

Algorithms for Storytelling

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ABSTRACT

We formulate a new data mining problem called *storytelling* as a generalization of redescription mining. In traditional redescription mining, we are given a set of objects and a collection of subsets defined over these objects. The goal is to view the set system as a vocabulary and identify two expressions in this vocabulary that induce the same set of objects. Storytelling, on the other hand, aims to explicitly relate object sets that are disjoint (and hence, maximally dissimilar) by finding a chain of (approximate) redescriptions between the sets. This problem finds applications in bioinformatics, for instance, where the biologist is trying to relate a set of genes expressed in one experiment to another set, implicated in a different pathway. We outline an efficient storytelling implementation that embeds the CARTwheels redescription mining algorithm in an A* search procedure, using the former to supply next move operators on search branches to the latter. This approach is practical and effective for mining large datasets and, at the same time, exploits the structure of partitions imposed by the given vocabulary. Three application case studies are presented: a study of word overlaps in large English dictionaries, exploring connections between genesets in a bioinformatics dataset, and relating publications in the PubMed index of abstracts.

Categories and Subject Descriptors: H.2.8 [Database Management]: Database Applications - Data Mining; I.2.6 [Artificial Intelligence]: Learning

General Terms: Algorithms.

Keywords: redescription, data mining, storytelling.

1. INTRODUCTION

Redescription mining is a recently introduced data mining problem [9, 10] that seeks to find subsets of data that afford multiple definitions. The input to redescription mining is a set of objects O (e.g., books, genes) and a collection of subsets \mathcal{S} defined over O . The goal is to view the set system as a vocabulary of descriptors and identify clusters of

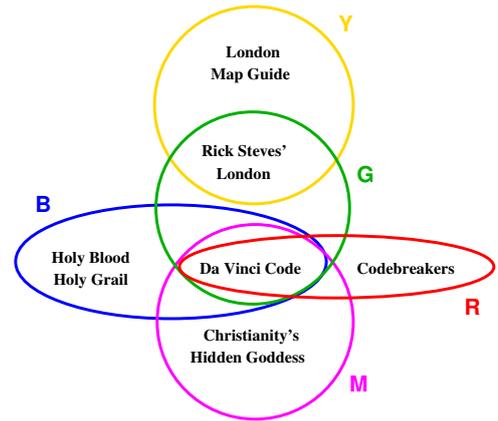


Figure 1: An example input to storytelling.

objects that can be defined in at least two ways using this vocabulary.

For instance, consider the set system in Fig. 1 where the six objects are books and the descriptors denote books about traveling in London (Y), books containing information about places where popes are interred (G), popular books about the history of codes and ciphers (R), books about Mary Magdalene (M), and books about the ancient Priory of Sion (B). An example redescription for this dataset is: ‘books involving Priory of Sion as well as Mary Magdalene are the same as non-travel books describing where popes are interred,’ or $B \cap M \Leftrightarrow G - Y$. This is an exact redescription and gives two different ways of defining the singleton set {‘The Da Vinci Code’}. The basic premise of redescription mining is that object sets that can indeed be defined in at least two ways are likely to exhibit concerted behavior and are, hence, interesting.

While traditional redescription mining is focused on finding object sets that are similar, storytelling aims to explicitly relate object sets that are disjoint (and hence, maximally dissimilar). Given start and end descriptors $X, Y \in \mathcal{S}$, the goal here is to find a sequence of descriptors Z_1, Z_2, \dots, Z_k where $Z_1 = X$, $Z_k = Y$, and every Z_i is an approximate redescription of Z_j , $1 \leq i < k, j = i + 1$. A redescription $Z_i \Leftrightarrow Z_j$ is approximate if its Jaccard’s coefficient $\frac{|Z_i \cap Z_j|}{|Z_i \cup Z_j|}$ is strictly between zero and one. An example story in the above dataset results when we try to relate London travel books to books about codes and cipher history: Some London travel books (Y) overlap with books about places where popes are interred (G), some of which are books about ancient codes (R). This story is a sequence

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obj.	\mathcal{S}_2	\mathcal{S}_3	\mathcal{S}_4	\mathcal{S}_5	\mathcal{S}_6	class
o_1	✓	×	×	×	×	$\overline{\mathcal{S}_1}$
o_2	✓	✓	×	×	×	$\overline{\mathcal{S}_1}$
o_3	✓	×	✓	×	×	$\overline{\mathcal{S}_1}$
o_4	×	✓	×	×	×	$\overline{\mathcal{S}_1}$
o_5	×	×	✓	✓	×	$\overline{\mathcal{S}_1}$
o_6	×	×	×	×	✓	$\overline{\mathcal{S}_1}$

obj.	\mathcal{S}_1	\mathcal{S}_3	\mathcal{S}_4	\mathcal{S}_5	\mathcal{S}_6	class
o_1	✓	×	×	×	×	$(\mathcal{S}_2 - \mathcal{S}_3)$
o_2	×	✓	×	×	×	$(\mathcal{S}_2 - \mathcal{S}_3)$
o_3	×	×	✓	×	×	$(\mathcal{S}_2 - \mathcal{S}_3)$
o_4	×	✓	×	×	×	$(\mathcal{S}_2 - \mathcal{S}_3)$
o_5	×	×	✓	✓	×	$(\mathcal{S}_2 - \mathcal{S}_3)$
o_6	×	×	×	×	✓	$(\mathcal{S}_2 - \mathcal{S}_3)$

Figure 3: (left) Dataset to initialize storytelling algorithm. (right) Dataset for the second iteration.

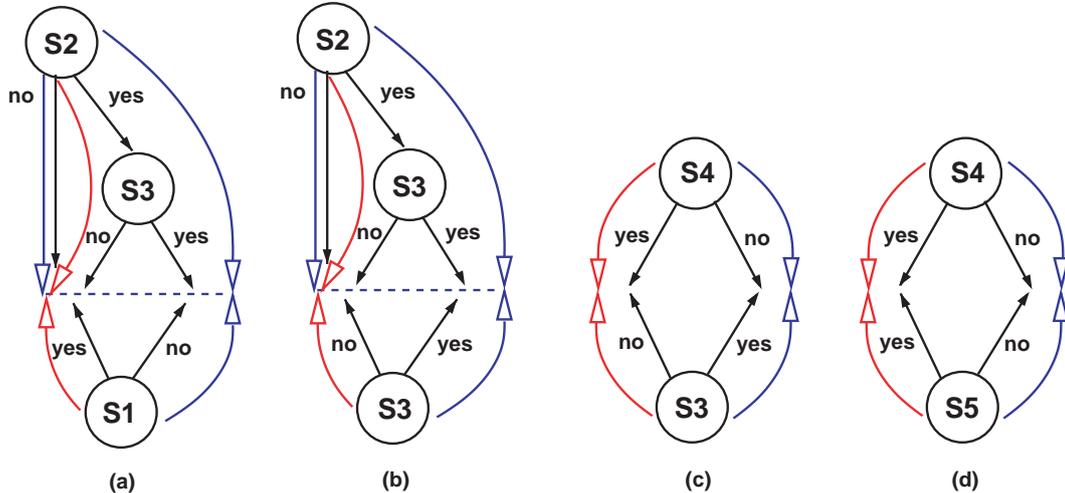


Figure 4: Storytelling using CARTwheels alternation. Beginning with \mathcal{S}_1 , the starting descriptor exposed by the bottom tree in (a), the alternation systematically moves toward \mathcal{S}_5 , the ending descriptor in (d). At each step we alternately keep one of the trees fixed and grow a new tree to match it. The story mined here is the sequence of redescrptions: $\mathcal{S}_1 \Leftrightarrow (\mathcal{S}_2 - \mathcal{S}_3) \Leftrightarrow \overline{\mathcal{S}_3} \Leftrightarrow \mathcal{S}_4 \Leftrightarrow \mathcal{S}_5$.

that imposes a bias \mathcal{B} over set expressions defined on \mathcal{S} ; and branching factor b that restricts the maximum number of possible next states from each state in the A^* search.

Our implementation can be divided into an Initialization step and an Alternation step. In the Initialization step, an empty open list (\mathcal{OL}) and closed list (\mathcal{IL}) required for A^* search are defined. Also, the decision tree induced by the starting class (a 1-level tree with the node X) is added to \mathcal{OL} along with its heuristic score obtained from the function *calculate_heuristic_score* as explained later. This tree provides the classes for the first step of the Alternation process. The class of interest (X) is marked as the one we want to find the closest match for.

At each alternation in the Alternation process, the first tree (t_N) in \mathcal{OL} provides the classification \mathcal{C} . The candidate set of features \mathcal{F} is made equal to all except the feature used at the root of the current tree providing the classes. b distinct trees of depth d are created using these definitions of \mathcal{C} and \mathcal{F} and Jaccard's coefficient as the metric. For each of the decision trees constructed, the Jaccard's coefficient between the current descriptor of interest and the union of the paths leading to it in the current tree is calculated. For each tree (t_j) for which this value is higher than or equal to θ , the *calculate_heuristic_score* is used to compute the heuristic score h_j .

If the heuristic evaluation h_j for the currently picked tree t_j is zero, we have arrived at a tree that has sufficient Jaccard's overlap with the end point of the story. We can then terminate by displaying the story by tracing back the sequence of mined redescrptions. If h_j is not zero, t_j is placed

in \mathcal{OL} and t_N is moved to \mathcal{CL} . For adding t_j to \mathcal{OL} , the heuristic score h_j is combined with cost expended so far (g_j) to arrive at the evaluation criterion s_j . Nodes are placed in \mathcal{OL} in ascending order of s_j . This completes one step in the Alternation process. The whole alternation process outlined is repeated until there is no tree left in \mathcal{OL} or a story has been found.

The heuristic function h is designed to systematically never over-estimate the number of redescrptions remaining and takes the value of zero for a tree whose partition has an overlap of at least θ with the ending descriptor. We now present details of h that clearly indicate its admissibility.

Table 1 outlines the approach to estimate h_j for tree t_j . This algorithm can be understood as follows. Assume that the new descriptor Z_j (provided by tree t_j) has f elements in common with the target descriptor Y and e elements that do not participate in Y . This means that Z_j must shed enough of the e elements and acquire enough of the $|Y| - f$ elements in order to have a Jaccard's threshold of $\geq \theta$ with Y . The goal of *calculate_heuristic_score* is to estimate the number of redescrptions required to shed the requisite number among e elements and acquire some of the necessary $|Y| - f$ elements. The procedure first conservatively estimates if the current discrepancies already correspond to a Jaccard's threshold of $\geq \theta$ with Y , in which case it returns zero. If this is not possible, the procedure estimates the shortest number of steps in which the deletions and additions can happen by a recursive computation. Two extremes are considered at each step – the case where we can acquire as many of the necessary new elements as dictated by θ without any

Table 1: Heuristic for storytelling A* search.

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calculate_heuristic_score( $t_j, C, Y, \theta$ ):
  set  $Z_{j-i}$  = target class from  $C$ 
  set  $Z_j$  = block from  $t_j$  that redescribes to  $Z_{j-1}$ 
  set  $f = |Z_j \cap Y|$ 
  set  $e = |Z_j - Y|$ 
  set  $h = 0$ 
  calculate  $h = \text{minpath}(f, e, |Y|, h, \theta)$ 
  return  $h$ 

minpath( $f, e, |Y|, h, \theta$ ):
  calculate  $\theta_Y = f/(e + |Y|)$ 
  if ( $\theta_Y \geq \theta$ )
    return  $h$ 
  else
    calculate  $\delta f_{max} = \lfloor \frac{(1-\theta)(f+e)}{\theta} \rfloor$ 
    calculate  $\delta e_{max} = \lfloor (1-\theta)(f+e) \rfloor$ 
    set  $h_{min} = \infty$ 
    for ( $i = 0; i \leq \delta f_{max}; i = i + 1$ )
      set  $done = \text{false}$ 
      for ( $k = \delta e_{max}; k \geq 0$  and !  $done; k = k - 1$ )
        calculate  $\theta_{new} = \frac{f+e-k}{f+e+i}$ 
        if ( $\theta_{new} \geq \theta$ )
          set  $done = \text{true}$ 
          set  $h_{curr} = \text{minpath}(f+i, e-k, |Y|, h+1, \theta)$ 
          if ( $h_{curr} < h_{min}$ )
            set  $h_{min} = h_{curr}$ 
          end if
        end if
      end for
    end for
  end if
  return  $h_{min}$ 
end if

```

removals, and the case where we can shed as many of the unnecessary elements as dictated by θ without any additions. This step provides us the bounds δf_{max} and δe_{max} in Table 1. We then search combinatorially within these ranges for the maximal number of deletions, for every possible number of additions, such that θ holds, akin to dynamic programming. The minimum number of redescriptions over all possibilities is then returned.

2.3 Data structures

The efficient implementation of our storytelling algorithm hinges on data structures for fast estimation of overlaps (e.g., see [7, 11]). In this paper, we combine an AD-tree data structure [6] with the signature tables [1] approach for efficient similarity search in categorical data. The signature table is constructed before the Initialization step mentioned earlier. Here, objects in the universal set are divided into a predefined number of clusters (c) on the basis of their co-occurrence frequencies, forming their signature. All descriptors and their co-occurrence frequencies (used in constructing a decision tree of depth more than 1) are also built into an AD-tree at this stage. The descriptors at the top-level of the AD-tree are additionally linked to their signatures. When a similarity search query is issued, only nodes that correspond to signatures of interest need to be investigated. At greater depths in the AD-tree, we can either construct individual signature tables for each node in the AD-tree or we can opt to use a traditional AD-tree node that contains descriptor names and co-occurrence frequencies. In our implementation, we used traditional AD-tree nodes at depth greater than 1.

Using these data structures, we can reduce the number of descriptors searched against at each step and improve the speed of computation of stories. For instance, in the first call to the function *construct_tree*, where we are looking for the best match for the class X from among the descriptor set D , we can reduce X to a vector of size c (X^c). Also, we keep a count of the number of objects in X that belong to each of the c clusters in the form of a frequency vector f^c . The optimistic Jaccard’s coefficient (\mathcal{OJ}) between X^c and a signature vector V_i^c corresponding to a set of descriptors can then be calculated by the formula

$$\mathcal{OJ}(X^c, V_i^c) = \frac{\sum_{j=1}^c (f^c[j] * X^c[j] * V_i^c[j])}{\sum_{j=1}^c f^c[j]}$$

We then compare X^c to all the signature vectors and retain only those for which the optimistic Jaccard’s coefficient is above θ . This narrows down our search to only those descriptors that have potential to provide the necessary overlap.

2.4 Assessing Significance of Stories

The significance of a story is assessed at the level of each redescription participating in the story. To assess the significance of redescription $X \Leftrightarrow Y$, we use the cumulative hypergeometric distribution to determine the probability of obtaining a rate of co-occurrence of X and Y (over the object domain), given their marginal occurrence probabilities, and comparing it to the observed rate of co-occurrence by chance. To account for multiple hypothesis testing, the significance threshold is determined by first characterizing the distribution for all descriptors tested and determining if the given redescription has a rate of occurrence more than four standard deviations above the mean.

3. EXPERIMENTAL RESULTS

Our three experimental studies are meant to illustrate different aspects of our storytelling algorithm and implementation. The first study characterizes word overlaps in large English dictionaries and illustrates scalability of the implementation and how the different parameter settings affect the quality of stories mined. The second study, involving gene sets in bioinformatics, showcases the constructive induction capabilities of CARTwheels when used for storytelling. This study and the third, which builds stories between PubMed abstracts, also illustrate interesting nuggets of discovered knowledge.

3.1 Word Overlaps

In our first study, we implement storytelling for the MorphWord puzzle wherein we are given two words, e.g., PURE and WOOL, and we must morph one into the other by changing only one letter at a time (meaningfully). One solution is: PURE \rightarrow PORE \rightarrow POLE \rightarrow POLL \rightarrow POOL \rightarrow WOOL. Here we can think of a word as a set of (letter, position) tuples so that all meaningful English words constitute the descriptors. Each step of this story is an approximate redescription between two four-element sets, having three elements in common. Note that words that are anagrams of each other (e.g., ‘ELVIS’ and ‘LIVES’) will *not* have a Jaccard’s coefficient of 1, since position is important.

We harvested words of length 3 to 13 words from the Wordox dictionary of English words (<http://www.esclub.gr/games/wordox/>), yielding more than 160,000 words. Con-

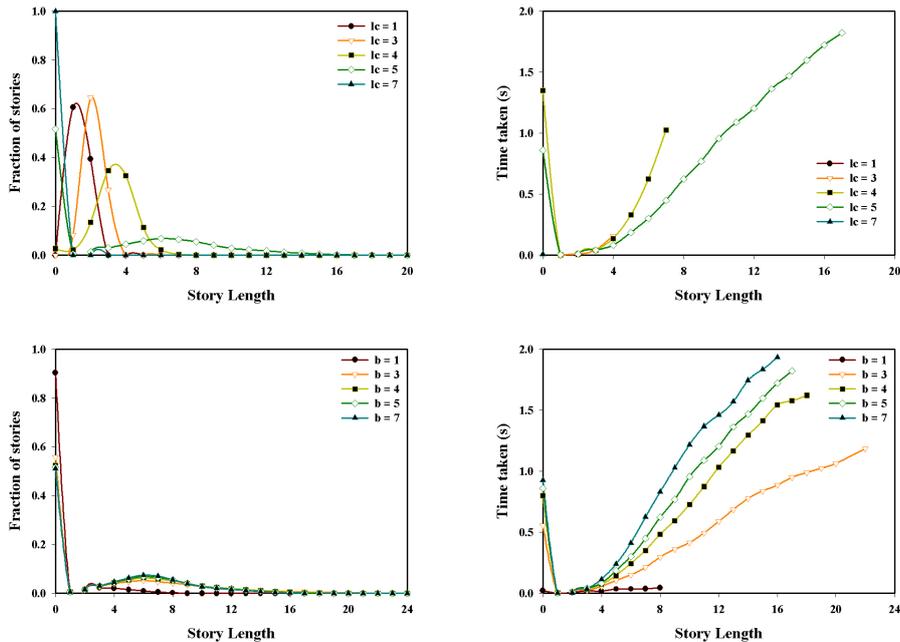


Figure 5: Fraction of stories mined as a function of story length, for different values of lc (Top left) and different values of b (Bottom left); Average time required to mine stories as a function of story length, for different values of lc (Top right) and different value of b (Bottom right); for L_{10} .

sistent with the MorphWord puzzle, we restrict all CARTs to be of depth $d = 1$ and study the effect of θ and b on the number of stories possible, length of stories mined, and time taken to mine stories. For ease of interpretation, we recast Jaccard’s thresholds in terms of the number of letters in common (lc) between two words. Although MorphWord is traditionally formulated with $lc = 1$, we explore higher lc values as well. Due to space restrictions, we present our results only on 10 letter words (L_{10}). We selected 100,000 pairs of words at random and tried to find stories between them, with different lc and b settings.

Fig. 5 (top left) depicts a plot of the fraction of stories (out of 100,000) mined with various story lengths as a function of lc , for a branching factor $b = 5$. In the plot, a story length of 0, rather counter-intuitively, implies that no story was found for the word pair considered. The critical story length where the majority of stories are mined steadily increases as lc is increased. This is because, as lc is increased, more overlap is required at each step of the story such that it takes longer for one word to morph into another. At the same time, the total number of stories mined decreases as lc is increased, due to the lack of viable redescrptions.

To study the effect of b on the length of stories mined, we focus our attention on lc value of 5 for L_{10} . Fig. 5 (bottom left) shows a plot of the fraction of stories mined with various lengths as a function of b . As before, a path length of 0 in the plots implies that no story was found for the word pair considered. Here, the lc value chosen contributes to a high probability of longer stories. As a result the branching factor b plays a crucial role. This is evident in the case of $b = 1$, where the excessively greedy strategy is often rendered futile. As b increases, the chances of going down toward the target word increases and more stories are mined.

To study the effect of these parameters on the time required to mine stories, we set $b = 5$ as before for understanding the role of lc . We computed the average time taken to mine a story, for various story lengths, across all pairs of words considered. Fig. 5 (top right) shows the plot of this average time against story lengths, for different lc values. The plots indicate that there is a near linear increase in time required, with steeper increases for lower lc values. This is because the lower lc values cause an increase in the number of possibilities (within the bound of $b = 5$) which must be explored before converging on the shortest path. Also observe the higher times for story lengths of 0, indicating it takes longer to conclude that stories do not exist. Similar linear trends are observed in time versus the role of b (Fig. 5, bottom right). Here, steeper profiles are witnessed for higher b values. Once again, this is due to the increase in the number of possibilities, although these increases appear to taper off quickly. These figures clearly indicate the underlying tradeoff in mining stories: time versus importance of optimal story lengths.

3.2 Gene Sets

In our second case study, we mine stories among descriptors defined over gene sets in the budding yeast *S. cerevisiae*. We draw our descriptors from various bioinformatics vocabularies (e.g., the Gene Ontology (GO), microarray experiment clusters, experiment ranges) as done in previous work [10]. An example significant story, between the GO categories protein modification and hexokinase, mined for $\theta = 0.5$, $b = 5$, and $d = 2$ is shown in Fig. 7. Observe that the second descriptor in the story involves a set intersection performed by CARTwheels. A unifying feature that links the genes in this story is their common role

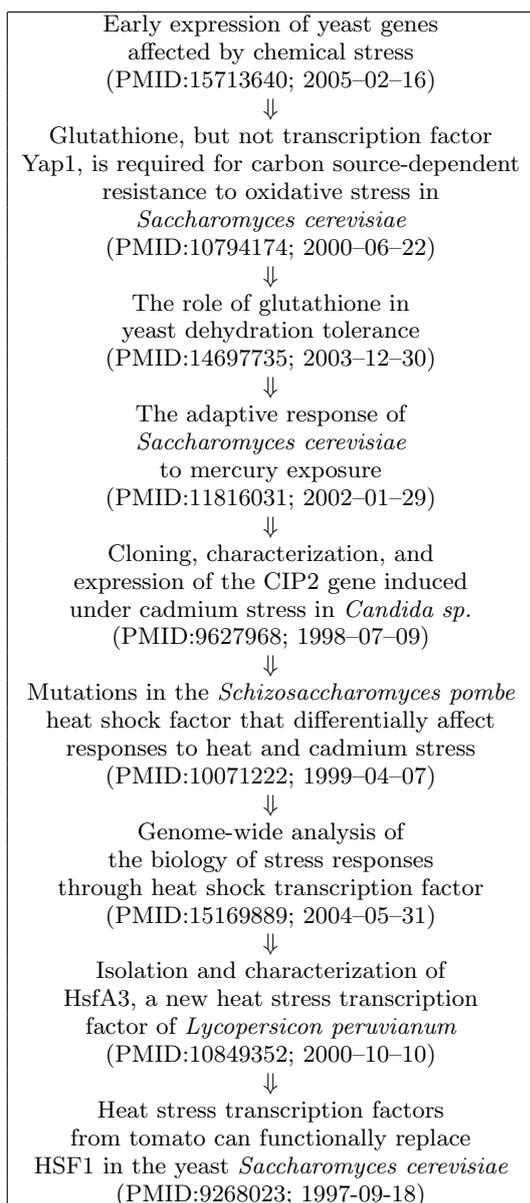


Figure 6: An example significant story among PubMed abstracts relating chemical stresses.

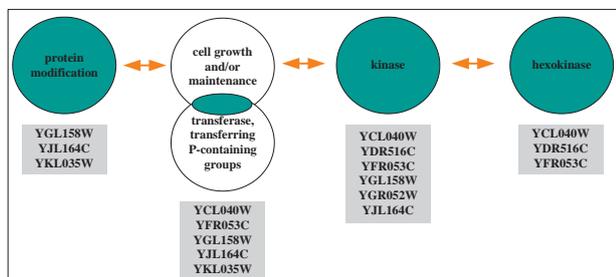


Figure 7: A significant story among gene sets from protein modification to hexokinase.

in nutrient control and carbohydrate metabolism, particularly metabolism of glucose-phosphate. Considering the three genes in the first descriptor, YKL035W is involved in the reversible conversion of glucose-1-phosphate to UDP-glucose via UTP; YJL164C is a cAMP dependent kinase and binds both YFL033C (glucose repressed, nutrient control) and YIL033C (glycogen accumulation); and YGL158W is a kinase that binds YGL115W (release from glucose repression). Two new genes enter the story with the first redescription, namely YCL040W (involved in phosphorylation of glucose) and YFR053C (a hexokinase also involved in the phosphorylation of glucose in the glycolysis pathway). In traversing the second redescription, two additional genes appear: YDR516C is involved in phosphorylation of glucose and, most importantly, also binds YCL040W (which is present in earlier redescrptions). YGR052W is a mitochondrial serine/threonine kinase of unknown function. Through the thread of the story we predict that YGR052W may also be involved in an aspect of glucose metabolism and/or nutrient control.

3.3 PubMed Abstracts

For our final case study, we consider the more than 140,000 publications about yeast in the PubMed index and focus on finding stories between publication abstracts. Each abstract is hence a descriptor over terms/keywords. We restrict our CARTs to be of depth 1 and also adopt a weighted Jaccard's measure that is more suited to measuring similarity between bags (details omitted due to space constraints). To generate keywords, we focused on the 3756 abstracts containing the keywords 'yeast AND stress' and applied stop word removal and Porter's stemming as well as manual inspection to cluster similar words together. Over 95% of the keywords were eliminated by significance testing over the values of $TF \cdot IDF$ (corresponds to a threshold of about 7), resulting in 6821 unique words.

For this application, it is important to note that the computation of the heuristic function would result in a combinatorial problem since each word does not uniformly have a weight of 1 in our Jaccard's calculation. For instance, elimination of different word subsets from a given descriptor, even if they are of the same size, will result in different Jaccard's coefficients; hence we will have to exhaustively search all combinations for removal and addition of keywords to determine the theoretically shortest possible storylength. Thus, for the case of the weighted Jaccard's coefficient, we used a simpler heuristic function wherein we estimate the maximum weight we can gain/lose at each step and calculated the number of steps required to gain enough of the weight for the final document and lose enough weight from the current document, to reach a Jaccard's coefficient above the threshold for the final document. An example of a significant story we mined using this function is given in Figs 6 (the PubMed IDs and publication dates are given alongside).

The story (see Fig. 6), mined with $\theta = 0.2, b = 5$, begins with a high throughput experiment that links chemical stress to gene expression in *Saccharomyces cerevisiae*, and ends with heat stress transcription factors in tomato. The 'story line' was initiated through comparisons between oxidative and heavy metal stresses. This led to a paper identifying a gene from *Candida sp.* that was expressed when the cells are exposed to cadmium but not copper, mercury, lead or manganese. Interestingly a BLAST search for the en-

coded protein sequence indicates that the protein is novel. The link between tomato heat stress transcription factors and a cadmium-specific gene with no known match in the current databases was through work with the fission yeast *Schizosaccharomyces pombe* where a study looked specifically at heat and cadmium stress responses. This story hence illustrates the key players in the systems biology of related chemical stresses.

4. RELATED RESEARCH

We briefly survey related research in three categories: storytelling in information visualization, approaches for topic tracking in documents, and link mining.

In the first category, storytelling has been viewed, not in a data mining context, but as an information organization tool based on narrative structures from real life. Kuchinsky et al. [4] propose an interactive approach for biological information management using three constructs – items, collections (of items), and stories. A ‘story editor’ is used to form an outline of the story using a template. The players (items and itemsets) are then used to fill in the template manually to complete the story.

Pertinent work in the topic tracking community, e.g., [3] focuses on post-processing search results into storylines by analyzing bipartite graphs of document-term relationships. Here a story is a thread of related documents with temporal as well as semantic coherence. Although similar to our PubMed abstracts case study, these works are focused on unsupervised discovery of all threads whereas we focus on directed storylines between given start and end points. Furthermore, as shown in our GeneSets case study, we allow arbitrary set constructions for the purpose of positing overlaps by casting stories as a generalization of redescription. The definition of a ‘thread’ is also different in this work and relies on the notion of node-disjoint directed paths.

Link mining [2] begins with data that can be modeled as a collection of links and, in this sense, storytelling can be approached as a problem of analyzing overlap relationships. However, the links used and sought by us are between sets of items rather than individual items, and these sets are not enumerated beforehand. The concept of stories is also inherently similar in spirit to relational knowledge discovery, e.g., [8], but observe that our vocabularies are primarily propositional in nature, and defined over a single domain of objects. In future work, we aim to generalize story telling into relational redescription mining where the stories can straddle different domains and employ relationships for navigating across domains.

Finally, the applications presented here suggest comparisons to classical discovery systems such as Swanson’s Arrowsmith [13] which can be viewed as seeking stories of length two. Our stories can be of arbitrary lengths with differing complexities of the participating descriptors.

5. DISCUSSION

By defining stories as chains of redescription, we have been able to design a storytelling algorithm as A* search around the outputs of a redescription mining algorithm. We have demonstrated the scalability of this approach using the Word overlaps case study and showcased its potential for knowledge discovery using the Gene sets and PubMed abstracts case studies.

In future work, we aim to investigate other metrics for evaluating stories besides story length, e.g., based on the number of objects temporarily brought into the story, the story’s conformance to prior background knowledge, or using overlap metrics that better mirror a domain scientist’s conception of set similarity. We also aim to explore connections to works that characterize the structure of partitions [5, 12] and investigate whether storylines can be designed around paths in such discrete structures. We also intend to generalize from propositional to predicate vocabularies and cast storytelling in the context of relational redescription. This will help provide structured stories that follow a template of connections. Our eventual goal is to establish storytelling as an important tool for reasoning with data and domain theories.

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