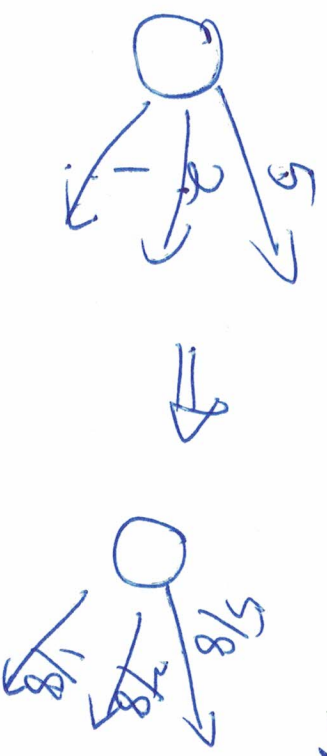


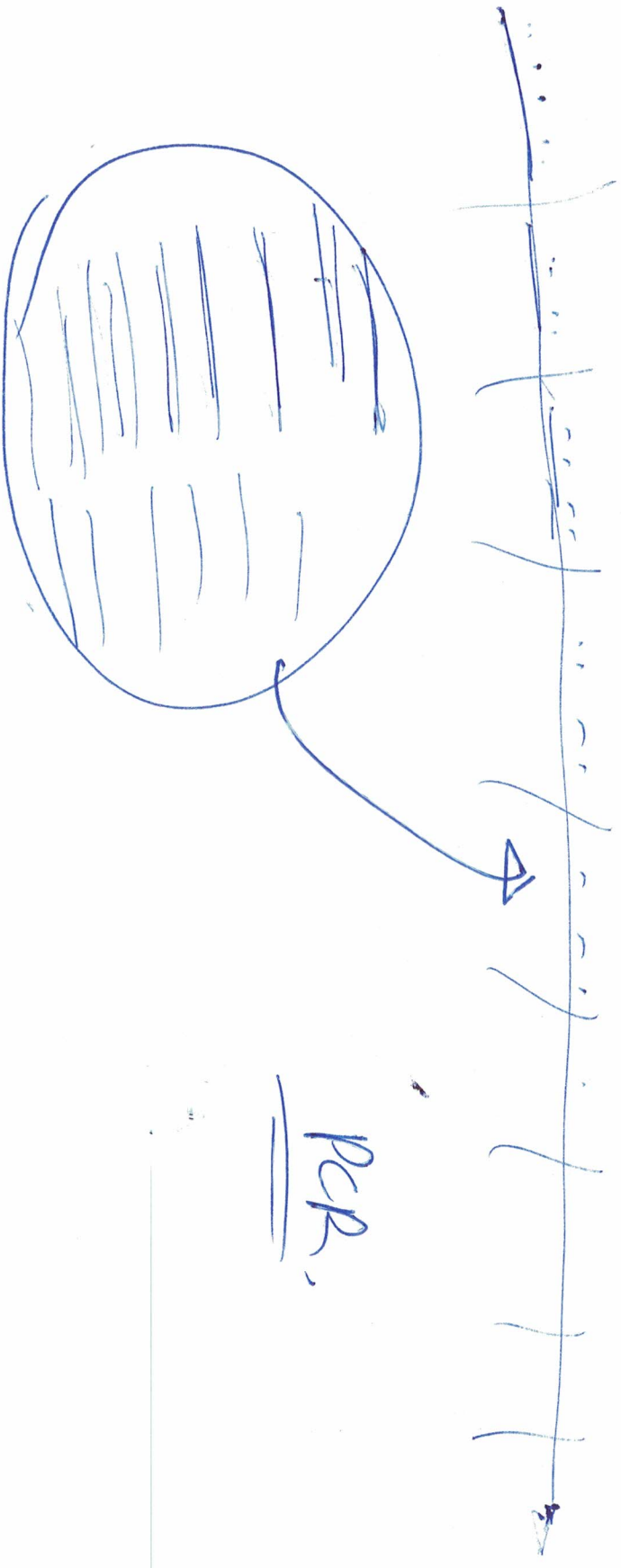
① in order to count it to Markov Chain, you put a count m to this edge, where m is the # of appearance of substring "abab" in the original sequence.

② Normalize it,

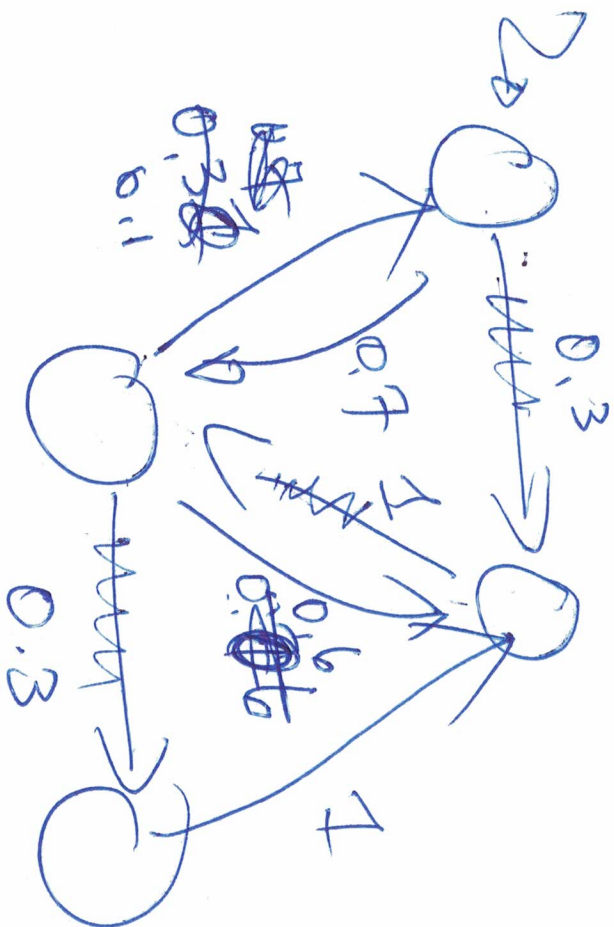


③ Use the small- ϵ trick (in Google Page Rank alg) to make the graph complete.

This de Bruijn graph can ~~also~~ also give you a way
to generate an approx. FA (with probability) from words
(sequences). (DNA assembly.)

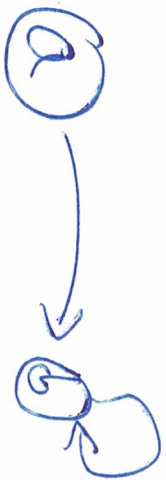


PCR.



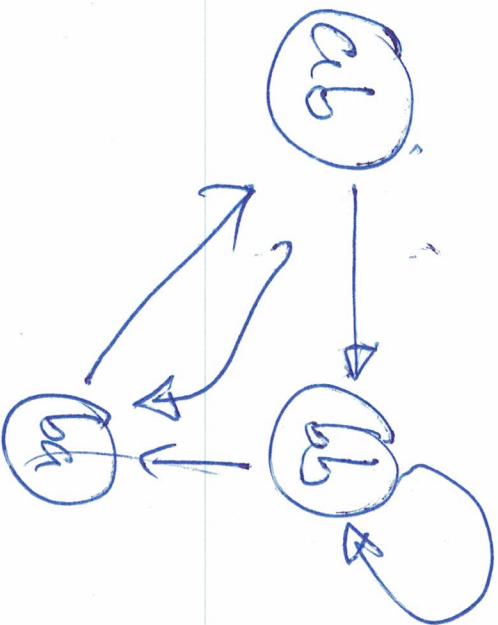
$$-\log(0.3 \cdot 1 \cdot 0.3) = \text{self-entropy}$$

a b b a b a b b a

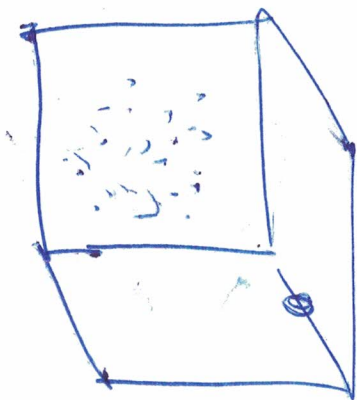


lose precision,

k=2



cofemba M.



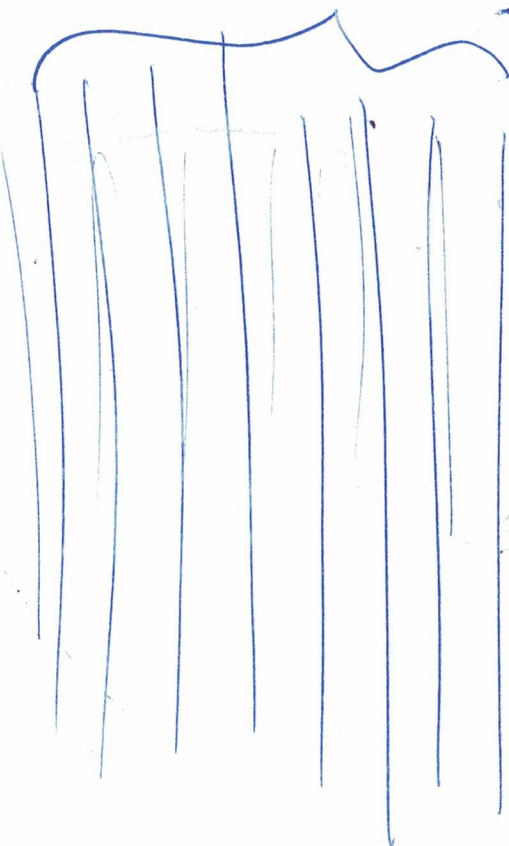
① M doesn't have spec.

② M is a blackbox, which is unchangeable

③

no no no

↓



user data

SI

④

Random int sequence?

Draw Back of de Bruijn Technique;

the sequence must be a discrete sequence
(over a finite alphabet).

Doesn't work for:

1.23 3.2 1.888 . - - -

→ need more work.

Does work for:

a b a b

fund
cur
} sector

back test

3SAT formula $F(x_1, \dots, x_m)$.

k is cover size C

Φ_C is cover iff

for each $(-v-v_-)$, at least

one of the literals in C .

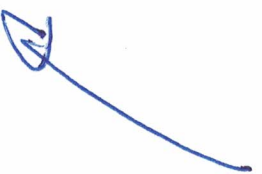
3SAT satisfiability is fixed parameter tractable in k .

\hookrightarrow Complexity $O(p(n) \cdot 2^k)$.

\hookrightarrow size of F .

F:

_____ \wedge _____ \wedge _____ \wedge _____



$(-V - V -)$

Cover C with size $|C| = k$. say $C = \{y_1, \dots, y_k\}$

↳ variables,

For each assert b_1, \dots, b_k to

$y_1, \dots, y_k,$

Check ~~if~~ F

$y_1 = b_1, \dots, y_k = b_k$

is sat, or not?

if yes, ret yes.
ret no.

This is
"SAT"

$$(F)_{y_1=b_1, \dots, y_k=b_k}$$

means to replace each var y_i in F with boolean value b_i .

Time: 2^k .

$f(n)$
 size of F .
 for solving "SAT is sat".

If you use others' ideas,

①. Cite

②. Explain clearly.