

Paper Type: Original Article

Game-Theoretic Approach to Weighted Rank Aggregation Based on Strategic Interactions among Rankers

Mohaddethe Nasrabadi^{1*} , Hamid Saadatfar², Mahdi Kherad³

¹ Department of Computer Engineering, Birjand Branch, Islamic Azad University, Birjand, Iran; Nasrabadi_Mohaddethe@iau.ac.ir.

² Department of Computer Engineering, Faculty of Electrical and Computer Engineering, University of Birjand, Birjand, Iran; Saadatfar@birjand.ac.ir.

³ Department of Computer Engineering and IT, University of Qom, Iran; m.kherad@stu.qom.ac.ir.

Citation:

Received: 08 February 2026

Revised: 13 April 2026

Accepted: 22 Jun 2026

Nasrabadi, M., Saadatfar, H., & Kherad, M. (2026). Game-theoretic approach to weighted rank aggregation based on strategic interactions among rankers. *Research Annals of Industrial and Systems Engineering*, 3(3), 212-227.

Abstract

Rank Aggregation (RA) refers to the process of combining multiple rankings from a set of candidate base rankers to achieve a better overall ranking. It has been widely applied across various domains and plays a critical role in integrating information from different biological studies addressing a common problem. In biological studies, due to the high heterogeneity of sources, the base rankers are often partial, lengthy, and of varying quality, and the ground-truth rankings are typically unavailable. This paper proposes a novel model for RA in biological and biomedical applications, modeling the combination of multiple rankings from different sources as a non-cooperative game among rankers. Unlike traditional methods that treat rankers as independent and passive entities, the proposed approach models each ranker as a strategic agent seeking to maximize its own utility and influence on the final aggregated ranking. The proposed utility function integrates similarity to the final ranking, agreement with other rankers, and the cost of generating a ranking. An iterative algorithm based on best-response dynamics is used to update each ranker's weight according to their current utility, leading to a stable aggregated output. To demonstrate the effectiveness of the proposed method in solving biological problems, three benchmark datasets—Breast, microRNA, and Prostate—were used. Experimental results indicate that the proposed method outperforms traditional RA techniques in both effectiveness and robustness.

Keywords: Rank aggregation, Biological studies, Game theory, Non-cooperative game, Strategic interaction, Biological data.

1 | Introduction

The problem of Rank Aggregation (RA) is the combination of multiple ordered lists of entities, as base rankers, to achieve a better ranking in the form of an aggregated ranker [1]. In one classification, RA can be

 Corresponding Author: Nasrabadi_Mohaddethe@iau.ac.ir

 <https://doi.org/10.22105/raise.vi.100>

 Licensee System Analytics. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0>).

divided into two categories [2]. In the first category, a score is assigned to each entity in each ordered list, and these scores are used for aggregating the lists, known as score-based aggregation. In the second category, only the rank of each entity in the ordered lists is used, known as order-based aggregation. RA has a rich history in information retrieval, marketing and advertising, sports competitions, applied psychology, social choice (political elections), and so on. In recent years, with the rapid development of technology, RA has faced new challenges in fields such as building search engines for web page ranking and identifying highly expressed genes in genomic studies, which is the main focus of this paper.

For an important biological question, large amounts of genomic data are often collected from various laboratories or research groups over time. Such data are inherently noisy due to the heterogeneity of different sources, including experiments, platforms, as well as different preprocessing procedures. For example, suppose data are available for gene copy number variation from Single-Nucleotide Polymorphism (SNP) arrays, gene expression from cDNA arrays, and protein-binding data from ChIP-seq; the goal is to find candidate genes whose function may be altered at a specific disease stage. Since the data come from different technological platforms that measure different aspects of the biological system, models that use raw data for all available information cannot be exploited.

To aggregate such data, researchers often use powerful meta-analytic approaches based on ranked lists [3], [4] which, without reverting to raw-data modelling, yield more reliable results and also increase the validity and reproducibility of individual studies [5]. For many such approaches, a core task is to perform RA. For analysing data from different biological experiments, an advantage of using a rank-aggregation-based method is that ranks are invariant to transformations and normalisations as long as the corresponding ranks are preserved. In other words, transformation and normalisation are usually not necessary for rank-based methods [6]. In practice, given the varying quality of base rankers, the RA problem can become even more challenging. For example, in biological studies, some laboratories collect or analyse data more efficiently than others.

In some cases, some base rankers may be meaningless or even misleading. Assigning different weights to base rankers, as mentioned in [2], [5], [7], appears to be the only available approach that accounts for the varying quality of base ranks. However, these approaches have a clear limitation: they lack a systematic, principled strategy for designing an appropriate weighting scheme for a practical problem, and they require strong initial assumptions and high computational complexity. Supervised RA may help to learn good weights, as presented in [8], but it requires a good training dataset, which is often unavailable. In most conventional rank-aggregation methods, it is assumed that base rankers (such as gene-analysis algorithms or outputs from different laboratories) are merely passive sources that provide their outputs independently and without interaction.

However, in many real-world applications, especially in biological and medical studies, rankers (or ranking sources) may use different data sources, different assumptions, and even diverse scientific objectives. This heterogeneity can lead to conflict, inconsistency, or purposeful alignment between rankers. In such situations, ignoring their interactive nature may lead to inefficient integration and inaccurate results.

Game theory is a branch of applied mathematics and economics that studies mathematical models of strategic interactions among rational agents. Applications of this theory in ensemble learning, expert opinion aggregation, multi-agent systems, and information-source combination show that modelling interactions among agents can lead to more stable solutions than classical non-interactive methods [9].

In this paper, we model RA within a game-theoretic framework. In this approach, each ranker is considered a strategic agent that tries to adjust its ranks so as to have the greatest impact on the final ranking while maintaining scientific accuracy. This competition or interaction among rankers can be modelled as a non-cooperative game, in which each player, considering the strategies of the others, makes the optimal decision. In the proposed model, the utility function of each ranker is designed to depend on three key factors: 1) the similarity of its provided ranking to the final ranking (as a measure of influence), 2) the degree of agreement

with other rankers (alignment), and 3) the cost of deviating from consensus. By defining this utility and analysing the dynamic behaviour of the rankers, a Nash equilibrium can be reached, which represents the final ranking. Thus, the final aggregation results from a stable, optimal interaction among data sources rather than a mere statistical combination of outputs. This model is not only theoretically innovative in the fields of artificial intelligence and game theory, but also, practically, for integrating heterogeneous results in genomic and biological studies, it provides a transparent, analysable, and adaptable structure.

The remainder of this paper is organised as follows. In Section 2, a review of the literature on the rank-aggregation problem and previous related research is presented. Then, in Section 3, the details of the proposed method are described. Section 4 is devoted to the details of the conducted experiments and the presentation of the obtained results. Finally, in Section 5, a summary of the paper's content will be provided.

2 | Related Works

Recently, many researchers have used RA in biological or medical problems. The authors of [10], using the RA method (TopKLists), combined data from six independent CRISPR experiments in the context of cancer immunotherapy. Their goal was to identify genes that improve the infiltration of T cells into tumours. The results showed that the RA method can reveal novel key genes such as AAK1, SPRR1B, and EHHADH, which are not observed in any single study alone. A new method called bootGSEA [11] has been introduced, in which, using the bootstrap technique, Gene Set Enrichment Analysis (GSEA) is performed multiple times, and then the results are combined using RA. This method has been used in the analysis of multi-omics data (such as transcriptomics and proteomics) in cancer and spinal muscular atrophy, and it has been shown that its results are more reproducible than traditional methods. A tool called GeneRaMeN [11] has been developed in the R-Shiny environment, which uses RA methods to analyse the results of multiple gene experiments. This tool was applied to the analysis of 24 CRISPR experiments for flaviviruses as well as 13 studies on SARS-CoV-2, and it was able to identify common key genes as well as those specific to particular conditions. This tool offers a novel approach for extracting shared and differentiated information in biological studies.

In another study [12], using the RRA method, transcriptomic data from various studies related to periodontitis (gum inflammation) were combined. The final results led to the identification of key genes such as C1QA, BST2, and an important lncRNA (LINC01133). This study demonstrated that RA can reliably integrate results from heterogeneous studies. Another paper [13] performed an RA of miRNAs involved in Mild Cognitive Impairment (MCI). They combined several independent studies using the RRA method. Although no significant markers were obtained from this aggregation, this work was recognised as an example of the challenges of aggregating heterogeneous clinical data and highlighted the importance of careful interpretation of results.

In a recent study [14], data from seven microarrays from patients with Alzheimer's disease were aggregated using RRA. The result was the identification of 473 significantly differentially expressed genes, with the TAC1 gene selected as one of the most important key genes, which was also validated in an animal model of Alzheimer's. This paper is a successful example of the application of RA in identifying novel genes in neurological diseases. These recent studies show that RA methods (especially RRA and TopKLists) are powerful tools for integrating heterogeneous biological data in various studies. From analysing CRISPR data to combining transcriptomic and microRNA results, these methods are increasingly being used in the discovery of key genes, disease pathways, and biomarkers. Given the presence of heterogeneous and sometimes conflicting ranking sources, traditional statistical approaches (such as Borda, RRA, or Stuart) may not be able to adequately model the complex interactions among ranking sources. Therefore, researchers have proposed using game theory to model these interactions. In this framework, each ranker is considered a rational player who chooses a ranking strategy with the aim of maximising its influence on the final ranking. This game can be non-cooperative, where each ranker acts independently to gain more benefit, or cooperative, where a group of rankers may form coalitions to exert greater influence [15]. In both cases, concepts such as

Nash equilibrium or the Shapley value are used to analyse the contribution and impact of each agent on the final output [16].

In a new line of research, the application of game theory to RA, particularly for analysing manipulation trends and strategic attacks on ranking systems, has attracted considerable attention. For example, Ma et al. [17] investigated targeted attacks against well-known RA algorithms based on pairwise comparisons, such as HodgeRank and RankCentrality, using a game-theoretic framework. They showed that the behaviour of the attacker and the ranking system can be modelled as a continuous game, and the Nash equilibrium defines the topology of the attack; consequently, the attacker, with complete or incomplete information, can impose a targeted ranking. Another important step in this area was taken by Mai et al. [18], who introduced the concept of sequential manipulation. In this study, an attacker manipulates pairwise comparisons online during the data collection process and uses a distributionally robust game-theoretic framework to model the game equilibrium under uncertainty. Their results show that the attacker's strategies under conditions of incomplete or complete knowledge can lead to equilibria that are skewed in favour of the attacker, and adaptability or strong stability has been demonstrated in this process. These two studies highlight the key role of game theory in understanding the stability, security, and strategic interaction among rankers. The models presented in these studies show that in order to design robust RA methods, one must engage in the analysis of dynamic equilibria and the strategic behaviour of agents—an approach that precisely forms our proposed path for adapting RA methods in the biomedical context with game theory.

3 | Proposed Method

Traditional RA methods usually assume that base rankers are independent and passive sources that provide their rankings without mutual interaction and solely based on the available data. However, in many biological and medical applications, rankers can represent algorithms, laboratories, or sources that interact with each other or strive to maximise their influence on the final outcome. In such situations, the assumption of independence among rankers is inefficient and may lead to incorrect or unstable integration of results. In order to model the interaction among rankers more realistically, this paper presents a novel framework based on game theory. In this framework, each ranker is modelled as a strategic agent that attempts to determine its rankings in such a way as to have the greatest impact on the final ranking while maintaining credibility and accuracy. This problem is modelled as a non-cooperative game in which agents, with relative awareness of others' strategies, seek to maximise their own utility.

The proposed model specifically analyses the strategic interaction between rankers and employs concepts such as Nash equilibrium to find a stable state in which no ranker has an incentive to change its strategy. Furthermore, for the practical implementation of this model, a utility function combining agreement and disagreement, along with an iterative optimisation algorithm, is used. In the following, the precise definition of the game, its elements, the utility function, and the solution process of the model are presented.

3.1 | Game Definition

In the proposed model, the RA process is modelled as a static non-cooperative game among a set of rankers. In this framework, each ranker is considered a decision-making agent (player) that, by choosing an appropriate strategy, seeks to maximise its utility in terms of influence on the final ranking.

Assume:

$N = \{1, 2, \dots, n\}$: Set of players (rankers).

$O = \{o_1, o_2, \dots, o_m\}$: Set of items (e.g., genes) to be ranked.

$R_i \in S_m$: Ranking provided by player i , which is a member of the set of possible permutations S_m .

$R = \{R_1, R_2, \dots, R_r\}$: Profile of strategies (rankings of all players).

R_{agg} : Final aggregated ranking from all rankers (by a specific mechanism).

Utility function: The objective of each player is to maximise a utility function that is a combination of agreement with the final ranking, agreement with other rankers, and reducing the cost of deviation from consensus. The utility function of player i is defined as follows:

$$U_i(R_i, R_{-i}) = \alpha \cdot \text{Sim}(R_i, R_{\text{agg}}) - \beta \cdot \frac{1}{n-1} \sum_{\substack{j=1 \\ j \neq i}}^n \text{Dis}(R_i, R_j) - \gamma \cdot C(R_i), \quad (1)$$

where:

$\text{Sim}(R_i, R_{\text{agg}})$: Similarity between the ranking of player i and the final ranking, e.g., using Kendall or Spearman Correlation (SC).

$\text{Dis}(R_i, R_j)$: The degree of inconsistency between ranker i and j .

$C(R_i)$: The cost for player i of producing a specific ranking (e.g., large deviation from a previous ranking or from the mean).

α, β, γ : Coefficients for adjusting the weight of each component.

Final ranking: The final ranking R_{agg} can be generated via weighted aggregation of rankings:

$$R_{\text{agg}} = \text{Aggregate}(R_1 \dots R_n; w_1 \dots w_n), \quad (2)$$

where the weight of each player can be determined proportionally to prior accuracy or current utility:

$$w_i = \frac{U_i}{\sum_{j=1}^n U_j}. \quad (3)$$

Nash equilibrium: A strategy profile $R^* = (R_1^* \dots R_n^*)$ is a Nash equilibrium if and only if:

$$U_i(R_i^*, R_{-i}^*) \geq U_i(R_i', R_{-i}^*), \quad \forall R_i' \in \mathcal{S}_m, \quad \forall i \in N, \quad (4)$$

That is, no player can obtain greater utility by changing its ranking unless the other players also change their strategies.

3.2| Game Solution Process and Proposed Algorithm

After defining the non-cooperative game among rankers, the goal is to find an equilibrium profile of strategies in which no ranker is willing to change its ranking unless others also change their strategies (Nash equilibrium). Because the strategy space is complex (all possible permutations), an analytical solution is difficult, and in practice it requires an iterative algorithm to approximate the equilibrium and estimate the final ranking. To solve this game, an iterative process based on Best Response Dynamics is used. In this method, at each step, rankers update their rankings in such a way as to maximise their current utility compared to other rankers. This process continues until convergence to a stable state. The proposed algorithm consists of the following steps:

- I. Input: The set of initial rankings $R_1^{(0)}, R_2^{(0)}, \dots, R_n^{(0)}$ provided by all rankers is collected. Also, the values of the parameters α, β, γ , the convergence threshold ϵ , and the maximum number of iterations are determined.
- II. Initial estimation of the final ranking: Using an equal-weighted average of all rankings, the initial final ranking is calculated:

$$R_{\text{agg}}^{(0)} = \text{Aggregate}(R_1^{(0)} \dots R_n^{(0)}; \text{weights}=1), \quad (5)$$

- III. Calculation of similarities and disagreements: For each ranker i , the similarity between its ranking and the current final ranking is calculated (e.g., using Kendall's or Spearman's coefficient). Also, the average

disagreement of each ranker's ranking with other rankers is computed in order to examine the conflicts among them:

$$\begin{aligned} \text{Sim}_i^{(t)} &= \text{Sim} \left(R_i^{(t)} \cdot R_{\text{agg}}^{(t)} \right), \\ \text{Dis}_i^{(t)} &= \frac{1}{n-1} \sum_{j \neq i} \text{Dis} \left(R_i^{(t)} \cdot R_j^{(t)} \right), \end{aligned} \quad (6)$$

IV. Calculation of each ranker's utility: The utility of each ranker is computed as a linear combination of similarity, disagreement, and cost:

$$U_i^{(t)} = \alpha \cdot \text{Sim}_i^{(t)} - \beta \cdot \text{Dis}_i^{(t)} - \gamma \cdot C \left(R_i^{(t)} \right), \quad (7)$$

V. Updating the weights: The utility of each ranker is normalised and considered as its influential weight in the next aggregation step:

$$w_i^{(t)} = \frac{U_i^{(t)}}{\sum_{j=1}^n U_j^{(t)}}, \quad (8)$$

VI. Calculation of the new final ranking: The new final ranking is calculated using the current rankings and the updated weights:

$$R_{\text{agg}}^{(t+1)} = \text{Aggregate} \left(R_1^{(t)} \dots R_n^{(t)}; w_1^{(t)} \dots w_n^{(t)} \right), \quad (9)$$

VII. Updating the rankings: Each ranker can choose a new ranking $R_i^{(t+1)}$ such that its utility increases compared to $R_i^{(t)}$ (e.g., by moving closer to $R_{\text{agg}}^{(t)}$).

VIII. Convergence check: If the change between two consecutive final rankings is less than the threshold ϵ , or if the number of iterations exceeds the maximum limit, the algorithm stops. Otherwise, it returns to Step 3.

IX. Final output: The stable final ranking R_{agg}^* , the final weight of each ranker w_i^* , the final utility, and the order of influence of the agents are presented as the final output of the algorithm.

This equilibrium process allows the final ranking to be obtained not merely as a statistical average of the rankings, but as a stable outcome of a strategic game among rankers with varying accuracies and perspectives. The pseudocode of the proposed algorithm is shown in Algorithm 1.

Algorithm 1. Pseudocode of the proposed algorithm.

Input :

$R = \{R_1^{(0)}, R_2^{(0)}, \dots, R_n^{(0)}\} \rightarrow$ Initial rankings by n rankers

$\alpha, \beta, \gamma \rightarrow$ Weight parameters

$\epsilon \rightarrow$ Convergence threshold

$\text{max_iter} \rightarrow$ Maximum number of iterations

Output :

$R_{\text{agg}}^* \rightarrow$ Final aggregated ranking

$W = \{w_1^*, w_2^*, \dots, w_n^*\} \rightarrow$ Final ranker weights

Begin

$t \leftarrow 0$

Compute initial aggregate ranking :

$R_{\text{agg}}^{(0)} \leftarrow \text{Aggregate}(R_1^{(0)}, \dots, R_n^{(0)})$ using equal weights

Repeat

For each ranker $i = 1$ to n do

$\text{Sim}_i \leftarrow \text{Similarity}(R_i^{(t)}, R_{\text{agg}}^{(t)})$ // e.g., Kendall or Spearman

$\text{Dis}_i \leftarrow (1 / (n - 1)) \times \sum_{j \neq i} \text{Dis}(R_i^{(t)}, R_j^{(t)})$ // Average pairwise disagreement

$\text{Cost}_i \leftarrow \text{Cost}(R_i^{(t)})$ // Optional cost function

$U_i \leftarrow \alpha \times \text{Sim}_i - \beta \times \text{Dis}_i - \gamma \times \text{Cost}_i$ // Utility of ranker i

Normalize weights:

For each i : $w_i \leftarrow U_i / \sum_j U_j$

Update aggregated ranking:

$R_{\text{agg}}^{(t+1)} \leftarrow \text{Aggregate}(R_1^{(t)}, \dots, R_n^{(t)}, \text{weights} = w_1, \dots, w_n)$

Optional: Each ranker updates $R_i^{(t+1)}$ to improve U_i (e.g., align with R_{agg})

$t \leftarrow t + 1$

Until convergence:

if $\|R_{\text{agg}}^{(t)} - R_{\text{agg}}^{(t-1)}\| < \epsilon$ or $t \geq \text{max_iter}$

Return R_{agg}^*, W

4 | Analysis and Evaluation

To demonstrate the efficiency of the proposed weighted RA method based on game theory, named MYRA, for solving biological problems, three datasets, Breast¹, microRNA [5], and Prostate [19], have been used. The Breast dataset consists of three lists of DNA microarray results (differentially expressed genes) obtained from three breast cancer studies: TransBig [20], MDCC [21], and Pusztai [22], with the aim of finding genes that are differentially expressed between breast cancer and normal breast tissues. Despite their common goal, these three studies were conducted in different laboratories and also differ in the materials and DNA microarray systems used, which makes it difficult to perform an integrated analysis of the data, given that the raw values are not directly comparable. Instead, we apply a high-level meta-analytic method such as the proposed RA to combine the top- k gene lists from each of the three studies. In this dataset, only the genes that are common to all studies are considered; therefore, each of the three lists has a length of $n=k=917$.

¹ <https://rdrr.io/rforge/TopKLists/man/breast.html>

Table 1 presents the gene rankings obtained by the three breast cancer studies, where the first column shows the gene ranks and the next three columns show the gene symbols obtained in the three studies.

The microRNA dataset pertains to an RA problem in the biological domain, aiming to aggregate results from several DNA microarray target prediction experiments. Today, there are several computational algorithms for predicting the genes whose messenger RNA (mRNA) are targets of DNA microarrays, but their results may differ widely [5]. Therefore, it can be useful to aggregate and filter the disparate results so that researchers can have greater confidence in the validity of these targets before conducting expensive experiments. Since the sensitivity and specificity of such algorithms are largely unknown, it seems more reasonable to regard each list obtained from each algorithm merely as a ranked list.

Table 1. Ranks of genes obtained by the three breast cancer studies (Breast dataset).

Rank	Transbig	Mdcc	Pusztai
1	ESR1	ESR1	ESR1
2	TBC1D9	TBC1D9	TBC1D9
3	SCUBE2	EVL	SCUBE2
4	EVL	SCUBE2	FBP1
5	NAT2	CIRBP	EVL
6	BTG2	FBP1	RHOB
7	GSTM3	FUT8	QDPR
8	FBP1	RHOB	CIRBP
9	CIRBP	KIAA1324	IDUA
10	ORC6L	BTG2	BTG2
11	BUB1	TBX3	FUT8
12	FUT8	C1orf106	YEATS2
13	PCSK6	QDPR	BLOC1S1
14	PFKP	IDUA	C1orf106
15	GPR126	PFKP	PCSK6
16	C1orf106	ADM	KRT18
17	TBX3	MZF1	PECI
18	YEATS2	NDRG1	SLC7A8
19	MZF1	KRT18	FBXL7
20	CENPA	HCFC1R1	PRKAG1
.	.	.	.
.	.	.	.
.	.	.	.
900	C7orf43	CALR	NCAM2
901	ALDH3A1	MBD3	SETDB1
902	AIPL1	EPB42	ACTN3
903	GABRR1	CAMK1	SFPQ
904	AFF4	C5AR1	BBC3
905	ZFY	FOXJ1	HGFAC
906	MC3R	HSF4	HSF4
907	ZFP30	UTP6	RASL11B
908	GTF2A2	TRO	DTL
909	TULP1	MEA1	CDC2L5
910	FBXW2	SFMBT1	INTS7
911	OR2H2	CLK3	C2orf42
912	ERCC3	GPR37L1	QPCTL
913	ZC3H7B	RPS6KB2	ASXL2
914	ZNF192	PSMD2	TNFRSF1A
915	FCER2	HBZ	USP39
916	USP2	SETDB1	NUP98
917	FZD10	MAPRE3	GALK2

The microRNA dataset includes three top-60 lists of DNA microarray target genes for miR-155 obtained from miRanda [23], TargetScan [24], and PicTar [25], shown with their rankings in *Table 2*.

Table 2. List of DNA microarray target genes obtained from three studies (microRNA dataset).

Rank	Miranda	Targetscan	Pictar
1	BACH1	ZNF537	ZNF537
2	SEMA5A	BACH1	BACH1
3	OR1K1	FGF7	IKBKE
4	JARID2	ZNF652	ASTN2
5	JARID1B	FLJ30435	AKAP10
6	SGKL	RAB11FIP2	MGC13272
7	OPRM1	ZIC3	FBXO11
8	RAPH1	MIDN	KBTBD2
9	CLCN5	ARID2	COL7A1
10	SPI1	PAPOLA	MAP3K10
11	TP53INP1	KIBRA	RNF123
12	STAC	PICALM	FLJ14299
13	CARHSP1	CAB39	SF3B1
14	PSKH1	CEBPB	KPNA1
15	MAP3K14	RNF123	CARHSP1
16	HBP1	SOCS1	EHD1
17	AGTRAP	SOX10	PAPOLA
18	KCNN3	SUFU	RAB34
19	TRIM32	MAP3K7IP2	GCN5L2
20	CSNK1G2	GPM6B	SOCS1
21	SOCS1	MLR1	ZIC3
22	CYR61	ASTN2	MLSTD2
23	DUSP14	FBXO11	SALL1
24	MGP	MAP3K14	ACTA1
25	SLC11A2	C10orf26	LRP1B
26	FGF7	TOMM20	C1QL2
27	PCDH9	C3orf18	LOC51161
28	DHX40	TLE4	CSNK1G2
29	KIAA0258	SGKL	FGF7
30	CEBPB	BCAP29	ADD3
31	GCET2	CARHSP1	MYB
32	ARL8	MYO1D	OLFML3
33	SEL1L	CSF1R	ARNTL
34	ZIC3	FLJ37543	COPS3
35	RREB1	SOX1	SMARCA4
36	MYPN	UPP2	SPRED1
37	RNF123	TP53INP1	CEBPB
38	C21orf107	MYO10	ARVCF
39	STARD6	SPI1	KCNN3
40	CDC37	DNCI1	CSF1R
41	AICDA	PRO1855	ZNF642
42	SATB2	LOC284058	KIBRA
43	FBXO33	ETS1	YWHAE
44	RPS6KA3	MLSTD2	ETNK2
45	FOS	GDF6	182-FIP
46	BIRC4	KIAA1889	SEPT11
47	NKX3-1	SMARCA4	SCG2
48	EIF2C4	RREB1	UBQLN1
49	LRP1B	ZNF236	ETS1
50	KIAA1411	DNAJB1	SIM2

Table 2. Continued.

Rank	Miranda	Targetscan	Pictar
51	CHAF1A	FLJ20273	KIAA0863
52	C10orf26	SIM2	AXOT
53	SGCZ	FBXO33	WIT-1
54	SDCBP	SBLF	ENTH
55	SMARCA4	SGCB	SKI
56	CUGBP2	AICDA	H3F3A
57	HRPT2	CARD11	MAP3K14
58	MEIS1	ETNK2	SLA
59	MEF2A	OLFML3	KIAA1274
60	SYPL	EHD1	NDFIP1

The Prostate dataset includes five top-25 lists of DNA microarray results obtained from five prostate cancer studies named Dhanasekaran [23], Luo [24], Welsh [25], Singh [26], and True [27], to find genes that are differentially expressed between prostate tumours and normal prostate tissues. *Table 3* presents the gene rankings obtained by the five prostate studies, where the first column shows the gene ranks, and the next five columns show the gene symbols obtained in the five studies.

Table 3. Ranks of genes obtained by the five prostate cancer studies (Prostate dataset).

Rank	Luo	Welsh	Dhanasekaran	Truee	Singh
1	HPN	HPN	OGT	AMACR	HPN
2	AMACR	AMACR	AMACR	HPN	SLC25A6
3	CYP1B1	OACT2	FASN	NME2	EEF2
4	ATF5	GDF15	HPN	CBX3	SAT
5	BRCA1	FASN	UAP1	GDF15	NME2
6	LGALS3	ANK3	GUCY1A3	MTHFD2	LDHA
7	MYC	KRT18	OACT2	MRPL3	CANX
8	PCDHGC3	UAP1	SLC19A1	SLC25A6	NACA
9	WT1	GRP58	KRT18	NME1	FASN
10	TFF3	PPIB	EEF2	COX6C	SND1
11	MARCKS	KRT7	STRA13	JTV1	KRT18
12	OS-9	NME1	ALCAM	CCNG2	RPL15
13	CCND2	STRA13	GDF15	AP3S1	TNFSF10
14	NME1	DAPK1	NME1	EEF2	SERP1
15	DRRK1A	TMEM4	CALR	RAN	GRP58
16	TRAP1	CANX	SND1	PRKACA	ALCAM
17	FMO5	TRA1	STAT6	RAD23B	GDF15
18	ZHX2	PRSS8	TCEB3	PSAP	TMEM4
19	RPL36AL	EMTPD6	EIF4A1	CCT2	CCT2
20	ITPR3	PPP1CA	LMAN1	G3BP	SLC39A6
21	GCSH	ACADSB	MAOA	EPRS	RPL5
22	DDB2	PTPLB	ATP6V0B	CKAP1	RPS13
23	TFCP2	TMEM23	PPIB	LIG3	MTHFD2
24	TRAM1	MRPL3	FMO5	SNX4	G3BP2
25	YTHDF3	SLC19A1	SLC7A5	NSMAF	UAP1

A primary task in many genetic studies, such as the two datasets mentioned, is to identify genes associated with certain complex human diseases. Given this, a good criterion for evaluating the performance of RA methods should assess the ability of each method to correctly rank the relevant genes. Suppose only a limited number of resources are available for further investigation of the studied genes; then, the ranking of genes that are at the top of the list is very important, whereas the order of genes near the bottom of the list is almost insignificant. In other words, instead of considering criteria such as the AUC measure, which can only evaluate full lists, in biological studies we need criteria that can also evaluate partial top-k lists [1]. Such criteria include Kendall Distance (KD), Spearman Distance (SD), Kendall Correlation (KC) (the ratio of the number of concordant pairs minus the number of discordant pairs to the total number of element pairs), and SC (applying Pearson correlation to the ranks of elements of two lists instead of to the values of the two lists). One advantage of correlation measures over distance measures is that they lie within a fixed range. Both KC

and SC fall within the range $[-1, 1]$. To use these criteria for evaluating aggregated rankers, the value of these measures is calculated between the aggregated ranker and each of the base rankers individually, and the sum is divided by the number of base rankers to obtain the final value of the criteria. Ultimately, the smaller the final value of the distance measures and the larger (closer to one) the final value of the correlation measures, the better the aggregated ranker.

To evaluate the proposed method, MYRA, it is applied to the Breast, microRNA, and Prostate datasets, and the obtained values of the four evaluation criteria, KD, SD, KC, and SC, are compared with the results of conventional RA methods, namely the Borda methods (Mean, MED, GEO, and L2), Markov chain-based methods (MC1, MC2, and MC3), and distribution-based methods (RRA and Stuart). The aggregated rankers obtained by each of the aforementioned methods, along with their evaluation criterion values, are shown for the Breast dataset in *Table 4*, for the microRNA dataset in *Table 5*, and for the Prostate dataset in *Table 6*. For the implementation and execution of the proposed method (RAA), the software Matlab R2019b¹ was used on a computer with 8 GB of RAM and a five-core 2.4 GHz processor. For running the RRA and Stuart methods, the ready-made software package RobustRankAggreg² in Matlab R2019b was used, and for running the Borda methods (Mean, MED, GEO, and L2) and the Markov chain-based methods (MC1, MC2, and MC3), the ready-made package TopKLists³ in R software was used.

Table 4. RA by different methods for the breast dataset.

Rank	Med	Mean	Geo	L2	Mc1	Mc2	Mc3	Stuart	Rra	Myra
1	ESR1	ESR1	ESR1	ESR1	ESR1	ESR1	ESR1	ESR1	ESR1	ESR1
2	TBC1D9	TBC1D9	TBC1D9	TBC1D9	FZD10	FZD10	FZD10	TBC1D9	TBC1D9	TBC1D9
3	SCUBE2	SCUBE2	SCUBE2	SCUBE2	ZNF192	ZNF192	ZNF192	SCUBE2	SCUBE2	SCUBE2
4	EVL	EVL	EVL	EVL	ZC3H7B	ZC3H7B	ZC3H7B	EVL	EVL	EVL
5	FBP1	FBP1	FBP1	FBP1	USP2	USP2	USP2	FBP1	FBP1	FBP1
6	CIRBP	CIRBP	CIRBP	CIRBP	FCER2	FCER2	FCER2	CIRBP	CIRBP	CIRBP
7	RHOB	BTG2	BTG2	BTG2	ERCC3	ERCC3	ERCC3	BTG2	BTG2	FUT8
8	BTG2	FUT8	FUT8	FUT8	OR2H2	OR2H2	OR2H2	FUT8	FUT8	BTG2
9	FUT8	C1orf106	RHOB	RHOB	FBXW2	FBXW2	FBXW2	C1orf106	C1orf106	C1orf106
10	QDPR	QDPR	C1orf106	C1orf106	TULP1	TULP1	TULP1	RHOB	ADM	KIAA1324
11	C1orf106	KIAA1324	QDPR	QDPR	GTF2A2	GTF2A2	GTF2A2	QDPR	KIAA1324	QDPR
12	IDUA	YEATS2	KIAA1324	KIAA1324	ZFP30	ZFP30	ZFP30	KIAA1324	YEATS2	TBX3
13	PCSK6	RHOB	YEATS2	ADM	MC3R	MC3R	MC3R	YEATS2	QDPR	IDUA
14	PFKP	TBX3	TBX3	TBX3	ZFY	ZFY	ZFY	TBX3	CENPA	PFKP
15	TBX3	ADM	ADM	MZF1	AFF4	AFF4	AFF4	ADM	TBX3	YEATS2
16	YEATS2	GSTM3	GSTM3	CENPA	AIPL1	AIPL1	AIPL1	PFKP	MZF1	ADM
17	KRT18	MZF1	IDUA	GSTM3	C7orf43	C7orf43	C7orf43	GSTM3	GSTM3	MZF1
18	MZF1	PFKP	PFKP	PFKP	CAPZB	CAPZB	CAPZB	IDUA	BLOC1S1	NDRG1
19	KIAA1324	PCSK6	PCSK6	MZF1	GABRR1	GABRR1	GABRR1	PCSK6	NDRG1	KRT18
20	PECI	CENPA	MZF1	PCSK6	SMPD2	SMPD2	SMPD2	MZF1	PFKP	NDRG1

¹ <https://www.mathworks.com/>

² <https://www.mathworks.com/matlabcentral/fileexchange/41835-rank-aggregation>

³ <https://rdrr.io/rforge/TopKLists/>

Table 4. Continued.

Rank	MED	Mean	GEO	L2	MC1	MC2	MC3	Stuart	RRA	MYRA
900	ASXL2	ARHGEF11	ARHGEF11	MLLT1	GPR20	GPR20	GPR20	UTP6	NUP98	CAMK1
901	VAMP1	MLLT1	VAMP1	SETDB1	KATNB1	KATNB1	KATNB1	FBXL12	NR0B1	EPB42
902	BNIP3	MGAT4A	MGAT4A	MGAT4A	C8G	C8G	C8G	MGAT4A	SP110	AQP3
903	NUP98	VAMP1	MLLT1	VAMP1	SF3B4	SF3B4	SF3B4	NUP98	SMPD2	FBXL12
904	CACNA1S	C7orf43	C7orf43	C7orf43	WDR46	WDR46	WDR46	CLK3	TBXAS1	FOXJ1
905	HIST1H3C	NKIRAS2	SFMBT1	NKIRAS2	PCTK1	PCTK1	PCTK1	C7orf43	AQP3	MBD3
906	HGFA	PSD	NKIRAS2	PSD	MMP25	MMP25	MMP25	APOA4	IRGC	HSF4
907	APOA4	SFMBT1	PSD	SFMBT1	MYL6	MYL6	MYL6	TBXAS1	VAMP1	UTP6
908	TRO	TBXAS1	TBXAS1	APOC3	EXOSC1	EXOSC1	EXOSC1	VAMP1	FBXL12	MEA1
909	ITFG2	APOC3	APOC3	TBXAS1	HBXIP	HBXIP	HBXIP	NR0B1	UTP6	TRO
910	ENO3	HIST1H2BB	HIST1H2BB	HIST1H2BB	PGLYRP4	PGLYRP4	PGLYRP4	IRGC	ERCC3	SFMBT1
911	C2orf42	SFRS4	SFRS4	SFRS4	PTPRJ	PTPRJ	PTPRJ	ERCC3	C7orf43	CLK3
912	NR0B1	NR0B1	NR0B1	NR0B1	RND1	RND1	RND1	AQP3	MBD3	GPR37L1
913	AQP3	AQP3	AQP3	AQP3	TACR2	TACR2	TACR2	MBD3	SETDB1	RPS6KB2
914	HBZ	IRGC	IRGC	IRGC	RPL24	RPL24	RPL24	SETDB1	CLK3	PSMD2
915	TNFRSF1A	MBD3	MBD3	MBD3	MUTYH	MUTYH	MUTYH	MAPRE3	MAPRE3	HBZ
916	SETDB1	TRO	TRO	TRO	MYO15A	MYO15A	MYO15A	SFMBT1	TRO	SETDB1
917	HSF4	APOA4	APOA4	APOA4	BAP1	BAP1	BAP1	TRO	SFMBT1	MAPRE3
KD	0.51129	0.48769	0.49988	0.48737	0.49786	0.49786	0.49786	0.50440	0.50200	0.45624
SD	0.67242	0.65223	0.66206	0.64886	0.66641	0.66641	0.66641	0.66926	0.66967	0.58995
KC	-0.02257	0.02461	0.00023	0.02526	0.00427	0.00427	0.00427	-0.00879	-0.00399	0.08752
SC	-0.03341	0.03658	0.00052	0.03850	0.00644	0.00644	0.00644	-0.01211	-0.00632	0.11611

In the tables, the best values of the criteria are shown underlined.

rank	MED	Mean	GEO	L2	MC1	MC2	MC3	stuart	RRA	MYRA
1	ZNF537	BACH1	BACH1	BACH1	ZNF537	ZNF537	BACH1	BACH1	BACH1	BACH1
2	BACH1	SOC81	ZNF537	SOC81	BACH1	BACH1	SOC81	ZNF537	ZNF537	SOC81
3	CARHSP1	FGF7	FGF7	CARHSP1	IKBKE	FGF7	FGF7	FGF7	FGF7	FGF7
4	RNF123	CARHSP1	ZIC3	FGF7	MGC13272	SOC81	CARHSP1	SOC81	FGF7	CARHSP1
5	PAPOLA	ZIC3	CARHSP1	ZIC3	KBTBD2	RNF123	ZIC3	CARHSP1	CARHSP1	ZIC3
6	SOC81	RNF123	RNF123	RNF123	COL7A1	ZIC3	RNF123	ZIC3	ZIC3	RNF123
7	ZIC3	CEBPB	SOC81	CEBPB	RAB34	CARHSP1	RNF123	CEBPB	CEBPB	ZNF537
8	ASTN2	MAP3K14	ASTN2	ZNF537	SALL1	CEBPB	CEBPB	CEBPB	RNF123	CEBPB
9	FBXO11	SMARCA4	CEBPB	MAP3K14	SEMA5A	PAPOLA	MAP3K14	ASTN2	PAPOLA	ASTN2
10	MAP3K14	ZNF537	MAP3K14	PAPOLA	OR1K1	ASTN2	ASTN2	MAP3K14	SEMA5A	PAPOLA
11	FGF7	ASTN2	FBXO11	ASTN2	JARID2	FBXO11	PAPOLA	PAPOLA	SMARCA4	MAP3K14
12	CSNK1G2	PAPOLA	PAPOLA	FBXO11	JARID1B	MAP3K14	FBXO11	FBXO11	IKBKE	SGKL
13	SGKL	FBXO11	SGKL	SGKL	RAPH1	SGKL	SEMA5A	SEMA5A	OR1K1	FBXO11
14	CEBPB	SGKL	SEMA5A	CSNK1G2	STAC	CSNK1G2	CSNK1G2	SGKL	ASTN2	CSNK1G2
15	TP53DN1	CSNK1G2	SP11	TP53DN1	PSKH1	KIBRA	TP53DN1	SMARCA4	MAP3K14	TP53DN1
16	KCNN3	TP53DN1	TP53DN1	SP11	MGP	SMARCA4	SP11	IKBKE	FBXO11	SP11
17	SP11	IKBKE	KCNN3	KCNN3	FGF7	TP53DN1	SMARCA4	SMARCA4	JARID2	KCNN3
18	CSF1R	KIBRA	OR1K1	KIBRA	ZNF652	SP11	KIBRA	JARID2	ZNF652	SEMA5A
19	KIBRA	KCNN3	KIBRA	MLSTD2	FLJ30435	MLSTD2	KCNN3	KCNN3	AKAP10	OR1K1
20	MLSTD2	MLSTD2	CSNK1G2	CSF1R	RAB11FIP2	KCNN3	MLSTD2	SP11	FLJ30435	KIBRA
21	SMARCA4	CSF1R	JARID2	SMARCA4	ZIC3	C10orf26	LRP1B	TP53DN1	JARID2	JARID2
22	RREB1	LRP1B	ZNF652	LRP1B	MIDN	CSF1R	EHD1	CSNK1G2	CSNK1G2	JARID1B
23	ETS1	EHD1	SMARCA4	C10orf26	ARID2	LRP1B	KIBRA	CSF1R	SGKL	IKBKE
24	LRP1B	C10orf26	AKAP10	RREB1	PAPOLA	EHD1	C10orf26	AKAP10	MGC13272	OPRM1
25	C10orf26	RREB1	FLJ30435	SEMA5A	KIBRA	RREB1	FLJ30435	RREB1	RAB11FIP2	AKAP10
26	SIM2	OLFML3	JARID1B	OR1K1	PICALM	ETS1	SEMA5A	JARID1B	OPRM1	RAPH1
27	FBXO33	ETS1	KCNN3	IKBKE	CAB39	OLFML3	OR1K1	MGC13272	KBTBD2	MGC13272
28	AICDA	FBXO33	MGC13272	JARID2	CEBPB	FBXO33	IKBKE	RAB11FIP2	MIDN	ZNF652
29	ETNK2	AICDA	RAB11FIP2	ZNF652	RNF123	AICDA	JARID2	KCNN3	RAPH1	CLCN3
30	OLFML3	ETNK2	EHD1	JARID1B	SF3B1	SIM2	JARID1B	OPRM1	TP53DN1	FLJ30435
31	EHD1	SIM2	MLSTD2	FLJ30435	KPNA1	ETNK2	ZNF652	KBTBD2	LRP1B	LRP1B
32	IS2-FIP	SEMA5A	OPRM1	AKAP10	SOC81	ARID2	OLFML3	MIDN	CLCN3	KBTBD2
33	ACTA1	IKBKE	KBTBD2	RAB11FIP2	SOX10	MIDN	AKAP10	RAPH1	COL7A1	RAB11FIP2
34	ADD3	OR1K1	MIDN	MGC13272	SUFU	RAB11FIP2	FLJ30435	MLSTD2	KCNN3	MLSTD2
35	AGTRAP	JARID2	RAPH1	MAP3K7P2	MAP3K7P2	FLJ30435	FLJ30435	ARID2	SP11	COL7A1
36	AKAP10	ZNF652	LRP1B	RAPH1	GPM6B	ZNF652	OPRM1	CLCN3	CSF1R	STAC
37	ARID2	AKAP10	ARID2	MIDN	MLR1	PICALM	RAB11FIP2	COL7A1	MAP3K10	SMARCA4
38	ARL3	FLJ30435	CLCN3	KBTBD2	ASTN2	CAB39	ETS1	CSF1R	KIBRA	MAP3K10
39	ARNTL	JARID1B	COL7A1	CLCN3	AKAP10	SOX10	RAPH1	EHD1	MLSTD2	MIDN
40	ARVCF	MGC13272	C10orf26	ARID2	FBXO11	SUFU	CLCN3	MAP3K10	FLJ14299	EHD1
41	AXOT	RAB11FIP2	CSF1R	COL7A1	MAP3K10	MAP3K7P2	KBTBD2	LRP1B	PICALM	PSKH1
42	BCAP29	OPRM1	MAP3K10	FLJ14299	MAP3K10	GPM6B	FBXO33	C10orf26	STAC	ARID2
43	BIRC4	KBTBD2	FLJ14299	EHD1	GCN5L2	MLR1	COL7A1	FLJ14299	CAB39	C10orf26
44	CIQL2	MIDN	PICALM	STAC	UBQLN1	IKBKE	MIDN	PICALM	SF3B1	FLJ14299
45	C10orf26	RAPH1	RREB1	PICALM	AXOT	MGC13272	AICDA	STAC	KPNA1	CSF1R
46	C3orf18	ARID2	STAC	FLJ14299	MAP3K14	AKAP10	MAP3K10	CAB39	PSKH1	SF3B1
47	CAB39	CLCN3	CAB39	CAB39	CYR61	C3orf18	ARID2	SF3B1	RREB1	HBP1
48	CARD11	COL7A1	SF3B1	SF3B1	SLC11A2	TLE4	STAC	ETS1	PICALM	PICALM
49	CDC37	MAP3K10	OLFML3	PSKH1	PCDH9	TOMM20	FLJ14299	KPNA1	LRP1B	RREB1
50	CHAF1A	PICALM	KPNA1	STARD6	KPNA1	PSKH1	PICALM	PSKH1	EHD1	KPNA1
51	CLCN3	STAC	PSKH1	HBP1	SATB2	SF3B1	SF3B1	HBP1	HBP1	AGTRAP
52	COL7A1	FLJ14299	ETS1	AGTRAP	RPS6KA3	FLJ14299	PSKH1	HBP1	C10orf26	CAB39
53	COPB3	CAB39	HBP1	SOX10	FOS	MAP3K10	SIM2	SIM2	SIM2	TRIM32
54	CUGBP2	SF3B1	FBXO33	SUFU	NKX3-1	COL7A1	ETNK2	OLFML3	FBXO33	RAB34
55	CYR61	KPNA1	AICDA	RAB34	EIF2C4	KBTBD2	CAB39	FBXO33	AGTRAP	GCN5L2
56	DHX40	PSKH1	AGTRAP	TRIM32	CHAF1A	BCAP29	KPNA1	AGTRAP	SOX10	SOX10
57	DNAJB1	HBP1	SOX10	MAP3K7P2	C10orf26	MYO1D	HBP1	SOX10	RAB34	CYR61
58	DNOC1	AGTRAP	RAB34	GCN5L2	TOMM20	UPP2	AGTRAP	AICDA	SUFU	OLFML3
59	DUSP14	SOX10	SUFU	GPM6B	C3orf18	SOX1	TRIM32	AICDA	SUFU	SUFU
60	EIF2C4	RAB34	ETS1	MLR1	TLE4	FLJ37443	RAB34	SUFU	GCN5L2	DUSP14
KD	1.1843	1.1291	1.1721	1.1566	1.1428	1.1436	1.1637	1.1197	1.1664	1.0852
SD	1.5448	1.3419	1.2376	1.2111	1.2067	1.2869	1.2224	1.2287	1.2463	1.1626
KC	-0.0121	-0.0339	-0.0026	0.0087	0.0200	0.0215	0.0023	0.0380	-0.0011	0.0689
SC	-0.0134	-0.0810	0.0020	0.0159	0.0272	0.0399	0.0128	0.0576	-0.0003	0.0968

Fig. 1. RA by different methods for the microRNA dataset.

Table 6. RA by different methods for the prostate dataset.

Rank	MED	Mean	GEO	L2	MC1	MC2	MC3	Stuart	RRA	MYRA
1	HPN	HPN	HPN	HPN	HPN	HPN	HPN	OGT	HPN	HPN
2	AMACR	AMACR	AMACR	AMACR	AMACR	AMACR	AMACR	HPN	AMACR	AMACR
3	FASN	GDF15	GDF15	GDF15	GDF15	GDF15	GDF15	AMACR	NME1	GDF15
4	KRT18	NME1	FASN	NME1	NME1	FASN	NME1	NME2	GDF15	NME1
5	GDF15	FASN	NME1	FASN	FASN	KRT18	FASN	LDHA	FASN	FASN
6	EEF2	EEF2	EEF2	KRT18	EEF2	NME1	EEF2	RPL15	KRT18	KRT18
7	NME1	KRT18	KRT18	EEF2	KRT18	EEF2	KRT18	CYP1B1	NME2	EEF2
8	UAP1	UAP1	UAP1	NME2	NME2	UAP1	UAP1	ATF5	EEF2	NME2
9	ACADSB	NME2	NME2	UAP1	SLC25A6	OACT2	NME2	BRCA1	OACT2	SLC25A6
10	ALCAM	OACT2	SLC25A6	OACT2	UAP1	NME2	SLC25A6	LGALS3	OGT	UAP1
11	ANK3	SLC25A6	OACT2	SLC25A6	OACT2	SLC25A6	OACT2	MYC	SLC25A6	OACT2
12	AP3S1	CANX	OGT	STRA13	CYP1B1	OGT	CANX	PCDHGC3	UAP1	OGT
13	ATF5	STRA13	CANX	CANX	ATF5	SAT	GRP58	WT1	CYP1B1	STRA13
14	ATP6V0B	GRP58	GRP58	GRP58	CANX	NACA	STRA13	GUCY1A3	STRA13	CYP1B1
15	BRCA1	SND1	MTHFD2	SND1	OGT	LDHA	SND1	OACT2	GRP58	CANX
16	CALR	ALCAM	STRA13	ALCAM	BRCA1	CANX	ALCAM	ATF5	ATF5	GRP58
17	CANX	MTHFD2	SND1	TMEM4	MTHFD2	SLC19A1	MTHFD2	MARCKS	CBX3	MTHFD2
18	CBX3	MRPL3	MRPL3	MTHFD2	LGALS3	ANK3	MRPL3	OS-9	SAT	SND1
19	CCND2	PPIB	ALCAM	MRPL3	GRP58	ALCAM	SLC19A1	CCND2	ALCAM	ATF5
20	CCNG2	SLC19A1	PPIB	SND1	SND1	GUCY1A3	TMEM4	CBX3	CANX	CBX3
21	CCT2	TMEM4	PPIB	OGT	CBX3	SND1	PPIB	GDF15	SND1	SAT
22	CXAP1	CCT2	CYP1B1	CYP1B1	MRPL3	MTHFD2	CCT2	FASN	BRCA1	ALCAM
23	COX6C	FMO5	TMEM4	SLC19A1	MYC	TMEM4	FMO5	ANK3	TMEM4	MRPL3
24	CYP1B1	OGT	ATF5	ATF5	STRA13	MRPL3	OGT	KRT18	CCT2	BRCA1
25	DAPK1	CYP1B1	CBX3	CBX3	ALCAM	GRP58	CYP1B1	SLC39A6	ANK3	SLC19A1
KD	1.745667	1.684	1.49	1.690667	1.627333	1.616	1.674	1.718333	1.736667	1.459667
SD	2.29568	1.18656	1.20128	1.3344	1.27488	1.08992	1.21344	1.45792	1.173568	1.25824
KC	0.016	0.0493333	0.1626666	0.0453333	0.0826667	0.0906667	0.0573333	0.0346667	0.0293333	0.1786666
SC	0.0247692	0.074	0.2158462	0.0783077	0.1153846	0.1190769	0.0898462	0.0532308	0.03	0.2343077

As can be seen in the tables, the aggregated ranker generated by the proposed method MYRA has smaller distance measure values (KD, SD) compared to the aggregated rankers of the other methods, meaning that the distance between the MYRA aggregated ranker and the base rankers is smaller, as is the difference between their ranks. On the other hand, it has larger correlation measure values (KC, SC) compared to the other aggregated rankers, meaning that the similarity between the MYRA aggregated ranker and the base rankers is greater and they are more correlated with each other. Another advantage of the proposed method over other methods is that it estimates the accuracy of each base ranker as its weight. These estimated accuracies can be used in biological problems to assess the reliability of various algorithms, experiments, platforms, and studies, such that those with much lower accuracy can be omitted from future research, and low-accuracy experiments and platforms can be improved. Table 7 shows the estimated accuracy (weight) by the proposed method MYRA for each of the studies used in the Breast, microRNA, and Prostate datasets.

Table 7. Estimated accuracy by the proposed method.

Prostate Dataset		MicroRNA Dataset				Breast Dataset				
Pusztai	MDCC	TransBig	PicTar	TargetScan	miRanda	Luo	Welsh	Dhana	Truee	Singh
0.6290	0.8700	0.7878	0.5997	0.9700	0.6570	1	1	0.6909	0.8000	0.6071

5 | Conclusion

RA has been widely used in various fields. RA is the process of combining several ranked lists into an aggregated ranker, which plays an important role in integrating information from different genomic studies addressing similar biological problems. In fields such as genetic and biological studies, researchers often generate several long ranked lists, but their true rank values are usually unavailable, and the quality of base rankers varies widely; in contrast, fields such as marketing and sociology generate many short ranked lists for which true rank values are usually available. Moreover, in biological studies, partial lists are more common than full lists due to the high heterogeneity of genomic studies and limited resources. Such inherent characteristics of data in the biological studies domain demand specific methods over others. Methods such as Markov chain, Stuart, CEMC, and RRA were initially developed for genetic experiment data. Also, methods such as Borda have been used for this domain. In this research, we present a novel framework for RA in

biological and biomedical applications, based on non-cooperative game theory. Unlike traditional methods that consider rankers as independent and static sources, in the proposed model, rankers are modelled as strategic agents that interact and compete with each other with the aim of maximising their own utility. In this framework, a utility function is defined for each ranker, which is a combination of similarity to the final ranking, the degree of agreement or conflict with other rankers, and the cost of producing the ranking. Using an iterative process based on best-response dynamics, the weight of each ranker is dynamically updated, and the final aggregated ranking is obtained as the stable outcome of a strategic game. The implementation of the proposed method for aggregating the results obtained from three breast cancer studies, aggregating the target prediction results of DNA microarrays by three different algorithms, and aggregating the results obtained from five prostate cancer studies demonstrates the efficiency and superiority of the proposed method over other conventional ranking methods, because the aggregated ranker resulting from it has lower distance measures and higher correlation measures with the base rankers. Overall, the game theory-based approach not only improves the accuracy of RA under conditions of source heterogeneity but also enables the analysis of interactions among sources and the design of mechanisms resistant to manipulation and biased ranking. Future development of this model could include the use of cooperative games, Markov dynamic games, and multi-agent reinforcement learning to enhance further dynamism and adaptability.

Acknowledgments

The authors sincerely appreciate the valuable contributions and support provided throughout this research.

Funding

No specific funding was received for this research.

Data Availability

The data used in this study are available from the corresponding author upon reasonable request

References

- [1] Li, X., Wang, X., & Xiao, G. (2019). A comparative study of rank aggregation methods for partial and top ranked lists in genomic applications. *Briefings in bioinformatics*, 20(1), 178-189. <https://doi.org/10.1093/bib/bbx101>
- [2] Deng, K., Han, S., Li, K. J., & Liu, J. S. (2014). Bayesian aggregation of order-based rank data. *Journal of the american statistical association*, 109(507), 1023-1039. <https://doi.org/10.1080/01621459.2013.878660>
- [3] Soneson, C., & Fontes, M. (2012). A framework for list representation, enabling list stabilization through incorporation of gene exchangeabilities. *Biostatistics*, 13(1), 129-141. <https://doi.org/10.1093/biostatistics/kxr023>
- [4] Chen, Q., Zhou, X. J., & Sun, F. (2015). Finding genetic overlaps among diseases based on ranked gene lists. *Journal of computational biology*, 22(2), 111-123. <https://doi.org/10.1089/cmb.2014.0149>
- [5] Lin, S., & Ding, J. (2009). Integration of ranked lists via cross entropy Monte Carlo with applications to mRNA and microRNA studies. *Biometrics*, 65(1), 9-18. <https://doi.org/10.1111/j.1541-0420.2008.01044.x>
- [6] Lin, S. (2010). Rank aggregation methods. *Wiley interdisciplinary reviews: computational statistics*, 2(5), 555-570. <https://doi.org/10.1002/wics.111>
- [7] Aslam, J. A., & Montague, M. (2001). Models for metasearch. In *Proceedings of the 24th annual international ACM SIGIR conference on Research and development in information retrieval* (pp. 276-284). <https://doi.org/10.1145/383952.384007>
- [8] Liu, Y. T., Liu, T. Y., Qin, T., Ma, Z. M., & Li, H. (2007, May). Supervised rank aggregation. *Proceedings of the 16th international conference on World Wide Web* (pp. 481-490). <https://doi.org/10.1145/1242572.1242638>
- [9] Aziz, H. (2010). Multiagent systems: algorithmic, game-theoretic, and logical foundations by y. shoham and k. leyton-brown cambridge university press, 2008. *ACM sigact news*, 41(1), 34-37. <https://dl.acm.org/doi/pdf/10.1145/1753171.1753181>

- [10] Vianzon, V. V, Hanson, R. M., Garg, I., Joseph, G. J., & Rogers, L. M. (2023). Rank aggregation of independent genetic screen results highlights new strategies for adoptive cellular transfer therapy of cancer. *Frontiers in immunology*, 14, 1235131. <https://doi.org/10.3389/fimmu.2023.1235131>
- [11] Hemandhar Kumar, S., Tapken, I., Kuhn, D., Claus, P., & Jung, K. (2024). bootGSEA: a bootstrap and rank aggregation pipeline for multi-study and multi-omics enrichment analyses. *Frontiers in bioinformatics*, 4, 1380928. <https://doi.org/10.3389/fbinf.2024.1380928>
- [12] Peng, C., Huang, J., Li, M., Liu, G., Liu, L., Lin, J., ... & Chen, X. (2024). Uncovering periodontitis-associated markers through the aggregation of transcriptomics information from diverse sources. *Frontiers in genetics*, 15, 1398582. <https://doi.org/10.3389/fgene.2024.1398582>
- [13] Vargas-Rondón, N., González-Giraldo, Y., García Fonseca, Á. Y., Gonzalez, J., & Aristizabal-Pachon, A. F. (2025). MicroRNAs signatures as potential molecular markers in mild cognitive impairment: a meta-analysis. *Frontiers in Aging Neuroscience*, 16, 1524622. <https://doi.org/10.3389/fnagi.2024.1524622>
- [14] Zhu, M., Tang, M., & Du, Y. (2023). Identification of TAC1 associated with Alzheimer's disease using a robust rank aggregation approach. *Journal of alzheimer's disease*, 91(4), 1339–1349. <https://doi.org/10.3233/JAD-220950>
- [15] Chebotarev, P., & Shamis, E. (2006). Characterizations of scoring methods for preference aggregation. *ArXiv preprint math/0602522*. <https://doi.org/10.48550/arXiv.math/0602522>
- [16] Rapoport, A. (2012). *Game theory as a theory of conflict resolution*. Springer Science & Business Media. https://doi.org/10.1007/978-94-010-2161-6_3
- [17] Ma, K., Xu, Q., Zeng, J., Li, G., Cao, X., & Huang, Q. (2022). A tale of hodgerank and spectral method: Target attack against rank aggregation is the fixed point of adversarial game. *IEEE transactions on pattern analysis and machine intelligence*, 45(4), 4090–4108. <https://doi.org/10.1109/TPAMI.2022.3190939>
- [18] Ma, K., Xu, Q., Zeng, J., Liu, W., Cao, X., Sun, Y., & Huang, Q. (2024). Sequential manipulation against rank aggregation: theory and algorithm. *IEEE transactions on pattern analysis and machine intelligence*, 46(12), 9353–9370. <https://doi.org/10.1109/TPAMI.2024.3416710>
- [19] DeConde, R. P., Hawley, S., Falcon, S., Clegg, N., Knudsen, B., Etzioni, R., & others. (2006). Combining results of microarray experiments: A rank aggregation approach. *Statistical applications in genetics and molecular biology*, 5(1), 1204. https://www.asc.ohio-state.edu/statistics/statgen/joul_win2008/DeConde.pdf
- [20] Desmedt, C., Piette, F., Loi, S., Wang, Y., Lallemand, F., Haibe-Kains, B., ... & TRANSBIG Consortium. (2007). Strong time dependence of the 76-gene prognostic signature for node-negative breast cancer patients in the TRANSBIG multicenter independent validation series. *Clinical cancer research*, 13(11), 3207–3214. <https://doi.org/10.1158/1078-0432.CCR-06-2765>
- [21] Shi, L., Campbell, G., Jones, W., Campagne, F., Wen, Z., Walker, S., ... & Peng, X. (2010). The MAQC-II Project: A comprehensive study of common practices for the development and validation of microarray-based predictive models. *Nature biotechnology*, 28(8), 827–838. *Nature biotechnology*, 28(8). 10.1038/nbt.1665%0A
- [22] Tabchy, A., Valero, V., Vidaurre, T., Lluch, A., Gomez, H., Martin, M., ... & Pusztai, L. (2010). Evaluation of a 30-gene paclitaxel, fluorouracil, doxorubicin, and cyclophosphamide chemotherapy response predictor in a multicenter randomized trial in breast cancer. *Clinical cancer research*, 16(21), 5351–5361. <https://doi.org/10.1158/1078-0432.CCR-10-1265>
- [23] Dhanasekaran, S. M., Barrette, T. R., Ghosh, D., Shah, R., Varambally, S., Kurachi, K., ... & Chinnaiyan, A. M. (2001). Delineation of prognostic biomarkers in prostate cancer. *Nature*, 412(6849), 822–826. <https://doi.org/10.1038/35090585%0A%0A>
- [24] Luo, J., Duggan, D. J., Chen, Y., Sauvageot, J., Ewing, C. M., Bittner, M. L., ... & Isaacs, W. B. (2001). Human prostate cancer and benign prostatic hyperplasia: molecular dissection by gene expression profiling. *Cancer research*, 61(12), 4683–4688. <https://aacrjournals.org/cancerres/article-pdf/61/12/4683/2486813/4683.pdf>
- [25] Welsh, J. B., & Sapinoso, L. M. (2001). Su AI, Kern SG, Wang-Rodriguez J, Moskaluk CA, Frierson HF, Hampton GM: Analysis of gene expression identifies candidate markers and pharmacological targets in prostate cancer. *Cancer res*, 61, 5974–5978. <https://doi.org/10.1186/1471-2407-10-165%0A%0A>

- [26] Singh, D., Febbo, P. G., Ross, K., Jackson, D. G., Manola, J., Ladd, C., ... & Sellers, W. R. (2002). Gene expression correlates of clinical prostate cancer behavior. *Cancer cell*, 1(2), 203-209. [https://www.cell.com/cancer-cell/pdf/S1535-6108\(02\)00030-2.pdf](https://www.cell.com/cancer-cell/pdf/S1535-6108(02)00030-2.pdf)
- [27] True, L., Coleman, I., Hawley, S., Huang, C. Y., Gifford, D., Coleman, R., ... & Nelson, P. S. (2006). A molecular correlate to the Gleason grading system for prostate adenocarcinoma. *Proceedings of the national academy of sciences*, 103(29), 10991-10996. <https://doi.org/10.1073/pnas.0603678103>