Master's Thesis

Mining Comparable Entities from the Web

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2012

웹에서 비교 가능한 개체의 마이닝

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by

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A dissertation submitted to the faculty of the Pohang University of Science and Technology in partial fulfillment of the requirements for the degree of Master of Science in the Division of Electrical and Computer Engineering (Computer Science and Engineering).

Pohang, Korea
Jun. 11, 2012
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Mining Comparable Entities from the Web

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Jun. 11, 2012

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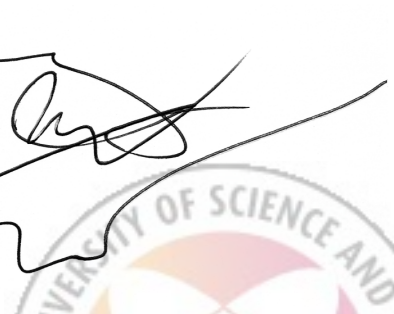

MECE 장명하, Myungha Jang,
20110716 Mining Comparable Entities from the Web,
웹에서 비교 가능한 개체의 마이닝,
Division of Electrical and Computer Engineering, 2012, 030P,
Advisor: Seung-won Hwang. Text in English.

ABSTRACT

Comparing entities is an important part of decision making. Several approaches have been reported for mining comparable entities from Web sources to improve user experience in comparing entities online. However, these efforts extract only entities explicitly compared in the corpora, and may exclude entities that occur less-frequently but potentially comparable. To build a more complete comparison machine that can infer such missing relations, here we develop a solution to predict transitivity of known comparable relations. Named CLIQUEGROW, our approach predicts missing links given a comparable entity graph obtained from versus query logs. Our approach achieved the highest F1-score among five link prediction approaches and a commercial comparison engine provided by *Yahoo!*.

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1 Introduction

To assist decision making, it is useful to compare entities that share a common utility but have distinguishing peripheral features. For example, when deciding on a new mobile device to purchase, a customer benefits from knowing products with similar specifications, *e.g.*, iPhone, Nexus One and Blackberry. Comparable entities need not be tangible; *e.g.*, comparing the health benefits of swimming and jogging.

One possible approach is *comparable entity mining*, which extracts comparable pairs that are explicitly compared on the Web corpus. Toward this goal, several approaches have been studied to mine comparable entities from Web sources [1, 2, 3]. Jindal et al. proposed supervised mining of comparable entities from comparative sentences. This method requires a comparative keyword set, which has to be manually defined. To overcome such a drawback, Li et al. proposed a weakly-supervised bootstrapping method for identifying comparable questions and extracting comparable entities. Recently, Jain et al. used pattern learning methods to extract comparable entities from both web documents and query logs. However, these techniques are limited by their ability to mine only entities explicitly compared in Web sources, excluding entities that are potentially comparable but are not currently explicitly compared in the corpora. However, for a fully-functional comparison suggestion system, such comparisons should not be disregarded. In fact, such missing links for comparable entities are inevitable even with large datasets.

An orthogonal approach is *predictive mining*, which can complement existing mining approach. It expands the known comparable relations using transitivity to infer the unknown relations. We stress that the two approaches are clearly different: for the task of classifying missing links into comparable and non-comparable ones, the former leads to zero precision and recall, whereas the predictive mining can classify them with rea-

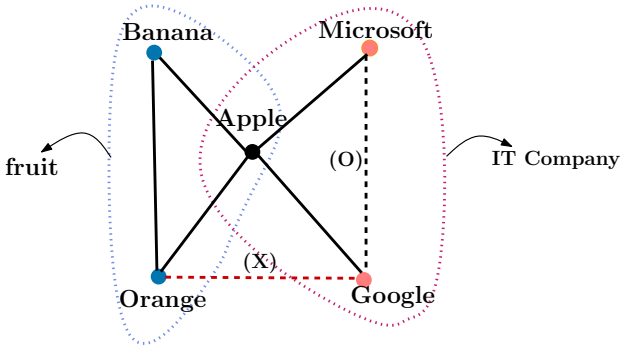

Figure 1: Two different sub-graphs of "fruit" and "IT Company" are connected by a bridge node "Apple"; (o) – comparable edge, (x) – non-comparable edge

sonable accuracy [1]. We first consider a *comparable entity graph (CE-graph)* containing these comparable entities and binary relations. It is an undirected graph $G = (V, E)$ where V is a set of named-entities, E is a set of edges where $(v_i, v_j) \in E$ indicates that v_i and v_j are comparable. An initial CE-graph can be constructed with entity pairs that are explicitly compared and mined by using techniques and resources proposed in comparable entity mining [1, 2, 3]. For an unconnected pair of nodes in a CE-graph, we should next determine the comparability of the pair, *i.e.*, we should predict a link between the nodes if the pair is comparable.

For an unconnected pair of nodes in a CE-graph, whether the pair (a) not comparable or (b) comparable but not observed from the corpus is unknown. Our task is to predict a link by distinguishing the above two cases. An example of (a) is (Orange, Google) and (b) is (Google, Mircrosoft) (Figure. 1). We study the two solutions to predict the links by inferring transitivity of comparable relationship in the CE-graph.

To infer such transitivity, two challenges must be overcome. First, ambiguous entities may serve as *bridge nodes* in a graph, which connect two semantically different subgraphs in a CE-graph. For example, *Apple* is the bridge node that connects two subgraphs, (Fruit: Apple, Banana, Orange) and (IT company: Apple, Microsoft, Google)

[1] Our proposed scheme achieved precision 83% and recall 19%.

(Fig. 6). Bridge nodes may cause an incorrect prediction deduced from a graph topology, such as (Orange, Google).

Second, the sparseness of an initial CE-graph offers little structural information for link prediction. For example, in a CE-graph obtained from Microsoft Live Search *versus* query logs collected over one month, the number of entity pairs explicitly compared is only 0.03% of all possible pairs of entities in the *versus* query logs (*i.e.*, 5,129 pairs among about 14 million possible pairs of 5,368 entities). Later we empirically show that applying generic link prediction algorithms to such a sparse graph achieves very low recall for prediction.

To predict the missing links considering these challenges, the three criteria listed below are required for a possible solution to properly expand known relations using transitivity.

- **Graph structure**: To infer transitivity of links in the given graph, graph structure should be considered to reflect how likely the two nodes are to be connected via neighbors.
- **Attributes**: To determine whether two nodes are comparable, attributes (*e.g.*, semantics) of nodes should be considered.
- **Disambiguation**: Graphs inevitably include ambiguous nodes, which should be disambiguated to prevent generation of heterogenous clusters.

In this paper, we present CLIQUEGROW, a new clustering algorithm that satisfies the three criteria.

2 Related Work

We survey two research areas related to our work: (1) comparable entity mining that complements our prediction work and (2) link prediction methods that compete with ours work.

2.1 Comparable Entity Mining

Several approaches exist to extract comparable entities from various web corpus. Jindal and Liu proposed supervised mining of comparable entities from comparative sentences [1]; their method uses a class sequential rule (CSR) to classify sentences into comparative or non-comparative. This method requires a comparative keyword set for training sequential rules; but keyword sets should be manually defined. To overcome this drawback, Li et al. proposed a weakly-supervised bootstrapping method to identify comparative questions and extract comparable entities [2]. Yang & Ko studied the automatic extraction of comparable entities using comparative type classification in Korean text [4]. Recently, Jain and Pennacchiotti used pattern learning methods to extract comparable entities from both query logs and web documents. Their experiments showed that query logs are superior to web documents as resources from which to extract comparable entities [5].

The above entity mining techniques focus on *mining* comparable pairs readily observed in the web corpus, but our work focuses on *predicting* pairs that cannot be observed from it. Our prediction work thus complements existing comparable entity mining; when used together, both approaches achieve the goal of obtaining a comparable entity set.

2.2 Link Prediction

In this section, we describe two main link prediction approaches–(1) using graph structure and (2) using clustering.

2.2.1 Using graph structure

This approach uses graph structure to solve link prediction problems. The type of graph structure used includes node neighbors and the ensemble of all possible paths. We introduce a few well-known generic link prediction algorithms.

- **CommonNeighbors:** It uses the number of neighbors that node x and y have in common as a similarity measure.

$$score(x, y) = |\Gamma(x) \cap \Gamma(y)| \tag{1}$$

  where $\Gamma(x)$ denotes the set of neighbors of x. This algorithm assumes that the probability that two nodes x and y form a link increases with the overlap of the sets of neighbors $\Gamma(x)$ and $\Gamma(y)$.

- **AdamicAdar:** It also takes a similar measure to CommonNeighbors, but this takes a weighted counting of rarer features rather than the simple counting of features.

$$score(x, y) = \sum_{z \in \Gamma(x) \cap \Gamma(y)} \frac{1}{log|\Gamma(z)|} \tag{2}$$

- **Preferential Attachment:** The basic assumption is that the probability that a new edge of node x is predicted is proportional to —$\Gamma(x)$—. This measure indicates that the probability of that a new link of x and y exists is correlated with the product

Table 1: Characteristics of clustering algorithms sorted by the three criteria

Method	Structure	Attribute	Disambiguation
MC-Cluster	√		√
TP-Cluster		√	√
SA-Cluster	√	√	
Our method	√	√	√

of number of neighbors of x and y.

$$score(x, y) = |\Gamma(x)| \cdot |\Gamma(y)| \tag{3}$$

- **Katz:** It is a measure that directly sums over all paths between x and y, exponentially decreased by the path length to count shorter paths more heavily.

$$score(x, y) = \sum_{l=1}^{\infty} \beta^l \cdot |paths_{x,y}^{<l>}| \tag{4}$$

where $paths_{x,y}^{<l>}$ is the set of all length-l paths from x to y.

2.2.2 Using clustering

For this approach, we specifically discuss three methods that come closest to meeting the three criteria listed above (Table 1).

MC-Cluster is a generic graph clustering that considers the presence of bridge nodes [6]. In the given graph, MC-Cluster generates clusters in which every pair of nodes in an Must-Link (ML) edge belong to the same cluster, and any nodes in an Cannot-Link (CL) edge cannot in the same cluster. A node is identified as a bridge node when it is connected to two nodes by ML edges and the two nodes are connected by a CL edge. The graph is disambiguated by cloning the bridge node to several nodes such that each belongs to one cluster (Figure 2).

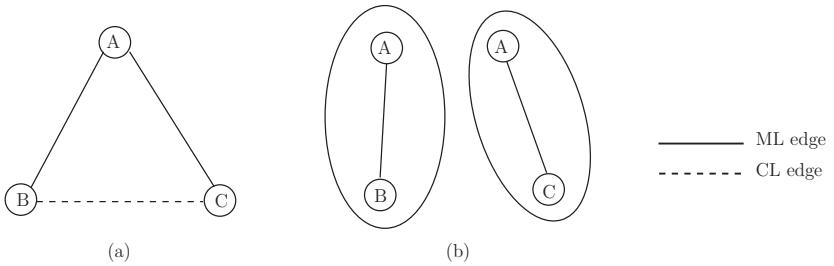

Figure 2: (a) A graph with two ML edges and one CL edge (b) Two clusters split from the graph by having the bridge node 'A' clonned

TP-Cluster was devised for a word sense induction problem that clusters semantically-similar words among a list of words that co-occurred with a given word. [7]. To disambiguate words, TP-Cluster creates all possible triplets from a list of words that the target word is co-occurred with. Each triplet contains the intersection of the co-occurrence list from each word; the intersection is used as a feature of the triplet. Two triplets are merged if they share similar features, until the algorithm converges. TP-Cluster is a context-based algorithm, so when clustering it considers node attributes, not graph structure.

SA-Cluster is a graph clustering algorithm that considers both structural and attributal properties [8]. SA-Cluster converts attributes to structural properties by inserting attribute

nodes that are connected to all nodes that have the corresponding attribute. They exploit a unified random walk distance on the augmented graph. We discovered that SA-Cluster shows a poor performance for our problem due to bridge nodes, and attribute nodes that are commonly-shared by many nodes. As a result, the augmented graph becomes very densely-connected, and may become one big heterogenous cluster instead of several homogenous clusters.

3 Our Approach: CLIQUEGROW

In this section, we introduce CLIQUEGROW, which is a clustering approach that is designed to meet the three criteria. CLIQUEGROW contains two phases: (1) graph enrichment and (2) clustering. In clustering, we aim to find clusters in which all entities within the same cluster are comparable to each other. Clustering is effective despite graph sparseness because all possible links are automatically inferred when an entity is included in the cluster.

3.1 Graph Enrichment

In this phase, a CE-Graph is enriched with semantic knowledge, namely *types*. Types describe the domains to which an entity belongs, and can be obtained from a taxonomy database (examples: Table 2). However, we cannot directly use such types to determine whether two entities are comparable–One may argue if they have the same type, they are comparable; but we find that this is not the case. Types are defined in varying granularity such that some types cover too broad a concept, so a pair having a common type might not be always comparable (i.e., false positive). Alternatively, some types are too narrow that a pair having different types might be comparable (i.e., false negative). To illustrate, in Freebase, 99% of non-comparable pairs would share the same Freebase type and thus would be falsely predicted to be comparable.

In this graph enrichment phase, we thus refine the type data by sorting and ranking to estimate the probability that two entities are comparable in clustering. The graph enrichment has four steps: Step 1 obtains the type, Steps 2 and 3 sort and rank them, and Step 4 extends the coverage of types in the graph.

Table 2: Types and Topic-indicative probabilities for the entity “Apple”.

Types (Step 1)	Collapsed Types (Step 2)	TI Probability (Step 3)
Company Business Organization	Company	0.68
Computer Electronics	Computer	0.20
Fruit	Fruit	0.11
Artist Person	Artist	0.01

3.1.1 Step 1: Adding Types to Entity Pairs

We first obtain types from a taxonomy such as Freebase [2], which is an open-sourced web-scale taxonomy for over 41 million entities. On average, each entity is associated with 15 types. We stress that although we use Freebase, our approach is not specific to this source and can be applied to other such resources.

We match an entity v_i to the entries in Freebase whose names are identical to that of entity v_i. We use a lemmatizer to cover the entities in several forms. An entity can have many types because it may be used in several contexts, or have several meanings (Table 2). A type set for each entity v_i in G is represented as a multi-dimensional binary vector t_i, in which t_i^k = 1 if an entity v_i has *k*-th type t^k, and t_i^k = 0 otherwise. After obtaining the types in the graph, we collapse dependent types (Step 2) and rank the most-likely type for the intent of the entity (Step 3).

3.1.2 Step 2: Collapsing Dependent Types

Types that are highly dependent on other types do not offer extra information, so we may collapse these dependent types to increase computational efficiency and efficacy.(Table 2). These dependencies occur when two types are (1) semantically similar

[2] `http://www.freebase.com`

(*e.g.*, "business" and "organization") (2) in the same hierarchy of concepts (*e.g.*, "athlete" and "person"). For example, "athlete" and "person" are in the same hierarchy of concepts because "athlete" is a sub-concept of "person". An example of semantically similar types is "business" and "organization". Such dependent types are redundant because it does not provide any new insight than the other type.

To remove such dependent types, we first check all pairs of types to see if one appears dependently to the other. We view these relations as directional dependency where one type dependently follows other type. We define a dependency score of t^i for t^j as:

$$dep(t^i \mid t^j) = \frac{co\text{-}occurence(t^i, t^j)}{occurence(t^j)} \tag{5}$$

where occurrence(t^i, t^j) is the number of entities that have both t^i and t^j, and occurrence(t^j) is the number of entities that have t^j. t_i is said to be dependent on t_j if $dep(t_i \mid t_j) >$ type removal threshold σ, which suggests all entities that have t_j also have t_i with a high probability. In this case, the existence of t_i is implied by the existence of t_j, which motivates us to remove such t_j (see 2nd column in Table 2).

If the dependency occurs in a bi-direction, the type whose dependency score is higher than the other type is removed.

Collapsing dependent types reduces computational cost by avoiding unnecessary comparisons and increases efficacy (Figure 5) by allowing the Topic-Indicative Probability (Step 3) to be properly calculated. Specifically, it reduces the cost of computation by avoiding unnecessary comparison between redundant types. Furthermore, the redundant types give too much emphasis on the concept referred to during entity disambiguation. As a result, it leads to the bias toward the concept in the distribution of topic-indicative probability of an entity to be discussed in the following section. This bias decreases the accuracy of our algorithms by resulting in inaccurate entity disambiguation and comparability computation (Figure 5).

3.1.3 Step 3: Topic-Indicative Probability of Types

The types attached to each entity must be ranked by how representative they are to the user's search objective. For example, when "Apple" was compared with many entities such as "Microsoft (in company)", "Banana (in fruit)", but not with any entity in "Artist", we can infer that "Apple" is likely to be used as "company" or "fruit" but highly unlikely to be used as "Artist" in the CE-graph.

For each type of entity in the CE-graph, we calculate topic-indicative ($\mathcal{TI}$) probability, which refers to the probability that the corresponding type is the representative intent of the entity in the CE-graph.

In existing work, such probability has been computed for a set of entities that belongs to the same concept, using a naive Bayes model [9]. However, in our problem context, identifying such a set is our problem goal. We thus modify the model to first infer the representative type for a given edge, which contains the smallest set of entities used in the same context:

$$P(t^k \mid (v_i, v_j)) = \frac{P((v_i, v_j)|t^k)P(t^k)}{p((v_i, v_j))} \tag{6}$$

$$P((v_i, v_j)|t^k)P(t^k) \propto \frac{t_i^k \cdot t_j^k \cdot W(v_i, v_j)}{\sum_{(v_p,v_q)\in E} t_p^k \cdot t_q^k \cdot W(v_p, v_q)}. \tag{7}$$

where $W(v_i, v_j)$ is the edge weight between v_i and v_j defined as occurrences of (v_i vs v_j) in the query logs.

After defining the types for each edge, we can use the probability of types in neighboring edges to infer the $\mathcal{TI}$ probabilities of each entity, because the likelihood that a type is a representative topic increases with the frequency at which it is compared to its neighbors. $\mathcal{TI}$ probability of type t^k for entity pair (v_i, v_j) is defined as:

$$P(t^k \mid v_i) = \frac{P(v_i \mid t^k)P(t^k)}{P(v_i)} = \frac{P(v_i, t^k)}{P(v_i)}, \tag{8}$$

In Eq. 8, we infer $P(v_i \mid t^k)$ from edges of v_i:

$$P(v_i, t^k) = \sum_{v_j \in N(v_i), (v_i, v_j) \in E} P(t^k \mid (v_i, v_j))P((v_i, v_j)). \tag{9}$$

$P(t^k|v_i)$ is normalized such that the sum of the probabilities for all types given the entity is one. To illustrate, $\mathcal{TI}$ probabilities for edges around "Apple" were calculated (see 3rd column in Table 2).

3.1.4 Step 4: Type Propagation

The CE-graph still includes unlabeled entities, *i.e.*, nodes that are not identified with any type. Unlabeled entities are intrinsic due to the dynamic nature of the Web whereby new entities are introduced continually. Manually-curated databases are not always up to date and unlabeled compound and misspelled words easily form, such as "intel processors" and "[John] macain", respectively. Since we use the types as semantic knowledge for entity disambiguation, we must propagate the types to unlabeled nodes to maintain accuracy. To propagate types, we adopt a state-of-the-art label propagation algorithm, Gaussian Random Field (GRF) [10]. A new challenge in our problem context is that more than one types are propagated; we straightforwardly address this by weighted propagation using type probability. More specifically, probabilistic label matrix Y is modified from a binary matrix in the original matrix, to $Y_{ij} = P(t^j \mid v_i)$.

3.2 Clustering

3.2.1 Algorithmic Framework

CLIQUEGROW is an agglomerative algorithm that aims to group nodes into clusters of mutually comparable entities, such that obtaining a transitive closure of each cluster would complete the CE-graph. Once clusters are identified, any two nodes belonging to the same cluster are comparable.

CLIQUEGROW starts with seed unit clusters and iteratively merges other base structures, until they converge to natural clusters. We use triangles (closed triplets) as initial seeds because a triangle is the basic unit of *transitive closure* that is observed. A triangle defines a unique topic among the three pairs of comparable entities of a triangle.

Using triangles as seeds, we gradually grow clusters, by connecting to neighboring entities. By the nature of an agglomerative approach, the topic purity is diluted as the cluster grows. We thus quantify the quality of triangles and populate a priority queue $\mathcal{H}$, to expand only high quality triangles. The quality is quantified as the lowest edge weight of a triangle, as a triangle with a high quality score corresponds to the clique in which every pair co-occurs frequently.

In this process, bridge nodes are first automatically disambiguated by being split into several triangles in the seeds, in which each triangle represents a single semantic. Link prediction is done in this process as well, as the cluster grows– When new entities are added, new links from all possible pairs of entities are inferred. We define and utilize a metric *comparability power* ($\mathcal{CP}$), to quantify the comparability of a a new base structure to the unit cluster that was grown from an initial seed.

Let A and B be groups, represented by a set of nodes, that have $\mathcal{TI}$ probability. $\mathcal{CP}$ is computed as:

$$\mathcal{CP}(A,B) = \sum_{i=1}^{m}\sum_{j=1}^{m} P(t_i,t_j)\cdot P(t_i \mid A)\cdot P(t_j \mid B), \tag{10}$$

where m denotes the number of types, $P(t_i \mid A)$ is a $\mathcal{TI}$ probability of t_i in a unit structure A, and $P(t_i, t_j)$ is a probability that t_i and t_j exist from each of comparable entities. In Eq. 10, $P(t_i \mid A)$ is computed as:

$$P(t_i \mid A) = \frac{\sum_{v_k \in A} P(t_i \mid v_k)}{|A|} \tag{11}$$

In Eq. 10, $P(t_i, t_j)$ is computed as:

$$P(t_i, t_j) = \frac{\sum_{v_p^i \wedge v_q^j = 1} W(v_p, v_q)}{\sum_{t_r^i \vee t_s^j = 1} W(v_r, v_s)} \tag{12}$$

With this metric defined, CLIQUEGROW iteratively identifies the highest-quality triangle seed and grows it into a cluster set by collecting qualifying neighboring base structures as follows:

1. Retrieve all triangle structures from the G and insert them into a priority queue $\mathcal{H}$, ordered by the minimum of the edge weights.

2. Pick the top seed (a triangle) in the sorted $\mathcal{H}$, and compute its $\mathcal{TI}$ probability (Eq. 11).

3. Compute $\mathcal{CP}(S, B)$ for each neighboring base structure B from seed S (Eq. 10). Include the corresponding structure in the cluster, if $\mathcal{CP}(S, B) >$ clustering threshold (CT) δ.

4. Update the $\mathcal{TI}$ probability for the expanded cluster at this iteration.

5. Go to Step 3 and repeat until expansion ceases.

6. Remove the clustered triangles from $\mathcal{H}$ go to Step 1 and iterate until $\mathcal{H} = \varnothing$.

3.2.2 Algorithm Implementations

Two implementations of CLIQUEGROW are possible, one using an edge as a base structure (CLIQUEGROW+E) and the other using a triangle (CLIQUEGROW+T).

CLIQUEGROW+E For each neighboring edge of the cluster (or seed at first), this algorithm calculates the $\mathcal{CP}$ between the edge and the cluster. Specifically, given a cluster S and an edge e_i, if $\mathcal{CP}(S, e_i) >$ threshold δ_e, a new node on the edge is included in the cluster.

CLIQUEGROW+T This algorithm inspects whether a neighboring triangle t_i is comparable to cluster S, such that $\mathcal{CP}(S, t_i) >$ threshold δ_t. However, triangle structures are rare in sparse graphs, so we add Step 0, prior to Step 1, to add triangles to the graph:

0. Retrieve all open triplets from graph G and calculate $\mathcal{CP}$ between the two edges from the triplet. If $\mathcal{CP}>$ seed transitivity threshold γ, and add a new edge for the missing link with a low weight (*e.g.*, zero) such that these triangles are considered after the original triangles are processed as seeds in the sorted $\mathcal{H}$.

4 Competing Algorithms

We compared our algorithms to six approaches: two from an approach that use a graph structure to predict links (LPREDICT, DLPREDICT), three that use a clustering approach (MC-Cluster, TP-Cluster, SA-Cluster), and one from a commercial service (Yahoo! versus query suggestion).

4.1 Link Prediction Algorithms using Graph Structure

We compare CLIQUEGROW with LPREDICT and DLPREDICT. LPREDICT is a generic link prediction algorithm that uses graph structure. We choose AdamicAdar algorithm, which our performance test showed had the best prediction accuracy in among nine existing algorithms (AdamicAdar, CommonNeighbor, PropFlow, RootedPageRank, IPageRank, IVolume, Preferential Attachment,IDegree, and JaccardCoefficient [11, 12, 13]). In this test, we used 80% of the graph as the training example and 20% as the test set, using an open-source solution for link [14] (Figure 4).

Since a generic link prediction algorithm does not consider the presence of bridge nodes, we design DLPREDICT, which combines graph disambiguation and a link prediction. The purpose of this approach is to show that a link prediction using only graph structure is not as efficient as CLIQUEGROW in our problem because the CE-graph is extremely sparse.

DLPREDICT contains three phases: graph enrichment; graph disambiguation; and link prediction.

4.1.1 Phase 1: Graph Enrichment

A graph is first enriched (Section 3.1) to be disambiguated.

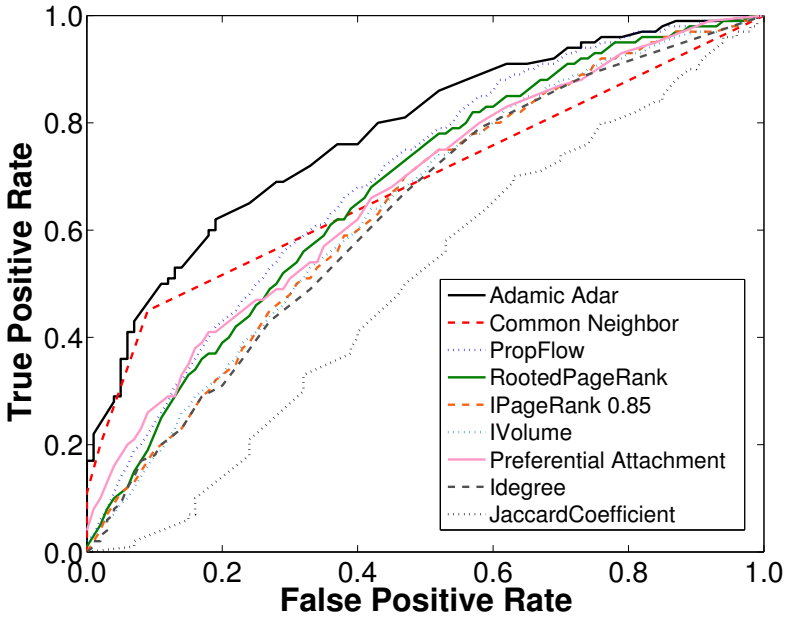

Figure 3: Receiver Operating Characteristics (ROC) of nine generic link prediction algorithms

4.1.2 Phase 2: Graph Disambiguation

Once edges are curated with $\mathcal{TI}$ probabilities in the enriched graph, we identify bridge nodes. For this purpose, we first perform *entity disambiguation* on edges to assign a *surface type* for each, out of many types associated with each edge. Then a bridge node is identified as a node connected to heterogeneous surface types. For example, the surface type is 'company' in (Apple, Microsoft) whereas it is 'fruit' in (Apple, Banana) in Figure 4.

Existing entity disambiguation methods leverage *context* of an entity to find its surface type [15, 16], *e.g.*, using Wikipedia disambiguation page [15]. Our work can be viewed as using an open-source taxonomy (*e.g.*, Freebase), as such context. Our preliminary study suggests that using such taxonomy achieves comparable accuracy to existing

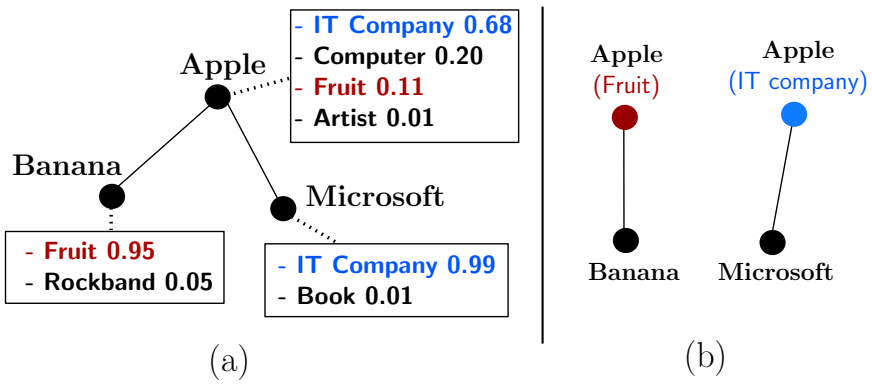

Figure 4: (a) before and (b) after the entity disambiguation of an entity "Apple"

approaches that require crawling of Wikipedia or a Web corpus, but we leave an extensive analysis as future work.

The surface type $t^{\widehat{k}}$ of edge (v_i, v_j) is defined with $\widehat{k}$:

$$\widehat{k} = \underset{k}{\operatorname{argmax}}\, min(P(t_k \mid v_i), P(t_k \mid v_j)) \tag{13}$$

Once the surface types are identified, a bridge node connected to neighbors with m heterogeneous types can be split into m clone nodes representing each type. The CE-graph is thus disambiguated in the form a few homogenous subgraphs.

4.1.3 Phase 3: Link Prediction

We apply a generic link prediction algorithm to the disambiguated CE-graph.

4.2 Clustering Algorithms

How each clustering method works was described in Section 2, so we only explain details relevant to implementation.

- **MC-Cluster** : We first sort edges by descending weight, then set the top 10% edge

weights as ML edges and the bottom 10% edges as CL edges.

- **TP-Cluster** : TP-Cluster was originally not graph-based but context-based, which requires a list of co-occurrence words obtained from external Web documents for each entity. However, we do not have such contextual data in our problem, so we modified TP-Cluster to be graph-based. Instead of a co-occurrence list, we used the list of neighboring nodes as a comparison list [7].

- **SA-Cluster** : We set $k = 200$ and density value $= 0.06$.

5 Algorithm Evaluation

5.1 Experiment Setup

5.1.1 Graph Construction

We used *versus query* logs to construct an initial CE-graph. Although more-sophisticated techniques or proprietary resources can be used to obtain a denser CE-graph, our focus is to show how we reinforce the given CE-graph. Thus we use readily available resource that does not require any complicated tool. These logs are Web queries in several forms such as "A [versus/vs/v.s] B". These versus query logs represent explicit user intention to make comparisons. We used Microsoft Live Search 2006 query logs[3], composed of 14.9×10^6 search queries collected over one month. The number of *versus* queries in the logs was 0.7×10^6; from these we constructed an initial graph that contained 9,574 entities and 15,287 edges.

5.1.2 Gold Standard

We manually labeled a gold standard set on comparable entities in the *versus* query logs. We labeled 7,233 pairs of entities in 447 clusters of mutually comparable entities.

To validate our gold standard, we performed a user study in which 10 human assessors were given 50 questions that ask to determine whether or not each entity pair is comparable. Twenty-five comparable and twenty-five non-comparable pairs were randomly selected from the gold standard. To qualitatively measure the agreement between the gold standard and assessors' answers, we use Cohen's kappa (K) [17] (Eq. 14).

$$\mathcal{K} = \frac{P_a - P_e}{1 - P_e} \tag{14}$$

where P_a is the proportion of agreement among users, and P_e is the proportion of ex-

[3]This log was awarded as a part of Microsoft Research Asia research award.

pected agreement. A kappa score close to 1 means assessors have a very good agreement, and a score close to 0 implies that they have a poor agreement. The following interpretation of Kappa score is suggested [18]:

- Poor agreement = less than 0.20
- Fair agreement = 0.20 to 0.40
- Moderate agreement = 0.40 to 0.60
- Good agreement = 0.60 to 0.80
- Very good agreement = 0.80 to 1.00

We obtained K = 0.9, which indicates that human assessors reached a very good agreement on our gold standard [19].

5.1.3 Evaluation Metric

We used two evaluation metrics depending on the purpose of the each experiment. To compare the effectiveness among DLPREDICT, CLIQUEGROW, Commercial service, we use precision, recall and F1-score. Precision is the number of correct links predicted divided by the number of links predicted by the algorithm. Recall is the number of correct links predicted divided by the number of links to be predicted in the gold standard.

To compare the effectiveness of CLIQUEGROW and other clustering algorithms, we adopted Extended-BCubed metrics [20] that is designed to evaluate the quality of overlapping clusters. The correctness of the relation between two entities e and e' is defined as:

$$\text{Correctness}(e, e') = \begin{cases} 1 & \text{iff } G(e) = G(e') \leftrightarrow C(e) = C(e') \\ 0 & \text{otherwise} \end{cases}$$

where G(e) denotes the gold-standard category and C(e) denotes the cluster to be evaluated. With this correctness function, BCubed precision and recall are:

$$\text{BC Precision} = \text{Avg}_e[\text{Avg}_{e'.C(e)=C(e')}[\text{Correctness}(e, e')]],$$

$$\text{BC Recall} = \text{Avg}_e[\text{Avg}_{e'.G(e)=G(e')}[\text{Correctness}(e, e')]]$$

Note that in our evaluation, we measure the recall only for the predicted pairs that did not appear in the original query graph (*i.e.*, log).

5.1.4 Parameter setting

We empirically set three types of parameters: (1) the type collapsing threshold (TCT) σ, (2) the clustering threshold (CT) δ_e and δ_t, and (3) seed transitivity threshold (STT) γ.

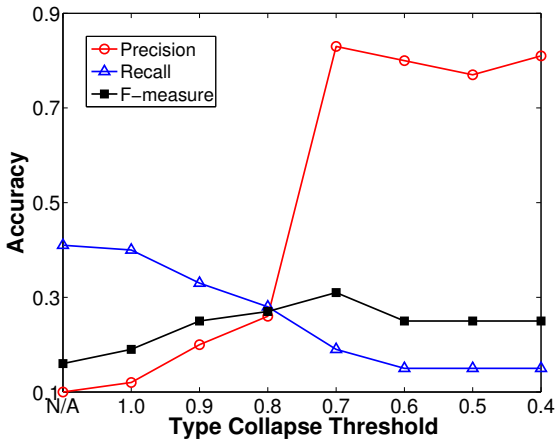

Figure 5: Clustering accuracy varies on TCT

(1) Choice of TCT (σ) We observed the change of accuracy as σ varied. The number of types collapsed increased as σ decreased. When $0.7 \geq \sigma \geq 0.4$, the precision was high; (average 80%). When σ = 0.8, the precision dramatically dropped to 26%. This shows that to achieve the best accuracy of the algorithm, the choice of an adequate type

removal parameter is important. Based on the experiment (Fig. 5), we set σ = 0.7.

(2) Choice of CT (δ) and STT (γ) We observed similar trade-offs between precision and recall for the remaining parameters, and similarly set the optimal parameters that gave the highest F-scores, *i.e.*, $\delta_e = 1.4$, $\delta_t = 0.5$, and $\gamma = 3.0$.

5.2 Evaluation Results

We performed two experiments to compare the effectiveness between (1) LPREDICT, DLPREDICT and CLIQUEGROW (2) CLIQUEGROW and other clustering algorithms, and (3) CLIQUEGROW and the commercial service provided by Yahoo!.

We did not compare ours with other comparable entity mining work such as [5], because we measured the number of correctly *predicted* edges that did not appear in the original log, and these pairs cannot be found from a mining-based approach (*i.e.*, recall of Jain's work in this scenario will be zero).

In each experiment, we measured the prediction accuracy by comparing results to the gold standard.

Table 3: Accuracy comparison of LPREDICT, DLPREDICT, and CliqueGrow

Method	Precision	Recall	F1-score
LPREDICT	0.6233	0.0246	0.0474
DLPREDICT	0.7721	0.0108	0.0213
CLIQUEGROW+E	**0.8310**	0.1941	**0.3146**
CLIQUEGROW+T	0.5234	**0.2160**	0.3059

5.2.1 (1) LPREDICT, DLPREDICT vs CLIQUEGROW

Among the three methods, CLIQUEGROW showed notably higher precision and recall than the other methods. Between LPREDICT and DLPREDICT, DLPREDICT improved precision by 15% but decreased recall by 1%, compared to LPREDICT (Table 3). Although graph disambiguation in DLPREDICT led to precise prediction, it produced

sparser graph by separating a graph component into several sub-graphs than the original graph, which resulted in a lower recall than in LPREDICT.

5.2.2 (2) CLIQUEGROW vs Clustering algorithms

Table 4: Comparison of six clustering methods by Extended B-Cubed metrics

Method	BC Precision	BC Recall	BC F1-score
TR-Closure	0.0068	0.7465	0.0119
MC-Cluster	0.8132	0.2351	0.3647
TP-Cluster	0.3183	0.2662	0.2899
SA-Cluster	0.0209	0.7782	0.0407
CLIQUEGROW+E	0.6006	0.4496	**0.5142**
CLIQUEGROW+T	0.4994	0.4498	0.4733

We compared CLIQUEGROW with MC-Cluster, TP-Cluster, SA-Cluster. The two CLIQUEGROW methods gave better results than the the other algorithms (Table 4). Although MC-Cluster showed the highest precision, it also showed the lowest recall. SA-Cluster failed to give a high precision, because its augmented graph resulted in many components, which were highly-connected by inserted type nodes that are commonly shared by many entities. CLIQUEGROW+E gave a higher precision but lower recall than did CLIQUEGROW+T.

5.2.3 (3) CLIQUEGROW vs Commercial Service

We crawled the list of *versus* query suggestion for each entity from Yahoo!, and compared the result with ours. Yahoo! automatically suggests a list of comparable entities that are extracted from various comparable queries when entity A is typed in with *'A versus ...'*. Since Yahoo! suggests maximum 10 comparable entities, the complete set of comparable entities is unknown when the number of comparable entities is ≥ 10. Hence, we identified entities with < 10 comparable entities; these comprise $\sim$20% of all entities, or $\sim$500 entities.

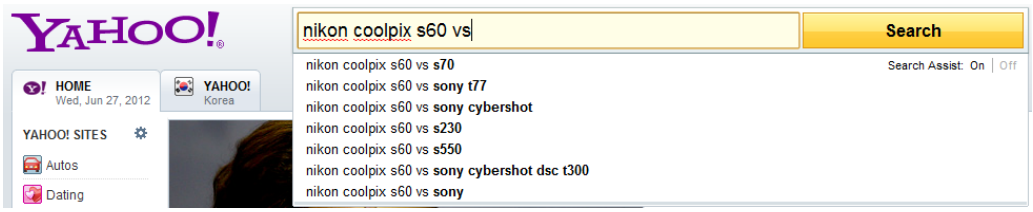

Figure 6: A snapshot of Yahoo! versus query suggestion service

Both CLIQUEGROW variants gave higher precision, recall, and F1-score than query suggestions provided by Yahoo! (Table 5). The result shows that our approach especially has an advantage when finding comparable entities in the long-tail queries.

Table 5: Comparison of CLIQUEGROW and Yahoo! query suggestion for entities in the long-tail queries

Method	Precision	Recall	F1-score
Yahoo!	0.3700	0.0637	0.1087
CLIQUEGROW+E	**0.9394**	0.1005	0.1816
CLIQUEGROW+T	0.7647	**0.1265**	**0.2171**

6 Conclusion

To predict missing links among a comparable entity graph obtained from the query logs, we developed CLIQUEGROW. In order to predict comparability both using graph structure and node semantics, our approach contains two phases, (1) graph enrichment and (2) clustering. In graph enrichment, we exploit type information to find semantics of entities. Once the graph is enriched with types, we apply our clustering algorithm CLIQUEGROW that clusters a set of comparable entities from the given graph while inferring the missing links. CLIQUEGROW was evaluated by a gold standard that is manually created and validated through a user study. CLIQUEGROW gave a higher F-measure than did five other link prediction approaches considered. Additionally, the accuracy of CLIQUEGROW is superior to results obtained from the commercial service of a search engine, Yahoo!. Our results are superior due to the predictive power employed, namely the ability to infer missing links between edges.

요 약 문

비교는 의사 결정에서 매우 중요한 과정이다. 기존에 웹에 존재하는 비교 가능한 두 개체들을 마이닝 하는 여러 연구들이 선행 되었으나, 기존의 연구들은 웹 코퍼스에서 명시적으로 비교된 두 개체를 문장에서 찾아내는 개체 추출 방식에 기반하고 있다. 이러한 추출 방식의 기법은 웹 문서에서 명시적으로 비교되지는 않았지만, 암묵적으로 비교 가능한 두 개체를 찾지 못한다는 한계점이 있다. 따라서, 완전한 비교 추천 시스템의 구현을 위해서는 이러한 암묵적인 비교 관계의 개체들을 찾는 문제가 중요하게 대두 된다. 본 논문에서는 주어진 비교 관계의 개체 그래프에서 숨겨진 비교 관계를 예측함으로써 비교 가능 개체를 마이닝하는 클러스터링 알고리즘 (CliqueGrow)를 제시하였다. 제안한 알고리즘은 기존에 연구된 링크 예측 알고리즘 및 클러스터링 알고리즘들과 비교하였을 때, 비교 관계의 예측에 대한 가장 높은 정확도를 보임을 실험으로 증명하였다. 또한, 제안한 알고리즘은 Yahoo!에서 현재 제공 되고 있는 'versus 쿼리 추천' 서비스와 비교하였을 때 역시 더 많은 비교 개체를 찾을 수 있었다.

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