Ahead of Time Mutation Based Fault Localisation using Statistical Inference

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***Abstract*—Mutation analysis can effectively capture the dependency between source code and test results. This has been exploited by Mutation Based Fault Localisation (MBFL) techniques. However, MBFL techniques suffer from the need to expend the high cost of mutation analysis after the observation of failures, which may present a challenge for its practical adoption. We introduce SIMFL (Statistical Inference for Mutation-based Fault Localisation), an MBFL technique that allows users to perform the mutation analysis in advance *before* a failure is observed, allowing the amortisation of the analysis cost. SIMFL uses mutants as artificial faults and aims to learn the failure patterns among test cases against different locations of mutations. Once a failure is observed, SIMFL requires either almost no or very small additional cost for analysis, depending on the used inference model. An empirical evaluation using DEFECTS4J shows that SIMFL can successfully localise up to 113 out of 203 studied faults (55%) at the top, and 159 (78%) faults within the top five, significantly outperforming existing MBFL techniques while using the results of mutation analysis that has been undertaken before the test failure. The amortised cost of mutation analysis can be further reduced by mutation sampling: SIMFL retains 80% of its localisation accuracy at the top rank when using only 10% of generated mutants, compared to results obtained without sampling.**

***Index Terms*—Fault Localisation**

I. Introduction

As software systems grow in size and complexity, automated fault localisation techniques [1] have received a lot of attention [2], [3], [4], [5], [6], [7]. There are two driving motivations for automated fault localisation. First, various studies have shown that developers can benefit from automated fault localisation technique if the location of a real fault can be narrowed down to a sufficiently small candidate set [8], [9]. Second, Automated Program Repair (APR), another technique increasingly in demand, depends on the accuracy of automated fault localisation for its success [10], [11], [12].

Mutation analysis has been successfully applied to fault localisation, resulting in a group of techniques called Mutation Based Fault Localisation (MBFL) [13], [14], [15], [16], [17]. Mutation analysis applies random syntactic modifications (each corresponding to a mutation operator) to existing code, and observes whether the changes in the program behaviour are detected via testing [18]. Existing MBFL techniques exploit the captured dependency between the artificial faults (i.e., mutants) and the changes in program behaviours (i.e., test results). For example, if mutating a program causes test cases to fail in a pattern similar to an observed failure, the mutant may be near the root cause of the observed failure [15], [16]. Alternatively, if mutating a program causes test cases to fail in a pattern very different from an observed failure, the mutant may be far from the location of the root cause [13].

Despite their success, MBFL techniques share a major weakness with mutation testing, which is the cost of test execution [18]. The more closely mutants approximate real faults, the more accurate MBFL techniques can be. As such, MBFL benefits from a large number of mutants, generated by a diverse set of mutation operators, to be analysed. However, this directly increases the cost of inspecting whether each mutant can be *killed* (i.e., whether the behavioural differences introduced by them are detectable), as this process requires the execution of the test suite per each mutant.

With large systems, this cost can grow significantly large, to the point that MBFL techniques cannot be used just-in-time after failures are observed. This is especially the case when MBFL techniques are used in the context of Continuous Integration (CI) [19], [20]. If developers encounter a failure during pre-commit testing, they are likely to want a just-in-time debugging technique that ensures fast and accurate feedback, so that they can remove the fault and continue to submit the changes. If, on the other hand, failure is observed during the post-commit testing initiated by the CI, it is still crucial for a fault localisation technique to be sufficiently fast so that developers do not wait hours for feedback [21]. The cost of having to re-run MBFL for each of the possibly many different failure patterns that can arise during pre- and post-commit testing efforts over, possibly, several commits could be truly staggering.

To overcome the high cost of mutation analysis in MBFL, we introduce SIMFL (Statistical Inference for Mutation-based Fault Localisation), an MBFL technique that allows developers to perform the mutation analysis in advance against an earlier version of the code. SIMFL constructs a kill matrix using a version of the System Under Test (SUT) before any test failures are observed. The matrix essentially captures which test cases fail when specific locations of SUT are mutated. Once an actual failure is observed, SIMFL builds predictive models and consults them using the information of which test cases pass and/or fail under the observed failure. Depending on the statistical inference technique, the actual post-hoc analysis, required after the observation of the failure, takes either virtually no time at all (Bayesian inference), or a small fraction of mutation analysis time (Logistic Regression or Multi-Layer Perceptron). SIMFL allows developers to amortise the cost of mutation analysis and use MBFL techniques in a just-in-time manner. By doing even the model building ahead-of-time the cost can be amortised further since we only need to use the previously built model and apply it to the specific failure patterns that are observed.

We have implemented and evaluated SIMFL using multiple modelling schemes and statistical inference techniques. The empirical evaluation studies real-world faults in DEFECTS4J benchmark [22], using the Major mutation tool [23]. SIMFL can successfully localise up to 113 out of 203 faults at the top, and 159 faults within the top five places. To reduce the cost of SIMFL even further, we also evaluate the impact of mutation sampling on the mutation analysis step of SIMFL. When using only 10% of the generated mutants for analysis, SIMFL can still achieve 80% of its localisation accuracy, compared to when not using sampling. The technical contributions of this paper are as follows:

- We introduce SIMFL, a Mutation Based Fault Localisation (MBFL) technique that allows ahead-of-time mutation analysis. Using the outcome of the mutation analysis, SIMFL builds a predictive model that allows developers to predict the location of actual future faults, using the test failure information as input. This process significantly amortises the cost of mutation analysis.
- We present the results of an empirical evaluation of SIMFL using the real world Java faults in DEFECTS4J benchmark. The empirical study concerns not only the localisation accuracy compared to the state-of-the-art FL techniques, but also various related aspects of SIMFL such as the impact of different modelling schemes, the viability of models built earlier than faults, and the impact of sampling rates.
- We discuss implications and characteristics of SIMFL and the impact of filtering mutants by their kill reason. Our observations suggest that mutant filtering has impact on localisation effectiveness of SIMFL and a potentially effective hybridisation would be possible between SIMFL and other fault localisation techniques.

The rest of the paper is organised as follows. Section II lays out the foundations of SIMFL by describing how the results of mutation analysis are formulated into predictive models for fault localisation. Section III presents the details of experimental design, including the protocols of the empirical study and research questions. Section IV presents and analyses results, while Section V discusses the results in the wider context of fault localisation. Section VI considers potential threats to validity, and Section VII presents related work. Finally, Section VIII concludes and presents future work.

II. METHODOLOGY

Intuitively, the underlying assumption of SIMFL is that, for a test that has killed the mutants located on a specific program element, the same program element should be identified as the suspicious location when the same test later fails again. This is based on the coupling effect hypothesis in mutation testing: essentially we *simulate* the occurrence of real faults with artificial faults with known locations, i.e., mutants, and build predictive models for actual future faults. This section describes the models and the statistical inference techniques used by SIMFL.

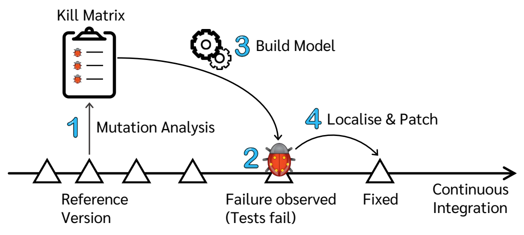


Fig. 1. Expected use case scenario of SIMFL

Figure 1 depicts the expected use case scenario of SIMFL, which includes four stages:

1) Perform mutation analysis for a version of SUT, and produce the kill matrix. The version is called the *reference* version.
2) While testing a subsequent version, a failure is observed.
3) Using the information of which test case(s) failed, as well as the kill matrix, build a predictive model for fault localisation.
4) Guided by the localisation result, patch the fault.

A. Mutation Analysis

We perform mutation analysis on the reference version of a program $\mathbf{P}$ with a test suite $\mathbf{T}$, and compute a kill matrix $\mathbf{K}$, which contains a complete report of all tests executed on all mutants. Let $\mathbf{K}_m$ denote a set of tests that kill mutant m, let $\mathbf{X}_e$ be a set of mutants located on a program element $e \in \mathbf{P}$, let M_e be an event that e is mutated, and let F_t be an event that a test case t fails on a given program. Based on the kill matrix $\mathbf{K}_m$, we can approximate the probability of test case t killing the mutants located on the program element e as follows:

$$Pr\left(F_t \mid M_e\right) \simeq \frac{\left|\{m \in \mathbf{X}_e \mid t \in \mathbf{K}_m\}\right|}{|\mathbf{X}_e|} \tag{1}$$

Note that this is strictly an *approximation* based on the observed kill matrix because it is impossible to produce and evaluate all possible mutants. The exact value of $Pr\left(M_e\right)$ is the ratio of the number of all possible mutants on e to the number of all possible mutants on $\mathbf{P}$; for $Pr\left(F_t \mid M_e\right)$, we need to calculate the number of all possible mutants in e that are killed by t. Neither is feasible. Consequently, we assume that we can analyse a *finite* set of mutants that allow us to approximate Equation 1.

Next, using Bayes' rule, we calculate the revised probability of the event that the program element e has been mutated, given that the test case t fails:

$$\begin{aligned} Pr\left(M_e \mid F_t\right) &= \frac{Pr\left(F_t \mid M_e\right) Pr\left(M_e\right)}{Pr\left(F_t\right)} \\ &\simeq Pr\left(\text{fault exists in } e \mid F_t\right) \end{aligned} \tag{2}$$

We argue that, if real faults are coupled to mutants, the probability above can approximate the likelihood that the fault is located on the program element e, when t is a failing test case in the future. This allows us to make ranking models that sort the program elements in descending order of the probability.

B. Ranking Models

We regard the probability in Equation 2 as the quantitative score representing how suspicious the program element e is for the failure observed via the failure of t. This section presents the formulations of ranking models based on the scores as well as more refined inference models based on kill matrix data.

1) Exact Matching (EM): This model is an extension of Equation 2 to a set of test cases. Let $\mathbf{T} = \{t_i \mid 1 \leq i \leq n \leq n'\}$ be the test set, which consists of two disjoint sets: $\mathbf{T}_f = \{t_1, \ldots, t_n\}$ is the set of failing test cases, and $\mathbf{T}_p = \mathbf{T} \setminus \mathbf{T}_f$ is the set of passing tests, on the faulty program. While there can be many different formulations of ranking models based on a set of test cases, we start by treating the set of all observed failures, $F_{\mathbf{T}_f}$, as a conjunctive event of individual test case failures, i.e., $F_{\mathbf{T}_f} = F_{t_1} \cap \cdots \cap F_{t_n}$. Our goal is to find the faulty program element $e_i \in \mathbf{P}$ with the highest probability of being the cause of the observed failure symptoms, that is, $Pr\left(M_{e_i} \mid F_{\mathbf{T}_f}\right)$. It follows that:

$$\underset{i}{\operatorname{argmax}}\, Pr\left(M_e \mid F_{\mathbf{T}_f}\right) = \underset{i}{\operatorname{argmax}} \frac{Pr\left(F_{\mathbf{T}_f} \mid M_e\right) Pr\left(M_e\right)}{Pr\left(F_{\mathbf{T}_f}\right)} \tag{3}$$

The denominator in Equation 3, $Pr\left(F_{\mathbf{T}_f}\right)$, can be ignored without affecting the order of ranking based on this score, because it is not related to a specific program element. Expanding the numerator yields the following:

$$\begin{aligned} &\underset{i}{\operatorname{argmax}}\, Pr\left(F_{\mathbf{T}_f} \mid M_{e_i}\right) Pr\left(M_{e_i}\right) \\ &= \underset{i}{\operatorname{argmax}}\, Pr\left(F_{t_1} \cap \cdots \cap F_{t_n} \mid M_{e_i}\right) Pr\left(M_{e_i}\right) \\ &= \underset{i}{\operatorname{argmax}} \frac{|\{m \in \mathbf{X}_{e_i} \mid \{t_1, \ldots, t_n\} = \mathbf{K}_m\}|}{|\mathbf{X}_{e_i}|} Pr\left(M_{e_i}\right) \\ &= \underset{i}{\operatorname{argmax}} \frac{|\{m \in \mathbf{X}_{e_i} \mid \mathbf{T}_f = \mathbf{K}_m\}|}{|\mathbf{X}_{e_i}|} \frac{|\mathbf{X}_{e_i}|}{|\mathbf{X}_{\mathbf{P}}|} \\ &= \underset{i}{\operatorname{argmax}} \frac{|\{m \in \mathbf{X}_{e_i} \mid \mathbf{T}_f = \mathbf{K}_m\}|}{|\mathbf{X}_{\mathbf{P}}|} \\ &= \underset{i}{\operatorname{argmax}}\, |\{m \in \mathbf{X}_{e_i} \mid \mathbf{T}_f = \mathbf{K}_m\}| \end{aligned} \tag{4}$$

Intuitively, Equation 4 counts the mutants on e that cause the same set of test cases to fail as the symptom of the actual fault, $F_{\mathbf{T}_f}$. We call this model the Exact Matching (EM) model with failing test cases, denoted by EM(F).

Alternatively, we can include passing tests in the pattern matching as well. Let P_t be an event that a test case t passes on a given program, then Equation 4 changes as follows:

$$\begin{aligned} &\underset{i}{\operatorname{argmax}}\, Pr\left(F_{\mathbf{T}_f} \cap P_{\mathbf{T}_p} \mid M_{e_i}\right) Pr\left(M_{e_i}\right) \\ &= \underset{i}{\operatorname{argmax}}\, Pr\left(F_{t_1} \cap \cdots \cap F_{t_n} \cap P_{t_{n+1}} \cap \cdots \cap P_{t_{n'}} \mid M_{e_i}\right) Pr\left(M_{e_i}\right) \\ &= \underset{i}{\operatorname{argmax}}\, |\{m \in \mathbf{X}_{e_i} \mid \mathbf{T}_f = \mathbf{K}_m \wedge \mathbf{T}_p = \mathbf{T} \setminus \mathbf{K}_m\}| \end{aligned} \tag{5}$$

Similarly to EM(F), this model is called EM(F+P): it counts the mutants on e that cause the same set of test cases to fail and pass exactly as the symptom of the actual fault. If, for example, a test case t passed under the actual fault, EM(F+P) model will not count any mutants that are killed by t.

2) Partial Matching (PM): The Exact Matching (EM) models lose any partial matches between the symptom and the mutation results. Suppose two test cases, t_1 and t_2, failed under the actual fault, but only t_1 killed a mutant on the faulty program element, i.e., $\exists t_1, t_2 \in \mathbf{T}_f, t_1 \in \mathbf{K}_m \wedge t_2 \notin \mathbf{K}_m$. The information that t_1 kills a mutant on the location of the fault is lost, simply because t_2 failed to do the same. To retrieve this partial information, we propose two additional models based on partial matches: a multiplicative partial match model and an additive partial match model.

- PM*(F): Multiplicative Partial Match Model w/ Failing Tests

$$\begin{aligned} &\underset{i}{\operatorname{argmax}} \prod_{t \in \mathbf{T}_f} \left(Pr\left(M_{e_i} \mid F_t\right) + \epsilon\right) \\ &= \underset{i}{\operatorname{argmax}} \prod_{t \in \mathbf{T}_f} \left(|\{m \in \mathbf{X}_{e_i} \mid t \in \mathbf{K}_m\}| + \epsilon\right) \end{aligned} \tag{6}$$

- PM$^+$(F): Additive Partial Match Model w/ Failing Tests

$$\begin{aligned} &\underset{i}{\operatorname{argmax}} \sum_{t \in \mathbf{T}_f} Pr\left(M_{e_i} \mid F_t\right) \\ &= \underset{i}{\operatorname{argmax}} \sum_{t \in \mathbf{T}_f} |\{m \in \mathbf{X}_{e_i} \mid t \in \mathbf{K}_m\}| \end{aligned} \tag{7}$$

Intuitively, instead of counting exact matches, we want to aggregate scores from the relationship between individual failing test cases and all mutants on a specific program element. PM*(F) and PM$^+$(F) respectively aggregate individual scores by multiplication and addition. Note that the PM*(F) model requires a small positive quantity ϵ to prevent the value of the entire formula from being zero when there exist one or more terms that evaluate to zero: the value of ϵ does not affect the ranking.

Similarly to the case of EM models, we can also include the information of test cases that pass under the actual fault. These two models are called PM*(F+P) and PM$^+$(F+P), and defined as follows:

- PM*(F+P): Multiplicative Partial Match Model w/ All Tests

$$\begin{aligned}&\operatorname*{argmax}_i \left(\prod_{t \in \mathbf{T}} (Pr\,(M_{e_i} \mid F_t) + \epsilon) \prod_{t \in \mathbf{T}_p} (Pr\,(M_{e_i} \mid P_t) + \epsilon) \right) \\ &= \operatorname*{argmax}_i \prod_{t \in \mathbf{T}} (|\{m \in \mathbf{X}_{e_i} \mid t \in \mathbf{T}_f \iff t \in \mathbf{K}_m\}| + \epsilon)\end{aligned} \tag{8}$$

- PM$^+$(F+P): Additive Partial Match Model w/ All Tests

$$\begin{aligned}&\operatorname*{argmax}_i \left(\sum_{t \in \mathbf{T}} (Pr\,(M_{e_i} \mid F_t)) + \sum_{t \in \mathbf{T}_p} (Pr\,(M_{e_i} \mid P_t)) \right) \\ &= \operatorname*{argmax}_i \sum_{t \in \mathbf{T}} |\{m \in \mathbf{X}_{e_i} \mid t \in \mathbf{T}_f \iff t \in \mathbf{K}_m\}|\end{aligned} \tag{9}$$

3) Linear and Non-linear Classifiers: Scores from the Bayesian inference models described in Section II-B1 and II-B2 are directly computed from the kill matrix, and requires virtually no additional analysis cost when scores are needed to be computed. However, all these models simply rely on counting matches between test results under the actual fault and kill matrix from the ahead-of-time mutation analysis.

To investigate if more sophisticated statistical inference techniques can improve the accuracy of SIMFL, we apply both linear and non-linear classifiers to build predictive models. These classifiers take the test results as input, and yield the most suspicious method, as well as the suspiciousness score of each method as output. Let $\alpha_{\mathbf{T_i}}$ denote a 0-1 vector of the test results of $\mathbf{T_i}$, where 0 indicates that test case fails, and 1 indicates that test case passes. We first build a training set using the kill matrix $\mathbf{K}$: test results per mutant $\mathbf{T_i}$ are transformed into $\alpha_{\mathbf{T_i}}$, and the class is labelled based on the method where the mutant is located.

We train representative linear and non-linear classifiers using Logistic Regression (LR) and Multi-Layer Perceptron (MLP) [24], [25]. For our study, we use a vanilla MLP that consists of one input layer, one hidden layer with 50 neurons, and one output layer. In the serving phase, we use the suspiciousness score of each program element, which is obtained before the model computes the most suspicious method. Only using the observed failures, we can compose 0-1 vectors (i.e., LR(F) and MLP(F)), or compose 0-1 vectors by including the information of passing tests (i.e., LR(F+P) and MLP(F+P)). Note that, unlike the Bayesian inference models described in Section II-B1 and II-B2, training these classifiers requires additional analysis cost to SIMFL, although the training cost of these models is much lower than the cost of mutation analysis.

III. Experimental Design

This section describes the design of our empirical evaluation, including the way we use DEFECTS4J benchmark, the research questions, as well as other environmental factors.

A. Protocol

One foundational assumption of SIMFL is that existing test cases can be fault revealing also for future changes. That is, for future faults to which SIMFL will be applied, test cases that would reveal them are available at the time of the ahead-of-time mutation analysis. We believe this is a likely scenario mainly in two contexts: regression faults, which are defined as failures of existing test cases, and pre-commit testing, for which developers depend on existing test cases for a sanity check. SIMFL is designed to reduce the cost of MBFL for these scenarios.[1]

However, this makes realistic experiments on real-world data challenging since a majority of failure triggering changes are not likely to have been committed to the main branch of the Version Control System (VCS): one of the purposes of Continuous Integration is to prevent such commits [21]. Consequently, fault benchmarks, such as DEFECTS4J, contain faults that have been reported externally (e.g., from issue tracking systems), and provide fault revealing test cases that have been added to the VCS with the patch itself [22]. This presents a challenge for the realistic evaluation of SIMFL in the context it was designed for. To address this issue, we introduce two experimental protocols.

1) Faulty Commit Emulation (FCE): This scenario emulates a faulty *commit* that would trigger failures of existing test cases simply by reversing a fix patch in DEFECTS4J. We take the fixed version (V_{fix}) in DEFECTS4J as the reference version and performs the mutation analysis, including the test cases from the same version. Subsequently, we reverse the fix patch, execute the same test cases, and try to localise the fault using the results with SIMFL.

We argue that this is more realistic than injecting mutation faults artificially to evaluate SIMFL. Since mutants are exactly what SIMFL uses to build its models, SIMFL may unfairly benefit if evaluated using mutants as faults. Instead, we emulate faulty commits using faults that some developers actually had introduced in real-world software. Existing work on test data generation has also used the fixed version as the reference version, against which a test generation tool is applied. The reversed fix patch is then used to emulate regression faults for the evaluation of the generated tests [26], [27]. Our approach with FCE is similar in the sense that we analyse the fixed version first, then use the outcome to localise the emulated regression fault.

2) Test Existence Emulation (TEE): This scenario uses original faulty commits that led to the faulty versions (V_{bug}) in DEFECTS4J, but simply *pretends* that the *fault revealing test cases existed earlier*. We have checked whether the fault revealing test cases in DEFECTS4J can be executed against versions that precede the actual faulty version. Since system specifications evolve over time, executing a future test case against past versions is not always successful: we have identi-

[1]Although we do note that the more mature a software system is and the stronger and more complete its test suite is, the more likely it is that these conditions hold and thus that the proposed approach can be useful.

fied 28 previous versions for which the future fault revealing test cases can be executed and *do not fail*. We use these 28 versions as references, and use their mutation analysis results to localise the corresponding faults that happened later. Compared to FCE, TEE follows the ground truth code changes, and only assumes the earlier existence of fault revealing test cases. We use TEE to complement the FCE scenario. Specifically, TEE can evaluate whether training SIMFL models with kill matrices of earlier versions degrades its localisation accuracy.

3) Experimental Premise: Building a full kill matrix requires huge computational cost: mutation analysis on all versions of Closure using Major exceeded our 24 hours timeout, and other subject programs also required significant amounts of analysis time. To address this practical concern, for empirical evaluation, we have constructed the kill matrix using only the *relevant test cases* as defined by DEFECTS4J[2], which include the failing test cases as well as any passing test cases that makes the JVM to load at least one of the classes modified by the fault introducing commit.

Note that this procedure has been adopted strictly to reduce experimental cost. Since we only have the kill matrix for the relevant test cases, models that use F+P test cases actually use the full set of relevant test cases. However, if construction of the full kill matrix is feasible, the same input used by SIMFL in this paper is naturally available. The F+P models can be trained either using the full set of test cases (increased training cost but also richer input information), or using the relevant test cases (relevancy information is still cheaper than full coverage instrumentation). We argue that, in general, the limitation to only the relevant test cases is a conservative one and should reduce rather than improve the fault localisation accuracy of SIMFL since other test cases could also be informative for its statistical models.

4) Using Test Runtime Information: The use case of SIMFL assumes that, while the actual mutation analysis can be performed in advance, the inference models are trained after the observation of a failure (see Figure 1). In practice, the observation of the behaviour of the failing test cases can provide information that is beyond the mutation analysis. Consequently, we exploit this additional information by collecting coverage reports of failing test cases using `Cobertura`. We then exclude any methods and mutants that are not covered by the failing test cases from model training and the final ranking.

TABLE I
SUBJECT PROGRAMS IN DEFECTS4J

Subject	# Faults	kLoC	# Methods	# Mutants	# Test cases
Commons-lang (Lang)	65	50	1,527	21,178	2,245
JFreeChart (Chart)	26	132	4,903	75,985	2,205
Joda-Time (Time)	27	105	1,946	21,689	4,130
Closure compiler (Closure)	133	216	5,038	58,515	7,927
Commons-math (Math)	106	104	2,713	79,428	3,602
Total	357	607	16,126	256,792	20,109

[2]See https://github.com/rjust/defects4j/tree/v1.3.1#export-version-specific-properties

B. Subject Programs

In our study, we use 357 versions of five different programs from the DEFECTS4J version 1.3.1. They provide reproducible and isolated faults of real-world programs. Table I summarises the subject programs we used with the average number of generated mutants, methods, lines of code, and test cases across all faults belonging to each subject respectively. We could not include Mockito as we failed to compile the majority of its versions and their mutants using the build script provided by DEFECTS4J on Docker containers.

C. Research Questions

RQ1. Localisation Effectiveness: *Does the models of SIMFL produce accurate fault localisation compared to the state-of-the-art FL techniques?* RQ1 is answered by computing the standard evaluation metrics on the eight models of SIMFL under the FCE scenario outlined in Section III-A1. We compare SIMFL with two MBFL techniques (MUSE and Metallaxis), two SBFL techniques (Ochiai and DStar), and two learning-to-rank based FL techniques (TraPT and FLUCCS).

RQ2. Model Viability: *How well does SIMFL hold up when applied using models built earlier?* RQ2 is answered by computing the standard evaluation metrics using prior models built under the TEE scenario outlined in Section III-A2.

RQ3. Sampling Impact: *What is the impact of mutation sampling to the effectiveness of SIMFL?* Since the cost of mutation analysis is the major component of the cost of SIMFL, we investigate how much impact different mutation sampling rates have. We evaluate two different sampling techniques: uniform random sampling, which samples from the pool of all mutants uniformly, and stratified sampling, which samples as the equal number of mutants from each method as possible.

D. Evaluation Metrics and Tie Breaking

We use three standard evaluation metrics:

- $acc@n$: counts the number of faults located within top n ranks. We report $acc@1$, $acc@3$, $acc@5$, and $acc@10$. If a fault is patched across multiple methods, we take the highest ranked method to compute $acc@n$.
- wef: approximates the amount of efforts wasted by developer while investigating non-faulty methods that are ranked higher than the faulty method.
- Mean Average Precision (MAP): measures the mean of the average precision values for a group of all faults.

If multiple program elements have the same score, resulting in the same rank, we break the tie using max tie breaker that places all program elements with the same score at the lowest rank.

E. Mutation Tool and Operators

In the study, we use Major version 1.3.4 [23] as our mutation analysis tool, and choose all mutation operators in Major. Note that some operators had to be turned off for specific classes

TABLE II
EFFECTIVENESS OF SIMFL MODELS USING FCE SCENARIO.

Model	Project	Total	acc				wef	MAP	Model	Project	Total	acc				wef	MAP
		Studied	@1	@3	@5	@10	med				Studied	@1	@3	@5	@10	med	
EM (F)	Lang	62 (65)	35	45	47	48	**0.0**	0.6176	EM (F+P)	Lang	61 (65)	36	41	43	44	**0.0**	0.5922
	Chart	26 (26)	**6**	**11**	**13**	15	5.0	0.3294		Chart	25 (26)	6	9	10	11	27.0	0.2917
	Time	26 (27)	**4**	9	9	13	8.5	0.2451		Time	26 (27)	10	13	14	15	3.0	0.3819
	Closure	132 (133)	10	31	41	57	17.0	0.1753		Closure	0 (133)	-	-	-	-	-	-
	Math	102 (106)	22	43	53	71	4.0	0.3404		Math	91 (106)	32	45	47	49	3.0	0.4098
	Total	348 (357)	77	139	163	204				Total	203 (357)	84	108	114	119		
PM* (F)	Lang	62 (65)	38	47	51	53	**0.0**	0.6732	PM* (F+P)	Lang	61 (65)	27	36	37	42	1.0	0.5264
	Chart	26 (26)	**6**	**11**	**13**	16	5.0	0.3562		Chart	25 (26)	7	9	12	14	6.0	0.3598
	Time	26 (27)	**4**	**10**	10	13	8.0	0.2549		Time	26 (27)	1	3	4	12	16.0	0.1172
	Closure	132 (133)	11	36	50	66	9.5	0.1982		Closure	0 (133)	-	-	-	-	-	-
	Math	102 (106)	23	**47**	59	77	3.5	0.3753		Math	91 (106)	14	26	33	42	12.0	0.2460
	Total	348 (357)	82	151	183	225				Total	203 (357)	49	74	86	110		
PM$^+$ (F)	Lang	62 (65)	40	48	52	53	**0.0**	0.6977	PM$^+$ (F+P)	Lang	61 (65)	19	31	33	37	2.0	0.4291
	Chart	26 (26)	**6**	10	**13**	**19**	**4.0**	**0.3697**		Chart	25 (26)	5	9	12	13	8.0	0.2712
	Time	26 (27)	**4**	**10**	10	13	8.0	0.2564		Time	26 (27)	0	2	3	5	40.5	0.0616
	Closure	132 (133)	**12**	**41**	**52**	65	11.0	0.2005		Closure	0 (133)	-	-	-	-	-	-
	Math	102 (106)	24	46	59	77	4.0	0.3845		Math	91 (106)	9	15	20	29	23.0	0.1574
	Total	348 (357)	86	**155**	**186**	**227**				Total	203 (357)	33	57	68	84		
LR (F)	Lang	62 (65)	**41**	49	**53**	**55**	**0.0**	**0.7179**	LR (F+P)	Lang	61 (65)	40	49	51	53	**0.0**	0.7017
	Chart	26 (26)	5	9	12	14	6.0	0.3175		Chart	25 (26)	8	14	14	16	**2.0**	0.4194
	Time	26 (27)	**4**	**10**	**12**	**14**	5.5	0.2668		Time	26 (27)	8	14	17	19	2.0	0.4094
	Closure	132 (133)	**12**	37	50	**68**	**9.0**	**0.2074**		Closure	0 (133)	-	-	-	-	-	-
	Math	102 (106)	**28**	**47**	59	75	**3.0**	**0.3976**		Math	91 (106)	32	43	47	51	3.0	0.4066
	Total	348 (357)	**90**	152	**186**	226				Total	203 (357)	88	120	129	139		
MLP (F)	Lang	62 (65)	39	**51**	**53**	**55**	**0.0**	0.7052	MLP (F+P)	Lang	61 (65)	**48**	**55**	**56**	**56**	**0.0**	**0.7882**
	Chart	26 (26)	5	10	12	15	6.0	0.3319		Chart	25 (26)	**9**	**13**	**15**	**19**	**2.0**	**0.4477**
	Time	26 (27)	**4**	**10**	**12**	**14**	**5.0**	**0.2710**		Time	26 (27)	**11**	**16**	**18**	**24**	**1.0**	**0.4847**
	Closure	132 (133)	11	33	41	60	12.0	0.1888		Closure	0 (133)	-	-	-	-	-	-
	Math	102 (106)	26	46	**62**	**79**	**3.0**	0.3941		Math	91 (106)	**45**	**61**	**70**	**82**	**1.0**	**0.5194**
	Total	348 (357)	85	150	180	223				Total	203 (357)	**113**	**145**	**159**	**181**		

so that Major does not generate an exceptionally large number of mutants.[3]

IV. RESULTS

Due to a space limit, we present the full results including all evaluation metrics online at https://coinse.github.io/simfl-results.

A. *Effectiveness (RQ1)*

We start by comparing different SIMFL models. Subsequently, using the best SIMFL model, we compare SIMFL to the state-of-the-art fault localisation techniques.

1) Comparison Between SIMFL Models: Table II shows the results of each evaluation metric for all studied faults, following the FCE scenario. The numbers $X(Y)$ in the column "Total Studied" represent the number of faults that we can localise (X), and the number of faults provided by DEFECTS4J (Y). Evaluation metric values representing the best outcome (i.e., the largest $acc@n$ and MAP, and the smallest wef) are typeset in bold. See Section III-B for the details of exclusion criteria we used: note that more faults are excluded from the study of F+P models shown on the right.

Overall, MLP(F+P) shows the best performance in terms of $acc@n$ metrics, placing 48 out of 61 faults at the first place for Lang, and 45 out of 91 faults at the first place for Math. Considering that MLP(F+P) is evaluated on fewer faults (203) than MLP(F) (348), the result suggests that MLP(F+P) shows better performance on average.

We argue that including results of passing tests gives richer information when compared to only using results of failing tests. However, we also note that only MLP significantly benefits from the additional information: MLP(F+P) places 28 more faults at the top than MLP(F). Two linear models, LR(F) and LR(F+P), on the other hand, do not show any significant difference in performance. This suggests that exploiting this information requires more sophisticated, non-linear inference methods.

The reason that PM$^+$(F) shows comparable results to MLP(F) may be that it is relatively easy to simply count the matching patterns of failing tests, which are much rarer than passing tests. We also note that PM*(F) and PM$^+$(F) both produce better results than EM(F), suggesting that partial matches are better than exact matches. This is because even the fault revealing test case may not be able to kill all mutations applied to the location of the fault. In such a case, the EM(F) model will lose the information, while the PM(F) models will benefit from other killed mutants from the same location.

Finally, the addition of passing test information to PM models actually degrades the performance significantly, as the metrics for PM*(F+P) and PM$^+$(F+P) show. Partially matching test cases that did not fail against the faulty version with test cases that did not kill mutants at the location of the fault will directly dilute the signal, as failing tests and killed mutants are likely to provide more information about

[3]Due to the internal design of Major, some classes that yield too many mutants may lead to the violation of bytecode length limit imposed by Java compiler. See https://github.com/rjust/defects4j/issues/62 for technical details.

the location of the fault in general.

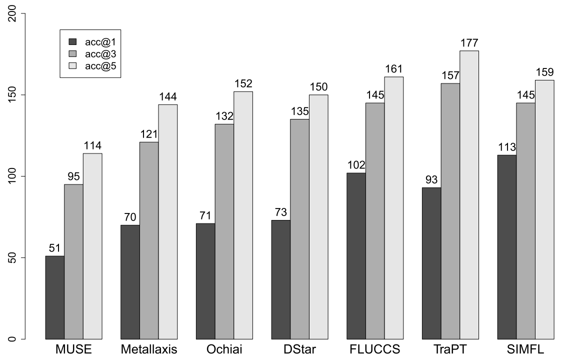


Fig. 2. Comparison to other FL techniques: $acc@n$ metric values without counts of Closure

2) Comparison to Other FL Techniques: To gain some insights into the trade-off between amortised modelling efforts and localisation accuracy, we compare the method-level fault localisation results of the state-of-the-art MBFL and SBFL techniques, the result of which is shown in Figure 2. We obtained the performance of the each model (i.e., $acc@n$) on DEFECTS4J from the literatures, and artefact of Zou et al. [28]. Based on the results of the comparison between SIMFL models, we choose MLP(F+P) to represent SIMFL. However, since Closure has been excluded from the evaluation of F+P models, we have excluded Closure from the results of other techniques for a fair comparison.

Figure 2 shows that MLP(F+P) is better than other techniques in terms of $acc@1$, but TraPT performs better in terms of $acc@3$ and $acc@5$. Although SIMFL does not make use of learning-to-rank technique to boost performance by fully including runtime information or suspiciousness scores of other FL techniques, SIMFL localises faults at the top better than others, and shows comparable results to the learning-to-rank techniques: FLUCCS and TraPT.

Based on this analysis, we answer RQ1 that SIMFL can localise faults accurately compared to the existing techniques: SIMFL places up to 25.86% (90 of 348 for LR(F)) of studied faults at the top using F models, and 55.67% (113 of 203 for MLP(F+P)) of studied faults at the top using F+P models.

B. Model Viability (RQ2)

Following the TEE scenario described in Section III-A2, we seek reference versions preceding the faulty version, i.e., the versions before the faulty version that pass all test cases of the fixed program, including the fault revealing test cases. Assuming that more recent versions are more likely to serve as references, given a faulty version n, we check $n-1$, …, $n-10$, $n-20$, and $n-30$ previous program versions, as it is impractical to inspect all of them. Starting from 357 faulty versions of subject programs, we found 28 preceding reference versions that correspond to seven different faulty versions. We have trained five F models on each of the 28 reference versions to localise the fault in the faulty version, resulting in 140 rankings based on TEE scenario. Note that we did not consider F+P models on these reference versions because they require more than 24 hours for mutation analysis, as described in Section III-B.

TABLE III
VIABILITY OF F MODELS USING TEE SCENARIO. THE RANKS THAT DO NOT HAVE SAME RANKS WITH FCE ARE TYPESET IN BOLD.

Fault		Commit (Δrev.)	Rank EM	PM*	PM$^+$	LR	MLP
Closure	21	FCE Rank	2	2	2	2	2
		32a12ba (2)	2	2	2	2	2
		43a5523 (3)	2	2	2	2	2
	61	FCE Rank	7	4	5	5	6
		f5529dd (3)	7	4	5	5	6
		b12d1d6 (4)	7	4	5	5	6
		245362a (7)	7	4	5	5	**7**
		8abd1d9 (8)	7	4	5	5	**8**
		37b0e1b (9)	7	4	5	5	6
	62	FCE Rank	1	1	1	1	1
		245362a (2)	1	1	1	1	1
		8abd1d9 (3)	1	1	1	1	1
		37b0e1b (4)	1	1	1	1	1
	115	FCE Rank	14	22	24	19	11
		b9262dc (5)	14	**19**	**22**	**18**	**13**
		911b2d6 (6)	14	22	24	19	**12**
	120	FCE Rank	7	7	7	6	6
		2aee36e (3)	**24**	**24**	**24**	**15**	**16**
Math	46	FCE Rank	188	188	188	47	85
		bbb5e1e (1)	188	188	188	**35**	**47**
		37680e2 (2)	188	188	188	**35**	**47**
		1861674 (3)	188	188	188	**35**	**27**
		f0b12de (4)	188	**1**	**1**	**3**	**1**
		8581b76 (5)	188	188	188	**35**	**41**
	89	FCE Rank	13	13	13	8	7
		43336b0 (1)	**12**	**12**	**12**	**2**	**3**
		cdd62a0 (2)	**14**	**14**	**14**	**2**	**5**
		90439e5 (3)	13	13	13	8	**11**
		36a8485 (4)	13	13	13	8	**13**
		dbe7842 (5)	13	13	13	8	7
		d84a587 (6)	13	13	13	8	**12**
		d27e072 (7)	13	13	13	8	**10**
		3590bdc (8)	13	13	13	8	**8**
		6b108c0 (9)	13	13	13	8	**13**
		9c55428 (10)	13	13	13	8	**12**

Table III shows the rank of the faulty method for each F model built on each preceding reference version. Out of 140 TEE based rankings produced by F models, 103 are identical to the corresponding FCE ranking. One notable exception is Math 46 (f0b12de) that shows a significant improvement over the FCE scenario rank. We have manually examined the kill matrix of this reference version, and found that some mutants in the future faulty method have been additionally killed due to timeout (enforced by Major itself), contributing to the high rank (these mutants were not killed in other preceding reference versions of Math 46). We suspect that this is due to the non-determinism in the process of building the kill matrix: the mutation may have brought in flakiness that has been removed for the original program. We study the impact of different kill reasons in Section V-C, and furthermore discuss this as one of the threats to internal validity in Section VI.

We answer RQ2 that performances of SIMFL using models built with preceding reference versions tend to be stable when compared to the FCE results: only 19 out of 140 cases show degraded performance since we used less recent mutation analysis results.

C. Sampling Impact (RQ3)

To investigate how the mutation sampling rates affect the performance of SIMFL, we attempt to localise the studied faults using mutants sampled with different rates. Table IV (left side) shows the uniform sampling results with rates of 0.1, 0.3, 0.5, and 0.7: all metric values are averaged across 20 different samples. Table IV also includes the results obtained without sampling (Full). The best results are typeset in bold.

As expected, the Full configuration often shows the best performance, followed by sampling rates of 0.7 and 0.5. Since we expect different mutants to contribute different amounts of information to localisation, we do not find it surprising that sampling rates down to 0.5 show comparable results with the Full configuration. However, the performance does not degrade

TABLE IV
UNIFORM AND STRATIFIED RANDOM SAMPLING

Ratio	Model	Total Studied	*acc* @1	*acc* @3	N (Ratio)	*acc* @1	*acc* @3
0.1	EM(F)	348	59.80	95.35	5 (0.27)	36.50	65.05
	PM*(F)	348	66.55	107.85		40.95	74.75
	PM$^+$(F)	348	68.40	108.50		40.05	75.00
	LR(F)	348	71.75	121.50		49.15	91.10
	MLP(F)	348	76.70	120.05		49.90	88.85
	EM(F+P)	203	46.35	56.55		39.50	57.05
	PM*(F+P)	203	45.45	66.65		65.70	100.25
	PM$^+$(F+P)	203	29.35	52.45		39.55	52.45
	LR(F+P)	203	70.70	93.30		75.95	114.40
	MLP(F+P)	203	83.60	111.30		78.15	118.20
0.3	EM(F)	348	72.25	118.55	10 (0.41)	45.60	80.95
	PM*(F)	348	78.90	132.15		49.65	93.50
	PM$^+$(F)	348	83.45	133.70		53.65	93.00
	LR(F)	348	84.85	142.15		59.95	106.60
	MLP(F)	348	82.45	139.40		56.90	102.60
	EM(F+P)	203	66.70	82.35		50.60	74.00
	PM*(F+P)	203	47.80	71.40		74.45	106.35
	PM$^+$(F+P)	203	31.75	55.45		39.20	55.05
	LR(F+P)	203	81.95	107.60		82.15	115.90
	MLP(F+P)	203	101.55	132.20		89.70	126.35
0.5	EM(F)	348	75.90	128.30	15 (0.50)	53.60	96.70
	PM*(F)	348	82.90	141.80		58.70	110.10
	PM$^+$(F)	348	86.30	143.80		62.20	109.15
	LR(F)	348	88.75	145.90		66.70	118.30
	MLP(F)	348	84.70	146.00		63.05	114.25
	EM(F+P)	203	73.90	93.10		57.35	82.65
	PM*(F+P)	203	47.55	72.70		78.75	109.90
	PM$^+$(F+P)	203	32.70	57.00		**42.15**	61.45
	LR(F+P)	203	86.35	112.15		86.95	116.95
	MLP(F+P)	203	104.90	138.65		94.80	134.60
0.7	EM(F)	348	**78.05**	133.55	20 (0.56)	55.80	105.80
	PM*(F)	348	**84.80**	147.75		64.95	121.45
	PM$^+$(F)	348	**88.15**	150.05		70.05	124.10
	LR(F)	348	89.65	148.50		74.35	127.05
	MLP(F)	348	84.30	144.60		69.70	124.70
	EM(F+P)	203	78.05	98.85		62.50	88.05
	PM*(F+P)	203	48.30	73.60		**81.55**	**110.15**
	PM$^+$(F+P)	203	32.90	**57.20**		40.55	**62.40**
	LR(F+P)	203	87.20	115.20		**90.70**	118.60
	MLP(F+P)	203	108.45	142.55		98.25	138.20
Full	EM(F)	348	77.00	**139.00**	Full	**77.00**	**139.00**
	PM*(F)	348	82.00	**151.00**		**82.00**	**151.00**
	PM$^+$(F)	348	86.00	**155.00**		**86.00**	**155.00**
	LR(F)	348	**90.00**	**152.00**		**90.00**	**152.00**
	MLP(F)	348	**85.00**	**150.00**		**85.00**	**150.00**
	EM(F+P)	203	**84.00**	**108.00**		**84.00**	**108.00**
	PM*(F+P)	203	**49.00**	**74.00**		49.00	74.00
	PM$^+$(F+P)	203	**33.00**	57.00		33.00	57.00
	LR(F+P)	203	**88.00**	**120.00**		88.00	**120.00**
	MLP(F+P)	203	**113.00**	**145.00**		**113.00**	**145.00**

at the same rate as the sampling rate, as can be seen from the results obtained using the sampling rate of 0.1.

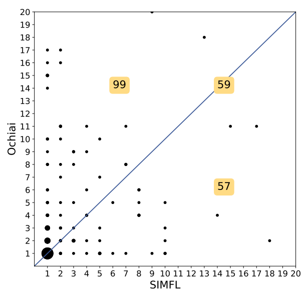
Since larger methods are likely to produce more mutants, uniform sampling will effectively sample more mutants for larger methods. We investigate whether this is disadvantageous for relatively smaller methods by evaluating stratified sampling: given the threshold parameter N, stratified sampling randomly chooses only N mutants from methods with more than N mutants, and chooses all mutants if their number is below N. Table IV (right side) contains the results obtained using stratified mutant sampling with $N \in \{5, 10, 15, 20\}$. The value in the parenthesis, i.e., "Ratio", is the average ratio of the number of mutants sampled by stratified sampling to the number of all mutants.

Compared to the Full configuration, the performance degradation as N decreases is notably worse than what has been observed from the results of uniform random sampling. However, even with $N = 5$, the sample ratio is 0.27 on average, higher than the smallest sampling rate for the uniform sampling. The comparison suggests that, contrary to our concern for a potential bias against smaller methods, stratified sampling is actually harmful to SIMFL. One interpretation of the result is that, if we assume that the location of a fault is a random variable, larger methods are by definition more likely to contain it.

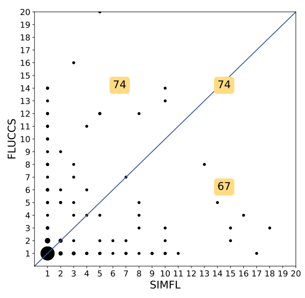
We answer RQ3 that the impact of mutation sampling is observable but not too disruptive. Using uniform sampling, on average 80% of the faults ranked at the top without sampling can still be localised at the top. However, stratified sampling actually harms SIMFL: larger methods need to be represented by more mutants.

V. DISCUSSION

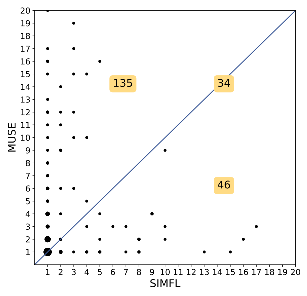
A. Relation with Other FL Techniques



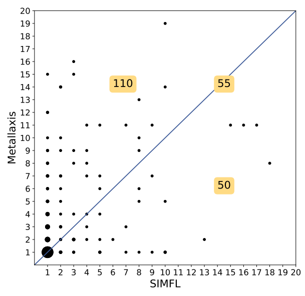
(a) Ochiai ($r = 0.215$)



(b) FLUCCS ($r = 0.105$)



(c) MUSE ($r = 0.072$)



(d) Metallaxis ($r = 0.130$)

Fig. 3. Comparison of MLP(F+P) and other FL techniques.

Two FL techniques can be complementary to each other if there is little overlap between faults ranked highly by each technique. To investigate whether the contribution of SIMFL is uniquely different from others, we investigate how individual faults are ranked differently by SIMFL and other FL techniques. SIMFL is represented by the MLP(F+P) model. We omit TraPT from this comparison as the individual rank information was not available from the paper; DStar is also excluded as its results are very similar to that of Ochiai.

Figure 3 plots each individual fault according to its rank by MLP(F+P) of SIMFL (x-axis) and its rank by the other FL technique (y-axis). Data points on the line $y = x$ represent faults that are ranked at the same place by both techniques, whereas the farther from the line a point is, the more differently it is ranked by two techniques. Plots only contain faults that are ranked within the top 20 places by at least one technique: the size of the dots corresponds to the number of faults plotted at the location of the dot. The numbers on the $y = x$ line as well as above and below the line show the total number of faults that belong to the corresponding parts, regardless of being ranked within the top 20 or not. For example, SIMFL ranks 135 faults higher than MUSE. The agreement between two techniques are measured using Pearson correlation coefficient (r): value 0 implies no correlation and, therefore, no agreement, whereas value 1 implies perfect correlation and, therefore, two identical rankings.

While there exist dense clusters of points near the top ranks around the $y = x$ line, there is no clear relationship between FL techniques. SIMFL shows low Pearson correlation coefficients against all compared techniques. Notably, SIMFL is significantly different from two existing MBFL techniques, MUSE and Metallaxis, suggesting that the way SIMFL captures the relationship between faults and tests differs significantly from existing MBFL techniques. SIMFL also ranks the most faults identically to FLUCCS, a technique that uses multiple SBFL scores as well as code and change metric, suggesting that mutation analysis can be a rich source of information for fault localisation. Overall, the results provide evidence that there exist faults that SIMFL can localise much more effectively than the other, and vice versa. The complementary nature also suggests the possibility of an effective hybridisation of SIMFL and other techniques, as recent work that combine multiple FL techniques suggest [28], [29], [3]. We leave the hybridisation as future work.

B. Test Case Granularity

TABLE V
THE RESULT OF ONE-TAILED t-TEST BETWEEN $W3$ AND $O3$.

Model	Project	$W3$ mean	$O3$ mean	p	Model	Project	$W3$ mean	$O3$ mean	p
EM(F)	Lang	5.5	10.0	**0.029**	EM(F+P)	Lang	6.2	7.9	0.238
	Chart	10.0	144.9	0.056		Chart	11.4	136.1	0.086
	Time	69.2	129.6	**0.002**		Time	103.7	113.7	0.320
	Closure	167.2	322.7	**0.000**		-	-	-	-
	Math	15.5	34.8	**0.000**		Math	20.5	28.5	0.056
PM*(F)	Lang	5.1	11.9	**0.002**	PM*(F+P)	Lang	4.7	9.8	**0.009**
	Chart	10.0	144.9	0.056		Chart	96.3	88.4	0.534
	Time	78.4	127.6	**0.009**		Time	20.0	120.3	**0.000**
	Closure	175.7	327.6	**0.000**		-	-	-	-
	Math	15.4	36.3	**0.000**		Math	15.2	28.2	**0.009**
PM$^+$(F)	Lang	5.1	12.4	**0.002**	PM$^+$(F+P)	Lang	4.4	9.2	**0.012**
	Chart	9.8	136.6	**0.072**		Chart	96.9	88.1	0.538
	Time	78.4	127.6	**0.009**		Time	0.5	117.7	**0.001**
	Closure	203.2	323.5	**0.000**		-	-	-	-
	Math	15.5	35.8	**0.000**		Math	11.5	27.1	**0.010**
LR(F)	Lang	4.9	13.5	**0.000**	LR(F+P)	Lang	5.5	12.2	**0.006**
	Chart	11.8	135.9	**0.087**		Chart	70.3	117.9	0.298
	Time	78.4	127.6	**0.009**		Time	90.8	129.6	**0.031**
	Closure	193.3	322.3	**0.000**		-	-	-	-
	Math	16.5	35.3	**0.000**		Math	17.3	31.0	**0.003**
MLP(F)	Lang	5.4	12.9	**0.003**	MLP(F+P)	Lang	5.9	13.3	**0.013**
	Chart	10.8	144.9	**0.066**		Chart	14.6	174.2	**0.032**
	Time	62.3	137.7	**0.000**		Time	95.1	130.5	**0.049**
	Closure	168.6	325.3	**0.000**		-	-	-	-
	Math	15.6	35.8	**0.000**		Math	17.0	40.9	**0.000**

A common pattern observed in all configurations of SIMFL is that it performs the best for Commons Lang. Following Laghari and Demeyer [30], we hypothesise that this may be related to the test case granularity: if each test case kills mutants that exist in only a few methods, SIMFL can benefit from this because failures of each test case will be tightly coupled with a few candidate locations.

To investigate the impact of test case granularity, we check whether the number of the methods that are relevant to failures caused by highly ranked faults is lower than the number of methods relevant to faults that are not ranked near the top. We define a method m to be relevant to the failure of a test case t if t kills a mutant in m. A finer granularity test case t is expected to be relevant to fewer methods. We categorise faults into those ranked in the top three places (set $W3$), and those that are not (set $O3$), and compare the number of relevant methods between $W3$ and $O3$.

Table V reports the result of one-tailed t-test on the number of relevant methods between $W3$ and $O3$: for 33 out of 45 cases, we accept the alternative hypothesis that the mean of $O3$ is significantly greater than $W3$. In other words, the faults in $W3$ are likely to be revealed by test cases with finer-granularity than the faults in $O3$. The test cases of Commons Lang have finer-granularity when compared to other subjects, leading us to conjecture that test case granularity is why SIMFL performs more effectively against Lang than others. However, the results also show that SIMFL is not simply reflecting a one-to-one mapping between methods (mutants) and their unit tests: failing test cases of Closure kill mutants in 203 methods on average, but PM$^+$(F) can still localise 41 out of 132 faults within the top three places (see Table II).

C. Kill Reason Filtering

TABLE VI
THE $acc@n$ METRIC VALUES AFTER FILTERING MUTANTS BASED ON THEIR KILL REASONS.

Model	Total Studied	Assertion			Timeout			Exception		
		@1	@3	@5	@1	@3	@5	@1	@3	@5
EM(F)	348	**100**	**163**	**179**	21	30	38	53	90	107
PM*(F)	348	**108**	**185**	**206**	23	35	44	60	97	117
PM$^+$(F)	348	**114**	**183**	**206**	22	36	45	61	99	119
LR(F)	348	**118**	**181**	**213**	40	79	88	66	109	131
MLP(F)	348	**121**	**189**	**210**	43	76	91	60	106	129
EM(F+P)	203	72	89	96	7	11	16	55	64	68
PM*(F+P)	203	**50**	**76**	**90**	23	42	57	49	71	80
PM$^+$(F+P)	203	**34**	57	**68**	20	34	50	**34**	**59**	**68**
LR(F+P)	203	**89**	117	128	23	41	51	77	104	115
MLP(F+P)	203	112	**147**	**160**	29	50	55	91	120	135

A mutated program can cause a test failure due to many different reasons, such as assertion (i.e., test oracle) violation, uncaught exception, or timeout. All these reasons are normally marked as a kill. While all three reasons do reveal some dependency between the mutated location and the test outcome (otherwise the mutant would not be killed), we suspect that different kill reasons may have varying degrees of importance for fault localisation. Assertion violations would imply that the test oracles actually capture the correct program behaviour. Uncaught exceptions and timeouts, however, may only show coincidental impacts of the mutation.

Considering the relative importance of different kill reasons, we investigate whether filtering out the kill matrix based on the exact reason of test failure has any impact on the localisation effectiveness. This is partly motivated by the use of failure messages by TraPT [31]. We train SIMFL models using one of three kill reasons, and compare their results to those of models trained using all three reasons. Kill reasons supported by Major are: assertion violations ("Assertion"), timeouts ("Timeout"), and uncaught exceptions ("Exception").

Table VI shows the results of $acc@n$ metrics for SIMFL models of three different kill reasons. For all F models, using only mutants killed due to the assertion failures shows the best performance in terms of $acc@1$ and $acc@3$, adding support to our assumption that assertion violations reflect test oracles of correct program behaviour better than others. Timeouts appear to be the weakest signal.

However, for F+P models, the unfiltered original results ("All") often show the best performance. This trend reveals a seemingly counter-intuitive, yet fundamental intuition about SIMFL: test cases in $\mathbf{T}_f$ and $\mathbf{T}_p$ contribute to localisation in different ways. If a test case t is in $\mathbf{T}_f$, all mutants killed by t earlier suggest that their locations may contain the fault. However, if $t \in \mathbf{T}_p$, all mutants killed by t earlier suggests that their locations may *not* contain the fault that is detected by $t' \in \mathbf{T}_f$. Consequently, kill reason filtering can make the contributions from tests in $\mathbf{T}_f$ more precise (i.e., to only reflect real fault detection), but may also reduce the total amount of contributions from tests in $\mathbf{T}_p$ because it removes potential locations that could have been *excluded* by being associated with a test in $\mathbf{T}_p$. This explains why, for F+P models, using only Assertion as the kill reason cannot dominate the results. Note that the distribution of kills between Assertion, Timeout, and Exception is likely not uniform, which we also think contributes to the mixed results of F+P models, combined with program semantics.

VI. Threats to Validity

Given the controlled setting for our experiments and the clearly defined objective measures, there are few threats to the internal validity of our study. There are some threats to internal validity that are inherent to any mutation analysis and hard to completely avoid, such as non-determinism caused by mutation and equivalent mutants, which have been discussed in Section IV. Similarly, we see few threats to the construct and conclusion validity. The metrics we used are standard in the fault localisation literature. We note that establishing one best technique is not our main goal here and we would likely need more study subjects for such a comparison to be meaningful.

Rather, the main threat of our study is to its external validity. Even though we studied five different subjects from the real-world Defects4J benchmark to mitigate this threat, this does not allow us to generalise to many, other programs and test suite contexts. Still, there was enough variation among the five subjects for us to identify SIMFL's dependence on the granularity of the test cases.

VII. Related Work

A number of Mutation Based Fault Localisation techniques have been proposed in the literature. Metallaxis uses SBFL-like formulas to measure the similarity between failure patterns of the actual fault and mutants [16], [15]. MUSE [13], and its variation MUSEUM [14], depend on two principles: first, if we mutate already faulty parts of the program, it is unlikely that we will observe more failing test cases, and we may even observe partial fixes, and second, if we mutate non-faulty parts, tests that used to fail are now likely to fail. MUSE and MUSEUM define their suspiciousness scores using the ratios of fail-become-pass and pass-become-fail tests. TraPT is similar to MUSE and MUSEUM in nature, but transforms both the output messages of failing tests, to distinguish different types of exceptions, and the test code itself, to prevent early program termination due to the assertion violation that precludes collecting information of other assertions [31]. All existing MBFL techniques mutate the faulty program once testing is finished. In contrast, SIMFL allows the mutation analysis to be performed ahead of time.

SIMFL was initially formulated based on Bayesian analysis to infer likely fault locations given test information. In the context of fault localisation, Abreau et al. [32] have introduced Barinel, an SBFL technique that adopts Bayesian reasoning to generate candidate sets of multiple fault locations. To the best of our knowledge, SIMFL is the first MBFL technique that uses Bayesian inference as well as other statistical inference techniques. While SIMFL also uses dynamic information from mutation, the mutation analysis can be performed ahead-of-time, which allows the cost to be amortised over multiple development iterations, and provides faster feedback.

VIII. Conclusion

This paper introduces SIMFL, a Mutation Based Fault Localisation (MBFL) technique that allows users to perform the mutation analysis in advance, before the actual failure is observed. SIMFL relies on statistical inference techniques to train predictive models that can be used with the actual failure information. This allows us to use the concrete and precise dependencies between source code and test cases for fault localisation, without having to expend the large cost of mutation analysis when failures are observed. We have empirically evaluated SIMFL using real-world faults from Defects4J benchmark. SIMFL can localise 113 faults at the top, and is capable of retaining 80% of its localisation accuracy at the top when we sample only 10% of all generated mutants.

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