# MinHash for overlapping and assembly

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National Biodefense Analysis & Countermeasures Center

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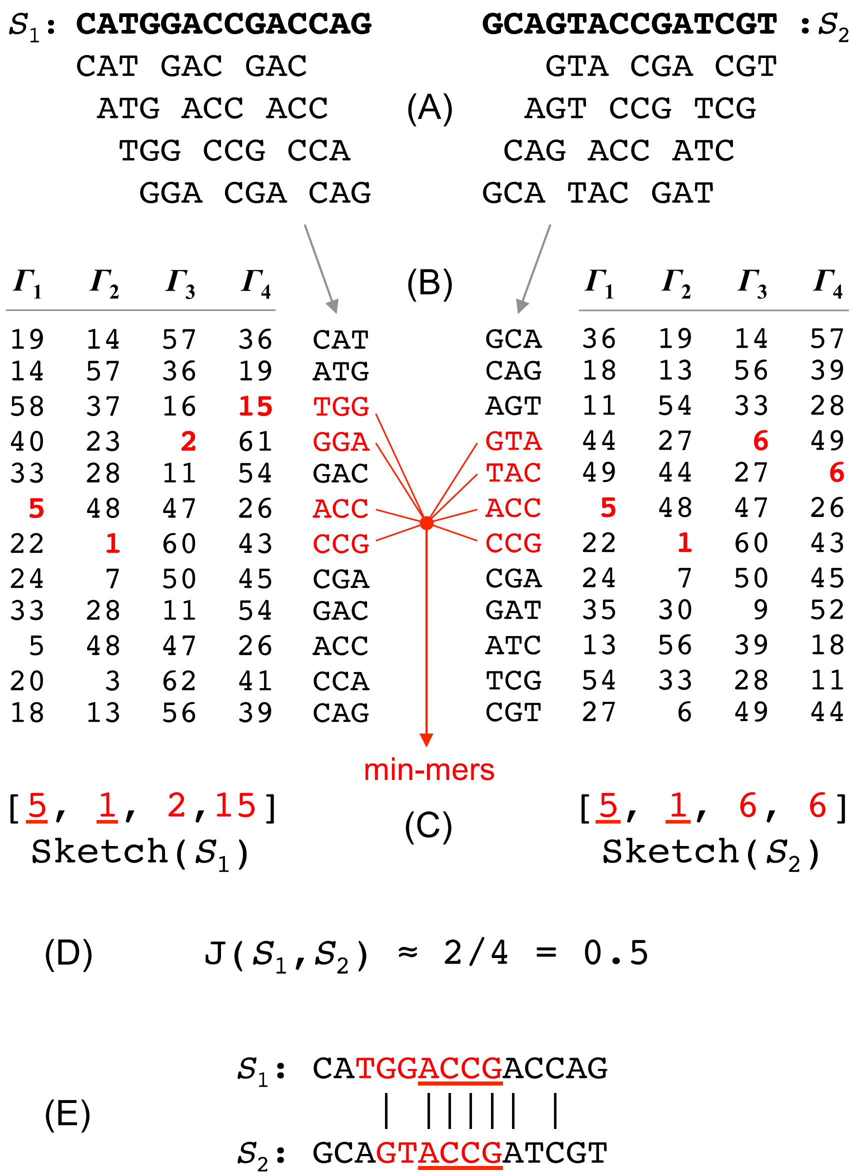


$S_1$: **CATGGACCGACCAG** GCAGTACCGATCGT : $S_2$

(A)

```
CAT GAC GAC          GTA CGA CGT
 ATG ACC ACC        AGT CCG TCG
  TGG CCG CCA      CAG ACC ATC
   GGA CGA CAG    GCA TAC GAT
```

(B)

| $\Gamma_1$ | $\Gamma_2$ | $\Gamma_3$ | $\Gamma_4$ | |
|---|---|---|---|---|
| 19 | 14 | 57 | 36 | CAT |
| 14 | 57 | 36 | 19 | ATG |
| 58 | 37 | 16 | **15** | TGG |
| 40 | 23 | **2** | 61 | GGA |
| 33 | 28 | 11 | 54 | GAC |
| **5** | 48 | 47 | 26 | ACC |
| 22 | **1** | 60 | 43 | CCG |
| 24 | 7 | 50 | 45 | CGA |
| 33 | 28 | 11 | 54 | GAC |
| 5 | 48 | 47 | 26 | ACC |
| 20 | 3 | 62 | 41 | CCA |
| 18 | 13 | 56 | 39 | CAG |

| | $\Gamma_1$ | $\Gamma_2$ | $\Gamma_3$ | $\Gamma_4$ |
|---|---|---|---|---|
| GCA | 36 | 19 | 14 | 57 |
| CAG | 18 | 13 | 56 | 39 |
| AGT | 11 | 54 | 33 | 28 |
| GTA | 44 | 27 | **6** | 49 |
| TAC | 49 | 44 | 27 | **6** |
| ACC | **5** | 48 | 47 | 26 |
| CCG | 22 | **1** | 60 | 43 |
| CGA | 24 | 7 | 50 | 45 |
| GAT | 35 | 30 | 9 | 52 |
| ATC | 13 | 56 | 39 | 18 |
| TCG | 54 | 33 | 28 | 11 |
| CGT | 27 | 6 | 49 | 44 |

min-mers

(C)

[5, 1, 2,15] Sketch($S_1$)

[5, 1, 6, 6] Sketch($S_2$)

(D) J($S_1$,$S_2$) ≈ 2/4 = 0.5

(E)

```
S1: CATGGACCGACCAG
       |  ||||| |
S2: GCAGTACCGATCGT
```

## ▪ The “AltaVista” algorithm

Invented in 1998 by Andrei Broder to detect duplicate web pages

Applied to DNA sequencing matching and alignment

– Quick estimator of Jaccard Similarity

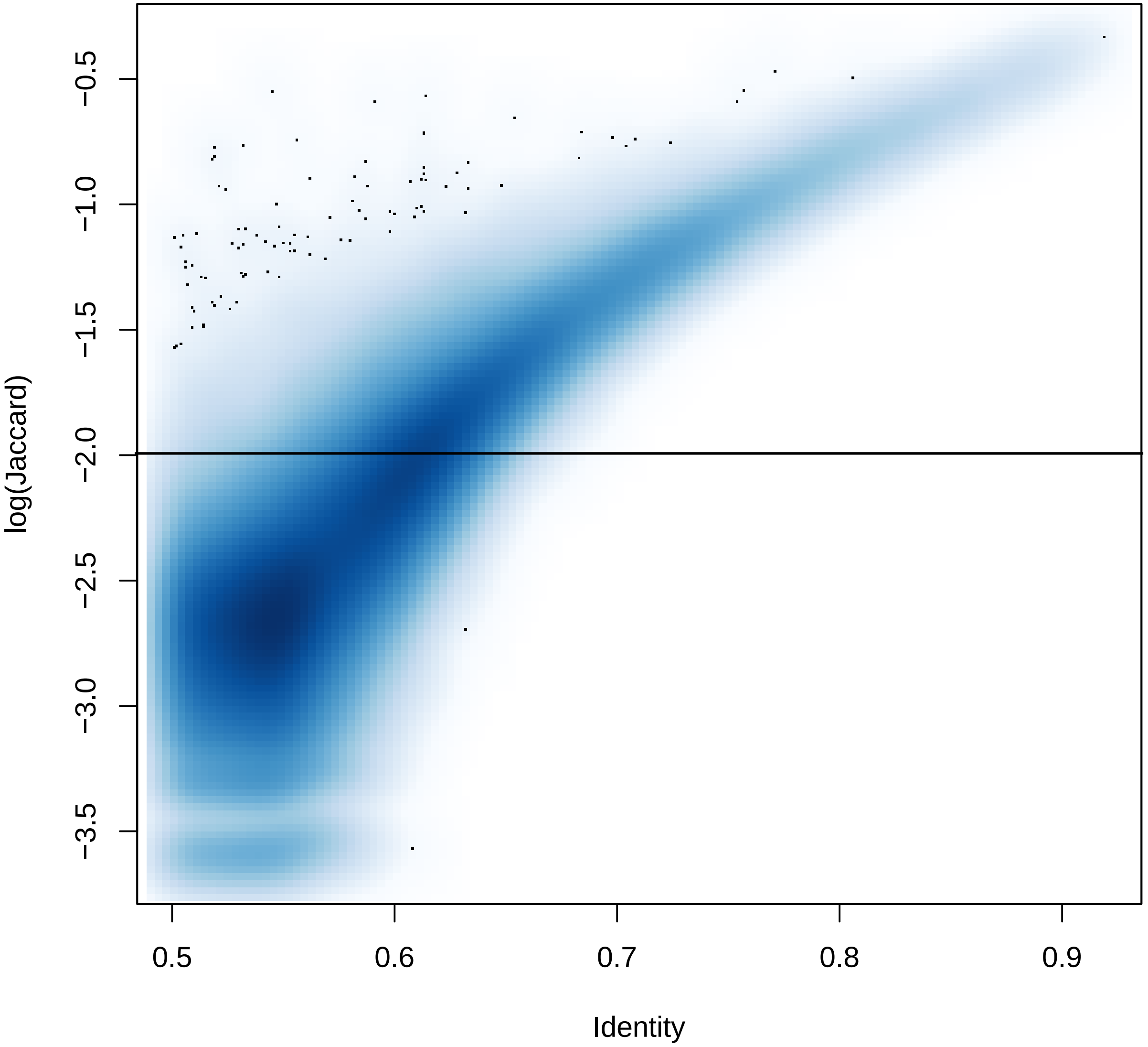
$$J(A,B)=\frac{|A \text{ Ç } B|}{|A \text{ È } B|}=\frac{4}{18}=0.22$$

- Position independent
- Length independent
- Correlated with identity

**Assembling Large Genomes with Single-Molecule Sequencing and Locality Sensitive Hashing**

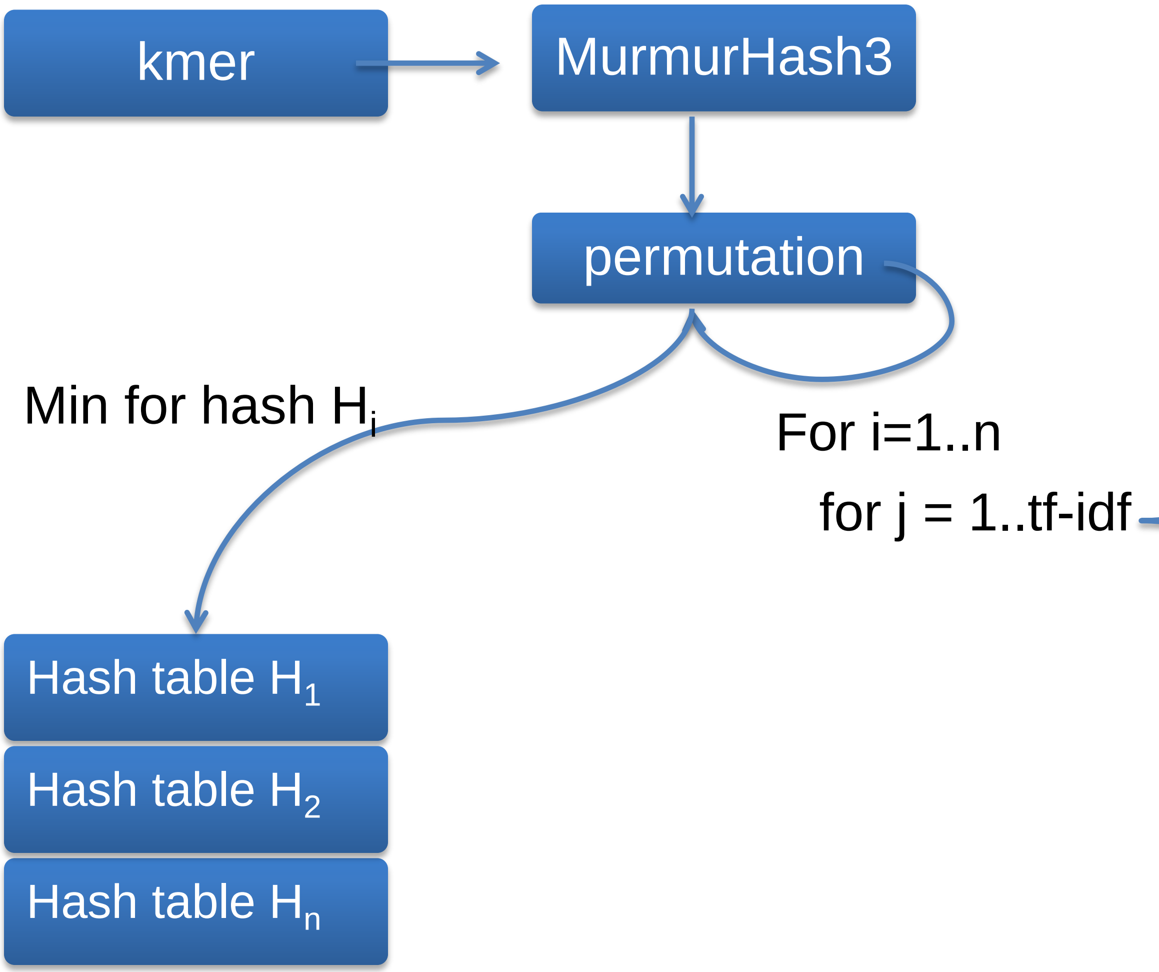
Berlin *et al.* (2015) *Nature Biotechnology*

# Jaccard score estimates identity



J=0.01

# In Practice, n hashes



kmer

MurmurHash3

permutation

Min for hash $H_i$

For i=1..n

for j = 1..tf-idf

Hash table $H_1$

Hash table $H_2$

Hash table $H_n$

## Tf-Idf Weight

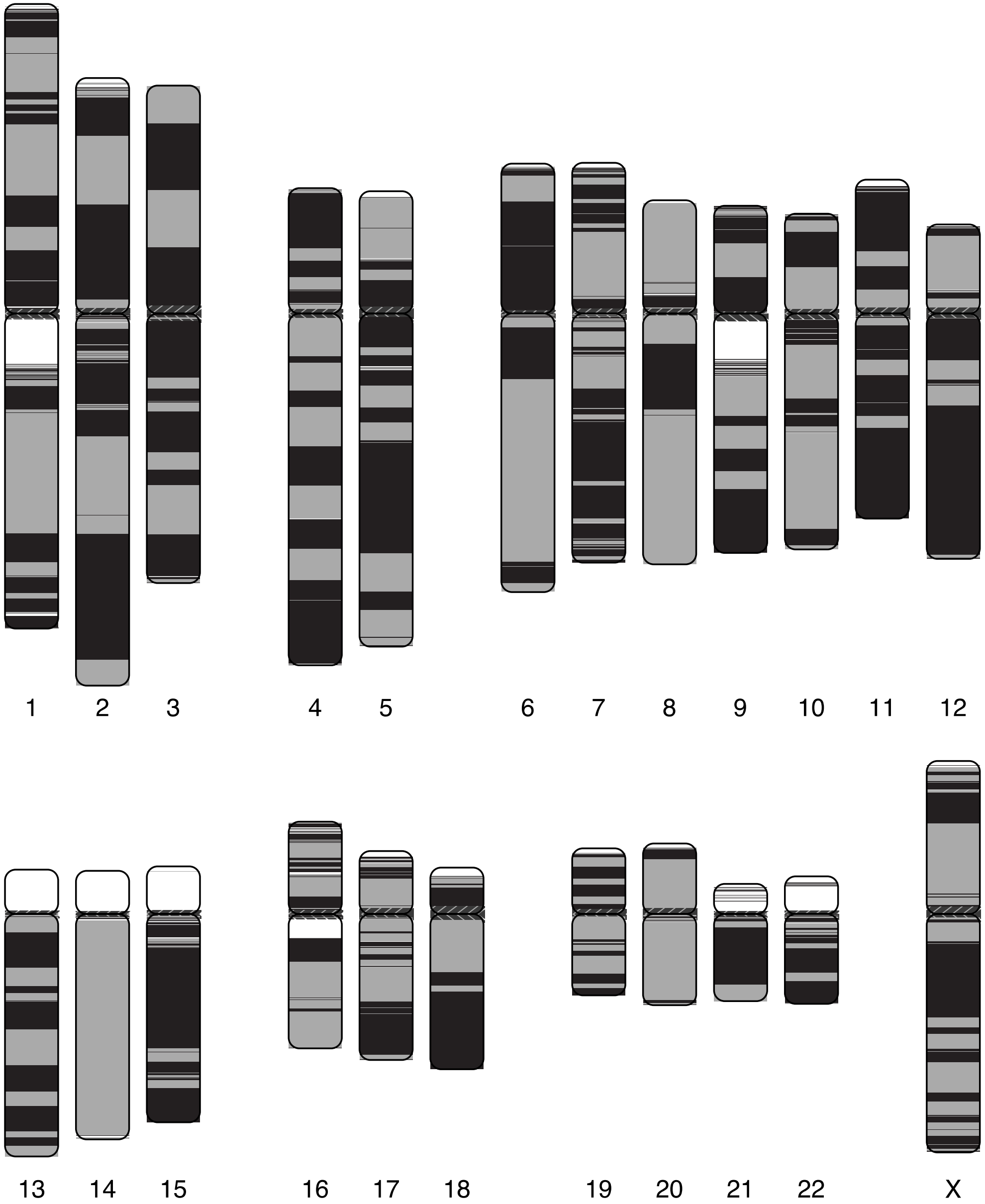
$$tf(kmer,r) = \#\ times\ kmer\ occurs\ in\ read\ r$$

$$f(kmer) = \sum_{r\ \in reads} tf(kmer,r)$$

$$idf(kmer) = \log\left(\frac{\max\,(f(kmer)\forall\ kmers}{f(kmer)}\right)$$

$$weight \propto tfidf = tf\ (kmer,read) *\ idf(kmer)$$

# Human Assembly, solved?



CHM13 CA 8.3

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  - Adam Phillippy
  - Konstantin Berlin
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- **Parsnp & Gingr**
  - Todd Treangen
  - Brian Ondov
- **Mash**
  - Brian Ondov

GitHub
/MarBL

Or just Google “PBcR MHAP”

- **Join Phillippy Lab/MarBL at NIH**
  - Looking for two postdocs, talk to myself or Adam

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# Human Assemblies with MHAP

| Genome | Chem | Cov | #Ctgs | Max (kb) | N50(kb) | Ovl CPU(h) |
|---|---|---:|---:|---:|---:|---:|
| CHM1 | P5 | 54X | 17,776 | 35,487 | 6,303 | 19,700 |
| CHM1 | P5+P6 | 120X | 8,011 | 143,469 | 23,254 | 26,305 |
| CHM13 | P5+P6 | 70X | 15,538 | 81,523 | 13,332 | 8,171 |
| | | | | | | |
| Trio HG002 | P5+P6 | 71X | 13,048 | 35,012 | 4,399 | 9,145 |
| Trio HG003 | P5+P6 | 33X | 23,493 | 9,815 | 912 | 30,625* |
| Trio HG004 | P5+P6 | 29X | 16,326 | 8,894 | 1,034 | 22,971* |

* Low coverage datasets run with sensitive parameters to improve assembly