Search and Ranking in Semantically Rich Applications

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ABSTRACT
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This thesis proposes novel search and ranking approaches for semantically rich application domains.

The central role of Data Management in today's society may be compared to the role of Physics in early 20th Century when it entered its Golden Age. Data is the raw matter of the Universe of Information, and, in a process analogous to nuclear fusion, data is transformed progressively into information, and then into knowledge.

The advent of the World Wide Web as an information exchange platform and a social medium, both on an unprecedented scale, raises the user's expectations with respect to the availability and ease of access to relevant information. Web users build persistent online personas: they provide information about themselves in stored profiles, register their relationships with other users, and express their preferences with respect to information and products. As a result, rich semantic information about the user is readily available, or can be derived, and can be used to improve the user's online experience, making him more productive, more creative, and better entertained online. There is thus a need for context-aware data management mechanisms that support a user-centric data exploration experience, and do so efficiently on the large scale.

In a complementary trend, scientific domains, most notably the domain of life sciences, are experiencing unprecedented growth. The ever-increasing amount of data and knowledge requires the development of new semantically rich data management techniques that facilitate system-wide analysis and scientific collaboration. Literature search is a central task in scientific research. Controlled vocabularies and ontologies that exist in this domain present an opportunity for improving the quality of ranking.

The Web is a multifaceted medium that gives users access to a wide variety of datasets,

and satisfies diverse information needs. Some Web users look for answers to specific questions, while others browse content and explore the richness of possibilities. The notion of relevance is intrinsically linked with preference and choice. Individual items and item collections are characterized in part by the semantic relationships that hold among values of their attributes. Exposing these semantic relationships helps the user gain a better understanding of the dataset, allowing him to make informed choices. This process is commonly known as data exploration, and has applications that range from analyzing the performance of the stock market, to identifying genetic disease susceptibility, to looking for a date.

In this thesis we propose novel search and ranking techniques that improve the user experience and facilitate information discovery in several semantically rich application domains. We show how the social context in *social tagging sites* can be used for user-centric information discovery. We also propose novel ontology-aware search and ranking techniques, and apply them to *scientific literature search*. Finally, we address data exploration in *ranked structured datasets*, and propose a rank-aware clustering algorithm that uses semantic relationships among item attributes to facilitate information discovery.

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In loving memory of my grandfather Zyama Avramovich Lurie.

Chapter 1

Introduction

The central role of Data Management in today's society may be compared to the role of Physics in early 20th Century when it entered its Golden Age. Data is the raw matter of the Universe of Information, and, in a process analogous to nuclear fusion, data is transformed progressively into information, and then into knowledge.

Information is, in fact, so important, that even philosophers are starting to get interested. An emerging discipline of *Philosophy of Information* [Floridi, 2009b] postulates that "to be is to be an informational entity" [Ess, 2009]. According to this new doctrine, history is synonymous with the information age, since prehistory is the age in human development that precedes the availability of recording systems.

The information-based nature of our society has only recently become apparent, and is clearly linked to the wide-spread adoption of the World Wide Web as a platform for information dissemination and sharing. Nowadays the most advanced economies highly depend on information technologies in their functioning and growth. It has been argued that the world's seven larges economies, formerly known as G7, qualify as information societies, because at least 70% of their gross domestic product depends on intangible information-related goods, not on material goods, which are the physical output of agricultural or manufacturing processes [Floridi, 2009a].

The World Wide Web is, without a doubt, one of the greatest inventions of the 20th century. The Web is a living and breathing organism that is interesting both as a phenomenon unto itself, and because of the multitude of other phenomena that it supports and enables. The advent of the World Wide Web sparked the generation and exchange of information on an unprecedented scale, presenting the data management community with vital opportunities and interesting challenges.

A central data management challenge that arises in the Internet age is the transformation of data into knowledge. A particular aspect of this challenge may be phrased as follows. *Provided that the burden of synthesizing knowledge from relevant information rests on the user, how can the system point the user towards the information that is relevant?* After all,

the complexity of finding a needle in a haystack increases with the size of the haystack.[1]

The young 21st century has already unveiled its first great discoveries, not last among which is the popularization of online social networking and of social content sites. Of these sites there is a great variety – from the versatile Facebook platform that supports many types of content and various degrees of user involvement, to the minimalist Twitter, in which users communicate by publishing laconic status updates, or tweets.

Social content sites are backed by the World Wide Web, and are responsible for enriching or, as some would say, polluting the global information space by orders of magnitude more data. These sites bring about a shift in the traditional paradigm of information dissemination, in which there are far fewer producers of information than there are consumers. In contrast to traditional media, and to Internet-based publishing of the pre-social era, users of social content sites are both producers and raters of information, as well as information consumers. The blurring of the line between producers and consumers of content results in *democratization of information*, providing a powerful participation incentive.

In a related trend, many scientific domains, most notably the domain of life sciences, are experiencing unprecedented growth. The recent complete sequencing of the Human Genome, and the tremendous advances in experimental technology, are rapidly bringing about new scientific knowledge. The ever-increasing amount of data and knowledge in life sciences in turn requires the development of new semantically rich data management techniques that facilitate scientific research and collaboration.

An important challenge posed by the data management needs of the scientific community may be phrased as follows. *Provided that high-quality knowledge bases are available that summarize the state of the art in a scientific field, how can the system use this knowledge to identify relevant information, enabling further scientific advances?*

The Web is a multifaceted medium that gives users access to a wide variety of datasets, and satisfies diverse information needs. Some Web users look for answers to specific questions, while others browse content and explore the richness of possibilities. The notion of relevance is intrinsically linked with preference and choice. Preferences are known to change based on temporal aspects, one of which is the change in availability of items (be it physical products of information entities), or in *a user's belief about the availability of items* [Hansson and Grüne-Yanoff, 2006]. The process by which a user ascertains the availability of items is known as *data exploration*.

Individual items and item collections are characterized in part by the semantic relationships that hold among values of their attributes. These relationships may be known *a priori*, e.g., all 10-story buildings in the US have an elevator. Alternatively, these relationships may need to be derived, using inference or statistical tools. Exposing semantic relationships that hold among item attributes helps the user gain a better understanding

[1] Proof is left as an exercise for the reader.

of the dataset, allowing him to make informed choices. Data exploration is a common task, with application ranging from analyzing the performance of the stock market, to identifying genetic disease susceptibility, to looking for a date.

Success of data exploration depends critically on the availability of effective analysis and presentation methods. An important data management question is then: *Provided that a user's preferences depend in part on the semantic relationships that hold among item attributes, how can the system effectively derive these relationships and present them to the user, facilitating data exploration?*

This thesis proposes novel search and ranking methods aimed at improving the user experience and facilitating information discovery in semantically rich applications. In the remainder of this section, we give an overview of the state of the art in related data management areas, and outline our contributions.

1.1 Information Retrieval and Web Search

In Information Retrieval (IR), a user expresses his information need with a query q. An IR system evaluates the query against a document corpus $\mathcal{D}$, and identifies a set of *answers* $\mathcal{A} \subseteq \mathcal{D}$ that are conjectured by the system to satisfy the user's information need. The documents in $\mathcal{A}$ are said to *match* the query q. The language used to express the query, and the mechanism by which answers are identified, depend on the retrieval model used by the IR system. We will describe several common retrieval models in Section 1.1.1.

In IR, documents are typically drawn from a large corpus, and relevant documents are identified. In real-world IR scenarios such as Web search, or scientific literature search, many more relevant documents are typically identified than any one user is willing to read. Further, not all documents that are identified as answers carry equal relevance to the user's query. Therefore, the system must choose a portion of the result set to present to the user, motivating the need for ranking. Results are commonly returned in the form of a ranked list, with the goal of presenting to the user documents that are conjectured by the system to have high relevance to the user's query. To this end, IR systems define a *ranking function* $R : \mathcal{D} \to \mathbb{R}$ that, for a fixed query, associates each document $d \in \mathcal{D}$ with a real number. R defines a natural ordering on the documents in the collection, and expresses the extent to which each document matches the query.

Information Retrieval methods were originally developed for searching document collections to which we currently refer as *Digital Libraries*, such as the on-line version of the Library of Congress (`www.loc.gov`) or the PubMed Central repository of scientific articles (`www.pubmedcentral.nih.gov`). These collections are curated and generally contain documents of high quality, in the sense that a document that covers a particular topic is usually authored by an expert on that topic. Further, the vocabulary used in a document is usually representative of the document's semantic content. This is to be contrasted with the

document corpus that is the World Wide Web, in which there is a high degree of variability with respect to the quality of information. Authors of Web content have a varying degree of expertise on the subjects they cover. Additionally, the words used on a particular web page may not truthfully reflect the semantic content of the page, a phenomenon known as *search engine spamming*. Based on these considerations, new IR methods were developed that incorporate both a document's textual relatedness to a user's query, and a document's *authority*. We will give an overview of these methods in Section 1.1.2.

An important and difficult question is how to properly evaluate the performance of an IR system. We discuss some approaches for evaluating the quality of retrieval and ranking in Section 1.1.3, and give an overview of performance-related issues in Section 1.1.4.

1.1.1 Information Retrieval Models

The IR models of this section represent queries and documents in a corpus as collections, such as sets or vectors, of *index terms*. Index terms $t_1, t_2, \ldots t_n$ are elements of a vocabulary $\mathcal{T}$ that typically corresponds to words in the natural language of the collection.

The *Boolean model* is based on set theory and Boolean algebra. In this model queries are specified as conjunctions (keyword *AND*), disjunctions (keyword *OR*), or negations (keyword *NOT*) of index terms. A query is an arbitrary Boolean expression over the terms from $\mathcal{T}$, which is converted by the system to *disjunctive normal form*. Each document $d \in \mathcal{D}$ is in turn represented as a conjunction of the terms that occur in the document.

Suppose that a vocabulary is given that consists of three terms; we represent the vocabulary as a set $\mathcal{T} = \{t_1, t_2, t_3\}$ [2]. Suppose also that a query is given by the Boolean expression $q = t_1 \wedge (t_2 \vee \neg t_3)$. This query can be equivalently re-written in disjunctive normal form as $q_{DNF} = (t_1 \wedge t_2 \wedge t_3) \vee (t_1 \wedge t_2 \wedge \neg t_3) \vee (t_1 \wedge \neg t_2 \wedge \neg t_3)$. Document $d_i = t_1 \wedge t_2$ will match the query, since it matches the second conjunctive term in q_{DNF}. On the other hand, document $d_j = t_1 \wedge t_3$ will not match q.

For each document $d \in \mathcal{D}$, the Boolean model will predict that the document is either relevant to a query q or that it is irrelevant.

The *vector space model*, which was first introduced in [Salton *et al.*, 1975], relaxes the assumption that a document is either relevant or irrelevant to a query. Unlike the Boolean model, the vector space model incorporates term weights, and supports partial matching.

In the vector space model, the vocabulary of index terms $\mathcal{T}$ is represented by a vector, with length equal to the size of the vocabulary. Queries and documents are represented by vectors of non-binary weights, with each position corresponding to a term in $\mathcal{T}$. The weights are used to compute the degree of similarity between a query and a document. So, for a query $\vec{q}$ and a document $\vec{d}$, we compute similarity as the cosine of the angle between

[2] This example is based on the example in Section 2.5.2 of [Baeza-Yates and Ribeiro-Neto, 1999].

these two vectors in the space of $\mathcal{T}$:

$$sim(\vec{d}, \vec{q}) = \frac{\vec{d} \bullet \vec{q}}{|\vec{d}| \times |\vec{q}|} \tag{1.1}$$

How well the model will match human intuition clearly depends on a meaningful choice for the weights. A classic weighting scheme, known as *tf-idf*, weights a document term according to how often the term appears in the document. This portion of the weight, called *term frequency*, or *tf*, models the intuition that a term that is mentioned in a document more often is more representative of the document's content than another term that is mentioned less often. The *tf* weight is normalized by the total frequency of the term in the corpus. This normalization, referred to as *inverse document frequency*, or *idf*, penalizes terms that frequently occur in the corpus, because such terms may be less informative.

We described two classical retrieval models in IR. Many other successful models exist and are used today in IR systems. The *probabilistic model* attempts to estimate the probability that the user will find the document d relevant to a query q, given the representations of d and q. A family of probabilistic IR models are the *language models* that are based on a probabilistic mechanism for generating text. Given a query q and a document d, the system computes the probability that q was generated by the language model of d, and ranks the retrieved documents on this probability [Croft and Lafferty, 2003].

The *fuzzy set model* assumes that each query term defines a fuzzy set, and that each document has a degree of membership (usually less than 1) in this set. The *extended Boolean model* allows for the weighting of Boolean terms. A variety of extensions, and of new models, have been considered in the literature. However, this thesis does not use any of the later models, and so a complete review is beyond the scope of this work. We refer the reader to [Baeza-Yates and Ribeiro-Neto, 1999; Manning *et al.*, 2008] for a comprehensive review of other approaches.

Most IR models lend themselves well to ranking, because they incorporate a notion of non-binary similarity between the query and the document. An exception is the Boolean retrieval model, which produces binary outcomes, and as such does not naturally support ranking. In addition to relevance, modern IR systems also incorporate a notion of *authority* into the ranking, and we discuss this topic next.

1.1.2 Link Analysis and Authority-Based Ranking

The World Wide Web became a prominent medium for information discovery in the early 1990s. By that time IR was already a mature field that developed primarily based on information discovery tasks over large curated document collections. The advent of the Web prompted the field of IR to adapt, and to develop techniques appropriate both for the ever-increasing size of this dynamic collection, and for the heterogeneity in information quality.

A crucial property of the Web that motivates some of the early advances in Web-based retrieval and ranking is that the Web has a natural graph structure. The Web is comprised of pages with hyperlinks to other pages. For example, a Web page of a Computer Science PhD student may contain a link pointing to her adviser's homepage:

```
<a href=''http://www.cs.columbia.edu/~kar''>Homepage of Kenneth A. Ross</a>
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A key observation made by Kleinberg in a seminal paper [Kleinberg, 1999] is that hyperlinks of this kind may be viewed as endorsements. A page that links to another page implicitly endorses the target page, giving it prominence, commonly referred to as *authority*.

At roughly the same time Brin and Page developed the PageRank algorithm [Brin and Page, 1998] that models the authority of a Web page based on the probability that it will be visited by a *random surfer* who uses the link structure of the Web. PageRank serves as basis for the search algorithm employed by Google, a leading Web search engine. We now give a brief description of these two influential algorithms.

The *Hyperlink-Induced Topic Search* (HITS) algorithm, also known as *Hubs and Authorities*, was proposed in [Kleinberg, 1999]. HITS uses the link structure of the web graph to identify, in a query-specific or topic-specific manner, a set of authoritative pages, and a set of hub pages that join the authorities into the link structure. The Web is modeled as a directed graph $G = (V, E)$, where nodes V correspond to pages, and a directed edge $(p, q) \in E$ indicates the presence of a link from page p to page q.

The algorithm starts by constructing a relatively small subgraph of the Web, called the *root set*, that contains a high number of query-relevant pages. The root set is then expanded to include adjacent pages – pages *pointed to* by the pages in the root set, and pages *pointing to* the pages in the root set. The resulting sub-graph of the Web graph, referred to as $\mathcal{G}_\sigma$, has a high chance of containing some authorities, and these authorities are identified using an iterative procedure.

Each web page p among the nodes of $\mathcal{G}_\sigma$ is assigned two weights – an *authority weight* $x^{\langle p \rangle}$ and a *hub weight* $y^{\langle p \rangle}$. Both kinds of weights are initialized uniformly for all pages, and are updated iteratively. The update procedure builds on the intuition that a page p that points to many pages should receive a high hub weight (y), while a page that is pointed to by many pages should receive a high authority weight (x). Given weights $\{x^{\langle p \rangle}\}$ and $\{y^{\langle p \rangle}\}$, two operations are applied in turn and update the weights as follows:

$$x^{\langle p \rangle} \leftarrow \Sigma_{q:(q,p)\in E} y^{\langle p \rangle} \tag{1.2}$$

$$y^{\langle p \rangle} \leftarrow \Sigma_{q:(q,p)\in E} x^{\langle p \rangle} \tag{1.3}$$

Weights are normalized after each iterative step. Eventually, the system converges to a solution and the iteration stops.

The *PageRank* algorithm, introduced in [Brin and Page, 1998], models the behavior of a *random surfer* who starts with a random Web page and visits other web pages by following outgoing hyperlinks. At some point the surfer may decide to start at another random page. The probability that a random surfer will visit a web page is the PageRank of that page.

Unlike HITS, PageRank is a query-independent measure of page authority. PageRank is computed iteratively over the entire Web graph, with the intuition that the authority of a page p depends on the number of incoming hyperlinks and on the authority of the page q from which the hyperlink to p originates. PageRank of a page p is computed by iteratively using the equation:

$$x^{\langle p \rangle} = (1-d)\Sigma_{q:(q,p)\in E}\frac{x^{\langle q \rangle}}{h_q} + d \tag{1.4}$$

Here, h_q is the outdegree of page q, and $d \in (0,1)$ is a dumping factor that represents the probability that the random surfer will get bored of hyperlinked browsing, and will jump to a random Web page. The computation eventually converges to an equilibrium solution.

An authority score of a page can be combined, for example in a multiplicative manner, with the query relevance score, allowing the system to rank results by a combination of query relevance and query-independent (in the case of PageRank) quality. The PageRank and HITS authority propagation measures have had extremely high impact, both academically and commercially. The practical value of link-based authority measures is best supported by the tremendous commercial success of Google and its wide adoption by everyday Web users. It may well be the case that the sustained growth of the Web is due, at least in part, to the fact that Web content can be discovered effectively using this generation of search technology.

Recently, a new style of Web search has emerged in which *semantic entities*, such as products or scholars, are returned by the system in response to a query. We will discuss the emergence of semantic Web technologies and their new search and ranking requirements in Section 1.2.1.

1.1.3 Evaluating the Quality of an Information Retrieval System

Evaluation of the effectiveness of an IR system typically incorporates relevance judgments that are issued by users against all, or some, documents in the corpus. Judgments rate the relevance of a document to a particular query on some scale, and may evaluate the textual relevance of a document to a query, the document's quality and trustworthiness, or both. In the simplest case, a document may be considered either relevant or irrelevant to the query, receiving a relevance score of 1 or 0, respectively. Sometimes more fine-grained relevance scores are used. For example, a document's relevance may be judged on a scale from 0 to 3, where 3 denotes high relevance, and 0 denotes no relevance.

1.1.3.1 Set-Based Measures

We now describe some typical ways that relevance judgments may be used to quantify the performance of an IR system. These and other methods are described in detail in [Baeza-Yates and Ribeiro-Neto, 1999]. Given a query q, and a document collection $\mathcal{D}$, we may use relevance judgments to partition the collection into two mutually exclusive sets: set $\mathcal{R}$ of relevant documents, and set $\mathcal{I}$ of irrelevant documents. To quantify the performance of a retrieval-only IR system (one that does not do any ranking), we may consider the set of all answers $\mathcal{A}$ conjectured by the system to be relevant to the query. We define *recall* as the fraction of the relevant documents that has been retrieved:

$$Recall = \frac{|\mathcal{R} \cap \mathcal{A}|}{|\mathcal{R}|} \tag{1.5}$$

We may also define *precision* as the fraction of the retrieved documents that are relevant:

$$Precision = \frac{|\mathcal{R} \cap \mathcal{A}|}{|\mathcal{A}|} \tag{1.6}$$

A variety of measures exist that combine precision and recall in various ways, such as the F-measure and the E-measure [Baeza-Yates and Ribeiro-Neto, 1999].

In order to make precision and recall appropriate for ranked retrieval, one can consider a modification of precision, recall and related measures, applying them at top-N, for various values of N. Then only the documents in the highest N positions in the list are considered when evaluating quality (we denote these documents by $top(\mathcal{A}, N)$), but these documents are still treated as a set, and the relative ordering of documents in the set is ignored. For example, precision at top-N may be defined as the fraction of the top-N that is relevant to the query:

$$Precision@N = \frac{|\mathcal{R} \cap top(\mathcal{A}, N)|}{|top(\mathcal{A}, N)|} \tag{1.7}$$

Recall, precision and related measures are based on the assumption that the set of relevant documents for a query is the same for every user. However, different users may have very different interpretations of relevance, and we will provide more background on this intuition in Section 1.3. Several user-oriented quality measures are in use in IR, including *coverage*, *novelty*, *expected search length*, *satisfaction* and *frustration* [Baeza-Yates and Ribeiro-Neto, 1999].

As before, for a given query, let $\mathcal{R}$ refer to the set of relevant documents in a collection, and let $\mathcal{A}$ be the set of answers retrieved by the IR method. Also let $\mathcal{U} \subseteq \mathcal{R}$ be the relevant documents known to the user. For example, $\mathcal{R}$ may represent all movies directed by Milos Forman, and $\mathcal{U}$ may represent the subset of Forman's movies that the user has seen. We

define *coverage* as the fraction of the documents known to the user to be relevant that has been retrieved:

$$Coverage = \frac{|\mathcal{U} \cap \mathcal{A}|}{|\mathcal{U}|} \tag{1.8}$$

Coverage is a user-oriented version of recall (see Equation 1.5), and we use this measure in Section 2.2. Another proposed quality measure is *novelty*, defined as the fraction of the relevant documents that were retrieved and were unknown to the user:

$$Novelty = \frac{|\mathcal{A} \setminus \mathcal{U}|}{|A|} \tag{1.9}$$

The novelty measure, while incorporating a user's point of view on relevance to some extent, still makes an implicit assumption that the set of relevant documents $\mathcal{R}$ is the same for all users, and that documents in this set simply have not been discovered, and judged, by all users. There is, however, increasing evidence that this assumption does not hold in practice, and we elaborate on this point in Section 1.3.2.

1.1.3.2 List-Based Measures

A crucial shortcoming of quality measures described above is that they do not naturally account for the *order of items* in the list. An intuitive argument can be made that, because a user is more likely to pay attention to the items that are returned higher in the list, i.e., at lower ranks, a successful IR method should return high-quality items closer to the top of the list. In the remainder of this section we describe several techniques proposed in [Järvelin and Kekäläinen, 2002] that incorporate this intuition. These techniques, particularly Normalized Discounted Cumulated Gain (NDCG), are used extensively throughout this thesis, both to assess the quality of proposed solutions, as in Chapters 2 and 4, and to develop new ranking methods, as in Chapter 5.

Other techniques for comparing ranked lists are described in the literature (see for example [Fagin *et al.*, 2003a]), but we focus on the techniques of [Järvelin and Kekäläinen, 2002] because, as we will show in subsequent chapters, they are efficient to compute and are a natural fit for our application scenarios.

The measures of [Järvelin and Kekäläinen, 2002] evaluate the quality of a ranked list with respect to information gain, or simply *gain*, that is cumulated by document rank. In other words, the relevance score of each document in the list is used to compute a gained value for its ranked position in the result, and the gain is then summed progressively from ranked position 1 to N. (Here, and in the remainder of this section, ranked lists are 1-based for convenience.)

Let us assume that relevance scores of 0 to 3 are used, with 3 denoting high relevance, and 0 denoting lack of relevance. A top-10 list of documents is represented as a gain vector

G of 10 components, each having a value of 0, 1, 2, or 3. For example:

$$G = \langle 3, 2, 3, 0, 0, 1, 2, 2, 3, 0 \rangle \tag{1.10}$$

The *cumulated gain* at ranked position i is computed by summing from position 1 to i, where i ranges from 1 to 10. Cumulated gain is represented by a vector CG, and is defined recursively as follows:

$$CG[i] = \begin{cases} G[1] & \text{if } i = 1 \\ CG[i-1] + G[i] & \text{otherwise} \end{cases} \tag{1.11}$$

For example, from the gain vector in Equation 1.10 we obtain the following cumulated again vector:

$$CG = \langle 3, 5, 8, 8, 8, 9, 11, 13, 16, 16 \rangle \tag{1.12}$$

The gain and cumulated gain vectors defined above incorporate the intuition that highly relevant documents are more valuable than marginally relevant documents. The next measure, *discounted cumulated gain*, builds on the intuitive idea that, the greater the ranked position of a relevant document, the less valuable the document is for the user. This is because the user is less likely to examine the document due to time, effort, and accumulated information from documents already seen. Discounted cumulated gain incorporates a rank-based discount factor.

The greater the rank, the smaller the share of the document in the cumulated gain score. A discounting function that progressively reduces the document's contribution to the score as its rank increases divides the gain of the document by the log of its rank. This discounting function is appropriate because, as argued in [Järvelin and Kekäläinen, 2002], it does not decrease the contribution too steeply (as would, for example, division by rank), allowing for user persistence in examining further documents. Selecting the base of the logarithm, sharper or smoother discounts can be computed to model varying user behavior. Denoting the base of the logarithm by b, we define the discounted cumulated gain vector DCG recursively as follows:

$$DCG[i] = \begin{cases} CG[i] & \text{if } i < b \\ DCG[i-1] + \frac{G[i]}{log_b i} & \text{if } i \geq b \end{cases} \tag{1.13}$$

For example, for $b = 2$, we derive the following DCG vector from CG in Equation 1.12:

$$DCG = \langle 3, 5, 6.89, 6.89, 6.89, 7.28, 7.99, 8.66, 9.61, 9.61 \rangle \tag{1.14}$$

The gain and cumulated gain measures, while insightful on their own, are most useful in our context because they allow us to compare the quality of two ranked lists. We now

show how these measures can be extended to allow a comparison between a ranked list and a theoretically best possible list, which we call *ideal*.

An ideal list is one in which entries are ordered by gain, in decreasing order. More formally, for a given query, let there be k, l, and m relevant documents at the relevance levels 1, 2, and 3, respectively. In the gain vector G^I that corresponds to the ideal list, positions $1, \ldots, m$ are filled by values 3, positions $m+1, \ldots, m+l$ are filled by values 2, positions $m+l+1, \ldots, m+l+k$ are filled by values 1, and the remaining positions are filled by values 0. A sample ideal gain vector, along with the corresponding cumulated gain, and discounted cumulated gain vectors, may contain the following values:

$$D^I = \langle 3, 3, 3, 2, 2, 2, 1, 1, 1, 1, 0, 0, \ldots \rangle \quad (1.15)$$

$$CG^I = \langle 3, 6, 9, 11, 13, 15, 16, 17, 18, 19, 19, \ldots \rangle \quad (1.16)$$

$$DCG^I = \langle 3, 6, 7.89, 8.89, 9.75, 10.52, 10.88, 11.21, 11.53, 11.83, 11.83, \ldots \rangle \quad (1.17)$$

The CG and DCG vectors may now be normalized by dividing each position in the vectors by the corresponding position in the ideal vectors CD^I and DCG^I. This normalization yields the following values for the vectors in our running example:

$$NCG = \langle 1, 0.83, 0.89, 0.73, 0.62, 0.6, 0.69, 0.76, 0.89, 0.84 \rangle \quad (1.18)$$

$$NDCG = \langle 1, 0.83, 0.87, 0.78, 0.71, 0.69, 0.73, 0.77, 0.83, 0.81 \rangle \quad (1.19)$$

Finally, as noted in [Järvelin and Kekäläinen, 2002], the area between the normalized ideal vector and the normalized (discounted) cumulated gain vector represents the quality of the IR technique. Normalized (D)CG vectors for two or more IR techniques also have a normalized difference. The average of an NCG vector, or of an NDCG vector (referred to jointly as V), up to a given rank N summarizes the performance of the technique, and is given by:

$$avg(V, N) = \frac{\Sigma_{i=1 \ldots N} V[i]}{N} \quad (1.20)$$

To summarize, the cumulated gain-based techniques of [Järvelin and Kekäläinen, 2002] evaluate the quality of a ranked list by considering the *gain* that is realized by the list, typically up to position i. The normalized techniques in this family compare the quality of a ranked list to that of an *ideal* list. We use these basic ideas throughout this thesis, though not always in a setting where the quality of items in a ranked list can be estimated based on user judgments. In situations where we depart from this typical setting, we specify an application-dependent formulation for the gain, along with an appropriate ideal list.

1.1.4 Efficiency of Processing

As mentioned throughout this section, both classic and Web-based Information Retrieval methods are usually applied to very large document collections, and are expected to yield sub-second response times in multi-user environments. Therefore IR methods must be built with efficiency considerations in mind.

The seminal work of Brin and Page [Brin and Page, 1998] in which the PageRank algorithm was first described also devotes significant attention to the scalable implementation of the Google prototype. This early paper outlines the challenges of large scale Web crawling, indexing, and searching, and presents the distributed file system construct fundamental to Google's architecture called *BigFiles*, a precursor of the *Google File System* (GFS) [Ghemawat *et al.*, 2003]. Google subsequently implemented *BigTable*, a proprietary database system built on GFS that departs from the typical convention of a fixed number of columns and is instead described by the authors as a sparse, distributed multi-dimensional sorted map [Chang *et al.*, 2006]. *BigTable* in turn supports the *MapReduce* framework, introduced by Google in [Dean and Ghemawat, 2006], which enables distributed computation over large scale datasets in a cluster environment.

The *MapReduce* framework supports two main operations: *Map* and *Reduce*. The *Map* operation is executed by the master node, which partitions the problem into sub-problems and assigns the sub-problems to worker nodes. The *Reduce* step involves combining the answers to sub-problems, and returning the combined solution as the final answer. The *MapReduce* framework is proprietary to Google.

Apache Hadoop is an open-source software framework that was inspired by *MapReduce* and by the *Google File System*.

An *inverted index*, also known as an *inverted file*, is a conceptual data structure used by many search algorithms in IR and Web search. An inverted index stores a mapping from content, such as vocabulary terms or phrases, to its location in a document, allowing full-text search. In [Zobel *et al.*, 1998] the performance of inverted files was extensively analyzed, demonstrating the scalability, space efficiency, and good update performance of this data structure.

Inverted files have been used in a variety of applications including some influential *top-K* processing algorithms. A seminal paper [Fagin *et al.*, 2003c] presents the *threshold algorithm* (TA), which is provably optimal in terms of run-time performance, and is used for aggregating scores over inverted file entries. Given a query q represented by a set of index terms, and a collection of inverted files, the TA algorithm determines the k items with the highest over-all score. The algorithm builds on an intuition that high-scoring items will appear closer to the top of all relevant inverted lists than would lower-scoring items.

1.2 Adding a Semantic Dimension to the Web

1.2.1 Semantic Web

Information Retrieval and Web search techniques outlined in Section 1.1 reason over queries and documents in a corpus by considering the terms that make up these queries and documents. These techniques manipulate terms as symbols, and do not consider the *semantics*, or *meaning* of the vocabulary.

The *Semantic Web*, or *a Web with meaning*, is an ambitious effort that aims to create a Web-wide machine-processable representation of real-world entities and of relationships between these entities. The World Wide Web Consortium (W3C) leads the Semantic Web effort, and gives the following definition of the initiative [3]:

The Semantic Web provides a common framework that allows data to be shared and reused across application, enterprise, and community boundaries.

According to the Wikipedia entry for Semantic Web (as of September 17, 2009): "At its core, the Semantic Web comprises a set of design principles, collaborative working groups, and a variety of enabling technologies. Some elements of the Semantic Web are expressed as prospective future possibilities that are yet to be implemented or realized. Other elements of the Semantic Web are expressed in formal specifications. Some of these include Resource Description Framework (RDF), a variety of data interchange formats (e.g., RDF/XML, N3, Turtle, N-Triples), and notations such as RDF Schema (RDFS) and the Web Ontology Language (OWL), all of which are intended to provide a formal description of concepts, terms, and relationships within a given knowledge domain."

For the promise of Semantic Web to be realized on the full scale of the Web, Web data should be published in languages specifically designed for semantic annotation such as RDF, OWL and XML, so as to enable semantic tagging of entities. For example, a Web page that mentions the entity *Cat* must use semantic mark-up that may look like[4]:

```
<item rdf:about=http://dbpedia.org/resource/Cat>Cat</item>
```

Semantic annotations of this kind refer to entries in an *ontology*, a formal representation of a set of concepts that defines the domain for each concept, and specifies the relationship between concepts. Ontologies provide a machine-processable representation, and support reasoning and inference.

While the goal of semantically annotating the whole Web remains elusive, due mostly to the high cost of adoption of a common representation framework, and to the difficulty (or perhaps impossibility) of schema design and maintenance at Web scale, Semantic Web technologies have been successfully used in certain domains. We describe some challenges

[3] Definition from `www.w3.org/2001/sw`, downloaded on September 17, 2009.

[4] This example is from `en.wikipedia.org/wiki/Semantic_Web`, downloaded on September 17, 2009.

related to the creation and maintenance of ontologies, and give examples of success stories, in the following section.

1.2.2 Ontologies

The building and maintenance of an ontology is a top-down process that requires an extensive amount of curation. Consider for example the process of creating and maintaining an ontology in the domain of life sciences. An ontology represents a consensus among domain experts regarding the state of knowledge in a particular field. This consensus is particularly difficult to achieve in dynamic fields where knowledge constantly evolves. At the same time, ontologies are most valuable in such fields, because they do not simply record the state of the art for posterity, but rather are aimed at supporting community-wide collaboration and the advancement of science.

In order to create an ontology, domain experts must first agree on the vocabulary. If an ontology represents a consensus view of several sub-fields within a field (e.g., an ontology of gene products across species), reaching an agreement with respect to a common vocabulary may be even more difficult. Having agreed on a vocabulary, the experts must next establish the hierarchical and semantic relationships that hold among entities in the domain. Relationships among entities in a scientific domain may be circular, context-sensitive, or otherwise complex, prompting difficult trade-offs between expressiveness and complexity of the resulting data model.

An ontology that represents the state of knowledge in a dynamic field must be maintained to incorporate advances in the field. This may require adding or retiring concepts, and changing the previously established relationships between concepts.

Because ontology creation is such an expensive process, ontology mining tools have been developed. OntoMiner [Davulcu *et al.*, 2004] and TaxaMiner [Kashyap *et al.*, 2005] automatically construct ontologies using bootstrapping, while Verity [Chung *et al.*, 2002] automatically constructs a domain-specific taxonomy using thematic mapping.

Despite the challenges that may hinder the creation and maintenance of ontologies, a number of ontologies have been created in the biomedical domain, and are being used by a variety of applications such as scientific literature search, biomedical text mining, and integration of experimental results. For example, the *Gene Ontology* (GO) [5] project is an effort to standardize the representation of genes and gene product attributes across species and datasets. GO annotations have been adopted by a variety of databases, and are the *de facto* standard in the domain. Another success story is the Medical Subject Headings (MeSH) ontology, developed and maintained by the National Library of Medicine [6]. MeSH is used by Entrez, the Life Sciences Search Engine, as part of the search functionality over

[5] `www.geneontology.org`

[6] `www.nlm.nih.gov/mesh`

resources such as PubMed.

1.2.3 Web 2.0

While some automatic ontology mining tools exist that derive new ontologies, or enhance existing ones, ontologies that are currently used successfully in scientific domains were created primarily by human experts in a top-down fashion. An alternative to the Semantic Web, in terms of both ontology creation and content annotation, is a trend commonly referred to as Web 2.0.

The term *Web 2.0* has no clear definition, but usually refers to the *emergence of semantics* brought about by the operation of Web-based communities. Examples of Web 2.0 applications include social networking sites, wikis, and blogs. In contrast to the Semantic Web, where an annotation schema, such as an ontology, must be defined before it can be used to annotate content, social content sites in Web 2.0 give rise to so-called *folksonomies* – hierarchical vocabularies of terms that are formed by collective use of the vocabulary.

The term folksonomy was coined by Thomas Vander Wal [Pink, 2005], and refers to a system of classification derived from the practice and method of collaboratively creating and managing tags to annotate and categorize content [7]. Folksonomies typically arise in the context of social tagging sites like *Delicious* (`delicious.com`), in which users bookmark and tag URLs that they find interesting. The tagging activity is social, in that URLs are tagged by users both for their own consumption, and for the consumption of other users of the site. The tagging vocabulary converges into a folksonomy particularly because of the social nature of tagging, since users want to enable others to locate their contributed content with ease.

Folksonomies contrast with taxonomies and traditional ontologies, which are typically created and maintained top-down, in a centralized manner.

In philosophy, *social epistemology* is the study of the social dimension of knowledge or information [Goldman, 2001]. Social epistemology dates back as far as Plato who, in his dialog *Charmides*, poses the question of how a layperson can determine whether to trust someone who claims to be an expert [Goldman, 2001]. The term *social epistemology* is used in two senses. The classical sense deals mostly with truth and belief, and is centered on the individual. Conversely, the anti-classical approaches focus on the process by which society as a whole synthesizes knowledge. This interpretation is directly applicable to the creation of folksonomies, and generally to Web 2.0.

[7] Definition from `en.wikipedia.org/wiki/Folksonomy`, downloaded on September 17, 2009.

1.3 Social Web

1.3.1 Social Content Sites

In Section 1.2.3 we discussed Web 2.0, a set of technologies that support, and embody, the social synthesis of knowledge. In this section we survey a particularly prominent part of Web 2.0, namely, the *social content sites*.

These sites bring about a shift in the traditional paradigm of information dissemination, in which there are far fewer producers of information than there are consumers. In contrast to traditional media, and to Internet-based publishing of the pre-social era, users of social content sites are both producers and raters of information, as well as information consumers. The wide-spread adoption of the social paradigm on the Web led to tremendous popularity and significant commercial success of these sites, and signaled a shift in the relationship between the Web and a typical Web user.

Many social content sites are in operation today, and many others are increasingly adding social features. Furthermore, many different kinds of social content sites exist, each catering to a particular activity or a set of activities, and to a particular user base.

For an example of successful social content sites consider *Facebook* (`facebook.com`) and *MySpace* (`myspace.com`), two sites that enable a full range of social behavior on the Web. Both sites support the posting and annotation of content, and the forming of social networks, and provide a range of direct inter-user communication options like messaging and various kinds of bulletin boards. In addition to direct communication, content is shared between users by means of information feeds. An interesting research question that arises in the context of these full-featured social content sites is how to best aggregate the heterogeneous data that comprises an information feed, improving the user experience on these sites and facilitating information discovery.

A recent success story is *Twitter* (`twitter.com`), a site aimed exclusively at inter-user communication via status updates. *Twitter* can be seen as the antithesis of full-featured sites like *Facebook* and *MySpace*, because of how limited an interaction it supports. Nonetheless, simple status update functionality seems to have hit a sweet spot in user needs, giving the site tremendous popularity.

An important category of social content sites focuses on a specific aspect of on-line social behavior, namely, the sharing and annotation of content. Prominent examples of such sites are *YouTube* (`youtube.com`) for videos, *Flickr* (`flickr.com`) for photos, *Delicious* (`delicious.com`) for URLs, and *CiteULike* (`citeulike.org`) for academic papers, to name just a few. These sites all allow users to annotate content with natural language keywords, or *tags*, and we refer to them jointly as *social tagging sites*. We give a more extensive description of social tagging sites, and particularly of *Delicious*, in Chapter 2.

Blogs and Wikis are yet another type of social content sites that gained tremendous popularity in recent years. Some prominent examples include *Wikipedia*, "the free ency-

clopedia that anyone can edit" (`en.wikipedia.org`), *LiveJournal* (`livejournal.com`), and *TechCrunch* (`techcrunch.com`). Users of these sites contribute free-text content that expresses opinions, descriptions of events, or other materials such as graphics of video. The term *blogosphere*, coined by Brad L. Graham[8], refers to the inter-connectivity among blogs, and implies that blogs exist together as a connected community, or as a social network in which everyday users can publish their opinions. Bloggers often publish news and editorial opinions on important local and national events, and this activity can be viewed as a kind of grass-roots journalism. Prominent blogging sites like *TechCrunch* are widely considered to be as authoritative as traditional news media on the topics they cover. Realizing the importance of blogging, many traditional media publishers such as *CNN*, *BBC* and others, incorporated blog features into their Web sites.

The final type of a social content site that we mention here deals with opinion aggregation. In sites like *Digg* (`digg.com`) and *StumbleUpon* (`stumbleupon.com`) users endorse (with a star or a thumbs-up) sites that they found interesting. The number of endorsements is aggregated, and a *hotlist* of the currently most popular sites is computed.

It is interesting to note that, while all social content sites are ultimately aimed at information sharing in large social groups, each caters to a different self-selected group of individuals. Recent reports [Richmond, 2009] point to a socio-economic divide between *Facebook* and *MySpace* users, with *Facebook* users more likely to come from families with higher levels of education. Other sites are also self-selecting. The prominence of technology-related content in *Delicious* draws technologically inclined users to that site, while the thematic focus of *Flickr* makes this site attractive to persons with an interest in photography.

The comedian Jerry Seinfeld famously said: "It's amazing that the amount of news that happens in the world every day always just exactly fits the newspaper". This joke expresses the intuition of why the social contribution of content has become so wide-spread. The blurring of the line between producers and consumers of content brings about *democratization of information*. Users are able to contribute news, commentary, and other types of information that are of interest to them and to other members of their social surrounding. An ability to tailor content to one's needs is an extremely powerful participation incentive, and serves as basis of a true *Information Society*.

1.3.2 Social Information Discovery

A factor that has high impact on the user experience on the Social Web is the ease of access to relevant content. This gives rise to a major difficulty, namely, how do we define *relevant content*?

Our personality, including interests and tastes, is shaped in large part by our membership in social groups. Throughout our lifetimes we belong to a variety of groups; our family,

[8]Information according to `en.wikipedia.org/wiki/Blogosphere`, downloaded on September 17, 2009.

our high school class, the social climate of the country in which we are brought up, and the circle of our professional peers all influence our opinions and preferences. Our taste in food, our choice of which electronics products to purchase, which books to read, and how to dress, are all influenced by our social context.

The Social Web allows us to behave socially on-line. However, the same mechanisms that govern our socially influenced choices in the physical world still apply to this new context. In many cases, users explicitly affiliate themselves with relevant and trusted sources of information. So, a person who considers himself a Liberal Democrat will read liberal media, and may attend gatherings of like-minded persons in his area. Likewise, a *blogger* interested in technology-related content may subscribe to *Slashdot* and *TechCrunch* updates through an RSS aggregator[9]. A physical-world endorsement of a friend's taste in food may translate to joining the friend's network of fans on *Delicious*, or following his status updates on *Twitter*.

Users who do not explicitly affiliate themselves with sources of relevant information, either via subscriptions or via the social networks mechanism, may still be able to discover information in a social manner. Namely, the system may deduce the user's preferences based on his content contributions. An important family of techniques that uses this idea is based on *Collaborative Filtering* (CF). The underlying assumption of CF is that people who agreed in the past tend to agree again in the future. Several CF approaches have been described in the literature, and we summarize one classic approach, referred to as *item-based CF*, here. In item-based CF, which was popularized by *Amazon.com* and is known as "people who bought x also bought y", the system first computes a matrix of item-to-item similarity. For example, similarity between items a and b may be computed as the angle between vectors $\vec{a}$ and $\vec{b}$, where i^{th} vector position is set to 1 if user i purchased the item, and to 0 otherwise. (Of course, weights may also be used instead of binary values.) Having constructed the item-to-item similarity matrix, the algorithm generates a prediction for a given user u. In an alternative approach, known as *user-based CF*, a user-to-user similarity matrix is built in the space of items.

An issue that arises in the context of content recommendation that is based on user behavior is privacy. Privacy is an active area or research, both as it relates specifically to Collaborative Filtering [Polat and Du, 2003; Canny, 2002], and in the broader context of privacy preserving data mining [Vaidya *et al.*, 2006].

While the personalization of content described here allows for access to highly relevant information, it comes with a significant drawback. Our brains have a natural tendency, based on the conservation of energy, to prefer recognition to discovery. This tendency leads us to trust familiar sources, and to become indoctrinated in familiar ideas. Receiving all information from a set of familiar sources may limit a person's horizons and prevent

[9]RSS stands for "Really Simple Syndication" and is a family of web feed formats used to publish frequently updated content. RSS feeds are read using aggregator software.

true information discovery. This pitfall, which exists both in the physical world and on the Social Web, can be avoided by social information processing systems, by diversifying offered content. We discuss this point further in Section 2.3.1.

Much of the information with which we come in contact every day is time-sensitive. Political news and commentary, party invitations, and restaurant openings are all examples of information that is relevant only when it is fresh. The assumption that information is time-sensitive underlies the design of most information presentation mechanism on the Social Web. For example, status updates on *Twitter*, RSS feeds of blog data, and status updates on *Facebook* all present data in time order. An interesting research question that arises in this context is how to determine whether or not a particular piece of information is time-sensitive, and how to present a combination of time-sensitive and time-invariant results to the user in an intuitive manner.

1.4 Result Presentation for Information Discovery

1.4.1 Shortcomings of Ranking

In Section 1.1 we argued that many more high-quality documents are typically identified by IR and Web search in real-life scenarios than any one user is willing to read, motivating the need for ranking. Ranking is intuitive, and is the predominant method or prioritizing results of potentially higher relevance over those of lower relevance in IR and search applications. The usefulness of ranking is widely recognized, and it has been applied in other domains, such as for improving the user experience in relational database applications; see for example [Ilyas, 2009].

Despite its wide-spread use, ranking has certain drawbacks. In particular, it is limited in its scope to information discovery tasks in which the user is well-aware of his information need, and is able to express that need with a query. Finding the phone number of the Computer Science Department at Columbia University, the date of birth of Albert Einstein, and a list of citations on the use of ranking in Database Systems are all information discovery tasks with a precisely phrased information need, and ranking is helpful for such tasks.

However, because only a limited portion of the result set is easily accessible in a ranked list (e.g., the top-10 or top-20 results), ranking is fundamentally inappropriate for *data exploration*. In data exploration a user is iteratively refining his understanding of the available data, and at the same time gradually re-defining his information need. An example of a task of this kind is deciding which Computer Science course to take during the current semester, or what style of shoes to buy this Fall. The commonality between these seemingly unrelated tasks (other than the reference to the Fall season) is that a query like "CS courses Fall 2009" or "Fall shoes" does not specify any properties of a desirable answer that can be used for relevance ranking. That is, according to the queries, all CS courses offered in the Fall of 2009 and all Fall shoes are equally relevant. The user may in fact have a rough

idea about the kinds of classes and shoes that he prefers, but he wishes to formulate his preference in a more informed manner, *based on the available items*.

In situations such as these the system must help the user formulate his information need, through an effective information presentation method appropriate for *data exploration*. Allowing the user to find relevant items is particularly important when the user is interacting with a large dataset.

1.4.2 Faceted Search

A popular presentation method appropriate for information discovery is *faceted search*, also called *faceted navigation* or *faceted browsing*. This method allows the user to access the items in a collection by facets, defined as mutually exclusive, and collectively exhaustive aspects, properties or characteristics [Wynar, 1992]. Faceted search is commonly used by on-line stores, like *Amazon.com* and *Best Buy*, for the representation of their product catalogs.

In faceted search systems navigation is typically limited to a single facet at a time. For example, the user may first choose to look at the "Automobiles" category, then at "Ferrari", then at "Red cars", and will finally arrive at the automobile that he wishes to buy. A summary statistic, such as the number of items that are classified under the current facet, is usually provided alongside the facet description.

Faceted search remains an active area of research, and many extensions of the basic model have been proposed, including a faceted query language [Ross and Janevski, 2004], an extension of the presentation to include statistics other than item counts [Ben-Yitzhak *et al.*, 2008], and dynamically suggesting which facet to explore next with the goal of minimizing navigation time [Roy *et al.*, 2008].

1.4.3 Clustering

Clustering has long been recognized as a valuable data exploration tool. Many general and domain-specific clustering algorithms exist and have been applied to the grouping together of similar Web documents, DNA samples, user preferences, etc. While an extensive survey of clustering is beyond the scope of this thesis, we briefly survey several application scenarios where clustering has been used for data exploration, and refer the reader to reviews of clustering [Jain *et al.*, 1999; Berkhin, 2002].

Clustering of text documents has been explored extensively in Information Retrieval, and we give a few examples here. It has long been recognized that partitioning large sets of results into coherent groups, and generating descriptions for these groups, greatly improves a user's ability to understand vast datasets. This intuition was supported experimentally in [Leuski, 2001] for collections of text documents. More recently, approaches have been explored [Bonchi *et al.*, 2008] that use search query logs to cluster search results into coherent well-separated sets for presentation purposes. In [Dakka and Gravano, 2007] the authors

combine an offline document clustering method and an online method to generate multi-document summaries of clustered news articles.

Subspace clustering is a feature selection technique that aims to uncover structure in high-dimensional datasets. Subspace clustering has been used extensively in data mining, following the introduction of CLIQUE [Agrawal *et al.*, 1998], an Apriori-style algorithm. Many extensions of CLIQUE, as well as a variety of new subspace clustering algorithms, have been proposed and are surveyed in [Parsons *et al.*, 2004; Kriegel *et al.*, 2008]. Subspace clustering algorithms can generally be classified as *bottom-up* and *top-down*. Most bottom-up algorithms, including CLIQUE, generate potentially overlapping clusters. In contrast, top-down subspace clustering algorithms usually assign an item to at most 1 cluster.

Clustering and data visualization have been used extensively for the analysis of biological data [Azuaje and Dopazo, 2005]. Clustering is used for tasks such as analysis of DNA microarrays, identification of biological networks and pathways, and validation of computational predictions.

Another wide-spread application of clustering relates to the understanding of complex networks such as the Web graph, a biological pathway, or a network of users of a collaborative tagging site. Graph clustering is aimed at finding sets of related vertices in a graph, where relatedness is application-dependent; see [Schaeffer, 2007] for a review.

1.5 Summary of Contributions and Thesis Outline

This thesis explores applied aspects of data management, aimed in particular at improving the user experience in on-line environments, with the goal of facilitating information discovery and furthering collaboration. We believe it essential to develop and validate our methods on real, rather than synthetic, datasets.

Because of the information-based nature of our society, information and knowledge are often a financial asset. Companies such as AT&T, Google, IBM, Microsoft, and Yahoo! achieved significant commercial success due in part to the multitude of valuable datasets that they own and support. All companies on this list, and many others, realize the value of academic research both for their own growth and for the development of the society at large, and invest significant resources to support research. Much of the work in this thesis is based on commercial datasets owned by Yahoo! We thank Yahoo! for giving us access to the *Delicious* and *Yahoo! Personals* datasets that serve as basis for our work in Chapters 2 and 5, respectively.

The World Wide Web is based on the idea of open information exchange. The Web itself, and many of its important subsets, are publicly available, and can be used as basis for scientific research. This thesis uses several datasets that fall into this category. The *PubMed* document corpus and the *Medical Subject Headings* ontology, both supported by the National Center for Biotechnology Information and the National Library of Medicine,

are used in Chapter 3. The English-language *Wikipedia* and an ontology of concepts called *YAGO* are used in Chapter 4.

We now briefly outline the technical contributions of this thesis.

In Chapter 2 we build on the intuition that ranking on the Social Web should take into account a user's social context. We start with a description of the goals and challenges of context-aware ranking, and present *Delicious*, a representative social tagging dataset that motivates our algorithmic work. We go on to analyze the types of social behavior in which *Delicious* users engage, and explore the potential of using this behavior for personalized content recommendation. Finally, we present the main algorithmic contribution of Chapter 2, a novel search paradigm referred to as *network-aware search*. We explore performance considerations of our approach, and propose optimizations that make network-aware search practical on the large scale.

In Chapter 3 we tackle the challenge of enhancing relevance ranking in scientific literature search. We describe *PubMed*, the largest bibliographic source in the domain of life sciences, and consider how a large high-quality ontology of *Medical Subject Headings* (MeSH) can be used to relate a user's query to the annotations of a document. We develop several relevance measures appropriate for ranking in this domain, and propose efficient evaluation algorithms for computing relevance on the scale of *PubMed* and *MeSH*. We also present results of a preliminary user study that evaluates the effectiveness of our techniques. In a final development, we go beyond list-based ranking, and present a two-dimensional visualization of query results that facilitates data exploration.

In Chapter 4 we build on the idea of using an ontology for relevance ranking, and present *EntityAuthority*, a framework for semantically enriched graph-based authority propagation. *EntityAuthority* operates over graphs that combine Web pages and semantic entities, and produces ranked lists of pages and entities as a result. We evaluate the effectiveness of our method on a graph that combines *Wikipedia* pages with entities from an automatically-derived ontology *YAGO*, and demonstrate an improvement in the quality of ranking.

In Chapter 5 we present *BARAC*, an algorithm for rank-aware clustering of structured datasets. We outline the challenges of data exploration in large multi-dimensional datasets in the presence of ranking, and propose to use clustering. We develop a family of clustering quality measures appropriate for this domain, and adapt an existing clustering algorithm to our scenario. We present an extensive experimental evaluation of the scalability of our techniques on *Yahoo! Personals* datasets. Finally, we discuss and experimentally validate the effectiveness of our methods.

Chapter 6 summarizes work that is not directly related to the main theme of this thesis, but that was carried out as part of doctoral research. In Section 6.1 we describe several approaches that address data modeling challenges in complex domains. In Section 6.2 we discuss how classification ensembles from Machine Learning may be used for Parametric Query Optimization in a Relational Database Engine. In Section 6.3 we describe *MutaGe-*

neSys, a system for estimating individual disease susceptibility based on genome-wide SNP arrays.

Chapter 7 concludes this thesis, summarizing our technical contributions and outlining directions for future work.

The contributions of this thesis are centered around adding a semantic dimension to search and ranking in a variety of application scenarios. The overarching goal of this work is to improve the user experience in richly structured data-intensive environments, facilitating information discovery. The datasets that motivate our work come from a variety of domains, but have two common features: they are large and richly structured. These properties lead us to develop techniques that utilize the rich semantic structure of the data, and that can be used efficiently on the large scale.

Our work is motivated by the intuition that ranking does not always have to mask the semantic richness of the data by mapping results onto a global one-dimensional line. In Chapter 2 we explore ways to partition the user base, and to customize ranking based on the semantics of a user's social behavior. In Chapters 3 and 4 we enrich the ranking function using ontological knowledge bases. In Chapter 5 we make the semantics of the relationship between the data and the ranking function explicit, and use this relationship to partition the dataset with respect to the ranking function.

Today's users live in a global society, and use data in ways that cross application and domain boundaries. In order to address the needs of users adequately, researchers must bridge the gap between areas that have historically been disjoint. The work of this thesis uses and extends techniques from a variety of research areas, such as database systems, information retrieval, data mining, and machine learning.

Chapter 2

Search and Ranking in Collaborative Tagging Sites

This chapter is based on joint work with Sihem Amer-Yahia, Michael Benedikt, Alban Galland, Cameron Marlow, Laks V.S. Lakshmanan, and Cong Yu. This work appeared in [Stoyanovich *et al.*, 2008a; Amer-Yahia *et al.*, 2008b; Amer-Yahia *et al.*, 2008a].

2.1 Introduction

2.1.1 Search and Ranking in the Social Context

As we argued in Chapter 1, the advent of the World Wide Web and the emergence of the Social Web brought about a paradigm shift in the relationship between users and content. The new breed of Social Web users have a more direct relationship with the content than do anonymous Web searchers modeled in traditional Information Retrieval. Users of the Social Web portals build persistent online personas: they provide information about themselves in stored profiles, register their relationships with other users, and express their preferences with respect to content. As a result, rich semantic information about the user is readily available, and can be used to improve the user's online experience, making him more productive, more creative, and better entertained online. Social Web users in fact have an expectation with respect to the quality of served content, and rely on the system to customize their online experience based on their social and informational context.

Collaborative tagging sites are a particular kind of social content site. In these sites, users form social networks, and produce content by tagging items with natural language keywords [Golder and Huberman, 2006]. What kinds of items are being tagged depends on the focus of the specific site; however, the types of social interaction and the ways of reaching content are consistent across sites. Some examples of collaborative tagging sites are *CiteULike*, which maintains a library of academic papers, *Delicious*, in which users

bookmark and tag web pages, *Flickr* and *Snapfish*, which focus on photos, and *YouTube*, which specializes in videos. The currently predominant ways of reaching content in these sites are:

- Browsing the most popular items;
- Browsing items by tag;
- Browsing by network.

For example, in *Delicious* users can view hotlists, which are lists of the currently most-popular sites. Users can also browse the most popular URLs by tag. Finally, users can befriend other users and subscribe to their friends' feeds, which list the latest bookmarked and tagged URLs.

As collaborative tagging sites grow in size, browsing-based information discovery becomes less effective. So, as the size of user's friendship network increases, managing the multitude of information feeds becomes more difficult. As more items are tagged by the user base, the 10 or so most popular items that comprise the hostlist become a less and less representative tip of the iceberg. As the community grows and includes users with varied interests, choosing tags by which to browse becomes challenging.

As the size of the data set increases, it is important to assist the user in finding relevant and interesting content. Further, the ability to define explicit social ties with other users raises users' expectations with respect to the quality of served content. In the remainder of this chapter we propose to leverage the user's social ties and tagging behavior for more effective data exploration. We will present two data exploration scenarios in which offered content is customized on a per-user basis, in accordance with the user's social and tagging contexts. The first scenario deals with customized content recommendation, while the second focuses on network-aware keyword search.

The models and algorithms in this chapter are supported by an experimental evaluation on datasets from *Delicious*, a representative collaborating tagging site. We start by describing the *Delicious* system and identifying the different types of behavior taken on by its users.

2.1.2 Delicious: a Collaborative Tagging Site

Delicious, formerly known as `del.icio.us`, is a social bookmarking and tagging service for storing, sharing, and discovering websites. *Delicious* is owned by Yahoo! and has more than five million users and 150 million bookmarked URLs[1].

[1]The statistics are as of August 18, 2009, according to `en.wikipedia.org`.

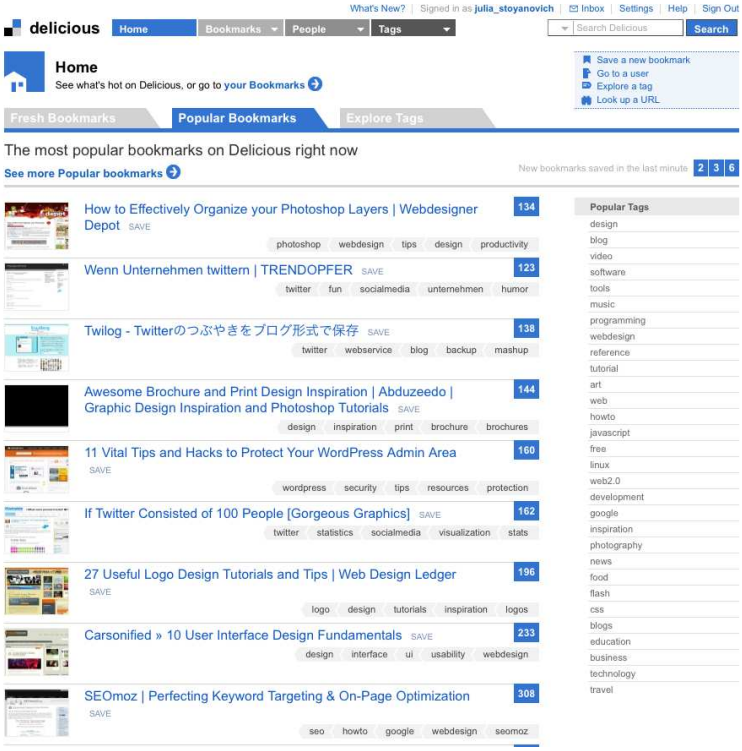


Figure 2.1: Popular bookmarks in *Delicious*.

Delicious users bookmark URLs, and optionally assign free-text index terms, called *tags*. Users can browse their own bookmarks, as well as bookmarks that were assigned by other users of the system.

Figure 2.1 presents a portion of a *hotlist*: a list of the currently most popular URLs, together with their popularity score (134 for the first URL), and a list of tags that were assigned to the URL by the user base[2].

In addition to browsing the most popular URLs, users can also browse content by tag. Figure 2.2 presents a *tag cloud*, a graphical representation of the most popular tags, with font size and color corresponding to the popularity of the tag in the system. (Tags that are popular in the system, and that are also part of the user's tagging vocabulary are highlighted in blue.)

Hotlists and tag clouds are both important means of information discovery in *Delicious* that rely on the system-wide, or global, popularity of URLs and tags, respectively. Additionally, to facilitate the *social sharing of bookmarks among pairs of users*, *Delicious* supports the creation of *networks*. A network is a directed graph in which users become *fans* of other users, and are then able to browse the recently bookmarked and tagged URLs

[2]All screenshots in this section were generated on August 16, 2009.

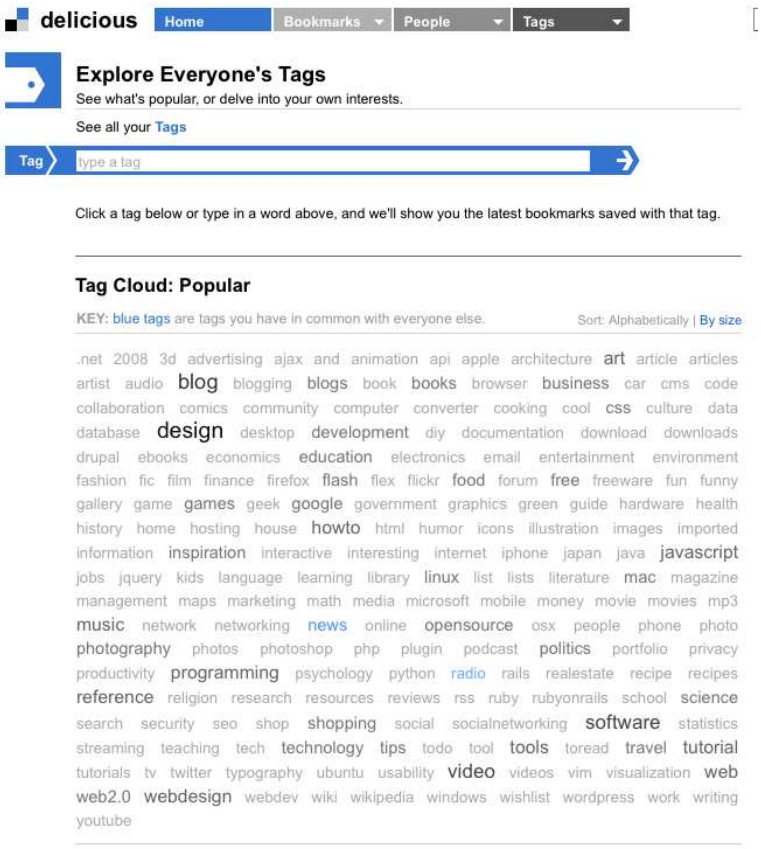


Figure 2.2: The *Delicious* tag cloud.

contributed by the individual members of their network.[3] We will sometimes refer to the explicit network of fans in *Delicious* as the *friendship network* for convenience. Figure 2.3 shows a list of recent bookmarks created by user *Cameron*. URLs are displayed in chronological order, and include a global popularity score (7 for the first URL in the list), and a list of tags that were assigned to the URL by all members of the user base.

In the remainder of this chapter we will develop a formalism for network-aware search and content recommendation. In order to present our approach, we now formally describe the data model. Our model is based on *Delicious*, but is applicable to other collaborative tagging systems that have a similar structure.

2.1.3 Data Model

We assume that three sets are given: a set of users $\mathcal{U}$, a set of items $\mathcal{I}$, and a set of tags $\mathcal{T}$. In *Delicious*, $\mathcal{U}$ includes all registered users, $\mathcal{I}$ corresponds to the set of URLs, and $\mathcal{T}$ is the

[3]It is also possible to browse bookmarks of users who are not in one's network. However, browsing a network member's URLs is easier because of more convenient navigation.

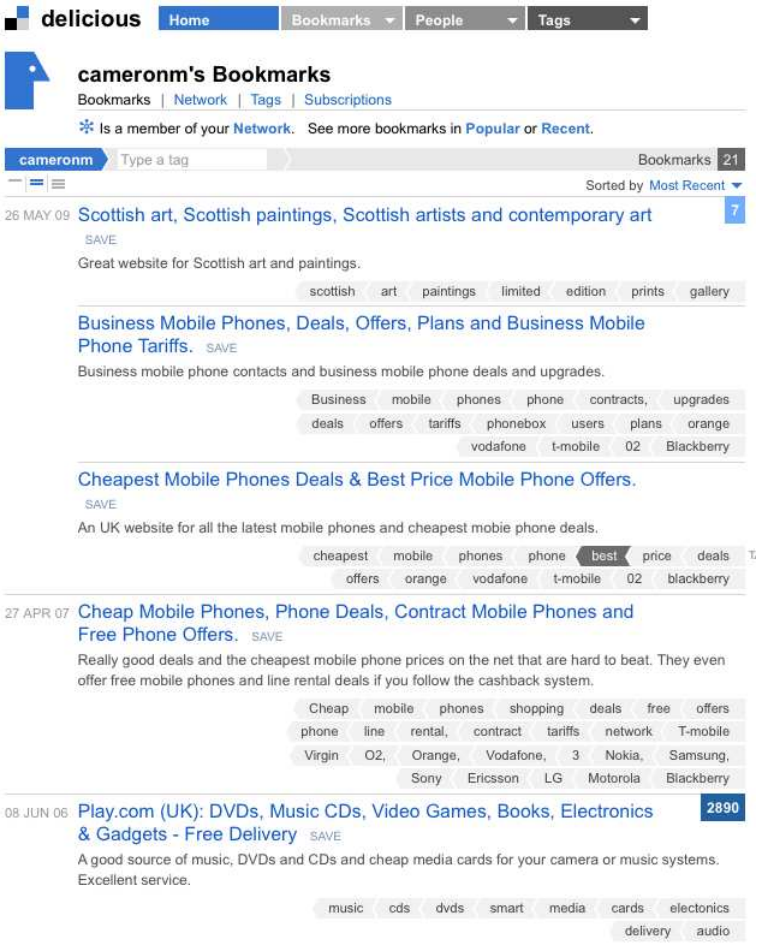


Figure 2.3: Browsing bookmarks of a network member.

set of all tags that were assigned by users to the URLs in the process of tagging. Tagging is the primary way in which users contribute content to the system. We will use the following notation to represent tagging.

- $\texttt{Tagged}(u, i, t)$ represents tagging actions: a user u tags an item i with a tag t.
- $\texttt{Tags}(u) \subseteq \mathcal{T}$ is the set of tags that were used by user u.
- $\texttt{Tags}(u, i) \subseteq \mathcal{T}$ is the set of tags that were used by user u to tag item i.
- $\texttt{Items}(u) \subseteq \mathcal{I}$ is the set items that were tagged by user u.
- $\texttt{Items}(u, t) \subseteq \mathcal{I}$ is the set items that were tagged by user u with tag t.
- $\texttt{Taggers}(i) \subseteq \mathcal{U}$ is the set of taggers of item i.
- $\texttt{Taggers}(i, t) \subseteq \mathcal{U}$ is the set of taggers of item i with tag t.

An additional activity that is complementary to tagging is the users' participation in social networks. A social network is a directed graph, in which nodes are users, and edges correspond to social ties between users. These ties may be explicit, such as friendship, similar age group, or geographic proximity. An example of an explicit tie in *Delicious* is when a user becomes a fan of another user. Social ties may also be implicit, and may be derived through data analysis. An example of an implicit tie is shared interest in a topic, and we will describe the semantics of shared interest in the following sections.

We use the following notation to represent a social network.

- $\texttt{Link}(u, v)$ represents a directional relationship between two users $u, v \in \mathcal{U}$, and denotes that there is an edge from u to v. For example, in *Delicious* such an edge may denote that u is a fan of v.

- $\texttt{Network}(u) \subseteq \mathcal{U}$ is the set of neighbors of u that is, $\texttt{Network}(u) = \{v \mid \texttt{Link}(u, v)\}$.

2.1.4 Description of the Experimental Dataset

The methods described in this chapter were evaluated over a sample of *Delicious* to which we were given access by the *Delicious* team. The dataset includes tagging actions during a one-month period in 2006. In addition to tagging actions, our dataset also includes a snapshot of the social network for the corresponding time period.

The dataset of tagging actions is very sparse and follows a long tail distribution [Kipp and Campbell, 2006; Golder and Huberman, 2006]: most URLs are tagged by only a handful of users, and many tags are only used by a few users. Sparse datasets are difficult to process efficiently, and we applied the following procedure to reduce the size of the dataset. First, we removed all URLs that were tagged by fewer than 10 distinct users. Additionally, we removed tagging actions that include uncommon tags: only tags used by at least 4 distinct users are included in our dataset. This cleaning procedure resulted in cutting the tail of URLs and tags. As a result, the dataset was reduced to 27% of its original size. Our cleaned dataset contains 116,177 distinct users who tagged 175,691 distinct URLs using 903 distinct tags, for a total of 2,322,458 tagging actions.

Reduction of the dataset size was done primarily to allow us to store and access the data more efficiently in a relational framework. However, while the size of the dataset was reduced dramatically by our cleaning procedure, the effect of this reduction on keyword search and content recommendation is limited. This is because only the URLs that were "unpopular" over all tags and all users were removed. Each of the removed tags was used by only a handful of *Delicious* users, and such tags have limited utility for content recommendation and search. More often than not such uncommon tags form part of a user's private vocabulary, and are not intended for social sharing of information. Some examples of such idiosyncratic tags are "Michael G's birthday party" and "bug #1293".

In the remainder of this chapter, we will focus on tagged URLs, and will neither explicitly represent nor use URLs that are bookmarked but not tagged. Additionally, because we will consider a user's tagging to verify the effectiveness of content recommendation, and, in some cases, to derive a social network, we focus our attention on taggers – users who contributed at least one tagging action to the cleaned dataset.

2.1.5 Chapter Outline

In the first part of this chapter (Section 2.2), we study the effectiveness of several *hotlist generation strategies* that take into account the user's tagging behavior, social ties, and interests. We conclude that leveraging context information significantly improves the quality of content recommendation.

In the second part of this chapter (Sections 2.3 through 2.6), we develop a novel paradigm of *network-aware search*, in which keyword search and ranking are executed over the content that is recommended by the user's network.

We review related work in Section 2.7 and conclude in Section 2.8.

2.2 Leveraging Semantic Context to Model User Interests

2.2.1 Introduction

In this section we study how the social context of a user can be used to improve the quality of content recommendations. In Section 2.1.2 we described the basic types of context that arise in collaborative tagging sites. In these sites users contribute content by tagging items, forming social networks, and consuming content, primarily by browsing. An important information discovery tool in collaborative tagging sites is a hotlist.

Hotlists are a means to expose vital content which has global popularity in the system. An example of a hotlist is presented in Figure 2.1. However, while globally popular items usually represent the consensus of many users, we experimentally observe in Section 2.2.3 that such items only account for a small fraction of any individual user's interests. We thus look for ways to account for user preferences during hotlist computation.

We first represent the interests of a user by the vocabulary he employs to tag URLs. The intuition is that if a significant portion of the user's tagging includes the tag "sports", the user is likely interested in sports-related content. This simple observation allows us to replace a single global hotlist by per-tag lists, and to suggest potentially interesting URLs by drawing from one or more per-tag lists in accordance with the user's preferences. As we demonstrate in Section 2.2.4, tag-driven customization significantly improves hotlist quality, but its success is still limited by the global aspect.

In the second approach, we propose to model interest using social ties. These ties are either explicitly stated or derived. An example of an explicit social tie is a network of fans.

We explore the utility of this network in hotlist generation in Section 2.2.5, and demonstrate that such ties can indeed be leveraged to generate higher quality hotlists.

Collaborative Filtering is a popular method that uses machine learning to determine interest overlap between users based on their behavior such as common ratings of items, or common purchasing and browsing patterns. We adopt an approach similar to Collaborative Filtering and construct a *common interest network* that links two users if the sets of URLs they tagged overlap significantly. We demonstrate in Section 2.2.6 how such networks can be used to construct personalized hotlists of very high quality.

One factor that limits the effectiveness of common interest networks in Collaborative Filtering is *sparsity*: there are often many more items than any one user is able to rate. This issue is further aggravated in the context of a collaborative tagging site such as *Delicious*, where the set of items corresponds to a potentially infinite set of Internet sites. Sparsity is one of the main reasons why using overlap in items to derive common interest networks is only effective for a subset of *Delicious* users in our experiments. Another important reason is that people rarely agree on everything: you may agree with your mother on cooking, and with your adviser on research, but your adviser's opinion on food is hardly relevant. We use this idea in Section 2.2.7 and demonstrate how tag and item overlap can be combined to construct per-tag common interest networks. Such networks have wider applicability than item-only networks, and can be used to construct hotlists of very high quality.

2.2.2 Formalism

We use the following terminology to describe a hotlist generation method M:

- The *scope* of M refers to the portion of the user base $\mathcal{U}_{scope} \subseteq \mathcal{U}$ to which the method can be applied. The larger the scope of a hotlist generation method, the more users can potentially benefit from it.
- The *seed* of M is the set of users $\mathcal{U}_{seed} \subseteq \mathcal{U}$ who are used to generate hotlists for $u \in \mathcal{U}_{scope}$. In order to produce high-quality hotlists the seed has to be both *representative* of a user's interests, and *focused* on his interests.

Given a set of items $\mathcal{I}$, and the seed set $\mathcal{U}_{seed}$, we define the score of an item $i \in \mathcal{I}$ as the number of users in $\mathcal{U}_{seed}$ who tagged item i:

$$\texttt{score}(i, \mathcal{U}_{seed}) = |\texttt{Taggers}(i) \cap \mathcal{U}_{seed}| \tag{2.1}$$

The goal of a method M is to produce a hotlist of items *HList*. Without loss of generality, we assume that we generate top-10 hotlists, $|HList| = 10$ for all methods.

We quantify the performance of M in terms of *coverage*, a normalized metric that represents the overlap between the hotlist and the items tagged by the user during the

specified time period.

$$\texttt{coverage}(HList, u) = \frac{|HList \cap \texttt{Items}(u)|}{MIN(|\texttt{Items}(u)|, 10)} \tag{2.2}$$

Coverage of a method M is the average of per-user coverage over all users in $\mathcal{U}_{scope}$.

$$\texttt{coverage}(M) = AVG_{u \in \mathcal{U}_{scope}} \texttt{coverage}(HList, u) \tag{2.3}$$

2.2.3 Using Global Popularity

We first consider the quality of hotlists that are based on global popularity of a URL (this is what is referred to as a "hotlist" by most systems). For this method, which we call `global`, the seed and the scope are the entire user base, while the score of an item i is simply the number of users who tagged that item.

$$\begin{aligned} \mathcal{U}_{seed} &= \mathcal{U}_{scope} = \mathcal{U} \\ score(i) &= |Taggers(i)| \end{aligned}$$

The top-10 best URLs computed using this method constitute the hotlist, and this hotlist is global, i.e. it is not customized per-user. The left hand-side of Figure 2.4 presents a *hypothetical* list of 10 most popular URLs, along with the number of users who tagged these URLs. The `global` method recommends the URLs in this list to each user in the system. Note that the popularity of each URL, recorded in the *Votes* column in Figure 2.4, reflects the total number of tagging actions that reference the URL, irrespective of the tag.

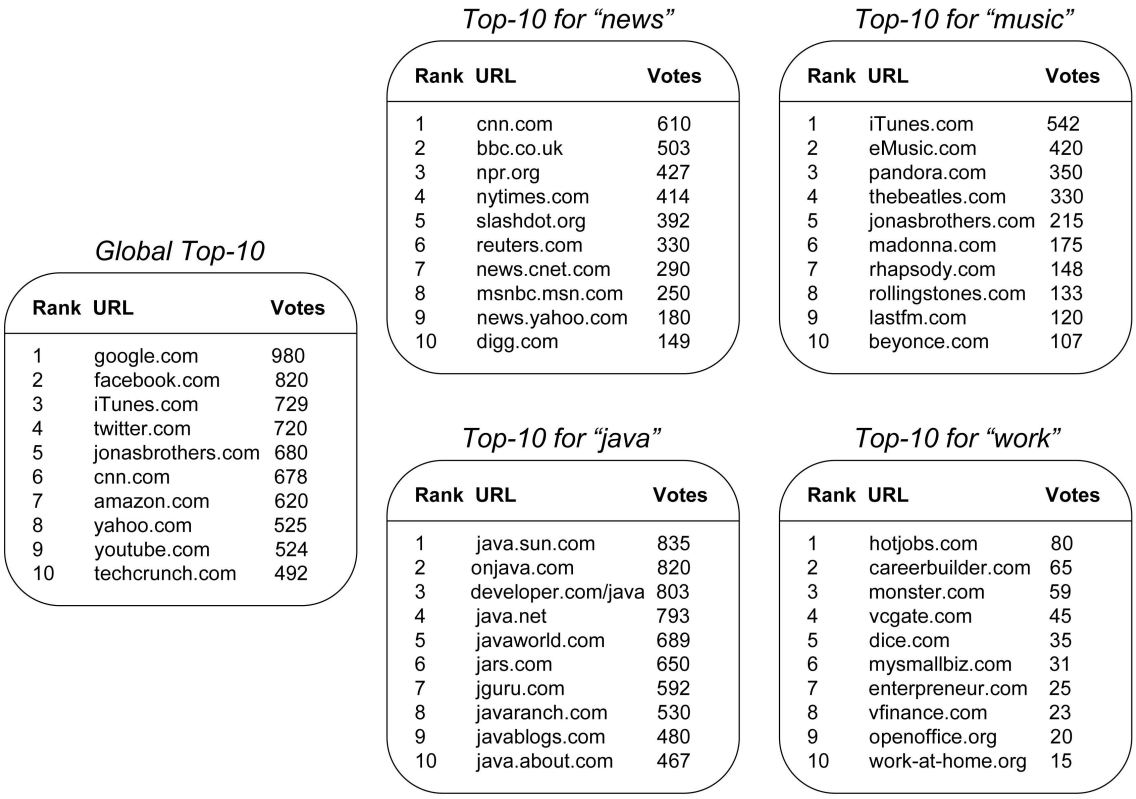
The average coverage of `global` over all 116,177 users in our experiments is 2.7%. This amount, while quite small, indicates that there is some correlation between the users' tagging behavior and globally popular URLs. It also argues for improving the method of producing hotlists by accounting for users interests.

2.2.4 Combining Global Popularity with Tags

We now model the interests of a user in terms of the user's tags, and define the *interest* of a user u for tag t as the fraction of u's tagging actions that include t.

$$\texttt{interest}(u, t) = \frac{|\texttt{Items}(u, t)|}{|\texttt{Items}(u)|} \tag{2.4}$$

Consider the tagging actions of four hypothetical users presented in Figure 2.5. *Ann* tags with "news" and "music" with equal frequency, and she uses no other tags. We compute $\texttt{interest}(Ann, \text{"music"}) = \texttt{interest}(Ann, \text{"news"}) = \frac{1}{2}$. *Dawn* also uses two tags, "work" and "play", but she tags with "work" more frequently: $\texttt{interest}(Dawn, \text{"work"}) = \frac{7}{8}$, while $\texttt{interest}(Dawn, \text{"play"}) = \frac{1}{8}$.



Global Top-10

Rank	URL	Votes
1	google.com	980
2	facebook.com	820
3	iTunes.com	729
4	twitter.com	720
5	jonasbrothers.com	680
6	cnn.com	678
7	amazon.com	620
8	yahoo.com	525
9	youtube.com	524
10	techcrunch.com	492

Top-10 for "news"

Rank	URL	Votes
1	cnn.com	610
2	bbc.co.uk	503
3	npr.org	427
4	nytimes.com	414
5	slashdot.org	392
6	reuters.com	330
7	news.cnet.com	290
8	msnbc.msn.com	250
9	news.yahoo.com	180
10	digg.com	149

Top-10 for "music"

Rank	URL	Votes
1	iTunes.com	542
2	eMusic.com	420
3	pandora.com	350
4	thebeatles.com	330
5	jonasbrothers.com	215
6	madonna.com	175
7	rhapsody.com	148
8	rollingstones.com	133
9	lastfm.com	120
10	beyonce.com	107

Top-10 for "java"

Rank	URL	Votes
1	java.sun.com	835
2	onjava.com	820
3	developer.com/java	803
4	java.net	793
5	javaworld.com	689
6	jars.com	650
7	jguru.com	592
8	javaranch.com	530
9	javablogs.com	480
10	java.about.com	467

Top-10 for "work"

Rank	URL	Votes
1	hotjobs.com	80
2	careerbuilder.com	65
3	monster.com	59
4	vcgate.com	45
5	dice.com	35
6	mysmallbiz.com	31
7	enterpreneur.com	25
8	vfinance.com	23
9	openoffice.org	20
10	work-at-home.org	15

Figure 2.4: Hypothetical top-10 hotlists.

We compute separate top-10 URL lists for each tag $t \in \mathcal{T}$. Figure 2.4 presents four hypothetical tag-specific hotlists for tags "news", "music", "java", and "work". The popularity of a particular URL in the *Votes* column reflects the number of tagging actions where the URL was tagged *with the particular tag*, and is typically lower than the global tag-unaware popularity. So, the popularity of `cnn.com` in the top-10 list for "news" is 610, which is lower than the popularity of this URL in the global top-10 list. This is because `cnn.com` was likely tagged with tags other than "news", such as "cnn", "toread", etc.

Observe that the popularity of items in the top-10 list for "work" is significantly lower than item popularity in other tag-specific lists. This is because the tag "work" is fairly broad and rarely describes the content of the URL it annotates. Tags like "work", "todo", "toread", and "nota_bene" are rarely used to assign semantic meaning to a URL. Rather, these tags are part of the user's private vocabulary, and are likely not intended for sharing.

With the tag-specific hotlists at our disposal, we experiment with two different ways of using these lists for user-specific hotlist generation. In the first approach, which we call `best_tag`, we identify, for each user u, a single tag from among $\texttt{Tags}(u)$ for which $\texttt{interest}(u, t)$ has the highest value, and use the global top-10 URLs for that tag as the user's hotlist. Ties are broken arbitrarily. More formally, for a given $t \in \mathcal{T}$,

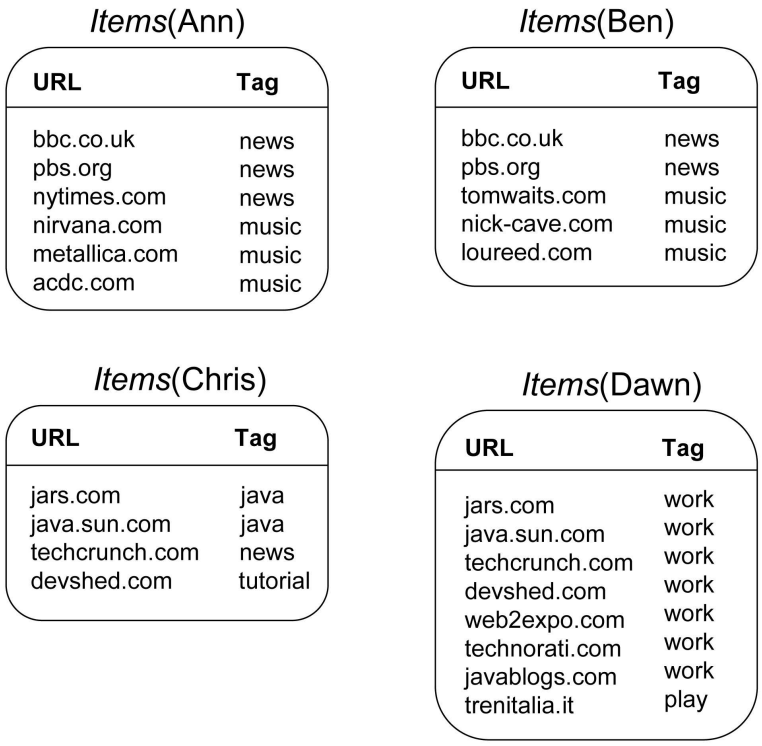


Figure 2.5: URLs tagged by four hypothetical *Delicious* users.

$$\mathcal{U}_{scope} = \{u \in \mathcal{U} | \quad \forall t' \in \texttt{Tags}(u), \quad \texttt{interest}(u,t) \geq \texttt{interest}(u,t')\}$$
$$\mathcal{U}_{seed} = \{u \in \mathcal{U} | \quad t \in \texttt{Tags}(u)\}$$

So, for *Ann* in Figure 2.5, either "news" or "music" may be used for `best_tag`. The tag "music" is the best tag for *Ben*, "java" is the best tag for *Chris*, and "work" is the best tag for *Dawn*.

The method `best_tag` can be used for all taggers $u \in \mathcal{U}$, and we report the average coverage over all users (116,177) for this experiment. Focusing on the single best tag brings coverage to 8.6%, a significant improvement over `global`. A deeper study of the data reveals that `best_tag` is most effective for users with comparatively higher values of $\texttt{interest}(u,t)$ for their best tag.

We draw two conclusions from our observation: first, that accounting for tagging behavior when computing hotlists does improve hotlist quality, and second, that a more general method for hotlist selection is needed, particularly for cases where no tag can be identified that clearly dominates a user's interests.

We thus propose another method, `dominant_tags`, where we identify taggers who have a strong interest in one or several tags, and then combine the best URLs from the per-tag

# dominant tags	$\lvert\mathcal{U}_{scope}\rvert$	coverage
1	36,736	10.4%
2	16,452	14.4%
3	6,466	17.8%

Table 2.1: Effect of the number of dominant tags on the performance of `dominant_tags`.

top-10 lists into a single custom top-10 hotlist. For a given tag $t \in \mathcal{T}$, and a threshold θ,

$$\begin{aligned} \mathcal{U}_{scope} &= \{u \in \mathcal{U} | \quad t \in Tags(u) \wedge \texttt{interest}(u,t) > \theta\} \\ \mathcal{U}_{seed} &= \{u \in \mathcal{U} | \quad t \in Tags(u)\} \end{aligned}$$

In the current set of experiments, we say that a user u has a strong interest in a tag t if $\texttt{interest}(u,t) > 0.3$. This threshold was determined empirically, and needs further validation in a future study. With an interest threshold set to 0.3, a user can have at most 3 dominant tags. If more than one tag passes the threshold, we draw an equal number of items from the top-10 lists that correspond to each dominant tag. If two tags t_1 and t_2 both pass the interest threshold for user $u \in U_{scope}$, the final list *HList* consists of the top-5 entries from $HList_1$ and the top-5 entries from $HList_2$. For users with 3 dominant tags, we choose the top-3 URLs from each $HList_1$, $HList_2$, and $HList_3$ and build a top-9 hotlist.

So, for users *Ann* and *Ben* in Figure 2.5, the hotlist is a combination of the top-5 URLs for "news" with the top-5 URLs for "music" (see Figure 2.4). *Chris* and *Dawn* both have a single dominant tag, and the top-10 list for these users is generated the same way as in the case of `best_tag`.

Table 2.1 presents the partitioning of the users in our dataset by the number of tags for which they have strong interest, and presents performance of `dominant_tags` for these users. Note that `dominant_tags` has less than perfect scope: the total number of users partitioned in this way is smaller than the entire user base; 49% of users in our dataset have no dominant tags.

The first row of Table 2.1 reports coverage as an average over the 36,736 users who have one dominant tag. For those users, the generated hotlist constitutes 10% of all URLs tagged by each user, on average. This number increases when users have 2 and 3 dominant tags. Clearly, the more dominant tags there are for a user, the better the coverage. However, a higher number of dominant tags corresponds to a more limited scope of applicability.

We now turn our attention to the relationship between the strength of a user's interest in a tag, and the coverage of the `dominant_tags` method. We do this for users with a single dominant tag (row 1 in Table 2.1). Table 2.2 summarizes our findings: as expected, the stronger the user's affinity for a tag, the better the coverage, but the more limited the scope.

Based on the data in Table 2.2 we observe that, while coverage increases with increasing

interest	$\lvert\mathcal{U}_{scope}\rvert$	coverage
30%	36,736	10%
40%	31,391	11%
50%	25,703	13%
60%	23,927	13%
70%	20,943	14%
80%	19,704	14%
90%	19,392	14%
100%	19,347	14%

Table 2.2: Effect of interest on the performance of `dominant_tags`.

affinity for a tag, a plateau is reached as interest reaches 60%. Hotlists generated by `dominant_tags` take into account a user's interests, as derived from his linguistic choices. However, items in the tag-specific top-10 lists still represent consensus of a very large group of users: $|\mathcal{U}_{seed}|$ is as large as 29,712 for the most popular tag in our experiments, i.e. 29,712 distinct users in our sample used this tag. For users with two or three dominant tags, multiple top-10 lists are combined, further increasing the size of $\mathcal{U}_{seed}$.

Conceptually, it is not the sheer size of the seed set, but rather the *subjective use of vocabulary* that limits the effectiveness of tag-based hotlist generation methods. This happens because vocabulary alone, in this case in the form of simple tags, cannot precisely capture meaning. Consider for example the sets of items that *Ann* and *Ben* tag with "music" in Figure 2.5. Under the assumption of tag-based hotlist generation methods, both users are interested in music. However, *Ann* and *Ben* are interested in different kids of music: *Ann* prefers alternative rock and heavy metal, while *Ben* likes bands that may be described as post-punk or alternative jazz.

Using tags to describe interests maps to the philosophical concept of *meaning by intention (connotation)*, where the meaning is defined or described. For example, a user may state that he is interested in music or in sports. Such a description may not be able to precisely define meaning because of implicit ambiguity. This is contrasted with *meaning by extension (denotation)*, where the meaning of a concept is expressed by pointing out examples of the concept. We will develop a hotlist generation approach that uses meaning by extension in Section 2.2.6, and will combine connotation and denotation in Section 2.2.7.

For reasons outlined above, the opinions and interests of individual users are approximated in large heterogeneous seed sets. The larger and the more heterogeneous the seed, the coarser the approximation. We call this effect *dilution*. To minimize dilution, given a user $u \in \mathcal{U}_{scope}$, a hotlist generation strategy needs to identify the seed set $\mathcal{U}_{seed}$ that is both representative of the interests of the user u, and focused on the user's interests.

In the remainder of this section, we seek to reduce dilution by considering explicit and

implicit social ties between users during hotlist generation.

2.2.5 Computing Hotlists Using the Friendship Network

The goal of this experiment is to explore the utility of the explicit friendship network in *Delicious* for hotlist generation. Of 116,177 taggers in our experiments, 36,248 (31%) also have a social network, and we term such users *friendly taggers*. Choosing the friendship network as $\mathcal{U}_{seed}$ is justified by the fact that *Delicious* users tend to pay attention to their friends tagging actions, which influence their own. In particular, users can subscribe to feeds and get notified whenever one of the users in their network tags a new URL.

For each friendly tagger, we generate a customized hotlist by drawing 10 URLs with highest popularity from among URLs tagged by the members of his network. We refer to this hotlist generation method as `friends`. The scope of `friends` is the set of friendly taggers, and the seed is defined, for a fixed user u, as the network of u.

$$\begin{aligned} \mathcal{U}_{scope} &= \{u \in \mathcal{U} \mid \exists v \in \mathcal{U} : v \in \texttt{Network}(u)\} \\ \mathcal{U}_{seed} &= \texttt{Network}(u) \end{aligned}$$

Consider again the hypothetical users in Figure 2.5, and suppose that *Chris* is a fan of *Ann* and *Ben*, that is, $\texttt{Network}(Chris) = \{Ann, Ben\}$. Then the hotlist for *Chris* would combine $\texttt{Items}(Ann)$ and $\texttt{Items}(Ben)$. In this list, `bbc.co.uk` and `pbs.org` would be ranked higher than the other URLs, since these items each have two votes, while other items each have one vote. Note that the coverage of the resulting hotlist with respect to $\texttt{Items}(Chris)$ is 0, signifying that, while *Ann* and *Ben* may be friends with *Chris* in real life, *Chris*'s interests diverge from those of his friends. Suppose now that *Chris* is a fan of *Dawn*, that is, $\texttt{Network}(Chris) = \{Dawn\}$. In this case the hotlist for *Chris* is $\texttt{Items}(Dawn)$, which attains a perfect coverage of 1. This example illustrates that explicitly declared networks, such as a network of fans, may or may not be indicative of the users' interests, and we now demonstrate this experimentally.

We focus on a random subset of friendly taggers, 4,644 in all, for our experiments in this section, and find the coverage of `friends` to be 42.9%, a significant improvement over `global`, which was 3.3% for the sample of friendly taggers in our experiments. Note that $AVG(|\mathcal{U}_{seed}|) = 4$ for our sample, multiple orders of magnitude less than for previous methods.

We now explore how tagging can be used to deduce interest overlap among users, and how such overlap can be used to generate hotlists of very high quality. We report two experiments: in the first, two users are said to have a social tie if the sets of URLs they tag overlap significantly; in the second, we enrich the set of derived ties by considering tag-specific overlap in URLs.

URL agreement	$\lvert\mathcal{U}_{scope}\rvert$	$AVG(\lvert\mathcal{U}_{seed}\rvert)$	coverage
30%	1,382	169.4	61.47%
50%	913	136.9	72.82%

Table 2.3: Effect of the agreement threshold on the effectiveness of `url_interest`.

2.2.6 Interest as Overlap in URLs

In this experiment we compute a *URL-interest network* by considering the overlap in tagged URLs between users. We quantify *URL-agreement* between users u and v as the fraction of URLs tagged by u that were also tagged by v.

$$\texttt{url\_agreement}(u,v) = \frac{|\texttt{Items}(u) \cap \texttt{Items}(v)|}{|\texttt{Items}(u)|} \tag{2.5}$$

When computing URL-based agreement between u and v we do not account for the tags that were assigned to the URLs in $\texttt{Items}(u)$ and $\texttt{Items}(v)$. So, u may have tagged the homepage of the Republican National Convention `www.gop.com` with the tag "good", while v may have tagged the same URL with "evil". Nonetheless, we assume that both u and v expressed an interest in `www.gop.com` by tagging that URL, irrespective of their sentiment.

Note that agreement is directional. If $\texttt{url\_agreement}(u,v)$ is above a certain *agreement threshold* θ, we will use URLs tagged by v to derive the hotlist for u. We refer to this method as `url_interest`. More formally, we first define the scope of the hotlist generation method as the set of users whose agreement with at least one other user in $\mathcal{U}$ is above the agreement threshold θ:

$$\mathcal{U}_{scope} = \{u \in \mathcal{U} \mid \exists v \in \mathcal{U} : \texttt{url\_agreement}(u,v) > \theta\}$$

We next define the seed for a fixed user $u \in \mathcal{U}_{scope}$:

$$\mathcal{U}_{seed} = \{v \in \mathcal{U} : \texttt{url\_agreement}(u,v) > \theta\}$$

Consider again four hypothetical users whose tagging actions are summarized in Figure 2.5. URL-agreement of *Chris* with *Dawn* equals 1, reflecting that URLs in $\texttt{Items}(Dawn)$ may be of interest to *Chris*. On the other hand, $\texttt{url\_agreement}(Dawn, Chris) = \frac{1}{2}$.

Table 2.3 summarizes the effectiveness of `url_interest` in terms of scope and coverage. We observe that, while the method achieves very good coverage, it is very limited in its scope: only 1,382 users can benefit from customized hotlists if 30% agreement is required. The scope is further limited to 913 users for a minimum agreement of 50%. Note also that $AVG(|\mathcal{U}_{seed}|)$ is lower for the 50% threshold. We believe this to be a case of lower dilution (fewer users in the $\mathcal{U}_{seed}$) leading to higher coverage.

The limited scope of `url_interest` is due to the fact that strong agreement of the kind required by this method is uncommon. To include an edge between two users in the interest network, we require that they agree on at least 30% of the tagged URLs over-all. We observe that, while agreement of this kind over all interests may be rare, people more commonly agree with others on only a part of their interests. We explore this idea in the next set of experiments.

2.2.7 Interest as Overlap in URLs and in Tags

We now propose to combine interest in a tag, as explored in `dominant_tags`, with agreement based on URL overlap, as in the previous section, to construct a *tag-URL-interest network*. We use tag interest to generate a global partitioning of tagging actions, and then search for URL-agreement within these partitions. We call this method `tag_url_interest`, and propose to use it for the taggers who show strong interest in one or more tags (see Equation 2.4). Thus, we define the scope of `tag_url_interest` as the set of taggers with strong interest in a tag, and with URL agreement, *for that tag*, with at least one other user. We first define a tag-specific version of agreement as:

$$\texttt{tag\_url\_agreement}(u, v, t) = \frac{|\texttt{Items}(u, t) \cap \texttt{Items}(v, t)|}{|\texttt{Items}(u, t)|} \tag{2.6}$$

The scope of `tag_url_interest` is then, for a fixed tag $t \in \mathcal{T}$:

$$\begin{aligned} \mathcal{U}_{scope} = \{u \in \mathcal{U} \quad | \quad & t \in \texttt{Tags}(u) \wedge \texttt{interest}(u, t) > \theta_{interest} \\ \wedge \quad & \exists v \in \mathcal{U} : \texttt{tag\_url\_agreement}(u, v, t) > \theta_{agreement}\} \end{aligned}$$

We next define the seed for a fixed $u \in \mathcal{U}_{scope}$, and for a fixed tag $t \in \mathcal{T}$ as the set of users who are in tag-url-agreement with u, and who have used t:

$$\mathcal{U}_{seed} = \{v \in \mathcal{U} | t \in \texttt{Tags}(v) \wedge v \in \texttt{tag\_url\_agreement}(u, v, t) > \theta_{agreement}\}$$

Consider users *Ann* and *Ben* in Figure 2.5. *Ben* is in perfect agreement with *Ann* on "news", and *Ann*'s news-related URLs should therefore be included into *Ben*'s hotlist. However, while both *Ann* and *Ben* tag with "music", their connotational agreement for this tag is 0; see Section 2.2.4 for a discussion. The `tag_url_interest` method recognizes this and will not recommend any of *Ann*'s music-related items to *Ben*.

We evaluated the effectiveness of `tag_url_interest` on a subset of users in our experiments: we choose users with strong interest in exactly 2 tags. Out of 16,452 users with strong interest in 2 tags, 1,235 were in the scope of `tag_url_interest`. We note that, while the scope of the current method is still limited, it greatly exceeds the scope of `url_interest`: only 205 users in the scope of `tag_url_interest` where also in the scope of `url_interest`.

method	$\lvert\mathcal{U}_{scope}\rvert$	$AVG(\lvert\mathcal{U}_{seed}\rvert)$	coverage
`dominant_tags`	1,235	26,855.5	17.2%
`tag_url_interest`	1,235	227.4	81.7%
`url_interest`	205	202.9	84.5%

Table 2.4: Relative performance of `dominant_tags`, `tag_url_interest`, and `url_interest`.

Table 2.4 summarizes the relative performance of `dominant_tags`, `url_interest` and `tag_url_interest` for the users in $\mathcal{U}_{scope}$ of `tag_url_interest`. The first line summarizes performance of `dominant_tags` for users in `tag_url_interest`. Because $\mathcal{U}_{scope}$ of `tag_url_interest` is a proper subset of $\mathcal{U}_{scope}$ of `dominant_tags`, we report performance of `dominant_tags` for all users in `tag_url_interest`. In this table, we use 30% as the threshold for both interest and URL agreement, wherever appropriate.

We note that `tag_url_interest` significantly outperforms `dominant_tags` in terms of coverage. However, for users who are in both `tag_url_interest` and `url_interest`, the latter does better. This represents 205 users for whom `tag_url_resource` achieves an 81.7% coverage while `url_resource` achieves an 84.5% coverage. This reinforces the idea that accounting for agreement over all URLs is stronger than agreement on one tag at a time. This result also supports our dilution hypothesis: $AVG(\lvert\mathcal{U}_{seed}\rvert)$ is smallest for `url_interest`, followed by `tag_url_interest`.

2.2.8 Discussion

As we demonstrated in this section, a user's tagging and social ties serve as a good indicator of his interests. Clearly, hotlists generated by observing explicit social ties, or by deriving social ties based on tagging, are of higher relevance than those produced by global hotlist generation strategies. In the remainder of this chapter we will expand on this intuition, and will develop network-aware search – a novel search paradigm where search results are computed with respect to a user's social network.

However, before we move on to network-aware search, we would like to make some observations regarding information discovery in collaborative tagging sites.

Social Information Discovery as a Participation Incentive

Delicious was originally conceived as an on-line bookmarking platform that allowed users to make their bookmarks portable. Bookmarking was initially viewed as a private activity, and tagging, particularly social tagging, gained prominence over time. While some users still view *Delicious* primarily as a private bookmarking platform, many enjoy the full range of social features of the site. This is evidenced by the extensive use of the *network feature*, and, perhaps most interestingly, by the fact that the tagging vocabulary in *Delicious*

converged to form a folksonomy. A folksonomy is a vocabulary, along with a classification system, that *emerges* in a bottom-up manner from the collaborative tagging practices of a social group. Users who tag socially tend to use folksonomy terms in their tagging, enabling other users to identify their content more easily.

In our work with the *Delicious* dataset we observed that participation in a network of fans and social tagging are complementary activities: users who form social networks are more likely to tag and vice versa [4].

As we just discussed, many *Delicious* users contribute content in a socially aware manner. Therefore, an important technical question, and one that may influence the very survival of social tagging sites like *Delicious*, is how to support social information discovery. In this section we described how a user's social behavior may be leveraged to generate high-quality hotlists, and we will present an algorithmic framework for network-aware search in the remaining sections of this chapter. However, the scope of applicability of our methods is limited to those users who choose to interact with the collaborative tagging platform in a collaborative, social manner. We believe that supporting socially aware information discovery will enrich the user experience, serving as a powerful incentive for continued user participation. This will, in turn, increase the scope of applicability of our methods.

Finally, we remark that the distinction between private tagging that involves idiosyncratic vocabulary, and public tagging that draws upon a folksonomy of terms, calls for the study of privacy in the context of collaborative tagging sites.

External Factors that Influence Interest

There are different reasons why a user would bookmark a URL and use specific tags to label it. Our evaluation of hotlist recommendation strategies shows that a user's interest in a URL is influenced by his social ties, many or all of which may be external: formed in real life, in another social content site, etc. Another external influence over a user's interest in a URL or in a tag is the general popularity of that URL or tag. Bursts in interest have been observed and studied in the past [Cohen and McCallum, 2003]. Indeed, some tags appear at certain periods of time and indicate a trend in the general public or among a community of users (e.g., people tend to visit travel sites more often during holiday time). Wars, health, and news also tend to follow similar trends, while other tags, such as cooking or professional photography, have a steadier popularity.

Persistence of Interest and Agreement

Collaborative Filtering is based on a strong underlying assumption that people who

[4] We do not provide actual figures here so as not to disclose Yahoo!'s sensitive statistics.

agreed in the past tend to agree again in the future, and conversely that items that are similar will continue to be similarly liked or disliked by a given user. Consequently, existing systems do little to detect or predict changes in user preferences. During our experimental evaluation we found that the assumption of persistence of interest and agreement does not always hold in *Delicious*. Derived social ties, particularly those based on resource agreement, were rarely conserved from one time period to the next. We identified the short lifespan of URLs as the main reason: many URLs are only tagged actively for a period of 1-2 weeks. A promising direction for future work is incorporating time into the analysis of interest and agreement. Another direction is to derive interest networks based on clusters of similar URLs, rather than on individual URLs. A similar approach is taken in [Wu *et al.*, 2006b], in which the authors study the relationship between items, tags, and users in scope of a unified probabilistic generative model.

2.3 Network-Aware Search

2.3.1 Introduction

In Section 2.1 we described collaborative tagging sites. These sites are gaining popularity, and while browsing is still the predominant way of reaching content, ranked keyword-based search will become more important as the size of networks and tagged content expand. An important question that we address in the remainder of this chapter is how to support *network-aware search* – a mechanism that will return the top-ranked answers to a query consisting of a set of tags, given a user with a particular network. Such a mechanism is important not only for supporting search within these sites, but also for incorporating a user's network and tagging behavior in general web search [Heymann *et al.*, 2008].

Information Retrieval generally assumes content to be relatively static, while user interests are dynamic, expressed via keyword queries [Baeza-Yates and Ribeiro-Neto, 1999]. On the other hand, the Publish/Subscribe model assumes static publisher needs and dynamic streaming content [Wu *et al.*, 2006a]. In collaborative tagging sites, *both content and interest are dynamic*. Users tag new photos on Flickr and new videos on YouTube every day and develop interest in new topics. In the remainder of this chapter we model collaborative tagging sites as follows: users in the system can be either *taggers* or *seekers*. *Taggers* annotate *items* with one or more *tags*. A query is composed of a set of tags and is asked by a *seeker*. A linking relation connects seekers and taggers, thereby forming the *network* associated with each seeker. In practice the set of seekers and the set of taggers may overlap, and our model and algorithms will not preclude this possibility.

Given a seeker, a network of taggers, and a query in the form of a set of tags, we wish to return a ranked list of most relevant items. In Section 2.2 we demonstrated that a user's social context, expressed by his network and tagging, can be used to improve the quality of content recommendation in collaborative tagging sites. In the remainder of this chapter, we

go on to formalize network-aware search in these sites, and define the problem of efficiently processing top-k queries in the presence of dynamic scores.

In this work we do not answer the orthogonal question of when search and ranking should be made network-aware, and when globally popular items should be returned as answers instead. Indeed, network-awareness may in some cases hinder true information discovery. A Liberal Democrat who wants to educate himself about the Republican view on health care reform is unlikely to find informative resources from among those tagged by his friends, also Liberal Democrats. Likewise, a Western physician looking to expand his horizons and learn about treatment protocols offered by the Eastern medicine must look beyond his immediate circle of colleagues for information. In such cases, the search system must realize that the user's information need cannot be satisfied when tapping the user's network alone, and must fall back on the content contributed by the user base at large for results.

Nonetheless, cases abound where network-aware search is the right choice. We discussed in Section 2.2.8 that users of collaborative tagging sites like *Delicious* already contribute content in a social manner. Therefore, allowing *socially aware consumption of content* is not only natural, but also makes socially aware tagging worth-while. As the size of the users' networks increases, so does the need for network-aware content aggregation. A programmer who adds several Java experts to his network expects to find Java-related content contributed by those experts with ease. A group of fans of a music band who live in close geographic proximity to each other expect to be notified of band-related news, parties, and performances that other fans endorse. Family members who live on several continents and in a variety of time zones expect to have easy access to photos from family gatherings.

In the following sections we introduce a general class of scoring functions that reflects this intuition. This class includes ranking functions that are appropriate in many application scenarios, such as hotlist generation, popularity among friends, and popularity among a network of peers in the same age group or geographic location. Our core question is then *how to achieve efficient top-k processing of network-aware search queries.*

We consider what sort of storage structures are needed to support such queries. In the network-unaware setting, one would use *per-tag inverted lists*, listing items ranked by their score. A naive extension of this is to generate similar lists for each *(tag,seeker)* pair since items have a different score per seeker's network. Items would then be sorted according to their network-aware score in each inverted list. The well-known top-k algorithms [Fagin, 2002] could then be directly applied to aggregate over tags in a query. We refer to this storage strategy as `Exact`, since it requires storing exact scores for each item for each *(tag,seeker)* pair. This strategy can clearly benefit from the efficiency of traditional top-k algorithms. However, materializing each of these lists would be prohibitive in terms of space, since there are potentially as many lists per tag as there are seekers. Consequently, we explore *dynamic computation* of scores, given a seeker's network and a tag, as a way of

achieving *a balance between processing time and storage space*. Note that while traditional top-k algorithms aggregate scores on different keywords at query time, they assume the inverted lists are ordered by exact scores, even if exact scores of list entries are not available. The most straightforward dynamic approach materializes only per-tag inverted lists. These inverted lists are seeker-independent, so their entries cannot contain exact per-seeker scores but only upper-bounds for each item, i.e., its max score over all seekers. We refer to this strategy as `Global Upper-Bound`. We develop generalizations of top-k processing algorithms to incorporate network-aware search. In particular, we modify the classic `NRA` (No Random Access) and `TA` (Threshold Algorithm) to account for score upper-bounds and dynamic computation of exact scores (Section 2.4).

The `Exact` and `Global Upper-Bound` strategies represent two extremes in the space-time trade-off. While `Global Upper-Bound` will offer considerable savings in space, we expect query processing to take much longer, since the upper-bounds may be very coarse. The finer the upper-bounds, the closer they are to exact scores for a given seeker, which affects the order of entries in the inverted lists. We explore two refinements in Section 2.5.

Our first refinement identifies groups of seekers whose "network-aware" scores are close. The score upper-bound computed for such a group will then be tighter than the global upper-bound. These groups represent seekers who exhibit *similar networking behavior*. We refer to this strategy as `Cluster-Seekers`. This strategy leads to one inverted list per *(tag,cluster)* pair. At query time, we find the *(tag,cluster)* inverted lists associated with that seeker and aggregate over them. We will see that the `Cluster-Seekers` strategy performs faster than `Global Upper-Bound` and consumes less space than `Exact`.

The performance of `Cluster-Seekers` depends on finding good clusterings. We explore quality metrics that measure how well the order of entries in a per-cluster inverted list reflects their order in a seeker-specific inverted list, for seekers who belong to that cluster.

Next, we explore `Cluster-Taggers`, a strategy that aims to group taggers in networks based on *similarity in their tagging behavior*. Each tagger cluster is associated with an inverted list, where items are ranked by their upper-bound within the cluster of taggers. At query time, we determine the tagger clusters associated with a given seeker and compute scores by aggregating over the inverted lists associated with these tagger clusters. Taggers in a seeker's network may belong to different clusters, and so multiple inverted lists per tag may be relevant for a given seeker. We thus may have to aggregate over a larger number of inverted lists, albeit with tighter upper-bounds per list. In our experiments, which we present in Section 2.6, we found that `Cluster-Taggers` imposes little space penalty compared to `Global Upper-Bound`, and outperforms `Cluster-Seekers` in both space overhead and query time. However, not every seeker will benefit from this approach.

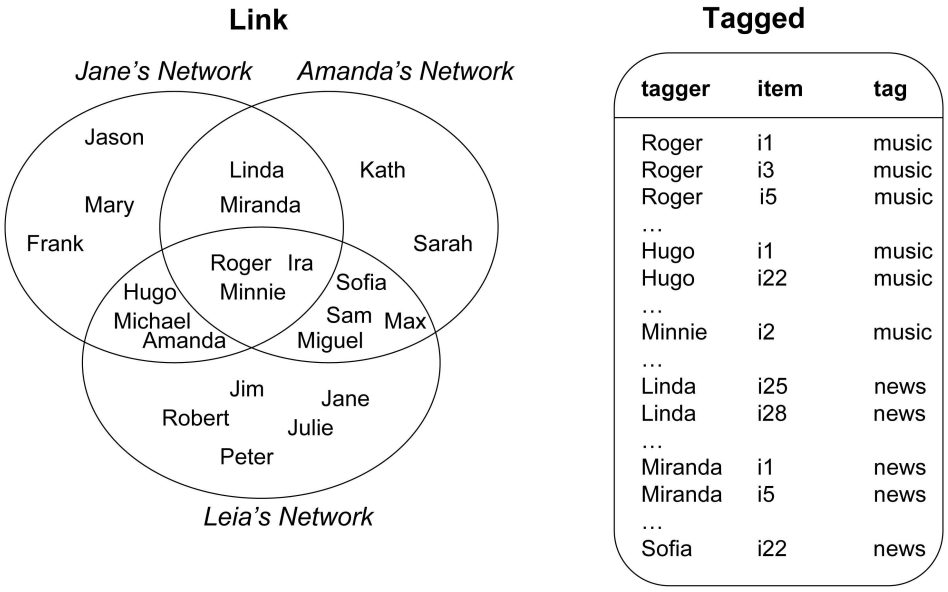


Figure 2.6: Seekers, networks and tagging actions.

2.3.2 Formalism

The data model uses as its starting point the formalism defined in Section 2.1.3, expanding it slightly to make notation more convenient. Here again, we assume that three sets are given: users $\mathcal{U}$, items $\mathcal{I}$, and tags $\mathcal{T}$. As before, we represents relationships between elements in these sets with two relations: $\texttt{Tagged}(u, i, t)$ and $\texttt{Link}(u, v)$.

Often we will be interested in iterating over all users in one of the projections of `Link` or `Tagged`. The projection on the first component of `Link` is the `Seekers` set; we will be interested in queries from these users. The projection on the first component of `Tagged` represents the `Taggers` set. We want the tags assigned by these users to influence the way answers to queries are scored. It is convenient to use the following notation.

Recall from Section 2.1.3 that, for a user $u \in \texttt{Seekers}$, $\texttt{Network}(u)$ is the set of neighbors of u, i.e., $\texttt{Network}(u) = \{v \mid \texttt{Link}(u, v)\}$. Recall also that we denote by $\texttt{Items}(u, t) = \{i \mid \texttt{Tagged}(u, i, t)\}$ the set of items tagged with t by tagger $u \in \texttt{Taggers}$.

We elaborate on a few natural implicit ties that may exist between users in G. Let $\texttt{Items}(v)$ be the set of items tagged by user v with any tag. Then we could define $\texttt{Link}(u, v)$ to mean that of the items tagged by u, a large fraction are also tagged by v, i.e., $|\texttt{Items}(u) \cap \texttt{Items}(v)|/|\texttt{Items}(u)| > \theta$, where θ is a given threshold. This type of a social tie was explored in Section 2.2.6, and we referred to is as the *URL-interest network*.

Alternatively, we could define $\texttt{Link}(u, v)$ if and only if v tags a sufficient fraction of the items tagged by u with the same tag as u, i.e., $|\{i \mid \exists t : \texttt{Tagged}(u, i, t) \wedge \texttt{Tagged}(v, i, t)\}|/|\{i \mid \exists t : \texttt{Tagged}(u, i, t)\}| > \theta$. We presented a similar relation as the *tag-URL-interest network*

in Section 2.2.7.

The techniques of this chapter do not assume any particular semantics of how the networks are obtained. Nonetheless, experimental results, which will be presented in Section 2.6, may be sensitive to the properties of the network, and performance trade-offs will need to be re-evaluated if semantics of the network change.

Figure 2.6 shows our running example of seekers, their networks, and their tagging actions. The network of seeker *Jane* overlaps with *Leia*'s and *Amanda*'s. This is reflected in `Tagged`, where taggers common to *Jane* and *Leia* tag various items.

Seekers issue queries in the form of a set of keywords. In order to focus on aggregation rather than the orthogonal text matching issues, we treat keywords and tags alike, and our scoring method is based on exact string matching. More specifically, given a seeker u and a query $Q = t_1, ..., t_n$, we define the score of an item i for u with respect to a tag t_j as a monotone function f of the number of taggers in u's network who tagged i with tag t_j:

$$\texttt{score}_{t_j}(i, u) = f(|\texttt{Network}(u) \cap \{v \mid \texttt{Tagged}(v, i, t_j)\}|) \tag{2.7}$$

We define the overall query score of an item i for a seeker $u \in \texttt{Seekers}$ as a monotone aggregation g of the scores for the individual keywords in the query:

$$\texttt{score}(i, u) = g(\{\texttt{score}_{t_1}(i, u), ..., \texttt{score}_{t_n}(i, u)\}) \tag{2.8}$$

While the framework is general enough to permit arbitrary monotone functions f and g, we will set f to be the identity function, and $g = sum$, for ease of exposition. As we demonstrated in Section 2.2, when content is recommended based on implicit common-interest networks, the resulting lists are good predictors of relevance to the seeker. Hence we use *common-interest networks* in our experiments.

2.3.3 Problem Statement

Given a query $Q = t_1, ..., t_n$, issued by user u, and a number k, we want to efficiently determine the top k items, i.e., the k items with the highest overall score.

In the next section, we address the following questions: given the input data modeled using the logical relations `Link` and `Tagged`, what information should we pre-compute in order that well-known top-k algorithms can be leveraged, and how should we adapt these algorithms to work correctly and efficiently in our setting?

2.4 Inverted Lists and Top-K Processing

We wish to compute the top-k items that have been tagged by people in a seeker's network with query relevant tags. As is typically done in top-k processing, we organize items in *inverted lists* and study the applicability of typical top-k algorithms in our setting.

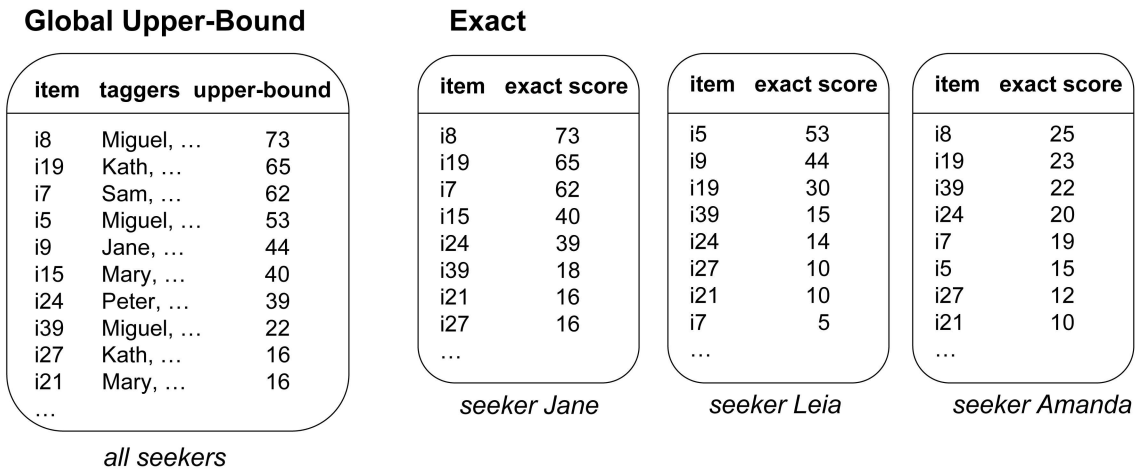


Figure 2.7: Inverted lists for `Global Upper-Bound` and `Exact`, for the tag *music*.

2.4.1 Computing Exact Scores

Typically, in Information Retrieval, one inverted list is created for each keyword [Baeza-Yates and Ribeiro-Neto, 1999]. Each entry in the list contains the identifier of a document along with its score for that keyword. Storing scores allows one to sort entries in the inverted list, enabling top-k pruning [Fagin *et al.*, 2003c]. While in classic IR each document has a unique score for a keyword (typically, *tf-idf* [Baeza-Yates and Ribeiro-Neto, 1999] or probabilistic [Fuhr and Rölleke, 1997]), one characteristic of our problem is that the score of an item for a tag depends on *who* is asking the query, i.e., on the seeker's network. One straightforward adaptation is to have one inverted list per *(tag,seeker)* pair and sort items in each list according to their score for the tag and seeker. Therefore, each item will be replicated along with its score in each relevant *(tag,seeker)* inverted list. We refer to this solution as `Exact`, and illustrate it on the right-hand side of Figure 2.7.

For each tag, `Exact` stores as many inverted lists as there are seekers. We will demonstrate in Section 2.6 that this approach leads to very high space overhead.

We now review top-k processing in the context of `Exact`.

2.4.2 Top-K Processing with Exact Scores

Existing top-k algorithms are directly applicable to `Exact`. Rather than describe them in detail, we give a brief overview of `NRA` (No Random Access) and `TA` (Threshold Algorithm) [Fagin *et al.*, 2003c], two representative algorithms.

In `NRA`, the inverted list for each query keyword is assumed to be sorted on the exact score of items. In the first phase, the algorithm maintains a heap which contains the current candidate entries for the top-k (there could be many more than k of these). The inverted

lists are scanned sequentially in parallel. When a new entry is found, it is added to the heap along with its partial (exact) score. If the item was seen before, its score in the heap entry is updated. For every heap entry, a worst-case score and a best-case score is maintained. The worst-case score is based on the assumption that the item does not appear in those lists where it is so far unseen. The best-case score assumes that the item's score in a list where it is unseen equals the bottom score of the heap (for that list). Items in the heap are sorted on their worst-case score, with ties broken using best-case scores, and subsequent ties broken arbitrarily. The algorithm stops when none of the entries outside of the top-k items examined so far has a best-case score higher than the worst-case score of the kth item in the buffer. The output of `NRA` consists of the set of top-k items in the buffer, for which we have only partial score and hence no rank information. Subsequent work (e.g., [Ilyas *et al.*, 2002]) has adapted `NRA` so as to obtain exact rank information.

`NRA` can be directly applied in the context of `Exact` by picking the lists which correspond to the current seeker and query keywords and aggregating over them as described above.

In `TA`, the inverted lists are sorted on score as for `NRA`, but random access is assumed in addition to sequential access. The algorithm accesses items in the various lists sequentially, and the lists are processed in parallel. `TA` maintains a heap, where items are kept sorted on their complete score. When a new entry is seen in any list under sequential access, its scores from other lists are obtained by random access. If its overall score is more than the score of the kth entry in the heap, the items are swapped. Otherwise this new entry is discarded. At any stage, the bottom score (seen under sequential access) is maintained for every list and is used to compute a threshold. No unseen item can have a score higher than the threshold, so if the score of the kth highest heap entry is greater than or equal to the threshold, then the algorithm stops. The output consists of the top-k list in the buffer, including items and their scores (and hence their ranks). Unlike in `NRA`, a far smaller portion of the lists needs to be explored, and the heap never needs to contain more than k items. However, this comes at the price of potentially many more random accesses.

`TA` can be applied directly in the context of `Exact`.

We now turn to describing our space-saving strategy and how top-k processing is adapted to fit it.

2.4.3 Computing Score Upper-Bounds

In order to save space in storing inverted lists, we factor out the seeker from each per-tag list and maintain entries of the form *(item,taggers)* where *taggers* are all taggers who tagged the item with the tag. In this case, every item is stored at most once in the inverted list for a given tag, as opposed to being replicated potentially once for each seeker. The question now is *which score to store with each entry.* The answer to this question will determine how the lists are ordered. Since scores are used for top-k pruning, it is safe to store, in each per-tag inverted list, the *maximum* score that an item could have for the tag *across all*

possible seekers. We refer to such maximum score as the *score upper-bound*. Given a query keyword t_j, the score upper-bound of an item i for t_j can be expressed as:

$$\texttt{ub}(i, t_j) = MAX_{u \in \texttt{Seekers}} |\{v \mid \texttt{Tagged}(v, i, t_j)\} \wedge v \in \texttt{Network}(u)|$$

In other words, the score upper-bound is the highest score an item could have for a tag. We refer to an inverted list organization based on these ideas as the `Global Upper-Bound` strategy. We will assume that the inverted lists are supplemented by the `Link` relation indexed by the seeker and the `Tagged` relation indexed by tag and item; these will support our equivalent of random access. They also support efficient computation of exact scores, given a seeker and an item.

Figure 2.7 shows the inverted list for tag *music* according to the `Global Upper-Bound` strategy and its counter-part in `Exact`. Notice that `Exact` may store one item multiple times across lists (e.g., item *i19* is stored with seekers *Jane*, *Amanda*, and *Leia*). In the case of `Global Upper-Bound`, an item is stored only once with its highest score (e.g., the score of item *i19* in `Global Upper-Bound` is higher than its score in the lists of *Leia* and *Amanda* since it corresponds to its score for *Jane*). While the per-seeker inverted lists in `Exact` are shorter than in `Global Upper-Bound`, the overall space consumption of `Exact` is expected to be much higher. However, the relative ordering of items in the inverted list for `Global Upper-Bound` does not necessarily reflect that of any per-seeker order in `Exact` (e.g., *i19* is scored lower than *i5* in *Leia*'s list while it is scored higher in the `Global Upper-Bound` list). This may cause `Global Upper-Bound` to scan many more entries in the inverted lists than `Exact`, thereby increasing query processing time. We next describe adaptations of `NRA` and `TA` that use score bounds; their application to the bounds in `Global Upper-Bound` will serve as another baseline (for processing time) in our experiments.

2.4.4 Top-k Processing with Score Upper-Bounds

We assume a function that does a "local aggregation", taking a seeker and a pair *(item, taggers)* from an inverted list and calculating the number of taggers that are friends of the seeker. We also assume a function $\texttt{computeExactScore}(i, u, t_j)$ that computes the value of Equation 2.8 by both retrieving the taggers of item i (for tag t_j) and counting the number of friends of u who tagged with t_j. Such a function can be implemented as a SQL aggregate query over the join of `Link` and `Tagged`.

2.4.4.1 NRA Generalization

Algorithm 1 shows the pseudo-code of `gNRA`. For any query, the inverted lists ($\texttt{IL}_t$) corresponding to each query keyword t are identified and are accessed sequentially in parallel, using a criterion such as round-robin. When an item is encountered in a list, we: (i) record the upper-bound of the item and (ii) compute the exact score of the item for that tag using

the *taggers* component of the IL entry. If the item has not been previously encountered, it is added to the heap along with its score. If it is already in the heap, the score is updated. Thus scores of items in the heap are partial exact scores and correspond to the notion of worst-case score of classic NRA. The set of bottom (i.e., last seen) bounds of the lists is used to compute best-case scores of items: for any item, its best-case score is the sum of its partial exact score and the bottom bounds of all lists where the item has not been seen. If an item is unseen anywhere, its partial exact score is 0 and its best-case score is the sum of bottom bounds over all lists. The heap is kept sorted on the worst-case score, with ties broken using best-case score, and then arbitrarily. The stopping condition is similar to that for classic NRA: none of the items outside the top-k of the heap has a best-case score that is more than the kth item's worst-case score. However, for classic NRA, it is sufficient to compare the kth item's worst-case score in the heap with the largest best-case score of an item in the heap outside of the top-k items. In our case, this would not be sound, since the lists are only sorted on bounds, not necessarily on scores. Thus, a completely unseen item can have a best-case score higher than the largest best-case score in the heap. Thus, we compare the maximum of the largest best-case score outside of top-k in the heap and the sum of all bottom bounds with the worst-case score of the kth item in the heap, stopping when the latter is higher.

Algorithm 1: Bounds-Based NRA Algorithm (gNRA)

Require: seeker u, Query Q;
1: Open inverted lists $\texttt{IL}_t$ for each keyword $t \in Q$;
2: **while** worstcase(kth heap item) $\leq max\{\text{BestcaseUnseen}, max\{\text{bestcase}(j) \mid j \in \text{heap} - \text{top-}k\}\}$ **do**
3: Get next list $\texttt{IL}_t$ using round-robin;
4: Get entry $e = (i, \texttt{ub}, \text{taggers})$ in $\texttt{IL}_t$;
5: Update the bottom bound of $\texttt{IL}_t$;
6: Compute partial exact score of i for t using itemTaggers;
7: If i is not in heap add it, otherwise update its partial exact score;
8: Update best-case scores of items in heap, and re-order heap;
9: BestcaseUnseen = sum of bottom bounds over all lists;
10: **end while**
11: Return top-k set of items from heap.

At this point, we are guaranteed that the set of items in the top-k of the heap belong to the final top-k list. If the exact score (and rank) is of interest, we need to compute the exact score of items in the heap on those lists where they are not seen. We can do this by computing exact scores (our analog of Random Access) for the remaining terms of the top-k heap items. [5]

[5] Thus, gNRA in our setting is really "generalized Not many Random Accesses".

Note that during exact score computation when a cursor is moved we get the entry $e = (i, \texttt{ub}, \text{itemTaggers})$ in memory without a search, and can thus get the exact score using a local exact score computation. We will reuse the term "sequential access" (and the abbreviation SA) to refer to the combination of advancement of a cursor and local exact score computation. In our algorithm, these two always occur in tandem. We will reuse the term "random access" (RA) to refer to the calls to `computeExactScore`, which in this algorithm occur only in phase 2. The ability to quickly get the scores to be aggregated in memory allows sequential access to be much more efficient than random access, as in the classical case. We discuss this further in Section 2.6.

Several optimizations are possible to the basic algorithm above. Clearly, we have no need to update scores of items in the heap whose best-case is below the worst-case of the kth highest heap item, nor do we need to re-order these as the lower bounds are updated. It is also possible to check whether an element is a candidate for entry into the top-k prior to performing an exact score computation, by checking its new upper bound against the worst-case score of the current k^{th} item; this optimization can be easily incorporated into the algorithm above.

2.4.4.2 TA Generalization

Algorithm 2: Bounds-Based `TA` Algorithm (`gTA`)

Require: seeker u, Query Q

Open inverted lists $\texttt{IL}_t$ for each keyword $t \in Q$;
while score(kth heap item) $\leq$ sum of bottom bounds over all lists **do**
  get next list $\texttt{IL}_t$ using round-robin;
  Let $e = (i, \texttt{ub}, \text{itemTaggers})$ be the next entry in $\texttt{IL}_t$;
  Update the bottom bound of $\texttt{IL}_t$;
  if i not in current top-k **then**
    Use local aggregation to get exact score of i in $\texttt{IL}_t$ using itemTaggers;
    Use `computeExactScore` to get exact score of i in other lists;
    if i's overall score $>$ kth score in heap **then**
      Swap kth item with i; keep top-k heap sorted;
    end if
  end if
end while
Output the heap as is.

We now present `gTA` – our adaptation of `TA` that works with score upper-bounds. Algorithm 2 shows the pseudo-code. Given a query Q from a seeker u, all relevant inverted lists are identified. We access them sequentially in parallel. When an entry is seen for the first time under sequential access in a list, we compute its exact score in that list (as part

of SA) and perform exact score computations on the other lists (a set of RAs). Thus, we always have complete exact scores for the items in the buffer. For each list, we remember the bottom bound seen. The threshold is the sum of the bottom bounds over all lists. The algorithm stops whenever the score of the kth item in the heap, which is kept sorted on score, is no less than the threshold. At this stage, we can output the top-k items together with their scores and hence rank them.

As with `gNRA`, there are slight modifications that can save accesses: when we find a new item i we could iteratively retrieve scores in other lists, curtailing the iteration if we find that the best-case of i is below the exact score of the kth item in the heap.

To summarize, both variants of `Global Upper-Bound` (`gNRA` and `gTA`) differ from `Exact` in that the former needs to compute the exact score of an item for a tag and seeker at query time. Using a simple variation of the argument in [Fagin *et al.*, 2003c], we can show that both `Global Upper-Bound` variants are *instance optimal* over all algorithms that use the same upper-bound based storage. In the case of `gTA`, this means that `gTA` based on a round-robin choice of cursors uses no more sequential accesses than any other "reasonable" algorithm, up to a linear factor. Reasonable here means that the algorithms cannot make a call to `computeExactScore` for an item until the item has been reached under sequential access. This is the analog of the "no wild guesses" restriction of [Fagin *et al.*, 2003c]. Similar statements can be made for `gNRA`: Algorithm 1 is optimal, up to a constant factor, in number of sequential accesses made, over algorithms that perform only sequential accesses. If we consider the optimization where exact score computations are done only for items that have a best-case score above the current kth highest-score, we find that it is optimal in terms of the number of exact score computations.

However, any of these optimality statements only justify the use of these query processing algorithms once a storage structure is fixed; they do not justify the storage structures themselves. The accuracy of upper-bounds in the inverted list is clearly the key factor in the efficiency of top-k pruning. The finer the upper-bound, the closer it is to the item's exact score and the faster an item can be pruned. Therefore, we need to explore further optimizations of our inverted list storage strategies. The clustering-based approaches introduced in the next section work by identifying upper-bound based inverted lists for a *(query,seeker)* pair and then applying either `gNRA` or `gTA`. They will differ on which lists are identified and on how the clusters are formed.

2.5 Clustering and Query Processing

As discussed in Section 2.4, the greater the difference between the score upper-bound and the exact score of an item for a tag, the more processing may be required to return the top k results for a given *(seeker,query)* pair. The aim of this section is to describe methods which *reduce the difference between exact scores and upper-bounds* by refining upper-bounds. The

core idea is to *cluster users* into groups and compute score upper-bounds within each group. The intuition is that by making a cluster contain users whose *behavior* is similar, the exact scores of users in the cluster will be very close to their upper-bound score. The remaining question is thus: *which users should the clustering algorithm group together to achieve that goal.*

2.5.1 Clustering Seekers

For a given seeker, the score of an item depends on the seeker's network of taggers. Therefore, a natural approach is to cluster the seekers based on similarity in item scores. Given any clustering of seekers, we form an inverted list $\texttt{IL}_{t,C}$ for every tag t and cluster C, containing all items tagged with t by a tagger in $\bigcup_{u \in C} \texttt{Network}(u)$, with the score of an item being the *maximum score over all seekers in the cluster*. That is, an item i in the list gets score $\max_{u \in C} \texttt{score}_t(i, u)$. Query processing for $Q = t_1 \dots t_n$ and seeker u proceeds by finding the cluster $C(u)$ containing u and then performing aggregation (using one of the algorithms in Section 2.4) over the collection of inverted lists $\texttt{IL}_{t_i,C(u)}$.

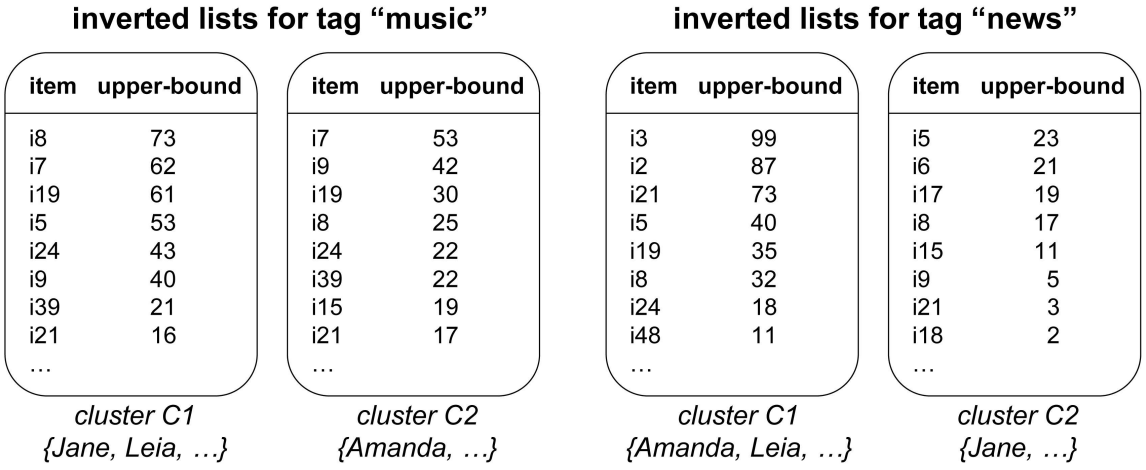


Figure 2.8: An example of `Cluster-Seekers`.

`Global Upper-Bound` is a special case of `Cluster-Seekers` where all seekers fall into the same cluster and the same cluster is used for all tags. That is not the case in general with `Cluster-Seekers` as illustrated in Figure 2.8, where *Jane* and *Leia* fall into the same cluster C_1 for the tag *music*, but into different clusters for the tag *news*. Clustering seekers independently for each tag allows for tighter upper-bounds, and thus for a better clustering outcome. This is because, while *Jane* and *Leia* may have highly overlapping networks of friends for *music*, resulting in a high overlap in the items and item scores, their networks for the tag *news* may be dissimilar.

Upper-bounds within each list are computed for members of the associated cluster, which

makes the bounds necessarily tighter. For example, item *i7* has a tighter upper-bound in cluster C_2 for tag *music* than in `Global Upper-Bound` in Figure 2.7. It is necessary to compute seekers' clusters on a per-tag basis in order to reflect (i) the overlap in networks among different seekers *and* (ii) the overlap in tagging actions of taggers in clusters. Indeed, if we generated a set of clusters which are agnostic to the tags, we could end up creating a cluster containing *Jane*, *Leia* and *Amanda* (since they share some taggers in their networks). The score upper-bounds for such a cluster would be coarser (e.g., *i19* would have a score upper-bound equal to 65 for tag *news* while it is equal to 30 in C_2!).

One can easily show that, for single keyword queries, as we refine the clustering, the upper bounds can only get tighter, and hence the processing time of the generalized threshold algorithms of the previous section can only go down, regardless of the seeker. In particular, `Exact` is optimal over all algorithms that use `Cluster-Seekers`, for any clustering, assuming single-keyword queries.

For multi-keyword queries, clustering, while resulting in tighter upper-bounds, may not always improve processing time. Consider a seeker u and a top-1 query $Q = t_1, t_2$. Assume that, for this seeker, the lists of scores for the two keywords are $IL_{t_1,u} = (x{:}10, i_1{:}3, i_2{:}2, \ldots)$, where the ... is a long tail of scores below 2; $IL_{t_2,u} = (i'_1{:}20, i'_2{:}19, \ldots, i'_{1000}{:}19, \ldots, x{:}15)$. Suppose a clustering puts this seeker in her own cluster, thus making the bounds exact for her! Under `gNRA`, we would have to keep making sequential accesses until we reach the entry x:15 in the second list. However, it is possible that in `Global Upper-Bound` (the coarsest possible clustering), the global inverted lists for the two keywords are: $IL_{t_1} = (x{:}10, i_1{:}3, i_2{:}2, \ldots)$; $IL_{t_2} = (x{:}22, i'_1{:}20, i'_2{:}19, \ldots, i'_{1000}{:}19)$. The entry x might have a much coarser (i.e., higher) bound in `Global Upper-Bound` and hence may bubble to the top of the second list. Now, `gNRA`, after one round-robin, gets the full exact score of x (still 25 for u). After this the algorithm will stop, since this score is higher than the sum of all bottom scores. This example shows that *an ideal clustering would take into account both the scores and the ordering.*

How do we cluster seekers? Ideally, we would find clusters that are *optimal* for the running time of one of our algorithms in Section 2.4. However, as we show in [Amer-Yahia *et al.*, 2008a], finding a clustering that would minimize the worst-case running time over all users is NP-hard. We also show that finding a clustering that minimizes the average-case running time is NP-hard.

Given these complexity results, we must rely on heuristic methods to find clusters of seekers. One natural approach is based on overlap of the seekers' networks. The intuition is that, given two seekers u and u', the higher the number of common taggers in their networks, the higher the chance that the score of an item for those networks be similar. However, two taggers may have different tagging behavior for different tags. Therefore, we propose to compute *per-tag network overlap* between seekers.

Given the set of all seekers in `Seekers` and a tag t, we can construct a graph where nodes

are seekers and an edge between two seekers u and u' is created if and only if $|\texttt{Network}(u,t) \cap \texttt{Network}(u',t)| \geq \theta$, where $\texttt{Network}(u,t)$ is the set of users in $\texttt{Network}(u)$ who tagged at least one item with tag t. The threshold θ is application-dependent. Once the graph is instantiated, we apply off-the-shelf graph clustering algorithms in Section 2.6 to generate clusters. We report the space/time performance of `Cluster-Seekers` in Section 2.6.4.

2.5.2 Evaluating and Tuning Clusters

The `Cluster-Seekers` approach depends on finding good clusterings, which in turn depends on being able to predict the performance of a clustering. Clearly, we cannot test a clustering on all keyword combinations for all users, and for all values of k. We begin with a measure comparing the orderings produced by the clustering with the exact orderings for a particular user; we will average this over users. Although many metrics that can be used to compare lists are considered in the literature (see for example [Fagin *et al.*, 2003a]), we need one that is both correlated with the performance of our algorithms and simple to compute. We discuss here one such measure, a variant of Normalized Discounted Cumulative Gain (NDCG). This measure was introduced in [Järvelin and Kekäläinen, 2002]), and is described in detail in Section 1.1.3.2.

Recall that NDCG compares the order of items in a ranked list to the order of items in an *ideal* list. For a tag t and a seeker u, let the ideal list L_{ideal} represent the list of items for u and t ranked by exact scores. Let L_{approx} represent the list of items in a cluster, ranked by score upper-bounds. Consider for example the inverted lists for the tag "music" presented in Figure 2.7. In order to quantify how well the `Global Upper-Bound` approach will perform for seeker *Jane*, we take *Jane*'s exact list as L_{ideal}, and compare it to the `Global Upper-Bound` list as L_{approx}.

Note that L_{approx} is not simply a reordering of L_{ideal}. Rather, the underlying domain of L_{approx} is the superset of the domain of L_{ideal}. This is because L_{approx} lists items that are relevant to any seeker in the cluster, not just to the particular seeker u. So, the global upper-bound list in Figure 2.7 includes the item $i9$ which is not present in *Jane*'s list.

Let D be a vector of length equal to the length of L_{ideal}, where, for each i, $D(i)$ records the *maximum over* $j \leq i$ of the position of the j^{th} item in L_{ideal} within L_{approx}. (All vectors are 1-based for convenience.) D will have the following values for *Jane* in our example: $\{1, 2, 3, 6, 7, 8, 10, 10, \ldots\}$. $D(i)$ represents the delay in getting to the top i items of L_{ideal}. We use D to assign values to the *gain vector* (see Section 1.1.3.2), with low gain corresponding to high delay and vice versa:

$$G(i) = \frac{i}{D(i)} \tag{2.9}$$

The delay for reaching item i is at least i, as was the case for the first three items for

Jane, and we set the corresponding value in the gain vector to 1 in such cases. If item i is reached after considering more than i items in L_{approx}, the gain will have a value between 0 and 1. Note that the delay vector for the ideal list is always $\{1, 2, 3, 4, \ldots\}$, and so the ideal gain vector has 1 in each position.

Intuitively, $G(i)$ represents the quality of the clustered list if we are looking for the seeker's top i items. For top-k multi-keyword queries, the highest scoring item may be significantly further down on an individual list than k. We will thus sum the quantity $G(i)$ over i, discounting higher values of i, since it is less likely that the tail of the seeker's list will be visited.

We use the gain vector described above to compute the *Normalized Discounted Cumulated Gain* (NDCG) as per Section 1.1.3.2, using a discount factor $b = 2$. NDCG measures the quality of a clustered list for a given seeker and keyword. A value of 1 is the optimum, which is realized by the ideal list, while values close to 0 indicate a list that is far from ideal. The quality over all seekers can be estimated by averaging over a randomly selected collection of seekers.

We will see in Section 2.6 that the performance of both NRA and TA variants for a clustering is correlated with a function of NDCG. Specifically, for a multi-keyword query Q, the performance of Q of the "aggregate NDCG of Q", where the aggregate averages over a sample of seekers and maximizes over the keywords in Q.

The NDCG can be used to compare two clusterings – for example, those done via different clustering algorithms, or different parameters within a clustering algorithm. It can also be used to decide whether increasing the number of clusters will significantly impact performance. Since the NDCG is a per-keyword quantity, it can be calculated offline.

2.5.3 Clustering Taggers

Another clustering alternative is to organize taggers into different groups which reflect overlap in their tagging behavior. We refer to this strategy as `Cluster-Taggers`. That is, for each tag t we partition the taggers into clusters. We again form inverted lists on a per-cluster, per-tag basis, where an item i in the inverted list for cluster C and tag t gets the score:

$$\text{MAX}_{u \in \texttt{Seekers}} |\texttt{Network}(u) \cap C \cap \{v \mid \texttt{Tagged}(v, i, t)\}|,$$

i.e., the maximum number of taggers in cluster C who are linked to u and tagged item i with tag t, over all of the seekers u. To process a query $Q = t_1 \ldots t_n$ for seeker u, we find the set of clusters of the taggers in `Network` (u), and then perform an aggregation over the inverted lists associated with all *(tag,cluster)* pairs. Members of a seeker's network may fall into multiple clusters for the same tag, thereby requiring us to process more lists for each tag (as opposed to one list per tag in the case of clustering seekers).

How do we cluster taggers? For some tag t, we instantiate an undirected graph where nodes are taggers and there exists an edge between two nodes v and v' if and only if: $|\texttt{Items}(v,t) \cap \texttt{Items}(v',t)| \geq \theta$ where t. Again, threshold θ depends on the application.

We now summarize the differences between clustering seekers based on network overlap (`Cluster-Seekers`) and clustering taggers based on overlap in tagging behavior (`Cluster-Taggers`). At query time, `Cluster-Seekers` identifies one inverted list per *(tag,seeker)* pair since a seeker always falls into a single cluster for a tag. In `Cluster-Taggers` there are potentially multiple inverted lists per *(tag,seeker)* pair, given that a seeker will generally have multiple taggers in his network which may fall into different clusters.

Unlike `Cluster-Seekers`, `Cluster-Taggers` does not replicate tagging actions over multiple inverted lists. In fact, we will show that there is no significant penalty in space of `Cluster-Taggers` over `Global Upper-Bound`. Space consumption of clustering is explored in Section 2.6.

As for processing time, while `Cluster-Seekers` benefits all seekers, `Cluster-Taggers` does not. Indeed, we find that `Cluster-Taggers` can hinder seekers that are associated with many tagger clusters and hence many inverted lists. Still, we show that there is a *significant* percentage of seekers that can benefit from `Cluster-Taggers` and that *this population can be identified in advance*. `Cluster-Taggers` also has advantages for maintenance under updates; while `Cluster-Seekers` requires multiple exact score computations and updates to maintain as new tagging events occur, `Cluster-Taggers` requires only a single exact score computation and a single update per tag, assuming to re-clustering. This is because in `Cluster-Taggers`, items are not replicated across clusters.

2.6 Experimental Evaluation

2.6.1 Implementation

We implement the `gNRA` and `gTA` algorithms in Java on top of an Oracle 10g relational database. Our experiments are executed on a MacBook Pro with a 2.16GHz Intel Core 2 Duo CPU and 1GB of RAM, running MacOS X v10.4. The database server is running on a 64-bit dual processor Intel Xeon 2.13GHz CPU with 4GB or RAM, running RedHat Enterprise Linux AS4. This platform, while not necessarily representative of production deployment, was sufficient for the purposes of our experimental evaluation which was conducted in a platform-independent manner (see Section 2.6.2).

Our schema consists of the following relations:

- `TaggingActions(itemId,taggerId,tag)` stores raw tagging actions.
- `Link(tag,seekerId,taggerId)` encodes the `Link` relation between seekers and taggers, on a per-tag basis. The network of a seeker is a union of all taggers associated to it.

- `InvertedList(tag,clusterId,itemId,ub)` stores inverted lists of items per tag, per cluster. A tree index is built on (tag, ub) to support ordered access. This table also stores per-tag inverted lists for `Global Upper-Bound`.
- `SeekerClusterMap(seekerId,clusterId,tag)` stores the assignment of seekers to clusters.
- `TaggerClusterMap(taggerId,clusterId,tag)` stores the result of clustering `Taggers`.

Given a seeker u, and a tag t, an SA is implemented as moving a cursor over the result of the query:

```
Select IL.itemId, IL.ub, count(*) as ‘‘score’’
From   InvertedList IL, TaggingAction T, Link L
Where  L.seekerId = :u And T.tag = :t
And    L.taggerId = T.taggerId And T.tag = L.tag
And    T.tag = IL.tag And T.itemId = IL.itemId
Group by IL.itemId, IL.ub
Order by IL.ub descending
```

Appropriate indexes are built on the selection and join columns to ensure efficient access. The role of aggregation in this query is to compute partial exact scores of items with respect to the current "inverted list". An RA, i.e., a calculation of `computeExactScore` on a single item i, is given as follows:

```
Select count(*) as ‘‘score’’
From   TaggingAction T, Link L
Where  L.seekerId= :u And T.tag= :t And T.itemId= :i
And    L.taggerId = T.taggerId And L.tag = T.tag
```

Both queries are for `Global Upper-Bound`, and are augmented by a join with `SeekerClusterMap` for `Cluster-Seekers`, and with `TaggerClusterMap` for `Cluster-Taggers`.

We use a SQL-based implementation for convenience only. The exact difference in cost between SAs and RAs, and hence the overall performance time of the algorithms, may vary significantly from a native implementation of the algorithms using inverted lists. In order to make the performance analysis implementation-independent, we will quantify the query execution time of all algorithms using the number of SAs and RAs. This will allow us to draw conclusions regarding the relative performance of our algorithms in comparison to `Exact` and in comparison to each other.

We found that, as is the case with traditional top-k algorithms, RAs in our implementation are significantly more expensive than SAs. The relative cost varies slightly depending on the tag, but a single RA is about 10 times more expensive than a single SA.

We use `Graclus` [Dhillon *et al.*, 2007], an efficient clustering implementation over *undirected weighted graphs*. `Graclus` provides two clustering methods. Ratio Association (ASC) maximizes edge density within each cluster, while Normalized Cut (NCT) minimizes the sum of weights on edges between clusters [Dhillon *et al.*, 2007]. More formally, given two sets of nodes $\mathcal{V}_i$ and $\mathcal{V}_j$, we denote by $links(\mathcal{V}_i, \mathcal{V}_j)$ the sum of edge weights between nodes in $\mathcal{V}_i$ and nodes in $\mathcal{V}_j$. We denote by $degree(\mathcal{V})$ the sum of weights on edges incident on the nodes in $\mathcal{V}$. The objective of ASC is:

$$\texttt{maximize} \sum_{i=1}^{n} \frac{|links(\mathcal{V}_i, \mathcal{V}_i)|}{|\mathcal{V}_i|}$$

The objective of NCT is:

$$\texttt{minimize} \sum_{i=1}^{n} \frac{|links(\mathcal{V}_i, \mathcal{V} \setminus \mathcal{V}_i)|}{degree(\mathcal{V}_i)}$$

2.6.2 Data and Evaluation Methods

We use a sample of *Delicious* for our experimental evaluation. Properties of the dataset are described in Section 2.1.4, and we recall here that the dataset contains 116,177 distinct users who tagged 175,691 distinct URLs using 903 distinct tags, for a total of 2,322,458 tagging actions.

We choose 4 tags (*software*, *programming*, *tutorial*, and *reference*) from the 20 most popular. Popularity of a tag is measured by the total number of tagging actions involving it: the most popular tag has been used about 100,000 times, while the 20th most popular was used about 34,000 times. We evaluate the performance of our methods over 6 queries of varying lengths, to which we refer by the first letters of each tag. The queries were *SP* for *software programming*, *TR* for *tutorial reference*, *PR* for *programming reference*, *SPT* for *software programming tutorial*, *SPR* for *software programming reference*, and *SPTR* for *software programming tutorial reference*. We chose these four tags because they are thematically related and may be meaningfully combined in a query.

As we described in Section 2.1.2, *Delicious* has an explicit notion of friendship. However, users may have various semantics for it. Since we are interested in networks that reflect affinities in item preference, in our experiments we use a network derived from the tagging data via *common interest*. This choice is supported by our experimental results in Section 2.2, where we find that a common-interest network reflects the user's interests more closely than does the explicit friendship network. In the network that was used for the purposes of our experimental evaluation, there is a link between a seeker and a tagger if they tagged at least *two* items in common with the same tag.

Due to the choice of the network, only seekers who are also taggers are included in the experimental evaluation. However, as mentioned in Section 2.3.2, the techniques of

tag	|Network|	AVG|Network|(v) |	MAX|Network|(v) |
Software	25545	8	607
Programming	21853	21	983
Tutorial	16895	23	1068
Reference	24697	34	1098

Table 2.5: Characteristics of `Network` for four tags.

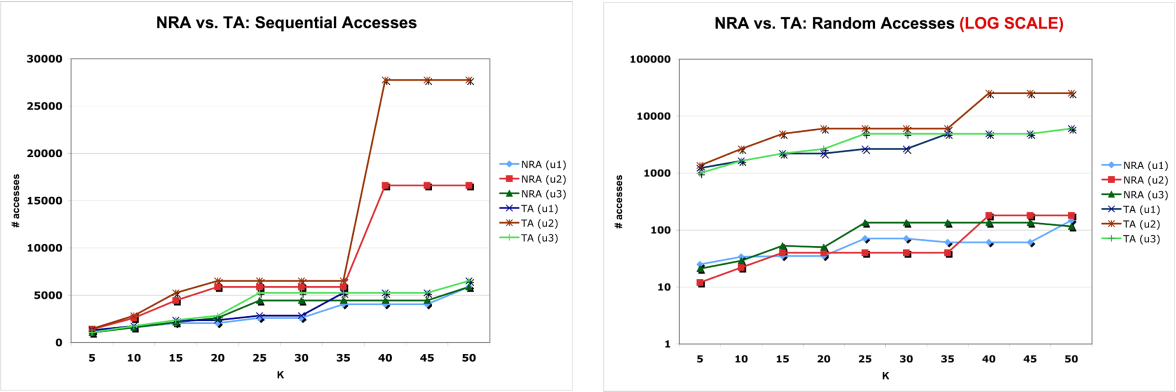


Figure 2.9: Performance of `gNRA` and `gTA` as k varies.

this chapter do not commit to any particular network semantics. This particular common-interest network is used for the purposes of our experimental evaluation only.

Table 2.5 lists the number of users per tag ($|Network|$), as well as the average and maximum cardinalities of `Link`, i.e., the size of a seeker's network. These numbers were computed with respect to our sample of *Delicious*.

We use the following sampling methodology to select users for our performance evaluation. For each tag and for each seeker we compute the total number of tagging actions that are relevant to that seeker (i.e., the total number of tagging actions by all taggers linked to the seeker), and rank seekers on this value. We notice that the top 25% of the seekers together correspond to 75%-80% of all tagging actions for the four tags in our experiments. For each query we identify three mutually exclusive groups of seekers: *Seekers-25* are in the top 25% of ranks for each query keyword, *Seekers-50* are in the top 50% of ranks for each query keyword, but not in the top 25%, *Seekers-100* are the rest. For each query we draw 10 seekers uniformly at random from each group, for a total of 30 seekers per query. This methodology allows us to capture the variation in performance for different types of seekers: popular tags correspond to many more items for `Seekers-25` than for `Seekers-100.`

We evaluate the performance of our algorithms with respect to two metrics.

- *Space overhead* is quantified by the number of entries in the inverted lists.

	Seekers-25		Seekers-50		Seekers-100	
query	**GUB**	`Exact`	**GUB**	`Exact`	**GUB**	`Exact`
SP	1674	52	12920	134	18036	61
PR	479	13	3923	87	12982	61
TR	1262	14	4813	92	18476	121
SPT	938	78	4107	112	17985	195
SPR	1495	67	8972	194	14976	131
SPTR	907	119	2229	119	10986	189

Table 2.6: Performance of `gNRA` for `Global Upper-Bound` and `Exact`.

- *Execution time* is expressed by the number of sequential and random accesses (SAs and RAs). The raw number of accesses varies significantly between seekers even when the query is fixed. Hence, we focus on *relative improvement* obtained by `gNRA` and `gTA` compared to `Global Upper-Bound`. Unless otherwise stated, we report average percent improvement over the baseline for 30 seekers per query, with separate averages given for *Seekers-25*, *Seekers-50* and *Seekers-100*. In order to reduce sensitivity to outliers, we use truncated mean, removing the minimum and maximum values before computing the average.

2.6.3 Performance of Global Upper-Bound

We start with some general comments about how the number of SAs and RAs increases with k, for both `gNRA` and `gTA`. The qualitative behavior depends on the characteristics of the seeker's network. Consider the query *software programming* for 3 selected users in Figure 2.9. For a fixed user, `gNRA` and `gTA` exhibit the same trend in both SAs and RAs. How the number of accesses increases with k is a function of the distribution of exact scores. For example, the number of SAs for `gNRA` for seeker u_2 increases dramatically for $k = 40$. When looking at the distribution of exact scores for this seeker we notice that the items can be classified into 3 categories with respect to their score: the first 36 items score higher than 3, followed by 60 items with a score of 2. The remaining 405 items (79%), have a score of 1, and constitute the tail of the distribution of scores for seeker u_2. The spike in accesses occurs when k becomes high enough that it becomes necessary to explore the long tail.

Space overhead. The space overhead of `Global Upper-Bound` is presented in Figure 2.10, displayed as a horizontal line marked `GUB`, and corresponds to 74,181 inverted list entries. We see that `Global Upper-Bound` achieves savings of about two orders of magnitude over `Exact` (a horizontal line marked `EXACT` that corresponds to 4,284,854 inverted list entries). However, as argued in Section 2.4, the `Global Upper-Bound` strategy, while optimal with respect to space overhead, may suffer from high query execution time.

Execution time. Table 2.6 compares the number of SAs for `gNRA` under `Global Upper-Bound` to the number of SAs for `Exact`. The numbers represent averages per query, per category of seekers. We observe that `Global Upper-Bound` under-performs `Exact` by up to two orders of magnitude, and that users in *Seekers-100* are at a particular disadvantage. `gTA` under `Global Upper-Bound` shows a similar trend.

2.6.4 Clustering Seekers

We experiment with 3 clustering algorithms: ASC, NCT (see Section 2.6.1) and a random clustering for reference, RND, which assigns seekers to random clusters. We cluster over the *common-interest network* of seekers: there is an edge between two nodes u and v if these users tagged at least one item in common. This graph is undirected, and edges are weighted by the number of items tagged in common.

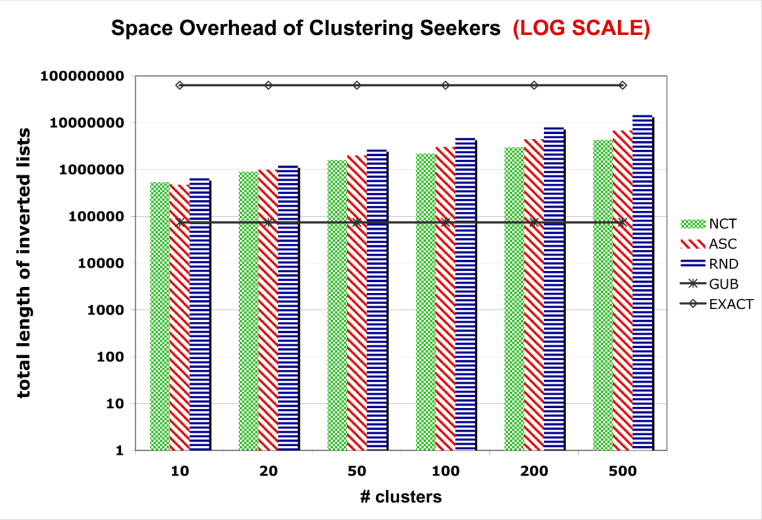


Figure 2.10: Space overhead of `Cluster-Seekers`.

Space Overhead. Figure 2.10 summarizes the space overhead of clustering seekers as the cluster budget varies from 10 to 500 clusters. `Global Upper-Bound` has lowest overhead, with 74,181 total inverted list entries, while `Exact` has 62,973,876 entries.

Space overhead of NCT ranges between 533,346 rows for 10 clusters and 4,284,854 rows for 500 clusters; ASC stores between 472,401 and 6,794,890 rows; while RND stores between 643,994 and 14,543,547 rows. ASC and NCT both achieve an order of magnitude improvement in space overhead over `Exact`. At this stage, we discard RND due to relatively poor space utilization, fix the number of clusters at 200, and continue our experiments with ASC (4,448,717 rows) and NCT (2,984,377 rows).

Execution Time. Tables 2.7 and 2.8 quantify the performance of `gNRA` and `gTA` with `Cluster-Seekers` when NCT and ASC are used for clustering. We list improvement in

	NCT (% improvement over GUB)						ASC (% improvement over GUB)					
	Seekers-25		Seekers-50		Seekers-100		Seekers-25		Seekers-50		Seekers-100	
query	SA	Total	SA	Total	SA	Total	SA	Total	SA	Total	SA	Total
SP	35	34	76	75	78	77	83	79	85	84	89	89
TR	54	53	78	77	78	80	80	72	76	75	85	84
PR	37	35	75	74	70	70	63	59	82	81	82	82
SPT	31	28	41	38	73	71	74	66	80	76	85	83
SPR	52	46	58	55	73	71	73	67	81	78	89	87
SPTR	40	34	49	45	64	60	68	56	78	70	82	77
Average	42	38	63	61	73	72	74	67	80	77	85	84

Table 2.7: Performance of `gNRA` for `Cluster-Seekers` with 200 clusters.

	NCT (% improvement over GUB)						ASC (% improvement over GUB)					
	Seekers-25		Seekers-50		Seekers-100		Seekers-25		Seekers-50		Seekers-100	
query	SA	Total	SA	Total	SA	Total	SA	Total	SA	Total	SA	Total
SP	36	34	66	65	73	73	80	80	82	81	87	87
TR	54	54	72	72	76	75	72	72	77	77	82	82
PR	38	37	74	74	68	67	64	64	81	81	79	78
SPT	34	35	46	45	74	73	72	73	81	80	84	84
SPR	53	52	57	56	67	66	74	74	78	77	85	85
SPTR	41	42	50	49	63	61	68	67	77	78	82	81
Average	43	42	61	60	70	69	72	72	79	79	83	83

Table 2.8: Performance of `gTA` for `Cluster-Seekers` with 200 clusters.

the number of sequential accesses (# SA) and in the **total** number of accesses, which is simply # SA + # RA. We observe that both `gNRA` and `gTA` with `Cluster-Seekers` significantly outperform `Global Upper-Bound` with both types of clustering. Consider the average improvement in the total number of accesses achieved by `gNRA` in Table 2.7. With NCT, `gNRA` makes 38-72% fewer total accesses compared to `Global Upper-Bound`, and with ASC the total number of accesses is improved by 67-87%. We observe a similar trend for `gTA`: NCT improves average total accesses by 42-69%, while ASC improves by 72-83%. Further, we observe that ASC outperforms NCT on both sequential and total accesses in all cases for `gTA` (Table 2.8), and in all cases except one in `gNRA`, query *TR* for *Seekers-50*, where NCT is better by 2%. Finally, note that in most cases percent-improvement over `Global Upper-Bound` is highest for *Seekers-100*, followed by *Seekers-50*. However, this trend needs to be related to the findings in Table 2.6: for *Seekers-100* `Global Upper-Bound` performs worst compared to `Exact`, and so there is significant room for improvement. Also note that improvement in # SA is similar to improvement in the total number of accesses. This is because performance of `gNRA` is heavily dominated by sequential accesses, while in `gTA`, # RA is bounded by $SA \cdot (n-1)$ for a query of length n.

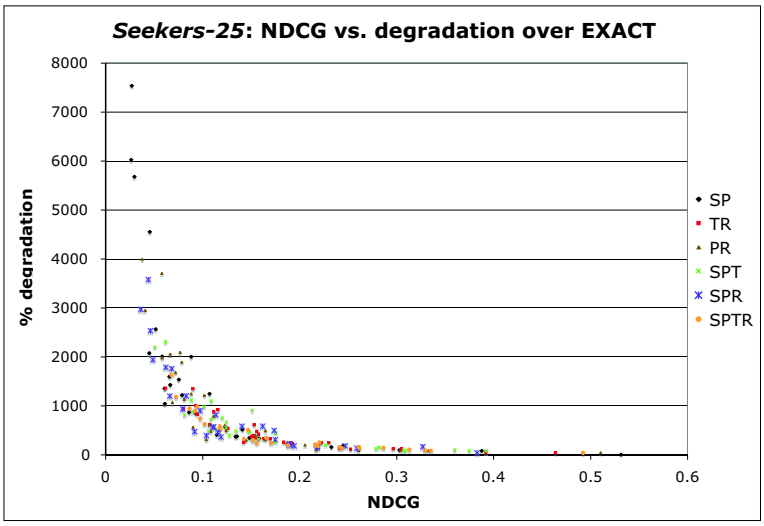


Figure 2.11: Correlation between NDCG and sequential accesses for *Seekers-25*.

2.6.5 Effectiveness of the Clustering Quality Metric

In Section 2.5.2 we described a clustering quality metric that uses Normalized Discounted Cumulative Gain (NDCG) (see Section 1.1.3.2) to quantify the run-time degradation of a cluster compared to `Exact`. We now demonstrate that our clustering quality metric correlates with the run-time performance of `gNRA`.

For `gNRA`, sequential accesses (SA) dominate the run time by a large margin, and we use SA to quantify run times in this experiment. Recall that `Exact` achieves best performance because inverted lists are ordered by exact score. Using the terminology of Section 2.5.2, `Exact` uses L_{ideal} lists. In contrast, `Global Upper-Bound` and `Cluster-Seekers` use inverted lists in which the order of items approximates the order in L_{ideal}, and we refer to such lists as L_{approx}. In the remainder of this section we will study the correlation between our variant of NDCG and the *percent degradation* in run time performance, compared to `Exact`, as measured by the number of sequential accesses.

Figure 2.11 presents the relationship between NDCG and run time performance for *Seekers-25*, for all clustering methods and all queries. We make the following observations based on these results. NDCG and percent degradation over `Exact` appear to be strongly correlated. As expected, a lower value of NDCG leads to a higher degradation over `Exact`, and vice versa. Using Spearman Rank Correlation, a non-parametric test appropriate for nonlinear correlations of the kind that is observed, we ascertain that the correlation is statistically significant. The two-sided p-value was less than $1.14 * 10^{-6}$ for individual queries, and less than $1.65 * 10^{-39}$ for the dataset as a whole. Similar results hold for the other groups of users in our experiments, *Seekers-50* and *Seekers-100*.

Tables 2.9, 2.11, and 2.12 lists average NDCG, and average percent degradation over

	Seekers-25					
	NDCG			% degr. over Exact		
query	GUB	NCT	ASC	GUB	NCT	ASC
SP	0.0575	0.0841	0.2232	2594	1128	306
TR	0.1155	0.1653	0.2602	796	382	180
PR	0.0796	0.1215	0.1745	2034	737	354
SPT	0.0936	0.1366	0.2963	963	569	123
SPR	0.0737	0.1283	0.2170	1571	626	286
SPTR	0.1098	0.1674	0.2883	739	362	135

Table 2.9: Using NDCG to predict performance of `Cluster-Seekers` for *Seekers-25*.

	Cluster-Seekers		Cluster-Taggers	
query	# SA	Total	# SA	Total
SP	82	82	97	97
TR	78	78	94	94
PR	82	82	97	96
SPT	83	83	97	97
SPR	86	86	95	95
SPTR	83	83	96	96

Table 2.10: Percent-improvement of `Cluster-Seekers` and `Cluster-Taggers`, compared to `Global Upper-Bound`.

`Exact`, with averages computed for each query and each clustering method. These results are in line with the performance numbers in Tables 2.6 and 2.7. Here, again, higher values of NDCG correlate with lower values of percent degradation compared to `Exact`. `Global Upper-Bound` has consistently lower NDCG, leading to poor query-execution times, while ASC has highest values of NDCG, and best run-time performance compared to other methods. A similar trend holds for `gTA`. The same trends hold when the total number of accesses rather than the number of SAs is used to measure run-time. Recall that NCT outperformed ASC for *Seekers-50* for query *TR* (see Table 2.8). NDCG captures this, assigning the highest value to NCT for this query and user sample. NDCG does mis-predict the relative performance of ASC and NCT in a single case, for the query *TR* on *Seekers-100*.

We established that our proposed clustering quality metric correlates with run time performance. This metric may be used in practice to tune clustering, or to trigger a re-clustering once NDCG drops below a certain threshold, which may be determined empirically. While the correlation between NDCG and run time performance is nonlinear, we can still conclude with confidence that higher values of NDCG correspond to better performance.

	Seekers-50					
	NDCG			% degr. over Exact		
query	GUB	NCT	ASC	GUB	NCT	ASC
SP	0.0270	0.0735	0.1088	8605	1893	1229
TR	0.0435	0.1206	0.1084	3935	728	813
PR	0.0391	0.0894	0.1093	4268	945	753
SPT	0.0459	0.0766	0.1436	3221	1735	537
SPR	0.0381	0.0846	0.1319	4039	1407	487
SPTR	0.0670	0.1099	0.1847	1684	766	154

Table 2.11: Using NDCG to predict performance for *Seekers-50*.

	Seekers-100					
	NDCG			% degr. over Exact		
query	GUB	NCT	ASC	GUB	NCT	ASC
SP	0.0100	0.0802	0.1080	26238	5388	2707
TR	0.0176	0.0728	0.0895	31835	4198	3609
PR	0.0183	0.0933	0.0430	19179	5051	3562
SPT	0.0261	0.0857	0.1023	7597	1664	977
SPR	0.0277	0.0833	0.1034	9293	1927	892
SPTR	0.0421	0.0914	0.1236	4103	1376	606

Table 2.12: Using NDCG to predict performance for *Seekers-100*.

2.6.6 Clustering Taggers

We cluster taggers using a variation of the underlying link relation in our experimental network: there is an edge between two taggers if they tagged at least one item in common with a given tag. Edges are weighted by the number of items tagged in common.

Space Overhead. Figure 2.12 presents the space overhead of `Cluster-Taggers` on a logarithmic scale. As expected, space overhead of this method is significantly lower than that of `Exact` and of `Cluster-Seekers`. Space overhead of NCT ranges from 115,168 rows for 10 clusters to 167,141 rows for 500 clusters; the overhead of ASC is between 100,922 and 180,881 rows; RND consumes between 160,432 and 259,216 rows. These numbers are all comparable to the optimal space consumption of `Global Upper-Bound`: 74,181 entries, which is explained by the lack of duplication of entries in the lists.

Execution Time. In the best case, given a keyword, all taggers relevant to a seeker will reside in a single cluster; then, only one inverted list will be processed at query time for that keyword. In the worst case, all taggers in the seeker's network will reside in separate clusters. For 200 clusters and tag *Reference*, there are 34 taggers per seeker, on average

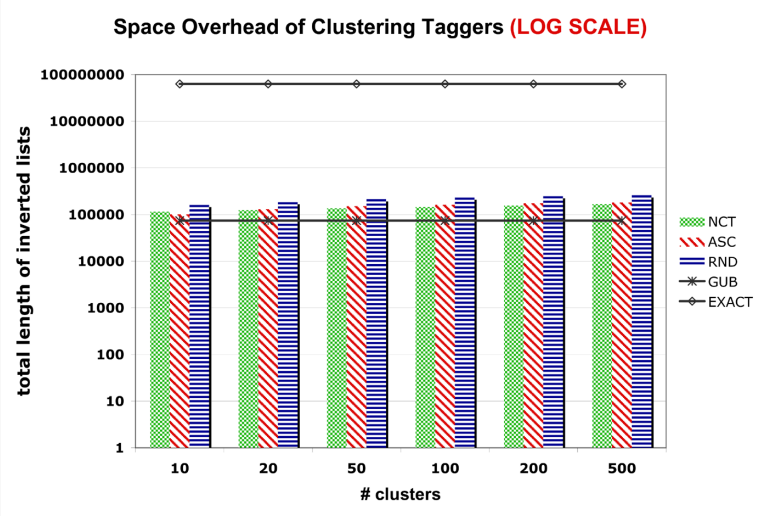


Figure 2.12: Space overhead of `Cluster-Taggers`.

(Table 2.5).

`Cluster-Taggers` has low space overhead; here, query execution time is the aspect of performance where we wish to realize an improvement. Since we found ASC to perform well in terms of time in other contexts (e.g., see Section 2.6.4), we now focus our attention on ASC with 200 clusters.

Even under the most effective clustering, a seeker may still be mapped to many clusters. An extreme case in our dataset is a seeker who mapped to 80 clusters for the two-keyword query *SP* (this seeker has 323 taggers). As a result, the number of SAs of `gNRA` increased 26 times compared to `Global Upper-Bound`, clearly an unacceptable performance. We observed empirically that `gNRA` with `Cluster-Taggers` outperforms `Global Upper-Bound` when at most $3*queryLength$ clusters are identified for the seeker. Therefore we propose to use `Cluster-Taggers` for a subset of the seekers – those who map to at most $3*queryLength$ clusters. In our dataset between 46-68% of seekers map to at most 3 clusters per tag. Using `Cluster-Taggers` for a subset of the seekers means that the outcomes of both clusterings, `Cluster-Seekers` and `Cluster-Taggers`, must be stored, bringing additional space overhead. However, storing `Cluster-Taggers` induces relatively low space overhead, and may result in superior processing times, which we demonstrate next.

Table 2.10 compares the run-time performance of `Cluster-Taggers` and `Cluster-Seekers` to `Global Upper-Bound`. We used ASC with 200 clusters for both `Cluster-Taggers` and `Cluster-Seekers`. We used a different sampling methodology for this experiment. For each query, we identified the set of seekers who map to at most 3 clusters for each keyword and sampled 10 seekers uniformly at random from that set. `Cluster-Taggers` outperforms `Cluster-Seekers` for all queries in our experiments, and achieves 94-97% improvement over

`Global Upper-Bound` for this class of seekers. This is because tagging actions of a particular tagger are not replicated across clusters in the `Cluster-Taggers` clustering scheme. As a result, per-cluster inverted lists in `Cluster-Taggers` are typically shorter, and upper-bounds are much closer to exact scores of the items.

2.7 Related Work

Top-k Processing: Top-k algorithms aim to reduce the amount of processing required to compute the top-ranked answers, and have been used in the relational [Carey and Kossmann, 1997], XML [Marian *et al.*, 2005], and other settings. The core ideas of these algorithms are overviewed in [Fagin *et al.*, 2003c; Fagin, 2002]. A common assumption is that scores are used to maintain dynamic thresholds during query processing, in order to efficiently prune low-scoring answers.

Even in work where the underlying query model is distributed [Michel *et al.*, 2005], or where the aggregation computation is expensive [Hwang and Chang, 2007], this assumption of pre-computation remains in place. In our work, we extend Fagin-style algorithms to process score *upper-bounds* – since pre-computed scores for each individual seeker are too expensive to store (given that they depend on a seeker's network) – and we explore clustering as a way to refine upper-bounds and reduce the size of the inverted lists.

Clustering: Graph clustering algorithms are plentiful and generally work on graphs with (possibly weighted) edges. Most of the work on clustering has focused on minimizing clustering time and considering additional constraints such as producing same-size clusters. In our experiments, we use Graclus, an open-source graph clustering software that is based on two variants of the popular k-means algorithms: normalized cut and ratio association [Dhillon *et al.*, 2007].

Socially Influenced Search: Although the potential of using social ties to improve search has been recognized for some time, this is still subject of ongoing work. Current research has focused on judging the impact of various notions of user affinity and socially-influenced scoring functions on search quality [Mislove *et al.*, 2006; Zhou *et al.*, 2008; Li *et al.*, 2008]. In contrast, our work develops indexing and query evaluation methods which apply to a wide class of scoring functions and networks.

User Experience in Collaborative Tagging Sites: The idea of motivating participation by displaying the value of contribution is characteristic of collaborative reviewing sites [Rashid *et al.*, 2006] but has received little attention in the study of collaborative tagging sites. Impact of reviews has been studied extensively in the e-commerce arena, and it has been shown that reviews impact sales [Chen *et al.*, 2007; Chevalier and Mayzlin, 2006;

Ghose and Ipeirotis, 2006]. Most of the current scientific literature dealing with user-contributed reviews concerns text analysis to distill reviews [Popescu and Etzioni, 2005], sentiment detection [Pang and Lee, 2004; Pang and Lee, 2005], and the impact of reviews on product sales [Bickart and Schindler, 2001; Ghose and Ipeirotis, 2007; Kim *et al.*, 2006; Lio *et al.*, 2007]. In contrast, very little has been done to extract value in collaborative tagging systems and provide participation incentives to users.

Deriving Semantics from Social Tagging: Wu et al. [Wu *et al.*, 2006b] present a probabilistic generative model that uses tagging to obtain the emergent semantics in social annotations. The authors study the relationship between resources, tags, and users by means of co-occurence analysis, and map these elements to a multi-dimensional *conceptual space*, where each dimension represents a category of knowledge. The authors demonstrate how these distributions may be learned and subsequently used to derive tag ambiguity information. They go on to show how their probabilistic model may be used for semantic search and discovery in social tagging sites like *Delicious*.

Collaborative Filtering: Collaborative Filtering (CF) is a popular method which is based on using machine learning to derive and compare user profiles in order to determine overlap of interest between users. A user profile is built from explicit or implicit data. The system can explicitly ask users to rate an item on a numerical scale, or to rank a collection of items from most to least favorite. The system can also record items that a user browsed or purchased, and analyze item viewing times. CF compares data collected from the user to similar data collected from others and calculates a list of recommended items for the user. Several methods have been developed to address data sparsity. Most of them (item-based and user-based) rely on statistical approximation [Bell *et al.*, 2007; Park and Pennock, 2007].

Our method differs from CF in that we express a user's interest qualitatively rather than quantitatively, using tags and derived ties. In [Agichtein *et al.*, 2006], it is shown that ranking in Web search can be improved by incorporating user behavior. Similarly, we show that incorporating tagging behavior improves ranking in producing hotlists. This motivates the need to better understand the principles behind designing a recommender tagging system, as was briefly discussed in [Golder and Huberman, 2006]. According to a study of del.icio.us tagging practices described in [Kipp and Campbell, 2006], tagging exhibits self-organizing patterns. In our work we explore how users can be classified into groups based on their tagging behavior, and how such groups can be used to improve the quality of recommended hotlists.

2.8 Conclusion

In this chapter we presented the types of semantic context that exist in collaborative tagging sites, and showed how such context can be used to improve the quality of search and ranking. We first explored how a user's social behavior and tagging can be used to produce high-quality hotlists. We then presented network-aware search, a first attempt to incorporate social behavior into searching in collaborative tagging sites.

We defined a model in which item scores are based on popularity among a network of related users, and formalized top-k processing in this context. We demonstrated how traditional algorithms can be extended to compute the best answers in a network-aware manner, and proposed clustering seekers and taggers as a way to balance between processing time and space consumption.

Incorporating a user's social context into search and ranking is central to supporting personalized social consumption of information, and provides a valuable participation incentive in collaborative tagging sites and beyond. A user who is able to access relevant information with ease in a social manner is likely to engage the system more actively, both by contributing content and creating social ties, and by consuming content provided by other users. Socially-influenced search uses the *semantics of social connections*, and has as one of its goals information discovery and the formation of knowledge. In the following chapter we will consider a different but related aspect of information discovery. There, search and ranking are likewise aimed at information discovery, and are based on the *semantic knowledge in domain ontologies*.

Chapter 3

Semantic Ranking for Life Sciences Publications

This chapter is based on joint work with Kenneth A. Ross and William Mee and will appear in [Stoyanovich *et al.*, 2010].

3.1 Introduction

Many scientific domains, most notably the domain of life sciences, are experiencing unprecedented growth. The recent complete sequencing of the Human Genome, and the tremendous advances in experimental technology are rapidly bringing about new scientific knowledge. The ever-increasing amount of data and semantic knowledge in life sciences requires the development of new semantically rich data management techniques that facilitate scientific research and collaboration.

Literature search is a central task in scientific research. In their search users may pursue different goals. For example, a user may need an overview of a broad area of research that is outside his main field of expertise, or he may need to find new publications in an area in which he is an expert. PubMed (`www.pubmed.gov`) is perhaps the most significant bibliographic source in the domain of life sciences, with over 18 million articles at the time of this writing. Indexed articles go back to 1865, and the number of articles grows daily, and increases steadily from year to year. PubMed articles are manually annotated with terms from the Medical Subject Headings (MeSH) controlled vocabulary. MeSH organizes term descriptors into a hierarchical structure, allowing searching at various levels of specificity. The 2008 version of MeSH contains 24,767 term descriptors that refer to general concepts like *Anatomy* and *Mental Disorders*, as well as to specific concepts like *Antiphospholipid Syndrome* and *Cholesterol*.

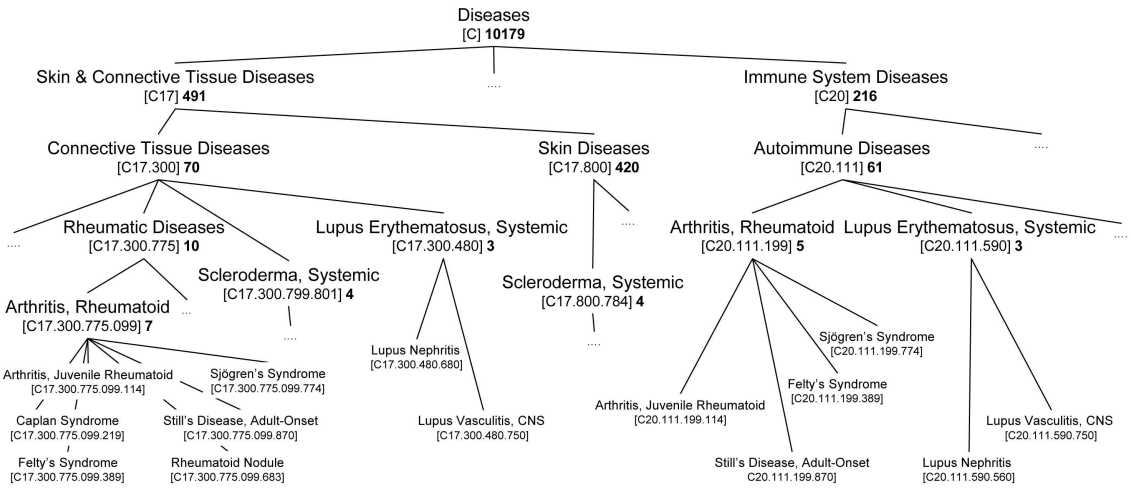


Figure 3.1: A portion of the MeSH polyhierarchy.

3.1.1 Overview of MeSH

MeSH terms are classified into an *is-a polyhierarchy*: the hierarchy defines is-a relationships among terms, and each term has one or more parent terms [Kaiser, 1911]. Figure 3.1 presents the portion of MeSH that describes autoimmune diseases and connective tissue diseases. The hierarchy is represented by a tree of *nodes*, with one or several nodes mapping to a single *term label*. For example, the term *Rheumatic Diseases* is represented by the node $C17.300.775.099$.

Interestingly, the MeSH hierarchy is *scoped*: two tree nodes that map to the same term label may not always induce isomorphic subtrees. The term *Rheumatoid Arthritis (RA)* maps to two nodes in Figure 3.1, and induces subtrees of different sizes. Node $C20.111.199$ represents the autoimmune aspect of RA and induces a subtree of size 5, while $C17.300.775.099$ refers to RA as a rheumatic disease, and induces a subtree of size 7. (Subtree size is noted next to the name of the node.) Scoping is an important technique for modeling complex polyhierarchies. Placing a concept in several parts of the hierarchy models different aspects of the concept, while accommodating different context in different parts of the hierarchy adds to the expressive power and reduces redundancy.

In MeSH it is almost always the case that if one term is a descendant of another in one part of the hierarchy, it will not be an ancestor of that same term in a different part of the hierarchy.[1]

PubMed and other NCBI-managed repositories can be searched with Entrez, the Life

[1]There is a single exception: *Ethics* is the parent of *Morals* in the *Humanities* branch of the hierarchy, while *Morals* is the parent of *Ethics* in the *Behavior and Behavioral Mechanisms* branch.

Sciences Search Engine[2]. Entrez implements sophisticated query processing, allowing the user to specify conjunctive or disjunctive boolean semantics for the search query, and to relate the search terms to one or several parts of the document: title, MeSH annotations, text of the document, etc. In order to improve recall, Entrez automatically expands query terms that are related to MeSH annotations with synonymous or near-synonymous terms. For example, the simple query *mosquito* will be transformed by Entrez to *"culicidae"[MeSH Terms] OR "culicidae"[All Fields] OR "mosquito"[All Fields].* Entrez also expands the query with descendants of any MeSH terms. For example, the query *"blood cells"[MeSH Terms]* will match articles that are annotated with *"blood cells"* or with *"erythrocytes"*, *"leukocytes"*, *"hemocytes"*, etc.

3.1.2 Challenges of Bibliographic Search

The need to improve recall differentiates bibliographic search from general web search. In web search it is often assumed that many documents equivalently satisfy the user's information need, and so high recall is less important than high precision among the top-ranked documents. Conversely, in bibliographic search the assumption (or at least the hope) is that every scientific article contributes something novel to the state of the art, and so no two documents are interchangeable when it comes to satisfying the user's information need. In this scenario the boolean retrieval model, such as that used by Entrez, guarantees perfect recall and is the right choice.

However, there is an important common characteristic of bibliographic and general web search: many queries return hundreds, or even thousands, of relevant results. Query expansion techniques that maximize recall exacerbate this problem by producing yet more results. For example, the fairly specific query *Antiphospholipid Antibodies AND Thrombosis*, which looks for information about a particular clinical manifestation of antiphospholipid syndrome, returned 2455 matches using the default query translation in January 2009. A more general query that looks for articles about connective tissue diseases that are also autoimmune returns close to 120,000 results.

Because so many results are returned per query, the system needs to help the user explore the result set. Entrez currently allows the results to be sorted by several metadata fields: publication date, first author, last author, journal, and title. This may help the user look up an article with which he is already familiar (i.e., knows some of the associated metadata), but does not support true information discovery.

A useful and well-known way to order results in web information retrieval is by query relevance. Retrieval models such as the Vector Space Model [Baeza-Yates and Ribeiro-Neto, 1999] have the query relevance metric built in, while the boolean retrieval model does not. In this chapter we propose to measure the relevance of a document to the query with respect

[2] `www.ncbi.nlm.nih.gov/sites/gquery`

to the MeSH vocabulary. We illustrate some semantic considerations and challenges with an example.

Example 3.1.1 *Consider the Entrez query* "Connective Tissue Diseases" [MeSH Terms] AND "Autoimmune Diseases" [MeSH Terms]*, evaluated against PubMed. Figure 3.1 represents these query terms in the context of the MeSH hierarchy. The query will match all documents that are annotated with at least one term from the induced subtrees of the query terms.*

One of the results, a document with pmid = 17825677*, is a review article that discusses the impact of autoimmune disorders on adverse pregnancy outcome. It is annotated with the query terms* "Autoimmune Diseases" *and* "Connective Tissue Diseases"*, and also with several terms from the induced subtrees of the query terms:* "Arthritis, Rheumatoid"*,* "Lupus Erythematosus, Systemic"*,* "Scleroderma, Systemic"*, and* "Sjögren's Syndrome"*. The article is also annotated with general terms that are not related to the query terms via the hierarchy:* "Pregnancy"*,* "Pregnancy Complications"*,* "Female"*, and* "Humans"*.*

Another result, an article with pmid = 19107995*, describes neuroimaging advances in the measurement of brain injury in Systemic Lupus. This article matches the query because it is annotated with* "Lupus Erythematosus, Systemic"*, which is both a connective tissue disease and an autoimmune disease. The article is also annotated with broader terms* "Brain"*,* "Brain Injuries"*,* "Diagnostic Imaging"*, and* "Humans"*.*

Based on this example, we observe that, while both articles are valid matches for the query, they certainly do not carry equal query relevance. The first article covers the fairly general query terms, as well as several specific disorders classified below the query terms in MeSH. In contrast, the second article answers a limited portion of the query, since it focuses on only one particular disorder. In this work we propose several ways to measure semantic relevance of a document to a query, and demonstrate how our semantic relevance can be computed efficiently on the scale of PubMed and MeSH.

An important dimension in data exploration, particularly in a high-paced scientific field, is time. An article that contributes to the state of the art at the time of publication may quickly become obsolete as new results are published. Semantic relevance measures of this chapter can be used to retrieve ranked lists of results, or they can be combined with data visualization techniques that give an at-a-glance overview of thousands of results. We develop a two-dimensional skyline visualization that plots relevance against publication date, and show how such skylines can be computed efficiently on the large scale.

Ranking that takes into account hierarchical structure of the domain has been considered in the literature [Rada and Bicknell, 1989; Lin, 1998; Ganesan *et al.*, 2003]. Such ranking typically relates two terms via a common ancestor; see Section 3.6 for a discussion of these methods. When terms appear in the hierarchy in multiple places, with subtly different meanings, it is unclear how such distance-based measures should be generalized. Instead,

in this chapter we develop new families of ranking measures that are aimed specifically at ranking with scoped polyhierarchies like MeSH, where terms may occur in multiple (partially replicated) parts of the hierarchy. We argue that the semantics of a term is best captured by its set of descendants across the whole hierarchy, and develop measures of relatedness that depend on the nature of the overlap between these sets of descendants.

Computing similarity based on sets of descendants is algorithmically more complex than simpler graph distance measures. We pay particular attention to efficiency, and provide an extensive experimental evaluation of our methods with the complete PubMed dataset and the full MeSH polyhierarchy, demonstrating that interactive response times are achievable.

3.1.3 Chapter Outline

The remainder of this chapter is organized as follows. We formalize semantics of query relevance for scoped polyhierarchies in Section 3.2. We present the data structures and algorithms that implement the query relevance measures on the large scale in Section 3.3. Section 3.4 describes an evaluation of efficiency, and Section 3.5 presents a user study. We present related work in Section 3.6, and conclude in Section 3.7.

3.2 Semantics of Query Relevance

We now formalize the data model, and define the semantics of several similarity measures, using the polyhierarchy in Figure 3.2 for demonstration. Term labels are denoted by letters $A, B, C, \ldots$, and nodes are denoted by numerical ids $1, 2, 3, \ldots$. Term $\top$ represents the root of the hierarchy, and maps to node 0.

3.2.1 Motivation

We wish to assign a score to documents whose MeSH terms overlap with the query terms. Our notion of "overlap" includes cases where a document term represents a sub-concept of a query term. If a query is $\{A, B\}$ in Figure 3.2, and the document contains MeSH terms C and D, then both C and D contribute to the overlap because they are sub-concepts of A and B. C is actually a subconcept of both A and B.

Our first similarity measure, which we formalize in Section 3.2.3, simply counts the number of elements in common between the descendants of the MeSH terms in the query and those in the document. According to this measure, concepts such as C that appear in multiple parts of the hierarchy count once. However, we might want to count C more than once because it contributes to the matching of both query terms.

The alternative of simply counting every occurrence of a term label can be naive. Suppose that the query is $\{C\}$ and that the document mentions term G but not C or H. One could argue that double-counting G is inappropriate, since the only reason we have two G

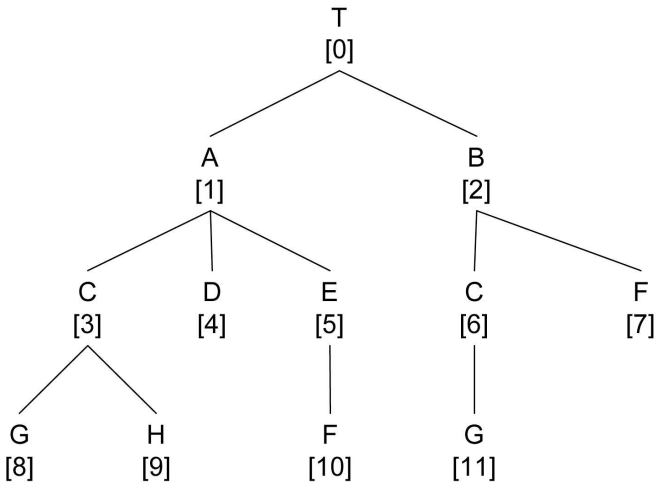


Figure 3.2: A sample scoped polyhierarchy.

instances is because C appears in multiple parts of the hierarchy. *Within the context of the concept C*, G really only appears once. This motivates us to refine the measure to only double-count when the ancestor concept in the query is different. We develop a similarity measure that models this intuition in Section 3.2.4.

The measures mentioned so far are sensitive to the size of the hierarchy. Because A has more descendants than B, an intermediate-level match in the A subtree may give a much larger score than a high-level match in the B subtree. The effect of this bias in scores would be that highly differentiated concepts in the hierarchy would be consistently given more weight than less differentiated concepts. To overcome this bias, we consider an additional scoring measure in Section 3.2.5 that weights matches in such a way that each term in the query contributes equally to the overall score.

3.2.2 Terminology

Definition 3.2.1 *A* scoped polyhierarchy *is a tuple $\mathcal{H} = \{\mathcal{T}, \mathcal{N}, ISA, L\}$, where $\mathcal{T}$ is a set of term labels, $\mathcal{N}$ is a set of nodes, $ISA : \mathcal{N} \to \mathcal{N}$ is a many-to-one relation that encodes the generalization hierarchy of nodes, and $L : \mathcal{N} \to \mathcal{T}$ associates a term with each node. When $ISA(n, n')$ holds, we say n' is a* parent *of n, and n is a* child *of n'. Every node except the root has exactly one parent node. n' is an* ancestor *of n if (n, n') is in the reflexive transitive closure of ISA. (Thus a node is its own ancestor and its own descendant.)*

We will use the following notation for convenience. For a term $t \in \mathcal{T}$, we denote by $N(t)$ the set of nodes n with label t (i.e., having $L(n) = t$). For a set of terms $T \subseteq \mathcal{T}$, we denote by $N(T)$ the set of nodes in $\bigcup_{t \in T} N(t)$. Likewise, for a set of nodes $M \subseteq \mathcal{N}$, we denote by $L(M)$ the set of labels of nodes in M.

Definition 3.2.2 *The* node-scope *of a term $t \in \mathcal{T}$, denoted by $N^*(t)$, is the set of nodes that have an ancestor with the label t: $N^*(t) = \{n | \exists n', t = L(n') \wedge ancestor(n', n)\}$.*

The node-scope *of a set of terms $T \subseteq \mathcal{T}$, denoted by $N^*(T)$, is the set of nodes that have an ancestor with the label in T: $N^*(T) = \bigcup_{t \in T} N^*(t)$.*

In Figure 3.2, the node-scope of the term C is $N^*(C) = \{3, 8, 9, 6, 11\}$, the same as the node scope of a set $\{C, G, H\}$.

Definition 3.2.3 *The* term-scope *of a term $t \in \mathcal{T}$, denoted by $L^*(t)$, is the set of term labels that appear among the nodes in $N^*(t)$: $L^*(t) = \bigcup_{n \in N^*(t)} L(n)$.*

We define the term-scope *of a set of terms $T \subseteq \mathcal{T}$ analogously, and denote it by $L^*(T) = \bigcup_{t \in T} L^*(t)$.*

The term-scope of the term C in Figure 3.2 is $L^*(C) = \{C, G, H\}$, while $L^*(\{B, C\}) = \{B, C, G, H, F\}$.

We use *node-scope* and *term-scope* to compare two sets of terms D and Q, where D is the set of terms that annotate a PubMed document, and Q is the set of query terms.

3.2.3 Set-Based Similarity

Our first measure, *term similarity*, treats the sets D and Q symmetrically, and quantifies how closely the two sets are related by considering the intersection of their *term-scopes*:

$$TermSim(D, Q) = |L^*(D) \cap L^*(Q)| \tag{3.1}$$

Term similarity may be used on its own, or it may be normalized by another quantity, changing the semantics of the score. For example, normalizing term similarity by the size of the *term-scope of the query* expresses the extent to which the query is answered by the document. We refer to this quantity as *term coverage*. Dividing the term similarity by the *term-scope of the document* expresses how specific the document is to the query. We refer to this quantity as *term specificity*. Finally, we may divide term coverage by the size of the union of the two term scopes, deriving *Jaccard similarity*.

$$TermCoverage(D, Q) = \frac{|L^*(D) \cap L^*(Q)|}{|L^*(Q)|} \tag{3.2}$$

$$TermSpecificity(D, Q) = \frac{|L^*(D) \cap L^*(Q)|}{|L^*(D)|} \tag{3.3}$$

$$TermsJaccard(D, Q) = \frac{|L^*(D) \cap L^*(Q)|}{|L^*(D) \cup L^*(Q)|} \tag{3.4}$$

3.2.4 Conditional Similarity

Set-based similarity treats the query and the document symmetrically, and may prioritize one set over the other in the final step, as is done in *term coverage* and *term specificity*. *Conditional similarity* prioritizes the query over the document from the start, by placing the term-scope of the document within the context of the term-scope of the query.

As we argued in Section 3.2.1, simply counting the paths between two terms can be naive, as we may be double-counting due to structural redundancy in the hierarchy. We thus define *conditional term-scope* by using ancestor-descendant pairs of terms, not full term paths. In the following definition, q is a query term and d is a document term.

Definition 3.2.4 *Let d and q be terms, and let $P_{d,q}$ be the set of node pairs (n_d, n_q) satisfying the following conditions:*

- *$n_d \in N^*(d)$, i.e., n_d has an ancestor with label d;*
- *$n_q \in N^*(q)$, i.e., n_q has an ancestor with label q;*
- *n_q is an ancestor of n_d.*

Conditional term-scope of d given q, denoted by $L^*(d|q)$, is the set of label pairs $(L(n_1), L(n_2))$, where $(n_1, n_2) \in P_{d,q}$.

Conditional term-scope of a set D given a set Q, denoted $L^*(D|Q)$, is the union of conditional term-scopes of all $d \in D$ given all $q \in Q$: $L^*(D|Q) = \bigcup_{d \in D, q \in Q} L^*(d|q)$.

For example, $L^*(G|C) = \{(C,G),(G,G)\}$, while $L^*(G|\{A,B\}) = \{(A,G),(B,G),(C,G),(C,G),(G,G)\}$. Note that $L^*(q|q)$ enumerates all pairs of terms (s,t), where $s,t \in L^*(q)$ such that there is a term-path from a node labeled with t to a node labeled with s. So, $L(C|C) = \{(C,G),(C,H),(C,C),(G,G),(H,H)\}$.

We define *conditional similarity* as:

$$CondSim(D,Q) = |L^*(D|Q)| \tag{3.5}$$

3.2.5 Balanced Similarity

Balanced similarity is a refinement of *conditional similarity* that balances the contributions of query terms to the score. Balanced similarity is given by the formula:

$$BalancedSim(D,Q) = \frac{1}{|Q|} \sum_{q \in Q} \frac{CondSim(D,q)}{CondSim(q,q)} \tag{3.6}$$

The relative contribution of each query term q to the score is normalized by the number of terms in the query, $|Q|$. For each term q, we compute the conditional similarity between the document D and the term q (as per Equation 3.5), and normalize this value by the

maximum possible conditional similarity that any document may achieve for q, which is $CondSim(q, q)$.

3.3 Efficient Computation of Query Relevance

In this section we describe the data structures and algorithms that support computing similarity measures of Section 3.2 at the scale of PubMed and MeSH. We do all processing in main memory to achieve interactive response time, and must control the size of our data structures so as to not exceed reasonable RAM size. Our data structures are at most linear in the size of PubMed, and at most quadratic in the size of MeSH.

We maintain annotations and publication date of PubMed articles in a hash table *Articles*, indexed by *pmid*. The version of PubMed to which we were given access by NCBI consists of about 17 million articles, published up to September 2007, and we are able to store publication date and annotations of all these articles in RAM. There are between 1 and 96 annotations per article, 9.7 on average.

In this work we focus on queries that are conjunctions or disjunctions of MeSH terms, and rely on the query processing provided by Entrez to retrieve query matches. We do not discriminate between AND and OR queries for the purposes of ranking. This is an item for future work. A query is represented in our system by a set of MeSH terms: $Query : \{t_1, \ldots, t_m\}$.

3.3.1 Exact Computation

We maintain the following data structures that allow us to compute values for the relevance metrics in Section 3.2. There are 24,767 terms and 48,442 nodes in MeSH 2008, the version of MeSH that we use in this work. For each term $t \in \mathcal{T}$, we precompute and maintain the following information in one or several hash tables, indexed on the term label.

- $N(t)$, the set of nodes that have t as its label. An average term labels 2 nodes. 50% of the terms label only a single node. The term *WAGR Syndrome* labels 19 nodes, the most of any term in MeSH.
- $L^*(t)$, the set of term labels in the term-scope of t (see Definition 3.2.3). An average MeSH term has 6.4 terms in its term-scope. The term *Amino Acids, Peptides, and Proteins* has the most terms in its term-scope: 2902. Recall that $t \in L^*(t)$; 67% of the terms have only their own label in their term-scope.
- $N^*(t)$, the set of nodes in the node-scope of t (see Definition 3.2.2). On average $|N^*(t)| = 9.6$. At least 1 and at most 6458 nodes are in the node-scope of any term in MeSH. The term *Amino Acids, Peptides, and Proteins* has the largest node-scope.
- $|L^*(t|t)|$, the size of conditional term scope of t, an integer value (see Definition 3.2.4).

For each node $n \in \mathcal{N}$, we maintain its term label $L(n)$, and the path from the top of the hierarchy to n.

- $L(n)$, the term label of n.
- The node-path from the top of the hierarchy to n. The average length of a node-path is 5, the longest path has length 12. (While one could traverse the hierarchy to construct this path as needed, it saves time to have all paths precomputed, and the space investment is modest.)

Algorithm 3: Procedure **TermSim**

Require: $Q = \{q_1 \dots q_n\}$, $R = \{pmid_1 \dots pmid_m\}$

1: Compute $L^*(Q) = \bigcup_i L^*(q_i)$
2: **for** $pmid \in R$ **do**
3: Retrieve $D = \{d_1 \dots d_m\}$ from *Articles*
4: Compute $L^*(D) = \bigcup_i L^*(d_i)$
5: $termSim(D, Q) = |L^*(D) \cap L^*(Q)|$
6: **end for**

Algorithm 3 describes how *term similarity* (Eq. 3.1) is computed for a query Q and a set of documents R. To compute the term-scope of a term t (lines 1 and 4), we retrieve $L^*(t)$ with a hash table lookup. Each lookup returns a set of terms, and the size of each such set is linear in the size of the hierarchy. In practice, for terms that denote general concepts, $L^*(t)$ may contain hundreds, or even thousands of term labels, while for terms that denote very specific concepts, $L^*(t)$ will contain only a handful of labels. Next, we take a union of the term-scopes of individual terms, which requires time linear in the size of the input data structures in our implementation. This computation happens once per query, and once for every document. Finally, having computed the term-scope of the document, we determine the intersection $L^*(D) \cap L^*(Q)$ (line 5). This operation takes time linear in the size of the data structures, and is executed once per document.

Algorithm 4 computes *conditional similarity* (Eq. 3.5) for a query Q and a document D. Term-scope and node-scope of Q are computed on lines 1 and 2. Then, for each document, we compute D_Q, the set of its terms that are in the term-scope of the query, and retrieve the node-scope of D_Q (lines 5 and 6). We then find all pairs of nodes $n' \in N^*(Q)$ and $n \in N^*(D_Q)$ such that there is a path from n' to n. Each document is processed in time proportional to $|N^*(Q)| \cdot |N^*(D_Q)|$, which can be high for queries and documents with large node-scopes.

Algorithm 5 computes *balanced similarity* (Eq. 3.6) by considering each query term q separately, and invoking *CondSim* for each document. Computing conditional similarity one

Algorithm 4: Procedure **CondSim**

Require: $Q = \{q_1 \dots q_n\}$, $R = \{pmid_1 \dots pmid_m\}$

Compute $L^*(Q) = \bigcup_i L^*(q_i)$
Compute $N^*(Q) = \bigcup_i N^*(q_i)$
for $pmid \in R$ **do**
  Retrieve $D = \{d_1 \dots d_m\}$ from *Articles*
  Compute $D_Q = D \cap L^*(Q)$
  Compute $N^*(D_Q)$
  $\mathcal{S} = \emptyset$
  for $n' \in N^*(Q)$ **do**
    for $n \in N^*(D_Q)$ **do**
      if $ancestor(n', n)$ **then**
        $\mathcal{S} = \mathcal{S} \cup (L(n'), L(n))$
      end if
    end for
  end for
  $condSim(D, Q) = |\mathcal{S}|$
end for

query term at a time has lower processing cost than the corresponding computation for the query as a whole, as is done in *CondSim*, as we will see during our experimental evaluation.

3.3.2 Computation with Score Upper-Bounds

In the previous section we saw that evaluating similarity of a set of documents with respect to a query can be expensive, particularly for queries and documents that are annotated with general MeSH terms. We now show how score upper-bounds can be computed more efficiently than exact scores.

Score upper-bounds can be used to limit the number of exact score computations in ranked retrieval, where only k best entries are to be retrieved from among N documents, and $k \ll N$. If score upper-bounds are cheaper to compute than actual scores, then we can compute score upper-bounds for all documents, order documents in decreasing order of score upper-bounds, and compute exact score values as needed, until the k best documents have been retrieved. Processing, and thus exact score computation, can stop when the score upper-bound of the document being considered is lower than the actual score of the current k^{th} best document. In addition to computing score upper-bounds for all documents, and evaluating exact scores for M documents, where $k \leq M \leq N$, the algorithm must perform a certain number of sorts, to determine the current k^{th} score at every round.

Consider again the computation of *term similarity* in Algorithm 3, which computes the

Algorithm 5: Procedure **BalancedSim**

Require: $Q = \{q_1 \dots q_n\}$, $R = \{pmid_1 \dots pmid_m\}$

Compute $weight_i = |Q| \cdot L^*(t|t)$ for each $q_i \in Q$
for $pmid \in R$ **do**
  $score = 0$
  for $q_i \in Q$ **do**
    $score = score + weight_i \cdot CondSim(q_i, pmid)$
  end for
  $balancedSim(D, Q) = score$
end for

value of the expression in Equation 3.1. We can transform this equation using distributivity of set intersection over set union, and observe that a natural upper-bound holds over the value of *term similarity*:

$$TermSim(D,Q) = |(\bigcup_d L^*(d)) \cap (\bigcup_q L^*(q))| =$$
$$|\bigcup_{d,q} L^*(d) \cap L^*(q)| \leq \sum_{d,q} |L^*(d) \cap L^*(q)|$$

The value of $TermSim(D, Q)$ cannot be higher than the sum of the sizes of pair-wise intersections of term-scopes of terms from D with terms from Q. To enable fast computation of this upper bound, we precompute $|L^*(s) \cap L^*(t)|$ for all pairs of terms s and t. The number of entries in this data structure, which we call *PairwiseTermSim*, is quadratic in the size of MeSH. In practice, we only need to record an entry for the terms s and t if $L^*(s) \cap L^*(t) \neq \emptyset$. There are over 613 million possible pairs of MeSH terms, but only 158,583 pairs have a non-empty intersection of their term-scopes.

For a query of size $|Q|$ and a document of size $|D|$, we need to look up $|Q| * |D|$ entries in *PairwiseTermSim*, and compute a sum of the retrieved values. The difference between the size of a set of terms, and the size of the term-scope of that set can be quite dramatic, and so computing upper-bounds is often much cheaper than computing actual scores. We will demonstrate this experimentally in Section 3.4.

Let us now consider how score upper-bounds can be computed for *conditional similarity* (Eq. 3.5), which counts the number of pairs of terms $q \in L^*(Q)$ and $d \in L^*(D)$ such that there is a node-path from $q \rightarrow d$. This quantity is bounded by the sum of sizes of $L^*(d|q)$ for all pair of terms d and q.

$$CondSim(D,Q) = |\bigcup_{d,q} L^*(d|q)| \leq \sum_{d,q} |L^*(d|q)|$$

To facilitate the computation of this upper-bound, we store the value of $L^*(s|t)$ for all pairs of terms s and t with intersecting term-scopes. We call this data structure *PairwiseCondSim*. This data structure has the same number of entries as *PairwiseTermSim*.

Finally, for *balanced similarity*, we observe that:

$$BalSim(D,Q) = \frac{1}{|Q|}\sum_{q}\frac{L^*(D|q)|}{L^*(q|q)} = \frac{1}{|Q|}\sum_{q,d}\frac{L^*(d|q)}{L^*(q|q)}$$

We re-use the *PairwiseCondSim* data structure for the computation of score-upper bounds for *balanced similarity*. We evaluate the performance improvements achieved by using score upper-bounds for ranked retrieval in Section 3.4.

3.3.3 Adaptive Skyline Computation with Upper-Bounds

As we argued in the Introduction, it is sometimes important to present more than a handful of query results. We propose to use a two-dimensional *skyline* visualization [Börzsönyi *et al.*, 2001] that is based on the familiar concept of dominance. A point in multi-dimensional space is said to belong to the skyline if it is not *dominated* by any other point, i.e., if no other point is as good or better in all dimensions, and strictly better in at least one dimension.

A skyline *contour* is defined inductively as follows:

- A point belongs to the first skyline contour if and only if it belongs to the skyline of the whole data set.
- A point belongs to the kth contour if and only if it belongs to the skyline of the data set obtained by removing points from the first through $k-1$st contours.

Skyline contours are useful for highlighting points that are close to the skyline, and that might be of interest to the user.

Publication date is a natural attribute in which to consider bibliography matches, and we use it as the x-axis of our visualization. The y-axis corresponds to one of the similarity measures described in Section 3.2. Figure 3.3 shows a skyline of results for the query *G-Protein-Coupled receptors*, for *term specificity* with 5 skyline contours. Points of highest quality are close to the origin on the x-axis and away from the origin on the y-axis. Points on the first contour are marked in white, points on the second contour are beige, and point on the last contour are red. When points are selected using the mouse, a window showing the full citation is displayed.

Our prototype implementation is running outside of the NCBI infrastructure, and we are using the Entrez query API, `eUtils`, to evaluate queries, and receive back ids of PubMed articles that match the query. The `eUtils` API can be asked to return query results in order of publication date. NCBI requests that large result sets be retrieved in batches, so

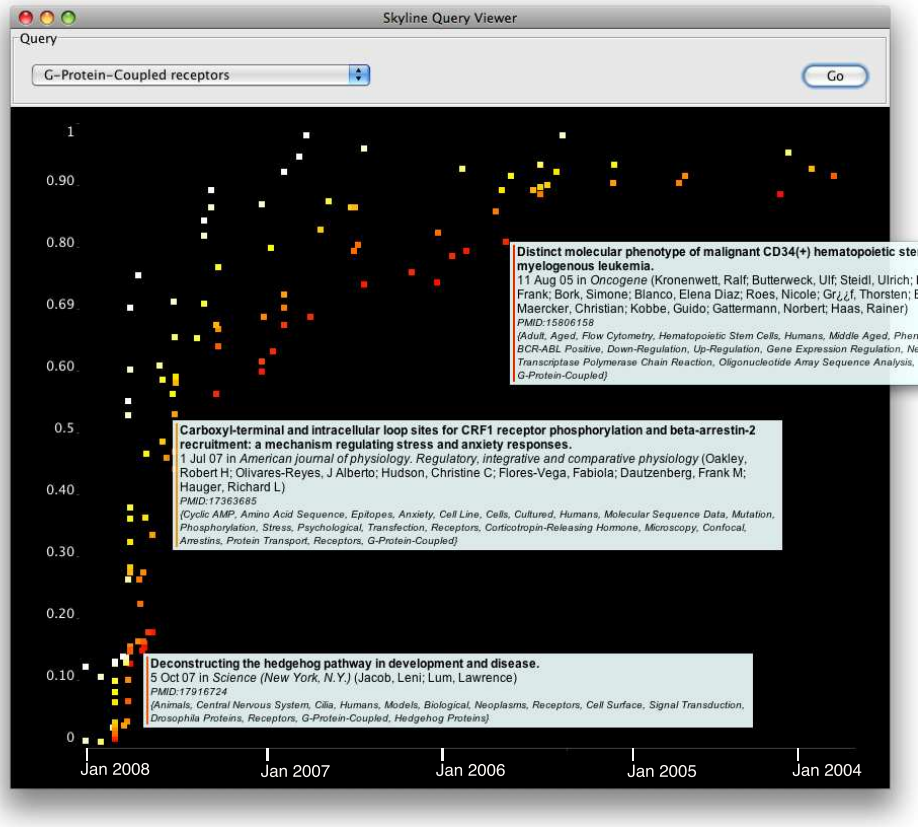


Figure 3.3: Two-dimensional skyline representation of results for the query *G-Protein-Coupled receptors*.

as not to overload their system. In the remainder of this section we describe a progressive algorithm that computes a two-dimensional skyline of results using score upper-bounds.

We implemented a divide-and-conquer algorithm based on the techniques in [Bentley, 1980]. Our algorithm processes results one batch at a time, with batches arriving in order of article publication date, from more to less recent. Articles within each batch are also sorted on publication date, and we use this sort order as basis for the divide-and-conquer.

The algorithm receives as input a sorted list of documents $R = \{pmid_1 \dots pmid_N\}$, the query $Q = \{q_1 \dots q_n\}$, an integer k that denotes the number of skyline contours to be computed, a similarity measure Sim, and $SkylineSoFar$: a list of documents, sorted on publication date, that were identified as belonging to the skyline when processing previous batches, along with contour number k. Note that a result that was assigned to the skyline during a previous batch will remain on the skyline, with the same contour number, for the remainder of the processing. This is because documents are processed in sorted order on the x-axis.

The divide-and-conquer algorithm processes the batch by recursively dividing the points along the median on the x-axis. When all points within an x-interval share the same x value, the algorithm sorts the points on the y coordinate, identifies contour points as the k best points in the interval, and assigns to each of the top-k points a contour number. Let us refer to this sub-routine as *AssignLinearDominance*. Contour number assignments are then merged across intervals, from left to right, and contour numbers of points on the right are adjusted. The $SkylineSoFar$ data structure is supplied to the left-most interval when a batch is processed.

The algorithm assumes that the values of the x and the y coordinates are readily available for each document. However, as we discussed in Section 3.3, the similarity score of the document may be expensive to compute, while the score upper-bound may be computed more efficiently. We therefore modify the *AssignLinearDominance* subroutine to use score upper-bounds as in Section 3.3.2. Exact scores are still computed, but the number of these computations is reduced. Using score upper-bounds allows us to compute the two-dimensional skyline more efficiently, as we demonstrate next.

3.4 Experimental Evaluation

In this section we present our experimental results that quantify the cost of exact score computation, and demonstrate the improvement achieved by using score upper-bounds in the computation. Techniques for this processing were described in Sections 3.3.2 and 3.3.3. Experiments in this section consider the run-time performance of three measures: *term similarity*, *conditional similarity*, and *balanced similarity*.

In the first set of our experiments, we study the advantage of using score upper-bounds for ranked list retrieval, for the various values of K. In the second set of experiments, we consider the performance improvement that is achieved when score upper-bounds are used for skyline computation, for various settings of the number of contours.

3.4.1 Experimental Platform

We evaluated the performance of our methods on a Java prototype. Figure 3.4 describes the system architecture and the data flow. Processing is coordinated by the *Query Manager* that receives a query from the user and communicates with PubMed via the `eUtils` API (arrow 1). Results are returned in batches, sorted in decreasing order of publication date (arrow 2). *Query Manager* receives results one batch at a time and communicates with the *In-Memory DB*, which implements the data structures and algorithms of Section 3.3. *In-Memory DB* and *Query Manager* communicate via Java RMI (arrows 3, 4). *In-Memory DB* runs on a 32-bit machine with a dual-core 2.4GHz Intel CPU and 4GB of RAM, with RedHat EL 5.1. Given a query and a list of PubMed ids, *In-Memory DB* can compute score upper-bounds or actual scores for each document, or it can compute the set of skyline

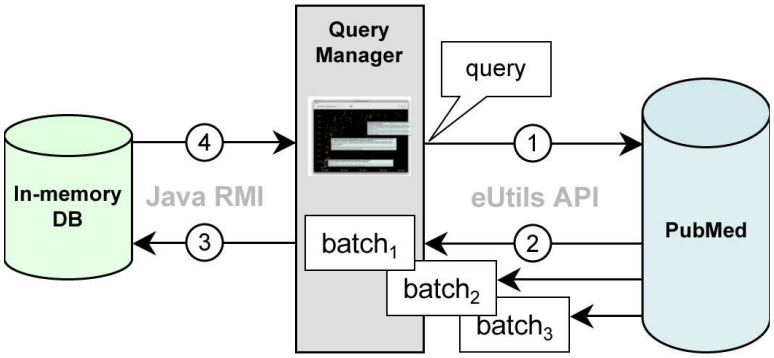


Figure 3.4: System architecture.

contours. Results are read by *Query Manager* (arrow 4), which can optionally pass them to the visualization component.

For the purposes of our evaluation all processing was done by *In-Memory DB*, to reduce communication cost. When a system like ours is deployed, some of the processing, e.g. skyline computation, can be moved to the client to reduce server load. All performance results are based on measuring processing times inside *In-Memory DB*. We report performance in terms of wall-clock time. All results are averages of three executions.

3.4.2 Workload

Our performance experiments are based on a workload of 150 queries. We were unable to get a real PubMed query workload from NCBI due to privacy regulations, and so we generated the workload based on pairwise co-occurrence of terms in annotations of PubMed articles. The rationale is that, if two or more terms are commonly used to annotate the same document, then these terms are semantically related and may be used together in a query. We generated the query workload as follows.

We took the set of all PubMed documents that were published during the month of January 2007, 124,413 documents in all, and computed pair-wise co-occurrence of terms in those documents. 20,848 out of a total of 24,767 MeSH terms are used to annotate documents in this sample. For all pairs of terms t_1 and t_2, we recorded the number of documents that are annotated with both t_1 and t_2, and compared this to the number of documents annotated with t_1 alone, and with t_2 alone. We refer to the sizes of these three document sets as $\mathcal{D}(t_1 \wedge t_2)$, $\mathcal{D}(t_1)$, and $\mathcal{D}(t_2)$, respectively.

Over 2.5 million pairs of terms were used together to annotate at least one document in our set. From among those, we selected pairs that contained terms that were neither too common not too uncommon. We removed terms that annotate more than 100 documents and fewer than 3 documents in the sample. Extremely common terms, such as *Human* and *Female* are likely too general to be used in a query. Very uncommon terms may be

# queries	150
size of $L^*(Q)$	2 to 454, avg 43, med 22
# results	1,024 to 179,450, avg 28,079, med 9,562

Table 3.1: Characteristics of the query workload.

	Term Similarity(sec)			
	med	**avg**	**min**	**max**
Score	0.412	1.342	0.013	13.238
UB	0.062	0.177	0.005	1.242
top-1	0.228	0.557	0.009	5.127
top-10	0.228	0.566	0.009	5.128
top-20	0.226	0.567	0.009	6.565
top-50	0.228	0.578	0.010	5.080
top-100	0.228	0.568	0.010	5.092

Table 3.2: Ranked retrieval: processing times of *Term similarity* for 150 queries.

informative, and could be used as part of a query. However, since the objective of our work is to assist the user in exploring large result sets, and since achieving good performance is more challenging for larger result sets, we decided to bias our experimental evaluation in that direction.

Further, to ensure that combining the terms is semantically meaningful, we selected pairs of terms that occur together at least 10% of the time that either of the terms occurs on its own. This is the case when $\frac{|\mathcal{D}(t_1 \wedge t_2)|}{|\mathcal{D}(t_1)|} \geq 0.1$ and $\frac{|\mathcal{D}(t_1 \wedge t_2)|}{|\mathcal{D}(t_2)|} \geq 0.1$. After this step we were left with 7958 pairs of terms.

From among 7958 pairs of terms (call this P), 487 were pairs with a common subtree in MeSH (call this P_O, for overlapping). These pairs are interesting because they can be meaningfully combined into an OR query. We thus chose 50 pairs of terms from $P \setminus P_O$ to create AND queries, 50 pairs from P_O for AND queries, and 50 pairs from P_O for OR queries.

Table 3.1 summarizes the properties of 150 queries in our workload. The number of results is calculated with respect to the entire PubMed corpus on which we run our performance experiments.

3.4.3 Ranked Retrieval with Score Upper-Bounds

Tables 3.2, 3.3, and 3.4 summarize the performance of 150 queries in our workload with *term similarity*, *conditional similarity*, and *balanced similarity*, respectively. We compare the execution time of computing exact scores for all results (**Score**) against the time of computing score upper-bounds for all results (**UB**). We then report the run-time of com-

	Conditional Similarity(sec)			
	med	**avg**	**min**	**max**
Score	0.387	4.408	0.004	274.230
UB	0.060	0.195	0.005	2.210
top-1	0.273	2.016	0.010	83.063
top-10	0.273	2.010	0.010	84.063
top-20	0.272	1.989	0.010	83.061
top-50	0.273	2.001	0.014	83.132
top-100	0.273	2.001	0.014	83.132

Table 3.3: Ranked retrieval: processing times of *Conditional similarity* for 150 queries.

	Balanced Similarity(sec)			
	med	**avg**	**min**	**max**
Score	0.372	3.760	0.006	195.420
UB	0.059	0.177	0.005	1.236
top-1	0.246	1.558	0.009	55.365
top-10	0.245	1.550	0.010	55.441
top-20	0.248	1.560	0.010	55.460
top-50	0.245	1.582	0.010	55.457
top-100	0.246	1.566	0.012	55.444

Table 3.4: Ranked retrieval: processing times of *Balanced similarity* for 150 queries.

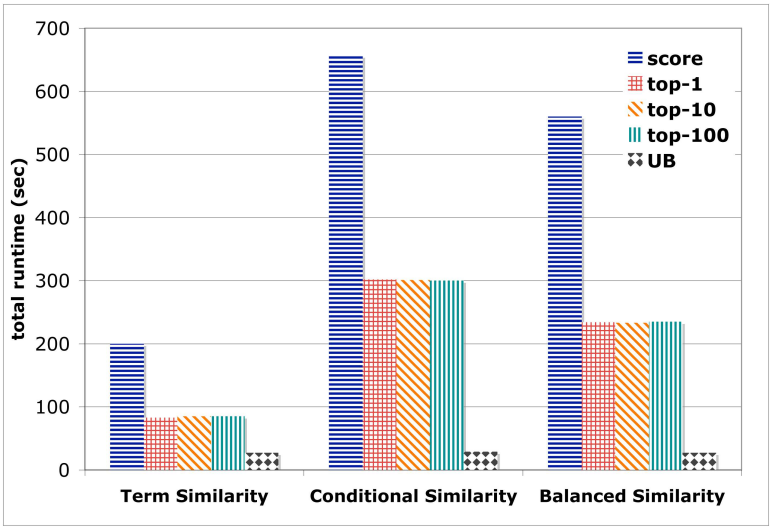


Figure 3.5: Total runtime of ranked retrieval.

puting the top-1, top-10, top-20, top-50, and top-100 results, in which upper bounds are computed for all items, and exact scores are computed for only the promising items. We observe that execution time of **Score** can be high, particularly for the conditional and balanced similarity metrics. In contrast, score upper-bounds can be computed about an order of magnitude faster, in interactive time even in the worst case. This behavior is expected, since, as we discussed in Section 3.3.2, the time to compute upper bounds is proportional to $|D| \cdot |Q|$, while computing the score is a function of the size of the term-scope of the query and of the document, which is typically much higher. According to our findings score upper-bounds can be computed about an order of magnitude faster than scores.

Figure 3.5 compares the *total run-time* of **Score**, **UB**, and ranked retrieval with $k = 1, 10, 20, 50, 100$, for all queries. Observe that *term similarity* computes fastest, while *conditional similarity* is slowest. It takes approximately the same amount of time to compute the top-k for different values of k.

Figures 3.6, 3.7 and 3.8 present run-time improvement of using score upper-bounds for top-k computation vs. computing exact scores, for three similarity measures. Performance of the vast majority of queries is improved due to using upper-bounds, for all similarity measures. The actual run-time improvement was up to 9.1 sec for *term similarity*, and between 0.7 and 0.8 sec on average for different values of k. For *conditional similarity*, the improvement was up to a dramatic 191 sec, and the average improvement was about 2.4 sec. For *balanced similarity*, using score upper-bounds improved run-time by up to 140 sec, and between 2.0 and 2.2 sec on average, for different values of k.

While performance improved for most queries, it degraded for some queries due to the overhead of sorting. This overhead was noticeable only in short-running queries, and abso-

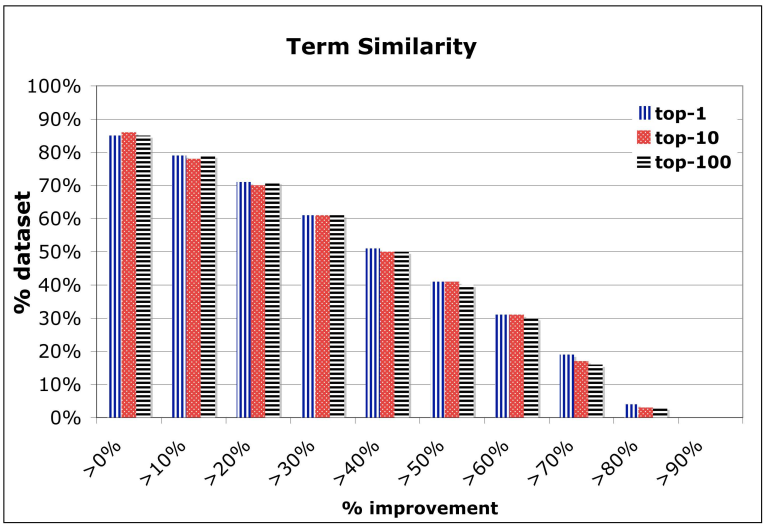


Figure 3.6: *Term similarity*: percent improvement in runtime of top-k when score upper-bounds are used.

lute degradation was insignificant: at most 0.081 sec for *TermSim*, 0.254 sec for *CondSim* and 0.213 sec for *BalancedSim*.

3.4.4 Skyline Computation with Upper-Bounds

In this section we consider the performance impact of using score upper-bounds for skyline computation, described in Section 3.3.3. We computed the skyline with 1, 2, 5, and 10 contours for 150 queries in our workload. Tables 3.5, 3.6, and 3.7 present the median, average, minimum, and maximum execution time for three similarity measures. For each number of contours, and for each similarity measure, we list two sets of numbers. The **Exact** line lists the performance of computing the skyline without the upper-bounds optimization, and the **UB** line lists the performance with the optimization. Recall that, whether we first compute exact scores for all documents (as in **Exact**), or first compute score upper-bounds for all documents, and then compute exact scores only for promising documents (as in **UB**), the result will be the same correct set of skyline points. So, the difference we are studying is with respect to performance only.

We observe that the **Exact** skyline performs in interactive time for the majority of queries, for all similarity measures. Median results are sub-second in all cases. We also observe that **UB** skyline outperforms **Exact** skyline. Note that these results are for the total execution of each query. Long-running queries typically execute in multiple batches, and The user is presented with the initial set of results as soon as the skyline of the first batch is computed, and does not have to wait for entire processing to complete.

In our experiments, we are able to predict whether a query will be long-running based

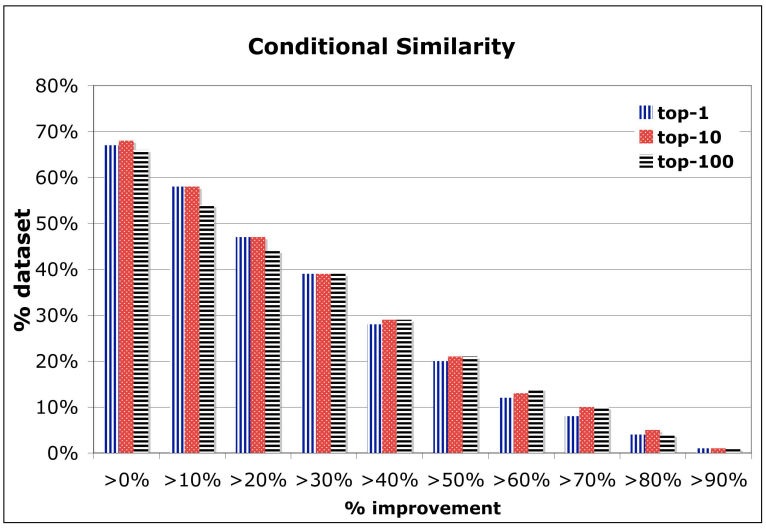


Figure 3.7: *Conditional similarity*: percent improvement in runtime of top-k when score upper-bounds are used.

on the number of results that the query returns. In fact, exact skyline computation for all queries that return fewer than 20,000 results completes in under 2 seconds. The information about the size of the result set is provided to us at the start of the execution by the **eUtils** API, and we can use this information to decide whether to apply the upper-bounds optimization. 45 out of 150 queries in our workload return over 20,000 results, and we refer to these as the *large queries* in the remainder of this section.

Figure 3.9(a) summarizes the total cumulative run-time of **Exact** and **UB** skylines for all queries in our experiments (*exact all* and *UB all* entries), and for the large queries (*exact large* and *UB large*), for the *term similarity* measure. We note that over 75% of the total time is spent processing 30% of the workload. We also observe that the time to compute the exact skyline stays approximately the same as the number of contours changes, both for the entire workload and for the large queries, while the time to compute the UB skyline increases with increasing number of contours. Finally, observe that UB skylines compute faster in total than their exact counterpart. The same trends hold for *conditional similarity* (Figure 3.10(a)) and *balanced similarity* (Figure 3.11(a)).

Figures 3.9(b), 3.10(b), and 3.11(b) plot the percent-improvement of **UB** skyline over **Exact** against the percentage of the *large queries* for which this improvement was realized. Query execution time was improved for the vast majority of large queries.

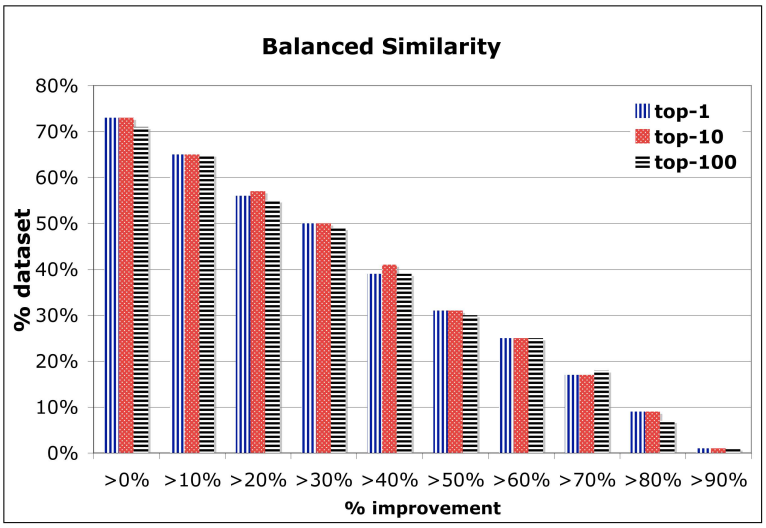


Figure 3.8: *Balanced similarity*: percent improvement in runtime of top-k when score upper-bounds are used.

3.5 Evaluation of Effectiveness

We now present a qualitative comparison between our similarity measures, and evaluate them against two baselines.

3.5.1 Baselines

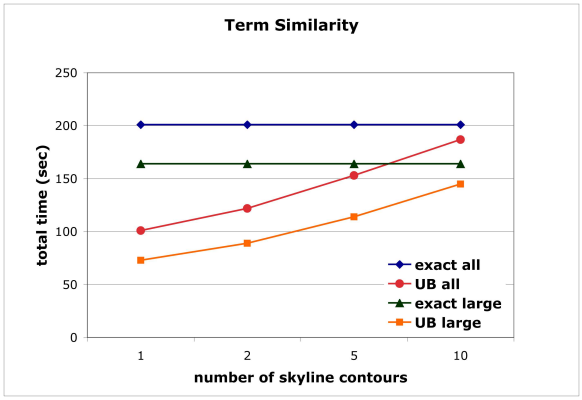
As before, we refer to the the set of MeSH terms derived from the query as Q, and to the set of MeSH terms that annotate a document as D.

Our first baseline is a *distance-based measure*, designed explicitly for MeSH, that compares two sets of terms based on the mean path-length between the individual terms [Rada and Bicknell, 1989]. For terms d and q, $dist(d, q)$ is the minimal number of edges in a path from any node in $N^*(d)$ to and node in $N^*(q)$. Consider nodes C and F in Figure 3.2. There are two paths between these nodes: $C \rightarrow A \rightarrow E \rightarrow F$ of length 3, and $C \rightarrow B \rightarrow F$ of length 2, and so $dist(C, F) = 2$. We define path-length as:

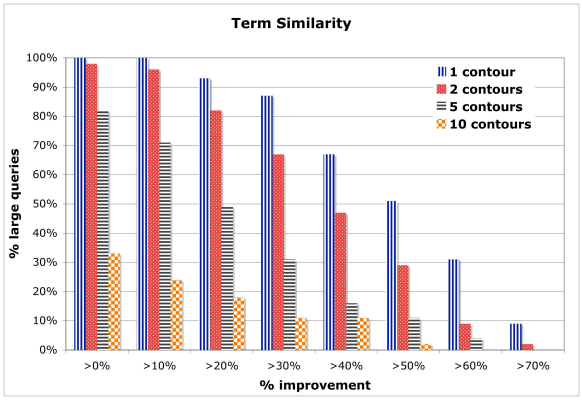
$$MeanPathLen(D, Q) = \frac{1}{|D||Q|} \sum_{d \in D} \sum_{q \in Q} dist(d, q) \tag{3.7}$$

This measure captures the distance between document D and query Q, and we transform it into a similarity:

$$MeanPathSim(D, Q) = \frac{1}{1 + MeanPathLen(D, Q)} \tag{3.8}$$



(a) Total run-time.



(b) % improvement with UB for *large queries*.

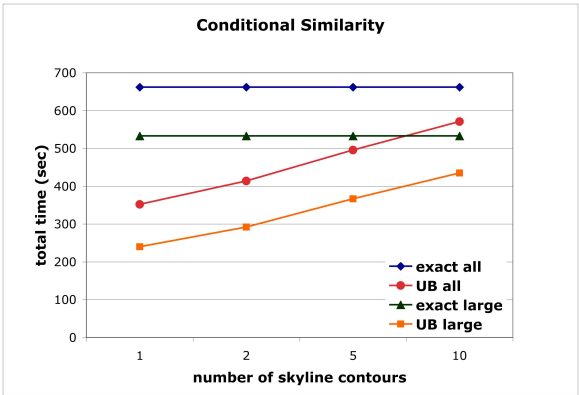
Figure 3.9: Run-time performance of skyline computation for *term similarity*.

	K	Term Similarity(sec)			
		med	avg	min	max
Exact	1	.4295	1.356	.016	13.225
UB	1	.299	.684	.014	5.687
Exact	2	.43	1.355	.016	13.202
UB	2	.3705	.825	.018	6.771
Exact	5	.4285	1.356	.016	13.209
UB	5	.448	1.036	.022	8.263
Exact	10	.4295	1.358	.016	13.222
UB	10	.4835	1.265	.022	9.647

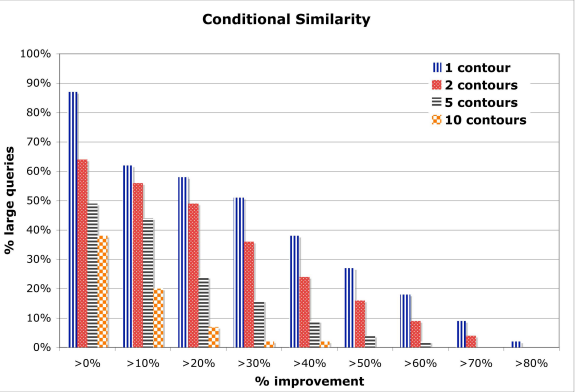
Table 3.5: Skyline computation: processing times for `TermSim` for 150 queries.

A known limitation of distance-based measures is an implicit assumption that edges in the taxonomy represent uniform conceptual distances, which does not always hold in practice. In Figure 3.2, the path distance between G and A is 2, the same as between G and B. However, one can argue that G is more closely related to B than to A because B has a smaller subtree, and so G represents a larger portion of the *meaning* of B than of A. Several information-theoretic measures have been proposed to overcome this limitation, and we use the one proposed by Lin [Lin, 1998] to derive our second baseline. Lin [Lin, 1998] demonstrated that his measure has a high degree of correlation with several other related measures [Resnik, 1995; Miller, 1990; Wu and Palmer, 1994].

For two taxonomy nodes s and t, we denote the lowest common ancestor by $LCA(s,t)$. The *information content* of a node s, denoted by $P(s)$, is the size of the subtree induced by s. Lin [Lin, 1998] defines similarity between nodes s and t as: $sim(s,t) = \frac{2 \times logP(LCA(s,t))}{logP(s)+logP(t)}$.



(a) Total run-time.



(b) % improvement with UB for *large queries*.

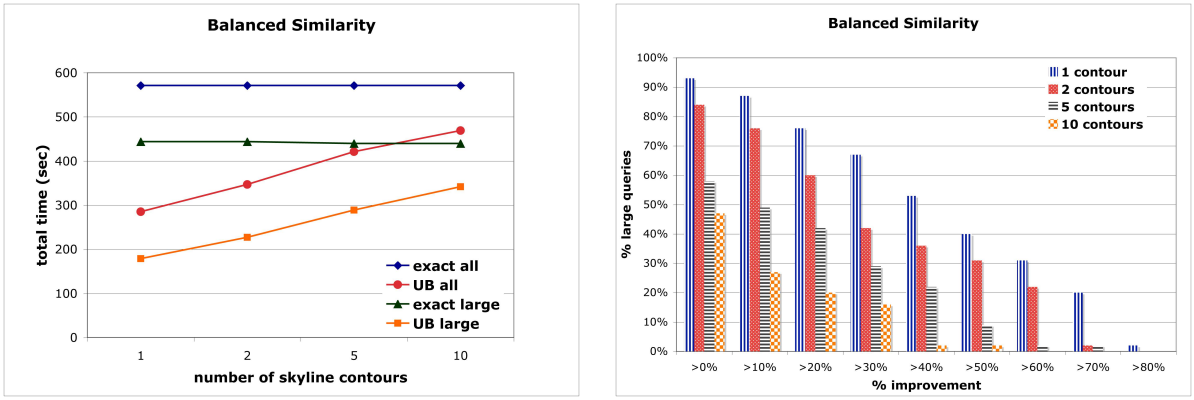
Figure 3.10: Run-time performance of skyline computation for *conditional similarity*.

	K	Conditional Similarity(sec)			
		med	avg	min	max
Exact	1	.4305	4.471	.009	274.301
UB	1	.343	2.377	.017	107.673
Exact	2	.424	4.471	.008	274.296
UB	2	.4055	2.796	.019	136.881
Exact	5	.4285	4.473	.009	274.311
UB	5	.4855	3.351	.019	167.917
Exact	10	.4275	4.472	.008	274.305
UB	10	.546	3.859	.019	197.304

Table 3.6: Skyline computation: processing times for `CondSim` for 150 queries.

To use this similarity for MeSH, we need to apply it to a polyhierarchy, with multiple nodes per term. We take a similar approach as in $MeanPathSim$, and say that the similarity between terms d and q is the highest similarity between any two nodes s and t, where $s \in N^*(d)$ and $t \in N^*(q)$. To handle multiple terms per query and per document, we define:

$$MeanInfoSim(D,Q) = \frac{1}{|D||Q|} \sum_{d \in D} \sum_{q \in Q} sim(d,q) \tag{3.9}$$



(a) Total run-time.

(b) % improvement with UB for *large queries*.

Figure 3.11: Run-time performance of skyline computation for *balanced similarity*.

	K	Balanced Similarity(sec)			
		med	avg	min	max
Exact	1	.4275	3.861	.01	199.521
UB	1	.3345	1.925	.018	72.955
Exact	2	.433	3.833	.01	195.194
UB	2	.389	2.345	.019	95.654
Exact	5	.4365	3.803	.01	195.13
UB	5	.4785	2.841	.02	116.974
Exact	10	.4365	3.806	.01	195.163
UB	10	.506	3.17	.019	132.334

Table 3.7: Skyline computation: processing times for `BalancedSim` for 150 queries.

3.5.2 User Study

3.5.2.1 Methodology

We recruited 8 researchers, all holding advanced degrees in medicine, biology, and bioinformatics. All are experienced PubMed users, with usage between several times a week and several times a day. Users were asked to come up with one query in their field of expertise, and to subsequently rate results returned by our system.

Rather than rating articles in the result, we asked our users to rate *annotation sets*: sets of MeSH terms that occur together as annotations of these articles. We opted for this kind of evaluation for several reasons. First, MeSH annotations of some articles are imprecise, that is, more general or more specific than the content of the article warrants. Second, abstracts of articles are often unavailable, making it difficult to judge the quality of content. Third,

presenting sets of MeSH terms for evaluation adds coverage and statistical power to our results, because we are deriving a judgment about a common class of annotations, which itself maps to a set of articles.

For a fixed query, and for a fixed similarity, all articles that are annotated with the same set of terms receive the same score. Additionally, several different annotation sets may map to the same score, and so ties are common. Scores are incomparable across measures, and we use ranks for our comparison.

Furthermore, *term similarity* typically assigns fewer distinct scores than other measures, and so its ranking is more discrete, while baselines generate more continuous ranks than do our measures. In order to meaningfully accommodate ties, and to make ranks comparable across measures, we assign ranks in the following way. To each result in a set of 1 or more ties, we assign the rank as the average row number of the ties. For example, if annotation sets s_1, s_2 and s_3 tie for the highest score, followed by sets s_4 through s_{10} that tie for the second highest score, then s_1, s_2 and s_3 are assigned a rank of $\frac{6}{3} = 2$, and the following 7 sets are assigned a rank of $\frac{49}{7} = 7$.

Many queries return thousands of results, and we cannot expect that the users will evaluate the quality of results exhaustively. We focus on a sub-set of results that is most informative about either the performance of a particular similarity measure, or about the relative performance of a pair of measures. Results are ranked according to $TermSim$, $CondSim$, $BalancedSim$, $MeanPathSim$, and $MeanInfoSim$. For a pair of measures $\mathcal{M}_1$ and $\mathcal{M}_2$, we choose 10 results from each of the following categories:

- *top*$\mathcal{M}_1$: in top 10% of ranks for $\mathcal{M}_1$ but not for $\mathcal{M}_2$
- *top*$\mathcal{M}_2$: in top 10% of ranks for $\mathcal{M}_2$ but not for $\mathcal{M}_1$
- *bot*$\mathcal{M}_1$: in bottom 10% of ranks for $\mathcal{M}_1$ but not for $\mathcal{M}_2$
- *bot*$\mathcal{M}_2$: in bottom 10% of ranks for $\mathcal{M}_2$ but not for $\mathcal{M}_1$

Results are chosen to maximize rank distances. So, a result that is at rank 1 for $\mathcal{M}_1$ and at rank 100 for $\mathcal{M}_2$ will be chosen before another result that is at rank 10 for $\mathcal{M}_1$ and at rank 100 for $\mathcal{M}_2$. Finally, we generate pairs of results to be compared to each other by the user. We never compare *top*$\mathcal{M}_1$ to *top*$\mathcal{M}_2$, and *bottom*$\mathcal{M}_1$ to *bottom*$\mathcal{M}_2$. Comparing top against bottom for the same method helps us validate that method on its own. Comparing top of one method against bottom of another allows us to compare a pair of methods against each other.

Figure 3.12 shows our evaluation interface. The user is presented with two annotation sets, **Match 1** and **Match 2**, and rates each set on a three-point scale. Clicking on a term name opens its definition in MeSH. Clicking on *example article* link shows the title and abstract (when available) of an article where the annotation set is used. The user also

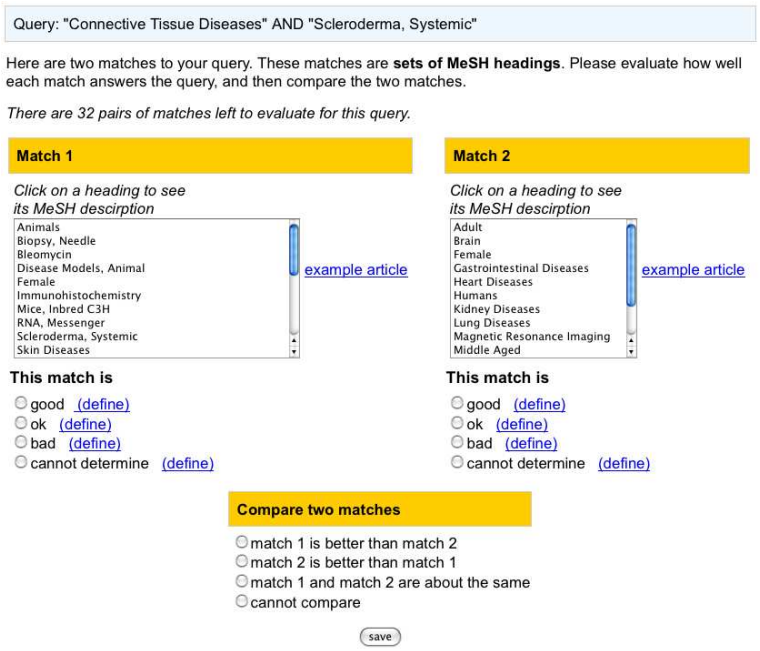


Figure 3.12: User study interface.

compares the matches with respect to how well they answer the query, on a three-point scale. Both scales include a "not sure" option, so as not to force a judgment when the user is not comfortable making one.

3.5.2.2 Results

Results in this section are based on 8 queries, each evaluated by a single user. We collected 670 individual judgments, and 335 pairwise judgments. In this section, we analyze the performance of each of our similarity measures individually, and then describe the relative performance of our measures, and compare them to the baselines. For results r_1 and r_2, user $\mathcal{U}$ issues a pair-wise relevance judgment $\mathcal{U} : r_1 = r_2$ if he considers results to be of equal quality, $\mathcal{U} : r_1 > r_2$ if r_1 is better, or $\mathcal{U} : r_1 < r_2$ if r_2 is better. (We exclude the cases where the user was unable to compare the results.) Likewise, a similarity measure $\mathcal{M}$ issues a judgment with respect to the relative quality of r_1 and r_2 by assigning ranks. Because users only judge a pair of results that are far apart in the ranking, the case $\mathcal{M} : r_1 = r_2$ never occurs.

A similarity measure may agree with the user's assessment, or it may disagree, in one of two ways: by reversing the rank order of r_1 and r_2, or by ranking r_1 and r_2 differently while the user considers them a tie. For ease of exposition, we incorporate all three outcomes: *agreement (A)*, *tie (T)* and *rank reversal error (E)*, into a single *agreement score*, defined as: $agreement(\mathcal{U}, \mathcal{M}, Q) = \frac{A+0.5 \cdot T}{A+T+E}$. Worst possible score is 0, best possible is 1. Table 3.8

	TermSim	**CondSim**	**Balmy**	**MeanPath**	**MeanInfo**
Q_1	0.56	0.51	0.51	**0.71**	**0.65**
Q_2	0.49	0.50	0.50	0.52	0.49
Q_3	**0.67**	**0.63**	**0.63**	0.39	0.48
Q_4	**0.66**	**0.66**	**0.66**	0.40	0.48
Q_5	0.42	0.43	0.43	0.33	**0.67**
Q_6	0.48	0.51	**0.60**	0.48	0.50
Q_7	0.43	0.45	0.45	**0.63**	0.44
Q_8	0.47	0.47	0.47	0.31	0.57
Avg	0.52	0.52	0.53	0.47	0.54

Table 3.8: Agreement between similarity measures and user judgments.

presents the agreement between the user and each similarity measure, for each query.

Due to the scale of our study we are unable to draw statistically significant conclusions about the relative performance of the measures. However, we point out some trends that emerge based on the data in Table 3.8, and which we plan to investigate further in the future, see Section 3.5.3 for a discussion. None of the measures seem to agree with user's judgment for queries Q_2 and Q_8. These queries do not exhibit polyhierarchy features: each term maps to a single node in MeSH. Our measures appear to outperform the baselines for queries Q_3, Q_4, and Q_6. All these queries include at least one term that exhibits polyhierarchy features: either the term itself *maps to two or more nodes* and *induces subtrees of different shape*, or its descendant terms do. Baselines appear to outperform our measures for queries Q_1, Q_5, and Q_7. Query Q_1 exhibits no polyhierarchy features. For a two-term query Q_8, each term maps to two nodes in MeSH, but the subtrees are isomorphic, i.e., there is *structural redundancy* in this part of the hierarchy. Query Q_5 exhibits true polyhierarchy features, yet the information theoretic baseline seems to be more in-line with the user's judgment for this query.

Table 3.9 presents the relative performance of our measures against the baselines. We present averages across queries, but note that performance for individual queries is in line with the trends in Table 3.8. Here, we are using judgments about a pairs of results such that one of the results has a high rank with respect to one method and a low rank with respect to another. We present the average percentage of user judgments that were in-line with the judgment made by the similarity measure. For example, in the entry for *TermSim* and *MeanPath* the user agreed with *TermSim* 46% of the time, and with *MeanPath* 28% of the time, and considered the remaining 26% of the cases as ties.

We also compared the relative performance of our measures for queries, for which there was a difference in performance. For Q_6, *BalancedSim* outperforms *CondSim*, which in turn outperforms *TermSim*. For Q_3, *TermSim* outperforms other measures. These findings are

	MeanPath	***MeanInfo***
TermSim	46% / *28%*	31% / *36%*
CondSim	41% / *31%*	36% / *36%*
BalSim	42% / *29%*	36% / *35%*

Table 3.9: *Term similarity*, *Conditional similarity* and *Balanced similarity* compared to baselines.

in line with results in Table 3.8.

3.5.3 Assessment of Results

Several issues make ranking difficult in our context. First, all results are already matches, i.e., all are in some sense "good". So, ranking by ontology is a second-order ranking among documents that may not be all that different from each other in terms of real relevance. However, as we demonstrate in Section 3.5.2.2, ontology-related score *is* correlated with quality as judged by the users in some cases. This occurs when terms appear in multiple tree locations and induce subtrees of different shape, a distinguishing feature in MeSH. Second, our user study is small, and so we cannot expect to demonstrate statistical significance. We plan to deploy the system and obtain more information by studying user feedback.

A user's perception of quality is informed by many aspects. Our work is motivated by the hypothesis that one of these aspects is captured by ontological relationships. This was supported by observations made by several users that they appreciated the presence of both general concepts, e.g., *Neurodegenerative Disease*, and related concepts that are more specific, e.g., *Alzheimer* and *Parkinson*.

Nonetheless, other aspects of user's quality perception may require a more sophisticated ontology than MeSH. Even when the ontology is helpful in principle, users may disagree with the classification, as observed by one user in our study. Semantic relationships, e.g., a connection between a protein and a disease, may be known to experts but are not present in MeSH, and are therefore unavailable for scoring. In future work, we plan to combine MeSH with other information sources that provide additional information about relationships between concepts. We also plan to incorporate weighting of terms, perhaps on a user-by-user basis, based on external information.

Due to the scale of our study, we do not establish which ranking is best for which kind of query, and when a query is amenable to ontology-aware ranking. We will investigate this in the future. For some queries our methods appear to do better, while for others the competing methods appear to do better. While no method dominates another for all queries, our methods seem to outperform the path-based overall, while performing comparably with the information theoretic measure.

3.6 Related Work

Ranking in Hierarchical Domains: Ranking that takes into account hierarchical structure of the domain has been considered in the literature. Ganesan et al. [Ganesan *et al.*, 2003] develop several families of similarity measures that relate sets or multisets of hierarchically classified items, such as two customers who buy one or several instances of the same product, or who buy several products in the same hierarchy. This work assumes that items in the sets are confined to being leaves of the hierarchy, and that the hierarchy is a strict tree. In our work we are comparing sets of terms in a scoped polyhierarchy, and we do not restrict the terms to being leaves.

Rada and Bicknell [Rada and Bicknell, 1989] consider the problem of ranking MEDLINE documents using the MeSH polyhierarchy, the same problem as we consider in our work. The authors propose to model the distance between the query and the document as the mean path-length between all pairs of document and query terms. This measure is one of several distance-based measures that have been proposed in the literature, see also [Lee and Myoung Ho Kim, 1993]. A known limitation of these measures is an assumption that links in the taxonomy represent uniform conceptual distances.

In an alternative approach, several information-theoretic measures have been proposed that can be used to measure semantic relatedness between concepts in hierarchical domains, see for example [Lin, 1998; Resnik, 1995]. These measures are similar to the distance-based methods in that they typically relate two concepts via a common ancestor. However, rather than simply counting the length of the path to the ancestor, the information content of the ancestor (the size of its subtree) is factored into the measure. The intuition is that a common ancestor that is very general is not as informative as one that is more specific.

In our work we propose several alternative ways to relate a document to a query, by measuring the overlap among common descendants (rather than ancestors) of all nodes labeled with two concepts. To the best of our knowledge, our work is the first to explicitly model semantic relatedness in a *scoped* polyhierarchy in which a term may appear in many parts of the hierarchy with subtly different meanings in each context. The question of how contributions of different terms, or different meanings of the same term, are reconciled in the final score is central to our approach. We explicitly model and explore alternative semantics of combining the contributions of individual pairs of terms to the over-all similarity score. Despite the extra computation needed for measures based on sets of descendants rather than ancestors, we demonstrate experimentally that interactive response times are still possible even when processing tens of thousands of documents.

Weighted Set Similarity: A number of efficient algorithms have been developed for the computation of similarity between weighted sets [Arasu *et al.*, 2006; Chaudhuri *et al.*, 2006; Sarawagi and Kirpal, 2004; Hadjieleftheriou *et al.*, 2008]. In [Sarawagi and Kirpal, 2004], inverted list indexes are constructed, and a variant of the Threshold Algorithm [Fagin

et al., 2003c] is used to allow for early termination of processing. In a recent work, Hadjieleftheriou et al. [Hadjieleftheriou *et al.*, 2008] develop indexing structures and processing algorithms for computing the similarity of weighted sets in order to evaluate set similarity selection queries. A query Q and a document D are compared based on corpus-derived weights of substrings of length q, termed q-grams, of which Q and D are comprised. The similarity between a query and a document is computed based on the combined weight of the q-grams that are common to D and Q, normalized by the weights of D and Q. This approach is conceptually similar to ours in that we also consider the set of elements, in our case MeSH terms, that are common to D and Q. However, unlike in [Hadjieleftheriou *et al.*, 2008], the elements we consider come from a hierarchy, and incorporating the structure of the hierarchy into the similarity score is central to our approach.

Techniques of [Sarawagi and Kirpal, 2004; Hadjieleftheriou *et al.*, 2008], and of other approaches that use inverted lists for processing, would require high space overhead in our setting. This is because an inverted index for a term must include not only the documents indexed with that term, but also the documents indexed with the term's descendants in MeSH. Processing with inverted lists is a *term-at-a-time* (TAAT) [Turtle and Flood, 1995] technique, in which query terms are processed one by one and partial document scores are accumulated. In our system we use *document-at-a-time* (DAAT) [Turtle and Flood, 1995] techniques, in which the documents are processed one by one and complete document scores are computed. DAAT strategies are known to be more appropriate for *context-sensitive queries*, in which score contributions from individual terms cannot be viewed independently, and score aggregation is crucial [Turtle and Flood, 1995], as is the case in our scenario.

Ontology Matching: Ontology matching uses a wide range of similarity measures to compare two or more ontologies. Ontology matching techniques in which comparison is based on taxonomic structure, bear some similarity to our approach. A particular class of similarity measures represents ontologies as labeled graphs and compares nodes in these graphs using lexical and structural features [David and Euzenat, 2008]. Pairwise node similarities are then aggregated into collection-wide measures. In our work we focus on structural similarity between sets of ontology terms, and consider them in the context of scoped polyhierarchies that do not naturally lend themselves to a graph-based representation.

Ontology Languages: The OWL Web Ontology Language was developed as part of the W3C Semantic Web Initiative[3], with the goal of assigning explicit semantic meaning to the information, and of presenting the semantics in machine-processable form. Hierarchies are modeled in OWL by means of the *rdfs:subClassOf* feature, and multiple inheritance is allowed. However, scoped polyhierarchies like MeSH cannot be expressed directly in OWL. Such hierarchies can be simulated with constructs *rdf:Property* and *rdfs:rdfssubPropertyOf*

[3] `http://www.w3.org/TR/owl-guide`

which are typically used to model relationships in OWL, and by restricting the scope of the inheritance relationship with *rdfs:domain*.

Skylines: Efficient computation of skyline results has been receiving significant attention of the database community. We build on the classic divide-and-conquer algorithm [Bentley, 1980], and adapt it to our application scenario and performance needs by incorporating processing with score upper-bounds. Tan et al. [Tan *et al.*, 2001] develop progressive skyline computation methods, while Jin et al. [Jin *et al.*, 2004] propose an efficient algorithm for the mining of thick skylines in large databases. In our work we also compute skylines progressively, by relying on a sort order in which results are supplied, and we are able to compute multi-contour skylines efficiently on the large scale. Our scenario differs from prior work in that coordinates of skyline points may be costly to compute, motivating us to use score upper-bounds.

Bibliographic Search in Life Science: A variety of web-based systems for bibliographic search in life sciences have been developed, see [Kim and Rebholz-Schuhmann, 2008] for a review. The system that is closest to our approach, GoPubMed [Doms and Schroeder, 2005], uses three ontologies - the Gene Ontology, MeSH and Uniprot, to organize PubMed query results. Results are presented in a faceted hierarchy that includes ontology terms, authors, journals, and publication dates. When multiple MeSH terms appear in the query or annotate query results, the system allows the user to navigate by each of these terms. Unlike in our work, no attempt is made to reconcile the contributions of multiple MeSH terms into a single score.

3.7 Conclusions

MeSH is a sophisticated, curated real-world ontology with about 25,000 terms. It has the interesting property that terms can appear in multiple parts of the hierarchy. Each time a term appears, its meaning is scoped, i.e., the meaning of the term depends on its position in the hierarchy. This observation challenges most past work which has been developed assuming that a term has a unique node in the generalization hierarchy.

We have attempted to capture the semantics of a term by looking at all of the term's descendants, across the whole hierarchy. We developed three similarity measures that relate sets of terms based on the degree of overlap between the sets of their descendants. We have demonstrated that each of these measures can be computed in interactive time for the complete MeSH ontology, at the scale of the complete PubMed corpus. We have also shown how computing score upper-bounds can be used to reduce the cost of identifying the best-matching documents, or of computing the skyline of the dataset with respect to score and publication date.

Enabling efficient and effective search and ranking that accounts for *semantic knowledge* is valuable for information discovery, particularly in domains in which high-quality

ontologies are available. Ontologies represent consensus of the scientific community with respect to the state of the knowledge in a particular domain. Wide-spread use of ontology-aware information discovery techniques is valuable not only for the end user, but also for the evolution of the ontologies: a community of users that sees a benefit in ontology-aware querying and ranking will keep the ontology up-to-date.

In this chapter we saw how a manually constructed ontology may be used for information discovery in an annotated document corpus, under the assumption that all documents in the corpus are of high quality. In the following chapter we will consider how ontologies can be used for search and ranking over the Wikipedia corpus, where there is a variation in both quality and relevance.

Chapter 4

Semantically Enriched Authority Propagation

This chapter is based on joint work with Srikanta Bedathur, Klaus Berberich, and Gerhard Weikum, which appeared in [Stoyanovich *et al.*, 2007].

4.1 Introduction

In Chapter 3 we presented a semantic framework that uses ontology annotations of scientific publications to rank query results. In the present chapter, we build on the idea of using an ontology for relevance ranking, and present *EntityAuthority*: a framework for semantically enriched authority propagation on graphs that combine documents, entities, and ontological concepts, in order to improve the ranking of keyword query results.

We apply the techniques of this chapter to Wikipedia, a community-curated encyclopedia corpus. Wikipedia may be considered as the middle ground between centrally-curated digital libraries like PubMed, in which documents are of high quality, and the World Wide Web, in which there is significant variation in document quality. Like the World Wide Web, Wikipedia gives rise to a natural link structure, and it is therefore appropriate to apply link analysis methods in this setting. Like PubMed documents, Wikipedia pages may be annotated with terms from a ontology, and it is therefore appropriate to use ontology-aware query processing and raking techniques.

4.1.1 Semantically Enriched Ranking

The classic link analysis methods, such as PageRank [Brin and Page, 1998] and HITS [Kleinberg, 1999], use the page-level Web graph for authority propagation. These approaches have been extremely influential. They are, however, fundamentally inappropriate for the emerging style of *semantic Web search* that aims to provide users with entities (e.g.,

products or scholars) and semantic attributes rather than pages [Cafarella *et al.*, 2007; Chakrabarti, 2004; Doan *et al.*, 2006a; Chu-Carroll *et al.*, 2006; Hearst, 2006; Madhavan *et al.*, 2007; Nie *et al.*, 2007]. Recently, techniques have been proposed for analyzing link structure, and for computing rankings of objects in relational databases or in entity-relationship graphs [Anyanwu *et al.*, 2005; Balmin *et al.*, 2004; Chakrabarti, 2007; Cheng and Chang, 2007]. However, these methods do not consider Web data or do not connect the object ranking back to the Web pages where the objects appear. In contrast, we jointly consider both the page-level and entity-level linkage structures and utilize their *mutual reinforcement* for ranking the results of keyword queries against Web data. We focus on keyword search as this is by far the most common information discovery method for most users. In our framework we consider two kinds of results: queries can return either pages or entities.

We utilize information-extraction techniques [Agichtein and Sarawagi, 2006; Cohen *et al.*, 2003; Cunningham, 2005; Doan *et al.*, 2006b] to identify semantic entities embedded in the text of Web pages, and to transform the page-level graph into a *generalized data graph*, with typed nodes that represent pages or entities, and with typed and weighted edges. We keep the entity part of this graph as noise-free as possible by mapping entities to nodes in a richly structured high-quality ontology that describes entities, concepts, and semantic relationships. More specifically, we use the popular open source GATE/ANNIE toolkit (`http://gate.ac.uk/`) for named-entity recognition, and various heuristics for entity disambiguation. According to a recent study that evaluates entity extraction systems [Marrero *et al.*, 2009], ANNIE supports 12 entity types, and achieves precision and recall in excess of 70%. While the study finds ANNIE to be inferior to several other systems because it produces a higher number of false positives, and is sensitive to orthographic features likes capitalization, this toolkit represented the state of the art at the time when this work was conducted, and is still among the highest-performing open source systems today.

For the ontology part of our generalized data graph we employ the YAGO knowledge base, which combines information from the Wikipedia category system and the WordNet thesaurus into a rigorously structured and highly accurate ontology [Suchanek *et al.*, 2007].

We assume and aim to exploit that there is mutual reinforcement between the authorities of pages and entities: pages become more valuable if they contain highly authoritative entities, and entities become more important if they are mentioned by highly authoritative pages. This resembles the HITS method [Kleinberg, 1999] for Web-graph link analysis and the ObjectRank method [Balmin *et al.*, 2004], but our approach operates on a generalized data graph that gives us a much richer substrate for ranking.

Consider for example the query "NBA team". When issued against a leading search engine on March 31st, 2007, this query returned links to the official homepage of the National Basketball Association, to the NBA-related area of `ESPN.com`, and to several team directories. The results were highly relevant but not specific to the user's information need:

it was not apparent from the top-10 results which teams play in the NBA, and there were no links to any of the teams' homepages. We observe that super-authorities dominated the query result, and team homepages did not start appearing until rank 38. (Results were very similar for the re-phrased query "National Basketball Association team".) We consider this and similar queries in our experimental evaluation and demonstrate how our EntityAuthority ranking methods can benefit such situations.

The results of such queries can be either entities or pages. The former may be preferred by a skilled user who has the proper context to interpret a concise list of entries such as "Miami Heat", "Dallas Mavericks", and "Chicago Bulls". The latter is appropriate for a non-expert user who wants to see an entire textual page, with relevant entities highlighted, providing him with at-a-glance contextual information. We will show that EntityAuthority ranking is beneficial for this type of Web-page ranking because it exploits the semantic connections and mutual authority propagation among pages, entities, and concepts.

4.1.2 Chapter Outline

In the remainder of this chapter we introduce *EntityAuthority*, and demonstrate its effectiveness on Wikipedia datasets. Section 4.2 presents the *generalized data graph*: a semantically-enriched model of the web graph that maintains information about web pages, and about the semantic entities that are contained in the pages. In Section 4.3 we describe several novel authority propagation measures that utilize the structure of the enriched web graph to a different extent. Section 4.4 details our prototype implementation, and Section 4.5 presents results of our experimental evaluation that demonstrate the effectiveness of our methods.

4.2 Data Model

In this work, we operate on a directed graph data model that integrates standard Web pages and their link structure with the entities extracted from these pages and with semantic relationships among entities. Figure 4.1 illustrates the key components in our data model using an example based on Web pages related to database research. The data model, which we call the *Generalized Data Graph*, or `GDG` for short, consists of three parts:

- the *Enriched Web Graph* that is derived using the underlying Web data collection
- the *Onto Graph*, which represents a richly structured ontological resource
- the *Onto Map*, a semantic layer that connects the Enriched Web Graph with the Onto Graph.

We now describe the Generalized Data Graph and its components in greater detail.

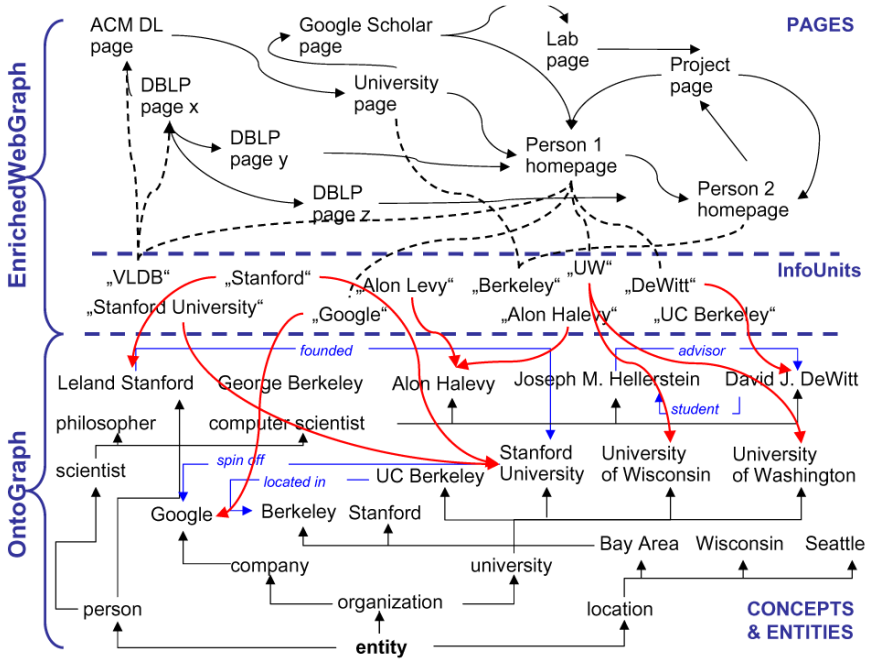


Figure 4.1: Example of a *Generalized Data Graph*.

4.2.1 Enriched Web Graph

Formally, Enriched Web Graph, or `EWG` for short, is a directed, labeled, and weighted graph $G_D = (V_D, E_D, L_v)$ where V_D is a set of nodes, $E_D \subseteq V_D \times V_D$ is a set of edges between nodes, and L_v is a set of node annotations. Each node $v \in V_D$ is assigned a label $l_v \in L_v$. These labels can simply be Page, InfoUnit, or richer concept names such as Person, Organization, etc., that can be obtained through a sophisticated information extraction software. Each edge $e = (v_1, v_2)$ also carries a weight whose value depends on the type of nodes v_1 and v_2.

`EWG` is the outcome of enriching the standard page-level content and link structure with entities that can be extracted from each page individually. Thus each node in the `EWG` corresponds to either a Web page or an information unit (an InfoUnit for short). An InfoUnit is a (short) textual snippet that is annotated as an instance of an entity by an information extraction tool such as GATE/ANNIE. This should be contrasted with the notion of an ontological entity/concept, which is the outcome of corpus-wide reconciliation of InfoUnits.

To make this distinction clear, consider two pages P_1 and P_2 that mention "UW" and "University of Washington" respectively. During the initial stage of information extraction, these text snippets are identified as potential entities and are thus marked as InfoUnits. Note that no effort at this stage is made to determine whether these two snippets refer to

the same entity or not.

4.2.2 Onto Graph

We model the underlying ontological resource as a directed, weighted graph $G_O = (V_O, E_O, L_e)$ on a set of nodes V_O which correspond to entities/concepts and E_O is a multi-set of edges between these entities. Note that we make no distinction between instances and concepts in this work. Each edge in E_O is annotated with a label from the set of labels, L_e that indicates the relationship between entities connected by the edge. For example, bornIn, locatedIn, and instanceOf are some of the labels available in YAGO – the precompiled ontology that we use. Each of these edges is assigned a weight representing the ontology's confidence in the relationship.

4.2.3 Onto Map

The next component in our model, *Onto Map*, forms the layer connecting the InfoUnits extracted from the corpus with entity and concept nodes in the ontology. Onto Map models a collection-wide entity reconciliation process that maps InfoUnits onto entities and concepts of the Onto Graph. This is represented in Figure 4.1 with solid edges from InfoUnits to Onto Graph layer. In order to support inherent ambiguities in the entity reconciliation process, our model allows for mapping of a single InfoUnit to more than one concept or entity. For example, the InfoUnit "UW" is mapped to both "University of Wisconsin" and "University of Washington".

4.2.4 Structure of the Generalized Data Graph

The Generalized Data Graph (GDG) that we obtain from extracting entities from pages, mapping them to the ontology, and connecting entities and concepts by semantic relationships, provides us with a rich cross-reference structure that reflects the authority of both pages and entities. This graph consists of the following kinds of typed and weighted, directed edges, where all weights are normalized so that the weights of a node's outgoing edges sum up to one:

- Hyperlinks between pages normalized by the source page's out-degree (as in standard PageRank);
- Edges from a page to each entity or concept that has been extracted from the page, weighted by the confidence in the extraction and mapping to the corresponding ontology node;
- Edges from entities to the concepts to which they belong, weighted with the ontology's confidence in the relationship and typed as an *isa* edge;

- Edges from an entity to each of the pages where it appears (i.e., backward pointers of the information extraction and mapping process), weighted by the extraction and mapping confidence.

Note that the weights on the edges from entities to pages are not necessarily the same as those from pages to entities, because of the normalization step: a page may contain only a few entities, but these entities may appear in many pages.

We do not currently include semantic relationship edges between entities and concepts, e.g.,*bornIn*, *locatedIn*, *childOf*, etc.

4.2.5 Query Result Graph

In Section 4.3 we will describe how the Generalized Data Graph may be used to compute authority of various graph nodes. At the high level, authority can reflect either a global query-independent importance, or it can be made query-dependent. A query-dependent ranking may be achieved by, for example, first applying a content-only retrieval procedure, and then ranking over the query-relevant subset of the data.

We now describe a heuristic procedure that constructs a *Query Result Graph*: a query-relevant subset of the Generalized Data Graph.

Suppose that we first evaluate a keyword query against both pages and ontology nodes, and compile a list of qualifying items. We consider an item as qualifying if it contains the query words or has a compact neighborhood in the data graph that contains them. We will describe how such a compact neighborhood may be identified in Section 4.4.2.

The resulting items – pages, entities, and concepts, may already carry their initial *relevance scores* that reflect frequencies or other kinds of prominence information. We can now construct a *Query Result Graph* (`QRG` for short) from these results, incorporating relevance scores into node weights.

The `QRG` consists of all initial results whose relevance score is above some predefined threshold. This threshold may be set to 0, capturing all qualifying items. Next, for each item we determine all its predecessors and all its successors in the `GDG` (these are nodes that point or are pointed to by the initial results), and we add these nodes to the `QRG`. We may then look up all successors of predecessors and all predecessors of successors and add them, too. How many sets of successors and predecessors will be added can be tuned heuristically.

Having identified a subset of `GDG` nodes that will be included into the `GRG`, we now add all edges from the `GDG` that connect two `QRG` nodes. This query-dependent graph construction is similar to the procedure proposed in the original HITS method [Kleinberg, 1999].

Edge weights can optionally be re-scaled by multiplying the weight of an edge $x \rightarrow y$ with the relevance score of the target node y, or with some minimum value μ if y was not among the initial query results. This is similar to a biased random-walk model in which a hypothesized Web surfer prefers target nodes whose contents has high relevance scores.

Regardless of whether this re-scaling is applied or not, edge weights need to be re-normalized because not all outgoing edges of a GDG node need be present in the QRG.

4.3 Authority Measures

We now present different models for computing page and entity authority values. The measures of this section can be applied to the complete Generalized Data Graph, or they can be applied to the Query Result Graph – a query-specific subset of the GDG.

One immediate candidate for computing a notion of importance on the graph would be to apply PageRank, or strictly speaking a weighted-edges variant of PageRank [Bharat and Henzinger, 1998; Borodin *et al.*, 2005] as if all nodes of the graph were pages. But we will see below that we can apply mathematically related but semantically more meaningful computations on this richer graph.

The following authority measures can be computed on either the GDG or the QRG. These measures utilize the rich structure of the graph to a different extent. The first measure uses only the page nodes of the graphs and then propagates page authority to entities and concepts; it is thus called *Page-Inherited Authority (PIA)*. The second measure, which is much more elaborate and one of this chapter's main contributions, uses the full graph and is coined *Entity-deriVed Authority (EVA)*.

4.3.1 Page-Inherited Authority

For *PIA* we consider only the pages in the GDG or the QRG and their incident page-to-page edges. For each page, we compute either the edge-weighted PageRank or the page authority according to HITS. Let $\mathcal{A}_P(p)$ denote the authority of page p, and let $\mathbf{P}(x)$ denote the set of pages that point to ontology node x in the GDG (i.e., the pages from which x has been extracted). Further, let $w(x \rightarrow y)$ denote the *weight* of the edge from x to y. We define the page-inherited authority of x as:

$$\mathcal{A}_P(x) = \sum_{p \in \mathbf{P}(x)} \mathcal{A}_P(p) \times w(p \rightarrow x)$$

According to *PIA*, an entity or concept is important if it appears in important pages, while the importance of a page is pre-determined by a page-links-only authority model.

4.3.2 Entity-Derived Authority

One can argue that importance of a page does not depend solely on the link structure of the web graph. So, a page may be viewed as important if it mentions important entities or concepts. This consideration leads to a mutual reinforcement model between pages and entities. For example, a Web page such as www.cs.stanford.edu is important because

it mentions authorities like *Jeffrey Ullman* and *Hector Garcia-Molina*, and that these are in turn authorities because they are referenced by many important Web pages such as `Citeseer-top-authors`, `DBLP-top-authors`, and `www.sigmod.acm.org`.

To express this intuition we propose an alternative authority propagation model, which we call *Entity deriVed Authority*, or *EVA*. *EVA* is defined by the following mutually-recursive equations that define $\mathcal{A}_P$ – the page-level authority score, and $\mathcal{A}_O$ – the entity-level authority score:

$$\mathcal{A}_P(p) = \sum_{x \in \mathbf{O}(p)} \mathcal{A}_O(x) \times w(x \to p) + \sum_{q \in \mathbf{P}(p)} \mathcal{A}_P(q) \times w(q \to p)$$

$$\mathcal{A}_O(x) = \sum_{p \in \mathbf{P}(x)} \mathcal{A}_P(p) \times w(p \to x) + \sum_{y \in \mathbf{O}(x)} \mathcal{A}_O(y) \times w(y \to x)$$

Here, p and q are pages, x and y are entities or concepts, $\mathbf{P}(z)$ denotes the set of pages to which a page, entity, or concept points, and $\mathbf{O}(z)$ denotes the set of ontology nodes to which a page, entity, or concept points.

This model is mathematically related to HITS, where there is mutual reinforcement between hubs and authorities, but the semantic interpretation of *EVA* is very different from HITS. The richer heterogeneous graph structure that we use in *EVA* also makes the computation itself more demanding.

The authorities of pages and ontology nodes $\mathcal{A}_P$ and $\mathcal{A}_O$ can be iteratively computed by the Orthogonal Iteration method [Kempe and McSherry, 2004]. In linear algebra notation, the two equations for $\mathcal{A}_P$ and $\mathcal{A}_O$ can be rewritten as follows. Let $\vec{P}$ be a vector of the pages' $\mathcal{A}_P$ values and $\vec{X}$ be a vector of the ontology nodes' $\mathcal{A}_O$ values. Suppose there are m pages and n ontology nodes in the underlying graph. Now let PP be an $m \times m$ matrix, PX an $m \times n$ matrix, XP an $n \times m$ matrix, and XX and $n \times n$ matrix with the following entries:

$$\begin{aligned}
PP_{ij} &= w(i \to j) \quad \text{for pages } i, j \text{ with } i \neq j \\
&= 0 \quad \text{for } i = j \\
PX_{ij} &= w(i \to j) \quad \text{for page } i \text{ and ontology node } j \\
XP_{ij} &= w(i \to j) \quad \text{for ontology node } i \text{ and page } j \\
XX_{ij} &= w(i \to j) \quad \text{for ontology nodes } i, j \text{ with } i \neq j \\
&= 0 \quad \text{for } i = j
\end{aligned}$$

Then the equations for $\mathcal{A}_P$ and $\mathcal{A}_O$ given above can be phrased in vector form as:

$$\vec{P} = XP \times \vec{X} + PP \times \vec{P} \tag{4.1}$$

$$\vec{X} = PX \times \vec{P} + XX \times \vec{X} \tag{4.2}$$

The computation is initialized by choosing arbitrary start vectors for P and X that are not linearly dependent on the eigenvectors of the matrices in Equations 4.1 and 4.2. It is not difficult to satisfy this start condition; for example, it is satisfied by choosing uniform start values in all but degenerate situations. Then we evaluate each of the two equations by substituting the current values of the two vectors in their right-hand side; the new values for the left-hand side then become the values for the right-hand side of the next iteration. Iteration repeats until the changes of the two vectors, as reflected either by their L1 norms, or by the relative ranking of their top-100 elements, drop below some threshold and become negligible. After each iteration step, the two vectors are re-scaled (i.e., multiplied by a normalization factor) so that their L1 norms become equal to one. This final step ensures convergence and result uniqueness for the Orthogonal Iteration method.

4.3.3 Untyped Authority

The *PIA* model computes a global authority score of an entity based on global authority of the page(s) from which the entity was extracted. In contrast, *EVA* models mutual reinforcement between pages and entities on the graph.

For completeness we also present a third ranking method, which we call *Un-Typed Authority*, or *UTA*. *UTA* serves as the middle-ground between *PIA* and *EVA*. Like *EVA*, *UTA* will operate over all nodes and edges of the `GDG`, or over the query specific `QRG`. However, unlike *EVA*, *UTA* simply runs an edge-weighted version of a standard ranking algorithm (e.g. PageRank or HITS) on this graph, ignoring node types.

We will compare the effectiveness of *PIA*, *UTA*, and *EVA* in Section 4.5.

4.4 System Implementation

This section describes the system architecture of our prototype implementation. Our prototype was evaluated on a part of the English-language Wikipedia.

4.4.1 Building the Generalized Data Graph

We use several existing tools to build the Generalized Data Graph, and while information annotation and extraction is not a major contribution of this work, we gained some insight into performing these tasks on a fairly large scale. We used the GATE/ANNIE toolkit to identify entities of types *Location*, *Person* and *Organization* in the corpus, and were able to automatically extract over 1.2 million annotations as InfoUnits. Entity annotation was time-consuming, forcing us to limit our experimental evaluation to a relatively small corpus.

However, while extraction may be a bottleneck in an academic setting, this process can be parallelized, and can be done on a large scale if enough hardware is available.

As the next step we group together InfoUnits that refer to the same real-life entity. For example, we would unify two occurrences of the same string (e.g. "Michael Jordan") into a single entity. We also attempt to identify InfoUnits that do not match literally, but are nonetheless likely to refer to the same real-life entity, e.g. "Michael Jordan" and "Mike Jordan". We rely on a combination of heuristics to identify groups of InfoUnits with high degree of string similarity. We consider strings that are at least 4 characters in length, and that match according to the SecondString[Cohen *et al.*, 2003] JaroWinkler-TFIDF metric, with a similarity of at least 0.95 out of 1.0. Additionally, we use the highly-accurate *means* relationship in YAGO [Suchanek *et al.*, 2007] to identify pairs of synonymous strings. Using these simple and efficient heuristics we map 1.2 million InfoUnits to 240 thousand entities.

Finally, we use the same string-based heuristics to map discovered entities to nodes in YAGO. If an entity maps to one or several nodes in the ontology, we add the appropriate mapping edges to the `GDG` (these are the solid arrows from InfoUnits to ontology nodes in Figure 4.1). If no node in the Onto Graph is identified as a target for mapping, we add discovered entities to the OntoGraph, placing them directly under *Person*, *Organization* or *Location*.

During the initial stages of this project, we considered more sophisticated (and less restrictive) ways of grouping together similar InfoUnits and of mapping such groups to ontology nodes. We eventually found that these techniques introduced a considerable amount of noise, causing topic drift. We conclude that more sophisticated context-aware tools are required to reliably match strings that do not pass the 0.95 similarity threshold. Using such tools (once they become available and are efficient enough to operate on the large scale) would benefit our method.

4.4.2 Query Processing

Our system processes keyword queries, and returns both pages and entities as query results. In this work we focus primarily on the construction of the data graph and on ranking, not on query processing, and we use a simple query processing method in our prototype implementation.

We store the Generalized Data Graph in an Oracle 10g RDBMS, and use Oracle Text to identify relevant pages and entities at query time. Matches are identified using a tf-idf-based algorithm that incorporates stemming and word proximity information. Relevant entries receive a non-zero relevance score from Oracle, and we normalize this score to the $(0, 1]$ range.

A page is considered relevant to a query if its body contains all words present in the query. The final score of a page is the product of its authority and relevance scores.

We identify entities that are relevant to a query using the OntoGraph built from YAGO. An entity is considered relevant to a query if at least one of the following conditions is met:

- The entity matches the query by name;
- The entity has strong string similarity with an ontology node that matches the query;
- The *thematic neighborhood* of the entity matches the query. Thematic neighborhoods are formed by combining all parents of an entity or concept, i.e. by following *is-a* and *instance-of* ontology edges.

Consider for example the Serbian basketball player Vlade Divac. YAGO assigns Vlade to several categories, including *Serbian basketball players*, *LA Lakers players*, and *Olympic competitors for Yugoslavia*. Vlade's thematic neighborhood includes all these category names. For this reason the entity *Vlade Divac* will be returned as a match for queries like "Serbian LA Lakers players" and "Olympic basketball competitors". Relevant entities are ranked according to their authority scores; the relevance score of the query with respect to the thematic neighborhood is discarded.

The identified relevant pages and entities are added to the Query Result Graph. The graph is then expanded by including predecessors and successors. The entire `QRG` is used for ranking, but only the relevant pages and entities are returned as the query result.

4.5 Experimental Evaluation

4.5.1 Experimental Setup

We evaluate the performance of our system on a subset of the English-language Wikipedia; we focus on two thematic slices: *Serbia* and *basketball*. Pages were included into the respective slice based on whether they contain the words "Serbia" and "basketball". The slices are comparable in size, and together include about 7800 Wikipedia articles.

We selected 20 keyword queries, 10 queries per slice, for our experimental evaluation. Queries ranged between 1 and 6 words in length. Some examples of queries are *lake*, *politician*, *physics*, *living writer prize winner* on the *Serbia* slice, and *NBA venue*, *college basketball*, *African American basketball player Olympic competitor* on the *basketball* slice. Queries were selected so as to have non-trivial recall in the ontology with respect to the slice: query terms had to match thematic neighborhoods of at least a few ontology nodes relevant to the slice. We allowed for significant variation in ontology recall: for some queries, hundreds of ontology nodes matched, while for others there were only a handful of matches. In the most extreme case, only one ontology node matched the query.

We compare four ranking methods in our experiments: one query-independent and three that re-rank results at query time. These are query-independent PageRank (PR) for pages,

and the corresponding Page-Inherited Authority (PIA) for entities. Query-time re-ranking methods include Un-Typed Authority with PageRank (UTA-PR) and with HITS (UTA-HITS), and Entity-Derived Authority (EVA). We consider top-20 pages and top-20 entities returned by each ranking method in our evaluation.

For a given query, top-ranking results were collected and pooled. The quality of each result was then evaluated by two of the co-authors of this work. Evaluators had no knowledge either of the method that retrieved the result, or of the result's rank. We used a simple *goodness* metric, a value between 0 and 2, in our evaluation, and averaged the goodness scores if there was disagreement. Goodness scores were assigned as follows: 0 for irrelevant, 1 for somewhat relevant or relevant but not very important, and 2 for very relevant. To judge goodness of an entity, the evaluator was asked to identify a Wikipedia page that was most relevant to the entity, and use the contents of the page to guide the evaluation. We also considered using a combination of metrics, such as coverage and specificity, to evaluate the results. However, these metrics were designed with documents (or parts of documents) in mind, and it was not clear how to apply them to entities and concepts.

We use four metrics to assess the performance of the ranking methods: discounted cumulated gain (*DCG*) [Järvelin and Kekäläinen, 2002], normalized discounted cumulated gain (*NDCG*) [Järvelin and Kekäläinen, 2002], precision, and recall. All metrics were applied at top-20. DCG and NDCG are described in detail in Section 1.1.3.2. Recall that DCG is a cumulative metric that weighs goodness scores by rank, penalizing entries that appear at later ranks. NDCG is an average metric that normalizes each entry in the DCG vector by the corresponding value in the ideal vector. We report DCG in addition to NDCG because it incorporates recall (a low-recall method may have a perfect NDCG score, but it will not have a perfect DCG score). As suggested in [Järvelin and Kekäläinen, 2002], we use $b = 2$ as the discount factor. For recall, we consider an entry to be relevant to a query if at least one of the two evaluators considered the entry relevant (goodness score ≥ 0.5). Precision is calculated with respect to the ideal: we pool together the relevant entries retrieved by all methods, order them by descending goodness scores, and calculate recall at top-20. Precision of a ranking method is then calculated as $recall_{method}/recall_{ideal}$.

4.5.2 Results and Discussion

Results of our experimental evaluation are summarized in Tables 4.1 and 4.2. All methods that involve query-time re-ranking operate on the Query Result Graph: a query-dependent subset of the Generalized Data Graph. Each entry represents an average among 20 queries in our experiments. We view results obtained by query-independent PageRank (*PR* entry in Table 4.2) as the base-line for our experiments. Note that NDCG, precision, and recall are normalized, and that perfect DCG is 15.63 in our setting.

We make the following observations from these results.

Method	DCG	NDCG	Recall	Precision
PIA	12.73	0.91	0.88	0.97
UTA-PR	12.67	0.91	0.88	0.96
UTA-HITS	11.17	0.78	0.82	0.91
EVA	11.95	0.86	0.90	0.99

Table 4.1: Ranking on entities.

Method	DCG	NDCG	Recall	Precision
PR	4.14	0.34	0.42	0.59
UTA-PR	2.90	0.26	0.35	0.53
UTA-HITS	2.62	0.24	0.30	0.47
EVA	7.61	0.60	0.67	0.89

Table 4.2: Ranking on pages.

- For the chosen queries, the set of highly ranked entities consistently and significantly outperforms highly ranked pages, according to all used metrics.
- EVA significantly outperforms other methods according to all metrics with respect to highly ranked pages.
- No conclusion can be drawn about the relative performance of ranking methods with respect to entities. All methods produce high-quality results.

Wikipedia contains a significant number of hubs (list pages that link to pages relevant to a topic) and super-authorities (e.g. country and major city pages). Such pages attain high query-independent PageRank scores, and appear in very high ranks in response to most queries. So, for the query *basketball* on the *Serbia* slice, query-independent PageRank returns the following pages in the top-20: "1977", "1990s", "Greece", and "Belgrade". Re-ranking on the combined page-entity graph with *UTA* leads to page matches that still have high global authority, but are more focused on the query: "List of athletes by nickname", "August 2004 in sports", and even a high-quality match "Basketball at the 2004 Summer Olympics (team squads)". Re-ranking with *EVA* returns pages that are very specific both to the query and to the slice: "Basketball in Yugoslavia", "Vlade Divac", "Basketball World Championship" and "National pastime". Entity matches are even better, and include "Michael Jordan", "LA Lakers", "NBA", "Madison Square Garden", "Belgrade Arena", and "Predrag Danilovic". The name "Vlade Divac" was not recognized by GATE, and we miss out on an entity that corresponds to this Serbian national hero in the top-20.

Our novel ranking technique, *EVA*, is not realizing its full potential when ranking on entities, most importantly because our current extraction and mapping techniques do not

allow us to include inter-entity edges into the QRG, limiting the flow of authority, particularly for entities.

The choice of relatively small thematic slices for our experiments makes the size of the Generalized Web Graph more manageable, but confines us to working with only a small subset of the ontology, limiting the recall of entity-based methods in some cases. For example, the query "orthodox monastery" on the *Serbia* slice was able to identify a single entity as a match – the monastery Hilandar. This happened because the ontology contained a limited amount of information relevant both to the query and to the thematic slice. The situation was further aggravated by the fact that the GATE/ANNIE Toolkit was not very successful when mining foreign-language names, and so many InfoUnits that could have been matched to relevant Onto Graph nodes went unnoticed.

4.6 Related Work

Link Analysis: Link analysis has come a long way since the seminal articles by Kleinberg [Kleinberg, 1999] and Page et al. [Page *et al.*, 1998] were published. These early approaches and their extensions, overviews of which are given in [Borodin *et al.*, 2005; Langville and Meyer, 2004], are based on a simple directed graph model. More sophisticated (e.g., weighted, multi-type, and labeled) graph models were considered in [Bhalotia *et al.*, 2002; Chitrapura and Kashyap, 2004; Geerts *et al.*, 2004; Guo *et al.*, 2003; Xi *et al.*, 2004]. More recently, the paradigm of link analysis has been carried over to graphs other than the Web graph, namely, relational databases with records and foreign-key relationships constituting the nodes and edges of the graph, and entity-relationship graphs that capture, for example, bibliographic data such as DBLP or Citeseer. Such settings have led to new forms of ObjectRank, PopRank, or EntityRank measures [Anyanwu *et al.*, 2005; Balmin *et al.*, 2004; Chakrabarti, 2007; Cheng and Chang, 2007; Nie *et al.*, 2005]. ObjectRank [Balmin *et al.*, 2004] resembles our approach because it is also inspired by HITS, but it does not address Web data at all. EntityRank [Cheng and Chang, 2007] addresses the ranking of entities extracted from Web pages, but its focus is on frequency-based content strength and it does not consider the graph structure of the Web and its embedded entities. PopRank [Nie *et al.*, 2005] is closest to our framework; it uses a "random object finder" model on an object-relationship graph and combines this with a prior popularity derived from pages' PageRank values (the latter is similar to our PIA method). Our approach is more powerful because we treat both pages and entities as first-class citizens in ranking, and because we also consider ontological relationships and confidence values from extraction and disambiguation.

Entity Search: Searching the Web at the finer and semantically more expressive granularity of entities (Web objects) and their relationships, instead of the coarser page granularity prevalent today, has been pursued in different variants like faceted search,

vertical search, object search, and entity-relationship search (e.g., [Chakrabarti, 2004; Chang, 2006; Doan *et al.*, 2006a; Hearst, 2006; Madhavan *et al.*, 2007; Nie *et al.*, 2005]. The approaches most closely related to our work are the Libra system [Nie *et al.*, 2007; Nie *et al.*, 2005], the EntitySearch engine [Cheng and Chang, 2007], and the ExDB system [Cafarella *et al.*, 2007]. All three systems extract entities and relations from Web data and provide ranked retrieval. Libra uses a variety of techniques for ranking, including the PopRank model mentioned above and a record-level statistical language model; the EntitySearch engine mostly relies on occurrence-frequency statistics; ExDB factors extraction confidence values into its ranking but does not consider any link information. None of these ranking models considers the mutual authority propagation between entities and pages that we exploit in our Generalized Data Graph.

4.7 Conclusions

In this chapter we developed an entity-aware ranking framework, and presented a novel ranking algorithm, EntityAuthority, that models the mutual reinforcement between pages and entities. We demonstrated how an ontology can be used for query processing and ranking in this setting. We presented a prototype implementation of our system, and experimentally demonstrated the improvement in query result quality.

EntityAuthority is an example of a search and ranking framework that can be used in a heterogeneous setting, where relevance and quality of a result is determined based on ontological relationships, link structure of page graph, etc. Techniques of this chapter may be combined with the similarity measures of Chapter 3, making the ontology-based portion of the ranking more sophisticated in presence of a scoped polyhierarchy. For example, an iterative authority propagation mechanism may be developed for PubMed, in which scores of documents would be initialized with similarity scores of Chapter 3, and documents and MeSH terms would then be re-ranked with EntityAuthority. Such re-ranking would operate over a linked graph of documents, with semantics of the links capturing the semantics of quality, or authority. For example, links between documents may be established based on co-authorship, citations, publication venues, or authors' affiliations.

Chapter 5

Rank-Aware Clustering of Structured Datasets

This chapter presents joint work with Sihem Amer-Yahia [Stoyanovich and Amer-Yahia, 2009]. We would like to thank Duncan Watts and Jake Hofman for their help and valuable discussions.

5.1 Introduction

In Chapter 2 we explored how *semantics of social connections* may be used for information discovery. In Chapters 3 and 4 we considered how *semantics of an ontology* may be used for search and ranking. In the present chapter we explore how *semantic relationships among item attributes* may be used for rank-aware information discovery.

In online applications that involve large structured datasets, such as *Yahoo! Personals* and *Trulia.com*, there are often thousands of high-quality items, in this case, persons and apartments, that satisfy a user's information need. Users typically specify a structured target profile in the form of attribute-value pairs, and this profile is then used by the system to *filter* items. On dating sites, a target profile may specify the age, height, income, education, political affiliation, and religion of a potential match. In real estate applications, a profile describes a user's dream home by its location, size, and number of bedrooms. The number of matches to a specific profile is often very high, making *data exploration* an interesting challenge.

Typically users also specify ranking criteria that are used to *rank* matches. For example, in *Yahoo! Personals*, potential matches can be ranked by decreasing income or increasing age, while in *Trulia.com*, available houses may be ranked by increasing price or decreasing size. Ranking helps users navigate the set of results by limiting the number of items that they see at any one time, and by making sure that the items users see first are of high quality (according to the ranking criteria). However, ranking also brings the disadvantage

of *match homogeneity*: the user is often required to go through a large number of similar items before finding the next different item. This is illustrated in the following fictional example inspired by *Yahoo! Personals*.

Example 5.1.1 *User* Mike *is looking for a date.* Mike *specifies that he is interested in women who are 20 to 30 years old and who have some college education, and requests that results be sorted on income in descending order. When inspecting the results,* Mike *notices that the top ranks are dominated by women in their late-twenties with a Master's degree. It takes* Mike *a while to scroll down to* the next set of matches *that are different from the top-ranking ones. In doing so, he skips over some unexpected cases such as younger women with higher education and income levels, or women with high income who did not graduate from college. After additional data exploration,* Mike *realizes that there is a* correlation *between age, education (filtering), and income (ranking). Such correlations would have been obvious if data were presented in* labeled groups *such as* `[20-24] year-olds with a bachelor's degree`, `[25-30] year-olds who make more than 75K`, *etc.*

A key point that arises from this example is that a user who is browsing a result set sequentially, item by item, is only able to infer some trends and correlations in the data after seeing a significant number of items. Sequential presentation is not very helpful if the user is trying to understand general properties of a dataset, i.e., explore the data, particularly if the dataset is large.

The complexity of manual data exploration increases with more sophisticated ranking. For example, *Mike*'s profile could provide a custom scoring function that computes a score which is inversely proportional to the distance from his geographic location to the location of his match, and directly proportional to the match's income. Helping the users better understand the results, which enables easier navigation and profile refinement, is even more important in this case, given that correlations between item attributes and the ranking function are less obvious.

5.1.1 Motivating User Study

In order to better understand the challenges of ranked data exploration, we interviewed six potential users. All users were male, and they were all members of *Yahoo! Research*. Users were asked to specify a realistic *Yahoo! Personals* profile, and to discuss their data exploration experience with us during the course of the interview. We conducted free-form interviews and did not use a questionnaire so as not to influence the users' statements by a limited menu of options. Users were allowed to select among a pre-specified set of ranking attributes.

User profiles were evaluated by our prototype implementation, against the *Yahoo! Personals* dataset. Profile matches were presented in two ways: *ranked list* and *clustered items*.

Three users were shown the *ranked list* first, followed by *clustered items*; the order was reversed for the other three users.

As the users were interacting with the *ranked list* interface, they noted that *results are homogeneous*: there was little variation in attribute values among top-ranked items. As a result, item attributes were ignored by most users, and the decision of whether to further explore a particular profile was based solely on the photo. All six users explicitly stated result homogeneity as a concern. The other key observation was that *ranking is opaque*. Indeed, item ordering was not considered helpful in data exploration and was not well-understood by some users. Even for single-attribute ranking, some users wanted to see items with a variety of values for the ranking attribute. Two users explicitly stated this limitation.

During their interaction with the *clustered items* interface users noted that *diverse results were more easily accessible*, and that *clustered items* helped them *refine their search preferences*. Three out of six users decided to refine their query moments after seeing clusters of results. Two of the three explicitly commented that the presentation enabled them to quickly understand the result set and to refine their query more effectively.

5.1.2 Limitations of Clustering Algorithms

Clustering is an effective data exploration method that is applicable to structured, semistructured, and unstructured data alike. Clustering algorithms assign N items to $K \ll N$ groups, where K is either known in advance or discovered by the algorithm. To be useful for data exploration, the algorithm must produce *meaningful descriptions* for the clusters. There are many families of clustering algorithms that can be used for this task. Some algorithms partition the dataset, while others assign each point to zero, one, or several clusters. Some algorithms operate over all item attributes, while others attempt *dimensionality reduction* techniques. In domains like *Yahoo! Personals*, where datasets are large and all items are described by a large number of attributes, it is intuitive to use *subspace clustering*.

Subspace clustering is an extension of traditional clustering that seeks to find clusters in different subspaces of a dataset [Parsons *et al.*, 2004]. Clusters of items are *high-quality* regions identified in multiple, possibly overlapping, subspaces. Many subspace clustering algorithms use the *density of a region* as a quality measure. In the simplest case, density is a percentage of data points that fall within a particular region, and the algorithm aims to find all regions that have density higher than a pre-defined threshold. We give an overview of one of the first subspace clustering algorithms, CLIQUE [Agrawal *et al.*, 1998], in Section 5.3.1, and we illustrate it here with an example.

Example 5.1.2 *Consider a fictional real estate example in Table 5.1: a database of 300 rental apartments, listing the number of bedrooms, number of bathrooms, size in ft^2, monthly rental price, and the number of such apartments currently on the market.* Mary *is looking*

# beds	# baths	size (ft^2)	price ($)	# apts
1	1	600	1800	5
	1.5	700	2100	55
	1	750	2900	25
2	1.5	700	2200	30
	1	800	2400	60
	2	800	2850	10
	2	950	3500	100
3	1.5	950	2900	5
	2	1000	3200	10

Table 5.1: A fictional real estate database.

for an apartment that is at least 600-ft^2 in size and has at least one bedroom, and she wants the matches sorted on price in increasing order. All apartments in Table 5.1 match Mary*'s profile.*

Assume a density threshold $\theta = 0.1$. A typical density-based subspace clustering algorithm starts by dividing the range of values along each dimension (attribute) into cells, and by computing the density in each cell. For example, each distinct value of `#beds`, `size`, and `#baths` may correspond to a cell, and `price` may be broken down into intervals $(1500, 2000]$, $(2000, 2500]$, $(2500, 3000]$, and $(3000, 3500]$. Cells that do not pass the density threshold are pruned at this stage. The algorithm immediately prunes 600-ft^2 apartments ($\frac{5}{300} < \theta$), 750-ft^2 apartments ($\frac{25}{300} < \theta$), 1000-ft^2 apartments ($\frac{10}{300} < \theta$), and apartments in the $(1500, 2000]$ price range ($\frac{5}{300} < \theta$). Given *Mary*'s interest in cheaper apartments (price is her ranking condition), it is problematic that the cheapest apartments in the dataset, the 600-ft^2 apartments that cost \$1800, are pruned.

Next, the algorithm progressively explores clusters in higher dimensions by *joining* lower-dimensional ones. For example, the 1-dimensional cluster of 800-ft^2 apartments (70 items) can be joined with the 1-dimensional cluster of apartments in the $(2000, 2500]$ price range (145 items). The result of this join is a region with 60 800-ft^2 2-bedrooms at \$2400 per month, which qualifies as a cluster since it passes the density threshold. However, the region that results from joining the 950-ft^2 apartments (105 items) with apartments in the $(2500, 3000]$ price range (40 items) does not qualify as a cluster (it contains only 5 items) and is pruned, losing the potentially interesting 3-bedrooms for a relatively low price (\$2900). Density decreases in higher dimensions and the algorithm stops when there are no more clusters to explore.

5.1.3 Challenges of Rank-Aware Clustering

A lower density threshold would evidently guarantee that some of the regions pruned using a higher threshold would be preserved. However, if the threshold is set too low, the algorithm would keep merging neighboring cells, ultimately identifying much larger clusters, and possibly one cluster containing the entire dataset. Moreover, not all regions that pass a typical clustering *quality metric*, e.g., density or entropy, are equally interesting to the user. Indeed, given a scoring function, some items, and hence some clusters, are more desirable than others (e.g., *Mary* has little interest in the 2-bedroom apartments that cost $3500, but would like to see the 1-bedrooms that cost $1800). Even when the density of a region is high, as is the case with 2-bedroom apartments for $3500, *Mary* would probably have less interest in them than in cheaper apartments. Therefore, we propose to explore *rank-aware clustering quality measures* which account for item scores and ranks in assessing cluster quality.

5.1.4 Chapter Outline

In the remainder of this chapter we present **BARAC**: a **B**ottom-up **A**lgorithm for **R**ank-**A**ware **C**lustering of structured datasets. We start by formalizing new clustering quality measures for rank-aware data exploration in Section 5.2, and develop an adaptation of a bottom-up APRIORI-style subspace clustering algorithm for this setting in Section 5.3. In Section 5.4 we present an extensive evaluation of the efficiency of **BARAC** on datasets from *Yahoo! Personals*, and show that our algorithm is efficient and scalable. We experimentally validate the effectiveness of our approach in Section 5.5, using both qualitative analysis, and results of a large-scale user study with a subset of *Yahoo! Personals* users.

5.2 Formalism

In this section we formalize rank-aware data exploration for structured datasets. We start by introducing the notion of a clustering quality measure, and then give the problem statement.

5.2.1 Regions and Clusters

We are given a dataset $\mathcal{D}$ where items are described by attribute-value pairs, including a special attribute *id* which uniquely identifies each item. Attributes belong to a set $\mathcal{A}$.

Definition 5.2.1 (Regions) *A region $\mathcal{G}$ is a set of items labeled with a conjunction of predicates over attributes in $\mathcal{A}$, which, if evaluated on the dataset $\mathcal{D}$, results in all items in the region. The dimensionality of a region is simply the number of predicates that describe that region.*

A predicate specifies a value, or a range of values, for an attributes. Note that a region may be described by the predicate $P = \top$, in which case it evaluates to the entire dataset.

The predicates that describe a region are the *region description*. We will often use *region* and *region description* interchangeably. The following conjunction of predicates specifies a two-dimensional region:

$$\mathcal{G} : age \in [25, 30] \wedge education = Bachelor's$$

Any subset of predicates that define a region $\mathcal{G}$ is a *sub-region* of $\mathcal{G}$ ($\mathcal{G}$ is a *super-region* of its sub-regions.) A *cluster* is a region that satisfies a *clustering quality measure*.

Definition 5.2.2 (Clustering Quality Measure) *A clustering quality measure $\mathcal{Q}$ is a predicate over the distribution of items in a* region *$\mathcal{G}$ that makes $\mathcal{G}$ interesting to a user for the purpose of data exploration.*

In this chapter we consider clustering quality measures that compare some statistic associated with the region to a threshold θ. Let us now give some examples of measures that were developed in data mining. Given a region $\mathcal{G} = P_1 \wedge \ldots \wedge P_n$, we denote by $p(P_i)$ the proportion of items satisfying P_i with respect to the entire dataset $\mathcal{D}$, i.e. $|P_i|/|\mathcal{D}|$.

A clustering quality measure may be stated with respect to the number of items in the region, as is the case with the *density measure* in CLIQUE [Agrawal *et al.*, 1998], e.g., "a cluster is a region that contains at least θ% of the total number of items":

$$\mathcal{Q}_{DENSE} : p(\mathcal{G}) \geq \theta \tag{5.1}$$

A clustering quality measure may encode *attribute correlation*,[1] i.e., higher-than-expected density of points, where the fraction of the observed number of items to the expected number is compared to a threshold θ.

$$\mathcal{Q}_{CORR} : \frac{p(P_1 \wedge \ldots \wedge P_n)}{p(P_1) \times \ldots \times p(P_n)} \geq \theta \tag{5.2}$$

A clustering quality measure may specify *entropy*, with the intuition that regions with lower entropy have higher density and higher attribute correlation, as was shown in ENCLUS [Cheng *et al.*, 1999]:

$$\mathcal{Q}_{ENT} : H(\mathcal{G}) = H(P_1, \ldots P_n) \leq \theta \tag{5.3}$$

Given a dataset $\mathcal{D}$, a clustering algorithm returns a set of regions that satisfy a clustering quality measure.

[1] Here and in the remainder of this chapter we use "correlation" loosely, in the sense of "departure from independence" (`http://en.wikipedia.org/wiki/Correlation`); we do not account for the direction of the relationship between random variables.

5.2.2 Rank-Aware Clusters

In an on-line data exploration scenario, a user specifies a profile composed of filtering and ranking criteria. We assume that the user's filtering conditions result in a dataset $\mathcal{D}$ (and can thus take users out of the notation since we are interested in one user at a time). Ranking is expressed by a scoring function $\mathcal{S}$ that assigns a score $i.score$ to each item $i \in \mathcal{D}$. We denote by $\mathcal{S}(\mathcal{D})$ the set of all items from $\mathcal{D}$ augmented with $i.score$. Typically, items are presented to the user as a single ranked list sorted by score.

We first argue that rank-unaware clustering measures (see Section 5.2.1) are inappropriate when users are interested in exploring ranked datasets.

Example 5.2.1 *Consider user* Mary *from Example 5.1.2.* Mary *is interested in seeing apartments ranked by price in increasing order.* Ann*, another user who shares* Mary*'s filtering conditions, may be interested in seeing the same apartments sorted by size in decreasing order. Which clusters are best for which user depends on the user's ranking preferences. One reasonable option is to cluster apartments based on the scoring attribute. In particular,* Ann *may appreciate seeing the 950-ft^2 apartments which cost \$2900 in the same cluster as the same-size apartments for \$3500, while* Mary *may prefer to see 950-ft^2 apartments grouped together with the same-priced 750-ft^2 apartments. A subspace clustering measure that does not account for item scores would not distinguish between these two users, and would therefore be inappropriate for rank-aware data exploration.*

The score of each item can be treated as an additional attribute and can thus be used for clustering. Items can be clustered using a quality measure of the kind described in Section 5.2.1. However, as we argue in the following example, using scores as an additional clustering dimension still fails to effectively address data exploration for ranked datasets.

Example 5.2.2 *Consider again Example 5.1.2, where* Mary *wants to sort apartments by price. If item price is used as a clustering dimension, in the same way as other attributes, then* Mary *may see a high number of clusters, not all of which are of potential interest to her: e.g. a cluster of expensive 2-bedroom apartments may appear alongside a cluster of cheap 2-bedrooms. If many clusters are discovered by the algorithm, the potentially more interesting ones may go unnoticed. Worse yet, the algorithm may decide to merge together intervals that are of high interest to* Mary *with those of low interest, resulting in a potentially large heterogeneous cluster with homogeneous results dominating the top ranks.*

Hence, we explore new clustering quality measures that use item scores and ranks to assess region quality.

Definition 5.2.3 (Rank-Aware Clustering Quality) *A rank-aware clustering quality measure is a predicate over $\mathcal{S}(\mathcal{G})$ for a region $\mathcal{G}$ and a scoring function $\mathcal{S}$.*

Here, $\mathcal{S}(\mathcal{G})$ denotes the set of all items from $\mathcal{G}$ augmented with $i.score$. We explore different types of rank-aware quality measures, building on the assumption that users are more interested in clusters that contain items with high scores, and that they will only explore the best items in those clusters. We use $\mathcal{S}(\mathcal{G}, N)$ to denote N highest scoring items in $\mathcal{S}(\mathcal{G})$. N is a parameter in our formalism that models the user's *attention span* – the number of items the user is likely to explore sequentially [Manber *et al.*, 2000]. This parameter can be customized per user, or it can be set to reflect the preferences of an average user.

The first measure, $\mathcal{Q}_{topN}$, states that a multi-dimensional region $\mathcal{G}$ is a cluster if it contains enough items that are in the top-N of each of its one-dimensional sub-regions.

$$\mathcal{Q}_{topN} : \frac{|\mathcal{S}(\mathcal{G}, N) \cap \mathcal{S}(P_1, N) \cap \ldots \cap \mathcal{S}(P_m, N)|}{|N|} \geq \theta \tag{5.4}$$

$\mathcal{Q}_{topN}$ aims to discover attribute correlations among the high-scoring items in the dataset. We illustrate how this measure compares to density using Example 5.1.2. Recall that user *Mary* specified price as the ranking condition.

The join of the 700-ft^2 cluster with the $(2000, 2500]$ price range cluster preserves the lower-priced 1-bedrooms, since the top-N items in the join correspond to the high-scoring items in the $(2000, 2500]$ cluster (one of the sub-regions) and to the high-scoring items in the 700-ft^2 cluster (its other sub-region). On the other hand, the join of 2-bathroom apartments with 950-ft^2 apartments would not contain any of the cheapest 2-bathroom apartments in its top-N and would thus not qualify as a cluster.

$\mathcal{Q}_{topN}$ is a generalization of density from CLIQUE [Agrawal *et al.*, 1998], where N is substituted by $|\mathcal{D}|$, making the numerator equal to $|\mathcal{S}(\mathcal{G})|$, or simply $|\mathcal{G}|$.

The next measure, $\mathcal{Q}_{SCORE}$, states that a region is interesting if it contains high-scoring items in its top-N. $\mathcal{G}$ will have the highest-scoring items in its top-N if the same high-scoring items are present in the top-N lists of all of its one-dimensional sub-regions $P_1 \ldots P_k$. In the best case, the top-N of the intersection of these regions will coincide with the top-N of their union, which gives rise to the formula:

$$\mathcal{Q}_{SCORE} : \frac{\Sigma_{i \in \mathcal{S}(\mathcal{G}, N)} i.score}{\Sigma_{i \in \mathcal{S}(\cup_k P_k, N)} i.score} \geq \theta \tag{5.5}$$

$\mathcal{Q}_{SCORE}$ can be used to compare regions with a different number of items in their top-N lists: a region with few high-scoring items in the top-N may be of equal interest to the user as one with many lower-scoring items. Suppose that *Mary*'s scoring function is $\mathcal{S}_{Mary} : i.score = \frac{3500 - i.price}{3500 - 1800}$. Then, under $\mathcal{Q}_{SCORE}$, the region formed by the five 600-ft^2 1-bedrooms has a quality score of five and is more interesting than the region formed by the ten 1000-ft^2 3-bedrooms with a score of 1.76.

Finally, we present a measure that models the relationship between item scores and ranks. The intuition is that a region with exceptionally high-scoring items in high ranks

may be just as interesting to the user as a region in which items have intermediate scores. We define this measure using NDCG (Normalized Discounted Cumulated Gain) [Järvelin and Kekäläinen, 2002], with $\mathcal{S}(\cup_k P_k, N)$ as the ideal vector. NDCG is described in detail in Section 1.1.3.2.

$$\mathcal{Q}_{SCORE\&RANK} : AVG_{r \leq N} NDCG(\mathcal{S}(\mathcal{G}, N), \mathcal{S}(\cup_k P_k, N))[r] \tag{5.6}$$

Consider again Example 5.1.2 and *Mary*'s scoring function $\mathcal{S}_{Mary}$, and let us take $N = 5$. Let us compute the NDCG for the 1.5-bathroom apartments with the size of 950-ft^2. The ideal gain vector consists of scores of the 5 best items that either have 1.5 bathrooms or are 950-ft^2 in size, namely, the 1.5-bath 700-ft^2 apartments that cost \$2100 per month ($i.score = 0.82$). With $b = 2$ we derive: DCG_{Ideal} = [0.82 1.64 1.55 1.64 1.77].

Let us now compute the NDCG for the 950-ft^2 1.5-bath apartments. The top-5 list of this region consists of five 3-bedroom apartments at \$2900 ($i.score = 0.35$). We derive DCG = [0.35 0.7 0.66 0.7 0.75]. We now normalize each position in DCG by the corresponding position in DCG_{Ideal}, average the values, and arrive at $NDCG = 0.43$.

5.2.3 Problem Statement

Definition 5.2.4 (Rank-Aware Clustering) *Given a dataset $\mathcal{D}$, a scoring function S, a rank-aware clustering quality measure $\mathcal{Q}$ and an integer N,* find all clusters *in $\mathcal{D}$, i.e., regions of any dimensionality that satisfy $\mathcal{Q}$.*

5.3 Rank-Aware Subspace Clustering

In this section, we give a brief overview of subspace clustering, formalize properties of our rank-aware subspace clustering algorithm, and finally present the algorithm.

5.3.1 Overview of Subspace Clusterings

We now give a general description of density-based bottom-up subspace clustering algorithms. The reader is referred to [Parsons *et al.*, 2004; Kriegel *et al.*, 2008] for comprehensive surveys.

Subspace clustering is a feature selection technique that aims to uncover structure in high-dimensional datasets [Parsons *et al.*, 2004]. Unlike Principal Component Analysis (PCA), where the goal is to identify the single best subset of features in which the dataset is then clustered, subspace clustering looks for multiple, possibly overlapping, subsets of features that are used to cluster different portions of the dataset.

Subspace clustering algorithms use several related quality measures, also referred to as clustering objectives, to guide the search. CLIQUE [Agrawal *et al.*, 1998], one of the first algorithms in this family, relies on a global notion of *density*, which is simply the

percentage of the overall dataset that falls within a particular region. A later algorithm, ENCLUS [Cheng *et al.*, 1999], uses information entropy as the clustering objective.

CLIQUE operates in three steps to which we refer as **BuildGrid**, **Merge** and **Join**.

1. **BuildGrid** builds a histogram in each dimension, counting the number of points that fall within each bucket. For example, if the dimension is *age*, the outcome of this phase is a set of non-overlapping age intervals and the number of matches in each interval.

2. **Merge** neighboring histogram buckets (within the same dimension) that pass the density threshold; discard buckets that do not pass the threshold.

3. **Join** dimensions APRIORI-style. This step computes clusters in higher dimensions by joining lower-dimensional clusters (e.g., $age \in [25-30]$ with $income \in [50K-80K]$), and only keeping higher-dimensional clusters that pass the density threshold. This step relies on the *downward closure* property of the clustering quality metric to prune the search space.

Several extensions of the original algorithm were developed: MAFIA [Nagesh, 1999] creates an adaptive grid that takes into account the data distribution, CLTree [Liu *et al.*, 2000] uses a decision-tree approach to identify high-density regions, while Cell-Based Clustering (CBF) [Chang and Jin, 2002] improves scalability by partitioning the data so as to produce fewer clusters.

5.3.2 Algorithm Properties

The **Merge** phase of our algorithm is different from the corresponding phase of density-based algorithms, and it relies on the notion of interval dominance with respect to a scoring function.

Definition 5.3.1 (Interval Dominance) *Given a scoring function $\mathcal{S}$, an integer N, an attribute a_i, and any two consecutive value intervals $\mathcal{I}_1$ and $\mathcal{I}_2$ in the set of values from domain(a_i), we say that $\mathcal{I}_1$* dominates *$\mathcal{I}_2$ with respect to $\mathcal{S}$ at top-N if and only if $\mathcal{S}(\mathcal{I}_1, N) = \mathcal{S}(\mathcal{I}_1 + \mathcal{I}_2, N)$. We denote this as $\mathcal{I}_1 \prec_{S,N} \mathcal{I}_2$.*

Here, $+$ is simply the concatenation of two consecutive intervals. The intuition is that the top-N items from the dominating interval are strictly better, with respect to the scoring function $\mathcal{S}$, than the items in the the top-N of the dominated interval. For example, if S ranks items in increasing order of age, then $\mathcal{I}_1 : age \in [25, 29]$ dominates $\mathcal{I}_2 : age \in [30, 34]$.

We refine this definition further. We say that $\mathcal{I}_1$ *dominates* $\mathcal{I}_2$ up-to a factor $\theta \in (0.5, 1]$, with respect to $\mathcal{S}$ at top-N if and only if

$$\frac{|\mathcal{S}(\mathcal{I}_1, N) \cap \mathcal{S}(\mathcal{I}_1 + \mathcal{I}_2, N)|}{N} \geq \theta$$

We denote this by $\mathcal{I}_1 \prec_{S,N,\theta} \mathcal{I}_2$.

Consider again the intervals $\mathcal{I}_1 : age \in [25, 29]$ and $\mathcal{I}_2 : age \in [30, 34]$, and a scoring function that orders items on a combination of income and education: $\mathcal{S} = 0.25 * income + 0.75 * education$ (higher values of attributes *income* and *education* correspond to higher income and education levels, respectively). Because age positively correlates with income and with education, it is likely that $\mathcal{I}_1 \prec_{S,N=10,\theta=0.75} \mathcal{I}_2$.

We are interested in bottom-up clustering algorithms which build clusters in higher dimensions from lower-dimensional clusters. Such algorithms rely on the *downward closure* property, which allows for pruning of the search space, resulting in better runtime performance.

Definition 5.3.2 (Downward Closure) *We say that* downward closure *holds for a clustering quality metric $\mathcal{Q}$ if and only if, for any region $\mathcal{G}$, if $\mathcal{Q}$ holds over $\mathcal{G}$, then it also holds over every sub-region of $\mathcal{G}$.*

The fact that downward closure holds for $\mathcal{Q}_{topN}$ follows directly from the definition of $\mathcal{Q}_{topN}$ and from set properties, namely, that $|A \cap B| \leq min(|A|, |B|)$. For a one-dimensional group P_k with N or more items, $\mathcal{Q}_{topN} = 1$. As dimensionality of the group increases, new sets are added to the intersection in the numerator of the expression. Thus the value of $\mathcal{Q}$ is strictly non-increasing with increasing dimensionality.

Downward closure holds for $\mathcal{Q}_{SCORE}$ and $\mathcal{Q}_{SCORE\&RANK}$. This is because the top-N of any region $\mathcal{S}(\mathcal{G}, N)$ consists of items that are either in the top-N of all its one-dimensional sub-regions ($i \in \cap_k \mathcal{S}(P_k, N)$), or of items that have lower scores ($j \in \cap_k(\mathcal{S}(P_k) \setminus \mathcal{S}(P_k, N))$). The portion of $\cap_k \mathcal{S}(P_k, N)$ in $\mathcal{S}(\mathcal{G}, N)$ does not increase as more one-dimensional groups are added to the intersection. Thus, the value of the numerator of the $\mathcal{Q}_{SCORE}$ expression, and the DCG values in $\mathcal{Q}_{SCORE\&RANK}$ are non-increasing in dimensionality of the group. At the same time, the denominator of $\mathcal{Q}_{SCORE}$, and the values of DCG_{Ideal} for $\mathcal{Q}_{SCORE\&RANK}$ are non-decreasing in the size of the union. Thus the values of $\mathcal{Q}_{SCORE}$ and $\mathcal{Q}_{SCORE\&RANK}$ are strictly non-increasing with increasing dimensionality.

5.3.3 Our Approach

Our proposed algorithm **BARAC**, **B**ottom-up **A**lgorithm for **R**ank-**A**ware **C**lustering, is an APRIORI-style algorithm with a flow that is similar to CLIQUE (Algorithm 6).

The procedure **BuildGrid** (Algorithm 7) starts by computing a score for each item $i \in \mathcal{D}$, and then sorts the items in decreasing order of score. As the dataset is scanned, all distinct values for each attribute $a_i \in \mathcal{A}$ are recorded as $domain(a_i)$. Next, we consider each attribute a_i with a corresponding $domain(a_i)$, and compute a *grid* data structure that is an array of one-dimensional histograms. If a_i is a categorical attribute with no natural ordering on its values (e.g. religion), a histogram bucket is created for each value $v_j \in domain(a_i)$.

Algorithm 6: **BARAC**: **B**ottom-up **A**lgorithm for **R**ank-**A**ware **C**lustering

Require: dataset $\mathcal{D}$, scoring function S, N, $\theta_{\mathcal{Q}}$, θ_{dom}, $maxBuckets$

1: $grid = \textbf{BuildGrid}(\mathcal{S}, \mathcal{D}, N, maxBuckets)$;
2: $mergedGrid = \textbf{Merge}(grid, N, \mathcal{S}, \theta_{dom})$;
3: $clusters = \textbf{Join}(mergedGrid, N, \mathcal{S}, \theta_{\mathcal{Q}})$;
4: **return** $clusters$

If a_i is numerical (e.g., age) or ordinal categorical (e.g., body type), $domain(a_i)$ is broken down into at most $maxBuckets$ intervals of consecutive values. Bucket j for attribute i is denoted by $grid[i][j]$. Having established interval boundaries for attribute a_i (lines 3-12), we assign to each interval the best N items in $\mathcal{S}(\mathcal{D})$ from among those that fall within the range of the interval (lines 13-15).

Algorithm 7: Procedure **BuildGrid**

Require: $\mathcal{S}(\mathcal{D}), S, N, maxBuckets$

1: compute a list of items S(D), sorted by i.score;
2: init $grid$, a matrix with one row per attribute $a_i \in \mathcal{A}$;
3: **for** $a_i \in \mathcal{A}$, where $|domain(a_i)| > 1$ **do**
4: **if** a_i is an unordered categorical attribute **then**
5: **for** $val_j \in domain(a_i)$ **do**
6: {allocate 1 column in $grid[i]$ per value val_j}
7: $grid[i][j].range = [val_j, val_j]$;
8: **end for**
9: **else**
10: divide $domain(a_i)$ into at most $maxBuckets$ consecutive intervals;
11: set $grid[i][j].range$ per interval;
12: **end if**
13: **for** each interval j **do**
14: $grid[i][j].items = S(\sigma_{grid[i][j].range}(D), N)$;
15: **end for**
16: **end for**
17: **return** $grid$

Merge runs multiple passes of the procedure **OnePassMerge** (Algorithm 8). **OnePassMerge** takes the $grid$ as input and expands the search space of the algorithm by considering, and possibly merging, runs of neighboring histogram buckets along the same dimension. Once the first run of **OnePassMerge** is done, it is invoked again on the output grid, and explores merging additional intervals.

The idea is that, for an attribute a_i, if neither of the two neighboring one-dimensional intervals $grid[i][j]$ and $grid[i][k]$ dominates the other (Definition 5.3.1), then it may be beneficial to consider their concatenation in the subsequent **Join** phase, in addition to considering both of them separately. This is because the top-N items of the concatenated interval are sufficiently different from the top-N items of the individual intervals, presenting additional clustering opportunities. If, however, one of the intervals dominates the other, then, by definition, the set of top-N items of the concatenated interval is very similar (or exactly the same) as the top-N items of the dominating interval, and so adding the concatenated interval to the search space is not helpful. We make two observations about **Merge**. First, the output grid is typically much larger than the original grid since all input intervals are also preserved in the result. Second, the lower the threshold θ_{dom}, the fewer intervals are generated. We explore the impact of θ_{dom} on efficiency in Section 5.4.

Algorithm 8: Procedure **OnePassMerge**

Require: $grid, N, \mathcal{S}, \theta_{dom}$

1: $mergedGrid = cloneGrid(grid)$;
2: **for** $a_i \in \mathcal{A}$ **do**
3: **for** $j = 1$ to $grid[i].length - 1$ **do**
4: {Check dominance among consecutive intervals.}
5: $k = j + 1$;
6: **if** not $(grid[i][j] \prec_{S,N,\theta dom} grid[i][k]) \wedge$ not $(grid[i][k] \prec_{S,N,\theta dom} grid[i][j])$ **then**
7: {+ denotes interval concatenation.}
8: $grid[i][j+k].items = \mathcal{S}(grid[i][j].items \cup grid[i][k].items, N)$;
9: $addToGrid(mergedGrid[i], grid[i][j + k]$;
10: **end if**
11: **end for**
12: **end for**
13: **return** *mergedGrid*

The procedure **Merge** returns the *mergedGrid*, which contains all one-dimensional clusters. The procedure **Join**, which is invoked next, computes clusters in higher dimensions by progressively joining together lower-dimensional clusters. This procedure is the same as the corresponding procedure in CLIQUE [Agrawal *et al.*, 1998], and we describe it here for completeness using our terminology.

Join repeatedly invokes the sub-routine **doJoin** and terminates when no more clusters are identified. Procedure **doJoin**, presented in Algorithm 9, takes $(k-1)$-dimensional clusters and a quality threshold as input, and returns a set of k-dimensional clusters. This is done by first identifying a candidate set of k-dimensional regions (lines 2-8), and then pruning the set by removing all regions that do not pass the quality threshold $\theta_{\mathcal{Q}}$ (line 9).

Algorithm 9: Procedure **doJoin**

Require: $Clusters_{K-1}$, $\theta_{\mathcal{Q}}$
1: $Regions_K = \emptyset$;
2: **for** $\mathcal{C}_1 \in Clusters_{K-1}$ **do**
3: **for** $\mathcal{C}_2 \in Clusters_{K-1}$ **do**
4: **if** $compatible(C_1, C_2)$ **then**
5: $append(Regions_K, joinClusters(C_1, C_2))$;
6: **end if**
7: **end for**
8: **end for**
9: $Clusters_K = prune(Regions_K, \theta_{\mathcal{Q}})$;
10: **return** $Clusters_K$;

We omit pseudo-code for some of the subroutines, but describe them verbally below.

Assume that the relation $<$ represents a lexicographic ordering on attribute names. Assume also that a cluster $\mathcal{C}$ is represented by a set of *intervals*, with the number of intervals in the set corresponding to the dimensionality of the cluster. Each interval records the attribute name (e.g., *age* or *income*), and the low and high values that specify the range. So, an interval $age \in [25, 29]$ has $attribute = age$, $low = 25$, and $high = 29$. Two intervals are considered equal if they reference the same attribute name and the same range of values.

Two $(k-1)$-dimensional clusters $\mathcal{C}_1$ and $\mathcal{C}_2$ are said to be *compatible* if they contain $k-2$ equal intervals, and if the $(k-1)^{st}$ interval of $\mathcal{C}_1$ is lexicographically lower than the $(k-1)^{st}$ interval of $\mathcal{C}_2$. The result of **joinClusters**$(\mathcal{C}_1, \mathcal{C}_2)$ is a k-dimensional region described by the union of the intervals of $\mathcal{C}_1$ and $\mathcal{C}_2$.

The quality measure $\mathcal{Q}$ can be any one of the measures defined in Definition 5.2.3. During the **Join** step, all measures are applied to $\mathcal{S}(\mathcal{G}, N)$, the top-$N$ items of each region $\mathcal{G}$. We compute the top-N lists for each grid interval in line 14 of Algorithm 7. As intervals are merged, and as clusters are joined to produce higher-dimensional clusters, top-N lists are re-computed (line 9 of Algorithm 8).

In the worst case **Join** will explore all combinations of dimensions. However, this worst case is very coarse. Actual run-time performance is highly data-dependent, as we show in the next section. **Join** terminates when there are no more pairs of compatible clusters which satisfy the quality threshold. This is guaranteed by the downward closure property (see Definition 5.3.2). The lower the value of $\theta_{\mathcal{Q}}$, the higher the number of clusters generated by our algorithm. We explore the impact of different threshold values on the run time performance in the next section.

5.4 Experimental Evaluation of Performance

We implemented **BARAC** with our three clustering quality measures (Section 5.2.2.) Since $\mathcal{Q}_{SCORE}$ behaved similarly to $\mathcal{Q}_{topN}$, we only report results with the latter and $\mathcal{Q}_{SCORE\&RANK}$. Our prototype is implemented in Java and operates on memory-resident data. All experiments were executed on a 64-bit machine with two Intel Xeon 2.13GHz processors and 4GB of RAM, running RedHat EL AS 4.

5.4.1 The Yahoo! Personals Dataset

Dataset. We evaluated the performance of **BARAC** on a dataset from a leading online dating service with millions of registered users. Users of the service create a *personal profile* in which they describe themselves using 30 structured attributes, e.g., age, height, occupation, education, income, etc. Users also commonly store one or several *target profiles*, expressed in terms of the same structured attributes. When specifying that profile, users designate attributes as *required* and *desirable*. Required attributes are used as *filtering* conditions for exact matching against personal profiles, while desirable attributes are used for *ranking* exact matches.

For the purpose of our experiments we focus on computing matches for male users, as there are at least one order of magnitude more males searching for females. We store a snapshot of *target profiles* of male users whom we call *seekers*, and of *personal profiles* of female users. The snapshot is as of a recent month in 2008, and contains all profiles that were registered with the dating service up to and including that month. We use 19 of the total 30 attributes, because there was no meaningful correlation between the ignored attributes (e.g. astrological sign) and other attributes, making them less suitable for clustering. Two of the 19 attributes, *has photo* and *gender*, have only two distinct values, and we use them for filtering, but not for clustering. So, there are 19 filtering attributes and 17 clustering attributes in our dataset. Therefore, for any given query, the number of clustering dimensions is at most 17.

User Sampling. We evaluated the performance for 100 target profiles. We chose a representative sample of profiles that cover a range of filtering and ranking attributes, as well as different number of matches. The chosen target profiles specify between 3 and 15 filtering attributes (median 5), and between 1 and 6 ranking attributes (median 3). Because data exploration is most meaningful for large datasets, we selected profiles with at least 1,000 matches for our evaluation. Our prototype operates on memory-resident data, and does all processing in memory. Due to a limitation in available RAM, we restrict our attention to users whose target profiles match up to 500,000 profiles. The chosen target profiles generated between 1,107 and 489,090 matches (median 102,492). Note that the size of the result set will often be reduced in practice by applying additional filtering criteria such as geographic distance between the seeker and the match, the freshness of the profile

filtering	*numerical*: age, height. *ordinal categorical*: body type, education level, income, religious services (attendance frequency). *categorical*: gender, sexual orientation, ethnicity, eye color, hair color, smoking, drinking, marital status, have kids, want more kids, employment status, profession, personality type, religion, political views.
ranking	age, height, body type, education level, income, religious services.
ignored	location, living situation, social personality, TV watching habits, languages, sense of humor, interests, love style, astrological sign.

Table 5.2: Structured attributes in the dating dataset.

of the match etc.

Ranking. The ranking functions we consider use 6 attributes: *age*, *height*, *body type*, *education*, *income*, and *religious services* (the frequency with which the user attends religious services). We chose these attributes because they are either continuous or ordinal categorical, thus inducing a natural order on their values. Which of the 6 attributes are included in the scoring function depends on which attributes are marked as *desirable* in the target profile.

The first scoring function we used, *attribute-rank*, assigns equal weights to each ranking attribute, and computes the score of an item as the sum of distances between the item and the ideal item along each attribute dimension. Here, an ideal item has the best possible value for each ranking attribute from among items in the filtered dataset. Distances along each dimension are normalized by the difference between extreme values for the corresponding attribute found in the filtered dataset. Note that this function is *personalized* in two ways. First, the user specifies which attributes are included in the scoring function. Second, the value of each ranking attribute contributes to the score based on how it compares to the best and worst values for that attribute, from among items that pass the filtering conditions of the target profile.

The second function, *geo-rank*, scales the value returned by *attribute-rank* by the geographic distance between the seeker and his match.

$$geo\_rank = \frac{attribute\_rank}{1 + (geo\_distance/100)} \tag{5.7}$$

We will discuss in detail in Section 5.5.2 that, because the clustering outcome depends

	Execution time(ms)			
	med	**avg**	**min**	**max**
BuildGrid	1756	2317	336	7814
Merge	13	23	6	119
Join	862	2912	258	37442
Total	3102	5499	600	40015

Table 5.3: Median, average, max and min processing times for $\mathcal{Q}_{topN}$ for 100 users, with $\theta_{dom} = \theta_Q = 0.5$.

on the combination of a user's filtering condition and the distribution of scores imposed by a particular scoring function, it is not always possible to find a meaningful clustering. The intuition is that rank-aware clustering does not apply if ranking does not discriminate well between high-quality and low-quality results, that is, if all, or most, of the items in the result set are tied for the same score. For example, selecting users with *income = 50K*, and then ranking on income, is not helpful, since all users will share the same score. Users whose scoring function assigned the top score to more than 30% of their profile matches were excluded from our evaluation.

5.4.2 Scalability

In the first part of our experiments, we study the behavior of **BARAC** with the $\mathcal{Q}_{topN}$ quality measure, and the *attribute-rank* scoring function. We analyze performance in terms of three distinct stages: **BuildGrid**, **Merge**, and **Join**. See Section 5.3.3 for a description of these stages.

BARAC takes several parameters as input. The parameter N models the user's *attention span* – the number of items the user is likely to explore sequentially [Manber *et al.*, 2000]. We used $N = 100$ for all experiments in this section. $maxBuckets$, used by the procedure **BuildGrid** (see Algorithm 7), specifies an upper bound on the number of intervals per dimension. We set it to 5. This value is chosen according to *age*, the attribute with highest cardinality, and is set so that the values falling into a particular age interval are perceived as similar by a typical user. For most other dimensions, the domain cardinality is lower than 5, and so the upper bound is never reached, and the actual domain cardinality is used instead. We study the scalability of **BARAC** as a function of the dominance and quality thresholds θ_{dom} and θ_Q. There are no additional parameters in our formalism.

In the first experiment, we ran **BARAC** for 100 users in the full space of 19 filtering attributes and 17 clustering attributes. Values of the dominance and quality thresholds were fixed at $\theta_{dom} = \theta_Q = 0.5$ for this experiment. Table 5.3 summarizes the median, average, minimum, and maximum run times of **BARAC**, with all times listed in milliseconds.

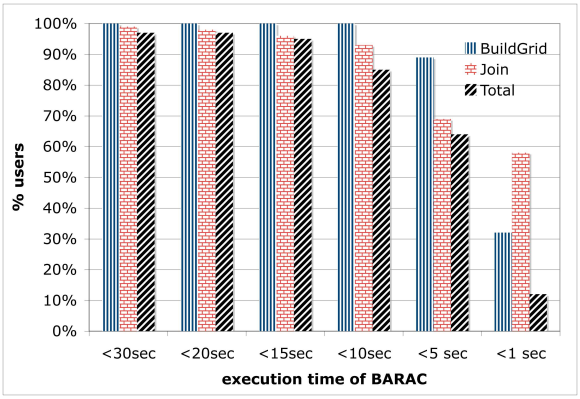


Figure 5.1: Performance of **BARAC** as percentage of cases that completed under a certain time limit.

According to Table 5.3, the median run time of **BARAC** is 3.1 seconds, and the average run time is 5.5 seconds. The run time of **BARAC** is dominated by **BuildGrid** and **Join**, while the execution time of **Merge** is negligible even in the worst case. While the maximum value for **Join** is quite high, motivating future performance optimizations, the run time reported in Table 5.3 may be unrealistically high. This is because, as discussed in Section 5.4.1, the actual clustering dimensionality is far lower than 17 for specific queries.

Figure 5.1 presents the run time of **BARAC** as the percentage of cases that completed under a certain time limit. **BARAC** completes in under 5 seconds in most cases, and takes longer than 10 seconds in only a handful of cases. In the remainder of this section we analyze the factors that contribute to the performance of **BuildGrid** and **Join**, and explore scalability as we vary the size of the dataset and the clustering dimensionality.

5.4.2.1 Varying Dataset Size

Figure 5.2 shows the performance of **BuildGrid** for 100 users as a function of dataset size – the number of items that pass the filtering conditions of the target profile. The data presented in this figure is the same as was used in Table 5.3 and Figure 5.1. Each data point corresponds to a particular target profile, and thus to a particular dataset size. All time measurements are in milliseconds. As before, the dominance and quality thresholds θ_{dom} and $\theta_{\mathcal{Q}}$ were both set to 0.5.

During **BuildGrid**, the seeker's filtering conditions are applied to memory-resident data in a single linear scan of the data, matches are identified, and a score is computed for every match. Items are then sorted on score in decreasing order. Finally, a data grid of matches is computed. We determined experimentally that score computation is the dominant factor in the execution time of **BuildGrid**. As Figure 5.2 demonstrates, the execution time of this stage increases linearly with the number of matches.

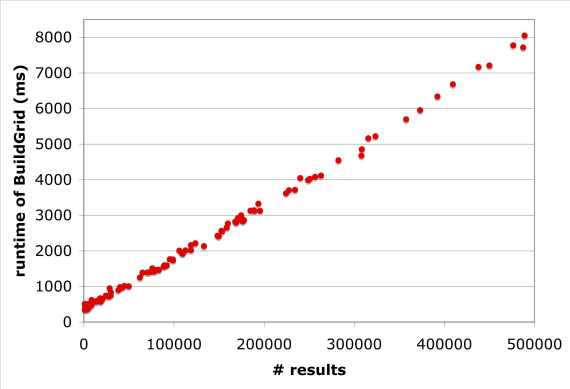


Figure 5.2: Execution time of **BuildGrid** as a function of dataset size.

5.4.2.2 Varying Clustering Dimensionality

We now explore the impact of dimensionality on the performance of **Join**. For this experiment, we fix $\theta_{dom} = \theta_Q = 0.5$ and vary the dimensionality of the clustering space from 3 to 17. The first 3 clustering attributes are selected, and attributes are added one at a time in subsequent rounds. Attributes are added in the same order for all users, but this order was chosen randomly. We have attempted several orders of adding attributes, and noticed no difference with respect to the performance trends of **Join**. We thus report our results with one particular order of adding attributes. Note that the filtering criteria and the scoring function are specified by the user's target profile, and are applied as before.

Figure 5.3 presents the execution time of **Join** as a function of clustering dimensionality. Each point is an average of execution times for the fixed dimensionality across all users. We observe that the average execution time of **Join** increases as the dimensionality increases, but that it increases more significantly in some cases than in others. The general trend, with the exception of attributes 12, 13, and 17, which we discuss below, seems to be that the execution time on **Join** increases approximately quadratically with increasing dimensionality.

Adding a clustering dimension to the set of dimensions *for a particular user* may or may not have an effect on the run time of the algorithm. For example, if we are adding the dimension *drinking*, but the user's filtering conditions are specifying a single value for this attribute, *drinking* = *no*, the attribute will not be added to the data grid, and so clustering will proceed as it did before the dimension was added. Attributes 12, 13 and 17 happen to be *marital status*, *wants more kids*, and *drinking*. These are all low-cardinality attributes, which users commonly restrict to a single value in their filtering conditions.

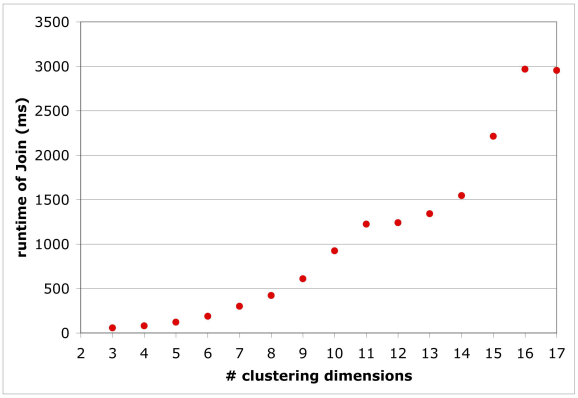


Figure 5.3: Execution time of **Join** as a function of clustering dimensionality.

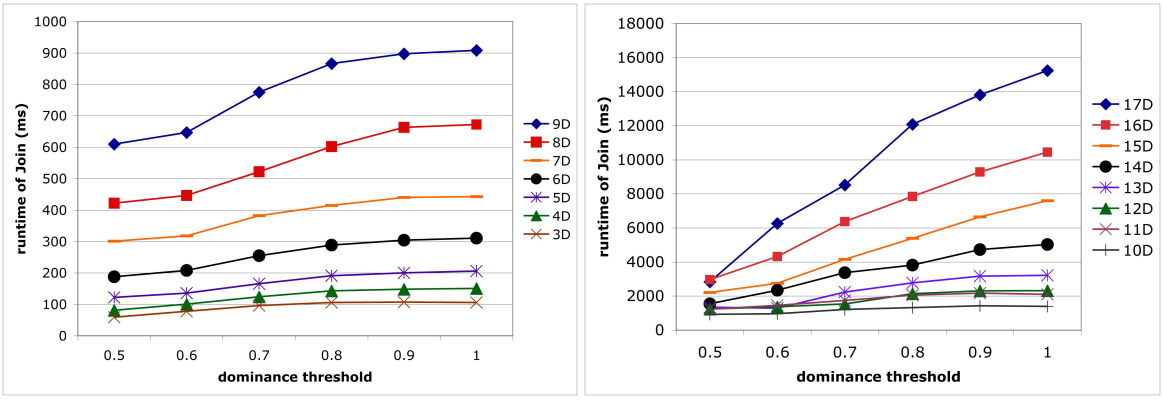


Figure 5.4: Execution time of **Join** as a function of θ_{dom}.

5.4.2.3 Varying Parameters of the Algorithm

Let us now see how the dominance and quality thresholds impact runtime performance. The dominance threshold θ_{dom} is used in **Merge**; the lower the threshold, the fewer intervals will **Merge** produce, and pass along to **Join**. Consequently, the run time of **Join** should increase as θ_{dom} increases. Figure 5.4 demonstrates that this trend holds for datasets of different dimensionality. Here, we fix $\theta_Q = 0.5$, and report the average run time of **Join** for each value of θ_{dom}, and for most dimensionality settings.

Varying the quality threshold θ_Q has the opposite effect on the run time of **Join**. This is because the higher the threshold, the fewer clusters are generated by **Join**, and the sooner it terminates. This intuition is supported by our experimental findings in Figure 5.5. Here, we set $\theta_{dom} = 0.5$ and present the average run time of **Join** for each value of θ_Q, and for most dimensionality settings.

In fact, for higher values of the quality thresholds it is often the case that no clusters at all

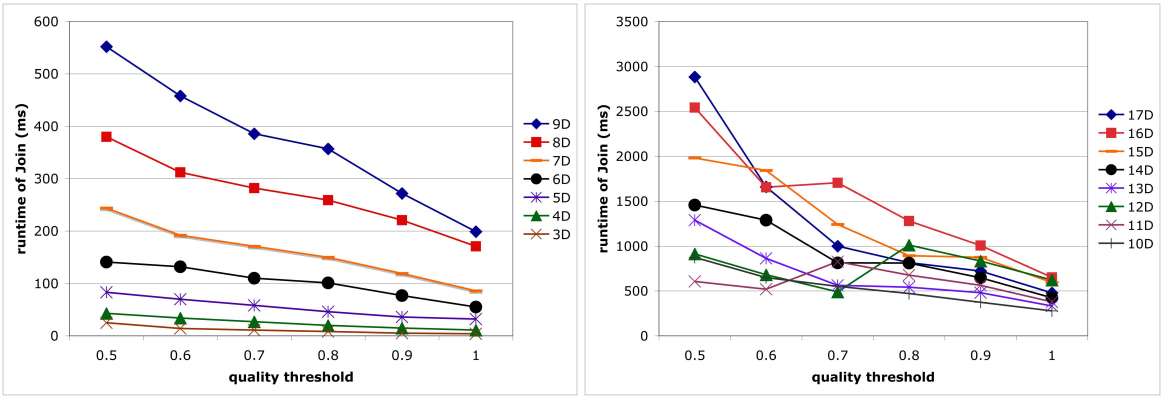


Figure 5.5: Execution time of **Join** as a function of θ_Q.

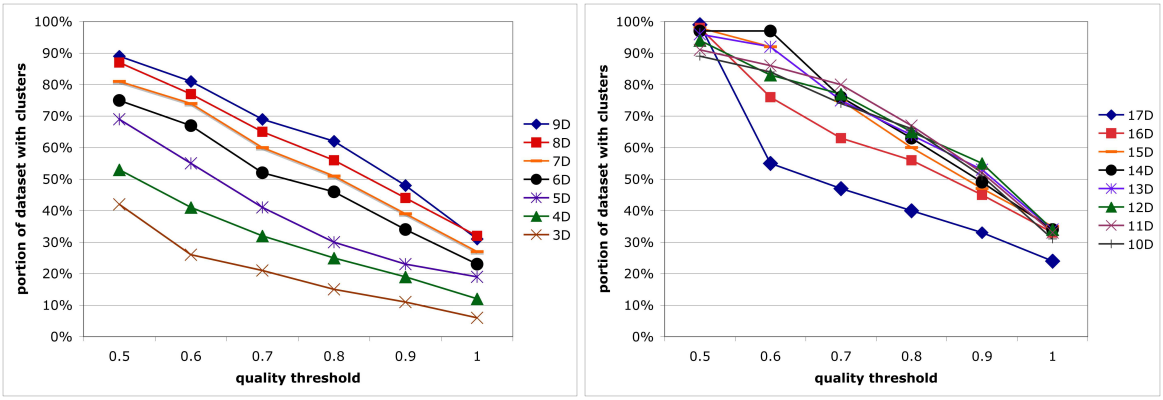


Figure 5.6: Percentage of users for whom **BARAC** identified clusters, as a function of θ_Q.

exist of sufficiently high quality. When this happens, **Join** terminates after its initial round of processing, in which it attempts to join 1D intervals into 2D clusters. In Figure 5.6 we plot the percentage of users for whom clusters were identified, as a function of the quality threshold θ_Q. We plot the same data here as in Figure 5.5, with the same dominance threshold setting, $\theta_{dom} = 0.5$.

All experiments so far dealt with the *attribute-rank* scoring function, and clustered items according to $\mathcal{Q}_{topN}$. In the following section, we explore the interplay between the quality thresholds, the distribution of scores induced by the ranking function, and the choice of a clustering quality measure.

5.5 Effectiveness of Rank-Aware Clustering: A Qualitative Analysis

5.5.1 Clustering Quality

We now give a qualitative intuition of the kinds of clusters that are discovered by **BARAC**. We use the Q_{topN} quality metric, and the *attribute-rank* ranking function for the purpose of this evaluation. We focus our attention on the following set of filtering conditions that are in-line with our motivating example in Section 5.1: *age* $\in$ *[25,35], height* $\in$ *[160cm, 175cm], education* $\geq$ *Bachelor's, ethnicity* = *Caucasian, body type* $\in \{$*slim, slender, average, athletic, fit*$\}$.

This set of filtering conditions returns over 30,000 matches. We rank the matches on a combination of *income* and *education*, both from higher to lower. There are about 100 top-matches: women with post-graduate education who make more than \$150K. About two thirds of the top matches are over 29 years old, and so younger matches would not be easily accessible if results were returned as a ranked list.

Let us now cluster the results of **BARAC**, using the Q_{topN} quality metric. The following are some of the clusters that are returned and that deal directly with the correlation between income and age, and income and education:

- $age \in [25, 27] \wedge income \in [\$35K, \$75K]$
- $age \in [28, 33] \wedge income \in [\$75K, \$150K]$
- $age \in [28, 33] \wedge income \geq \$150K$
- $age \in [31, 35] \wedge income \geq \$75K$
- $age \in [28, 33] \wedge education = post\ graduate$
- $age \in [31, 35] \wedge education = post\ graduate$

Note that two clusters are returned that contain different sets of matches with age between 28 and 33. Note also that the younger matches, aged between 25 and 27, are returned as a cluster with relatively lower income. These matches would not have been easily accessible in a single ranked list. **BARAC** also returned several clusters that are not directly related to the ranking conditions, but for which a correlation was detected among attributes at top ranks. So, there was a cluster of matches who are politically *very conservative* or *conservative* and who attend religious services *more than once a week* or *weekly*. Another cluster consisted of matches who are politically *middle of the road* or *liberal* and who attend religious services no more often than *monthly*.

Recall that **BARAC** does not partition the dataset. That is, an item may be returned as part of one or several clusters. This is a feature of our approach that bears some similarity to

faceted navigation [Wynar, 1992], a popular browsing and information discovery paradigm. In rank-aware clustering and in faceted navigation alike, the user may encounter the same item through different paths, with each path describing a particular aspect of the item that the user may find interesting.

As we illustrated, the clustering outcome depends on the ranking attributes, and how they correlate with other attributes in the data. We now explore the effect of different quality measures on the clustering outcome.

5.5.2 Choosing a Clustering Quality Metric

We now demonstrate the qualitative difference between two proposed quality measures, $\mathcal{Q}_{topN}$ and $\mathcal{Q}_{SCORE\&RANK}$. We use the profile of one particular user, whom we call $user_1$, as an example in this section. $user_1$ is a representative user with about 60,000 profile matches.

As we discussed in Section 5.2, $\mathcal{Q}_{topN}$ favors regions that contain many items that are in the top-N lists of their sub-regions, irrespective of the scores and ranks of those items in top-N lists of the sub-regions. Conversely, $\mathcal{Q}_{SCORE\&RANK}$ assigns a higher quality score to a region in which top-N lists of the sub-regions intersect at top ranks, particularly if top-ranked items have significantly higher scores.

Ideally, a rank-aware clustering quality measure should be rich enough to capture the distribution of scores imposed by the scoring function. $\mathcal{Q}_{topN}$ treats all items with N highest scores equally, and is thus appropriate for scoring functions where the best N items have higher scores than the rest of the items, but where *there is no significant variability in scores among the top-N*. The scoring function *attribute-rank* is one such function.

Conversely, $\mathcal{Q}_{SCORE\&RANK}$ is most meaningful if there is a significant variability in scores among items in the top-N. For example, for $N = 100$ it should hold that the first 10 items have much higher average scores than the following 10 items etc. The scoring function *geo-rank* is one such function. We plot the distribution of the top-100 scores of $user_1$'s items for the two ranking function in Figure 5.7.

We now demonstrate that $\mathcal{Q}_{SCORE\&RANK}$ is more appropriate to use in conjunction with the *geo-rank* scoring function for $user_1$. We fix $\theta_{dom} = 0.5$ and $\theta_Q = 0.7$, and compare the sets of clusters that were identified by $\mathcal{Q}_{topN}$ and $\mathcal{Q}_{SCORE\&RANK}$. $\mathcal{Q}_{topN}$ identified 11 clusters, while $\mathcal{Q}_{SCORE\&RANK}$ identified 33 clusters. One of the clusters returned by $\mathcal{Q}_{topN}$ was not returned by $\mathcal{Q}_{SCORE\&RANK}$, we call it $\mathcal{G}_{topN}$. $\mathcal{Q}_{SCORE\&RANK}$ found 23 clusters that were not found by $\mathcal{Q}_{topN}$. We refer to the highest- and lowest-quality clusters from this set as $\mathcal{G}^+_{SCORE\&RANK}$ and $\mathcal{G}^-_{SCORE\&RANK}$. We summarize some properties of $\mathcal{G}_{topN}$, $\mathcal{G}^+_{SCORE\&RANK}$ and $\mathcal{G}^-_{SCORE\&RANK}$ in Table 5.4, where we compare the top-N list of each cluster to the ideal top-N list in terms of ranks and scores. The value in the column "score loss at 10" contains the difference between the total scores of the top-10 items from the ideal (the union of top-N items of the individual predicates forming each cluster), and

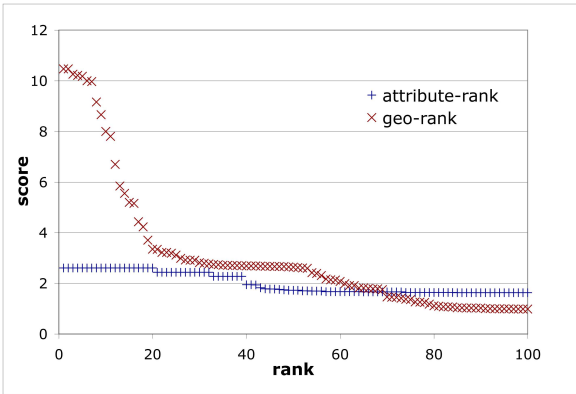


Figure 5.7: Top-100 scores for *attribute-rank* and *geo-rank* for $user_1$.

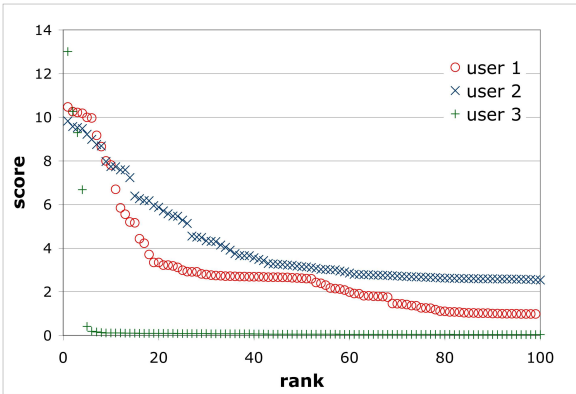


Figure 5.8: Top-100 scores for *geo-rank* for three users.

the top-10 items for the cluster.

$\mathcal{G}_{topN}$ is a two-dimensional cluster on attributes *height* and *income*. The top-N list of $\mathcal{G}_{topN}$ contains items that were in ranks 1 through 47 in the top-N list on *height* (median rank 27), but in ranks 8 through 100 on *income* (median rank 70). So, while the intersection happens at the top of the top-N on *height*, it is closer to the bottom of the top-N on income. This cluster seems less valuable than the other two clusters in the table, based on both the lower score loss, and the lower (worse) median rank.

$\mathcal{Q}_{SCORE\&RANK}$ is sensitive to the distribution of scores. The same scoring function, e.g. *geo-rank*, may not generate a distribution of scores that is appropriate for $\mathcal{Q}_{SCORE\&RANK}$ for all users because their filtering conditions may differ. For users who live in sparsely-populated areas this function may produce very few high-scoring items. Consider the distribution of top 100 scores for three users in Figure 5.8. Users $user_1$ and $user_2$ have similar distributions, while $user_3$ only has four high-scoring items in his top-100, followed by 96 items with similar low scores. $user_3$ is not a good candidate for $\mathcal{Q}_{SCORE\&RANK}$, and a

	best rank	**worst rank**	**median rank**	**score loss at 10**
$\mathcal{G}_{topN}$	8	100	70	1.77
$\mathcal{G}^{+}_{SCORE\&RANK}$	1	98	40	5.61
$\mathcal{G}^{-}_{SCORE\&RANK}$	1	99	40	5.42

Table 5.4: Characteristics of some groups identified by $\mathcal{Q}_{topN}$ and $\mathcal{Q}_{SCORE\&RANK}$.

score-insensitive quality measure like $\mathcal{Q}_{topN}$ should be used instead.

5.6 Related Work

Clustering Web Documents: The motivation for this work is similar to ours, namely, that grouping results and generating descriptions for these groups greatly improves the user's ability to understand vast datasets. Clustering of text documents has been explored extensively in Information Retrieval [Leuski, 2001; Dakka and Gravano, 2007; Bonchi *et al.*, 2008]. Leuski [Leuski, 2001] experimentally demonstrates that presenting clusters of documents can be significantly more effective than presenting a ranked list. He also shows that clustering can be as effective as the interactive relevance feedback approach based on query expansion. In [Dakka and Gravano, 2007] the authors combine an offline (query-independent) document clustering method and an online (query-dependent) method to generate multi-document summaries of clustered news articles. Bonchi et al [Bonchi *et al.*, 2008] use search query logs to cluster search results into coherent well-separated sets for presentation purposes. In contrast, our work focuses on the interaction between structure and ranking in clustering.

Clustering Relational Data: Li et al. [Li *et al.*, 2007] argue for native support of clustering and ranking operators in relational databases. The authors demonstrate how clustering can be implemented by means of a bitmap index over a summary grid. In their framework, the grouping (clustering) and ordering attributes, as well as the number of clusters, are specified by the user, and the focus of the work is on efficiency. The focus of our work is, in addition to efficiency, on automatically determining which clustering attributes are meaningful given a scoring function.

Faceted Navigation: This methods facilitates information discovery over large datasets. Faceted classification defines items using mutually exclusive, collectively exhaustive properties [Wynar, 1992], and has been used in faceted navigation, where items are classified simultaneously along multiple facets, and item counts are presented per facet. A strong limitation is that a facet is a single attribute, and no attribute correlations are captured. Several extensions of the faceted data model were proposed. Ross and Janevski [Ross and Janevski, 2004] developed *entity algebra*, a faceted query language that supports operators

such as selection and semi-join. Ben-Yitzhak et al. [Ben-Yitzhak *et al.*, 2008] extended faceted navigation to include quantitative summary information other than item counts, such as average price and rating, and developed methods for efficient computation of such statistics over correlated facets.

Roy et al. [Roy *et al.*, 2008] proposed techniques that dynamically suggest facets for database exploration, with the goal of minimizing navigation time. At every step, the system asks the user a set of questions about his information need, and dynamically fetches the next most promising set of facets. In [Dash *et al.*, 2008], the authors extend Solr, a popular search engine, with dynamic faceted search for exploring data with both textual content and structured attributes. Given a keyword query, the system selects a small set of interesting attributes, where interestingness measures the difference between expected and actual attribute values.

Our work is complementary to faceted navigation. While we focus on attribute correlations, our analysis can be used to propose to the user which, among many attributes, may be more interesting to explore in a particular dataset.

The Many-Answers Problem: In [Chaudhuri *et al.*, 2004] the authors state the *Many-Answers Problem* and show how correlations among attribute values in a structured datasets can be used to automatically derive a suitable ranking function. To this end, the authors develop a comprehensive probabilistic information retrieval ranking model and present efficient processing techniques. A related *Empty-Answers Problem* is discussed in [Agrawal *et al.*, 2003]. Here, the authors present an adaptation of *inverse document frequency* (IDF) that is used for automatic ranking of results. The authors also propose to incorporate workload information into the ranking.

Rank Aggregation: Fagin et al. [Fagin *et al.*, 2003b] propose rank aggregation, in which ranked exploration of large high dimensional datasets is viewed as a similarity search problem. Given a ranking function on d attributes, the algorithm considers d ranked lists, and aggregates these lists using a variant of the threshold algorithm [Fagin *et al.*, 2003c]. An approximation based on dimensionality reduction is also proposed, in which projections along random lines in the d-dimensional space are taken, and the computation is carried out on the projection.

Our work differs from [Fagin *et al.*, 2003b] in that we consider non-ranking attributes in addition to the ranking attributes. Rather than computing a global aggregate rank or similarity score, we consider the correlations that hold among attributes of the data in various projections of the space, and identify items, or groups of items, that are best from among comparable, given the ranking function.

Skyline Operator: A alternative result presentation method in presence of multi-dimensional ranking functions is the skyline [Börzsönyi *et al.*, 2001]. A point in multi-dimensional space is said to belong to the skyline if it is not dominated by any other point, i.e., if no other point is as good or better in all dimensions, and strictly better in at least

one dimension. In Chapter 3 we presented a skyline visualization of ranked results in a two-dimensional space. Skylines are a valuable data visualization tool, however, the results of this visualization are difficult to interpret for datasets of high dimensionality. The notion of dominance may be applicable to other aspects of our work, such as cluster selection, and we plan to consider this direction in the future.

Integrating Ranking with Clustering: Sun et al. [Sun *et al.*, 2009] recently presented RankClus, a framework that integrates ranking with clustering in a heterogeneous information network such as DBLP. RankClus is based on a mixture model that uses mutual reinforcement between clustering and ranking. Our high-level motivation is also to treat clustering and ranking as parts of a unified framework. However, our application domain (structured datasets with user-defined ranking functions) and technical approach are very different.

5.7 Conclusion

In this chapter we introduced rank-aware clustering, a novel result presentation method for large structured datasets. We developed rank-aware clustering quality measures, and proposed BARAC: a Bottom-up Algorithm for Rank-Aware Clustering, an Apriori-style algorithm geared specifically at such quality measures. We presented an extensive experimental evaluation of scalability, and gave an intuition of the effectiveness of BARAC on *Yahoo! Personals* datasets. A large-scale user study is currently underway in scope of the *Yahoo! Research Sandbox* project. The goal of the study is to ascertain the effect of our result presentation method on the user experience. We look forward to reporting these results in a subsequent study. In the future we will consider performance optimizations, and will explore the applicability of our methods to other large structured datasets. We will also explore user interface design issues such as cluster selection.

Chapter 6

Other Contributions

This chapter summarizes some work that is not directly related to the main theme of this thesis, but that was carried out as part of the doctoral research.

6.1 Data Modeling in Complex Domains

6.1.1 Schema Polynomials and Applications

This section is based on joint work with Kenneth A. Ross and appeared in [Ross and Stoyanovich, 2008].

Conceptual complexity is emerging as a new bottleneck as database developers, application developers, and database administrators struggle to design and comprehend large, complex schemas. Applications in domains as diverse as medicine, archaeology, and astronomy often rest on database schemas with hundreds of relations and thousands of columns. The schema design and maintenance, as well as application development, are all extremely challenging for schemas of this size.

The conciseness of a schema depends critically on the idioms available to express the schema. As an analogy, consider the class of boolean expressions with conjunction and disjunction. It is well known that there are formulas that are compact in one representation (say disjunctive normal form) but exponentially bigger in another (say conjunctive normal form), and vice versa.

Three well-known formalisms for writing schemas are the relational, the object-oriented, and the faceted approaches. Each of these is very good at expressing certain classes of schema, but poor at expressing certain other classes of schema. Object-oriented schemas allow the factorization of common attributes into an inheritance hierarchy. Faceted schemas allow the orthogonal composition of many independent attributes; in an e-commerce application, for example, a product may be independently classified by size, by brand, and by color. Traditionally, one has been limited to just one of these design methodologies when

creating schemas. However, even if part of the schema is compactly represented using that methodology, other parts may not be.

We define a higher-level conceptual data representation language that allows the schema to be manipulated in ways that expose the strengths of each of these data modeling approaches. If a schema has parts that are compact when expressed according to one approach, then that part of the schema should be expressed using that approach, even if other parts of the schema use a different approach. We propose a formal language for representing schemas, and derive a set of properties that allow one to manipulate schema expressions while preserving the set of representable tuples. We propose that standard design methodologies such as entity-relationship modeling [Ramakrishnan and Gehrke, 2003], modeling in UML [Booch *et al.*, 2005], faceted modeling [Wynar, 1992], and relational normalization [Ramakrishnan and Gehrke, 2003], produce outputs in this framework rather than going directly to a physical relational schema, with the following advantages:

- One can explore a variety of physical representations obtained using different equivalent expressions for a schema.
- One can derive an unambiguous logical representation that allows transformations, such as attribute factorization and subtraction, that are not straightforward for sets of physical tables.
- Different users can orient the schema to their own points of view. One user may impose an inheritance hierarchy (e.g., factoring out the location of manufacture) while another may impose an alternative hierarchy (e.g., factoring out the product-type). These conceptual views are compatible, and can be automatically translated into the chosen physical representation.
- Users can project out parts of the schema that they are not interested in. The remaining portion can be simplified using various equivalences, leading to a description that is much easier to understand than a schema with hundreds of tables and thousands of columns.

Our novel schema modeling framework, which we call *schema polynomials*, reasons over schema expressions. The basic notion in describing schemas is the *attribute*: a label, along with a data type, that represents an aspect of a concept. Examples of attributes are "age", "height", "company-name", etc. We use attributes to define *tuple-descriptors*:

Definition 6.1.1 *A* tuple-descriptor T *is defined recursively with the context free grammar:*

$$T \quad ::= \quad 0 \mid 1 \mid A \mid B \mid C \mid \ \ldots \ \mid TT \mid T+T \mid T-T$$

We will describe the concatenation TT *as* multiplication. A, B, C, $\ldots$ *are the attribute names,* 1 *is a special symbol denoting an empty product (i.e., the empty set of attributes), and* 0 *is a special symbol denoting an empty sum.* □

In [Ross and Stoyanovich, 2008] we demonstrate how tuple-descriptors may be used to concisely represent schemas, and we illustrate this here with an example. Consider the following schema expression.

$$ABCD + ABG + ACD + AG + BCH \tag{6.1}$$

When we write $ABCD$ in Expression 6.1 we mean that tuples with attribute names A, B, C, and D are valid for this schema. When we write $S_1 + S_2$ we mean that a tuple is valid for either S_1 or S_2. Our schema could be mapped to a collection of five stored tables **ABCD**, **ABG**, **ACD**, **AG**, and **BCH**. We use bold script to describe physical level structures such as tables, and math script for conceptual level expressions. We could alternatively factorize the schema into the representation:

$$A(B + 1)(CD + G) + BCH \tag{6.2}$$

This representation has fewer syntactic elements than Expression 6.1. Common occurrences of some attributes have been factored out. The $B + 1$ subexpression allows tuples having either a valid or a null value for attribute B. Expression 6.2 does not have a direct relational interpretation, since there is no relational construct to express $CD + G$. Nevertheless, one can map this expression to a set of tables for storage as follows: Add a new unique identifier column (say I) to represent the link between the $A(B + 1)$ subexpression and the $(CD + G)$ subexpression, to yield tables **ABI**, **ICD**, **IG** and **BCH**, where B can be null in **ABI**. This transformation is correct only with constraints on the new attribute I. The constraint for I in **ABI** says that the value of I must appear in exactly one of **ICD** and **IG**. There must also be foreign key constraints on I into **ABI** from both **ICD** and **IG**.

An alternative rewriting of Expression 6.2 is:

$$A(B + 1)[(CD + 1)(G + 1) - CDG - 1] + BCH \tag{6.3}$$

The subtractions in Expression 6.3 can be interpreted as constraints stating that (a) C, D, and G cannot all be non-null, and (b) C, D, and G cannot all be null. This expression can be mapped to a physical schema **ABCDG**, **BCH**, where **ABCDG** has various null/not-null constraints on B, C, D, and G. If one cared only about attributes A, B, and C in this schema, one could project out the other attributes to obtain from Expresssion 6.1 the simpler expression $ABC + AB + AC + A + BC$, which could again be factorized in various ways. Yet another factorization of Expression 6.1 is:

$$C(ABD + AD + BH) + ABG + AG \tag{6.4}$$

This would be a natural factorization in a hierarchical or object-oriented view in which C is the primary dimension of classification and is inherited from a higher-level entity. Unlike traditional object-oriented data modeling that imposes a single hierarchical structure, our

approach allows different users with different points of view to "orient" the schema according to the dimensions they are most interested in. In such a case, the measure of simplicity for a user might give added weight to the absence of redundancy for the C attribute in Expression 6.4, since the user cares more about C than the other attributes.

In [Ross and Stoyanovich, 2008] we present rewrite rules that generate efficient physical representations of schema expressions. We develop several schema factorization heuristics, and present an experimental evaluation on a large real-life relational schema, demonstrating a significant improvement in schema compactness. Finally, we introduce an application of schema polynomials to the representation of relationships with constraints.

6.1.2 Symmetric Relationships and Cardinality-Bounded Multisets

This section is based on joint work with Kenneth A. Ross and appeared in [Ross and Stoyanovich, 2004].

Complex application domains often require the modeling of relationships, some of which are symmetric. In a binary symmetric relationship, A is related to B if and only if B is related to A. Symmetric relationships between k participating entities also arise naturally in real-world applications, and can be represented as multisets of cardinality k. For example, in a law-enforcement database recording meetings between pairs of individuals under investigation, the "meets" relationship is symmetric. This relationship can be generalized to allow meetings of up to k people. The k-ary meeting relationship would be symmetric in the sense that if $P = (p_1, \ldots, p_k)$ is in the relationship, then so is any column-permutation of P.

As another example consider a database recording what television channel various viewers watch most during the 24 hourly time-slots of the day. For performance reasons, the database uses a table $V(id, date, C_1, \ldots, C_{24})$ to record the viewer (identified by id), the date, and the twenty-four channels most watched, one channel for each hour of the day. (A conventional representation as a set of slots would require a 24-way join to reconstruct V.) This table V is not symmetric, because C_i is not interchangeable with C_j: C_i reflects what the viewer was watching at time-slot number i. Nevertheless, there are interesting queries that could be posed for which this semantic difference is unimportant. An example might be "Find viewers who have watched channels 2 and 4, but not channel 5." For these queries, it could be beneficial to treat V as a symmetric relation in order to have access to query plans that are specialized to symmetric relations.

Sets and multisets have a wide range of uses for representing information in databases. Bounded cardinality multisets would be useful for applications in which there is a natural limit to the size of multisets. This limit could be implicit in the application (e.g., the number of players in a baseball team), or defined as a conservative bound (e.g., the number of children belonging to a parent).

Storing a symmetric relation in a conventional database system can be done in a number

of possible ways. Storing the full symmetric relation induces some redundancy in the database: more space is required (up to a factor of $k!$ for k-ary relationships), and integrity constraints need to be enforced to ensure consistency of updates. Updates need to be aware of the symmetry of the table, and to add the various column permutations to all insertions and deletions. Queries need to perform I/O for tuples and their permutations, increasing the time needed for query processing.

Alternatively, a database schema designer could recognize that the relation was symmetric and code database procedures to store only one representative tuple for each group of permuted tuples. A view can then be defined to present the symmetric closure of the stored relation for query processing. The update problem remains, because updates through this view would be ambiguous. Updates to the underlying table would need to be aware of the symmetry, to avoid storing multiple permutations of a tuple, and to perform a deletion correctly. For symmetric relations over k columns, just defining the view using standard SQL requires a query of length proportional to $k(k!)$.

For both of the above proposals, indexed access to an underlying symmetric relationship would require multiple index lookups, one for each symmetric column.

A third alternative is to model a symmetric relation as a set [Date, 2003] or multiset. Instead of recording both $R(a, b, c, d, e)$ and $R(b, a, c, d, e)$, one could record $R'(q, c, d, e)$, $S(a, q)$, and $S(b, q)$, where q is a new surrogate identifier, and R' and S are new tables. The intuition here is that q represents a multiset, of which a and b are members according to table S. Distinct members of the multiset can be substituted for the first two arguments of R. To represent tuples that are their own symmetric complement, such as $R(a, a, c, d, e)$, one inserts $S(a, q)$ twice. This representation uses slightly more space than the previous proposal, while not resolving the issue of keeping the representation consistent under updates. Further, reconstructing the original symmetric relation requires joins.

In [Ross and Stoyanovich, 2004] we argue that none of these solutions is ideal, and that the database system should be responsible for providing a *symmetric table type*. We propose techniques to enable such a table type, and provide:

- An underlying abstract data type to store the *kernel* of a symmetric relation, i.e., a particular non-redundant subset of the relation. We show how updates on this data type would be handled by the database system. We describe how relational normalization techniques should take account of symmetric relations during database design. Both normalization and the proposed representation of symmetric relations aim to remove redundancy, so combining these two approaches should be beneficial.

- An extension of the relational algebra with a symmetric closure operator γ. We show how to translate a query over a symmetric relation into a query involving γ applied to the kernel of the relation. We provide algebraic equivalences that allow the rewriting of queries so that work can be saved by applying γ as late as possible.

- A method for inferring when a view is guaranteed to be symmetric. By using this method, the database system has the flexibility to store a materialized view using the more compact representation.

- A syntactic extension to SQL that allows the succinct expression of queries over symmetric relations.

6.1.3 A Faceted Query Engine Applied to Archaeology

This section is based on joint work with Kenneth A. Ross and Angel Janevski, and appeared in [Ross *et al.*, 2005; Ross *et al.*, 2007].

A number of application domains require the modeling of complex entities within classification hierarchies. For many of these domains, the hierarchy and the entity structure are the main sources of complexity, while other features of the domain, such as relationships between entities, are relatively simple. In such domains it is natural to make the set of entities the basic conceptual structure.

Faceted classification was introduced by an Indian librarian and classificationist S.R. Ranganathan, and was first used in his Colon Classification in the early 1930s. Faceted classification treats entities or groups of entities as collections of clearly defined, mutually exclusive, and collectively exhaustive aspects, properties or characteristics, called facets [Wynar, 1992]. For example, in an archaeology domain, we may classify artifacts along multiple orthogonal dimensions: by time period, by culture, by material, or by geographic location.

Recent work, see for example `flamenco.berkeley.edu` and `facetmap.com`, proposes search facilities for hierarchical data using faceted hierarchies. Ross and Janevski [Ross and Janevski, 2004] developed a faceted data model, and proposed a query language, called *Entity Algebra*, that is appropriate for faceted domains. The primary goal of their work was to create a data model and a query language that is understandable to non-technical users, while still allowing one to compose complex queries from simple pieces.

Building on the work of [Ross and Janevski, 2004] we developed the *Faceted Query Engine*. Our work was part of an inter-disciplinary project that aims to apply computational tools from Robotics, Virtual Environments, and Databases to modeling, visualizing, and analyzing historical and archaeological sites (see `www.learn.columbia.edu/nsf`). We collaborated with archaeologists to create a collection of orthogonal hierarchical classifications of finds from two archaeological excavations: a large-scale dig of ancient artifacts in Memphis, Egypt [Giddy, 1999], and a medium-scale dig of iron-age finds from Thulamela, South Africa. Our system provides a web-based user interface, and allows one to query thousands of objects from the two locations with respect to any of the facets, and to perform spatial and temporal analysis of the data. Users of our system can access text, images, and multimedia data related to the finds.

Figure 6.1 provides a screenshot of our system with data from the Thulamela excavation.

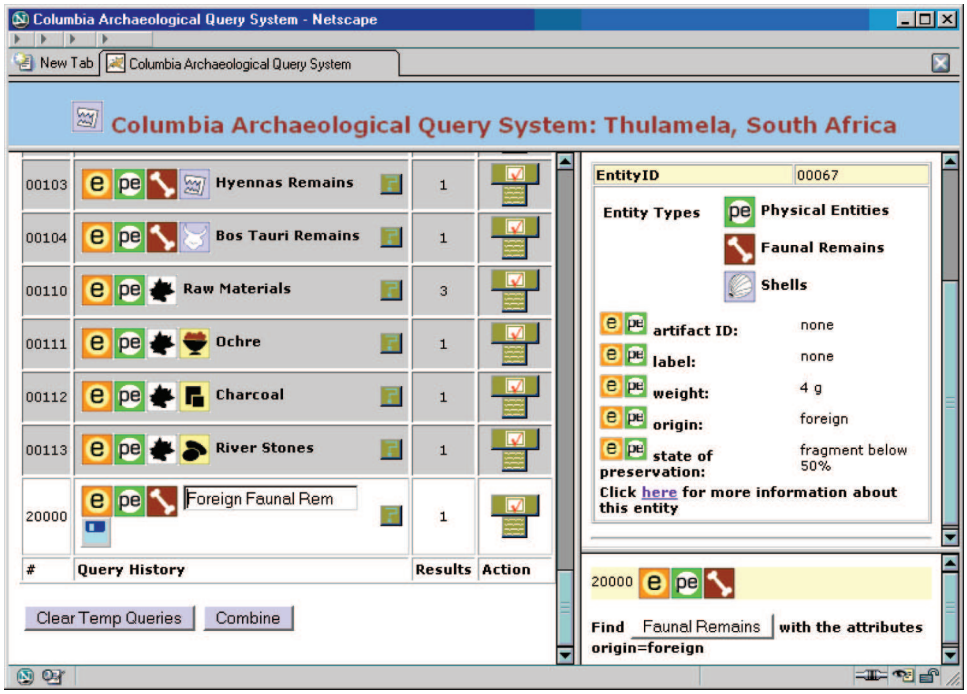


Figure 6.1: A screenshot of the *Faceted Query Engine*.

Our system implements the full Entity Algebra [Ross and Janevski, 2004] and supports the following operators: selection, union, intersection, set difference, and semi-join.

6.2 ReoptSMART: a Learning Query Plan Cache

This section is based on joint work with Kenneth A. Ross, Jun Rao, Wei Fan, Volker Markl, and Guy Lohman. It appeared in [Stoyanovich *et al.*, 2008b].

6.2.1 Introduction

Query optimization is central to the efficient operation of a modern relational database system. The query optimizer is typically invoked every time a new query enters the system. The optimizer identifies an efficient execution plan for the query, based on available database statistics and cost functions for the database operators. In commercial systems, great care has been taken to reduce the overhead of query optimization. However, the task of the optimizer is complex, and the join ordering problem alone has complexity that is exponential in the number of tables [Ioannidis *et al.*, 1997]. As a result, the cost of optimization may represent a significant fraction of the elapsed time between query submission and answer generation.

If identical queries are submitted, the database system can cache the optimizer's plan the first time, and avoid re-optimization for subsequent query invocations. The query processor merely has to check for syntactic identity of the query with the cached query. This idea can be generalized to queries with parameters. Constants in the query are replaced with "bind variables" to generate a query template, in which the bind variables are parameters. The query processor can then cache a plan for a query template rather than for a query. As a result, frequently-submitted queries that differ only in the constants can avoid the cost of query optimization. Oracle provides such a facility, as do IBM DB2 and Microsoft SQL Server.

There is a potential problem with this approach. A single plan is chosen for all instances of a query template. This plan, while optimal in a particular region of the parameter space, may be sub-optimal in another region. Savings achieved by not invoking the query optimizer may be nullified by the choice of a sub-optimal execution plan. In fact often the difference in cost between the optimizer's plan and the cached plan exceeds the optimization time.

Modern transaction processing systems are often required to handle thousands of transactions per second. Consider for example a web-based OLTP application, such as an on-line book store described by the TPCW benchmark (`www.tpc.org/tpcw`). The system executes canned queries that share a small number of pre-defined templates, such as queries generated by the same HTML form, but differ in parameter values. An interactive system is expected to complete query processing and return results to the user in a short amount of time, often less than a second. A single user's queries may exhibit locality in the values of the submitted parameters, in which case a single query execution plan may be good enough. However, this locality is lost when many users interact with the system at any given time. Therefore, to ensure that an optimal plan is chosen for every query invocation, every instance of the query must be optimized anew. Many of these queries involve joins of several database tables and are thus non-trivial to optimize. In this setting, query optimization may add significant overhead to the overall execution time.

Parametric query optimization (PQO) models the distribution of plans chosen in different regions of the parameter space of a query template [Hulgeri and Sudarshan, 2003], or of a set of templates [Ghosh *et al.*, 2002]. A PQO system is *trained* off-line using a number of invocations of the query optimizer on instances of the query template. The result of such training is a function that, given an instance of the query parameters, identifies a plan that is likely to be the optimizer's choice. To be useful, this function must execute quickly, much faster than the optimizer itself. The function must also have a compact representation, so that a collection of such functions can be managed in memory by the database system.

In [Stoyanovich *et al.*, 2008b] we present *ReoptSMART*, a parametric query optimization framework that uses machine learning techniques to analyze the training set, and to generate a set of classifiers that map parameter instances to plans.

Compared with earlier geometric approaches [Hulgeri and Sudarshan, 2003], machine

```
Select i_title, a_lname, i_publisher
From Author, Item
Where a_id = i_a_id And i_stock < :b1 And i_page < :b2
```

Figure 6.2: The query template for TPCW-1.

learning techniques that we use have the advantage of being effective with much less training data, and of automatically handling non-linear boundaries in plan space. Due to the compactness of the models, our classifiers have modest space requirements linear in the number of classes, and typically on the order of 10 KB per class. Our techniques apply for both qualified and categorical attributes of any data type. We demonstrate experimentally that our methods accurately predict plans for uniform as well as for skewed data distributions. We demonstrate that the testing functions (i.e., identifying a plan given parameter values) can be performed in less than a millisecond per query. This is typically much cheaper than the cost of query optimization.

We apply two state-of-the-art ensemble methods, *AdaBoost* [Freund and Schapire, 1999] and *Random Decision Trees* [Fan *et al.*, 2005], to the problem of Parameteric Query Optimization, and we review each of these in turn.

6.2.2 AdaBoost

Boosting is a general and provably effective method for improving the accuracy of any learning algorithm. AdaBoost [Freund and Schapire, 1999] is a widely accepted boosting algorithm that can improve the accuracy of a collection of "weak" learners and produce an arbitrarily accurate "strong" learner. The weak learners are only required to be slightly better than random guessing, i.e., more than 50% accurate in the case of binary classification.

AdaBoost is a binary classifier, while PQO is a multi-class problem. Rather than opting for the "one-vs-all" approach, which does not provide a measure of classification confidence, we use AdaBoost in scope of *error-correcting output codes* [Dietterich and Bakiri, 1995].

A critical modeling question that must be answered in order to apply AdaBoost to a particular application domain, in this case PQO, is *what is the right choice for a weak learner*. Our choice of a weak learner was guided by the observation that the selectivity of a single parameter can be used to discriminate between an optimal and a sub-optimal plan for a query in a particular selectivity region.

Consider the query in Figure 6.2 based on the TPCW benchmark. The plan space for this query according to the DB2 Universal Database version 8.2 optimizer is represented in Figure 6.3. In this example the optimizer chooses the optimal plan based on the product of the selectivities of the two parameters. Plan 1 executes a nested loops join with the

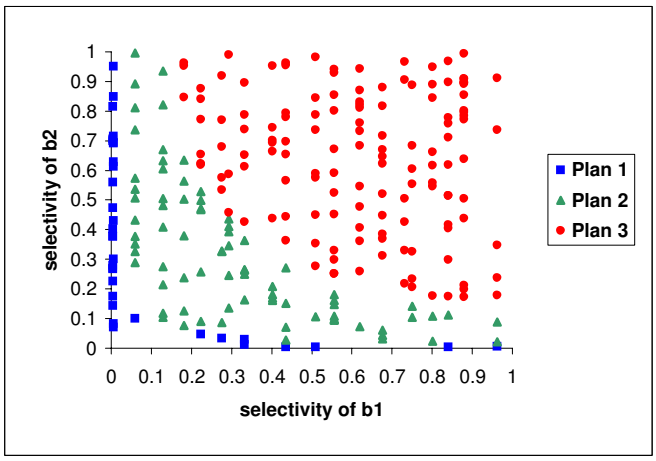


Figure 6.3: Optimal plan space for query TPCW-1.

relation `Item` as the outer, and is chosen by the optimizer when the product of selectivities of $b1$ and $b2$ is very low. This happens when one or both of the selectivities are close to 0, and their product does not exceed 0.01. Plan 2 performs a hash join with `Item` as the build input. This plan is chosen for intermediate values of the two selectivities, with their product between 0.01 and 0.13. Plan 3 utilizes a hash join between the two relations with `Author` as the build input. This plan is optimal when both selectivities are higher than 0.2 and their product is above 0.13.

For queries with d parameters, the optimizer chooses a query execution plan based on individual selectivities and/or on products of any subset of the d selectivities. Products of selectivities naturally correspond to estimates of the relative size of intermediate or final results during plan execution. Explicit enumeration of all possible products (i.e. of all possible subsets of parameters) is exponential. We design our weak learners to avoid the exponential explosion and consider the selectivity of one parameter at a time. For Plan 1 we observe that the product of the selectivities is low if either one of the selectivities is less than 0.004, in which case the selectivity of the other parameter is immaterial, or if both $selectivity(b1) \epsilon [0, 0.06]$ and $selectivity(b2) \epsilon [0, 0.05]$.

The design of our weak learners is based on the above observation. Each weak learner is a discrete vector of weighted probabilities. The probabilities represent the likelihood that a particular plan is chosen by the optimizer when the selectivity falls within each bucket. The weights are adjusted over time by the AdaBoost meta-learner. A weak learner of this kind is defined for each parameter, and for each plan.

6.2.3 Random Decision Trees

A *decision tree* is a classifier with a hierarchy of decisions made at each node of the tree. One traverses the tree from root to leaf, choosing the appropriate child based on the decision criterion coded into each node. For example, a node might have children for different ranges of the selectivity of the first predicate of a query template.

The Random Decision Tree (RDT) method constructs multiple decision trees *randomly*. The construction selects a feature (in our case a predicate selectivity) at random from among those features not yet used in higher levels of the tree. A partitioning value for that feature is also selected at random from some distribution. Training data points from the node are then distributed to the node's children. Construction stops when the depth reaches a certain limit, when the number of data points in a node is sufficiently small, or when all points in a node have the same label (pure node).

During the on-line phase, each tree is traversed using the actual query selectivities, to arrive at a leaf node L containing a number of plans. A posterior probability is calculated for each plan P. This probability is simply the proportion of the training points in L that are labeled with P. The posterior probabilities are averaged across all trees, and the plan with the highest average is output. RDT has been shown to reliably estimate probabilities, closely approximate non-linear boundaries, and reduce variance when the number of training examples is small [Fan *et al.*, 2005].

To adapt RDT for query plan prediction, we make one important improvement based on our knowledge about the behavior of the optimizer. While predicates are still chosen at random, the decision threshold is no longer chosen at random. Instead, for a randomly chosen predicate, we compute a threshold with the highest information gain [Mitchell, 1997]. This way we are more likely to generate pure nodes, which leads to smaller trees.

6.2.4 Results

Figures 6.4 and 6.5 present the decision boundary learned by AdaBoost and RDT, respectively, for query TPCW-1. The color of a region indicates the learned plan for that region.

In [Stoyanovich *et al.*, 2008b] we present an experimental evaluation of ReoptSMART on the DB2 Universal Optimizer over *selected* queries from two workloads: the TPCW and the Dutch DMV. Our results demonstrate a new win over the baseline methods, and indicate that Random Decision Trees outperform AdaBoost in our framework.

6.3 Estimating Individual Disease Susceptibility Based on Genome-Wide SNP Arrays

This section presents *MutaGeneSys*, and is based on joint work with Itsik Pe'er that appeared in [Stoyanovich and Pe'er, 2007].

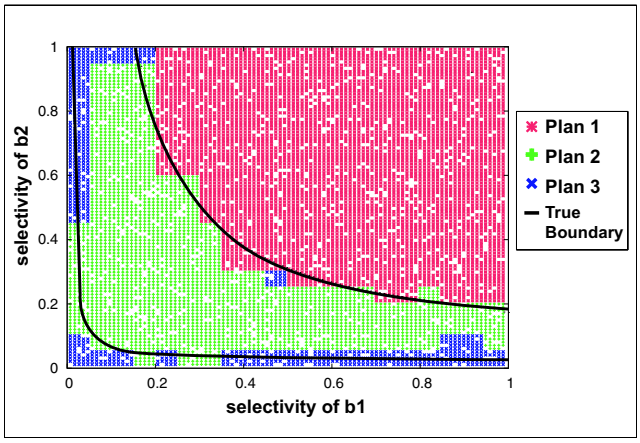


Figure 6.4: AdaBoost decision boundary for TPCW-1.

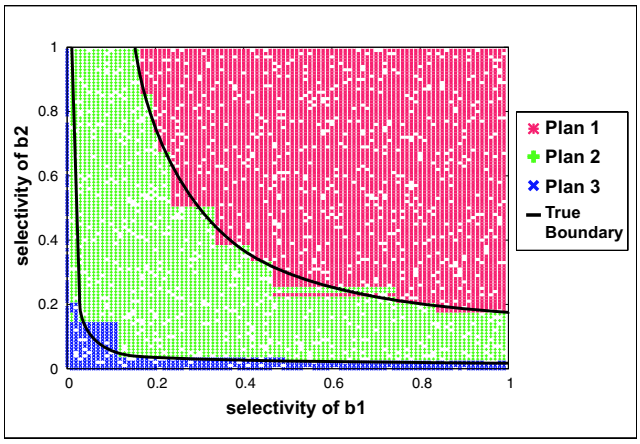


Figure 6.5: RDT decision boundary for TPCW-1.

6.3.1 Introduction

Availability of genetic information continues to revolutionize the way we perceive medicine, with an ever stronger trend towards personalized diagnostics and treatment of heritable conditions. One challenge towards this goal is per-patient evaluation of susceptibility to disease and potential to gain from treatment based on single nucleotide polymorphisms (SNPs) – DNA sequence variations occurring when a single nucleotide in the genome differs between individuals. Significant attention of the research community is devoted to determining *direct causal association* between the genotype and the phenotype, and many interesting associations have already been reported. The Online Mendelian Inheritance in Man (OMIM) database (`www.ncbi.nlm.nih.gov/omim`) is currently the most complete source of such associations. A text search of OMIM yields, for example, a correlation between a C/T SNP (rs908832) in exon 14 of the ABCA2 gene and Alzheimer disease and a

connection between a SNP in the IFIH1 gene, rs1990760, and type-I diabetes.

Much individual genetic data is now being collected in the context of association studies, typing thousands of individuals for millions of variants. Yet, fully exploiting genetic information for disease prediction is difficult for two reasons. First and foremost, genetic information remains expensive to collect, and it is currently economically prohibitive to make a complete set of an individual's genotypes of SNPs available for analysis. Cost-effective methods such as SNP arrays currently exist, and are used for collecting genetic data from 1-5% of all 11 million human SNPs. This calls for the development of techniques that can effectively utilize partial genetic information for disease prediction. The second reason that makes personalized disease prediction difficult is the limited amount of cross-referencing between OMIM and other NCBI databases. This motivates the development of an integrated framework geared towards personalized genome-wide disease prediction. In this section we describe *MutaGeneSys*, a system that can be seen as a first step towards such a framework.

Several studies, culminating with the International HapMap project [HapMap, 2005], report on a significant amount of correlation among markers in the genome [Pe'er *et al.*, 2006]. This genomic redundancy enables one to experimentally type an incomplete set of SNPs, and to expand this set by including correlated proxies. *Indirect association* between proxy genotype and phenotype thus facilitates effective and efficient association analysis.

In the simplest case, SNPs are correlated pairwise, and one of them may be predicted by the other; such correlations are referred to as *single-marker predictors*. Many two-marker and three-marker predictors are also known. Correlations between causal SNPs and their proxies are associated with a coefficient of determination (squared Pearson's correlation coefficient) $r^2 \epsilon [0, 1]$. Marker correlation is population-dependent [de Bakker *et al.*, 2006]; the typed SNPs, and hence, the allowed predictors also depend on the genotyping technology. For example, according to our marker correlation dataset [Pe'er *et al.*, 2006], we can best predict the minor allele T of rs1205 on chromosome 1 based on the the Affymetrix GeneChip 500K genotyping technology, and the prediction accuracy is $r^2 = 0.733$ (in the Japanese and Chinese population). OMIM links the predicted SNP rs1205 with Systemic Lupus Erythematosus (SLE) and antinuclear antibody production.

Genome-wide correlation can be used to augment an individual's genetic information, greatly enhancing its diagnostic value. In the example above, if rs1205 was not typed, but rs12076827 and rs1572970 were, probabilities for the presence of the SLE-associated variant may be estimated. Our project is the first step in this direction. Our goal is to stream-line the process of correlating SNP information with heritable disorders, and to enable real-time retrieval of disease susceptibility hypotheses on genome-wide scale.

6.3.2 Methods

We integrate three datasets: the International HapMap project [HapMap, 2005], Online Mendelian Inheritance in Man (`www.ncbi.nlm.nih.gov/omim`), and a dataset of marker

correlations [Pe'er *et al.*, 2006]. We use HapMap – a comprehensive repository of SNP genotypes, to compile population-specific lists of SNP alleles and frequencies. Our prediction dataset consists of single-marker and two-marker correlations; consequently, these are the types of correlation that our system supports.

Both HapMap and marker correlation datasets are clean, non-redundant, and available in machine-processable form. The challenge with these datasets is the sheer volume of data. However, while there is a lot of information regarding correlations along the genome (the marker correlation dataset is large), relatively little is still known about correlations between SNPs and heritable disorders. We observe that our system can take advantage of marker correlations only if they ultimately lead to a hypothesis of disease susceptibility, and so we use available marker-to-disorder data as the limiting factor. In other words, a correlation between SNP_1 and SNP_2 is only useful in our processing if at least one of these SNPs is associated with a heritable disorder.

We currently use OMIM, a repository of publications about human genes and genetic disorders, as our data source for marker to disorder associations. Associations between SNPs and diseases are not readily available in machine-processable form, and we resort to parsing this information from the text. We process OMIM record by record, looking for occurrences of *rs* numbers (cross-references from OMIM to dbSNP). We then assume that the mentioned SNP is associated with the heritable trait to which the current OMIM record pertains.

6.3.3 Results

Our database contains a significant amount of SNP and marker correlation data, but only a limited number of SNP to OMIM associations. Across all populations and platforms we store over 10 million SNPs, close to 50 million single correlations, and over 20 million two-marker correlations. OMIM contains about 18,000 scientific articles, many of which are not relevant to association studies. However, we still identify 187 articles that mention associations between heritable disorders and SNPs, with 133 unique participating SNPs. Combining OMIM with marker correlation data, we are able to estimate disease susceptibility for additional 328 unique single-marker pairs, and 396 double-marker sets. The dataset is enriched with a total of 1,312 population-specific correlations. The number of susceptibility hypotheses will grow as more information about direct associations between SNPs and heritable disorders becomes available.

For an example of the effectiveness of MutaGeneSys, consider age-related macular degeneration (ARMD). According to OMIM, two SNPs are implicated in this disorder: rs3793784 in the ERCC6 gene and rs380390 in the CFH gene. MutaGeneSys associates 72 additional SNPs with ARMD. As another example, Systemic Lupus Erythematosus (SLE) is associated with two CRP polymorphisms in OMIM; MutaGeneSys uses 15 additional SNPs to indicate potential susceptibility to SLE.

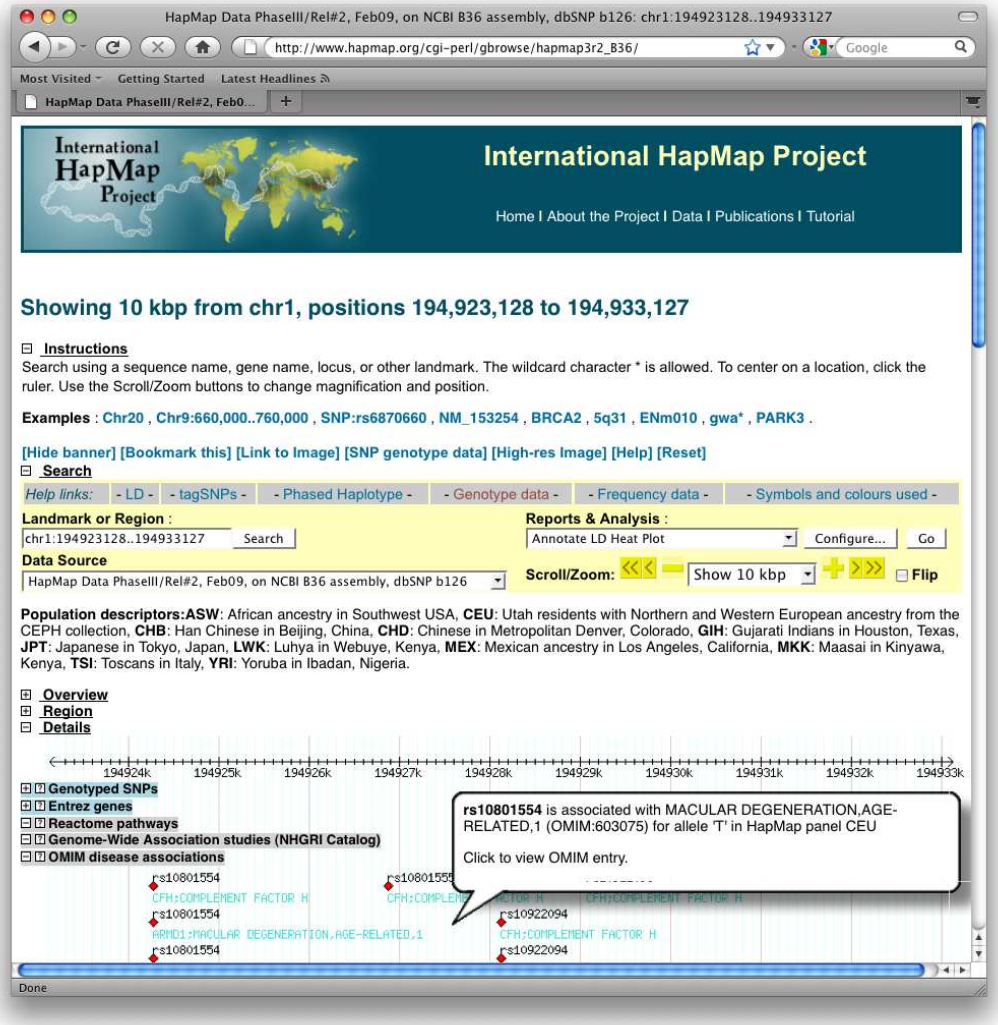


Figure 6.6: Results of MutaGeneSys in scope of the HapMap genome browser.

The complete version of our system is available at `maget.c2b2.columbia.edu/mutagenesys`. The web interface accepts genotype queries specific to an individual, and estimates potential disease susceptibility by looking for population-specific disease associations that also meet the specified correlation coefficient cut-off. The system reasons with both single-marker and two-marker correlations. Results include the causal and the proxy SNPs, the correlation coefficient, and provide a link to the relevant OMIM record and to the portion of the genome in HapMap GBrowse. The system generates HTML and XML output.

Our findings have also been incorporated directly into the HapMap genome browser and into James Watson's personal genome sequence browser, as the *OMIM disease association track*. These sites only use single-maker correlations, and display links to potentially rele-

vant OMIM records irrespective of the population and of the coefficient of determination. Figure 6.6 presents a view of our findings for a particular region on Chromosome 1, as part of the HapMap genome browser.

6.3.4 Discussion

MutaGeneSys cannot yet be considered a source of diagnostic predictions, because of a number of uncertainties involved in going from a specific marker to disease. Given the available data, we made our best effort to control for population and correlation-specific effects: marker associations are computed separately for different populations, and susceptibility results include correlation parameters. For lack of information, *we make two assumptions about OMIM markers: that they are causal, and that they correspond to the minor allele.* (We incorporate allele frequencies from HapMap to determine which allele to consider as minor in a particular population.) Another source of uncertainty is that specific markers may have different levels of penetrance, and therefore have different value as diagnostic predictors. Because of these factors we are currently only able to estimate, not diagnose, individual disease susceptibility.

Chapter 7

Conclusion

In this thesis we proposed novel search and ranking techniques that improve the user experience and facilitate information discovery in several semantically rich application domains. We showed how the social context in *social tagging sites* can be used for user-centric information discovery. We proposed novel ontology-aware search and ranking techniques, and applied them to *scientific literature search* and to ranking in *Wikipedia*. We addressed data exploration in *ranked structured datasets*, and proposed a rank-aware clustering algorithm that uses semantic relationships among attributes of high-quality items to facilitate information discovery.

7.1 Summary of Contributions

We now elaborate on our technical contributions and outline some promising future directions.

In Chapter 2 we described the goals and challenges of context-aware ranking on the Social Web. We showed how a user's social behavior in a collaborative tagging site can be used to improve the quality of content recommendation. We presented *network-aware* search, a novel search paradigm where the score of an item is computed based on a user's social network. We showed how the standard top-K processing algorithms can be used for network-aware search, and presented performance optimizations that explore the trade-off between query processing time and space overhead. We provided an extensive experimental evaluation of our techniques on a dataset from *Delicious*, a leading social tagging site.

Our techniques improve the current state of the art in search and ranking on the Social Web, but also reach beyond social tagging sites, and towards incorporating the social dimension into general Web search.

In Chapter 3 we tackled the challenge of enhancing relevance ranking in scientific literature search. We describe *PubMed*, the largest bibliographic source in the domain of life sciences, and consider how a large high-quality ontology of *Medical Subject Headings*

(MeSH) can be used to relate a user's query to the annotations of a document. We observed that the MeSH hierarchy is *scoped*, i.e., terms may appear in multiple places in the hierarchy, and the meaning of a term depends on its position. This observation challenges most past work which has been developed assuming that a term has a unique node in the generalization hierarchy.

We developed several relevance measures appropriate for ranking in the domain at hand, and proposed efficient evaluation algorithms for computing relevance on the scale of *PubMed* and *MeSH*. We have demonstrated that our measures can be computed in interactive time using score upper-bounds. We presented a two-dimensional Skyline visualization of query results that facilitates data exploration, and demonstrated that it, too, can be computed efficiently on the scale of *PubMed* and *MeSH*.

We also presented results of a preliminary user study that evaluates the effectiveness of our techniques. The small scale of our study and the complexity of evaluation do not allow us to draw statistically significant conclusions about the relative performance of our methods and baselines. In the future we plan to make our software available to the scientific community. This will increase the practical impact of our research and will allow us to gather more information about the effectiveness of our methods.

In Chapter 4 we developed an entity-aware ranking framework, and presented a novel ranking algorithm, EntityAuthority, that models the mutual reinforcement between pages and entities. We demonstrated how an ontology can be used for query processing in this setting. We presented a prototype implementation of our system, and experimentally demonstrated the improvement in query result quality.

In Chapter 5 we introduced rank-aware clustering, a novel result presentation method for large structured datasets. We developed rank-aware clustering quality measures, and proposed a Bottom-up Algorithm for Rank-Aware Clustering (BARAC), an Apriori-style algorithm geared specifically at such quality measures. We presented an extensive experimental evaluation of scalability, and gave an intuition of the effectiveness of BARAC on Yahoo! Personals datasets.

A large-scale user study is currently underway in scope of the Yahoo! Research Sandbox project. The goal of the study is to ascertain the effect of our result presentation method on the user experience. In the future we will consider performance optimizations, and will explore the applicability of our methods to other large structured datasets. We will also explore user interface design issues such as cluster selection.

7.2 Future Research Directions

7.2.1 Combining Different Types of Semantic Context

Using semantic context for search and ranking has potential for high impact, both in terms of scientific advances in Data Management and by enabling end-users. An important ques-

tion that I will address in the future is how to combine various types of context into a single model, achieving higher expressive power, and ultimately supporting a better user experience.

The techniques described in this thesis can be extended and applied to the domain of life sciences, with the goal of facilitating customized content recommendation and scientific collaboration. In a hypothetical system called *PubMed Social*, a scientist's profile may include ontology terms that describe his research interests. The scientist may establish a network of collaborators, and may choose to customize his search and information discovery experience by incorporating his semantic (ontology-based) or social (network-based) context. In addition to consuming available content, the scientist may use the system to disseminate his findings. He will do so by annotating results, and by sharing them with other members of his network. Depending on the stage of the project, the scientist may choose to share results with a small group of collaborators, or with the scientific community at large.

In certain situations, the quality of ranking in search and in content recommendation may be improved by incorporating the user's mental context, or *intent*, into the model. This is based on the observation that the information need may be different for the same user in different situations: I may ask my mother's advise on cooking, and my academic adviser's opinion on research. Likewise, a user of *PubMed Social* who participates in interdisciplinary research, or who is active in multiple research areas, may need help from the system when choosing and aggregating information from multiple sources. To this end, I will explore how structured contextual information about the user, about a particular task, and about the nature of the user's relationship with the content, can be used to better organize *information feeds*.

The paradigm of an information feed, or channel, has emerged as the de-facto standard for information aggregation and sharing in syndicated and collaborative environments. Some examples include the use of RSS for blog aggregation, Facebook's news feed functionality, and status updates on Twitter. Feeds are typically used to aggregate and serve recent information, and are well-suited for accessing information in order of publication time, from more to less recent. However, important information that was published outside the most recent visible time window may be missed. Further, while organizing information solely by time is appropriate for time-centered tasks in information discovery, such as following breaking news, upcoming events, and status updates, it is less appropriate for more semantically-centered tasks. In my future work I plan to build on and extend the ideas of this thesis to combine the time dimension with context-aware semantic relevance.

Using context, and particularly intent, in data management applications, brings about new challenges with respect to privacy. I will consider the privacy implications of explicitly modeling intent, and will explore the privacy vs. expressiveness trade-offs in this setting.

7.2.2 Semantics of Provenance

An important type of context that arises in biological data management is the *provenance of schema and data*. In addition to recording the history of data and operations that led to the creation of a particular data product, provenance often contains semantic annotations that are either automatically derived or assigned by a user. Beyond data provenance, we may think about *schema provenance*, i.e. a record of schema creation and evolution. Both data and schema provenance can give important insights into the phenomenon being modeled, and hence can be used to improve queries on data and schema as well as the ranking of results.

A particular kind of schema that is widely used in scientific applications is a *workflow schema*. A workflow is a procedural schema that describes both the data that it admits and the order of operations over that data. Scientific workflows are complex, and it is therefore essential to enable sharing and re-use of existing workflows in collaborative environments. I plan to build on the insights of Chapters 3 and 4 and explore how semantic annotations that are part of data and schema provenance can be used to improve the quality of similarity search in this domain. A *PubMed Social* user may, for instance, have a file that contains a set of typed single nucleotide polymorphisms (SNPs), which he needs to transform into hypotheses of susceptibility to a particular family of genetic disorders. A novice user may not know which processing modules to invoke, and in which order, and how to format the input data. The user may have an easier time searching for an existing workflow that was designed for similar types of input and output data, and had similar goals. Whether an existing workflow is a likely match can be determined based on the semantic annotations of the match, and on other provenance information, such as its source and recency of use.

Provenance information can also be used to compare workflows, and to summarize a single workflow, or a workflow repository, using a hierarchical view. In Section 6.1.1 we show how complex relational, object-oriented and faceted schemas can be summarized in multiple alternative ways, making the schemas more concise and easier to understand, while also reflecting the user's perspective regarding which elements of the schema are central, and which are subsidiary. In the future I plan to explore an application of this work to the summarization of workflows.

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