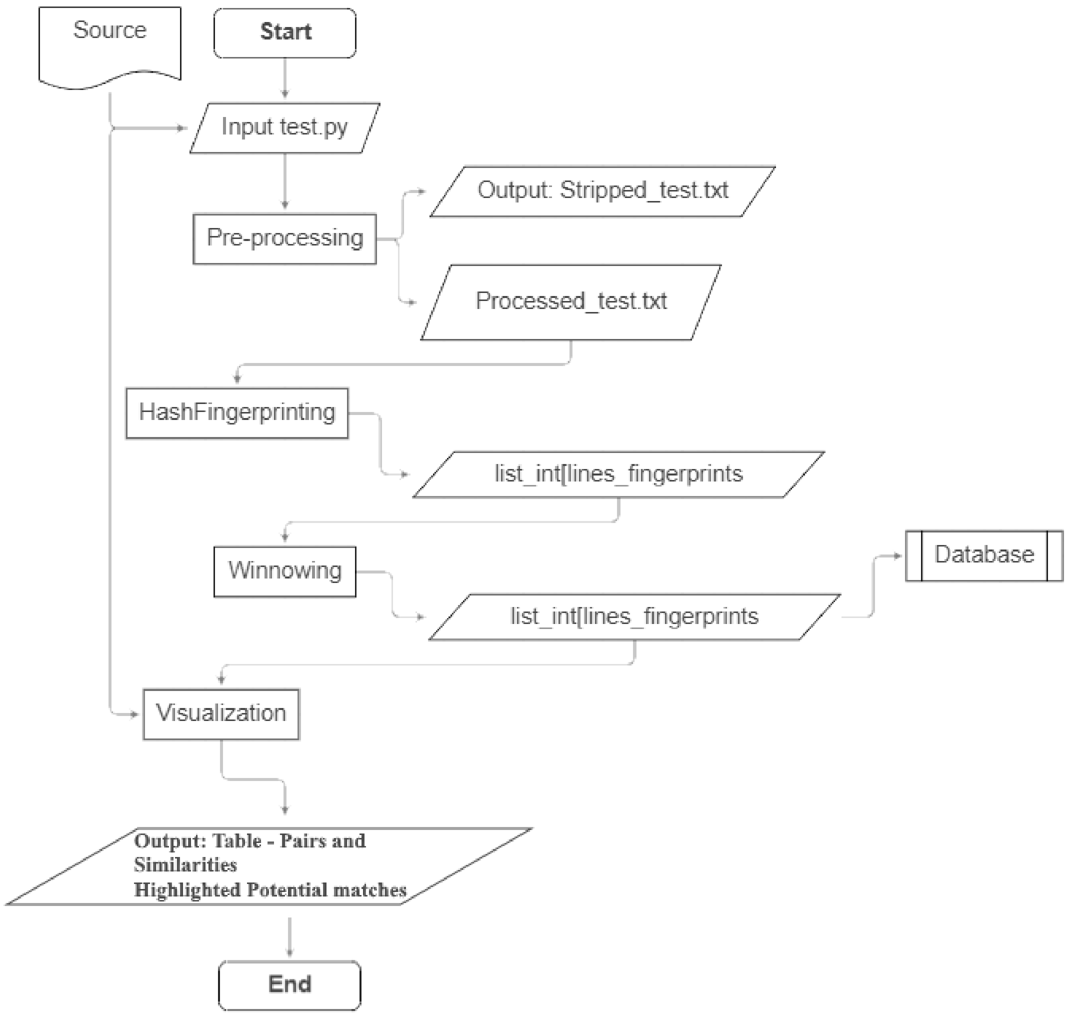
Preprocessing - Chase Jamieson
Hashing/Fingerprinting & Visual - Tracy Hotchkiss & Vinh Duong
Winnowing - Trevor Holland

Pipeline of Plagiarism Detector

Pipeline Interface



Source

Start

Input test.py

Pre-processing

Output: Stripped_test.txt

Processed_test.txt

HashFingerprinting

list_int[lines_fingerprints

Winnowing

list_int[lines_fingerprints

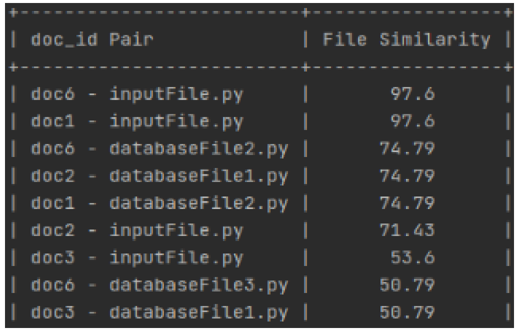
Database

Visualization

Output: Table - Pairs and Similarities
Highlighted Potential matches

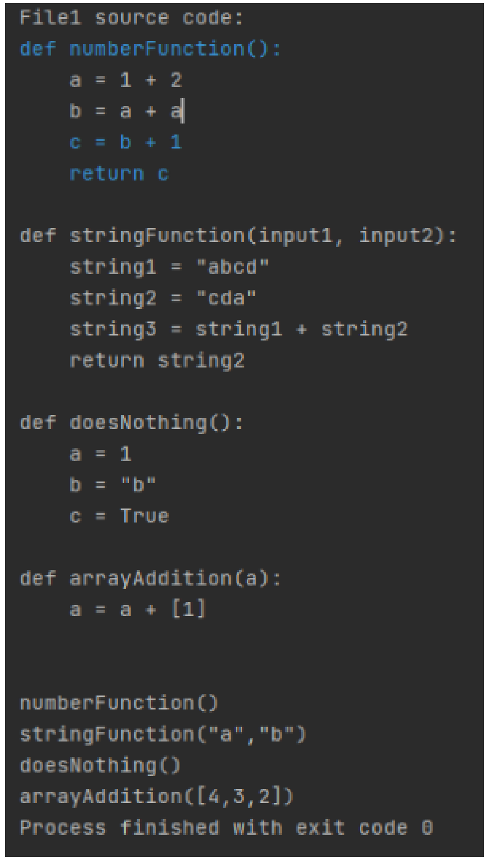
End

Sample of Table: Pairs and Similarities



```
+-------------------------+-------------------+
| doc_id Pair             | File Similarity |
+-------------------------+-------------------+
| doc6 - inputFile.py     |       97.6        |
| doc1 - inputFile.py     |       97.6        |
| doc6 - databaseFile2.py |      74.79        |
| doc2 - databaseFile1.py |      74.79        |
| doc1 - databaseFile2.py |      74.79        |
| doc2 - inputFile.py     |      71.43        |
| doc3 - inputFile.py     |       53.6        |
| doc6 - databaseFile3.py |      50.79        |
| doc3 - databaseFile1.py |      50.79        |
```

Sample of Highlighted Potential Match's

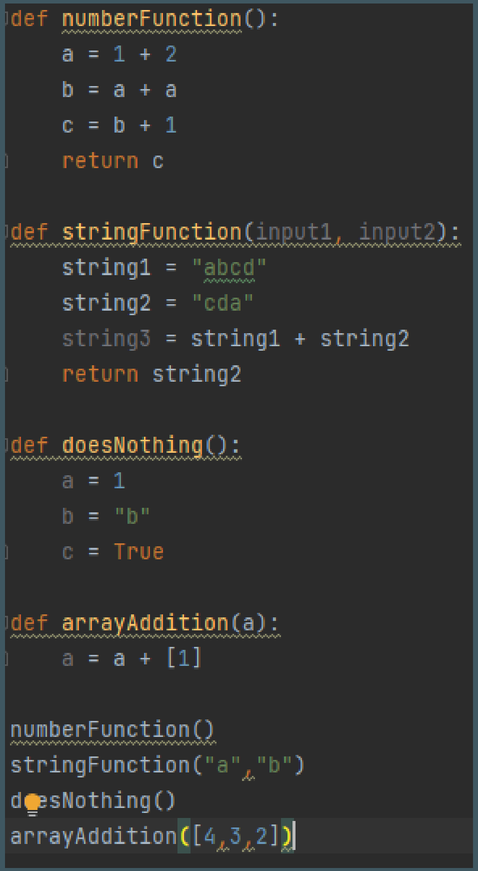


```
File1 source code:
def numberFunction():
    a = 1 + 2
    b = a + a
    c = b + 1
    return c

def stringFunction(input1, input2):
    string1 = "abcd"
    string2 = "cda"
    string3 = string1 + string2
    return string2

def doesNothing():
    a = 1
    b = "b"
    c = True

def arrayAddition(a):
    a = a + [1]


numberFunction()
stringFunction("a","b")
doesNothing()
arrayAddition([4,3,2])
Process finished with exit code 0
```

Contracts

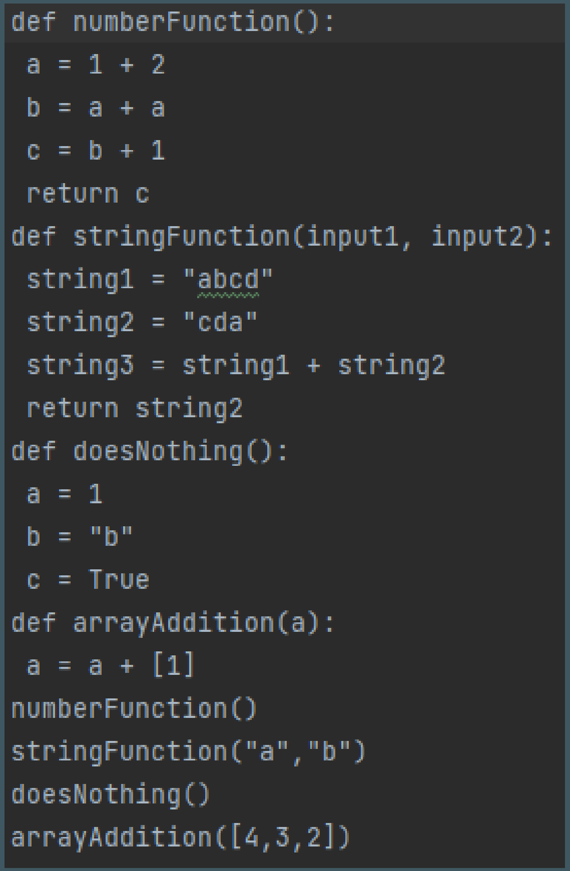
Preprocessing	
Input: source file	Example1 (‘databaseFile1.py’)
Output: stripped source file	Example2 (databaseFile1.py_Stripped)
Output: processed source file	Example3 (Str[processed])

Example1



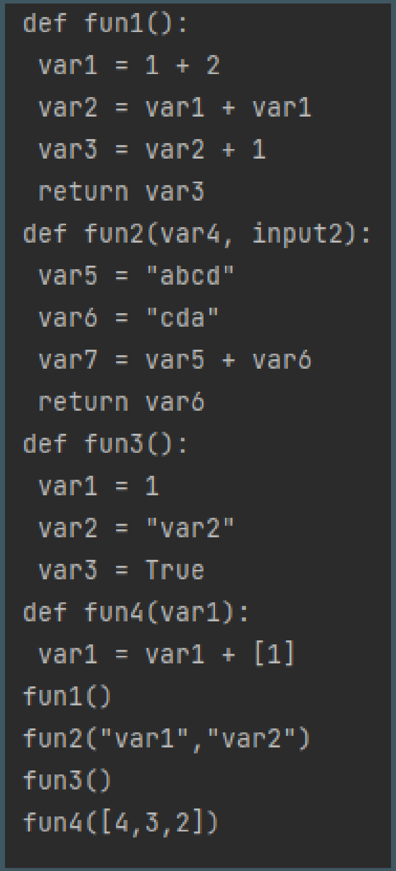
```
def numberFunction():
    a = 1 + 2
    b = a + a
    c = b + 1
    return c

def stringFunction(input1, input2):
    string1 = "abcd"
    string2 = "cda"
    string3 = string1 + string2
    return string2

def doesNothing():
    a = 1
    b = "b"
    c = True

def arrayAddition(a):
    a = a + [1]

numberFunction()
stringFunction("a","b")
doesNothing()
arrayAddition([4,3,2])
```

Example2



```
def numberFunction():
 a = 1 + 2
 b = a + a
 c = b + 1
 return c
def stringFunction(input1, input2):
 string1 = "abcd"
 string2 = "cda"
 string3 = string1 + string2
 return string2
def doesNothing():
 a = 1
 b = "b"
 c = True
def arrayAddition(a):
 a = a + [1]
numberFunction()
stringFunction("a","b")
doesNothing()
arrayAddition([4,3,2])
```

Example3

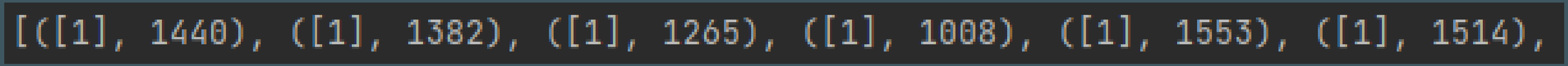


```
def fun1():
 var1 = 1 + 2
 var2 = var1 + var1
 var3 = var2 + 1
 return var3
def fun2(var4, input2):
 var5 = "abcd"
 var6 = "cda"
 var7 = var5 + var6
 return var6
def fun3():
 var1 = 1
 var2 = "var2"
 var3 = True
def fun4(var1):
 var1 = var1 + [1]
fun1()
fun2("var1","var2")
fun3()
fun4([4,3,2])
```

Contracts

HashFingerprinting	
Input: processed source file	Example3 ('str[processed]')
Output: fingerprints source file	Example4 (list_int[lines_fingerprints])

Example4

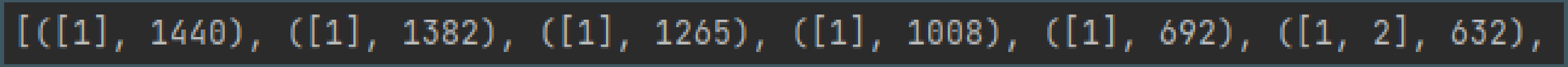


```
[([1], 1440), ([1], 1382), ([1], 1265), ([1], 1008), ([1], 1553), ([1], 1514),
```

Contracts

Winnowing	
Input: fingerprints source file	Example4 (list_int[lines_fingerprints])
Output: list lines and fingerprints	Example5 (list_int[lines_fingerprints])

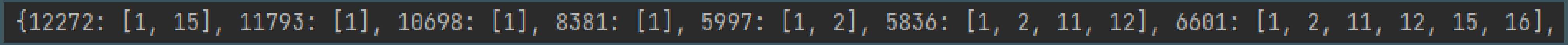
Example5



```
[([1], 1440), ([1], 1382), ([1], 1265), ([1], 1008), ([1], 692), ([1, 2], 632),
```

Build Inverted Index For Each File in Repo

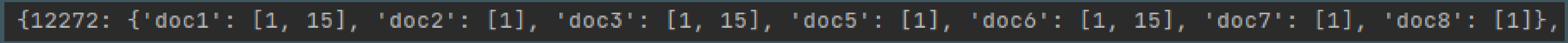
Sample of inverted index



```
{12272: [1, 15], 11793: [1], 10698: [1], 8381: [1], 5997: [1, 2], 5836: [1, 2, 11, 12], 6601: [1, 2, 11, 12, 15, 16],
```

Build Into a Corpus

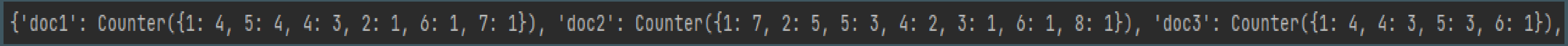
Sample of Corpus



```
{12272: {'doc1': [1, 15], 'doc2': [1], 'doc3': [1, 15], 'doc5': [1], 'doc6': [1, 15], 'doc7': [1], 'doc8': [1]},
```

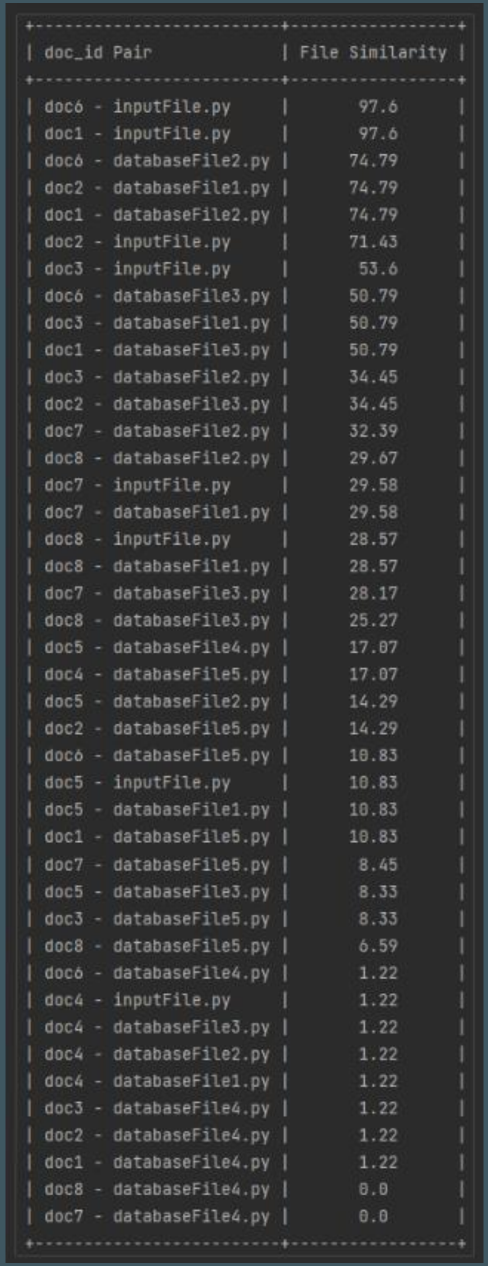
Query a File

Sample of Masterlist



```
{'doc1': Counter({1: 4, 5: 4, 4: 3, 2: 1, 6: 1, 7: 1}), 'doc2': Counter({1: 7, 2: 5, 5: 3, 4: 2, 3: 1, 6: 1, 8: 1}), 'doc3': Counter({1: 4, 4: 3, 5: 3, 6: 1}),
```

Output: doc_id Pair | File Similarity



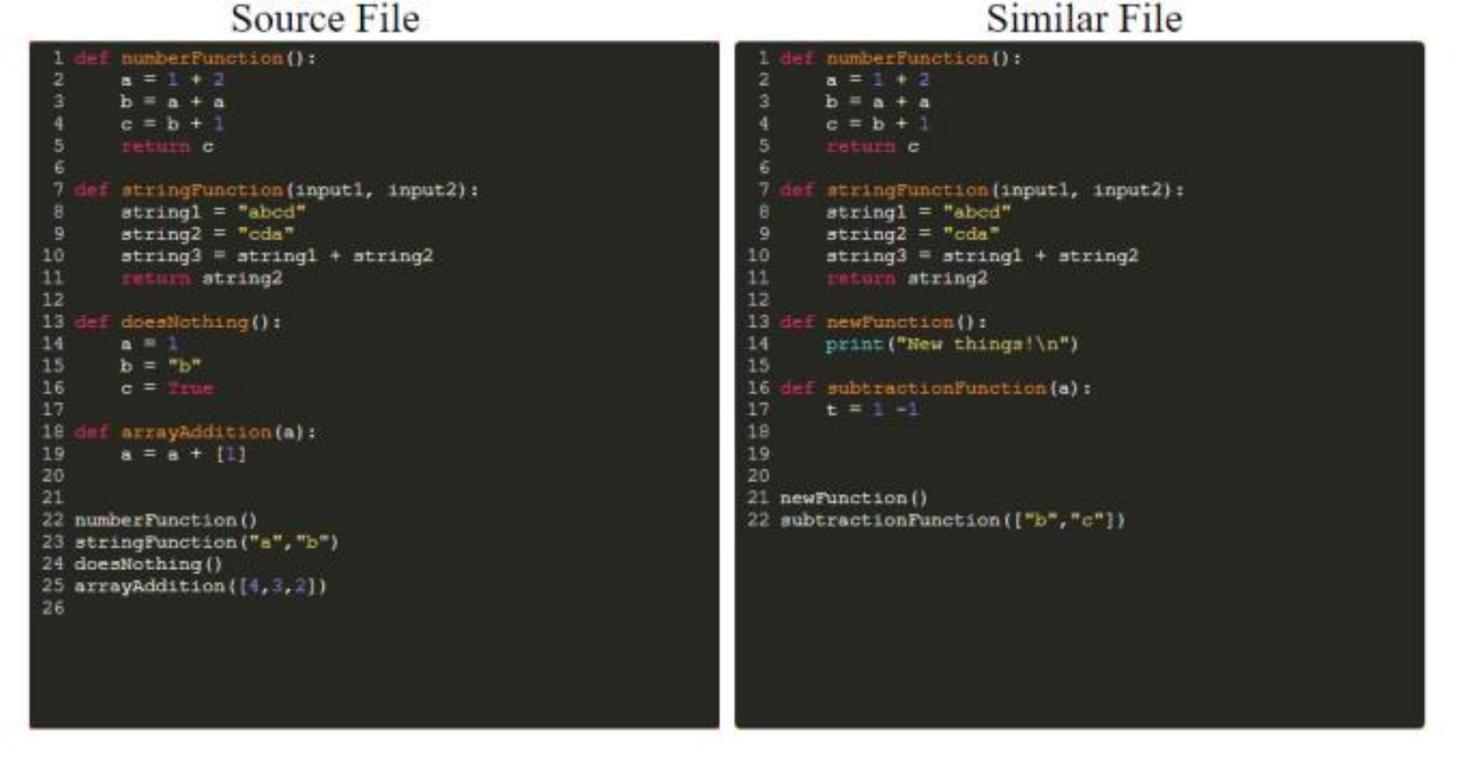
```
+-------------------------+-----------------+
| doc_id Pair             | File Similarity |
+-------------------------+-----------------+
| doc6 - inputFile.py     |       97.6      |
| doc1 - inputFile.py     |       97.6      |
| doc6 - databaseFile2.py |      74.79      |
| doc2 - databaseFile1.py |      74.79      |
| doc1 - databaseFile2.py |      74.79      |
| doc2 - inputFile.py     |      71.43      |
| doc3 - inputFile.py     |       53.6      |
| doc6 - databaseFile3.py |      50.79      |
| doc3 - databaseFile1.py |      50.79      |
| doc1 - databaseFile3.py |      50.79      |
| doc3 - databaseFile2.py |      34.45      |
| doc2 - databaseFile3.py |      34.45      |
| doc7 - databaseFile2.py |      32.39      |
| doc8 - databaseFile2.py |      29.67      |
| doc7 - inputFile.py     |      29.58      |
| doc7 - databaseFile1.py |      29.58      |
| doc8 - inputFile.py     |      28.57      |
| doc8 - databaseFile1.py |      28.57      |
| doc7 - databaseFile3.py |      28.17      |
| doc8 - databaseFile3.py |      25.27      |
| doc5 - databaseFile4.py |      17.07      |
| doc4 - databaseFile5.py |      17.07      |
| doc5 - databaseFile2.py |      14.29      |
| doc2 - databaseFile5.py |      14.29      |
| doc6 - databaseFile5.py |      10.83      |
| doc5 - inputFile.py     |      10.83      |
| doc5 - databaseFile1.py |      10.83      |
| doc1 - databaseFile5.py |      10.83      |
| doc7 - databaseFile5.py |       8.45      |
| doc5 - databaseFile3.py |       8.33      |
| doc3 - databaseFile5.py |       8.33      |
| doc8 - databaseFile5.py |       6.59      |
| doc6 - databaseFile4.py |       1.22      |
| doc4 - inputFile.py     |       1.22      |
| doc4 - databaseFile3.py |       1.22      |
| doc4 - databaseFile2.py |       1.22      |
| doc4 - databaseFile1.py |       1.22      |
| doc3 - databaseFile4.py |       1.22      |
| doc2 - databaseFile4.py |       1.22      |
| doc1 - databaseFile4.py |       1.22      |
| doc8 - databaseFile4.py |      0.0        |
| doc7 - databaseFile4.py |      0.0        |
+-------------------------+-----------------+
```

Interface Plans Research:

- Codemirror
- Pywebio
- Dynamic HTML

Interface Plans Research:

- Codemirror



Source File

```
def numberFunction():
    a = 1 + 2
    b = a + a
    c = b + 1
    return c

def stringFunction(input1, input2):
    string1 = "abcd"
    string2 = "cda"
    string3 = string1 + string2
    return string2

def doesNothing():
    a = 1
    b = "b"
    c = True

def arrayAddition(a):
    a = a + [1]


numberFunction()
stringFunction("a","b")
doesNothing()
arrayAddition([4,3,2])

```

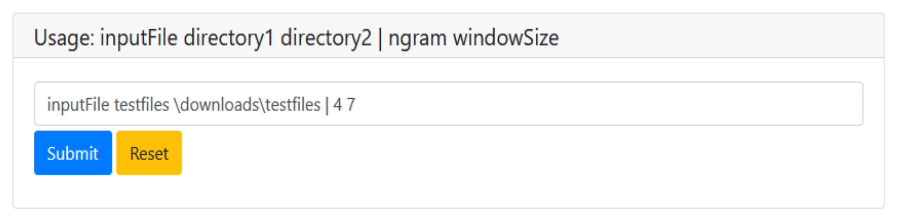
Similar File

```
def numberFunction():
    a = 1 + 2
    b = a + a
    c = b + 1
    return c

def stringFunction(input1, input2):
    string1 = "abcd"
    string2 = "cda"
    string3 = string1 + string2
    return string2

def newFunction():
    print("New things!\n")

def subtractionFunction(a):
    t = 1 -1



newFunction()
subtractionFunction(["b","c"])
```

Pywebio:

- Uses imperative API to call functions, text, images, tables, and other content to a browser window.
- Provides support for click events, layout, and CSS style
- Input
- Output

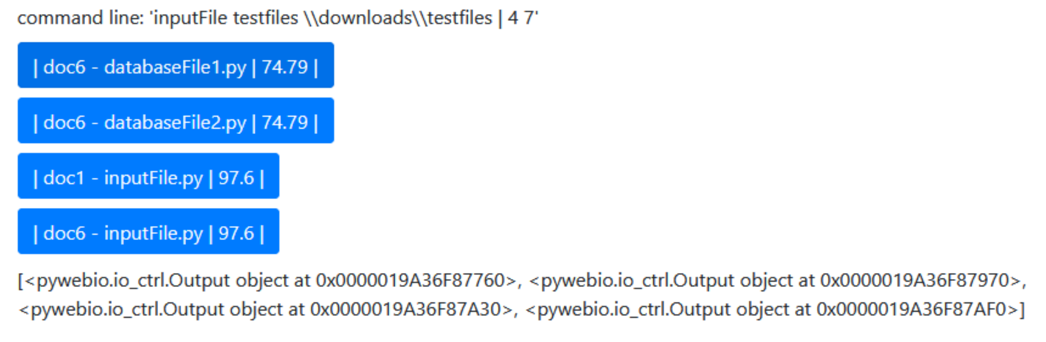
Input example 1



Usage: inputFile directory1 directory2 | ngram windowSize

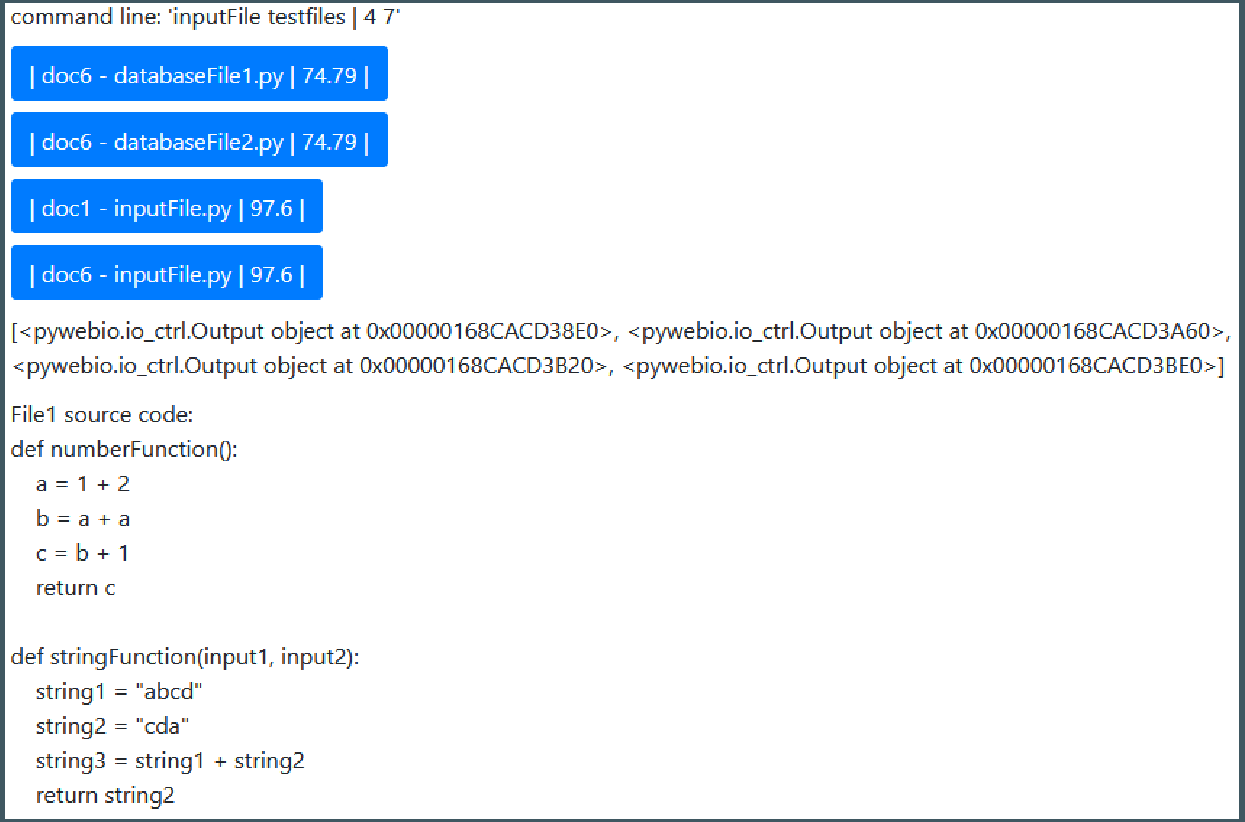
inputFile testfiles \downloads\testfiles | 4 7

Input example 2



```
command line: 'inputFile testfiles \\downloads\\testfiles | 4 7'
| doc6 - databaseFile1.py | 74.79 |
| doc6 - databaseFile2.py | 74.79 |
| doc1 - inputFile.py | 97.6 |
| doc6 - inputFile.py | 97.6 |
[<pywebio.io_ctrl.Output object at 0x0000019A36F87760>, <pywebio.io_ctrl.Output object at 0x0000019A36F87970>,
<pywebio.io_ctrl.Output object at 0x0000019A36F87A30>, <pywebio.io_ctrl.Output object at 0x0000019A36F87AF0>]
```

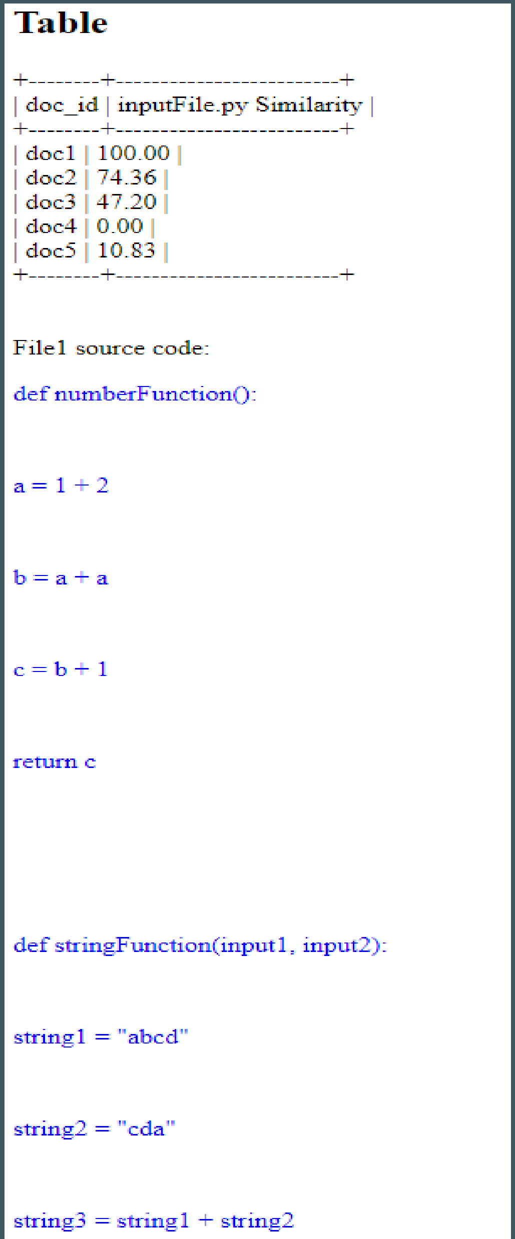
Output example



```
command line: 'inputFile testfiles | 4 7'
| doc6 - databaseFile1.py | 74.79 |
| doc6 - databaseFile2.py | 74.79 |
| doc1 - inputFile.py | 97.6 |
| doc6 - inputFile.py | 97.6 |
[<pywebio.io_ctrl.Output object at 0x00000168CACD38E0>, <pywebio.io_ctrl.Output object at 0x00000168CACD3A60>,
<pywebio.io_ctrl.Output object at 0x00000168CACD3B20>, <pywebio.io_ctrl.Output object at 0x00000168CACD3BE0>]
File1 source code:
def numberFunction():
    a = 1 + 2
    b = a + a
    c = b + 1
    return c

def stringFunction(input1, input2):
    string1 = "abcd"
    string2 = "cda"
    string3 = string1 + string2
    return string2
```

Reference guide: https://pywebio.readthedocs.io/en/latest/guide.html
Additional info: https://gittysatyam.medium.com/python-pywebio-input-method-10756d664ecf

Interface Plans Research:
- Dynamic HTML



Table

```
+--------+-------------------------+
| doc_id | inputFile.py Similarity |
+--------+-------------------------+
| doc1 | 100.00 |
| doc2 | 74.36 |
| doc3 | 47.20 |
| doc4 | 0.00 |
| doc5 | 10.83 |
+--------+-------------------------+
```

File1 source code:

```
def numberFunction():

a = 1 + 2

b = a + a

c = b + 1

return c



def stringFunction(input1, input2):

string1 = "abcd"

string2 = "cda"

string3 = string1 + string2
```

Testing Plans:

- Changing Winnowing Window Size, N-Gram, Highlight Counter Parameters

- Block Detection (cosine similarity for line blocks)

- More thorough check of all hashes after winnowing