminary Results (cont)

Core sets - No operators common to all

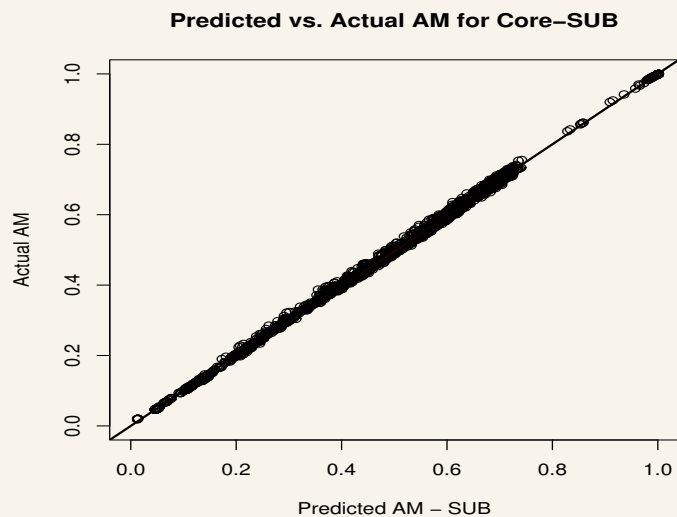
core-SUB	Mutants	core-EBC	Mutants	core-CA	Mutants
I-DirVarAriNeg	44	I-IndVarAriNeg	19	I-CovAllEdg	12
I-DirVarRepReq	220	I-IndVarLogNeg	19	I-DirVarRepCon	38
I-IndVarLogNeg	19	II-ArgRepReq	5	I-IndVarAriNeg	19
I-IndVarRepReq	91	u-OALN	2	I-RetStaDel	17
u-OABN	3	u-OASN	2	II-ArgIncDec	54
u-OLSN	34	u-OCNG	8	u-OABN	3
u-VDTR	111	u-OLLN	17	u-OALN	2
u-VGSR	794			u-OASN	2
u-VTWD	74			u-OCNG	8
II-ArgLogNeg	3			u-OLNG	51
				u-ORSN	30
				u-SRSR	60
				u-STRP	70
Total	1393	Total	72	Total	366

Preliminary Results (cont)

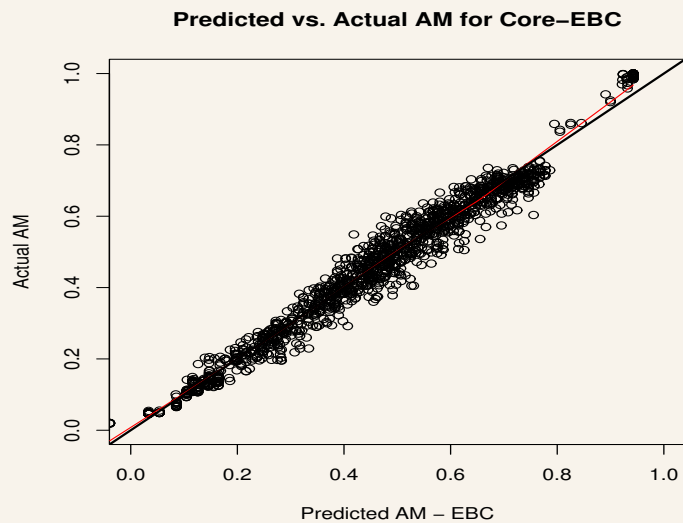
Comparison of core sets

	Core-SUB	Core-EBC	Core-CA
Mutants	1393	72	366
%Total	28.22%	1.45%	7.41%
%Saving	71.78%	98.55%	92.59%
Operators	10	7	13
%Total	9.25%	6.48%	12.03%
%Saving	90.75%	93.52%	87.97%

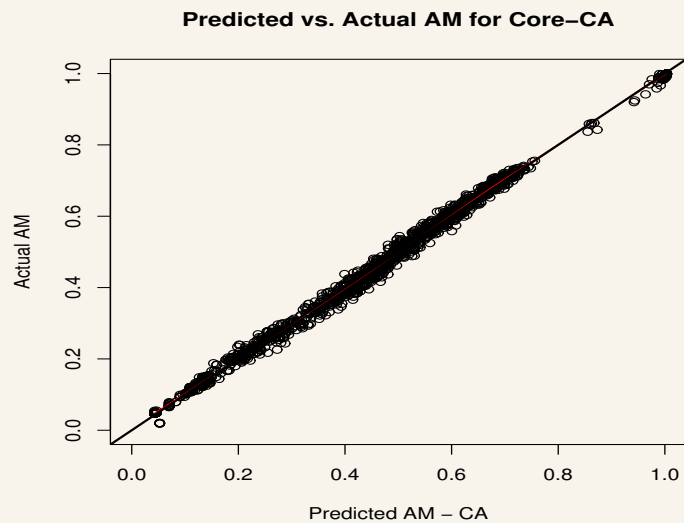
Preliminary Results (cont)



Preliminary Results (cont)

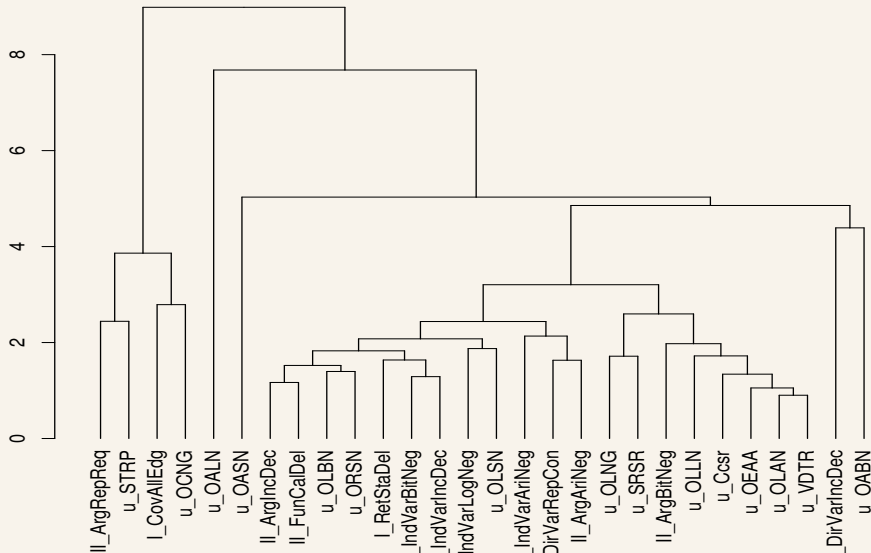


Preliminary Results (cont)



Preliminary Results (cont)

Similarity of Sufficient Mutation Operators for tcas-100



Discussion

Threats to Validity

- Analysis for tcas.c so far
- The correctness of the mutant generation and scripting processes
 - Rely on Proteum and our shell scripts
- Use of C programs

Data Combination and Analysis

- The order of activities:
 1. Combining Data from subject program
 2. Statistical Analysis
 3. Combine data from test suite groups
 4. Fit linear models

Conclusion and Future Work

Conclusion

- Applying variable reduction techniques to address sufficient mutation operators problem
 - Subset selection analysis considers AM as target
 - Correlation and cluster analyses try to identify the most distinct set of operators
- Our experiment reveals valuable information

Future Work

- Extend to all seven Siemens programs
- Study of possibilities of finding non-linear relationships among mutation operators
- Identifying one or several sets of mutation operators as sufficient

Thanks

*Questions
and
Answers*