De Bruijn Graphs

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Outline

De Bruijn Sequences

De novo Genome Assembly

Section 1

De Bruijn Sequences

Problem Statement

For $n \geq 1$, does there exist a circular sequence S that contains all n-length binary strings exactly once?

Examples

For $n = 1$, we uniquely have

$$10$$

For $n = 2$, we uniquely have

$$1100$$

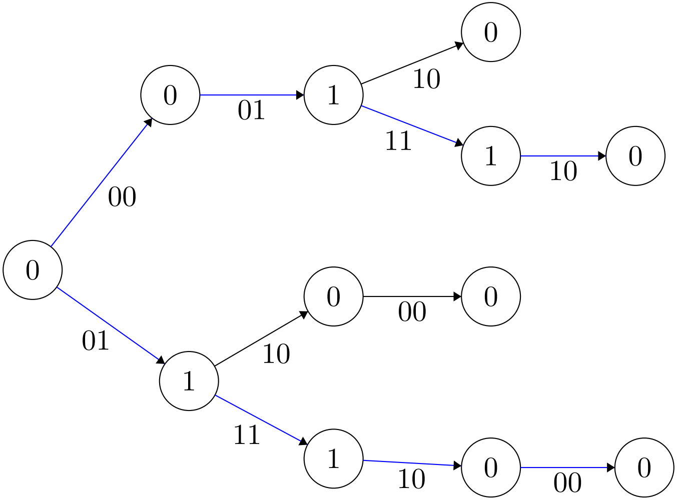
For $n = 3$, we have

$$11100010 \qquad 11101000$$

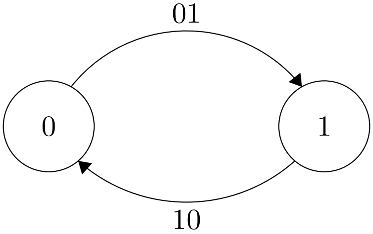
Observations

- S must have length exactly 2^n
- Every $(n-1)$-length substring occurs exactly twice
- The first n bits are arbitrary

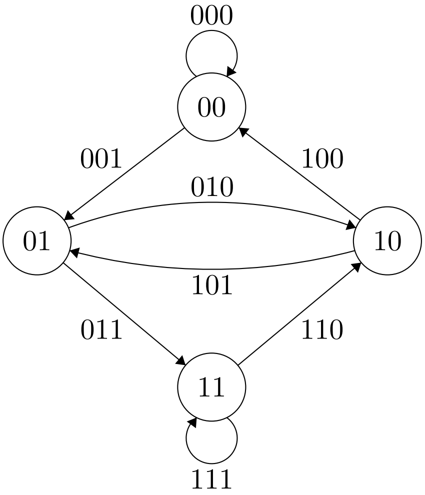
A Graph Representation



A Better Graph Representation



A Better Graph Representation



De Bruijn Graph

Let $n \geq 1$.

$$V = \mathbb{F}_2^{n-1}$$

$$u \to v \text{ if } \textit{suffix}(u) = \textit{prefix}(v)$$

What graph problem are we solving?

Eulerian Circuit

Definition (Circuit)

A *circuit* is a closed walk that uses an edge at most once.

Definition (Eulerian Circuit)

A circuit is *Eulerian* if it uses all edges exactly once.

Eulerian Graphs

We say a (simple) (di)graph is Eulerian if it has an Eulerian circuit.

Theorem (Eulerian Graphs)

G is Eulerian if $\mathrm{indeg}(v) = \mathrm{outdeg}(v)$ *for all* $v \in V(G)$.

Eulerian Graphs Sufficiency

```
FindEulerianCircuit($G$):
    $T \leftarrow$ maximal trail in $G$
    $G' \leftarrow G \setminus T$
    $C \leftarrow$ FindEulerianCircuit($G'$)
    return $T \cup C$
```

Eulerian Graphs Sufficiency

Proof.

Suppose G is balanced. Then, T must be a circuit. G' must be balanced. Then, $T \cup C$ is Eulerian, by induction. □

Claim

The above algorithm runs in $O(|E|)$ time.

De Bruijn Sequences

Claim

For all n, De Bruijn sequences exist.

Proof.

Consider G, the De Bruijn graph. For all $v \in V(G)$,

$$\mathit{indeg}(v) = \mathit{outdeg}(v) = 2$$

Thus, G is Eulerian. □

Additional Results

- There are $2^{2^{n-1}-n}$ such circular sequences
- Considering not-circular, there are $2^{2^{n-1}}$ sequences
- There is a bijection between pairs of De Bruijn sequences, and all binary 2^n sequences.

Section 2

De novo Genome Assembly

Sequencing Is Hard

- First generation (Sanger) sequencing: Sorting Based
- Next generation sequencing: Synthesis Based

We get short k-mers, rather than long sequences.

Problem Statement

There is a model string T. Given all k-mers, estimate T.

Law of Assembly

If $\mathit{suffix}(A) = \mathit{prefix}(B)$, they might overlap.

$$ACG \cup CGT \implies ACGT$$

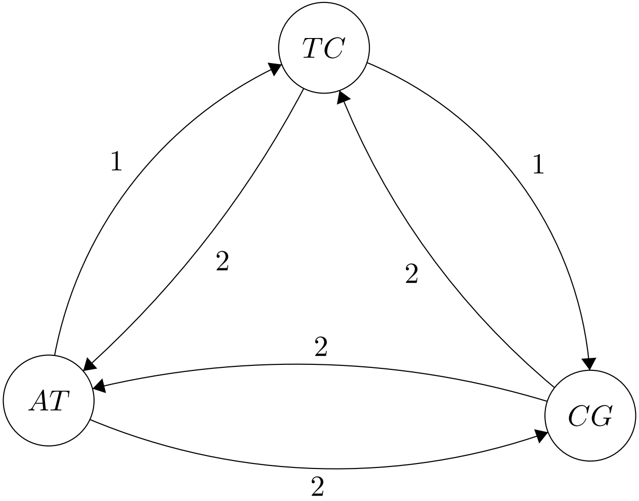
Overlap Graphs (SCS)

Form a connected graph $G = K_n$.

$$w(A, B) = \mathit{suffix}(A) = \mathit{prefix}(B)$$

We want to find the shortest common superstring.

Overlap Graphs (SCS)



Overlap Graphs (SCS)

This is the *Traveling Salesman Problem*. It is *NP-Hard*

We may approximate with greedy Nearest Neighbor. This is a $\log n$ approximation.

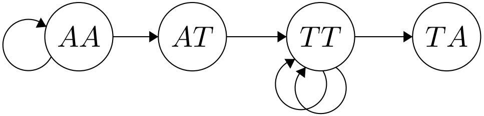
Additional Remarks

- Determining Overlaps: bloom filters
- Tandem Repeats: $AAAAA$

De Bruijn Graphs

Break all k-mers into 2 $(k-1)$-mers. Create De Bruijn graph.

If the genome is $AAATTTA$, for $k = 3$,

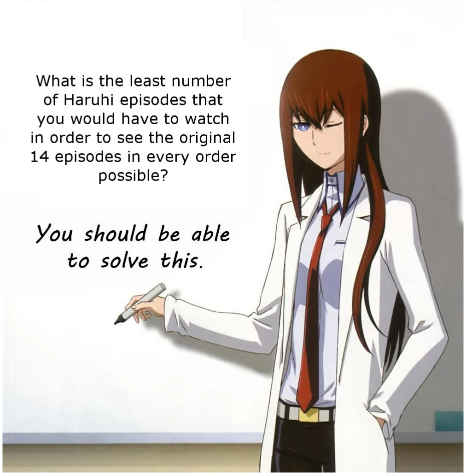


We want to find an *Eulerian Trail*.

Additional Remarks

- Unequal coverage, repeats
- Error correction,
- Bubbles, islands

Brainteaser


What is the least number of Haruhi episodes that you would have to watch in order to see the original 14 episodes in every order possible?
You should be able to solve this.

WAGA WAGA

— Sariel Har-Peled (2024)

Bibliography I

- Ben Langmea (JHU), https://www.langmead-lab.org/teaching.html
- Lionel Levine (MIT), https://pi.math.cornell.edu/~levine/18.312/