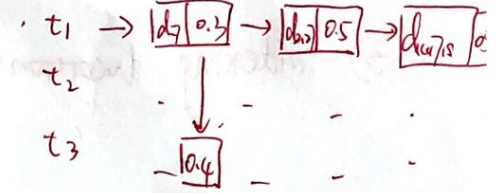


efficiency?

- space
- query pro

$q = t_1, t_2, t_3, \dots$

list



or. docs. $[d_1, d_3, \dots, d_n]$

$t_1 \rightarrow [0.3]$

t_2

$t_3 \rightarrow [0.4]$

$\sum_{t \in q} \text{nd.}$

start from term of query.

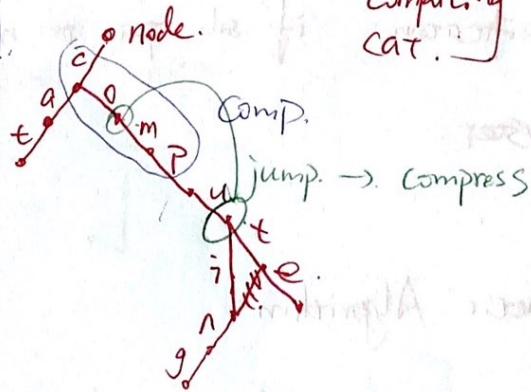
$\text{find}(t, \text{list})$

\downarrow
sorted list - $O(\log N)$.

Index?

- hashing
- B+ tree
- trie

compute computing cat.



\rightarrow parallelization: $\vec{d} \quad \vec{q}$
 (t_1, t_2, t_3, \dots)

$\rightarrow t_1 \quad t_2$

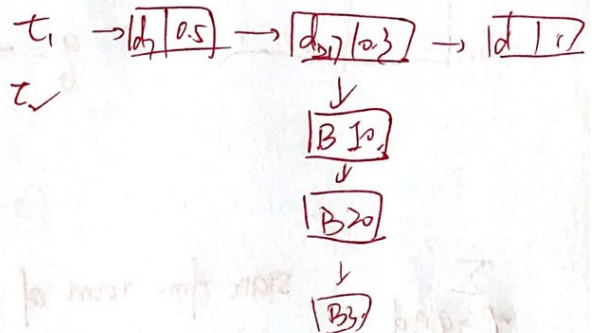
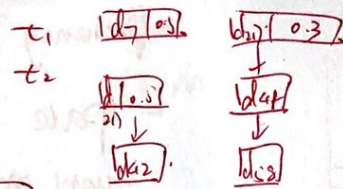
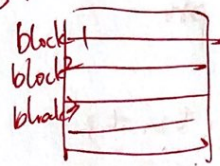
$t_1 \quad \text{NEAR} \quad t_2$
within 10 terms

run time. \leftarrow ad: not need to change index.

- look up t_1
 - look up t_2
 - intersection
 - check position
- disord: very common or very less docs will cost a lot to find one.
- 3rd-Nov IR-1

2). Index phrase.

3). indexing locations.



Or can also store the GAP between the index locations so that we can save more space.

IR: (Learning process).

classification: if sth span or not / \neq relevance or not.

cluster:

Genetic Algorithm:

Start with a random set of sols.

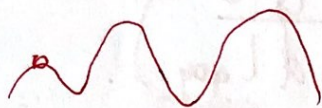
Calculate the fitness

• Disad.: will have convergence on a certain weight.

mutation: mutate operators.

df x idf.

term weighting scheme.



$T = \{ df, cf, \dots, N, V, C, \dots, 1, 10, 0.5 \}$
doc frequency cross frequency values of df, cf.

$F: \{ \dots \}$
factor operators.

There is no bias. \Rightarrow

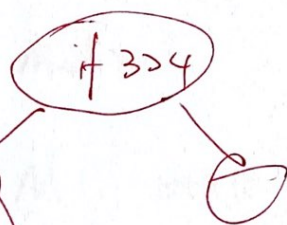
N : num of doc. cf : document frequency

df : doc frequency,

term density

$w_3 := \sqrt{\dots}$

ISSUE:



have no effect
on the whole

if tree ^{generally} too large: cut the subtree
if the fitness ^{for} is the same:
keep the shortest ^{sub} tree

IR-3.

BM 25

Pivot normalisation.

$$\sqrt{\left(\frac{d \cdot l}{d \cdot l_{avg}}\right)}.$$

There is no turning involved.

100%