A Theoretic Framework For Evaluating Similarity Digesting Tools

By

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Presented At

The Digital Forensic Research Conference

DFRWS 2015 EU Dublin, Ireland (Mar 23rd- 26th)

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A Theoretic Framework for Evaluating Similarity Digesting Tools

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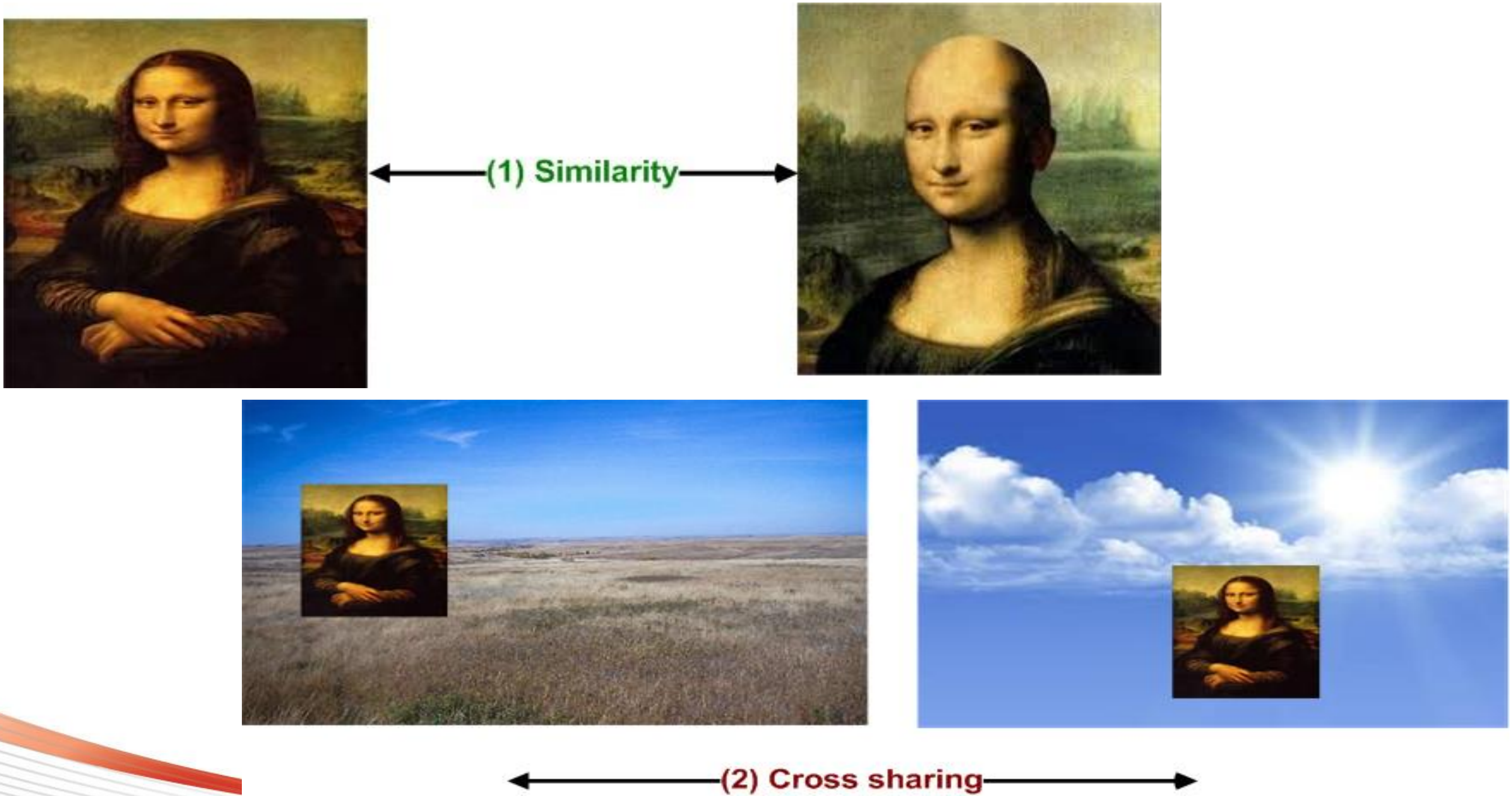
DFRWS EU 2015, Dublin, Ireland, March, 2015

Agenda

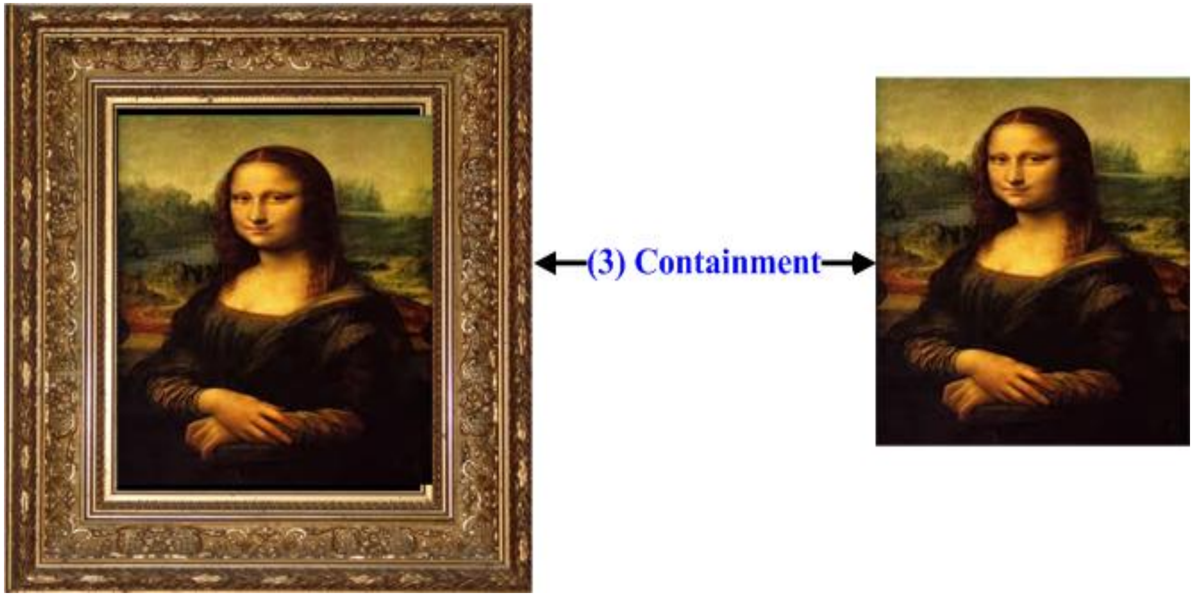
- Byte-wise Approximate Matching
- Similarity Digesting Tools
- Mathematical Models for Byte-wise Similarity
- Tool Evaluation with Theoretic Analysis
- Tool Evaluation with Data Experiment
- Further Research for Approximate Matching

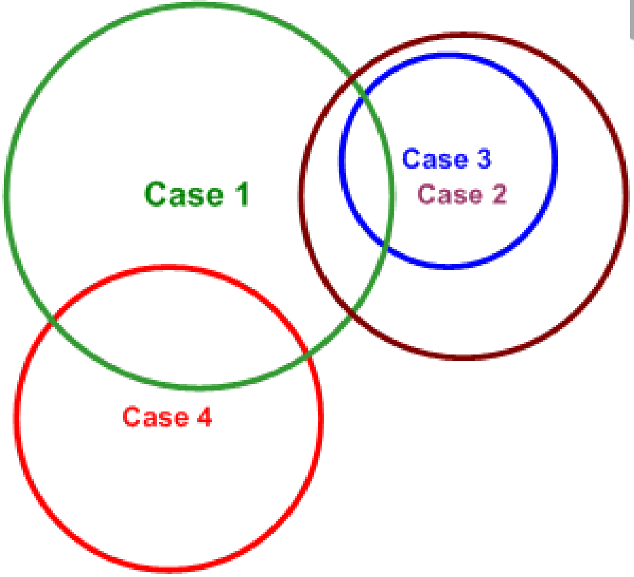
Byte-wise Approximate Matching

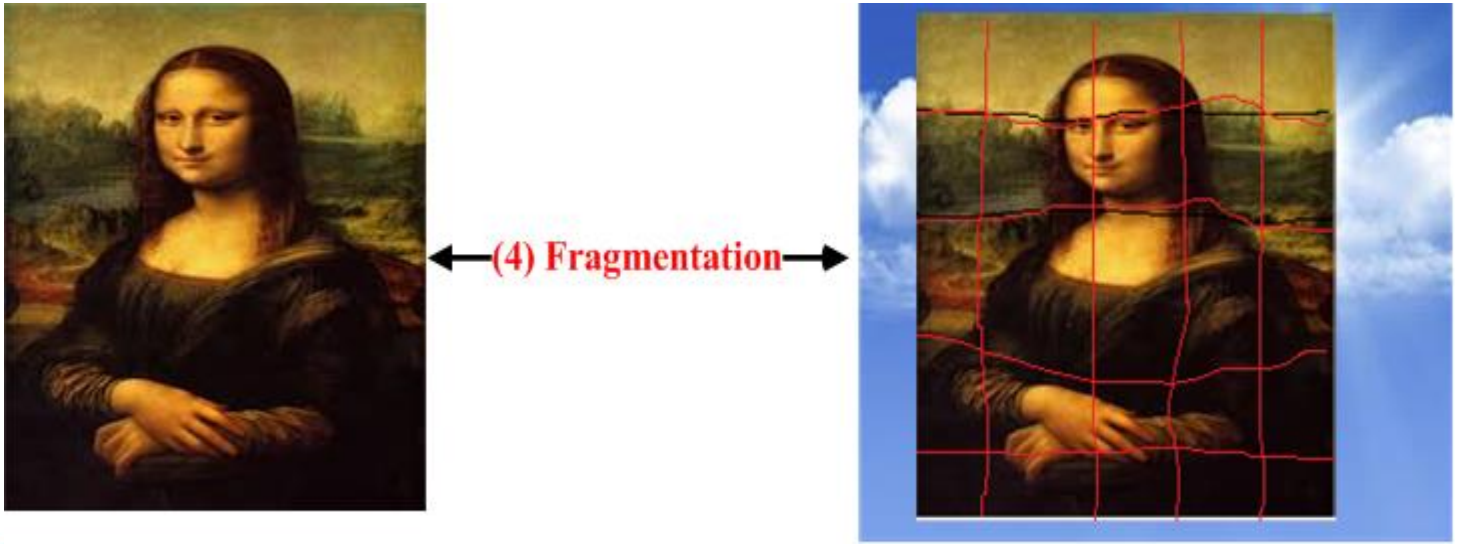
- Byte-wise similarity & approximate matching.
  - What is byte-wise similarity ?
- 4 Use Cases specified by *NIST*:



Byte-wise Approximate Matching

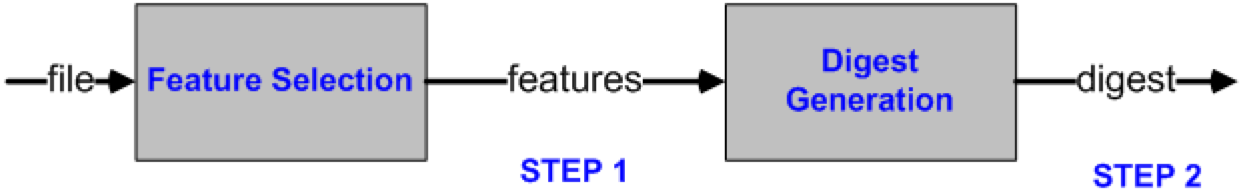






Similarity Digesting Tools

- **Similarity digesting :**
  - A class of hash techniques or tools that preserve similarity.
  - Typical steps for digest generation:

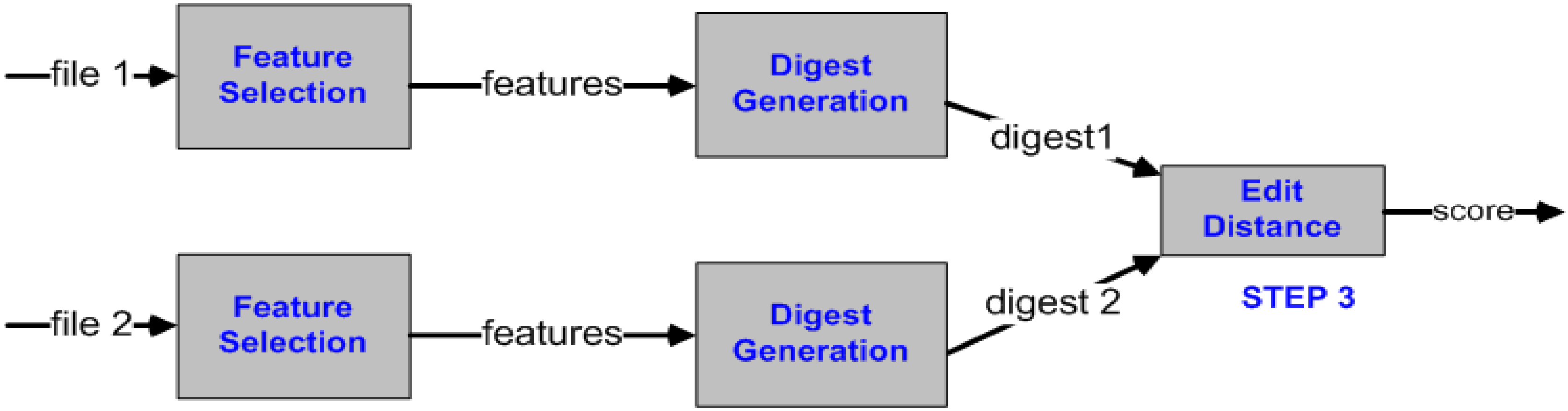


file → Feature Selection → features → Digest Generation → digest

STEP 1

STEP 2

  - Detecting similarity with similarity digesting:



file 1 → Feature Selection → features → Digest Generation → digest1

file 2 → Feature Selection → features → Digest Generation → digest 2

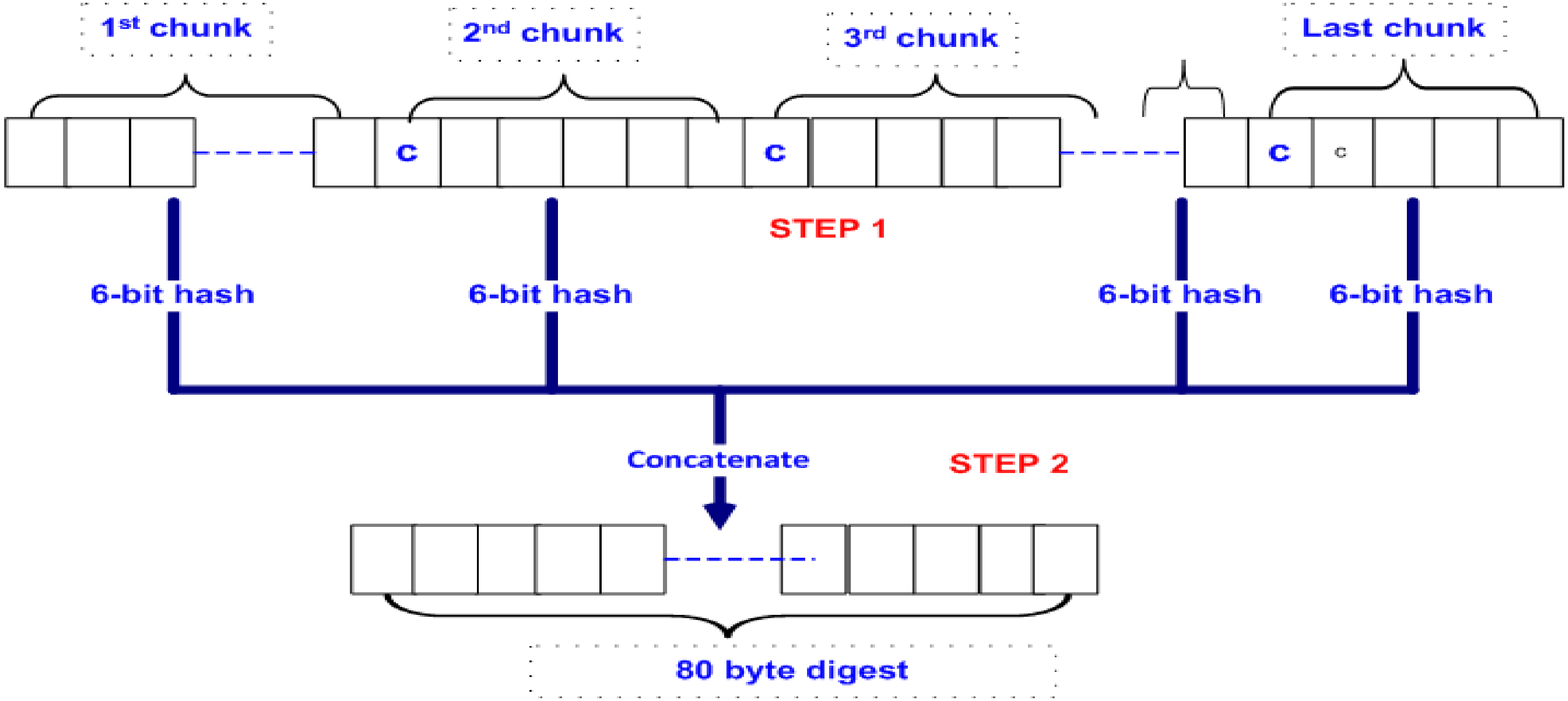
digest1, digest 2 → Edit Distance → score

STEP 3

- **Three similarity digesting algorithms and tools:**
  - ssdeep, sdhash & TLSH

Similarity Digesting Tools

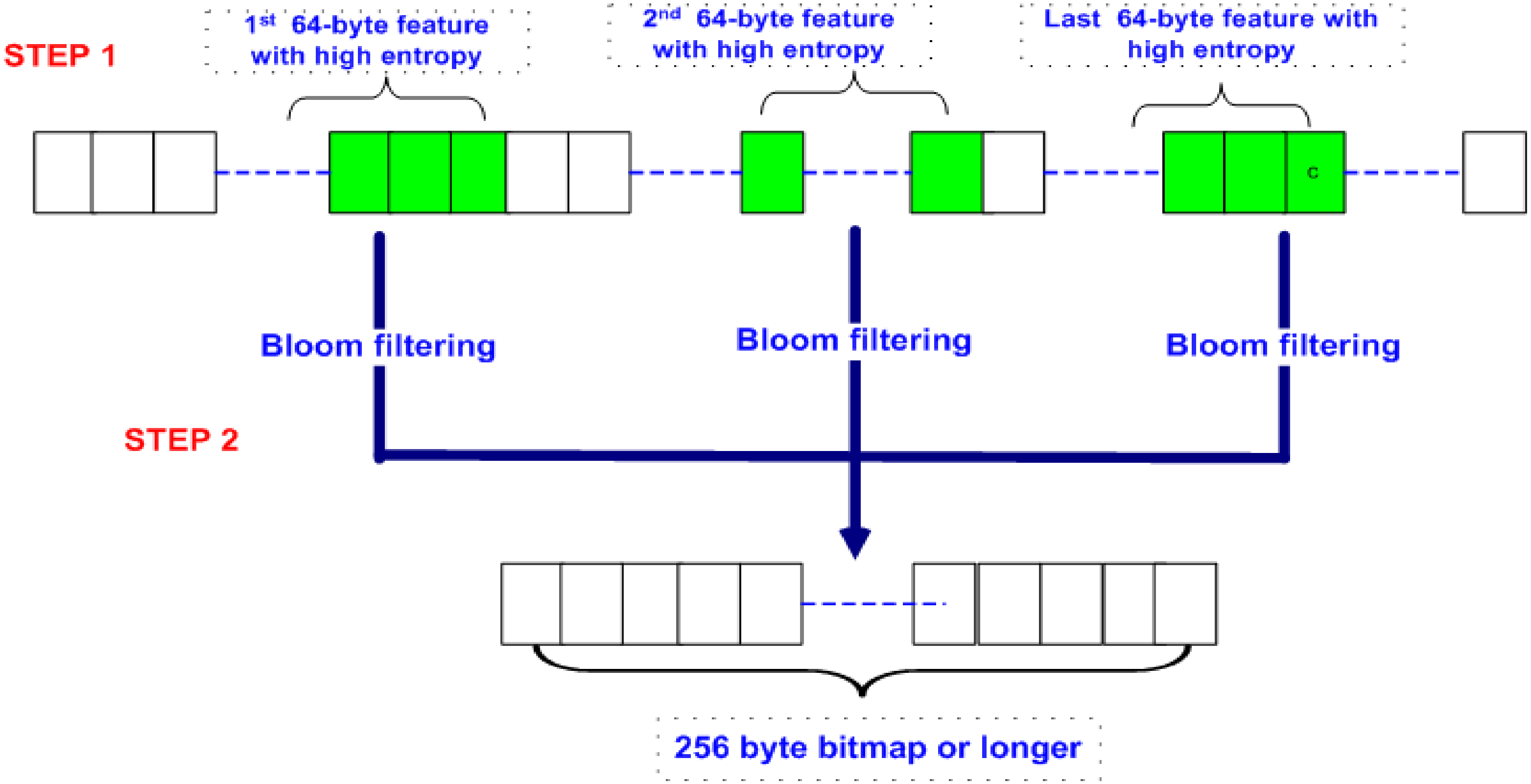
- ssdeep
  - Two steps for digesting:



  - Edit Distance: Levenshtein distance

Similarity Digesting Tools

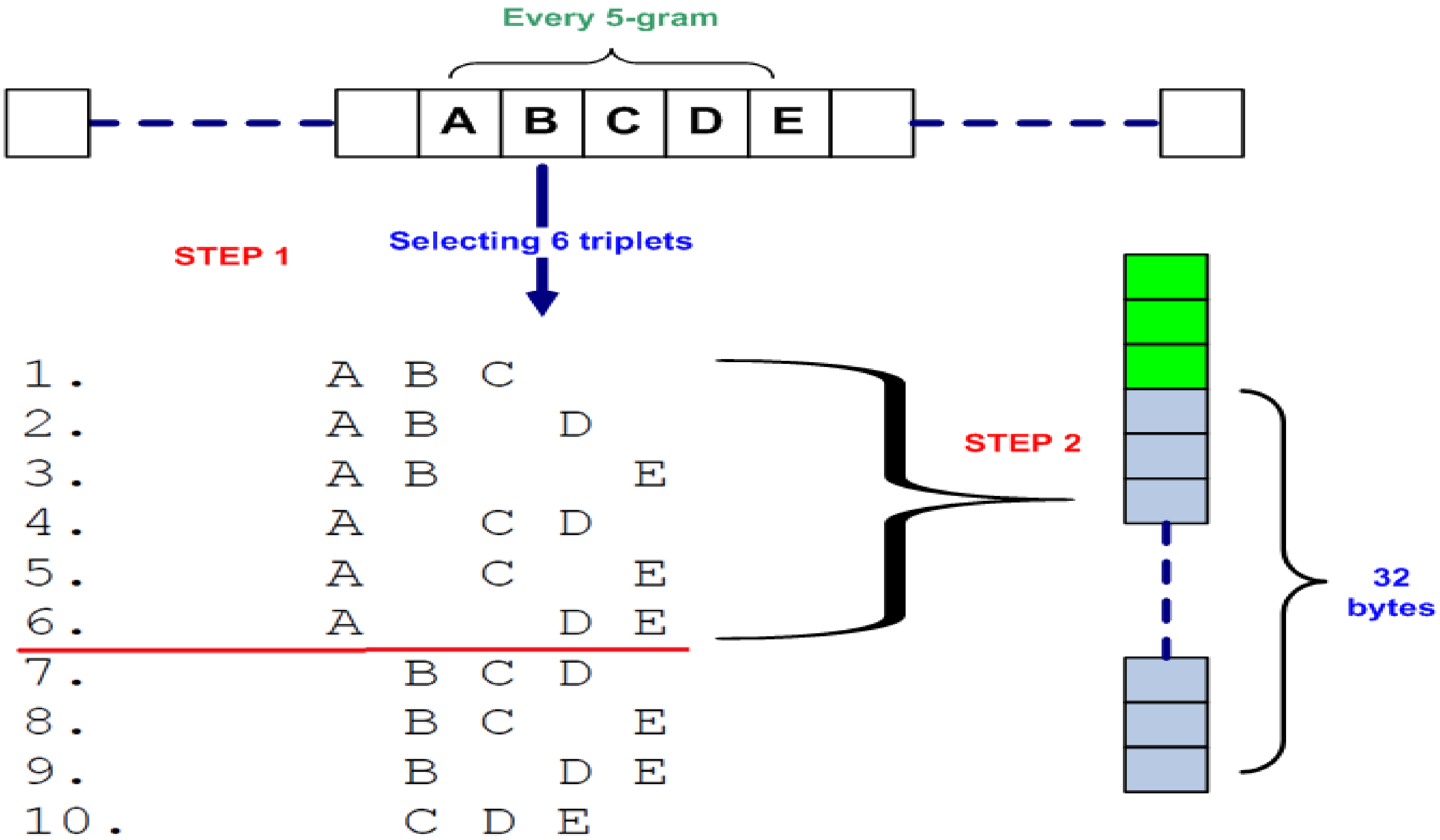
- sdhash
  - Two steps for digesting:


STEP 1
1st 64-byte feature with high entropy
2nd 64-byte feature with high entropy
Last 64-byte feature with high entropy
c
Bloom filtering
Bloom filtering
Bloom filtering
STEP 2
256 byte bitmap or longer

  - Edit Distance: Hamming distance

Similarity Digesting Tools

- TLSH
  - Two steps for digesting :



Every 5-gram

A B C D E

Selecting 6 triplets

STEP 1

1. A B C
2. A B D
3. A B E
4. A C D
5. A C E
6. A D E
7. B C D
8. B C E
9. B D E
10. C D E

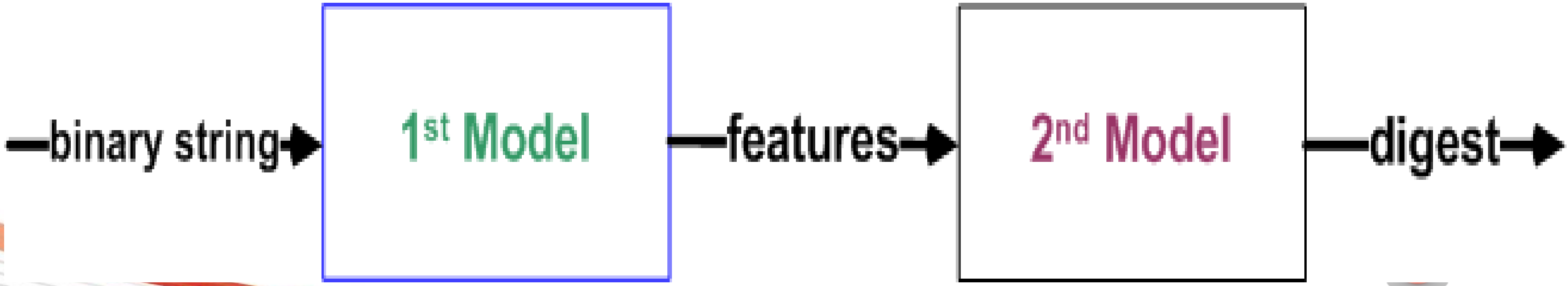
STEP 2

32 bytes

  - Edit Distance: A diff based evaluation function

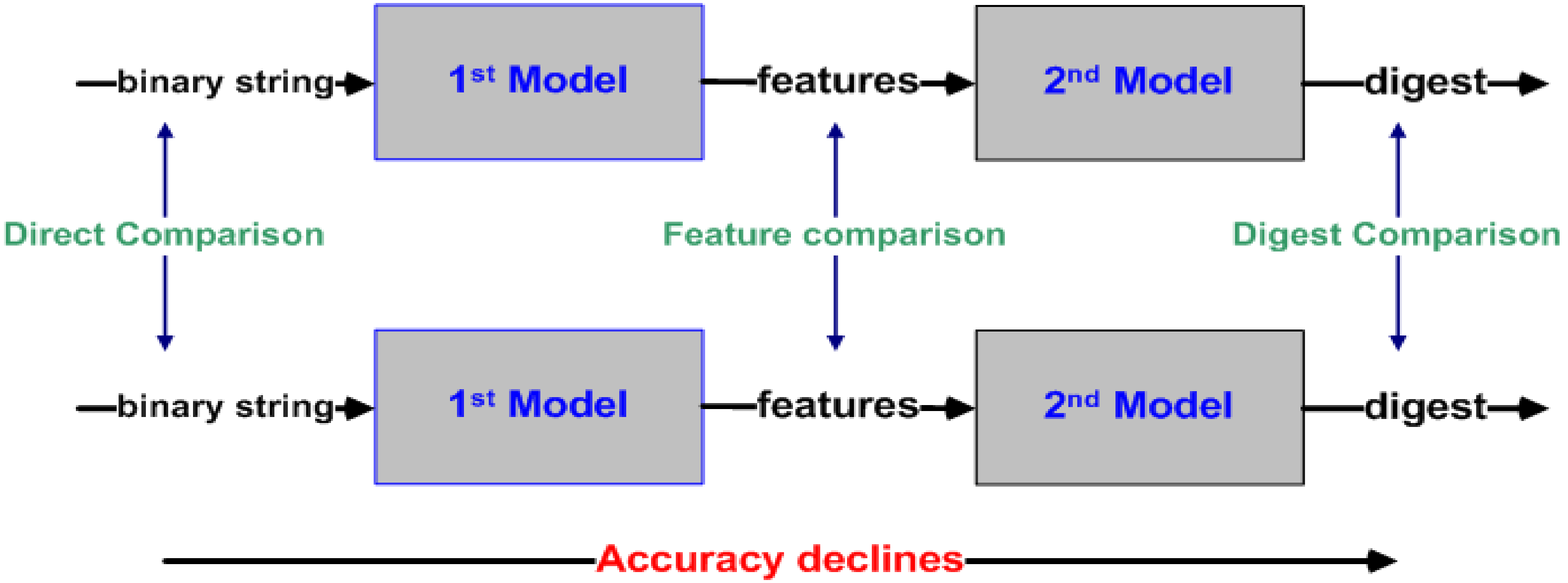
Mathematical Models for Byte-wise Similarity

- **Summary of Three Similarity Digesting Schemes:**
  - Using a **first model** to describe a binary string with ***selected features***:
    - ssdeep model: a string is a ***sequence*** of ***chunks*** (split from the string).
    - sdhash model: a string is a ***bag*** of ***64-byte blocks*** (selected with entropy values).
    - TLSH model: a string is a ***bag*** of ***triplets*** (selected from all 5-grams).
  - Using a **second model** to map the selected features into a digest which is able to preserve similarity to certain degree.
    - ssdeep model: a sequence of chunks is mapped into a 80-byte digest.
    - **sdhash model**: a bag of blocks is mapped into one or multiple 256-byte bloom filter bitmaps.
    - TLSH model: a bag of triplets is mapped into a 32-byte container.



Mathematical Models for Byte-wise Similarity

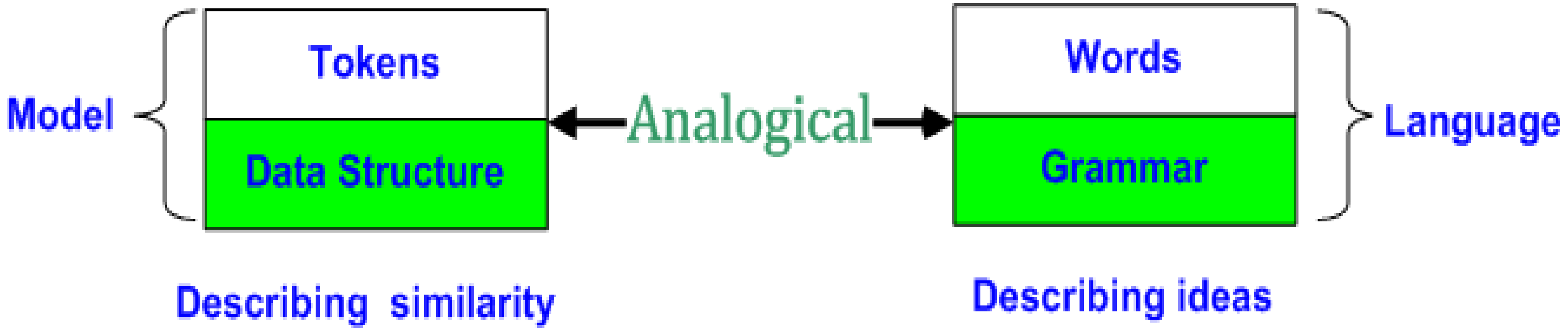
- Three approaches for similarity evaluation:



- 1st model plays critical role for similarity comparison.
  - Let focus on discussing various 1st models today.
    - Based on a unified format.
- 2nd model saves space but further reduces accuracy.

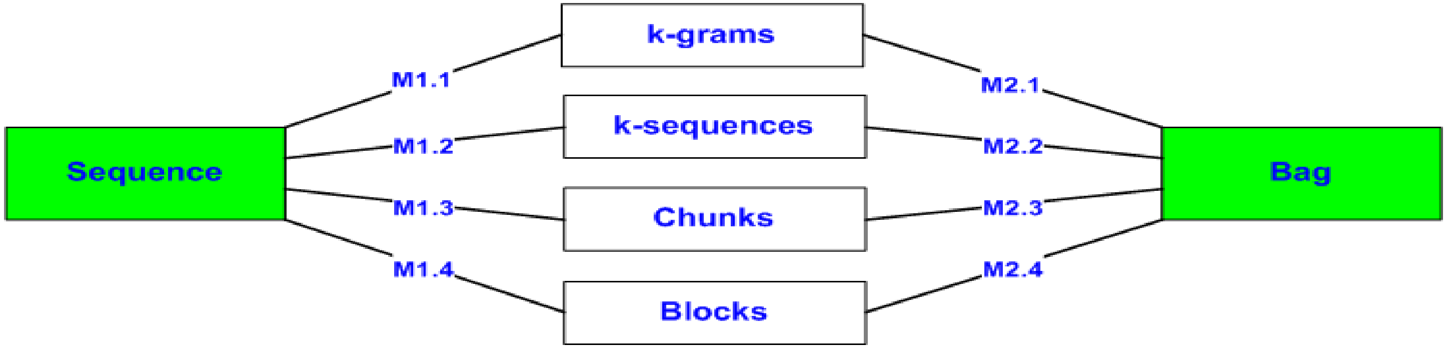
Mathematical Models for Byte-wise Similarity

- **Unified format for 1st model:**
  - A string is described as a collection of **tokens** (aka, features) organized by a **data structure:**
    - ssdeep: a sequence of chunks.
    - sdhash: a bag of 64-byte blocks with high entropy values.
    - TLSH: a bag of selected triplets.
  - Two types of data structures: sequence, bag.
  - Three types of tokens: chunks, blocks, triplets.
- **Analogical comparison:**



Mathematical Models for Byte-wise Similarity

- **Four general types of tokens from binary strings:**
  - k-grams where k is as small as 3,4,…
  - k-subsequences: any subsequence with length k. The triplet in TLSH is an example.
  - Chunks: whole string is split into non-overlapping chunks.
  - Blocks: selected substrings of fixed length.
- Eight different models to describe a string for similarity.



- Analogical thinking:
  - we define different distances to describe a metric space.

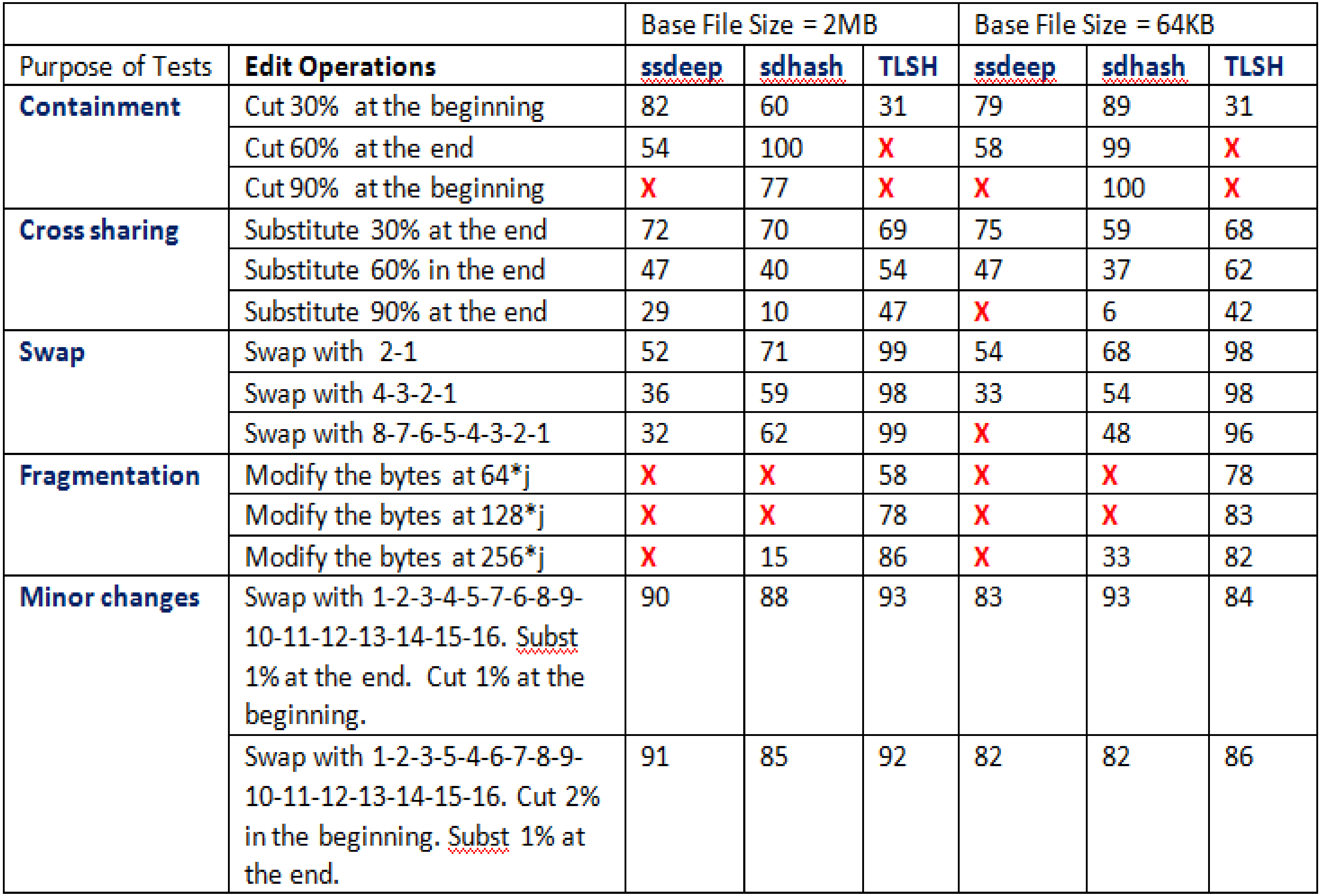
Tool Evaluation with Theoretic Analysis

- **Data Structure:**
  - **Bag**: a bag ignores the order of tokens. It is *good at handling content swapping.*
  - **Sequence**: a sequence organizes tokens in an order. This is *weak for handling content swapping.*
- **Tokens**:
  - **k-grams**: Due to the small k (3,4,5,…), this fine granularity is *good at handling fragmentation*.
  - **k-sequences**: Due to the small k (3,4,5,…), this fine granularity is *good at handling fragmentation* .
  - **Chunks**: This approach takes account of every byte in raw granularity. It should be *OK at handling containment* and *cross sharing*
  - **Blocks**: Depending on different selection functions, even though it does not take account of every byte, but it may present a string more efficiently and that is good for generating similarity digests. Due to the nature of fixed length blocks, it is *good at handling containment* and *cross sharing*.

Tool Evaluation with Theoretic Analysis

Tool	Model	Minor Changes	Containment	Cross sharing	Swap	Fragmentation
ssdeep	M1.3	*High*	*Medium*	*Medium*	*Medium*	*Low*
sdhash	M2.4	*High*	*High*	*High*	*High*	*Low*
TLSH	M2.2	*High*	*Low*	*Medium*	*High*	*High*
Sdhash + TLSH	Hybrid	*High*	*High*	*High*	*High*	*High*

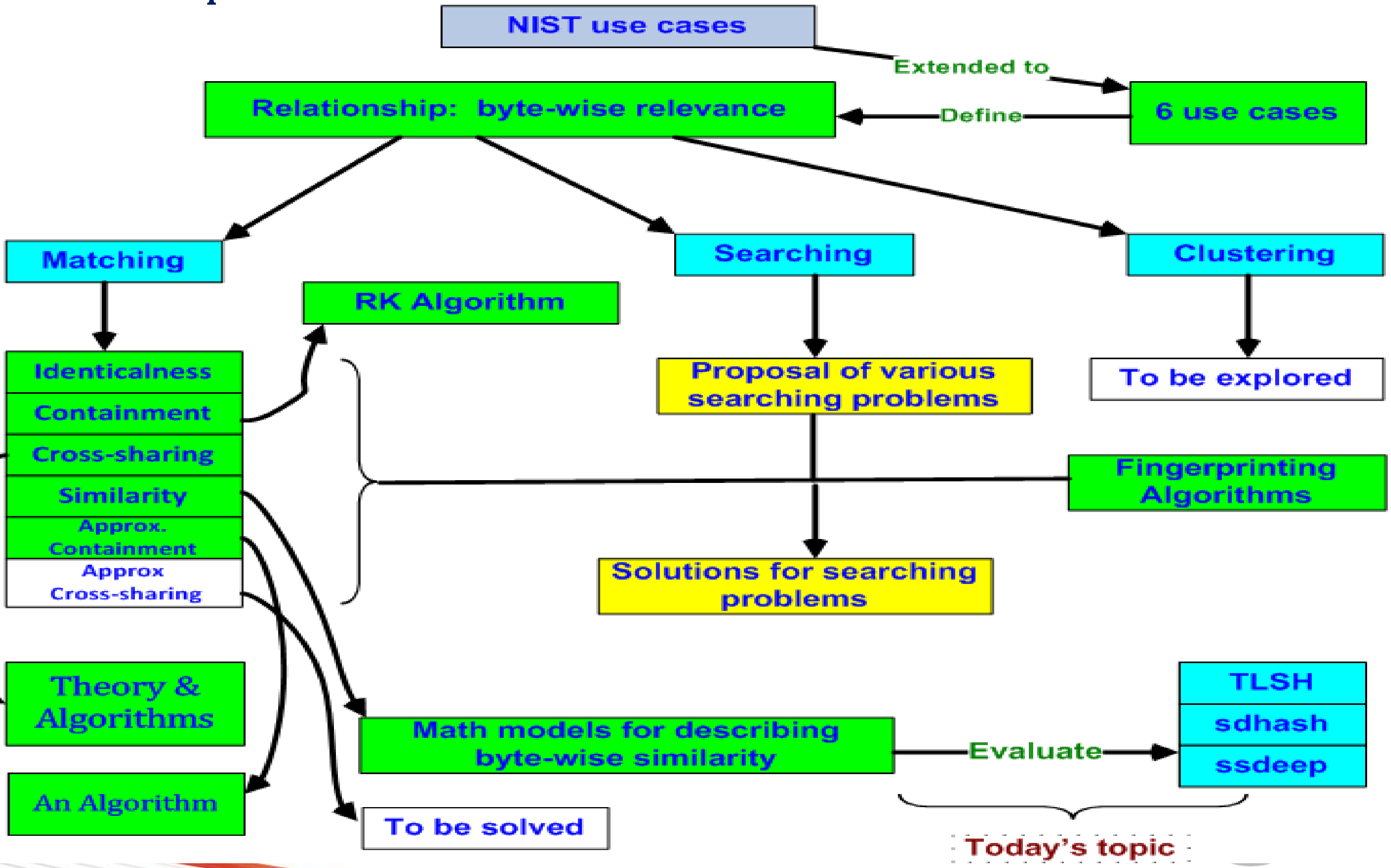
Tool Evaluation with Data Experiment



		Base File Size = 2MB			Base File Size = 64KB		
Purpose of Tests	**Edit Operations**	**ssdeep**	**sdhash**	**TLSH**	**ssdeep**	**sdhash**	**TLSH**
Containment	Cut 30% at the beginning	82	60	31	79	89	31
	Cut 60% at the end	54	100	X	58	99	X
	Cut 90% at the beginning	X	77	X	X	100	X
Cross sharing	Substitute 30% at the end	72	70	69	75	59	68
	Substitute 60% in the end	47	40	54	47	37	62
	Substitute 90% at the end	29	10	47	X	6	42
Swap	Swap with 2-1	52	71	99	54	68	98
	Swap with 4-3-2-1	36	59	98	33	54	98
	Swap with 8-7-6-5-4-3-2-1	32	62	99	X	48	96
Fragmentation	Modify the bytes at 64*j	X	X	58	X	X	78
	Modify the bytes at 128*j	X	X	78	X	X	83
	Modify the bytes at 256*j	X	15	86	X	33	82
Minor changes	Swap with 1-2-3-4-5-7-6-8-9-10-11-12-13-14-15-16. Subst 1% at the end. Cut 1% at the beginning.	90	88	93	83	93	84
	Swap with 1-2-3-5-4-6-7-8-9-10-11-12-13-14-15-16. Cut 2% in the beginning. Subst 1% at the end.	91	85	92	82	82	86

Further Research for Approximate Matching

- A Roadmap for Further Research :



Q&A

- Thank you for your interest.

- Any questions?

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