Design of Web Ranking Module using Genetic Algorithm

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ABSTRACT
Crawling is a process in which web search engines collect data from the web. Focused crawling is a special type of crawling process where crawler look for information related to a predefined topic[1].In this paper a method for finding out the most relevant document among a set of documents for the given set of keyword is presented. Relevance checking is done with the help of Rogers-Tanimoto, MountFord and Baroni-Urbani/Buser similarity coefficients. The method uses genetic algorithm to show that the average similarity of documents to the query increases when Probability of mutation is taken as low and Probability of crossover is taken as high. The method does the performance analysis of different similarity coefficients on the same set of documents and applies ranking to the documents whose relevancy is highest among the three coefficients.

General Terms
Growth, retrieval, crawl, engine

Keywords
Relevancy, similarity, coefficients, genetic

1. INTRODUCTION
Design of most focused crawlers is based on the vector space model. The model is used to judge the evenness of web pages and general web search algorithms. The relevance in turn work as guide in following target links [2]. One of the most important module of search engine is ranking module. The task of ranking module is to assign some ranking score to relevant pages using some criterion. Output of ranking module is an ordered set of pages according to their rank i.e. pages with high rank are near the top of the list and low rank pages are at the bottom of the list. These pages are then presented to the user in their ranking order. A GA based approach using Rogers-Tanimoto, MountFord and Baroni-Urbani/Buser similarity coefficients is taken in this paper for ranking the retrieved documents.

2. GENETIC ALGORITHM
GAs are search algorithms that follow the concept of natural selection and genetics [3]. GA are powerful and very efficient search and optimization techniques motivated by the natural selection theory of Darwin [4].
Genetic Algorithms **[5]** are based on the principle of heredity and evolution which claims "in each generation the stronger individual survives and the weaker dies". Therefore, each new generation would contain stronger (fitter) individuals in contrast to its ancestors. The process of GA's is iteration based of constant population size of candidate solutions. In each generation/iteration each chromosome's fitness in the current population is evaluated and new population evolves. Chromosomes with higher fitness values goes through reproduction phase in which selection, crossover and mutation operators are applied to get new population. Chromosomes with lower fitness values are discarded. Again this generated new population is evaluated and selection, crossover, mutation operators are applied. This process continues until we get an optimal solution for the given problem

2.1 Fitness Evaluation
Fitness function is a function which is responsible for evaluating some value to indicate among number of solutions which one is optimum. It can also be considered as a measure of performance or fitness to show how fit is the candidate solution. The problem of IRS using GA is to retrieve documents using this fitness function. For finding the relevant document on the basis of some similarity measures we can have number of relevancy methods.

Table 1: Coefficients Used As Fitness Function In Research [6]

S.N	Cofficient Name	Similarity Formula
1.	Rogers & Tanimoto	$(p+s) / (p+2*(q+r)+s)$
2.	Baroni-Urbani/Buser	$(p+sqrt(p*s)) / (p+q+r+sqrt(p*s))$
3.	Mountford	$2*p/(2*q*r+p*q+p*r))$

For the calculation of similarity metric we define few parameters p,q,r and s as (n = p+q+r+s).

p= (x=1 and y=1) (total match)
q= (x=1 and y=0) (single match)
r= (x=0 and y=1) (single match)
s= (x=0 and y=0) (no match)
This is shown in table 2, where

Table 2: Variables Used to Calculate Binary Similarities/Dissimilarities[7,6,8]

	y=1	y=0
x=1	p=1/1 in both A and B	q=1/0 only in A
x=0	r=0/1 only in B	s=0/0 in none of A and B

Where A and B may be any query or document represented in binary form.

2.2 Selection

Once the fitness evaluation process is done next step is to perform selection operation. Process of selection operation is based on the principle of ''survival of the fittest'. Higher fitness valued chromosomes goes through reproduction. Lower fitness valued chromosomes are discarded. There are number of ways to implement this operator, but all relies on the concept that candidates with good fitness values are to be preferred over poor fitness values. The idea is to give preference to better individuals. This selection operation does the replication of candidate chromosomes with good fitness values and eliminating those with poor fitness values [9].

Individual	Fitness
A	8
B	7
C	3
D	5

Individual	Fitness
A	8
B	7
A	8
D	5

Fig 1: Selection Operator on a Population of 4 Individuals[9]

The research work uses roulette wheel selection method as selection operator [10]. It is also known as fitness proportionate selection method.

2.3 Crossover[3,11]

In the crossover operation mating of two chromosomes is performed that gives birth to two new offspring. This operation of crossover always happens with one parameter that is known as probability of crossover (ProC). When ProC is say 0.8 it means only 80% of the total population goes for crossover operation. Rests 20% chromosomes remain abstain from this operation and has no effect of crossover. Motive behind performing crossover operation is to explore new solutions and exploit use of old solutions. GA forms an optimum solution by mating two fit chromosomes together. Chromosomes with higher fitness will always have good selection probability then others with lower fitness values, thus a good solution moves from one generation to next generation

One point crossover (crossover point 7)

Doc1	1	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0
Doc2	0	0	1	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	1

After crossover

Doc1	1	0	1	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	1
Doc2	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0

Fig 2: Single Point Crossover Explained

2.4 Mutation[3,11]

Mutation involves changing one bit of a chromosome from 0 to 1 or viceversa. This is performed under the constraint parameter called probability of mutation (ProM). For example if ProM is 0.10 then 10% genes of total chromosomes will go for mutation. The concept of mutation is based on this natural theory that varying breeds are possible only by varying gene values. After this operation fitness quality of new chromosomes may be high or low then old ones. In case new chromosomes are poor then old ones they are removed during selection process. The motive behind mutation is regaining the lost and discovering varying breeds. For example: randomly mutate chromosome at position 5

Doc1	1	0	1	0	0	0	1	0	1	0	0	1	0	0	0	0	0	1	0	0	0

After mutation (bit number 5 is mutated i.e. bit is negated)

Doc1	0	0	1	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1

Fig 3: Mutation Operation Explained

3. RESEARCH TOOLS

This section is about the introduction of tools which helped us to find the top keywords from relevant document. These keywords actually used for making the chromosomes; backbone of GA in which the research implementation work was carried out. We discuss a brief introduction of tools Text Analyzer and Keyword Density Checker. Both the tools were used to find out top most keywords present on webpage with highest frequency.

3.7.1 Textalyser

Textalyser[12] is tool for analyzing text or website online. The tool can be used for calculating detailed statistics of text like frequency of top occurring words in text or webpage etc. The tool has good application for translation purpose and webmasters for ranking webpages, for simply normal users to know about top keywords from a text. Using this tool keyword density can be easily found out. Further relative importance of word or expressions can also be found out. Webmasters can use this tool for the analysis of the links on their pages.

3.7.2 Keyword Density Checker

The keyword density checker tool [13] is an online tool which can be used for finding density of top occurred keywords. These keywords are then displayed at the top . Input to the tool can be URL only against both URL and text for textalyser tool. The tool crawls the given URL , bring out words normally as done by search engine , remove punctuations and return result in the form of density of the top URL keywords in the form of keyword cloud.
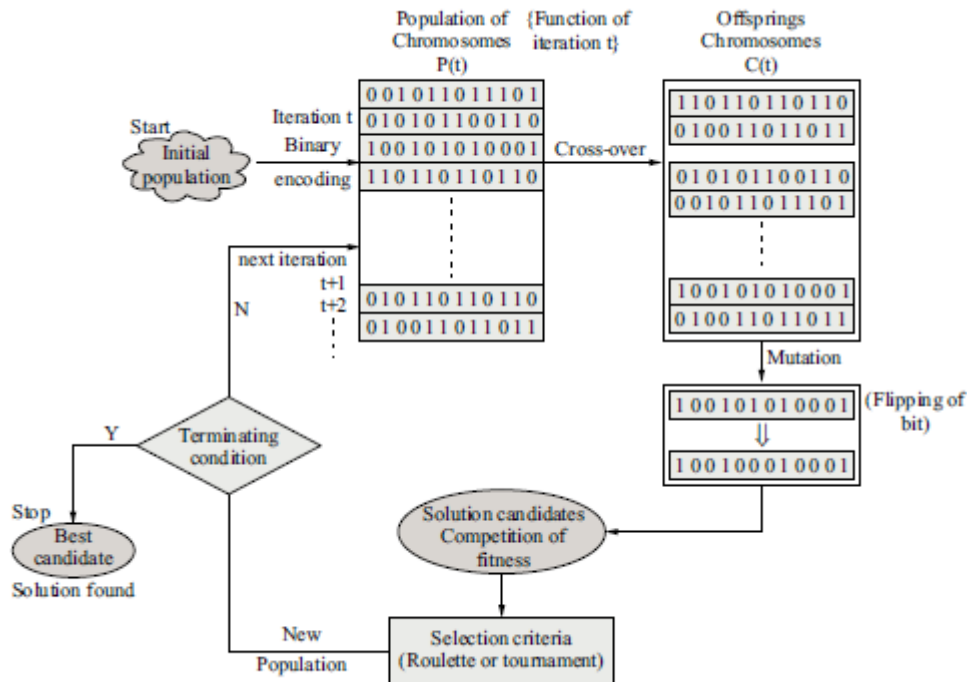.

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Fig 4: Basic Operation of Genetic Algorithm[14]

4. EXPERIMENTAL SETUP & RESULTS

In general the web documents are encoded in strings of 0's and 1's as shown in the figure 1. The documents have been obtained using some search query. The set of documents also contains some non relevant documents too. In the experimental setup of GA 50 documents have been retrieved for each different query. This set of 50 documents serves as document database. The query is also encoded in terms of string of 0 and 1. Process of experiment is as follows:

i. Query is input to the Google search engine.
ii. Top frequent keywords of each retrieved document are extracted using Textalyser or Keyword Density Checker online tool as discussed in chapter 3 and making list of keywords.
iii. Generate initial population by encoding retrieved documents to chromosomes for each query.
iv. Initial population now consists of these encoded documents. Pass this initial population to GA algorithm.
v. Either some maximum generation or some predefined fitness value is not achieved repeat step 4. At the end of this step we get an optimized document for retrieval.
vi. Optimized document chromosome can be decoded and document can be retrieved from stored documents related to each query.
vii. Rank the documents on the basis of fitness value as obtained in step 4.

4.1 Experimentation

The research work conducted the tests for 15 different queries and 30 documents for each query. The experimentation tests for all 15 queries with RT, MF and BUB coefficients chosen as fitness function. A complete MATLAB code has been written with roulette wheel selection operator, random point crossover with different rates of crossover and mutation. Experiment conducted with various GA parameters as :

probability of crossover ProC = 0.7, 0.8 and 0.9 along with probability of mutation (ProM =0.01, 0.10, 0.30) to do performance analysis of this GA based retrieval system. The efficiency parameter is average relevance. Average relevance from three fitness functions are compared and best combination for crossover and mutation probability for any one among three similarity function is selected as best . Using this best selected similarity function the document's rank before and after the algorithm are checked and new ranks to document are assigned. The retrieval process now retrieves documents using this new ranking scheme.

Table 3: Queries Used in Research Work

S.N	Chromosome Length	Keywords
1.	33	Delhi, Gang, Rape, Case
2.	39	Bomb, Blast, Boston, Marathon
3.	37	Search ,Engine, Optimization,Seo
4.	49	Anna, Hazare, Anti, Corruption
5.	53	Osama, Bin, Laden, Death, Killed
6.	47	Stock, Market, Mutual, Fund
7.	55	Fiber, Optic, Information, Technology
8.	66	Health, Medicine, Medical,Disease
9.	44	Artificial,Intelligence,Neural, Network

| 10.	40	Rajasthan, Royals,Amity,University
11.	49	Remote, Method, Invocation, RMI
12.	61	Gang, Rape, Kangaroo, Court
13.	69	Aam, Aadmi, Party, Arvind, Kejriwal
14.	50	Genetic,Algorithms,Optimization, Techniques
15.	64	Search, Engine, Web, Crawler

4.2 Results

In this section we show the results in tabular and graphical form for all three similarity coefficients viz. RT, MF and BUB. We vary probability of mutation ProM from 0.01 to 0.10 and 0.30 and keep ProC=0.5, 0.7 and 0.9 for all the values of ProM. Keeping together ProC and ProM we get total nine possible combinations for checking the performance of said similarity coefficients on retrieved documents. Out of nine possible results we got best was for ProC=0.9 and ProM=0.1. Tables and figures for rest eight combinations have not been shown.

Table 4: Maximum Average Relevancy with ProC = 0.9 and ProM = 0.01

|	ProC=0.9		ProM=0.01
	RT	MF	BUB
Query1	0.6309	0.2948	0.6141
Query2	0.5442	0.2307	0.5446
Query3	0.5729	0.1871	0.5462
Query4	0.5541	0.1503	0.4695
Query5	0.5381	0.1258	0.4509
Query6	0.5348	0.1337	0.4702
Query7	0.5462	0.1182	0.4507
Query8	0.5268	0.088	0.4113
Query9	0.5852	0.1666	0.5198
Query10	0.5838	0.2001	0.5171
Query11	0.5604	0.1356	0.4397
Query12	0.5294	0.0848	0.4641
Query13	0.5345	0.0815	0.4241
Query14	0.5552	0.1457	0.4808
Query15	0.4987	0.088	0.4518

Further it was observed that best average maximum fitness is given by Rogers-Tanimoto coefficient. Figure plotted using the above table is shown in Fig 4
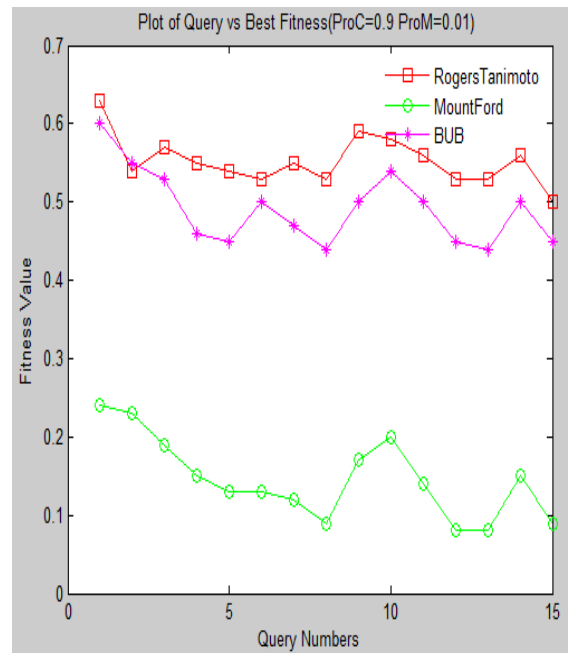
Fig 5:Query vs best fitness for ProC=0.9,ProM=0.01 using RT,MF and BUB

4.3 Ranking of Documents

To rank the documents using GA on the basis of fitness obtained using RT for the above parameters of GA for all queries, we run the MATLAB code for a fixed number of generations for RT and obtain the fitness values for each documents. The documents are ranked on the basis of this obtained fitness values. We show this only for first query Q1={ Delhi, Gang, Rape, Case} in table . The hyperlinks for each of the documents are not shown in fact we name them as Di (i=1 to 30).
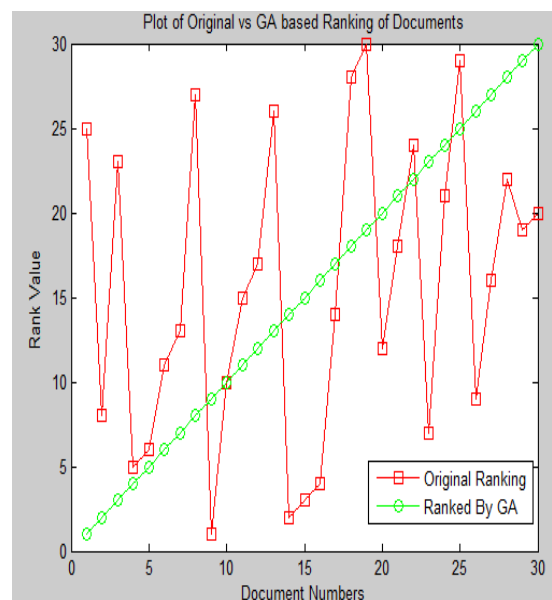
Fig 6: Comparative ranking of Original and GA based using RT similarity coefficient

Table 5: New and Old Ranking of Documents Using GA and % increase /Decrease

Docs	Original Ranking	New Ranking	%Increase / Decrease in Ranking
Doc 1	25	1	80
Doc 2	8	2	20
Doc 3	23	3	66.67
Doc 4	5	4	3.33
Doc 5	6	5	3.33
Doc 6	11	6	16.67
Doc 7	13	7	20
Doc 8	27	8	63.33
Doc 9	1	9	-26.67
Doc 10	10	10	0
Doc 11	15	11	13.33
Doc 12	17	12	16.67
Doc 13	26	13	43.33
Doc 14	2	14	-40
Doc 15	3	15	-40
Doc 16	4	16	-40
Doc 17	14	17	-10
Doc 18	28	18	33.33
Doc 19	30	19	36.67
Doc 20	12	20	-26.67
Doc 21	18	21	-10
Doc 22	24	22	6.67
Doc 23	7	23	-53.33
Doc 24	21	24	-10
Doc 25	29	25	13.33
Doc 26	9	26	-56.67
Doc 27	16	27	-36.67
Doc 28	22	28	-20
Doc 29	19	29	-33.33
Doc 30	20	30	-33.33

The comparison of old and new rankings and percentage improvement is shown graphically in the figures below:
The figure 4.23 and 4.24 shows that document having rank 25 has got new rank 1 and percentage improvement in rank is 80. Similarly another document having old rank as 8 has moved to new rank 2 and got 20 % increment in rank because of our applied GA with RT.

We have also checked online by opening pages with new rank and they were providing the good result as required by the corresponding query. Similar type of work was carried out for other queries and their related documents but as not to extend the length of this research paper we have provided ranking table and figure only for one query.
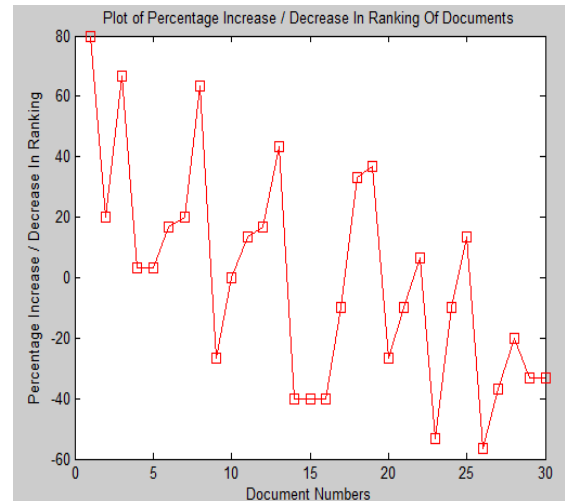
Fig 7: Percentage Increase/Decrease in Ranking of Documents

6. CONCLUSION
The research work has calculated average maximum fitness value using RT, BUB and MF similarity coefficients. In the work ProC and ProM was varied from 0.7-0.9 and {0.01, 0.10, 0.30} respectively. It has been shown that average relevancy of retrieved document increases when PC is increased and ProM is decreased. Using the best average fitness value among RT, MF and BUB the research work applies new ranking to retrieved documents. The goal was to design the web ranking module using genetic algorithm and focused crawling and good results are a manifest to this research work. In this way searching has been made easy, so more relevant document or web pages can be retrieved easily. Results show that average relevance of document increased up to 63%. In this way if focused crawler have key set with more relevancy then the retrieved data is more relevant for local collection of a search engine which improves the crawling performance.

7. REFERENCES
[1]. B. Novak "A Survey Of Focused Web Crawling Algorithms", Proceedings of SIKDD, pp. 55–58, 12-15 Oct 2004.

[2]. http://www.wikipedia.org/Web_Crawler

[3] B.Klabbankoh, O.Pinngern. "applied genetic algorithms in information retrieval" Proceeding of IEEE ,pp.702-711,Nov 2004

[4] S.S.Satya and P.Simon, "Review on Applicability of Genetic Algorithm to Web Search," International Journal of Computer Theory and Engineering, vol. 1, no. 4, pp. 450-455, 2009.

[5] Shokouhi, M.; Chubak, P.; Raeesy, Z " Enhancing focused crawling with genetic algorithms"Vol: 4-6, pp.503-508,2005.

[6]www.sequentix.de/gelquest/help/distance_measures.htm

[7] V.Consonni and R. Todeschini ,"New Similarity Coefficients for Binary Data", Communications in Mathematical and in Computer Chemistry, pp.581-592, 2012

[8] H.Wolda, "Similarity Indices, Sample Size and Diversity", OecoIogia-Springer-Verlag ,pp. 296-302,1981

[9] M.A.Kauser, M. Nasar, S.K.Singh, "A Detailed Study on Information Retrieval using Genetic Algorithm", Journal of Industrial and Intelligent Information vol. 1, no. 3, pp.122-127 Sep 2013.

[10]http://en.wikipedia/wiki/Fitness_Proportionate_Selection

[11] J.R. Koza, " Survey Of Genetic Algorithms And Genetic Programming", Proceedings of the Wescon, pp.589-595,1995

[12] http://textalyser.net/

[13]http://www.webconfs.com/keyword-density-checker.php.

[14] V.Thada, V.Jaglan, "Use of Genetic Algorithm in Web Information Retrieval", International Journal of Emerging Technologies in Computational and Applied Sciences, vol.7,no.3,pp.278-281, Feb,2014