Data Structures and Algorithms MinHash Sketch

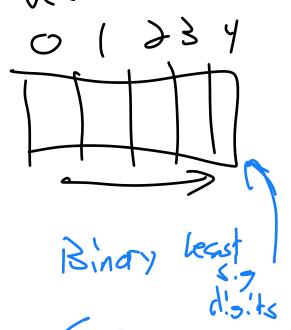
CS 225

Vector Solomon

Vector Solomon

O (> 3 4

November 8, 2023





Department of Computer Science



Extra Credit Project — Next Steps



If you were not approved, its just means you will not receive extra credit

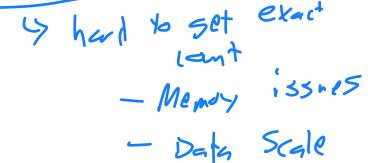
Mentors will be notifying you sometime this week

Be sure to submit a weekly development log! Schedule a check-in meeting!

Learning Objectives # ~ wight Hems

Review the concept of cardinality and cardinality estimation

Improve our cardinality estimation approach

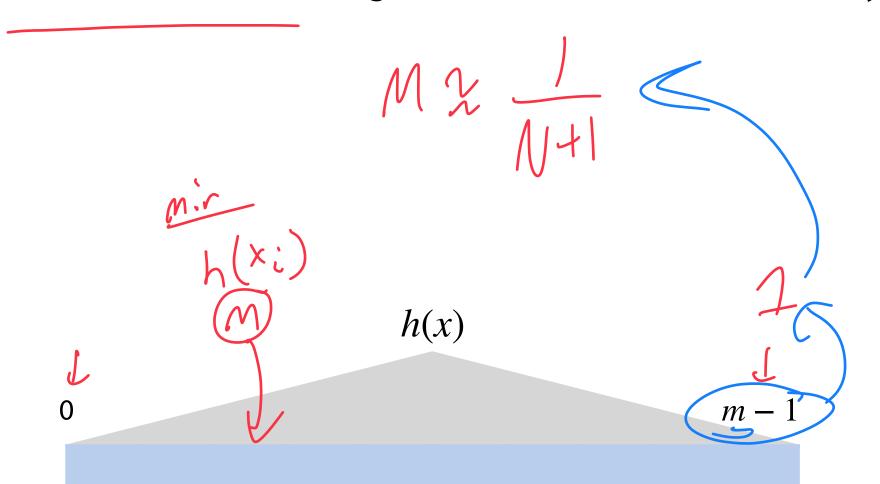


Demonstrate the relationship between cardinality and similarity

Introduce the MinHash Sketch for set similarity detection

Cardinality Estimation 5 = (40.000)

Given a SUHA hash h over a range m, we can estimate cardinality:



Let $M = min(X_1, X_2, ..., X_N)$ where each $X_i \in [0, 1]$ is an uniform independent random variable

Claim:
$$\mathbf{E}[M] = \frac{1}{N+1}$$



 $\mathbf{E}[M]$ defines the range from 0 to the min value $\left(M = \min_{1 \leq i \leq N} X_i\right)$

Consider an
$$N+1$$
 draw: $X_1 X_2 X_3 \cdots X_N X_{N+1}$ by Pin Prob (X_{N+1} is min) = M

Cardinality Sketch wifers inde X: is equally likely to be in

Consider an N + 1 draw:

Define an **indicator:**

$$I_i = \begin{cases} 1 & \text{if } X_i < \min_{j \neq i} X_j \\ 0 & \text{otherwise} \end{cases}$$

$$\mathbf{E}[I_i] = \xi \operatorname{Prob} - v = \operatorname{Pr}(X_i \subset M) \cdot 1 + 0 \cdot \xi \operatorname{Pr}(X_i \cap A \subset M)$$



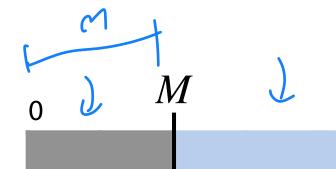


Claim:
$$\mathbf{E}[M] = \mathbf{E}[I_{N+1}] - \sqrt{4}$$

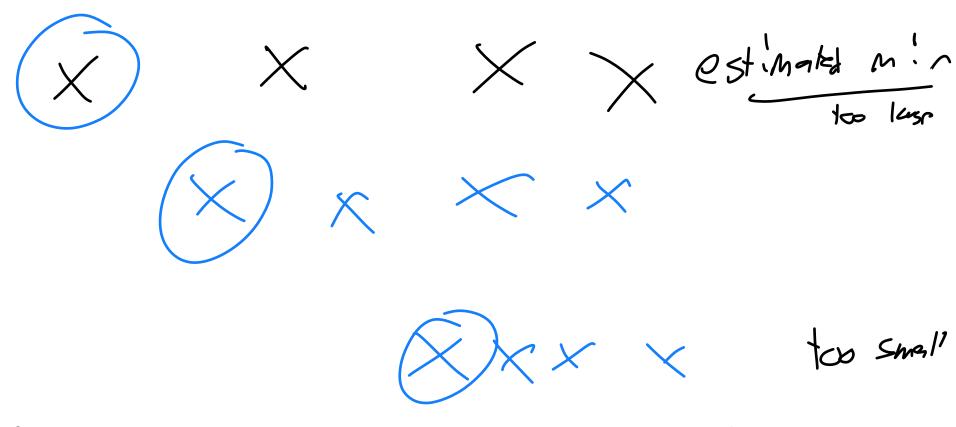
$$I_1 \qquad I_N \qquad I_{N+1}$$

$$X_1 \qquad \dots \qquad X_N \qquad X_{N+1} \qquad M = \min_{1 \le i \le N} X_i$$

By definition,
$$\mathbf{E}[I_{N+1}] = \Pr(X_{N+1} < M) = \frac{1}{N+1}$$



The minimum hash is a valid sketch of a dataset but can we do better?



0

Claim: Taking the k^{th} -smallest hash value is a better sketch!

Claim:
$$E[M_k] = \frac{1}{N+1}$$

$$\frac{1}{N+1}$$

Claim: Taking the k^{th} -smallest hash value is a better sketch!

Claim:
$$\frac{\mathbf{E}[M_k]}{k} = \frac{1}{N+1}$$
$$= \left[\mathbf{E}[M_1] + (\mathbf{E}[M_2] - \mathbf{E}[M_1]) + \dots + (\mathbf{E}[M_k] - \mathbf{E}[M_{k-1}]) \right] \cdot \frac{1}{k}$$

$$M_1$$

$$M_2$$

$$M_3$$
 ..

$$M_{k-1}$$

$$M_k$$

$$\frac{1}{N+1} = \frac{\mathbf{E}[M_k]}{k}$$

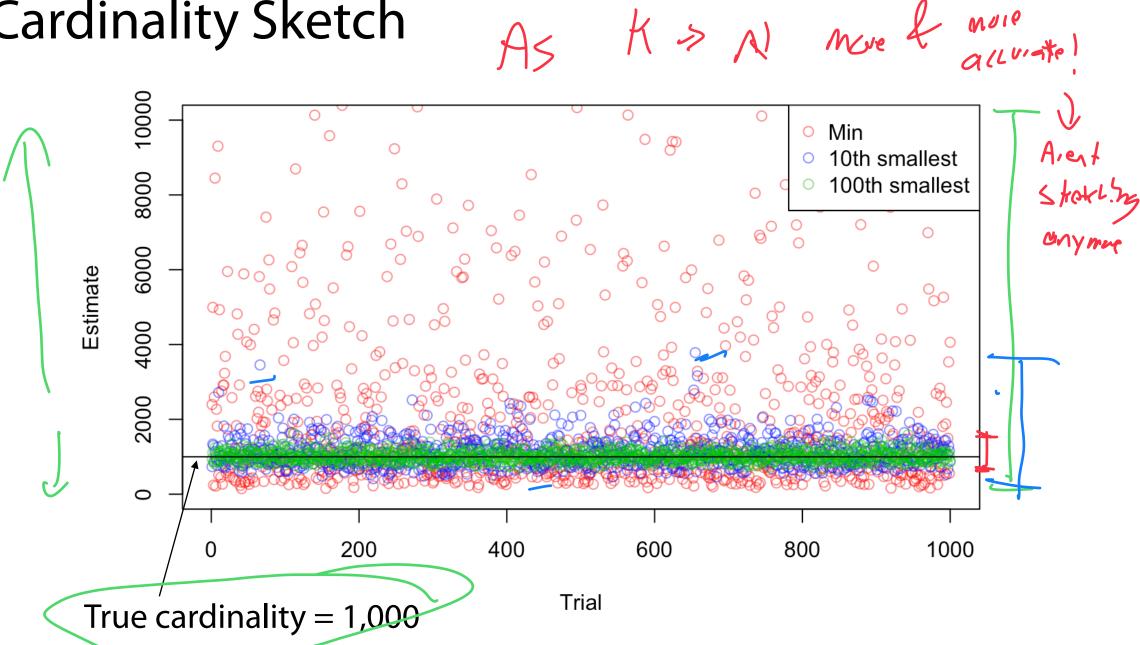
$$= \left[\mathbf{E}[M_1] + (\mathbf{E}[M_2] - \mathbf{E}[M_1]) + \dots + (\mathbf{E}[M_k] - \mathbf{E}[M_{k-1}])\right] \cdot \frac{1}{k}$$

$$M_1 \quad M_2 \quad M_3 \quad M_{k-1} M_k$$

$$k^{th} \text{ minimum}$$

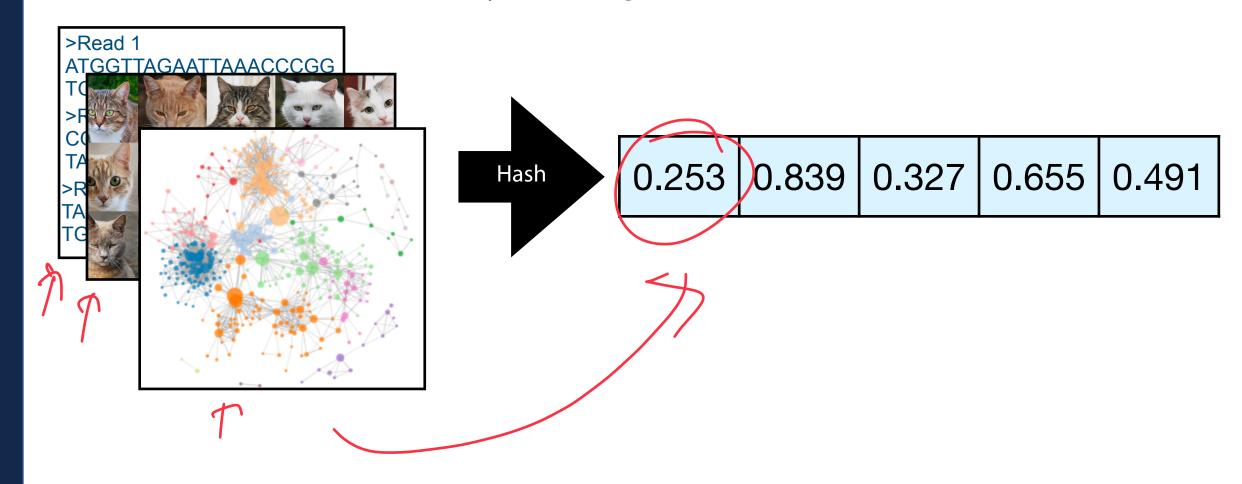
$$\text{value (KMV)}$$

$$Averages \ k \text{ estimates for } \frac{1}{N+1}$$





Given any dataset and a SUHA hash function, we can **estimate the number of unique items** by tracking the **k-th minimum hash value**.



Applied Cardinalities



Cardinalities

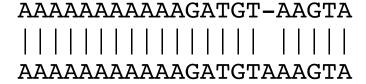
 $|A \cap B|$

$$O = \frac{|A \cap B|}{\min(|A|, |B|)}$$

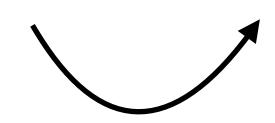
$$J = \frac{|A \cap B|}{|A \cup B|}$$

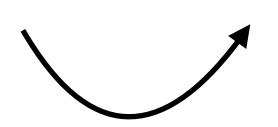
Real-world Meaning



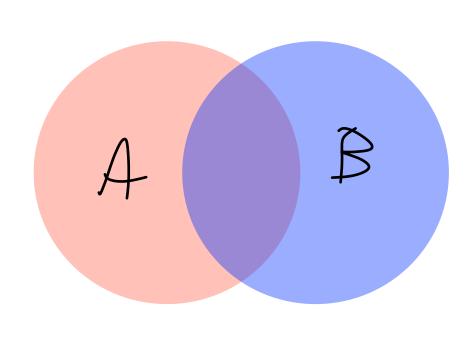


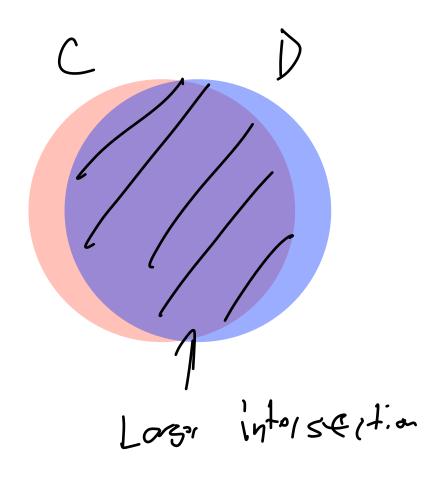




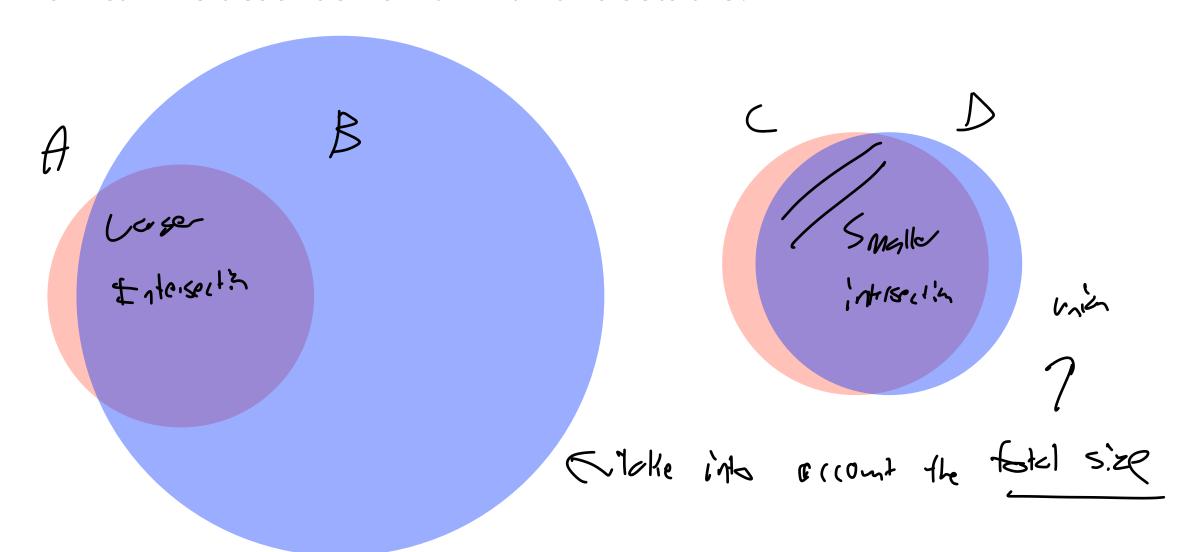


How can we describe how *similar* two sets are?

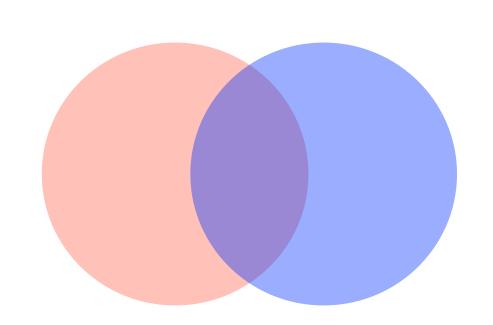




How can we describe how **similar** two sets are?



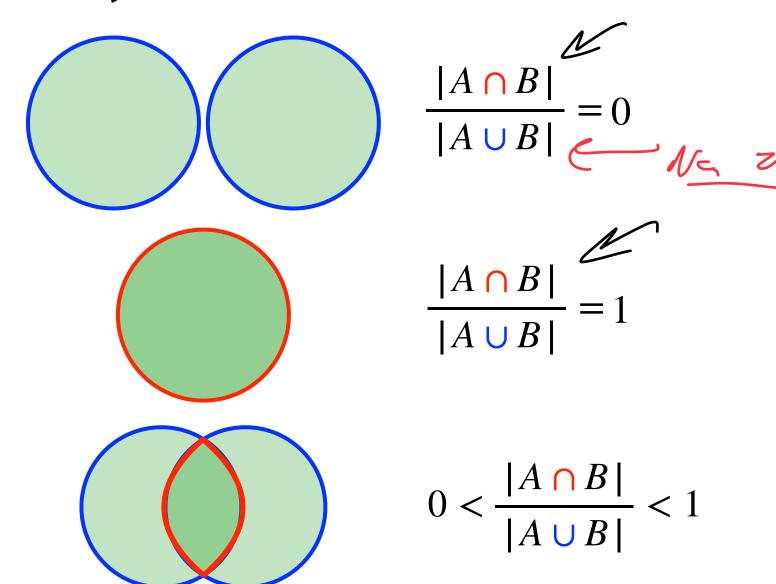
To measure **similarity** of A & B, we need both a measure of how similar the sets are but also the total size of both sets.



$$J = \frac{|A \cap B|}{|A \cup B|} \leq u_{A} \leq u_$$

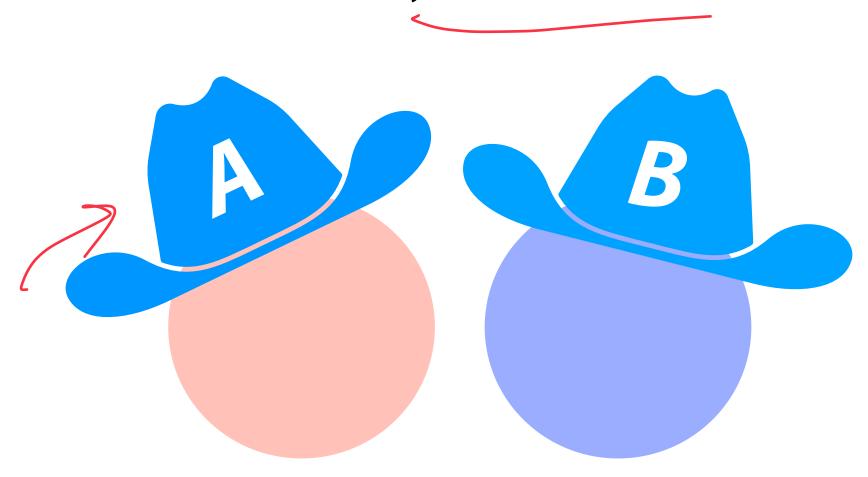
J is the **Jaccard coefficient**





Similarity Sketches

But what do we do when we only have a sketch?



Similarity Sketches

Imagine we have two datasets represented by their kth minimum values

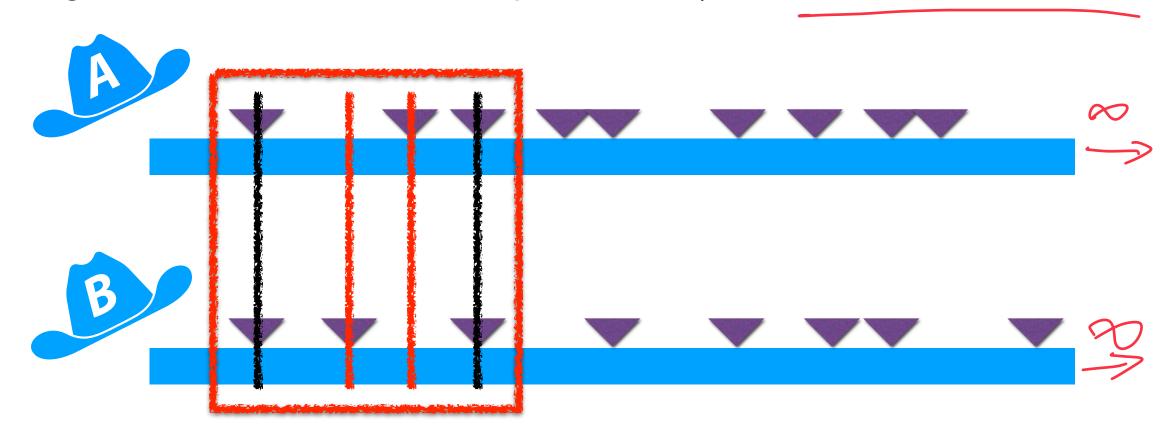


Image inspired by: Ondov B, Starrett G, Sappington A, Kostic A, Koren S, Buck CB, Phillippy AM. **Mash Screen:** high-throughput sequence containment estimation for genome discovery. *Genome Biol* 20, 232 (2019)

Similarity Sketches

Claim: Under SUHA, set similarity can be estimated by sketch similarity!

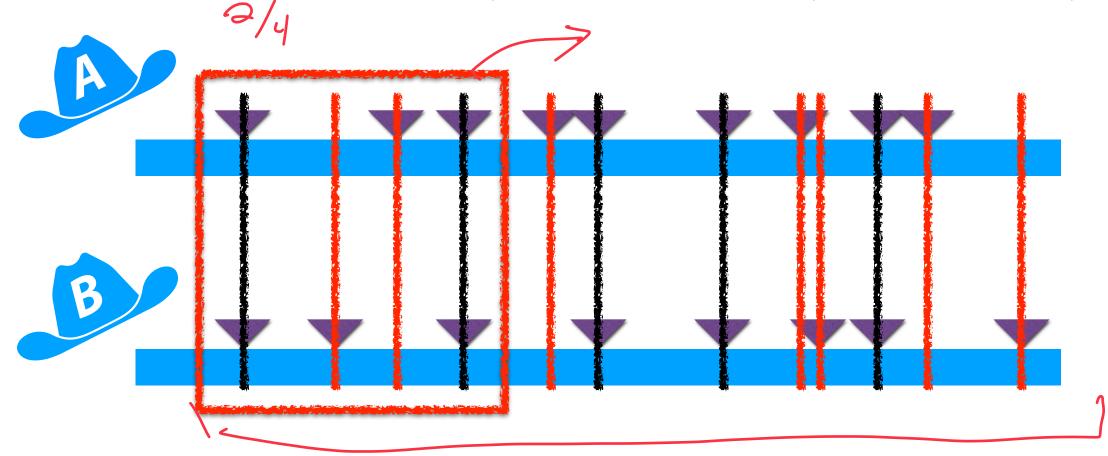
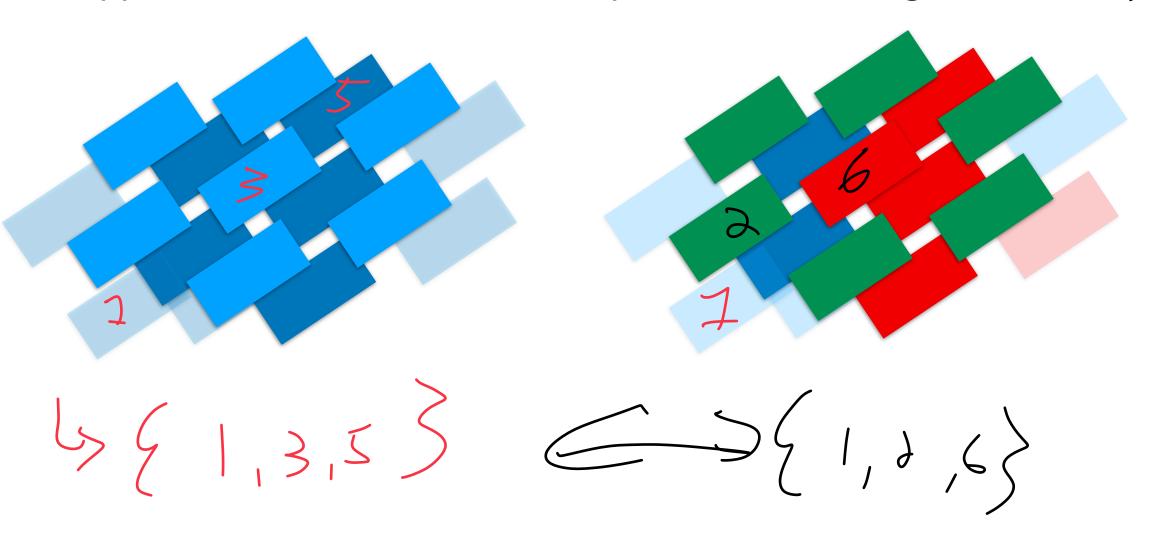


Image inspired by: Ondov B, Starrett G, Sappington A, Kostic A, Koren S, Buck CB, Phillippy AM. **Mash Screen:** high-throughput sequence containment estimation for genome discovery. *Genome Biol* 20, 232 (2019)

Minhash Sketch

An approximation for a full dataset capable of estimating set similarity



Minhash Sketch 'ADT' (Use Cases)

Constructor > K min Valves

Cardinality Estimation — Sen Ms

Set Similarity Estimation

MinHash Construction

A MinHash sketch has three required inputs: (*** Completes**)

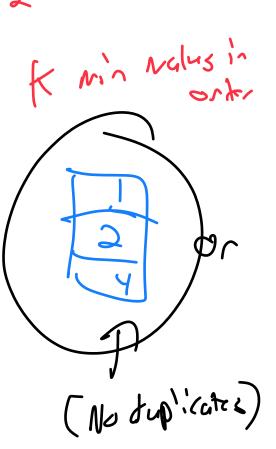
MinHash Construction

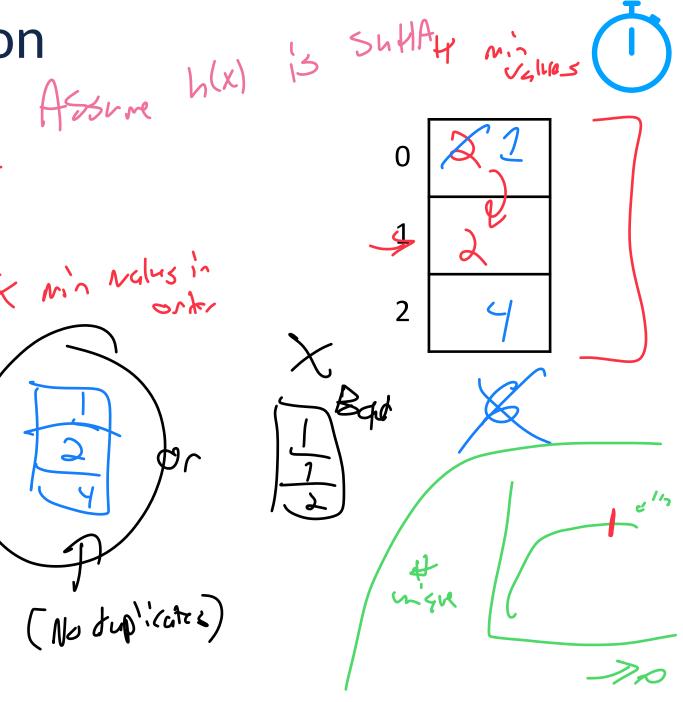
$$S = \{ 16, 8, 4, 13, 15 \}$$

$$h(x) = x \% 7$$

$$k = 3$$

Minhosh Sketch is





MinHash Cardinality Estimation

of unique . tems

$$h(x) = x \% 7 \implies \{0, 1, 3, 5, 4, 5, 6\}$$

$$k = 3$$

$$Ma^{-2}/6 = \frac{\lambda}{\Lambda/4}$$

Maz Y/6 = 3 & Normalizate & Haw to calc Kinin values

Let's assume we have sets A and B sampled uniformly from [0, 100).

Instead of storing A & B, we store the bottom-8 MinHash

Already hashel

Sketch A

3	15
7	17
8	22
11	23

Sketch B

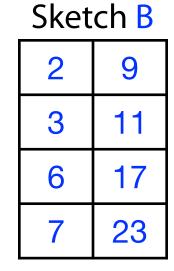
2	9
3	11
6	17
7	23

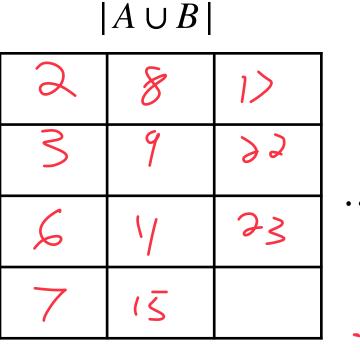
()					8			1	6		24	
Α			3		7	8		11	15	17	22 23	3	 \geqslant
В		2	3	6	7		9	11		17	23	3	7



What do we know about $|A \cup B|$?

Sketch A					
3	15				
7	17				
8	22				
11	23				







8 min items

We dont $know \mid A \cup B \mid$, but we can estimate it!

Sketch of $A \cup B$

Sketch A					
3	15				
7	17				
8	22				
11	23				



Sketch B					
2	9				
3	11				
6	17				
7	23				

7	8
M	9
Q	11
7	15

	0			8	3		1	6	24	
Α		3		7 8	3	11	15	17	22 23	•••
В	2	3	6	7	9	11		17	23	



We can estimate the cardinality of $|A \cup B|$ from this sketch.

Sketch of $|A \cup B|$

- 6

KMV

Our sets sampled from [0, 100).

$$15/99 = \frac{8}{111}$$

$$15/99 = \frac{8}{1/11}$$

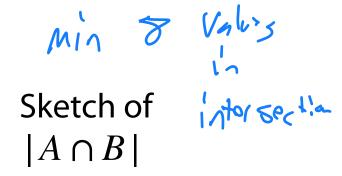
Can we build a 8-Minhash of $|A \cap B|$?

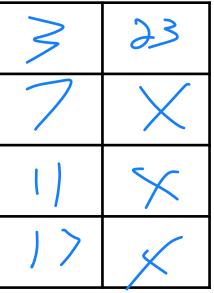
Sket	Sketch A					
3	15					
7	17					
8	22					
11	23					



2	9					
3	11					
6	17					
7	23					

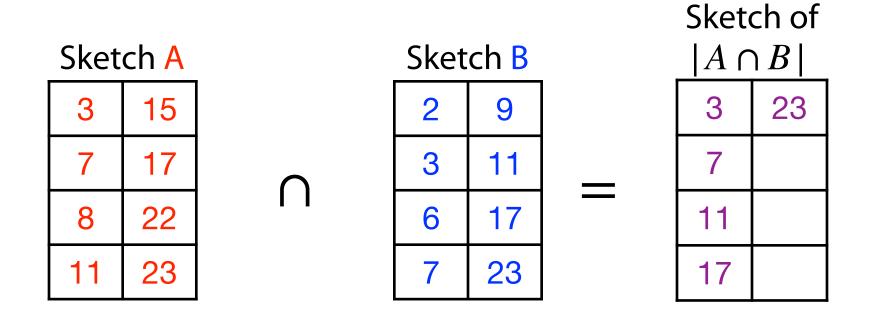
Sketch B

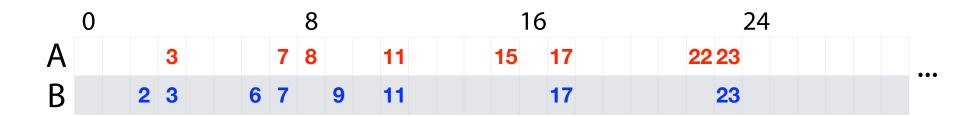






We are not guaranteed to be able to get a full sketch of the intersection!

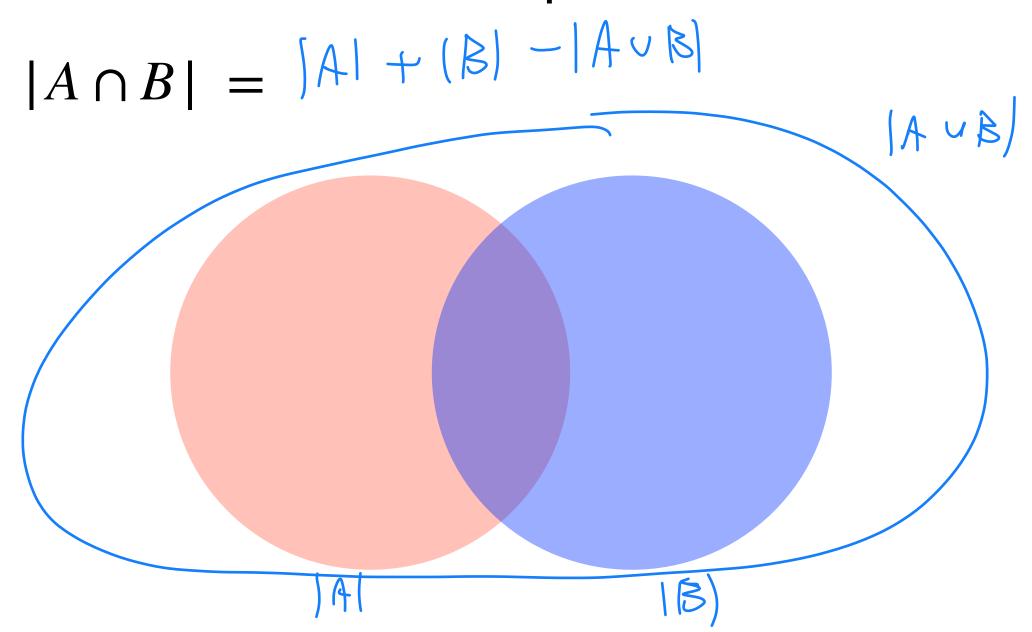




Using MinHash sketches, we can estimate |A|, |B|, and $|A \cup B|$

Is this enough to estimate the Jaccard?

Inclusion-Exclusion Principle



MinHash Jaccard Estimation Math Lable therk

$$\frac{|A| \cap |B|}{|A| \cup |B|} = \frac{|A| + |B| - |A \cup B|}{|A \cup B|}$$

k = 8 MinHash sketches Our sets sampled from [0, 100]

Sketch A

3	15
7	17
8	22
11	23

Sketch B

JACTON					
2	9				
3	11				
6	17				
7	23				

Sketch of

$$|A \cup B|$$

 2
 8

 3
 9

 6
 11

 7
 15

$$= \frac{(800/23-1) + (800/23-1) - (800/15-1)}{800/15-1}$$

$$=\frac{34.782 + 34.782 - 53.333 - 1}{53.333 - 1} \approx 0.29$$

The MinHash Sketch

We can also estimate cardinality directly using our sketches!

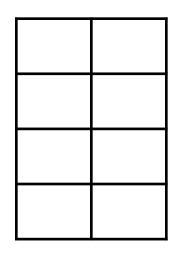
Sketch A

3	15
7	17
8	22
11	23

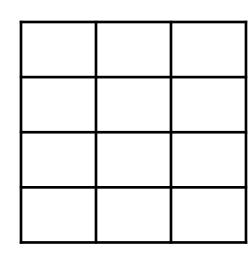
Sketch B

2	9
3	11
6	17
7	23

Intersection



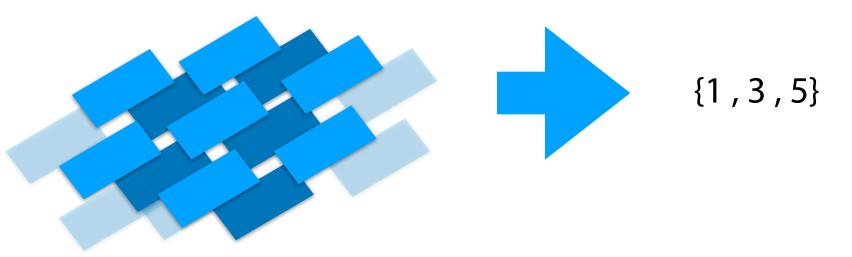
Union



MinHash Sketch



We can convert any hashable dataset into a MinHash sketch



We lose our original dataset, but we can still estimate two things:

1.

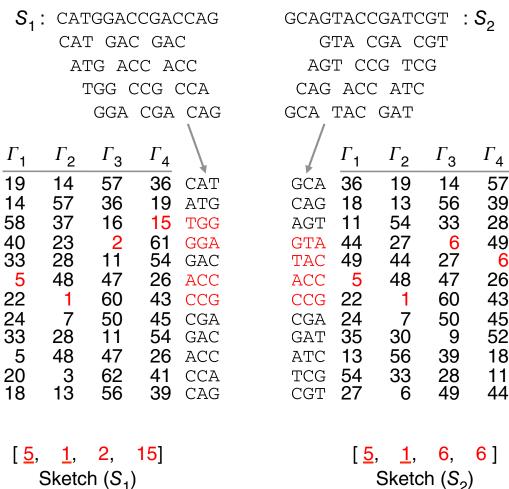
2.

Alternative MinHash Sketch Approaches

The **easiest** version of MinHash uses k hashes. How might this work?

- 1) Sequence decomposed into **kmers**
- 2) Multiple hash functions (**Γ**) map kmers to values.

- 3) The smallest values for each hash function is chosen
- 4) The Jaccard similarity can be estimated by the overlap in the **Min**imum **Hash**es (**MinHash**)



Sketch
$$(S_1)$$

$$J(S_1, S_2) \approx 2/4 = 0.5$$

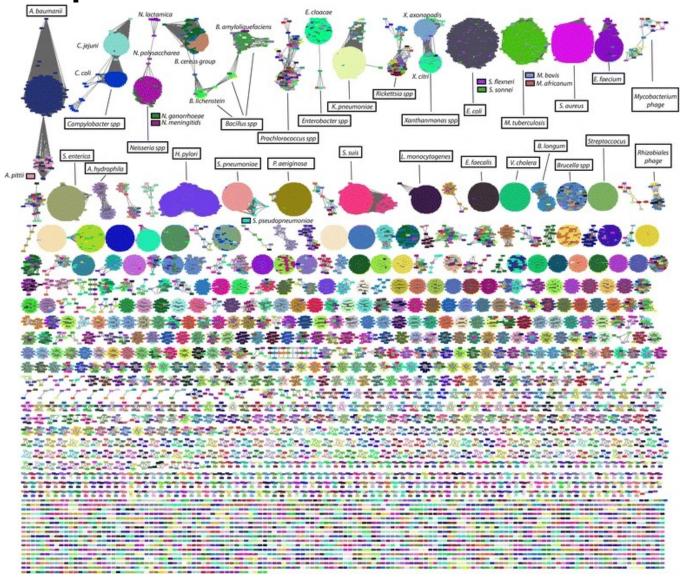
$$S_1: \text{CATGGACCGACCAG}$$

$$| | | | | |$$

$$S_2: \text{GCAGTACCGATCGT}$$

Assembling large genomes with single-molecule sequencing and locality-sensitive hashing Berlin et al (2015) *Nature Biotechnology*

MinHash in practice



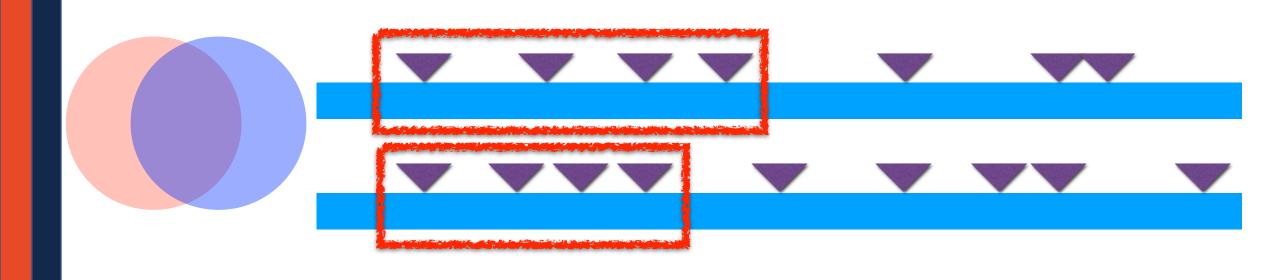
Mash: fast genome and metagenome distance estimation using MinHash Ondov et al (2016) *Genome Biology*

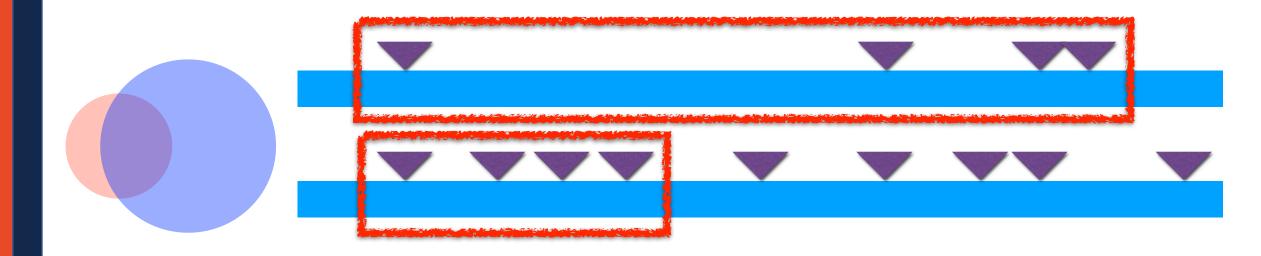
Alternative MinHash Sketch Approaches

What if I have a dataset which is **much** larger than another?

```
S_1 = \{ 1, 3, 40, 59, 82, 101 \}

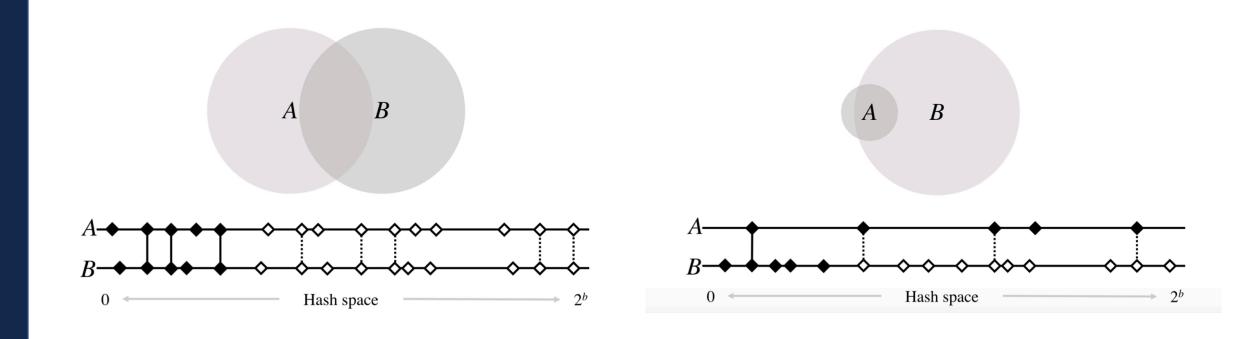
S_2 = \{ 1, 2, 3, 4, 5, 6, 7, ... 59, 82, 101, ... \}
```





Alternative MinHash sketches

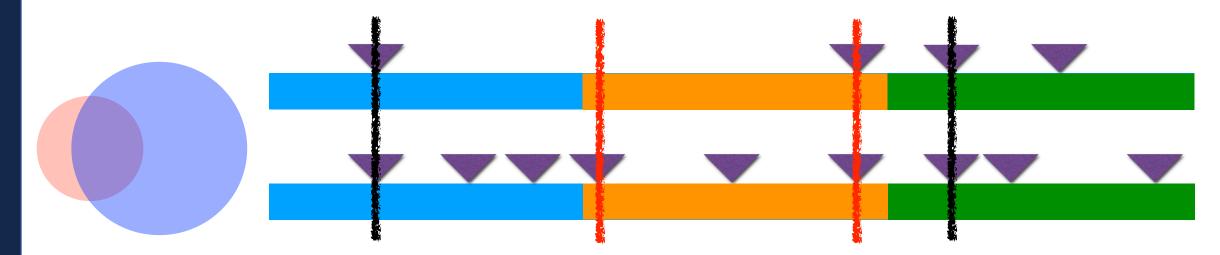
Bottom-k minhash has low accuracy if the cardinality of sets are skewed



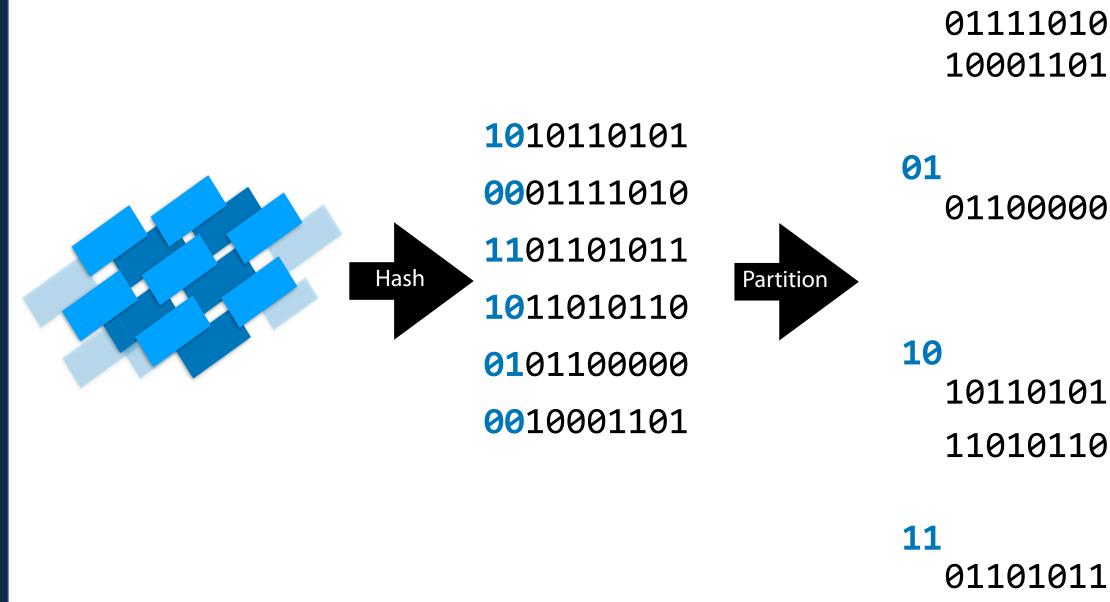
Ondov, Brian D., Gabriel J. Starrett, Anna Sappington, Aleksandra Kostic, Sergey Koren, Christopher B. Buck, and Adam M. Phillippy. **Mash Screen: High-throughput sequence containment estimation for genome discovery**. *Genome biology* 20.1 (2019): 1-13.

Alternative MinHash Sketch Approaches

If there is a large cardinality difference, use k-partitions!



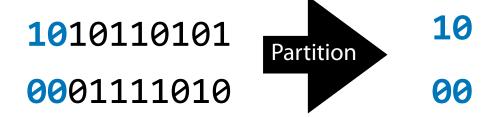
K-Partition Minhash



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K-Partition Minhash

Hint: What bitwise operator will allow me to do this?



What information do I need to do this in general?

MP_Sketching: A MinHash experiment

Using legitimate hashes, write MinHash sketch three ways:

```
std::vector<uint64_t> khash_minhash(std::vector<int> inList, std::vector<hashFunction> hv);
std::vector<uint64_t> kminhash(std::vector<int> inList, unsigned k, hashFunction h);
std::vector<uint64 t> kpartition minhash(std::vector<int> inList, int part bits, hashFunction h);
```

MP_Sketching: A MinHash experiment

Use MinHash sketches to estimate PNG similarity



Mosaics (Discord: Bose)



Mosaics (Discord: LightningStorm)

MP_Sketching: A MinHash experiment

Build a weighted graph of every possible pairwise comparison!