

# Replication Utilities

This repository contains the resources and steps required to replicate our study.

The replication package consists of two major stages:

1. **Stage 1** – Evaluation and refinement of the multi-language design smell detector.
  2. **Stage 2** – Re-analysis of smell prevalence and their relation to software fault- and change-proneness.
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## 1. Detection of Multi-Language Design Smell Occurrences

**Location:** Stage 1/

**Includes:**

- **Dataset/** – Scripts and metadata to fetch and prepare the 60 open-source multi-language projects.
- **Ground Truth/** – Manual annotations for each smell, labeling guidelines, and validation data.
- **Detection Approach Revised/** – Refined implementation of the detector.
- **Results/** – Detection results and precision/recall comparison.

### Getting Started

#### Running the Detector

1. Navigate to:

```
cd Stage\ 1\Detection\ Approach\ Revised\mlssdd\
```

2. Open `DetectCodeSmellsAndAntiPatterns.java`.
3. Comment out all smell detectors except the one to be executed.
4. Compile and run:

```
javac mlssdd/DetectCodeSmellsAndAntiPatterns.java  
java mlssdd.DetectCodeSmellsAndAntiPatterns
```

5. The output CSV files are generated under:

```
Stage 1/Results/results_of_revised_technique_on_new_data/[SmellName]/
```

#### Example:

To detect *Unused Parameter*, uncomment:

```
new UnusedParameterDetector().runDetection();
```

and rerun the above commands.

**Comparison:**

Baseline and refined detector accuracy are summarized in `precision_recall_baseline.csv` and `precision_recall_refined.csv`.

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## 2. Prevalence Analysis

**Location:** Stage 2/Prevalence Results/

**Includes:**

- `general_smelly/` – Files affected by  $\geq 1$  smell (per release).
- `smelly/` – 15 subfolders, one per smell type.
- Aggregated results:
  - `percentage_of_general_smelly_files_releasewise.csv`
  - `percentage_of_smelly_files_affected_by_each_smell.csv`
  - `difference_of_prevalence_by_both_techniques.csv`

### Getting Started

Each CSV file reports prevalence metrics per release and per smell.

These can be analyzed directly using R or Python (e.g., `pandas`, `matplotlib`).

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## 3. Change-Proneness Analysis

**Location:** Stage 2/Change-Proneness Results/

**Includes:**

- `changedJNI/` – Lists of changed JNI files per release.
- `general_smelly/` and `JNIfiles/` – Supporting data.
- `scripts/` – Scripts for extracting changes and running Fisher's exact tests.
- `fisher_results_change.csv` – Final computed test results.

### Getting Started

1. Ensure Python  $\geq 3.8$  is installed.
2. Run the provided scripts sequentially:

```
python scripts/extract_changed_files.py
python scripts/fisher_change_analysis.py
```

3. The resulting CSV provides odds ratios, p-values, and confidence intervals.
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## 4. Fault-Proneness Analysis

**Location:** Stage 2/Fault-Proneness Results/

**Includes:**

- `faultyJNI/` – Lists of faulty JNI files (per release).
- `scripts/` – Scripts for fault extraction and Fisher tests.
- `fisher_results_fault.csv` – Final computed test results.

### Getting Started

```
python scripts/extract_faulty_files.py  
python scripts/fisher_fault_analysis.py
```

Outputs mirror the structure of the change-proneness results.

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## 5. Dependencies

- **Java 8 +**
- **Python 3.8 +** with pandas, numpy, scipy
- **srcML** (for code parsing)
- **Apache Commons Compress** (for archive handling)

Download srcML: <https://www.srcml.org>