Chapter 6

DRACoR: A Multi-level Fusion Based Collaborator Recommender System

"In nature we never see anything isolated, but everything in connection with something else [· · ·]"

-Jahann wolfgang von Goethe (1749-1832)

6.1 Introduction

In academia, researchers collaborate with their peers to improve the quality of research and thereby enhance academic profiles. However, information overload in big scholarly data poses a challenge in identifying potential researchers for fruitful collaboration. In this article, we introduce a multi-level fusion based model for collaborator recommendation, DRACoR (Deep learning and Random walk based Academic Collaborator Recommender).

DRACoR fuses deep learning and biased random walk model to provide the recommendation for potential collaborators that share similar research interests at the peer level. We run a topic model on abstracts and Doc2Vec on titles on year-wise publications to capture dynamic research interests of researchers. Author-author cosine similarity is computed from the feature vectors extracted from abstracts and titles and is then used to weigh edges in the author-author graph (AAG). We also aggregate various meta-path features with profile-aware features in order to bias the random walk behavior. Finally,

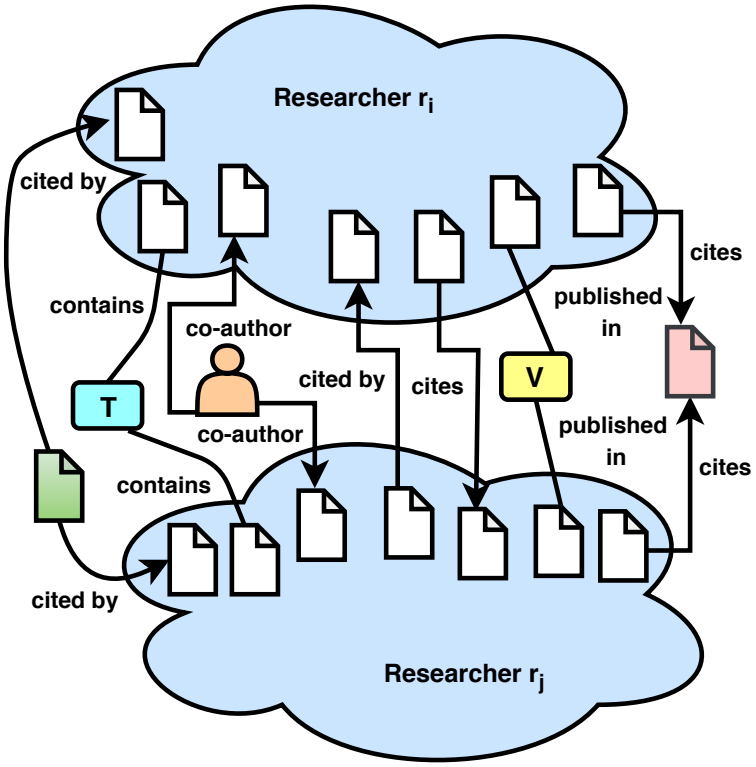


Figure 6.1: Graphical representation of SIN graph. P_main paper is the paper written by either of the disparate researchers under study and latent metapaths between P_main papers may be formed via various vertices types: cited by P_main (P_ref), cites a P_main (P_cite), researcher (R), term (T), and venue (V).

we employ a random walk with restart(RWR) to recommend top N collaborators where the edge weights are used to bias the random walker's behavior.

6.2 Problem Statement and Other Definitions

Academic collaboration recommendation is different from traditional social recommendation. In addition to similar research interests, academic collaboration is also governed by the accessibility of the collaborator and other scholarly influence-aware features. In this segment, we exhibited the problem description and discussed various notations and terminology. A heterogeneous network is a special kind of information network, which either contains multiple types of objects or multiple types of links.

Definition 10 *Heterogeneous Information Network (HIN) [173, 174]. It is defined as a graph* $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ *with a node type mapping function* $\delta : \mathcal{V} \rightarrow \mathcal{A}$ *and a link type mapping*

function $\mu : \mathcal{E} \rightarrow \mathcal{R}$. Each node $v \in \mathcal{V}$ belongs to one particular node type in the node type set $\mathcal{A}$: $\delta(v) \in \mathcal{A}$, and each link $e \in \mathcal{E}$ belongs to a particular link type in the link type set $\mathcal{R}$: $\mu(e) \in \mathcal{R}$. Here both type of nodes $\mathcal{A}$ and type of edges $\mathcal{R}$ depend on the domain in question. Note that both $|\mathcal{A}| > 1$ and $|\mathcal{R}| > 1$.

Due to the complexity of HIN and also to understand the node types and link types clearly in the network, meta level (schema-level) description is provided. So the concept of network schema is proposed to describe the meta structure of a network [175].

Definition 11 *(HIN Schema) [173]. The HIN schema denoted as $\mathcal{S} = (\mathcal{A}, \mathcal{R})$, is a meta template for an information network $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ with a node type mapping function $\delta : \mathcal{V} \rightarrow \mathcal{A}$ and a link type mapping function $\mu : \mathcal{E} \rightarrow \mathcal{R}$, which is a directed graph defined over node types $\mathcal{A}$ and type of edges $\mathcal{R}$.*

Definition 12 *Scholarly Information Network (SIN) [176]. SIN graph is an instance of HIN. Here both type of nodes $\mathcal{A}$ and type of edges $\mathcal{R}$ are related to a scholarly network (academia).*

Example. In a SIN, $\mathcal{A}$ can be either authors, papers, publication venues, terms etc. Similarly, type of links $\mathcal{R}$ can be any type of relations between a pair of members in $\mathcal{A}$ like paper-paper, author-author, paper-author, paper-venue, author-venue, paper-terms, author-terms, venue-terms etc. In Fig. 6.1, we show graphical representation of a SIN with all of its vertices types and their relationship. Here we have six type of nodes $\mathcal{A}$, such that $\mathcal{A} = P\_main \cup P\_ref \cup P\_cite \cup R \cup T \cup V$ and seven type of links $\mathcal{R}$ (Table 6.2). The meaning of each type of node is defined in Table 6.1. P_main paper is the paper written by either of the disparate researchers under study. In Fig. 6.1, P_main papers are those papers written by either researcher r_i or researcher r_j or both. P_ref denotes the set of papers cited by a P_main paper whereas P_cite indicates to a set of papers that cite at least a P_main paper.

Definition 13 *Co-authorship Networks (CN) [83]. Let $G_a = (V_a, E_a)$ be the original co-authorship bibliographic network, with l authors. $V = \{r_1, r_2, \cdots, r_l\}$. Each edge $e = (r_i, r_j) \in E$ represents a co-authorship of r_i with r_j in one or more papers.*

Definition 14 *Author-Author Graph (AAG). Let $G' = (V', E')$ be the newly generated author-author graph (AAG) from SIN based on the similarity score of abstract and title.*

Table 6.1: Type of vertices used in SIN

No.	Vertices Type
1	P_main={set of papers written by a researcher}
2	P_ref= {set of papers cited by a P_main paper}
3	P_cite= {set of papers that cites a P_main paper}
4	R (researcher)= {authors of P_main, P_cite, P_ref}
5	T (term)={terms appearing in P_main papers}
6	V (venue) = { Venues of P_main papers}

Table 6.2: Type of edges used in SIN

No.	Edges Type
1	$n_1 \xrightarrow{written\_by} n_2 : \delta(n_1) \in \{P\_main, P\_ref, P\_cite\}, \delta(n_2) = R, n_1, n_2 \in N$
2	$n_1 \xrightarrow{published\_by} n_2 : \delta(n_1) \in \{P\_main, P\_ref, P\_cite\}, \delta(n_2) = V, n_1, n_2 \in N$
3	$n_1 \xrightarrow{contains} n_2 : \delta(n_1) \in \{P\_main, P\_ref, P\_cite\}, \delta(n_2) = T, n_1, n_2 \in N$
4	$n_1 \xrightarrow{cites} n_2 : \delta(n_1) \in \{P_main\}, \delta(n_2) =P_ref, n_1, n_2 \in N$
5	$n_1 \xrightarrow{cited_by} n_2 : \delta(n_1) \in \{P_main\}, \delta(n_2) =P_cite, n_1, n_2 \in N$
6	$n_1 \xrightarrow{cites} n_2 : \delta(n_1) \in \{P_main\}, \delta(n_2) =P_main, n_1, n_2 \in N$
7	$n_1 \xrightarrow{cited_by} n_2 : \delta(n_1) \in \{P_main\}, \delta(n_2) =P_main, n_1, n_2 \in N$

$V' = \{r_1, r_2, \cdots, r_l\}$. *Each edge* $e = (r_i, r_j) \in E'$ *represents a currently similar research interest of* r_i *with* r_j *based on their past publications. There is an edge* $e = (r_i, r_j) \in E'$ *exists if the similarity score among researcher* r_i *and* r_j *is greater than average similarity score. We weight the edges of the network AAG using content similarity (linear combination of abstract and title) in order to provide a single score as explained in Sec.* 6.5.

Example. In Fig. 6.1, there will be an edge (r_i,r_j) that exists between researcher r_i and researcher r_j if their similarity score will be greater than the average similarity score. In AAG there will be only one type of nodes $\mathcal{A}$ researcher (researcher associated with only P_main).

In AAG, two researchers can be connected via different semantic paths, which are called meta-paths.

Definition 15 *Meta-path [201]. A meta-path* $\mathcal{M}$ *is a path defined on the SIN graph introduced in Sec. 12 . It joins two or more vertices using one or more edges such that* $\mathcal{M} = n_1 \xrightarrow{l_1} n_2 \xrightarrow{l_2} ... \xrightarrow{l_t} n_{t+1}$, *where the starting and ending vertices are of same vertex type* P_main, $\delta(n_1) = \delta(n_{t+1})$ *and both belong to* P_main, $P\_main \in \mathcal{A}$, $\mu(l_1, l_2, ..., l_t) \in \mathcal{R}$.

Example. In Fig. 6.1, There will be a meta path between researcher r_i and researcher r_j via the meta path $r_i \overset{writes}{\rightarrow} P\_main \overset{citedby}{\rightarrow} P\_cite \overset{cites}{\rightarrow} P\_main \overset{writtenby}{\rightarrow} r_j$.

Definition 16 *Random Walk [178]. A random walk is defined as a node sequence* $S_r = \{r_1, r_2, r_3, \cdots, r_l\}$ *wherein the i-th node* r_i *in the walk is randomly selected from the neighbors of its predecessor* r_{i-1}.

Definition 17 *Collaborator Recommendation. Given a set M of m target researchers* $M = \{r_1, r_2, \cdots, r_m\}$,$(m << l)$, *the collaborator recommendation task is to recommend a list of potential collaborators* $K_i = \{r_{i1}, r_{i2}, ..., r_{in}\}$, $(r_{ij} \in V')$ *related to each target researcher* r_i *where the list is in decreasing order of relevance* $(K_i \subset V')$.

A collaborator recommendation problem is essentially a link prediction problem. In an author-author graph (AAG) for a pair of researchers (r_i, r_j), predict whether the node pair can collaborate in the near future (irrespective of the fact whether the pair collaborated earlier or not). However, we are more interested in predicting new collaborators (co-authors) in addition to the existing ones, to the target researcher.

6.3 The Functional Architecture of DRACoR

We propose DRACoR comprised of two blocks: Block-I and Block-II as depicted in Fig. 6.2. To reduce computational overhead and to make it independent and autonomous target researchers, particularly Block-I is developed once for the entire dataset. Later on, we will utilize the target researcher as an input to interact with Block-II to extract meaningful recommendations from both the MRCR model and DBCR model. We present a layered architecture where each layer realizes a specialized task. The system contains four essential layers, where Layer-1 to Layer-3 associated with Block-I and the rest Layer-4 goes under the classification of Block-II. Four essential layers are portrayed as given underneath:

(i) *D*ata Preprocessing **(Layer-1)**: This step aims to structure the dataset into a formal model for processing. Mainly it is used for faster extraction of researcher-year wise, relevant papers for further use **(BLOCK I)**.

(ii) *F*eature Representation Layer **(Layer-2)**: This layer is mainly introduced to extract current research interest by computing Author2Vec approach and also to transform

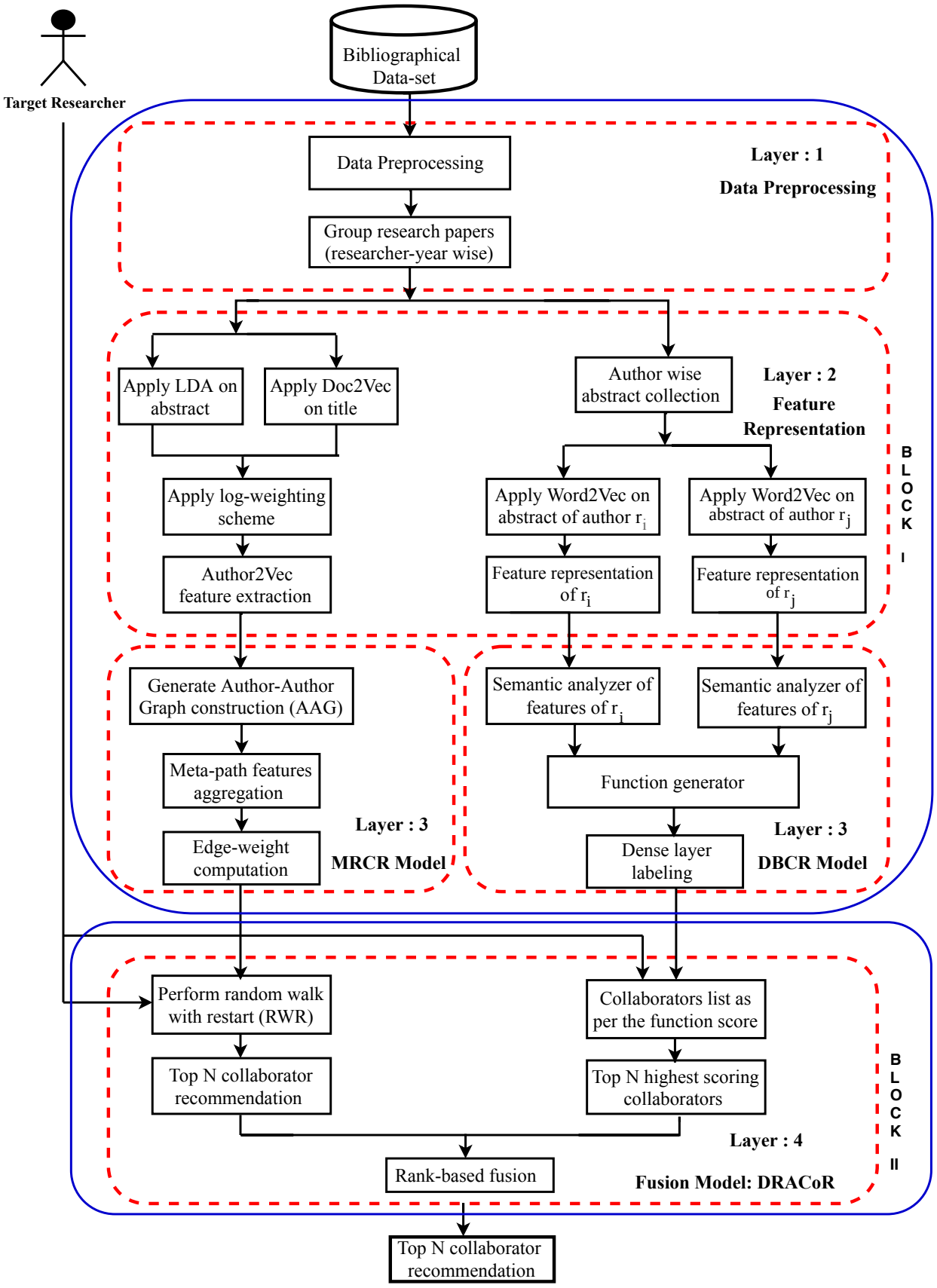


Figure 6.2: Functional architecture of DRACoR

raw data (words in abstract) to a meaningful alignment of word vectors in the embedding space of each researcher by Word2Vec approach **(BLOCK I)**.

(iii) *M*RCR Model **(Layer-3)**: This model improves the performance of basic random walk based approach by exploiting meta-path features such as previous publication content, citations, co-citations and other similarity (venue, co-author and term) and scholarly influence-aware features such as percentage of collaboration and level similarity in order to recommend MPC collaborators **(BLOCK I)**.

(iv) *D*BCR Model **(Layer-3)**: To reflect the semantics such as interesting topics shared by two researchers and furthermore to capture hidden relationship among them, LSTM model based deep learning architecture is incorporated. It utilized previous publications content as word embedding layer and meta-path features are exploited to set dense layer labeling among researchers to recommend highly personalized MVC collaborators **(BLOCK I)**.

(v) *F*usion Model **(Layer-4)**: To provide a diversified personalized recommendation, the MRCR model and DBCR are utilized to firstly make predictions individually and later on a fusion model is applied to integrate the strengths of both the models and to reduce their weaknesses. The outcome acquired from these two models is fused by the standardized Borda count method. We propose this fusion model as DRACoR **(BLOCK II)**.

6.4 Data Preprocessing Layer (Layer-1)

This step plans to structure the dataset into a formal model for preprocessing. Fundamentally, it is utilized for faster extraction of relevant papers. In the DBLP-citation-network V10 [1] dataset, there were 3,079,007 rows and 7 columns. After dropping all the Nan (not a number) values, we left with 2,408,010 rows. We drop all the rows which were left blank in the references column as it will create unnecessary hindrance during training. Similarly, we preprocessed the hep-th (Theoretical High Energy Particle Physics) dataset provided by KDD Cup 2003 [2]. After data preprocessing as above, we get 1,922 concurrent authors

[1]https://aminer.org/citation

[2]https://www.cs.cornell.edu/projects/kddcup/datasets.html

from 20,961 publications. We have split the authors into different columns with the paper information, and we now have a separate row for authors of every paper. Finally, we removed all the noise in abstracts to get the experimental dataset. The detail statistics and data collection of DBLP and hep-th are described in Sec. 2.7.2.

6.5 Feature Representation Layer (Layer-2)

Generally, the abstract provides a summary containing the main idea of a paper. We use the LDA model on the abstract to generate the feature description [132]. LDA is used for automatically identifying topics and to derive hidden patterns exhibited by a text corpus. We have chosen LDA over other methods to discover coherent topics and their distribution in the abstract. Doc2Vec is used to extract the feature description from the title of a paper as Doc2Vec captures contextual information of words occurring in titles [179]. It is mainly used to generate sentence/document embeddings [180]. It is chosen over other methods due to its potential to overcome the weaknesses such as the ordering of words, semantic of the words, data sparsity, and high dimensionality in bag-of-words models.

The feature extraction for DBCR model is based on a trained Word2Vec skip-gram model with negative sampling, which uses the dataset made using abstracts as the training dataset. The core idea behind Word2Vec is this, a model that is able to predict a given word, given neighboring words, or vice versa, predict neighboring words for a given word is likely to capture the contextual meanings of words very well. The reason to adopt skip gram model are:

(i) Skip-gram model can capture the semantics for a single word.

(ii) Generally skip-gram with negative sub-sampling outperforms every other methods.

6.5.1 Topic Distribution of Research Interest

We cluster the abstract of publications for each researcher. To measure a researcher's dynamic research interest, we first build academic documents for each researcher by joining the abstract of the researcher's publication in each year by space. Therefore, for each researcher, we get a set of documents corresponding to each year. Then, we run the LDA model with a special parameter k on the generated documents set which contains the

documents from all researchers. The parameter k represents the clustered topic number in LDA. The LDA gives the probability distribution of a researcher's interest over k topics in each year. We treat this as a feature vector of length k.

We follow a similar procedure with publication titles as well. Doc2Vec is used to extract feature vectors from titles in this work [202]. In this work, vector length for Doc2Vec and LDA have been kept the same to reduce the number of parameters in preliminary experimentation and can be tuned separately in future works.

6.5.2 Researcher's Interest Variation with Time

Topic distribution of abstract and title embeddings in recent years can describe the current research interest of a researcher more accurately. Hence, to capture the dynamic research interest, we propose a weighted addition of vectors that we get after LDA and Doc2Vec. The vectors in recent years are given more weight, and the weight decays in the decreasing order of the years. For each author, we have two sets of vectors: one from LDA on year-wise abstracts and the other from Doc2Vec on year-wise titles.

The results from LDA and Doc2Vec can be considered as two sets of vectors. L_i^r represents the vector of year-wise topic distribution vectors and D_i^r represents the vector of year-wise title embeddings vectors as depicted in Eqn. 6.1 and Eqn. 6.2. The years considered are 2000, 2001, ..., 2012. Each year-wise vector is again a vector of k different topics as given in Eqn. 6.6 and Eqn. 6.7.

$$\boldsymbol{L}_i^r = [L_{2000i}^r, L_{2001i}^r, \cdots, L_{2012i}^r] \tag{6.1}$$

$$\boldsymbol{D}_i^r = [D_{2000i}^r, D_{2001i}^r, \cdots, D_{2012i}^r] \tag{6.2}$$

Now, we employ a weighted addition of vectors from each set to get one vector for abstract similarity and one vector for title similarity. We use inverse log-weighting to give more weight to the current year vectors, and the weight reduces in the decreasing order of the years. For each researcher r_i, we get a vector A_i^r for abstract similarity and vector T_i^r for title similarity.

$$\boldsymbol{A}_i^r = \sum_{y_i \in Y} \frac{L_{y_i}^r}{log_2(y_o - y_i + 2)}, \text{ and} \tag{6.3}$$

$$\boldsymbol{T}_i^r = \sum_{y_i \in Y} \frac{D_{y_i}^r}{log_2(y_o - y_i + 2)} \text{ where} \tag{6.4}$$

Table 6.3: Research topic distribution of researcher r_i

Year	$Topic_1$	$Topic_2$	$Topic_3$	$Topic_4$	$Topic_5$
2008	0.1	0.2	0.5	0	0.2
2009	0.4	0.2	0.3	0.1	0
2010	0.3	0.1	0.2	0.2	0.2
2011	0.1	0.3	0.1	0.3	0.2
2012	0	0.1	0.3	0.3	0.3

Table 6.4: Weighted score of topic distribution of researcher r_i

Year	$Topic_1$	$Topic_2$	$Topic_3$	$Topic_4$	$Topic_5$
2008	0.03	0.07	0.19	0	0.07
2009	0.17	0.08	0.12	0.04	0
2010	0.15	0.05	0.1	0.1	0.1
2011	0.06	0.18	0.06	0.18	0.12
2012	0	0.1	0.3	0.3	0.3

$$Y = \{2000, \cdots, 2012\} \text{ and } y_o \text{ is the latest year in } Y. \tag{6.5}$$

$$L^r_{y_i} = [a_{1i}, a_{2i}, \ldots, a_{ki}] \tag{6.6}$$

$$D^r_{y_i} = [a_{1i}, a_{2i}, \ldots, a_{ki}] \tag{6.7}$$

Using A^r_i and T^r_i for a researcher r_i, we compute cosine similarity with their counterpart from the seed paper (r_j) as discussed in next section Author2Vec edge weighting.

Example: Table 6.3 shows the topic distributions for five topics of researcher r_i and Table 6.4 shows the topic distribution after the log weighting scheme has been applied to each year. Eqn. 6.8 shows the topic distribution vector of researcher r_i in year 2009. The vector after inverse log-weight has been applied is depicted in Eqn. 6.9.

$$A^r_{2009k} = [0.4, 0.2, 0.3, 0.1, 0] \tag{6.8}$$

$$\frac{A^r_{2009k}}{log_2(5)} = [0.17, 0.08, 0.12, 0.04, 0] \tag{6.9}$$

Furthermore, we adopt a weighted addition of vectors to obtain the final vector as mentioned in Table 6.4. The final vector A_i for researcher r_i after weighted addition will be:

$$A^r_i = [0.41, 0.48, 0.77, 0.62, 0.59] \tag{6.10}$$

If we had applied a simple vector addition without any weights, we would have got a vector $A_i^{r\prime}$ as:

$$A_i^{r\prime} = [0.9, 0.9, 1.4, 0.9, 0.9] \tag{6.11}$$

We can clearly see the difference between A_i^r and $A_i^{r\prime}$. It clearly indicates the influence of topic distribution vector of recent year 2012 in the calculation of A_i^r where as in $A_i^{r\prime}$, all the year wise vectors contribute equally. Furthermore, researcher-researcher similarity is done among venues exploiting their corresponding weighted vector A_i^r and T_i^r respectively.

6.5.3 Author2Vec Edge Weighting

Using A_i and T_i for a researcher r_i, we compute cosine similarity between any two researchers. We get two cosine similarities, $Sim_a(r_i, r_j)$ and $Sim_t(r_i, r_j)$, for a pair of researchers, r_i and r_j, using (A_i, A_j) and (T_i, T_j) respectively.

$$Sim_a(r_i, r_j) = \frac{\boldsymbol{A_i^r . A_j^r}}{|\boldsymbol{A_i^r}||\boldsymbol{A_j^r}|} = \frac{\sum_{b=1}^{k}(a_{b,i} * a_{b,j})}{\sqrt{\sum_{b=1}^{k} a_{b,i}^2} * \sqrt{\sum_{b=1}^{k} a_{b,j}^2}} \tag{6.12}$$

$$Sim_t(r_i, r_j) = \frac{\boldsymbol{T_i^r . T_j^r}}{|\boldsymbol{T_i^r}||\boldsymbol{T_j^r}|} = \frac{\sum_{b=1}^{k}(t_{b,i} * t_{b,j})}{\sqrt{\sum_{b=1}^{k} t_{b,i}^2} * \sqrt{\sum_{b=1}^{k} t_{b,j}^2}} \tag{6.13}$$

Now we utilize these two similarity metrics to get one final metric, $Sim(r_i, r_j)$ with the help of an adjustment parameter m as:

$$Sim(r_i, r_j) = m * Sim_a(r_i, r_j) + (1 - m) * Sim_t(r_i, r_j) \tag{6.14}$$

where $m \in [0, 1]$. We consider these similarity scores as contextual similarity features (CSF). The influence of m is discussed in Sec. 6.9.5. Note that, we can use the above similarity score $Sim(r_i, r_j)$ to create the AAG and also to compute the edge-weight among researchers.

6.6 The Architecture of MRCR Model (Layer-3)

The process of MRCR model mainly consists of four steps.

(i) Generation of Author-Author Graph (AAG)

(ii) Meta-path Features Aggregation (MPF)

(iii) Scholarly Influence-aware Features (SIF)

(iv) Recommendation of biased RWR model

We are attempting to discover inherent community structures in an Author-Author Graph (AAG) to understand the network more profoundly and reveal interesting concept shared among researchers.

Table 6.5: Meta-paths used in DRACoR model

No.	Meta-path	Description
1.	*common_author*	Core researcher's share an author (R)
2.	*common_venue*	Core researcher's share a venue (V)
3.	*common_term*	Core researcher's share a term (T)
4.	*direct_cites*	Core researcher cites a paper written by core researcher (P_{main})
5.	*direct_cited_by*	Paper written by a core researcher cited by a core researcher (P_{main})
6.	*citation_paper*	Core researcher's share a reference (P_{ref})
7.	*co_citation_paper*	Papers written by core researcher's co-cited together (P_{cite})

6.6.1 Generation of Author-Author Graph (AAG)

In this section, we will create a homogeneous undirected Author-Author Graph (AAG) from SIN graph in order to recommend relevant collaborators for a target researcher. We define this graph as an undirected graph $G' = (V', E')$ as defined in Definition 14. AAG is a type of SIN with a node type mapping function δ and an link type mapping function μ as defined in Definition 10. Here, we have one types of vertex V' for each researcher. V'=$\{$set of researchers associated with P_main papers$\}$. The type of edge E' is defined as: $v'_1 \xrightarrow{connects} v'_2 : \delta(v'_1), \delta(v'_2) \in \{P\_main\}, v'_1, v'_2 \in V'$. It joins two researchers using only one type of link edge such that $v'_1 \xrightarrow{e'_1} v'_2$, where $\mu(e'_1) \in E'$.

Computation of Edge-weight of AAG

After creating the Author-Author Graph (AAG), we need to compute the edge-weight among researchers in AAG. Initially, CSF score $Sim(r_i, r_j)$ as computed in Sec. 6.5.3 among researchers (pairwise) is used to create the AAG graph. The average CSF score is used as a threshold to create an edge between researchers. There is no edge that exists with less than average CSF score found among researchers. Initially, this score is used to

recommend top N collaborators for a target researcher. This approach is purely content-based so-called TBRec model, and we will use it as a baseline in Sec. 6.9. Further, we have calculated the combined weighted score $CWS(r_i, r_j)$ between any two researchers r_i and r_j by integrating both Meta-path features (MPF) and Scholarly Influence-Aware features (SIF).

Combining Different Meta-path Features into AAG

Since meta-paths are mostly composite relations of various links type in a SIN graph, they can capture the various relationship between SIN nodes [177]. We assume that a meta-path connects two different P_main papers x, y, which are written by two disjoint core researchers r_i, and r_j, respectively.

We observe that meta-path features with more than two degrees are not much meaningful in our work and are not able to create much difference to compute the similarity among researchers. To reduce the time complexity and to obtain a tightly coupled relationship among researchers, only one-degree[3], and two-degree meta-path features are incorporated into this MRCR model.

6.6.2 Meta-path Features (MPF)

Table 6.5 lists all types of meta-paths defined in our model. We are extracting the researcher of P_main and considering as a core researcher in order to maintain a homogeneous AAG graph. The following kinds of similarity scores are exploited in order to compute the meta-path features (MPF).

(i) Co-author Similarity (C_S)

(ii) Term Similarity (T_S)

(iii) Venue Similarity (V_S)

(iv) Direct Citation Based Similarity (DC_S)

(v) Co-citation Based similarity (CC_S)

[3]The degree of a meta-path indicates its length and the distance between two main papers (P_main).

The calculation of these above scores is elucidated in the later sections. We use this cumulative score of the $sim(r_i, r_j)$ to bias the behavior of the random walk such that it will more easily traverse to positive collaborators in the AAG graph. Finally, we generated a list of recommended potential collaborators after the random walk converges.

Computing Meta-path Edge Weights as Features

In order to discover the latent association between researchers, we have divided the above seven meta-paths as depicted in Table 6.5, into the following categories of edge weighting.

(i) Co-author Similarity (C_S): We observe that if two researchers have a similar co-authors profile, it makes it easy for researchers to connect. We consider the co-authors profile C_i of a researcher r_i as a vector of length L, equal to the total number of authors. Each dimension of the vector represents an author. The value of C_i at jth index will be 1 if r_i and r_j have worked in the past where r_j represents the author at dimension j and zero if they haven't. Index i represents author r_i, and the value at index i for C_i is kept 1.

We calculate the co-author similarity between two authors r_i and r_j by calculating the cosine of the angle between C_i and C_j. Therefore, we can write the co-author similarity $sim_{C_S}(r_i, r_j)$, between r_i and r_j as:

$$sim_{C_S}(r_i, r_j) = \frac{\sum_{l=1}^{L}(C_{i,l} * C_{j,l})}{\sqrt{\sum_{l=1}^{L} C_{i,l}^2} * \sqrt{\sum_{l=1}^{L} C_{j,l}^2}} \tag{6.15}$$

In reality, none of the similarity scores among two researchers will get a perfect score of 1 and also random walk is sensitive to higher probability score. To avoid such issue, normalization of data within a uniform range (e.g., (0-1)) is essential to prevent larger applies to the output variables. One way is to scale input and output variables (z) in the interval $[\rho_1, \rho_1]$ corresponding to the range of the transfer function [186]. Before adding any individual meta-path score into the model, we are individually applying the normalization to be in the range of [0.1-0.95] as shown in Eqn. 6.16.

$$z_i = \rho_1 + (\rho_2 - \rho_1)\frac{(x_i - x_i^{min})}{(x_i^{max} - x_i^{min})} \tag{6.16}$$

where z_i is the normalized value of x_i, and x_i^{max} and x_i^{min} are the maximum and minimum values of x_i in the database.

Algorithm 8: Pseudo-code of MRCR model

Input: The AAG Graph with $V' = \{r_1, r_2, \cdots, r_l\}$; a given target reseacher r_i

Output: Top N recommended list of collaborators

Initialize Q based on a given target researcher r_i

$R_0 \leftarrow$ Q

Initialize NumIteration

Initialize MinDelta for break

$Sim(r_i, r_j)$, $Avg\_Similarity$=0

for $i \leftarrow 0$ **to** $|r_l| - 1$ **do**

  for $j \leftarrow 0$ **to** $|r_l| - 1$ **do**

    if *(i==j)* **then**

      $Sim(r_i, r_j) \leftarrow 0$

    else

      Compute $Sim(r_i, r_j)$ by using Eqn. 6.14

      $Avg\_Similarity \leftarrow Avg\_Similarity + Sim(r_i, r_j)$

    end

  end

end

$Avg\_Similarity \leftarrow \frac{Avg\_Similarity}{|r_l| * (|r_l| - 1)}$

for $i \leftarrow 0$ **to** $|r_l| - 1$ **do**

  for $j \leftarrow 0$ **to** $|r_l| - 1$ **do**

    if $Sim(r_i, r_j) > Avg\_Similarity$ **then**

      Create an edge (r_i, r_j) among r_i and r_j in AAG

    else

      Discard the edge (r_i, r_j) from AAG

    end

  end

end

foreach *edge* (r_i, r_j) *in AAG* **do**

  Compute $CWS_{MPF}(r_i, r_j)$ by using Eqn. 6.23

  Compute $CWS_{SIF}(r_i, r_j)$ by using Eqn. 6.27

  Compute $CWS(r_i, r_j)$ by using Eqn. 6.28

end

foreach *neighbor* $N(r_i)$ *of target researcher* r_i **do**

  Compute w_{r_i, r_j}(edge weight) by using Eqn. 6.30

  $S_{i,j} = w_{r_i, r_j}$

end

for $k \leftarrow 0$ **to** $NumIteration - 1$ **do**

  difference=0

  for $i \leftarrow 0$ **to** $len(Q) - 1$ **do**

    $R_{k_i} = \alpha \sum_{j=o}^{len(Q)-1} S_{i,j} R_j + (1\text{-}\alpha) Q_i$

    difference=difference+$(R_{k_i}\text{-}R_{k-1_i})$

  end

  if *(difference* $<$ *MinDelta)* **then**

    break

  end

end

Sort collaborators in the decreasing order of their ranking scores

Prepare the final list of top N collaborators for r_i

After applying this normalization, we will get a normalized $sim_{C_S}(r_i, r_j)$ score $sim'_{C_S}(r_i, r_j)$ among two researchers r_i and r_j.

(ii) Venue Similarity (V_S): Venue plays a crucial role in the collaboration of two researchers. When the researchers publish at the same venue, it implies that the research areas are the same. Also, there is a chance that they met at the venue and this might result in their future collaboration with each other. To calculate the venue similarity, we followed a similar approach as Eqn. 6.15. After applying the normalization defined in Eqn. 4.27, we will get a normalized $sim_{V_S}(r_i, r_j)$ score $sim'_{V_S}(r_i, r_j)$ among two researchers r_i and r_j.

(iii) Term Similarity (T_S): Term appearing in titles or abstracts of a P_main paper after stop word removal and stemming are taken into consideration for this similarity computation. We use snowball stemmer to get the root words [151]. Jaccard similarity coefficient [159] is used to calculate $sim_{T_S}(r_i, r_j)$(Eqn. 6.17). Here set E and F denote sample terms occur in all abstracts and titles published by researchers r_i and r_j respectively.

$$sim_{T_S}(r_i, r_j) = \frac{|E \cap F|}{|E \cup F|} \tag{6.17}$$

where $0 \leq J(E, F) \leq 1$. After applying the normalization defined in Eqn. 4.27, we will get a normalized $sim_{T_S}(r_i, r_j)$ score $sim'_{T_S}(r_i, r_j)$ among two researchers r_i and r_j.

(iv) Direct citation based similarity (DC_S): It is experimentally observed that, if two researchers are citing each other very frequently then there is a very high probability that they will work together again. So, we are calculating the number of times they co-cited each other and give the weight-age to the researcher-researcher links. We have used meta-paths such as direct cites and direct cited-by to compute the similarity among researchers. The computation of edge weighting of DC_S is defined below:

$$sim_{DC_S}(r_i, r_j) = Count_1(r_i \rightarrow r_j) + Count_2(r_j \rightarrow r_i) \tag{6.18}$$

where $Count_1(r_i \rightarrow r_j)$ is the number of times author r_i cites a set of papers written by author r_j and vice versa. After applying the normalization defined in Eqn. 4.27, we will get a normalized $sim_{DC_S}(r_i, r_j)$ score $sim'_{DC_S}(r_i, r_j)$ among two researchers r_i and r_j.

(v) Co-citation based similarity (CC_S): It is experimentally observed that, if two researchers get co-cited by some other paper then there is a very high probability that they can work in the future as their research area might be the same. Similarly, if two researchers are frequently citing common papers, they may work in the future as their research area might be the same. We have used meta-paths features such as co-cites and co-cited-by to compute the similarity among authors. The computation of edge weighting of CC_S is defined below:

$$sim_{CC_S}(r_i, r_j) = Sum_1(r_i, r_j \rightarrow p_i) + Sum_2(p_j \rightarrow r_i, r_j) \tag{6.19}$$

where $Sum_1(v_i \rightarrow v_j)$ is the number of times set of papers belongs to a particular venue, v_i cites a set of papers which are also cited by the set of papers belongs to venue v_j and vice versa. After applying the normalization defined in Eqn. 4.27, we will get a normalized $sim_{CC_S}(r_i, r_j)$ score $sim'_{CC_S}(r_i, r_j)$ among two researchers r_i and r_j.

The link weight between any two researchers will be computed through the addition of link weighting scores discussed above. We add each meta-path features into the model and will analyze their effect on the recommendation quality. We already have initial edge weighting score CSF, which is computed by log-weighting based abstract and title similarity as computed in Eqn. 6.14. It was purely based on the contextual similarity. After applying the normalization defined in Eqn. 6.16, we will get a normalized CSF score $CSF^{'}(r_i, r_j)$ among two researchers r_i and r_j. Initially the recommendation will be provided on the basis of this normalized score.

$$CWS(r_i, r_j) = CSF'(r_i, r_j) \tag{6.20}$$

MPF-based Combined Weighted Score $CWS_{MPF}(r_i, r_j)$

We need to combine individual meta-path scores into the model, and we call it as the combined weighted score (CWS) as depicted in Eqn. 6.23 to use it as a probability score between researchers in AAG graph as computed using Eqn. 6.30 to apply random walk with restart.

$$CWS_{CF}(r_i, r_j) = sim'_{C_S}(r_i, r_j) + sim'_{T_S}(r_i, r_j) + sim'_{V_S}(r_i, r_j) \tag{6.21}$$

$$CWS_{OF}(r_i, r_j) = sim'_{DC_S}(r_i, r_j) + sim'_{CC_S}(r_i, r_j) \tag{6.22}$$

$$CWS_{MPF}(r_i, r_j) = CWS_{CF}(r_i, r_j) + CWS_{OF}(r_i, r_j) \tag{6.23}$$

In addition to normalized CSF score obtained in Eqn. 6.20, all normalized scores obtained from Eqn. 6.15, score obtained from normalized venue similarity (V_S), Eqn. 6.17, Eqn. 6.18, and Eqn. 6.19 are added to obtain the meta-path based combined weighted score $CWS_{MPF}(r_i, r_j)$.

6.6.3 Scholarly Influence-aware Features (SIF)

To discover the patterns in researcher association over time and to get the latent association between researchers. Specifically, we have explored a few scholarly influence-aware features. The following scholarly influence-aware features are taken into consideration.

(i) Percentage of collaboration (PC_S)

(ii) H-Index based level similarity (L_S)

Percentage of Collaboration

How frequently a researcher collaborates with another researcher can also indicate the likelihood of collaboration shortly. Moreover, a researcher with whom an author has frequently collaborated can lead to collaboration with other researchers as well. Our idea is that a researcher's frequently collaborated co-authors can play a role in his/her future collaborations.

Let the total number of publications of author r_i be m and the total number of publications of author r_j be n. The number of publications they have in common be p. Then, we define the percentage of collaboration $sim_p(r_i, r_j)$ between r_i and r_j as:

$$sim_{PC_S}(r_i, r_j) = \frac{p}{m} + \frac{p}{n} \tag{6.24}$$

$$= p\big(\frac{1}{m} + \frac{1}{n}\big) \tag{6.25}$$

Observe that the first term in Eqn. 6.24, represents the fraction of the publications that r_i shares with r_j .i.e., p out of all the publications of r_i .i.e., m and analogously, the second term represents the fraction of the publications that r_j shares with r_i .i.e., p out of all the publications of r_j .i.e., n. After applying the normalization defined in Eqn. 4.27, we will get a normalized $sim_{PC_S}(r_i, r_j)$ score $sim'_{PC_S}(r_i, r_j)$ among two researchers r_i and r_j.

H-Index Based Level Similarity (L_S)

Normally, researchers having the same academic level imply future collaboration. We have calculated the level similarity among two researchers by using two parameters:

(i) Number of citations

(ii) H-index with individual citations

The level similarity is calculated using the formula:

$$sim_{L_S}(r_i, r_j) = \frac{min(h_i, h_j)}{\sum_{k=1}^{min(h_i,h_j)} \log_2 (|C_{i_k} - C_{j_k}| + 2)} \tag{6.26}$$

Here L_S represents Level similarity between two authors r_i and r_j having h-index h_i and h_j respectively. The C_{i_k} and C_{j_k} are the citations of Author r_i and Author r_j of k_{th} paper when papers are sorted in decreasing order of their citations. After applying the normalization defined in Eqn. 4.27, we will get a normalized $sim_{L_S}(r_i, r_j)$ score $sim'_{L_S}(r_i, r_j)$ among two researchers r_i and r_j.

SIF-based Combined Weighted Score $CWS_{SIF}(r_i, r_j)$

We need to combine cholarly influence-aware features (SIF) based similarity scores into the model, and we call it as combined weighted score $CWS_{SIF}(r_i, r_j)$ as depicted in Eqn. 6.27 to use it as a probability score between researchers in AAG graph as computed using Eqn. 6.30 to apply random walk with restart.

$$CWS_{SIF}(r_i, r_j) = sim'_{PC_S}(r_i, r_j) + sim'_{L_S}(r_i, r_j) \tag{6.27}$$

As we mentioned earlier, individual scores mentioned above are normalized before computing the combined weighted score as described in Eqn. 4.27.

Cumulative Combined Weighted Score $CWS(r_i, r_j)$

In addition to $CWS_{MPF}(r_i, r_j)$ score $CWS_{SIF}(r_i, r_j)$ scores are added to obtain the final CWS(r_i, r_j) in order to enhance the probability of recommending relevant collaborators during recommendation.

$$CWS(r_i, r_j) = CWS_{MPF}(r_i, r_j) + CWS_{SIF}(r_i, r_j) \tag{6.28}$$

6.6.4 Recommendation of MRCR Model

To exploit both collaboration network information along with publication content, we employ a popular network-based approach known as a random walk with restart (RWR). The pseudo-code of the MRCR model is given in Algo. 8.

Random Walk with Restart (RWR)

RWR provides a good way to measure how closely related two nodes are in a graph [187]. The core equation of the RWR model is shown in Eqn. 6.29.

$$R^{(t+1)} = \alpha \mathbf{S} R^{(t)} + (1 - \alpha) Q \tag{6.29}$$

where $\mathbf{S}$ is the transfer matrix, representing the probability for each node to jump to other nodes. $R^{(t)}$ is the rank score vector at step t and Q is the initial vector of the form $(0, , \cdots, 1, \cdots, 0)$.

We use the weighted combined score (CWS) found after aggregating various meta-path features and scholarly influence-aware features in Eqn. 6.28, to bias the walker towards researchers with higher content as well as semantic similarity. Each entries $S_{i,j}$ in S is the transition probability for each researcher r_i in AAG skipping to next researcher r_j. It can be computed as edge weight w_{r_i,r_j} as shown in the equation below:

$$w_{r_i,r_j} = \frac{CWS(r_i, r_j)}{\sum_{r_x \in N(r_i)} CWS(r_i, r_x)} \tag{6.30}$$

where $N(r_i)$ is set of neighbors who have incoming links from r_i.

Initially, the rank score of the target node is 1, while others are 0. Initially, the vector Q is initialized to $R^{(0)}$, α is the damping coefficient. With probability $(1 - \alpha)$, walker restarts from the start node. RWR is an iterative process. After certain iterations, $R^{(t)}$ converges to a steady-state probability vector. We use $R^{(t+1)}$ researcher-rank score vector to give our final top N recommendation.

6.7 The Architecture of DBCR Model (Layer-3)

In this section, we introduce the basics of RNNs and LSTMs and provide the details of our proposed model based on deep learning to provide a diversified personalized collaborator recommendation.

6.7.1 Basics of RNNs and LSTMs

Recurrent Neural Networks are the state of the art algorithm for sequential data. In RNN, the information cycles through a loop. It decides by considering the current input and also what it has learned from the inputs it received before. Mathematically, Recurrent Neural networks can be expressed as:

$$L^{(t)} = g(L^{(t-1)}, c^{(t)}, \alpha) \tag{6.31}$$

where $L^{(t)}$ represents the state of the RNN at timestep t which equals the application of transformation g applied considering the state of RNN at timestep $(t-1)$, the current input $c^{(t)}$ and the network parameter α which are shared through each timestep t = 1,2,$\cdots$,T. As a result, RNNs takes into account the current input and also what it has learned from the inputs it received earlier, as well.

LSTMs enable RNNs to memorize their inputs over a long interval of time. This is because LSTMs contain their information in a memory, that is much like the computers memory because the LSTM can read, write and delete information from its memory. Fig. 2.3 describes the computational graph of LSTM at time step t. In this article, we will show how LSTMs will be used to learn embeddings for the textual content describing the items recommended by the content based recommender system. The optimization objective of the skip-gram model is to maximize the following log-likelihood function:

$$L = \sum_{w \epsilon C} logP(context(w)|w) \tag{6.32}$$

The key point is to construct and calculate the conditional probability function $P(context(w)|w)$. For skip-gram model, given the central word w, we need to predict the words in context(w). Most of the parameter for Word2Vec is taken as default value except for the vector size which is set to be a relatively larger value so that the proposed model can take the entire sentence as context while training a word of the sentence.

6.7.2 Label Selection

In the case of a collaborator recommender system, there are no user ratings, unlike other content-based recommender systems. In a supervised deep learning-based recommender system, we have to give the label so that the model can learn the training parameters.

To achieve this, we have taken various parameters by history among researchers. The features used here are similar to the features adopted in the MRCR model except for content similarity, which is as follows:

(i) Venue similarity (V_S)

(ii) Direct citation based similarity (DC_S)

(iii) Co-citation based similarity (CC_S)

(iv) Percentage of collaboration(PC_S)

(v) H-Index based level similarity(L_S)

Calculation of these above mentioned features has been shown in the Sec. 6.6.2. Individual scores mentioned above are normalized before computing the $S(r_i, r_j)$ by Eqn. 4.27. So this normalized $S(r_i, r_j)$ is considered as the label for the DBCR model.

$$S(r_i, r_j) = V_S + DC_S + CC_S + PC_S + L_S \tag{6.33}$$

6.7.3 Proposed Architecture

The architecture of DBCR model is shown in Fig. 6.3. This architecture can predict a score S(r_i,r_j) to define the probability that the pair of authors r_i and r_j will collaborate in the future. Briefly, this approach is based on two different word embeddings for two different authors.

This word embeddings can jointly learn continuous vector representations for a pair of authors $r_i \in R$ and $r_j \in R$ that are used to feed a classifier which generates the score which is a probability of their future collaboration. Overall, the proposed architecture consisting of the following six layers:

(i) **Embedding Layer**: Generates the matrix associated with author's content from trained Word2Vec model.

(ii) **LSTM Layer**: An RNN network with LSTM units.

(iii) **Mean Pooling Layer**: Calculates the mean of the input vectors.

(iv) **Concatenation Layer**: Concatenates the input vectors.

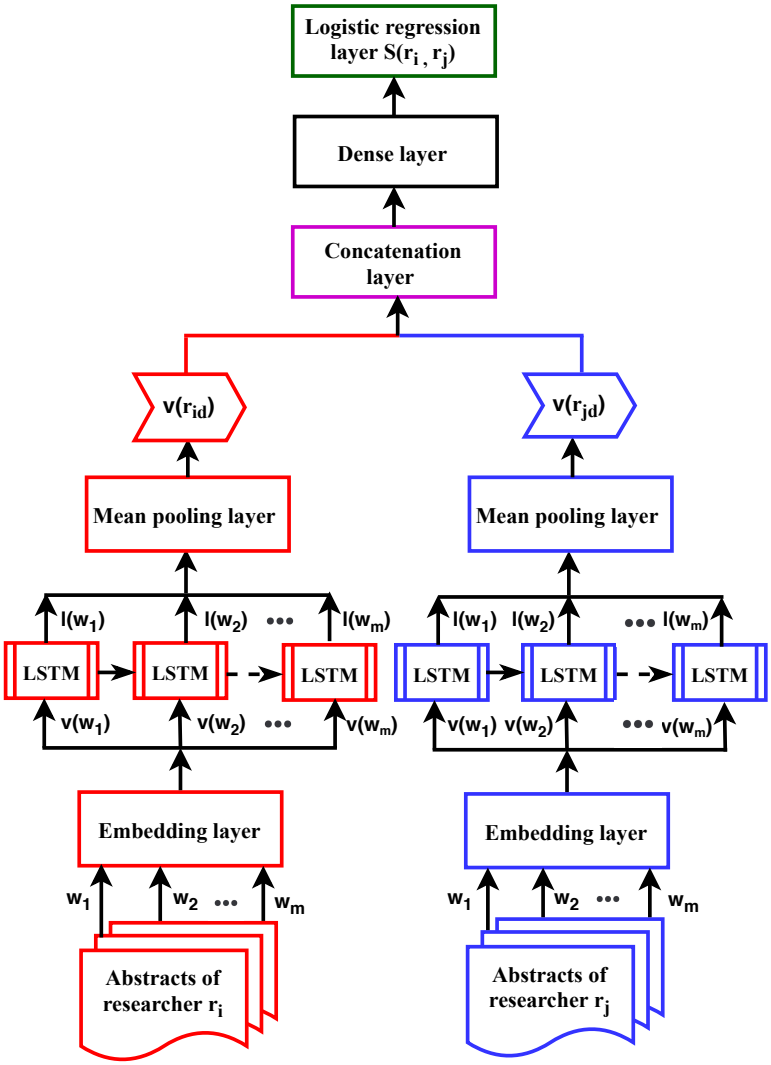


Figure 6.3: The architecture of DBCR model

(v) **Dense Layer**: Deep Neural network with hidden layers.

(vi) **Logistic Regression Layer**: Exploits logistic regression to calculate the score for the pair of authors.

Embedding Layer

An important component of DBCR model is the embedding layer, which generates the dense representations of its input. This is our input layer through which abstracts $w_1, w_2, w_3, \cdots, w_m$ of the papers written by authors are passed. It will generate the matrix associated with the author's content from the trained Word2Vec model. Word-embedding techniques help extract information from the pattern and occurrence of words to decode the context of the words, thereby providing more relevant and important features to the

model. Given a set of elements R, each of them can be represented as an x-dimensional vector contained in a $E \in \mathbb{R}^{|R| \times x}$ embedding matrix generated using Word2Vec. Each pair of authors is given in input to an embedding layer, which generates an x-dimensional author embedding E.

LSTM Layer

This layer contains a RNN network with a few LSTM units. After getting the word embedding matrix, each word representations are sequentially passed through a Long Short Term Memory(LSTM) network with t hidden units which generate for each of them a t-dimensional latent representation L using a LSTM cell. The objective of LSTM mode is to capture the word sequence information and semantic information of each word representation that are useful to generate the latent representation. Here, LSTM model is used to capture the long-term temporal dependencies and the positional relation of features along with significant global features from each obtained word representation. As stated in the introduction, several works already showed that LSTM could overcome shallow models. Moreover, we chose LSTM since such networks are very effective when sequences of input have to be shaped.

Given that the textual description of the input can be easily viewed as a sequence of words, it was straightforward for us to investigate the adoption of LSTMs in a content-based recommendation scenario. We have used tanh as activation function in LSTM. The tanh activation function is defined as:

$$f(x) = tanh(x) = \frac{e^x - e^{-x}}{e^x + e^{-x}} \tag{6.34}$$

We have used sigmoid as recurrent activation in LSTM. The sigmoid activation function is defined as:

$$f(x) = \frac{1}{1 + e^{-x}} \tag{6.35}$$

Mean Pooling Layer

In recurrent-neural-network-based models, pooling is often used to aggregate hidden states at different time steps (i.e., words in a sentence) to obtain sentence embedding. It is used to compress our features to lower fidelity. A mean-pool layer compresses by taking the mean activation in a block. It calculates the mean of the input vectors. After the latent

representation are computed by the LSTM network, the item embedding $E(i)$ is obtained by a mean pooling layer which averages the latent representations $\mathrm{l}(w_k)$ for all the words in the textual description of the item. $\mathrm{M} \in \mathbb{R}^{L*S}$ is the input matrix for mean pooling layer.

The pooling layer has two hyperparameters, the spatial extent of the filter f and the stride s. It takes M, an input volume of size mx (x is the size of the vector generated by Word2Vec) and provides an output volume of size $\bar{m}\bar{x}$ (where $\bar{m} = \frac{m-f}{s+1}$, and $\bar{x} = \frac{x-f}{s+1}$). The pooling layer operates by defining a window of size f*f and reducing the data within this window to a single value which is the average of all values in case of mean pooling layer. The window is moved by s positions after each operation, and the reduction is repeated at each position of the window until the entire activation volume is spatially reduced.

Concatenation Layer

This layer mainly concatenates the input vectors resulting after mean pooling layer. We have specifically used this layer to compare them using a deep neural network. The resulting vectors $v(i)$ and $v(j)$ of the pair of authors respectively are then concatenated through a concatenation layer [here $v(i)$ stands for $v(r_i)$ and vice versa].

Dense Layer

Dense layer is used to compare the feature vectors after Concatenation. Also, the dimensionality of this output until now does not equal to the dimensionality of the desired target. This layer consists of deep neural network with hidden layers. The resulting $(t_i + t_j)$-dimensional feature vector is given as input to the dense layers to generate the functions to find the relation between them. We have used sigmoid as activation in the dense layer.

Logistic Regression Layer

Exploits logistic regression to calculate the score for the pair of authors. Finally, it is passed through the logistic regression layer to predict the score $\mathrm{S}(r_i, r_j)$. Mathematically this can be expressed as:

$$S(r_i, r_j) = sigmoid(W_{ih}[v(i), v(j)] + b_{ih}) \tag{6.36}$$

Algorithm 9: Fusion of MRCR and DBCR models

Input: Given target reseacher r_i for the recommendation

Output: Top N recommended list of collaborators

Initialization

let R= r_1, r_2...,r_N be the set of target researchers

Perform MRCR model at target author r_i in order to Compute top N similar collaborators

$\mathcal{U}_i$ = Ordered list of unique collaborators found by MRCR model (Sec. 6.6)

$= \{a_1, a_2, \ldots, a_N\}$

Perform DBCR in order to Compute top N similar collaborators

$\mathcal{V}_i$ = Ordered list of unique collaborators found by MRCR model (Sec. 6.7)

$= \{b_1, b_2, \ldots, b_N\}$

for $i \leftarrow 0$ **to** $|a_N| - 1$ **do**

    Borda Count $B_c(a_i) \leftarrow N - i + 1$

end

for $j \leftarrow 0$ **to** $|b_N| - 1$ **do**

    Borda Count $B_c(b_j) \leftarrow N - j + 1$

end

k=0, $counter(a_i)$=false, $counter(b_j)$=false

for $i \leftarrow 0$ **to** $|\mathcal{U}_i|$-1 **do**

    for $j \leftarrow 0$ **to** $|\mathcal{V}_i|$-1 **do**

        if $(a_i == b_j)$ **then**

            Boda Count $B_c(v_k) \leftarrow B_c(a_i) + B_c(b_j)$ /* same collaborator so add their Borda Count */

            k=k+1

            $counter(b_j)$=true

        else

            $B_c(v_{k+1}) \leftarrow B_c(a_i)$ /*individually consider Borda Count of a_i*/

            k=k+1

        end

    end

end

for $j \leftarrow 0$ **to** $|\mathcal{V}_i|$-1 **do**

    if $(counter(b_j) != true)$ **then**

        $B_c(v_{k+1}) \leftarrow B_c(b_j)$ /*individually consider Borda Count of b_j*/

        k=k+1

    end

end

Sort collaborators in the decreasing order of Boda count $B_c(v_k)$

Prepare the final list of top N collaborators recommendation

where $W_{ih} \in \mathbb{R}^{(d_i+d_j)\times 1}$ is a weight matrix, $b_{ih} \in \mathbb{R}$ is a bias term and the sqaure bracket denotes the concatenation operation between two vectors.

The logistic regression layer can learn its parameters W_{ih} and b_{ih} according to the relationship between the authors r_i and, r_j. To generate the top-N recommendations for author r_i, the recommender system generates a list for an author with all other authors sorted in descending order of score $\mathrm{S}(r_i, r_j)$. We have used mean squared error as loss function. The mean squared error is defined as:

$$\text{Mean squared error(MSE)} = \frac{1}{n}\sum_{i=1}^{n}(Y_i - \bar{Y_i})^2 \tag{6.37}$$

where Y_i is the observed value and $\bar{Y_i}$ is the predicted value.

6.8 Fusion Model: DRACoR (Layer-4)

The main assumption of fusion-based approach can be stated that "hybrid recommendation approaches can provide more accurate recommendation than a single approach and the disadvantages of one approach can be overcome by the other approach" [27, 203]. On the other hand, hybrid approach is a promising alternative to traditional approach. It has shown excellent performance in the field of recommendation [27, 204–206]. Data combination has also been widely investigated in the recommendation community. They were often divided into two categories: score-based and ranking-based [169, 189]. Ranking-based combination methods require rank or position information to integrate different candidates ranking lists, such as Borda fusion, Condorcet fusion, and MAPFuse.

The MRCR and DBCR models which have been improved with previous publication content, meta-paths features aggregation, random walk with restart, LSTM based deep learning method are integrated into a fusion model based collaborator recommendation approach, i.e., DRACoR. We employed a rank-based fusion technique Borda Count to integrate the existing prediction lists generated by the MRCR model and DBCR model respectively. To be more specific, the predictions resulting from the MRCR and DBCR are firstly produced separately with the purpose of allowing us to leverage the individual strengths of both approaches since there is no interdependency between them, then we are fusing the results with standardized Borda Count technique as mentioned in Algo. 9.

6.9 Experiments

In this section, we present the experiments of the proposed fusion model DRACoR, where initial two sections present the experimental datasets and evaluation metrics. Then the baseline methods, experimental setting, performance comparison and study of the proposed approach are described in further section. The following experiments are performed on a laptop with 64-bit windows 10 operating system, Intel i7-3540M CPU@3.00 GHz, and 32 GB memory. All the programs are implemented in Python.

6.9.1 Data Collection

We use two real-world datasets such as DBLP-citation-network V10 [4] (Sec. 2.7.2) and hep-th (Theoretical High Energy Particle Physics) (Sec. 2.7.3) provided by KDD Cup 2003 [5] to demonstrate the effectiveness of our proposed method.

6.9.2 Evaluation Metrics

We employed various evaluation metrics such as Precision, Recall, F1-score, nDCG, and MRR, which are quite popular in recommender systems to demonstrate the effectiveness of DRACoR (Sec. 2.6). For clarity, we further explained Precision, Recall, F1-score as follows.

(i) Precision, Recall and F1-score: We can divide all nodes(researchers) into four groups according to the following four cases:

- A: collaborating with the target node and recommended;
- B: collaborating with the target node but not recommended;
- C: not collaborating with the target node but recommended;
- D: not collaborating with the target node and not recommended.

$$Precision = \frac{|A|}{|A + C|} \tag{6.38}$$

$$Recall = \frac{|A|}{|A + B|} \tag{6.39}$$

$$F1 = \frac{2(Precision * Recall)}{Precision + Recall} \tag{6.40}$$

[4] https://aminer.org/citation

[5] https://www.cs.cornell.edu/projects/kddcup/datasets.html

6.9.3 Baseline Methods

To measure effectiveness of the proposed system DRACoR, we compare our results with various state-of-the-art methods such as CNRec, RWR, TBRec, MVCWalker, CCRec, BCR, and RWR-CR (Sec. 2.8.2).

6.9.4 Experimental Setting

While preparing the test dataset, we considered two scenarios: firstly, due to operational constraints, 14 sub-domains of computer science: information retrieval, image processing, security, wireless sensor network, machine learning, software engineering, computer vision, artificial intelligence, data mining, algorithms and theory, databases, natural language processing, parallel and distributed systems, and multimedia were selected as the testing dataset in our experiment.

Secondly, while identifying the target researchers, the following conditions are taken into consideration to measure the effectiveness of DRACoR to handle cold start issues like a new researcher or researcher with less number of publications or collaborations. To validate the effectiveness of DRACoR against new researcher or researchers with fewer collaborations, primarily the below two categories are taken into consideration. There are two major categories, i.e., (a) number of citations (n_c), and (b) target nodes degree (n_d). Generally, n_c denotes the number of citations of individual researchers and n_d denotes the number of collaborators or degree of target researchers. The following two categories are discussed below.

(a) *T*arget researcher's academic level (Number of citations)

   (i) *Primary Level* ($2 \leq n_c < 6$)

   (ii) *Intermediate Level* ($6 \leq n_c < 26$)

   (iii) *Advanced Level* ($26 \leq n_c$)

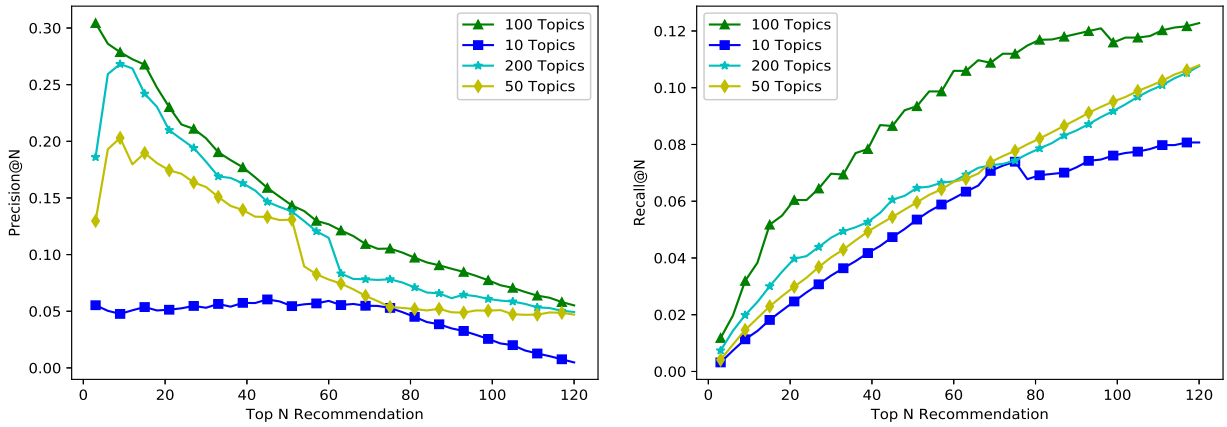
(b) *T*arget researcher's degree (Number of collaborations)

   (i) *Group I* ($1 \leq n_d < 10$)

   (ii) *Group II* ($10 \leq n_d < 19$)

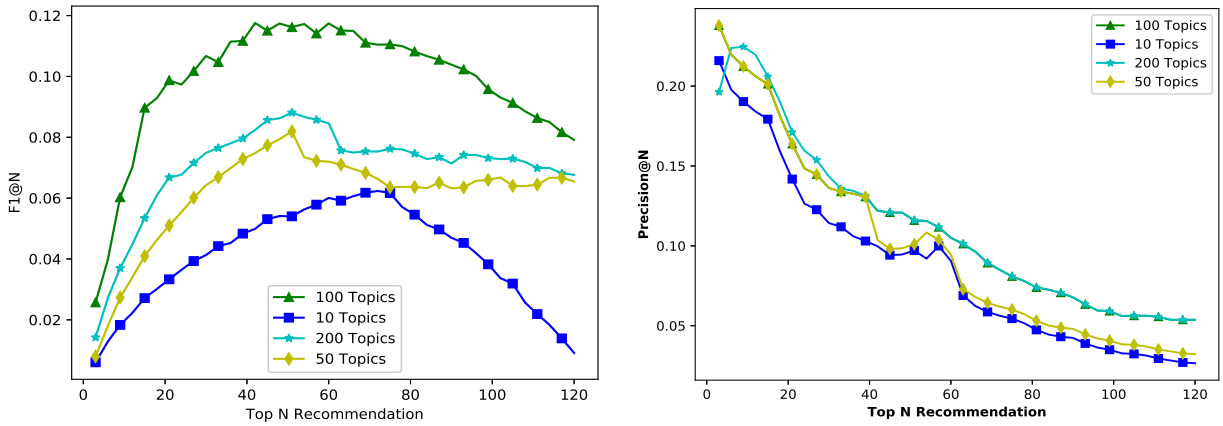
   (iii) *Group III* ($20 \leq n_d < 29$)

(iv) *Group IV ($30 \leq n_d$)*



(a) (b)

Figure 6.4: Influence of vector dimensions on: (a) Precision (hep-th) (b) Recall (hep-th)



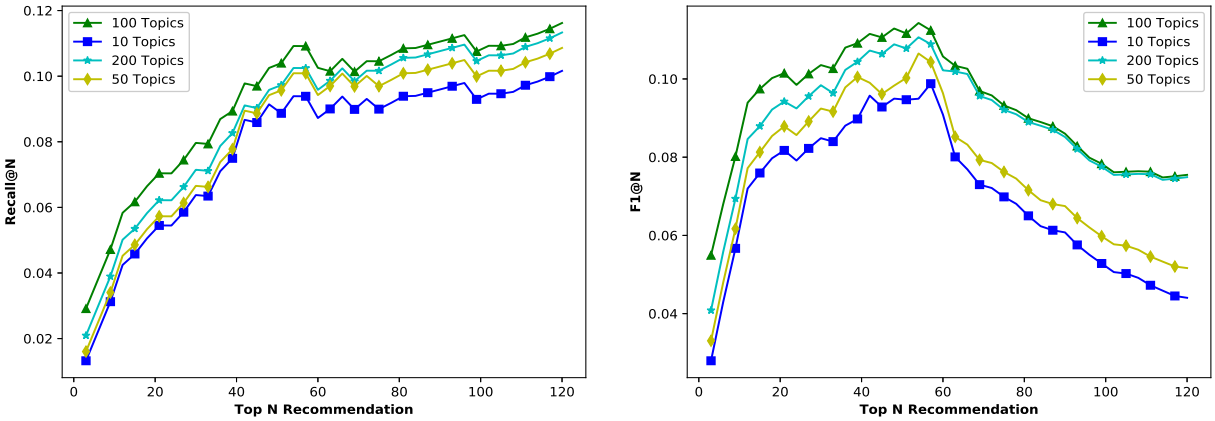
(a) (b)

Figure 6.5: Influence of vector dimensions on: (a) F1 (hep-th) (b) Precision (DBLP)

In this experiment the relevance value r is binary, i.e., r $\in$ {0 or 1}. It is set to 1 if the recommended collaborators are matching with the ground truth data and set to 0 if the recommended collaborators are not collaborating with the target node in reality.

To comprehensively evaluate our proposed method and more specifically, to address the broad research questions (RQs) discussed in Sec. 1.5, we prefer to examine the following sub-queries (SQs):

SQ1: How does different parameter selection affect the performance of DRACoR?



(a) (b)

Figure 6.6: Influence of vector dimensions on: (a) Recall (DBLP) (b) F1 (DBLP)

Table 6.6: Experimental parameter settings

Parameter	Range	Default
Vector dimension (A_i and T_i)	(10-200)	100
Adjustment parameter (m)	(0.1-0.95)	0.7
Damping constant (α)	(0.1-0.95)	0.8
Target researcher's academic level (n_c)	≥ 0	(6-24)
Target researcher's degree (n_d)	≥ 0	≥ 30
Number of iteration	(10-100)	25
Number of recommended nodes	(5-150)	120

SQ2: How does DRACoR handle cold-start issue for new researcher and other issue like diversity ?

SQ3: How effective is DRACoR in comparison to other state-of-the-art methods ?

6.9.5 Parameter Tuning and Optimization

In this section, we demonstrate the impact of various experimental parameter settings, including vector dimension (A_i and T_i), adjustment parameter (m), damping constant (α), target researcher's academic level (n_c), target researcher's degree (n_d), and number of iteration. The ranges and default values of the parameters are depicted in Table 6.6. When the effect of the parameter is under examination, the other parameters are set to default values. During the assessment, best results and the second-best are marked by 'bold-face' and '+' symbol respectively.

Influence of Vector Dimension

In order to find the ideal dimension for vectors A_i and T_i, we conduct experiments on four values for vector dimension , i.e. {10,50,100,200}. The value of the adjustment parameter is set to be 0.7, and α is set to be 0.8.

We choose 140 researchers randomly as the target nodes and run DRACoR model for both the datasets of DBLP and hep-th. This is done to calculate the average precision, recall, and $F1$ over these recommended collaborators. We conducted extensive experiments with different recommendation lists in length to evaluate the influence of the vector dimension on the result. Fig. 6.4a and Fig. 6.5b show the performance of our model in terms of precision for different vector dimensions. Similarly Fig. 6.4b, Fig. 6.6a and Fig. 6.5a, Fig. 6.6b, demonstrate the effectiveness of DRACoR in terms of both recall and F1 respectively.

During the experiments on DBLP and hep-th datasets, it can be seen that the model performs best, in terms of precision, when the value of the vector dimension is 100 and performs a downtrend with the recommendation list increasing. In the case of recall evaluation, the overall results show an upward trend and then slightly flattens out at the end of the recommendation list. The best performance of recall is achieved with a vector dimension of 100. The F1 score performs the upper convex curve, rapidly rising and then shows a slight decline. The best performance of F1 score is achieved with a vector dimension of 100. So considering the above performance, in this experiment, the value of the vector dimension has been taken as 100.

Table 6.7: Influence of adjustment parameter on MRR

Adjustment	MRR						
prob.(1-m)	$2<=n_c<6$	$6<=n_c<25$	$26<=n_c$	$2<=n_d<10$	$10<=n_d<20$	$20<=n_d<30$	$30<=n_d$
0.5	0.0793	0.0849	0.0853	0.0854	0.0861	0.0864	0.0895
0.45	0.0798	0.0879	0.0851	0.0853	0.0893	0.0847	0.0853
0.4	0.0867	0.0905	0.0893	0.0915	0.0841	0.0859	0.0874
0.35	0.0972	0.0895	0.0949	0.0858	0.0903	0.0885	0.0896
0.3	**0.1093**	**0.1197**	**0.1267**	**0.1134**	**0.1127**	**0.1185**	**0.1189**
0.25	0.0976^{+}	0.1014^{+}	0.1258^{+}	0.1016^{+}	0.1039^{+}	0.1073^{+}	0.1052^{+}
0.2	0.0668	0.0848	0.1132	0.0894	0.0917	0.0995	0.0987
0.15	0.0526	0.0773	0.0866	0.0739	0.0877	0.0914	0.0923
0.1	0.0473	0.0637	0.0725	0.0683	0.0746	0.0828	0.0848
0.05	0.0437	0.0591	0.0683	0.0565	0.0677	0.0769	0.0787

Influence of an Adjustment Parameter (m)

This parameter has a realistic significance as it controls how an abstract and a title of research papers published by a researcher determines the area of interest of a researcher. In this section, we analyze how the adjustment parameter (m) influences the performance of the algorithm concerning nDCG and MRR. In order to find the ideal value of m to get the efficient combined score of vectors A_i and T_i, we conducted experiments on 10 possible values for adjustment parameter, i.e. {0.5, 0.45, 0.4, 0.35, 0.3, 0.25, 0.2, 0.15, 0.1, 0.05 }. The value of vector dimension (A_i and T_i) is set to be 100 and α is set to be 0.8.

From Table 6.7, we can observe that the variation tendency of MRR score performs roughly consistent. We can see that the MRR shows an overall upward trend with the increasing value of adjustment parameter m of value 0.7. The model performs the best while the value of the adjustment parameter (m) is 0.7 as marked in bold text. This is because, in most of the cases, the abstract is giving a better clarity of topic similarity while in a few cases the title is resulting better. So considering this experiment in a similar nature, the value of (1-m) has been taken as 0.3.

Influence of Damping Constant (α)

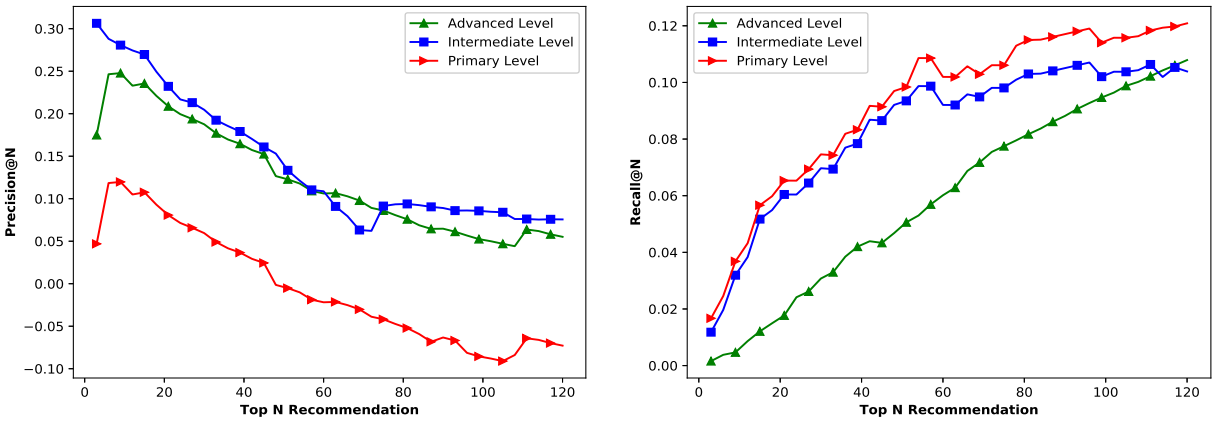
This parameter has a realistic significance as it controls how far the random walker reaches. In this section, we analyze how the damping coefficient influences the performance of the algorithm concerning nDCG and MRR. With higher values of α, the probability of random walker reaching far away nodes increases. Hence, the number of new collaborators, i.e., researchers who have not collaborated with the target researcher in training set but have done so in the test set, increases. It is evident from Table 6.8, that as the damping constant increases there is a drastic increase in MRR and nDCG for new collaborators and a negligible decrease in MRR and nDCG for overall (new+old) collaborators.

The table displays the influence of restart probability $(1 - \alpha)$ on the algorithm. This parameter setting gives the highest nDCG of 0.162 and 0.419 for both new and old collaborators. Similarly, while evaluating MRR, we can see that the overall results of MRR for both new and old collaborators are 0.179 and 0.494 respectively. The second-best performer is indicated with a + marks sign. Considering the above results of both nDCG and MRR for new and old collaborators, in this experiment, the value of (1-α) has

Table 6.8: Influence of restart probability on nDCG and MRR

Restart prob. (1-α)	nDCG (New)	nDCG (O)	MRR(N)	MRR(O)
0.5	0.009	0.338	0.005	0.419
0.45	0.010	0.337	0.023	0.407
0.4	0.017	0.339	0.046	0.418
0.35	0.026	0.339	0.051	0.418
0.3	0.036	0.343	0.078	0.426
0.25	0.104	0.348^{+}	0.084	0.428^{+}
0.2	**0.162**	**0.419**	**0.179**	**0.494**
0.15	0.107^{+}	0.297	0.127^{+}	0.417
0.1	0.089	0.254	0.123	0.329
0.05	0.061	0.226	0.119	0.121

been taken as 0.2.



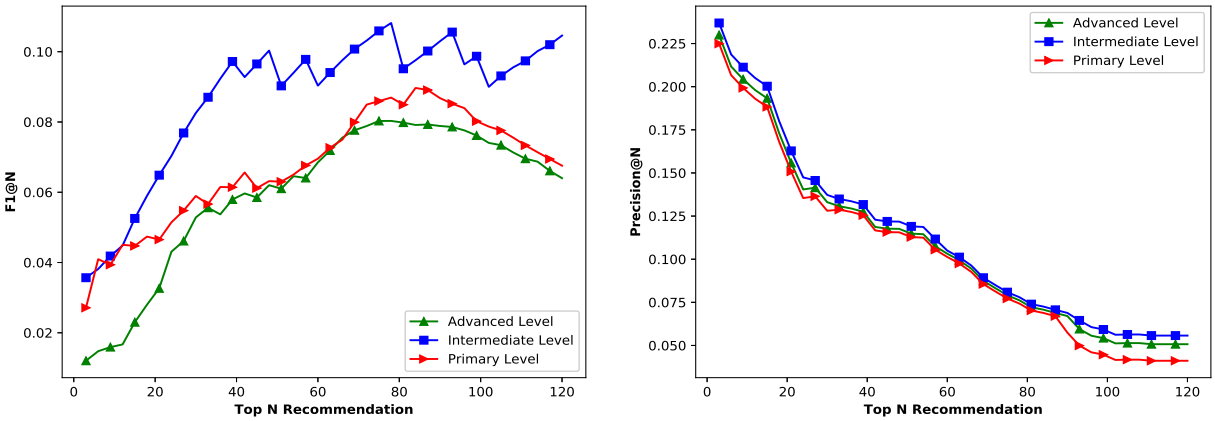
(a) (b)

Figure 6.7: Influence of academic level on: (a) Precision (hep-th) (b) Recall (hep-th)

Influence of Target Researcher's Academic Level

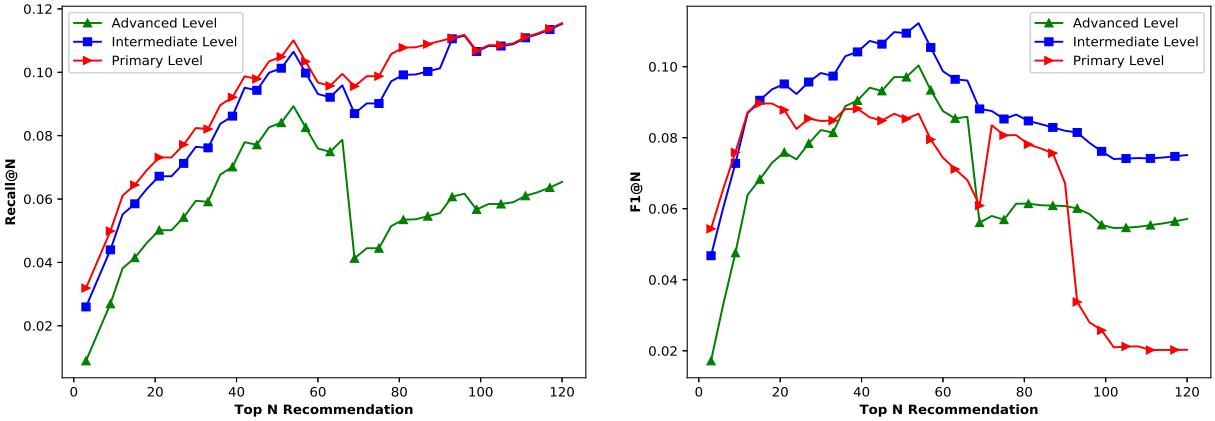
In this section, we demonstrate the overall performance of the DRACoR model against varying academic levels of target researchers. The experimental settings are the same as other groups of experiments. The vector dimension is 100, the adjustment parameter is 0.7, and the damping constant was 0.8 during the experiment.

DRACoR performs better in terms of precision on recommending potential collaborators for intermediate and advanced level researchers on both hep-th and DBLP datasets (Fig. 6.7a, and Fig. 6.8b). For the primary level researchers, it shows a relatively low



(a) (b)

Figure 6.8: Influence of academic level on: (a) F1 (hep-th) (b) Precision (DBLP)



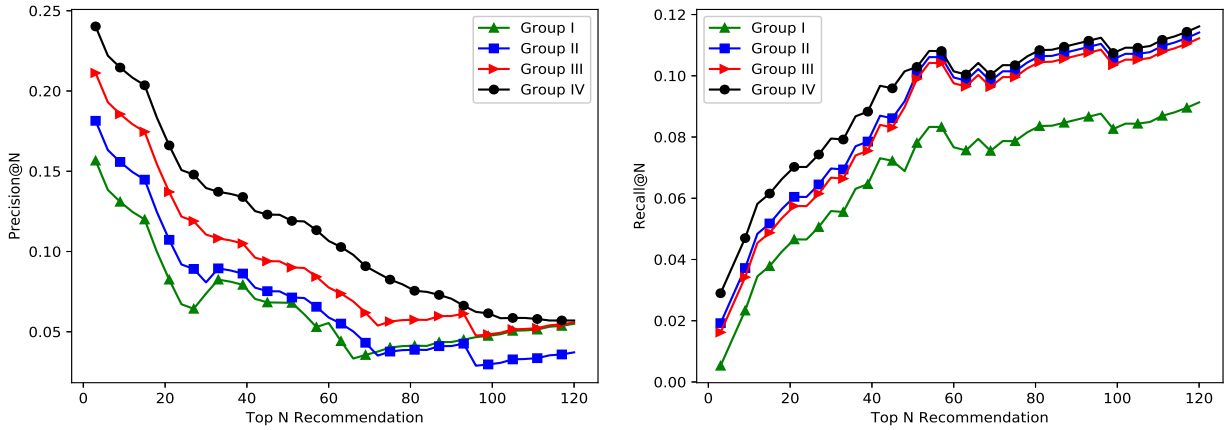
(a) (b)

Figure 6.9: Influence of vector dimensions on: (a) Recall (DBLP) (b) F1 (DBLP)

precision value. However, according to Fig. 6.7b; and Fig. 6.9a, DRACoR is good at recommending for those primary level researchers in terms of recall. However, the performance of DRACoR shows the worse for advanced-level researchers.

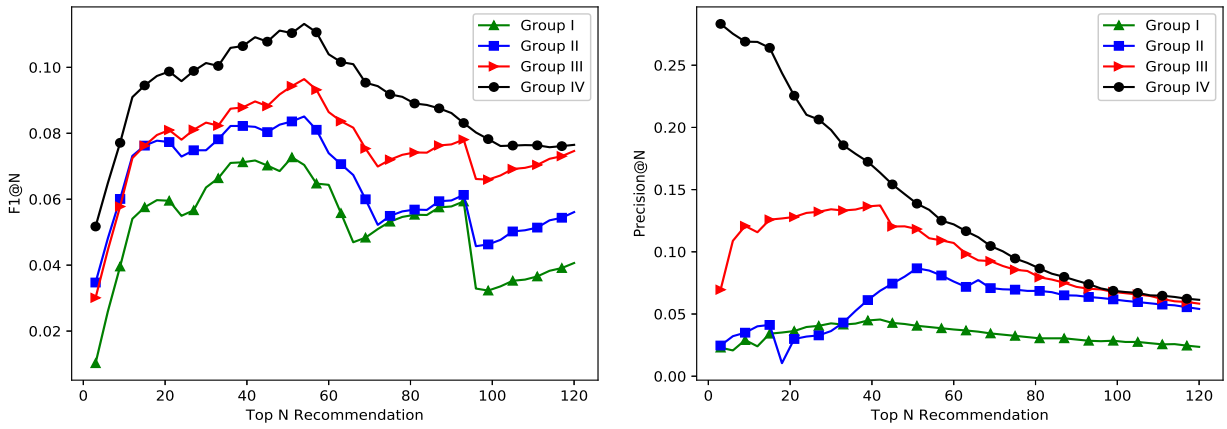
DRACoR shows higher F1 score on recommending for the intermediate level researchers compared to the primary and advanced-level researchers (Figs. 6.8a, and 6.9b). After seeing all the analysis of the results, we observe that the academic level of target researchers has a great impact on the performance of DRACoR. If we focus more on the overall metric F1 rating, the DRACoR is higher at recommending potential collaborators for the one's intermediate level researchers.

Influence of Target Researcher's Degree



(a) (b)

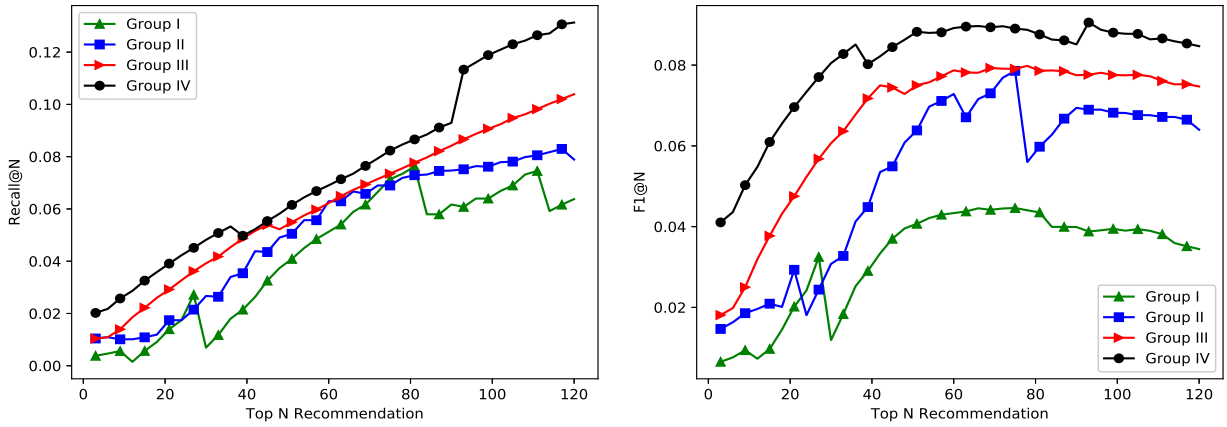
Figure 6.10: Influence of target researcher's degree on: (a) Precision (hep-th) (b) Recall (hep-th)



(a) (b)

Figure 6.11: Influence of target researcher's degree on: (a) F1 (hep-th) (b) Precision (DBLP)

In terms of precision, the larger the target node's degree, the better the model's performance (Figs. 6.10a; and 6.11b). Besides, we can see that DRACoR has relatively higher precision with group IV than all other groups. At the range from 0 to 10, DRACoR performs the worst. But when the target node's degree gets larger than 30, the precision performs better as compared to other groups of target researchers. Thus we can conclude



(a) (b)

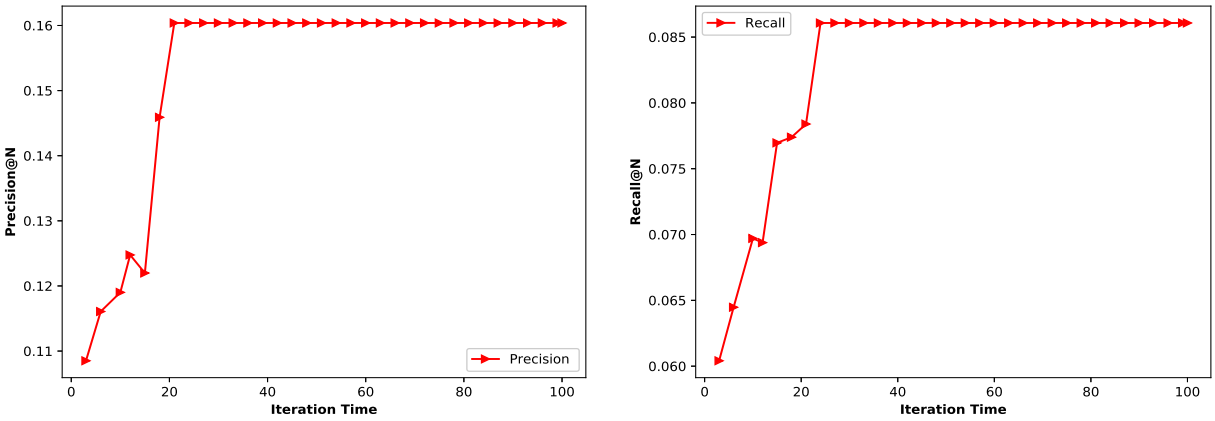
Figure 6.12: Influence of target researcher's degree on: (a) Recall (DBLP) (b) F1 (DBLP)

that DRACoR has higher precision for strong nodes but performs almost the same for weak nodes.

Fig. 6.10b, and Fig. 6.12a show the comparison of recall rate with the changing degree. Similar to the results of precision, when the degree becomes larger than 30, the corresponding recall rate of DRACoR increases. Besides, we can see that DRACoR has a relatively higher recall with group IV than all other groups. Fig. 6.11a, and Fig. 6.12b show the comparison of F1 with the changing degree. But when the target node's degree gets larger than 30, the F1 performs better as compared to other groups of target researchers. Thus we can conclude that DRACoR has a higher recall for strong nodes but performs almost the same for weak nodes.

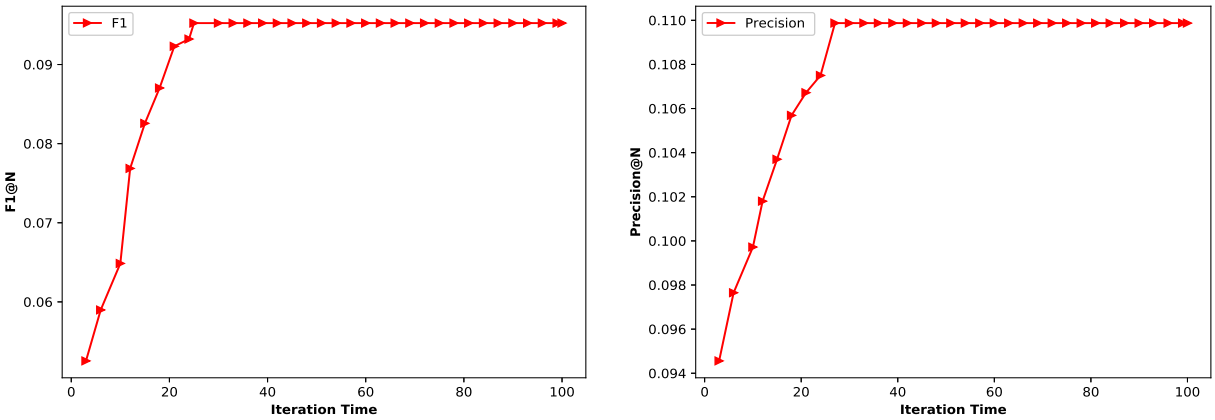
Impact of Number of Iteration on Overall Results

In this work, the higher the number of iterations, the higher the number of matrix multiplication operations done by RWR before getting the recommended list. While evaluating the overall performance of DRACoR, it has been observed that, there is no significant changes occurring when iteration times get bigger. As shown in Fig. 6.13a, and Fig. 6.14b, the model achieves a maximum precision of 16% and 11% at iteration 21 and 23 in both hep-th and DBLP respectively. There are similar behavior observed by the model in case of recall and $F1$ until 23 iterations as shown in Fig. 6.13b, Fig. 6.15a, Fig. 6.14a, and Fig. 6.15b. Afterward, the model becomes convergent. So there is no need to execute the



(a) (b)

Figure 6.13: Influence of iteration on: (a) Precision (hep-th) (b) Recall (hep-th)



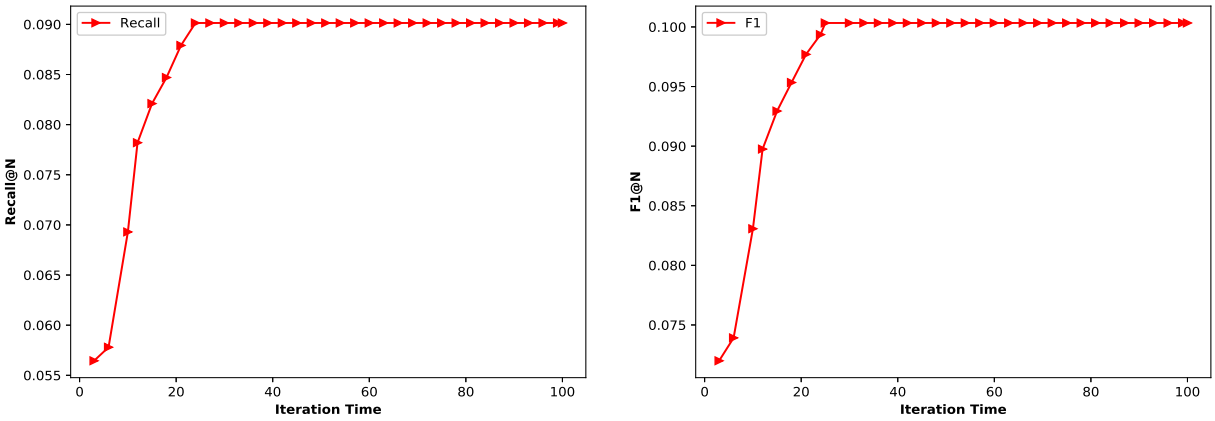
(a) (b)

Figure 6.14: Influence of iteration on: (a) F1 (hep-th) (b) Precision (DBLP)

model with many iterations. Based on the above experiments, we have set the iteration time as 25.

6.9.6 Parameter Tuning of DBCR Model

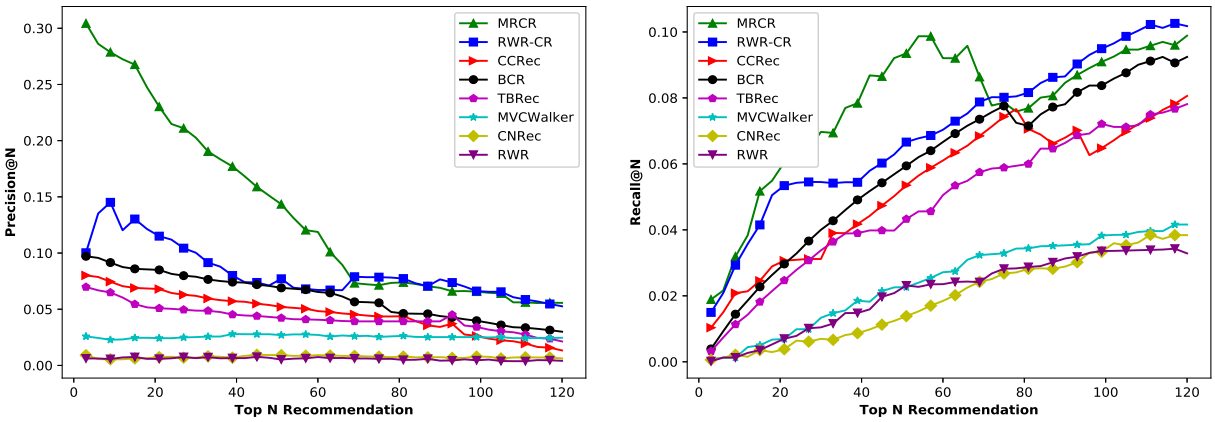
The model is trained using RMSProp as an optimizer. The parameter α is set to be 0.9, and the learning rate is set to 0.0001. Models are trained for 50 epochs, by setting batch sizes to 512. As for cost function, we choose the mean squared error, which is typically used for regression tasks since it tries to minimize the mean squared error in the regression. Due to the computational costs requested by the models, the dimension of the



(a) (b)

Figure 6.15: Influence of iteration on: (a) Recall (DBLP) (b) F1 (DBLP)

learned embeddings r_i and r_j are fixed to 50.

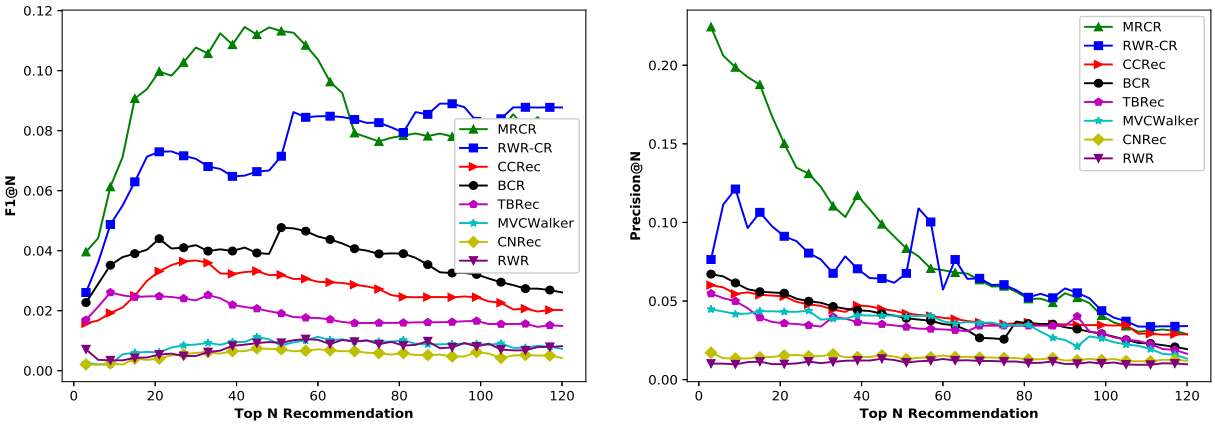


(a) (b)

Figure 6.16: MRCR performance in terms of: (a) Precision (hep-th) (b) Recall (hep-th)

6.10 Results and Discussions

In this section, we evaluated the effectiveness of DRACoR against existing state-of-the-art methods. Before evaluating the performance of the fusion model, DRACoR individual performance analysis of MRCR and DBCR models are estimated.



(a) (b)

Figure 6.17: MRCR performance in terms of: (a) F1 (hep-th) (b) Precision (DBLP)

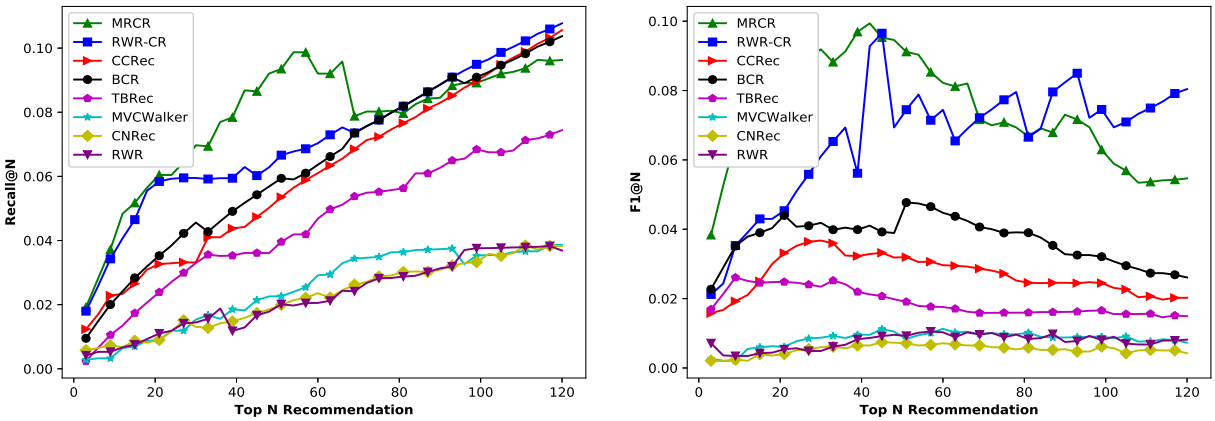
6.10.1 Results Analysis of MRCR Model

The detailed results are shown in Fig. 6.16, Fig. 6.17 and Fig. 6.18 respectively. While evaluating on the hep-th dataset, the MRCR model achieves the highest precision of 0.304 at first recommendation, and slowly, it shows a downward trend and reaches a precision value of 0.055 at position 120 as shown in Fig. 6.16a. Similarly, the MRCR model achieves the highest precision of 0.224 at first recommendation, and slowly it shows a downward trend and reaches a precision value of 0.028 at position 120 on DBLP dataset, as shown in Fig. 6.17b.

In the case of recall evaluation on hep-th, the MRCR model performs an upward trend and reaches the highest recall of 0.098 at position 54, and afterward again it shows a downward trend and reaches a recall of 0.075 at position 78. Then it slowly increases and achieves the highest recall of 0.098 at position 120, as shown in Fig. 6.16b. It provides a similar nature of performance on DBLP dataset too. As shown in Fig. 6.18a, it recommends with a higher recall of 0.098 at position 56, and afterward, it seems very like a trend of decline on recall to a certain degree and reaches a recall of 0.096 at position 120.

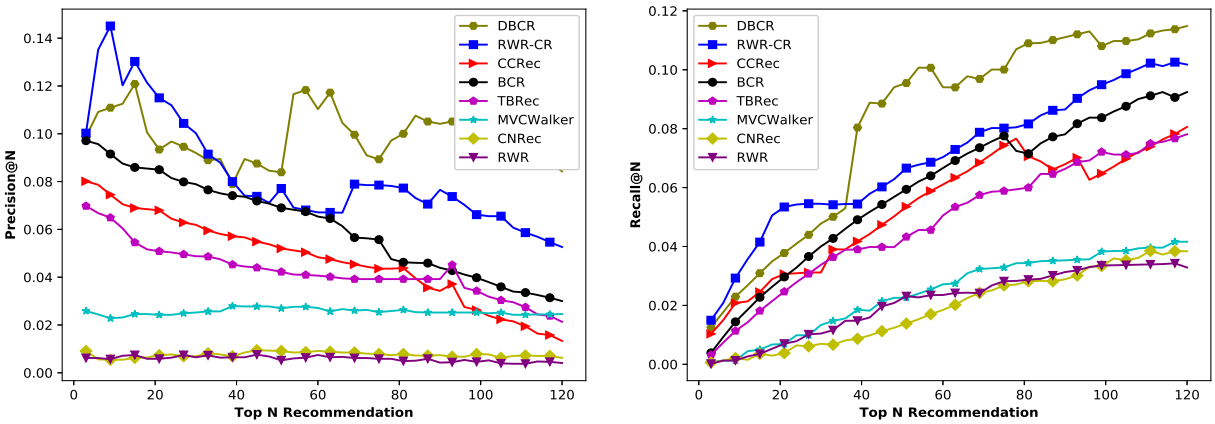
Similarly, while evaluating the performance on hep-th, the MRCR model performs an upward trend from the beginning and achieves the highest F1 of 0.113 at position 50. It shows a downward trend and reaches a F1 of 0.078 at position 80. Then it shows a steady performance over the recommendation list and finally reaches a F1 of 0.079 at

position 120 as shown in Fig. 6.17a. But in case of DBLP dataset the model shows an upward trend from the beginning and reaches a F1 of 0.091 at position 50, and slowly it shows a downward trend and finally achieves a F1 of 0.054 at position 120 as shown in Fig. 6.18b. During the initial recommendation, the MRCR model made a significant improvement on evaluation metrics, such as precision, recall and F1 over the standard approaches.



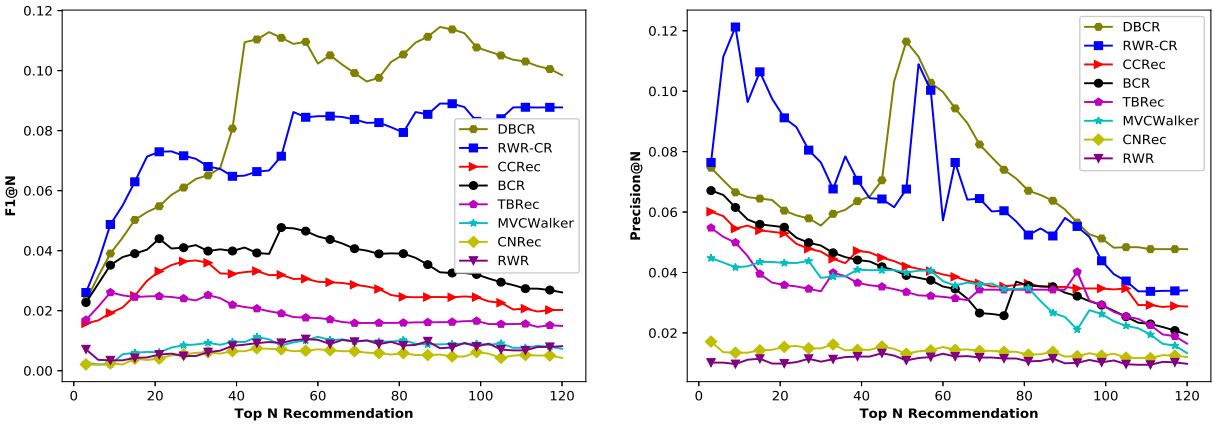
(a) (b)

Figure 6.18: MRCR performance in terms of: (a) Recall (DBLP) (b) F1 (DBLP)



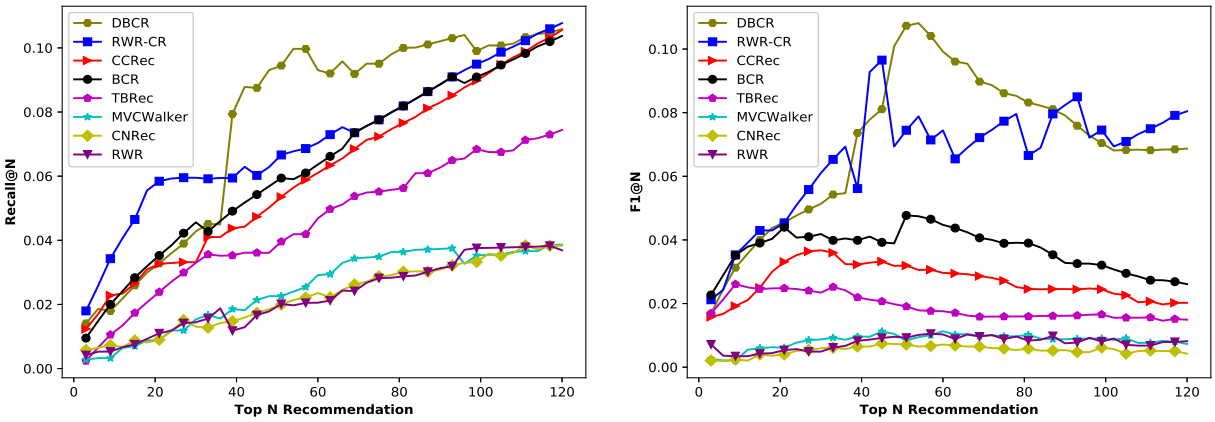
(a) (b)

Figure 6.19: DBCR performance in terms of: (a) Precision (hep-th) (b) Recall (hep-th)



(a) (b)

Figure 6.20: DBCR performance in terms of: (a) F1 (hep-th) (b) Precision (DBLP)



(a) (b)

Figure 6.21: DBCR performance in terms of: (a) Recall (DBLP) (b) F1 (DBLP)

6.10.2 Results Analysis of DBCR Model

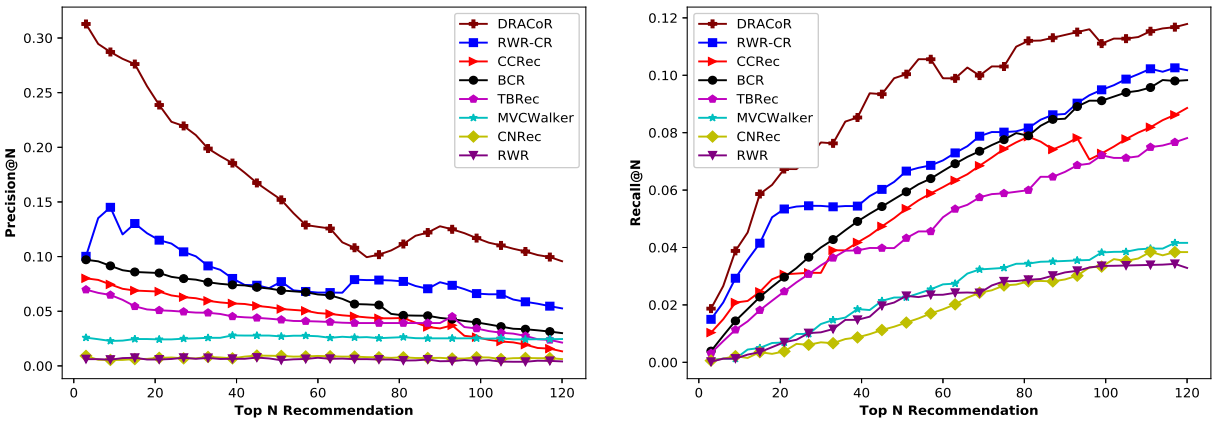
The detailed results are shown in Fig. 6.19, Fig. 6.20 and Fig. 6.21 respectively. We have experimented on the hep-th dataset, and observed that DBCR model, achieves the highest precision of 0.098 at first recommendation and slowly shows a downward trend and reaches a precision value of 0.084 at position 120 as shown in Fig. 6.19a. Similarly, it achieves the highest precision of 0.073 at first recommendation and shows a downward trend and reaches a value of 0.047 at position 120 on DBLP dataset as shown in Fig. 6.20b.

In the case of recall evaluation on hep-th, the DBCR model performs an upward trend and reaches a recall of 0.101 at position 56 and then slowly increases and achieves a recall

of 0.114 at position 120 as shown in Fig. 6.19b. The DBCR model shows a similar nature of performance on DBLP dataset too. As shown in Fig. 6.21a, it recommends with a higher recall of 0.099 at position 56, and afterward, it seems like a trend of decline on recall to a certain degree and reaches a recall of 0.105 while recommending 120 collaborators.

Similarly, while evaluating the performance on hep-th, the DBCR model performs an upward trend from the beginning and achieves the highest F1 of 0.111 at position 50. Then it shows a downward trend and reaches a F1 of 0.098 at position 120 as shown in Fig. 6.20a. But in case of DBLP dataset, the model shows an upward trend from the beginning and reaches a F1 of 0.106 at position 50, and it shows a downward trend slowly and finally achieves a F1 of 0.068 at position 120 as shown in Fig. 6.21b.

We observed that during the mid-end stages of the recommendation, DBCR model made a significant improvement on evaluation metrics like precision, recall and F1 over the standard approaches.

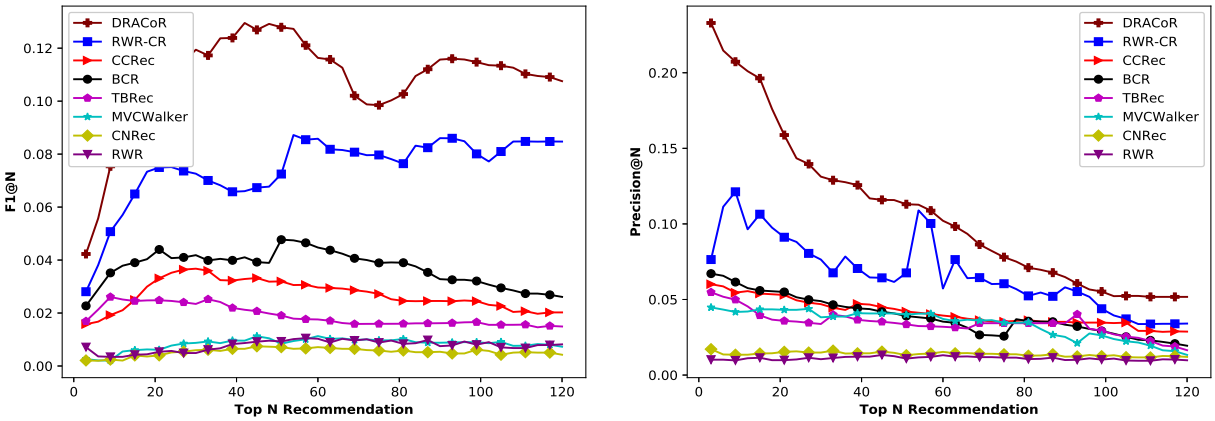


(a) (b)

Figure 6.22: DRACoR performance in terms of: (a) Precision (hep-th) (b) Recall (hep-th)

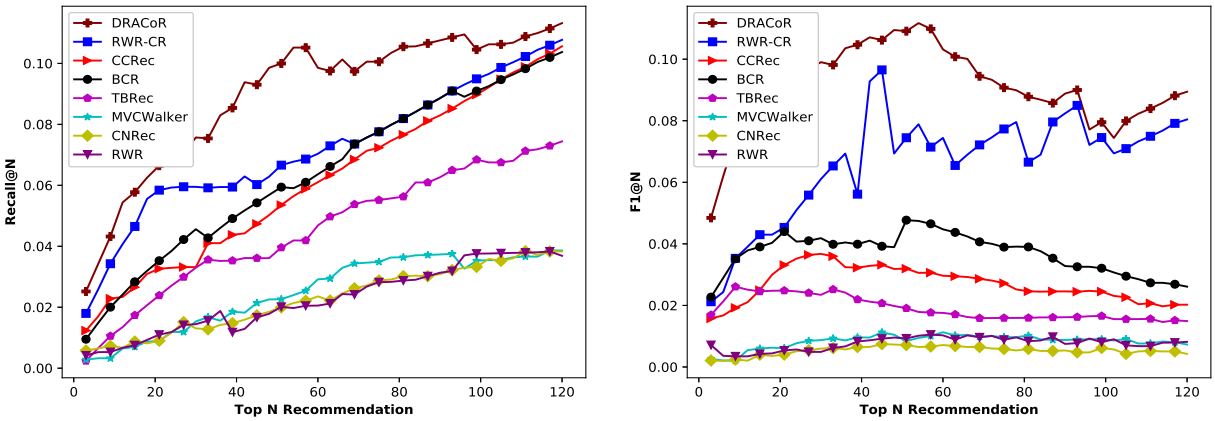
6.10.3 Results Analysis of DRACoR Model

The detailed results are shown in Fig. 6.22, Fig. 6.23 and Fig. 6.24 respectively. We have experimented on hep-th dataset and observed that proposed model DRACoR exhibits the highest precision of 0.287 after recommending the top 10 potential collaborators and then slowly it shows a downward trend and reaches a precision value of 0.095 at position 120 as shown in Fig. 6.22a. Similarly, it achieves the highest precision of 0.207 at position



(a) (b)

Figure 6.23: DRACoR performance in terms of: (a) F1 (hep-th) (b) Precision (DBLP)



(a) (b)

Figure 6.24: DRACoR performance in terms of: (a) Recall (DBLP) (b) F1 (DBLP)

10 and then slowly shows a downward trend and reaches a precision value of 0.051 at position 120 on DBLP dataset as shown in Fig. 6.23b.

In case of recall evaluation on hep-th, the proposed model DRACoR performs an upward trend and reaches a recall of 0.098 at position 54 and then slowly increases and achieves a recall of 0.117 at position 120 as shown in Fig. 6.22b. The DRACoR model shows a similar nature of performance on DBLP dataset too. As shown in Fig. 6.24a, it recommends with a higher recall of 0.098 at position 60 and finally reaches a recall of 0.113 while recommending 120 collaborators.

Similarly, while evaluating F1 on hep-th the DRACoR model performs an upward

trend from the beginning and achieves a F1 of 0.127 at position 50. Then it shows a downward trend and reaches a F1 of 0.107 at position 120 as shown in Fig. 6.23a. But in case of DBLP dataset the model shows an upward trend from the beginning and reaches a F1 of 0.109 at position 50, and slowly it shows a downward trend and finally achieves a F1 of 0.089 at position 120 as shown in Fig. 6.24b.

Table 6.9: F1-score results of DRACoR and other approaches (hep-th)

Methods	F1@10	F1@20	F1@30	F1@40	F1@50	F1@60	F1@80	F1@100	F1@120
CNRec	0.0024	0.0040	0.0059	0.0064	0.0071	0.0071	0.0058	0.0061	0.0042
RWR	0.0034	0.0053	0.0048	0.0082	0.0092	0.0102	0.0083	0.0080	0.0081
MVCWalker	0.0020	0.0061	0.0087	0.0096	0.0084	0.0112	0.0101	0.0090	0.0072
TBRec	0.0260	0.0248	0.0234	0.0219	0.0190	0.0175	0.0159	0.0165	0.0149
CCRec	0.0192	0.0331	0.0367	0.0322	0.0319	0.0296	0.0245	0.0244	0.0202
BCR	0.0351	0.0439	0.0418	0.0398	0.0477	0.0448	0.0390	0.0320	0.0260
RWR-CR	0.0487^{+}	0.0729^{+}	0.0706^{+}	0.0647^{+}	0.0714^{+}	0.0848^{+}	0.0793^{+}	0.0833^{+}	0.0877^{+}
MRCR	0.0612	0.0997	0.1077	0.1086	0.1131	0.1037	0.0783	0.0795	0.0793
DBCR	0.0390	0.0548	0.0639	0.0806	0.1109	0.1023	0.1053	0.1077	0.0984
DRACoR	0.0753*	0.1120*	0.1194*	0.1238*	0.1278*	0.1163*	0.1026*	0.1147*	0.1075*

'*' denotes statistical significance (α=0.05) over the best among state-of-the-art ('+')

The complete results of MRR and nDCG are depicted in Table 6.11 and Table 6.12. It is evident from Table 6.11 that, proposed approach shows a consistent nDCG and MRR over all other standard approaches on hep-th dataset. The proposed approach shows an MRR of 0.457 indicates the effectiveness of correctly predicting the first collaborators within top 2 recommendations. While evaluating the performance analysis in terms of nDCG, DRACoR shows the highest nDCG of 0.299 at position 10 then slowly it decreases and achieves an nDCG of 0.1509 at position 120 as shown in Table 6.11.

In the case of MRR evaluation on the DBLP dataset, DRACoR shows an MRR of 0.410, which indicates the effectiveness of correctly predicting the first collaborators within the top 2 recommendations. Similarly, for nDCG evaluation on DBLP, it is visible that the proposed model DRACoR exhibits a significant improvement of nDCG over all other state-of-the-art methods. It is clearly shown in Table 6.12 that the nDCG results of DRACoR are consistent and show the highest nDCG of 0.279 at position 10 and display the worst nDCG of 0.140 at position 120.

We also conduct pairwise t-tests on overall F1, MRR, and nDCG for both hep-

Table 6.10: F1-score results of DRACoR and other approaches (DBLP)

Methods	F1@10	F1@20	F1@30	F1@40	F1@50	F1@60	F1@80	F1@100	F1@120
CNRec	0.0021	0.0038	0.0057	0.0061	0.0074	0.0066	0.0061	0.0062	0.0040
RWR	0.0032	0.0051	0.0045	0.0079	0.0089	0.0100	0.0081	0.0077	0.0076
MVCWalker	0.0018	0.0058	0.0084	0.0093	0.0082	0.0109	0.0098	0.0087	0.0069
TBRec	0.0257	0.0246	0.0231	0.0215	0.0186	0.0172	0.0157	0.0161	0.0145
CCRec	0.0188	0.0326	0.0363	0.0318	0.0314	0.0291	0.0242	0.0239	0.0201
BCR	0.0348	0.0433	0.0413	0.0393	0.0472	0.0443	0.0384	0.0315	0.0256
RWR-CR	0.0352^{+}	0.0453^{+}	0.0610^{+}	0.0561^{+}	0.0744^{+}	0.0741^{+}	0.0665^{+}	0.0745^{+}	0.0804^{+}
MRCR	0.0656	0.0891	0.0918	0.0969	0.0911	0.0822	0.0664	0.0629	0.0546
DBCR	0.0312	0.0455	0.0513	0.0736	0.1073	0.0991	0.0831	0.0704	0.0686
DRACoR	0.0744*	0.0966*	0.0990*	0.1046*	0.1090*	0.1031*	0.0878*	0.0795*	0.0894*

'*' denotes statistical significance (α=0.05) over the best among state-of-the-art ('+')

Table 6.11: MRR and nDCG results of DRACoR and other approaches (hep-th)

Methods	MRR	nDCG@10	nDCG@20	nDCG@30	nDCG@40	nDCG@60	nDCG@80	nDCG@100	nDCG@120
CNRec	0.1615	0.0055	0.0054	0.0049	0.0056	0.0049	0.0045	0.0041	0.0039
RWR	0.1798	0.0228	0.0219	0.0174	0.0156	0.0127	0.0119	0.0096	0.0082
MVCWalker	0.1974	0.0239	0.0248	0.0277	0.0269	0.0268	0.0258	0.0226	0.0197
TBRec	0.2208	0.0508	0.0487	0.0452	0.0406	0.0392	0.0332	0.0249	0.0231
CCRec	0.0679	0.0673	0.0548	0.0477	0.0429	0.0358	0.0341	0.0324	0.0319
BCR	0.1971	0.0775	0.0746	0.0668	0.0644	0.0697^{+}	0.0473	0.0597^{+}	0.0496^{+}
RWR-CR	0.2247^{+}	0.1703^{+}	0.1687^{+}	0.1459^{+}	0.1002^{+}	0.0695	0.0639^{+}	0.0591	0.0492
MRCR	0.4292	0.2576	0.2663	0.2669	0.2108	0.1749	0.1386	0.1252	0.1196
DBCR	0.2038	0.1645	0.1856	0.1747	0.1793	0.1966	0.1686	0.1593	0.1478
DRACoR	0.4578*	0.2993*	0.2892*	0.2886*	0.2372*	0.2019*	0.1837*	0.1693*	0.1509*

'*' denotes statistical significance (α=0.05) over the best among state-of-the-art ('+')

th and DBLP datasets between DRACoR and the third-best performers at 5% level of significance. This is because for most of the cases, the second best was either proposed DBCR or MRCR models. The complete results are shown in Tables 6.9, 6.10, 6.11, and 6.12 respectively.

6.10.4 Study of the Proposed Approach

The main findings concerning our various SQs are summarized below.

Table 6.12: MRR and nDCG results of DRACoR and other approaches (DBLP)

Methods	MRR	nDCG@10	nDCG@20	nDCG@30	nDCG@40	nDCG@60	nDCG@80	nDCG@100	nDCG@120
CNRec	0.1536	0.0042	0.0049	0.0052	0.0055	0.0047	0.0041	0.0039	0.0035
RWR	0.1589	0.0215	0.0219	0.0169	0.0149	0.0121	0.0115	0.0089	0.0079
MVCWalker	0.1878	0.0219	0.0235	0.0265	0.0251	0.0255	0.0247	0.0219	0.0189
TBRec	0.2338^{+}	0.0497	0.0469	0.0431	0.0389	0.0392	0.0319	0.0225	0.0218
CCRec	0.0643	0.0652	0.0519	0.0439	0.0407	0.0348	0.0331	0.0309	0.0298
BCR	0.1877	0.0691	0.0729	0.0615	0.0598	0.0654	0.0435	0.0516	0.0448
RWR-CR	0.1975	0.1694^{+}	0.1589^{+}	0.1424^{+}	0.0984^{+}	0.0583^{+}	0.0616^{+}	0.0536^{+}	0.0467^{+}
MRCR	0.4005	0.2449	0.2573	0.2557	0.2012	0.1674	0.1211	0.1226	0.1098
DBCR	0.1985	0.1544	0.1769	0.1693	0.1671	0.1849	0.1537	0.1493	0.1368
DRACoR	0.4109*	0.2793*	0.2787*	0.2804*	0.2295*	0.1982*	0.1768*	0.1578*	0.1406*

'*' denotes statistical significance (α=0.05) over the best among state-of-the-art ('+')

SQ1: How Does Different Parameter Selection Affect the Performance of DRACoR?

We have evaluated the impact of various experimental parameter settings, including vector dimension (A_i and T_i), adjustment parameter (m), damping constant (α), target researcher's academic level (n_c), target researcher's degree (n_d), number of iteration, and partitioning time point on DRACoR. The overall results are shown in Sec. 6.9.5.

SQ2: How Does DRACoR Handle the Cold-start Issue for the New Researcher?

We conducted an extensive experiment to prove the efficacy of the proposed model DRACoR against new collaborators. Our model recommends collaborators, including new and old irrespective of target researchers' degree and academic level. To validate the effectiveness of DRACoR, we experimented with varying academic level (n_c) of a target researcher as explained in Sec. 6.9.5. We also evaluated with varying target researcher's degree (n_d) as described in Sec. 6.9.5.

SQ3: How Effective is DRACoR in Comparison to Other State-Of-The-Art methods ?

The complete results of F1 are depicted in Table 6.9 and Table 6.10. It is evident that the proposed approach DRACoR shows a consistent F1 over all other standard approaches

on the hep-th dataset and DBLP dataset. The complete results of MRR and nDCG are depicted in Table 6.11 and Table 6.12. It is evident that, proposed approach shows a consistent nDCG and MRR over all other standard approaches on hep-th dataset and DBLP dataset.

6.10.5 Some Insights

The overall performance results obtained showcase the efficacy of the proposed DRACoR. The good overall precision, recall, F1, MRR, and nDCG verify that the models can effectively recommend the relevant collaborators. However, there are a few limitations to our work.

(i) As we have considered only top 100 topics for each researcher. As a result, it may fail to recommend relevant collaborators where a target researcher is associated with multiple research areas.

(ii) We do not consider the affiliation data, due to which in few cases both MRCR model and DBCR models exhibit the worst performance in a few positions over state-of-the-art methods.

(iii) We have considered multiple factors to enhance the link importance among researchers but the individual MRCR or DBCR model is not stable throughout the recommendation. We also notice that the model MRCR can give better results to position 60. But afterward, it exhibits the worst performance over other standard methods.

(iv) As we adopted RWR model to recommend collaborators in MRCR Model which can jump with a probability of α, and restart probability of 1-α. We have set the value of α as 0.8 due to which after recommending 60 collaborators, the chances of getting relevant researchers are quite rare. The chances of getting other researchers (researcher with other research areas) will be more, and this might be the reason for obtaining the worst results after position 60 in MRCR model.

(v) Although we have used deep learning in DBCR model to capture hidden relationships mostly, the model performs worst till position 30, and afterward, it displays effective results over state-of-the-art methods.

6.11 Conclusions

In this work, we focus on recommending MICs (MPCs+MVCs), which can help researchers benefit more from collaboration based on the big scholarly data. We mainly focused on recommending potential collaborators based on similar research interests and social accessibility. We propose a multi-level fusion-based academic collaborator recommender system DRACoR (Deep learning and Random walk based Academic Collaborator Recommender). Mainly, it fuses Meta-path aggregated Random walk based Collaborator Recommendation (MRCR) that finds out MPCs with Deep learning-Boosted Collaborator Recommendation (DBCR) models that find MVCs so that their combination (MICs) can be recommended.

The proposed model DRACoR works irrespective of researchers' past publication records and is entirely biased towards the current works. Isolated researchers, researchers with less number of co-authors, or researchers with fewer publication records are also getting an equal chance of inclusion in the final recommendation. Individually, we have considered a few factors, namely meta-path features, dynamic interest, research content, scholarly influence-aware features, and hidden relationship to determine the similarity between two researchers.

We conducted extensive experiments on a subset of hep-th and DBLP dataset to evaluate the performance of DRACoR against various state-of-the-art methods. The proposed system DRACoR outperforms other state-of-the-art models when compared in terms of precision, recall, F1, MRR, and nDCG, respectively. The proposed model reveals that the combination of topic distribution and co-authorship networks based models can significantly improve the effectiveness of the academic collaborations.

Nonetheless, there is still room for future studies in this direction. Besides, there can be many latent reasons behind the collaboration of two researchers. They might have met at a meeting or are from the same institution. Additionally, many other features such as researcher age, education, institution, acknowledgment details, the personal profile should be explored to improve upon our model. Collaboration can also be for cross-domain research. The relationship among co-authors of a paper is far more complicated than what we have imagined.