

# Relational Retrieval Using a Combination of Path-Constrained Random Walks

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2010.9.22

# Outline

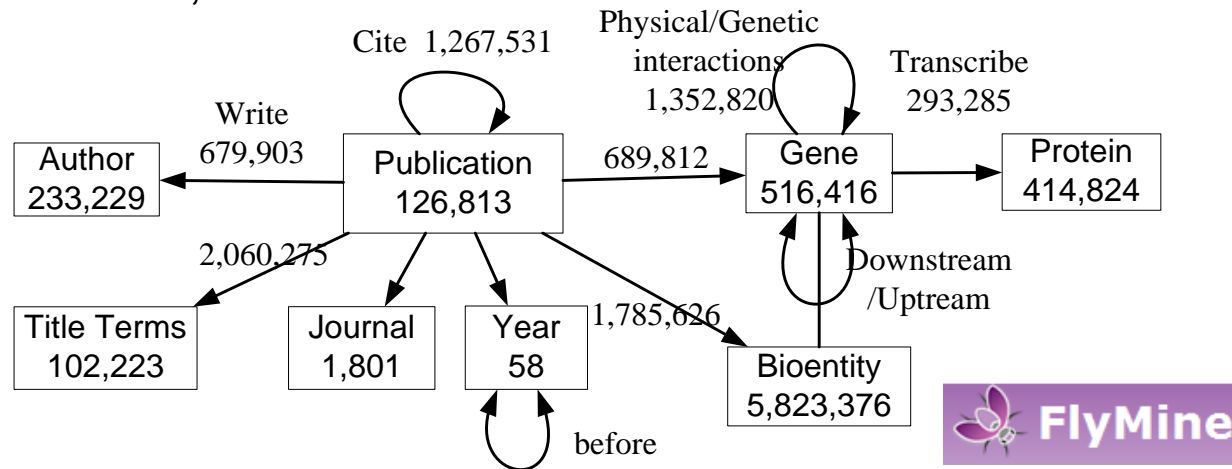
- Relational Retrieval Problems
  - Path-constrained random walks
  - The need for retrieval strategy mining
- Retrieval Models with PCRW
  - Path Ranking Algorithm (PRA)
  - Ext.1: query-independent experts (generalization of PageRank)
  - Ext.2: popular entity experts
- Experiment

# Relational Retrieval Problems

- Data of many retrieval/recommendation tasks can be represented as **labeled directed graphs**
  - E.g. scientific literature
  - Typed nodes: documents, terms, metadata
  - Labeled edges: citation, authorOf, datePublished
- Can support a family of *typed proximity queries*
  - ad hoc retrieval: term nodes → documents
  - Reference (citation) recommendation: topic → paper
  - Expert finding: topic → user
  - Collaborator recommendation : scientist → scientist
- How to measure the proximity between **query** and **target** nodes?

# Biology Literature Data

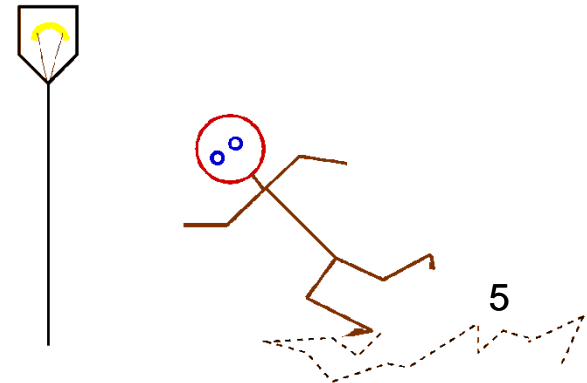
- Data of this study
  - Yeast: 0.2M nodes, 5.5M links
  - Fly: 0.8M nodes, 3.5M links



- Tasks
  - Gene recommendation: author, year → gene
  - Reference recommendation: title words, year → paper
  - Venue recommendation: genes, title words → journal
  - Expert-finding: title words, genes → author

# Random Walks with Restart (RWR) as A Proximity Measure

- RWR is a commonly used similarity measure on Labeled Graphs
  - Topic-sensitive Pagerank (Haveliwala, 2002)
  - Personalized Pagerank (Jeh & Widom, 2003)
  - ObjectRank (Balmin et al., 2004),
  - Personal information management (Minkov & Cohen, 2007)
- RWR can be improved by supervised learning of edge weights
  - quadratic programming (Tsoi et al., 2003),
  - simulated annealing (Nie et al., 2005),
  - back-propagation (Diligenti et al., 2005; Minkov & Cohen, 2007),
  - limit memory Newton method (Agarwal et al., 2006)



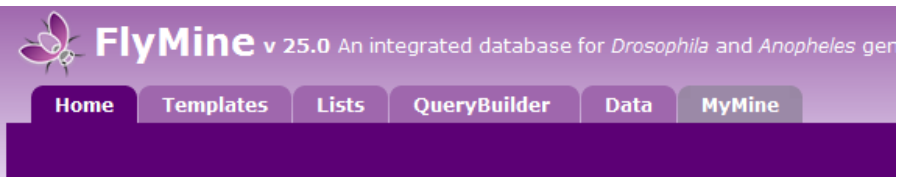
# The Limitation of RWR

- **One-parameter-per-edge label** is limited because the **context** in which an edge label appears is ignored
  - E.g. (observed from real data)

Path	Comments
$author \xrightarrow{Read} paper \xrightarrow{Contain} gene \xrightarrow{Contain^{-1}} paper$	Don't read about <b>genes</b> which I have already studied
$author \xrightarrow{Read} paper \xrightarrow{Write^{-1}} author \xrightarrow{Write} paper$	Read about my favorite <b>authors</b>
Path	Comments
$author \xrightarrow{Write} paper \xrightarrow{Contain} gene \xrightarrow{Contain^{-1}} paper$	Read about the <b>genes</b> that I am working on
$author \xrightarrow{Write} paper \xrightarrow{publish^{-1}} institute \xrightarrow{publish} paper$	Don't need to read paper from <b>my own lab</b>

# The Need for Retrieval Strategy Mining

- A ramification of considering paths on heterogeneous graph with complex schema
- Consider non-expert users....
  - Who are willing to give some labels



[Contact Us](#)

You can create a MyMine account and log in to save queries and lists permanently.

## Data Categories

Select a category to see more information about the data sets included. Each category includes associated templates and lists.



Genomics



Comparative Genomics



Proteins



Protein Structure



Interactions



Gene Ontology



Gene Expression



Transcriptional Regulation



Phenotypes



Pathways

## News

- **FlyMine 25.0** - Thu May 13  
In Release 25.0 we have u data from FlyBase to relea FB2010\_04 and updated s sets to their most recent v Please see the data sectio for more details. DATA NEV

[more...](#)

## Templates

Templates are predefined queries, in the QueryBuilder, if you log in y

Example templates (205 total):

## Lists

You can run queries on whole list: identifiers. Click on a list to view g save lists permanently.

## Query Builder

You can use the flexible query into start is by editing an existing tem

Start a query from: Gene. Prote

University of Cambridge

A screenshot of the FlyMine Query Overview page. The page title is "Query Overview" and the breadcrumb is "FlyMine &gt; QueryBuilder &gt; Query builder ?". Below the title, it says "Click on a class name below to view its fields". The main content is a list of classes with their fields and associated actions (delete, edit, etc.). The classes listed are: TFBindingSite, dataSets DataSet collection, factor Gene, gene Gene, and regulatoryRegions TFBindingSite collection. Each class has a list of fields, some of which are highlighted in green. The fields are: primaryIdentifier, title, name, organism, primaryIdentifier, symbol, primaryIdentifier, title, name, and name. The fields are associated with various actions like 'x' (delete), 'e' (edit), and 'D' (delete). The fields are also associated with various labels like (A), (B), (C), (D), (E), and (F). The constraint logic is shown at the bottom: "Constraint logic: A and B and E and F and C and D".

# The Proposed Approach

- Automatically generate, evaluate and combine different retrieval strategies (paths)
- An example -- reference recommendation
  - In the TREC-CHEM Prior Art Search Task, researchers found that it is more effective to first find patents about the topic, then aggregate their citations
  - Our proposed model can discover this kind of retrieval schemes and assign proper weights to combine them. E.g.

## Weight Path

272.4 *word*  $\xrightarrow{HasTitle^{-1}}$  *paper*  $\xrightarrow{Cite^{-1}}$  *paper*  $\xrightarrow{Cite}$  *paper*

156.7 *word*  $\xrightarrow{HasTitle^{-1}}$  *paper*  $\xrightarrow{Cite}$  *paper*

41.4 *word*  $\xrightarrow{HasTitle^{-1}}$  *paper*



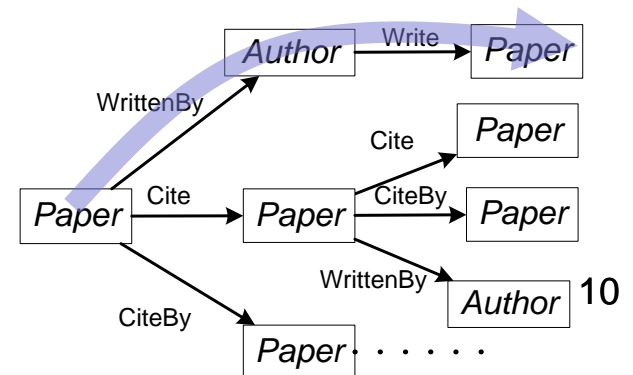
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  - Path-constrained random walks
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# Definitions

- An *Entity-Relation graph*  $G=(\mathbf{T},\mathbf{E},\mathbf{R})$ , is
  - a set of *entities types*  $\mathbf{T}=\{T\}$
  - a set of *entities*  $\mathbf{E}=\{e\}$ , Each entity is typed with  $e.T \in \mathbf{T}$
  - a set of *relations*  $\mathbf{R}=\{R\}$
- A *Relation path*  $P=(R_1, \dots, R_n)$  is a sequence of relations
  - E.g.  $year \xrightarrow{PublishedIn^{-1}} paper$
  - $year \xrightarrow{PublishedIn^{-1}} paper \xrightarrow{Cite} paper$
- *Path Constrained Random Walk*
  - Given a query  $q=(\mathbf{E}_q, T_q)$
  - Recursively define a distribution for each path

$$h_{E_q, P}(e) = \sum_{e' \in range(P')} h_{E_q, P'}(e') \cdot \frac{I(R_\ell(e', e))}{|R_\ell(e')|}$$



# Supervised PCRW Retrieval Model

- A retrieval model can rank target entities by linearly combine the distributions of different paths

$$score(e, \theta, D) = \sum_{P \in \mathbf{P}(q, D)} h_P \cdot \theta_P$$

– or in matrix form  $s=A\theta$

- This mode can be optimized by maximizing the probability of the observed relevance

$$p_e^{(m)} = p(y_e^{(m)} = 1 | q^{(m)}; \theta) = \frac{\exp(\theta^T A_e^{(m)})}{1 + \exp(\theta^T A_e^{(m)})}$$

– Given a set of training data  $D=\{(q^{(m)}, A^{(m)}, y^{(m)})\}$ ,  $y_e^{(m)}=1/0$

# Parameter Estimation (Details)

- We can define a **regularized** objective function

$$O(\theta) = \sum_{m=1..M} o_m(\theta) - \lambda_1 \|\theta\|_1 - \lambda_2 \|\theta\|_2 / 2$$

- Use **average log-likelihood** as the objective  $o_m(\theta)$

$$o_m(\theta) = |P_m|^{-1} \sum_{i \in P_m} \ln p_i^{(m)} + |N_m|^{-1} \sum_{i \in N_m} \ln(1 - p_i^{(m)})$$

$$p_i^{(m)} = p(y_i^{(m)} = 1 | q^{(m)}; \theta) = \frac{\exp(\theta^T A_i^{(m)})}{1 + \exp(\theta^T A_i^{(m)})}$$

- $P(m)$  the index set of relevant entities,
- $N(m)$  the index set of irrelevant entities (sampled)

# Parameter Estimation (Details)

- Selecting the negative entity set  $N_m$ 
  - Few positive entities vs. thousands (or millions) of negative entities?
  - First sort all the negative entities with an initial model (uniform weight 1.0)
  - Then take negative entities at the  $k(k+1)/2$ -th position,
- The gradient

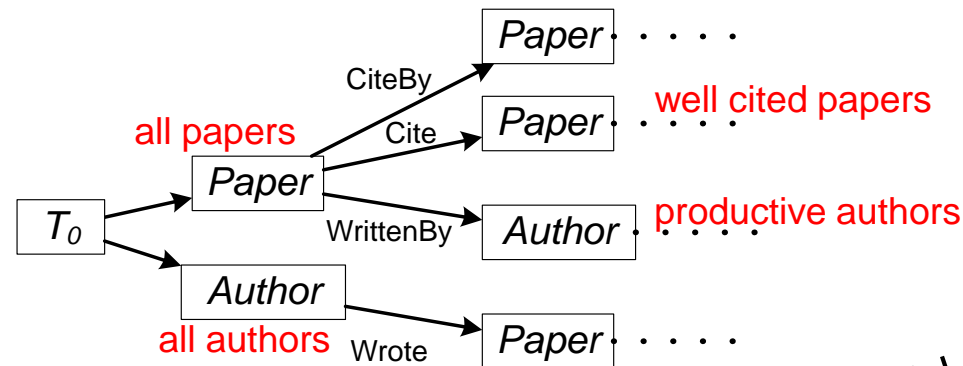
$$\frac{\partial o_m(\theta)}{\partial \theta} = |P_m|^{-1} \sum_{i \in P_m} (1 - p_i^{(m)}) A_i^{(m)} - |N_m|^{-1} \sum_{i \in N_m} p_i^{(m)} A_i^{(m)}$$

- Use orthant-wise L-BFGS (Andrew & Gao, 2007) to estimate  $\theta$ 
  - Efficient
  - Can deal with L1 regularization

# Ext.1: Query Independent Paths

- PageRank
  - assign an **importance score** (query independent) to each web page
  - later combined with **relevance score** (query dependent)
- Generalize to **heterogeneous graph**
  - We include to each query a special entity  $e_0$  of special type  $T_0$
  - $T_0$  has relation to all other entity types, and  $e_0$  has links to all entities
  - Therefore, we have a set of **query independent relation paths**
  - (distributions of which can be calculate offline)

- Example



Simple yet powerful idea

## Ext.2: Popular Entity Biases

- There are **entity specific** characteristics which cannot be captured by a general model
  - E.g. log mining
  - Some document with lower rank to a query may be interesting to the users because of features not captured in the data
  - E.g. personalization
  - Different users may have completely different information needs and goals under the same query
  - The **identity** of **entity** matters

## Ext.2: Popular Entity Biases

- For a task with query type  $T_0$ , and target type  $T_q$ ,
  - Introduce a bias  $\theta_e$  for each entity  $e$  in  $I_E(T_q)$
  - Introduce a bias  $\theta_{e',e}$  for each entity pair  $(e',e)$  where  $e$  in  $I_E(T_q)$  and  $e'$  in  $I_E(T_0)$
- Then 
$$s(e; \theta) = \sum_{P.T_{last}=T_q} h_P^T(e)\theta_P + \theta_e + \sum_{e' \in \mathcal{E}_q} \theta_{e',e}$$
  - Or in matrix form  $s = A\theta + \theta^{(b)} + \Theta q$
- Efficiency consideration
  - Only add to the model top  $J$  parameters (measured by  $|\mathcal{O}(\theta)/\theta_e|$ ) at each LBFGS iteration



# Outline

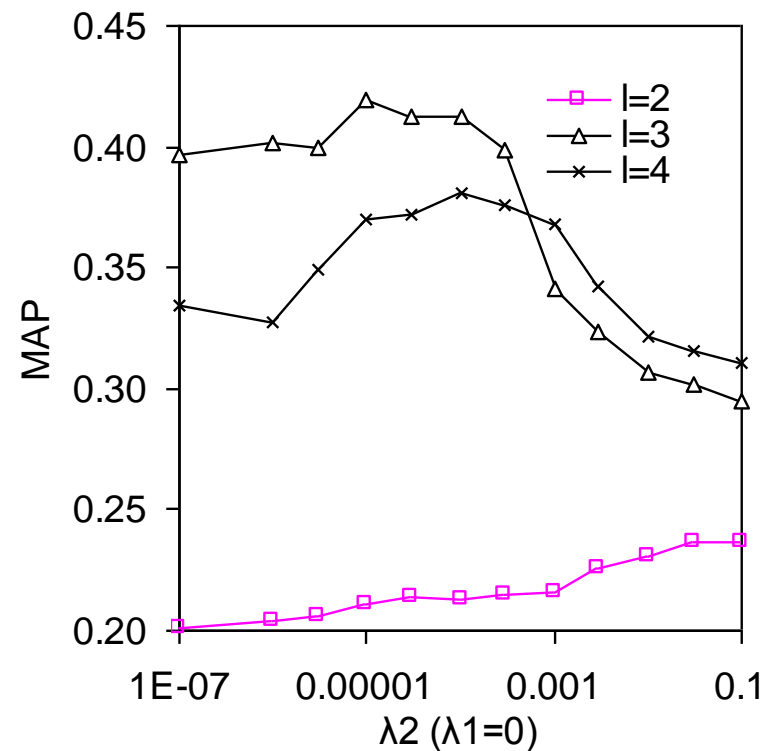
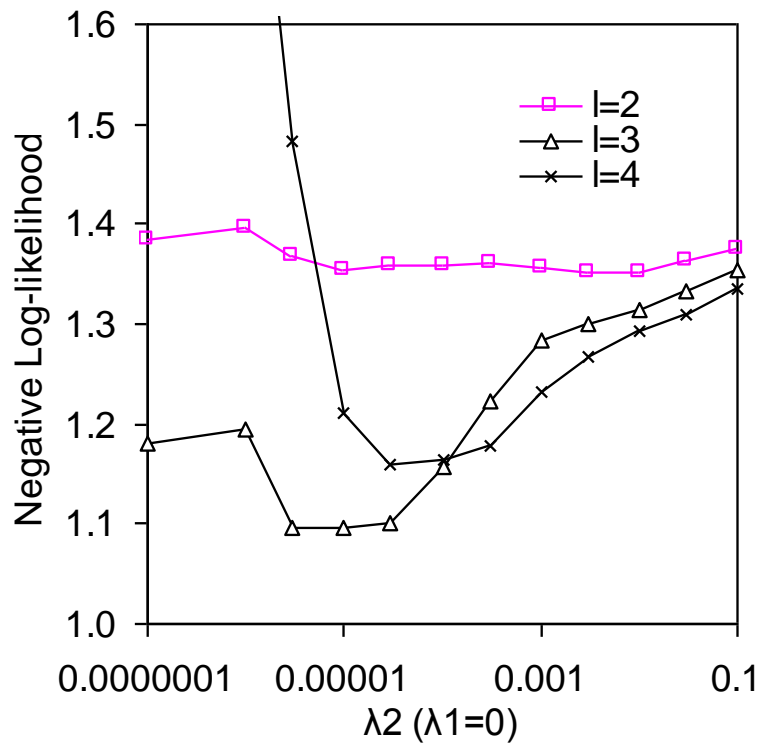
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# Setup

- Data sources for bio-informatics
  - PubMed on-line archive of over 18 million biological abstracts
  - PubMed Central (PMC) full-text copies of over 1 million of these papers
  - Saccharomyces Genome Database (SGD) a database for yeast
  - Flymine a database for fruit flies
- Tasks
  - Gene recommendation: author, year → gene
  - Venue recommendation: genes, title words → journal
  - Reference recommendation: title words, year → paper
  - Expert-finding: title words, genes → author
- Data split
  - 2000 training, 2000 tuning, 2000 test
- Time variant graph (for training)
  - each edge is tagged with a time stamp (year)
  - only consider edges that are earlier than the query during random walk

# L2 Regularization

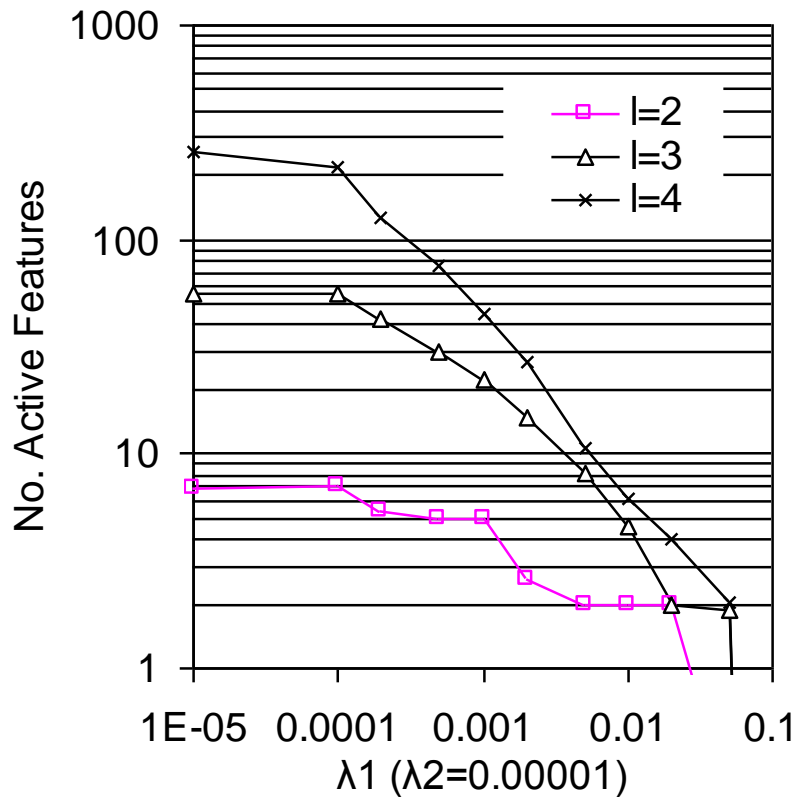
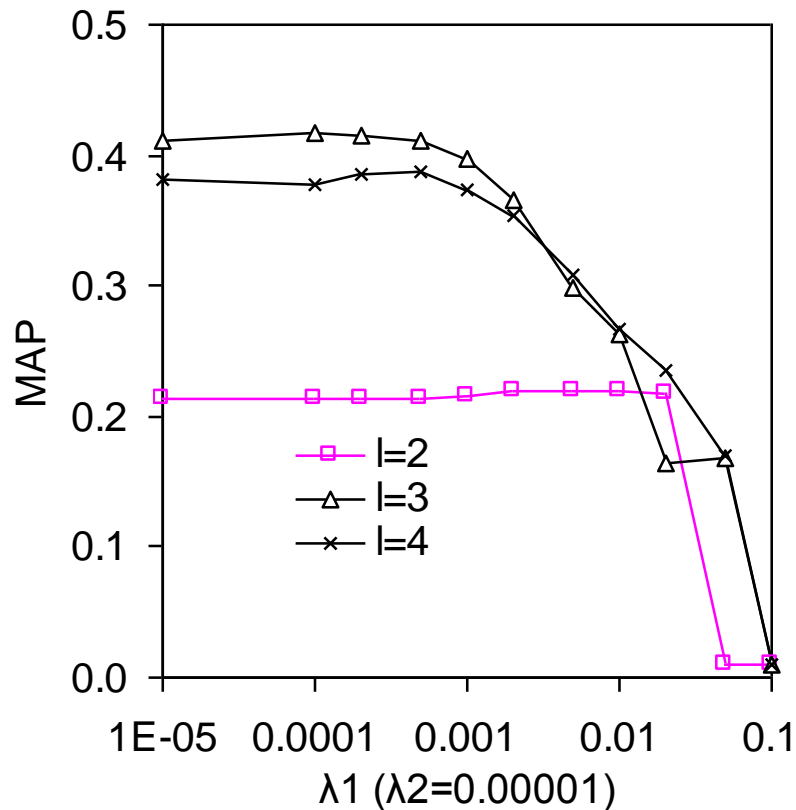
- Improves retrieval quality



On the personal paper recommendation task

# L1 Regularization

- Can help select features



# Example Features

ID	Weight	Feature	
1	272.4	$word \rightarrow paper \xrightarrow{Cite^{-1}} paper \xrightarrow{Cite} paper$	1) Papers co-cited with the on-topic papers
2	156.7	$word \rightarrow paper \xrightarrow{Cite} paper$	2) Aggregated citations of the on-topic papers
3	100.5	$gene \rightarrow paper \xrightarrow{Cite^{-1}} paper \xrightarrow{Cite} paper$	
4	83.7	$word \rightarrow paper \xrightarrow{Cite^{-1}} paper$	
5	50.2	$gene \rightarrow paper \xrightarrow{Cite} paper$	
6	41.4	$word \rightarrow paper$	6) Resembles an ad-hoc retrieval system
7	29.3	$year \rightarrow paper \xrightarrow{Cite} paper$	
8	13.0	$year \xrightarrow{Before^{-1}} year \rightarrow paper \xrightarrow{Cite} paper$	7,8) Papers cited during the past two years
	...		
9	3.7	$T^* \rightarrow paper \xrightarrow{Cite} paper$	9) Well cited papers
10	2.9	GAL4>Nature. 1988. GAL4-VP16 is an unusually potent transcriptional activator.	
11	2.1	CYC1>Cell. 1979. Sequence of the gene for iso-1-cytochrome c in Saccharomyces cerevisiae.	
	...		10,11) (Important) early papers about specific query terms (genes)
12	-5.4	$year \xrightarrow{Before^{-1}} year \rightarrow paper$	12,13) General papers published during the past two years
13	-39.1	$year \rightarrow paper$	
14	-49.0	$T^* \rightarrow year \rightarrow paper$	14) old papers

A model trained for reference recommendation task on the yeast data

# Evaluations

- Compare the MAP of PCRW to
  - Random walk with restart (RWR) model
  - Query independent paths (qip)
  - Popular entity biases (pop)

Corpus Task		RWR	PRA			
		trained	trained	+qip	+pop	+qip+pop
yeast	Ven	44.2	45.7 (+3.4)	46.4 (+5.0)	48.7 (+10.2)	49.3 (+11.5)
yeast	Ref	16.0	16.9 (+5.6)	18.3 (+14.4)	19.1 (+19.4)	19.8 (+23.8)
yeast	Exp	11.1	11.9 (+7.2)	12.4 (+11.7)	12.5 (+12.6)	12.9 (+16.2)
yeast	Gen	14.4	14.9 (+3.5)	15.1 (+4.9)	15.1 (+4.9)	15.3 (+6.3)
fly	Ven	48.3	50.4 (+4.3)	51.1 (+5.8)	50.7 (+5.0)	51.7 (+7.0)
fly	Ref	20.5	20.8 ( <sup>†</sup> +1.5)	21.0 (+2.4)	21.6 (+5.4)	21.7 (+5.9)
fly	Exp	7.2	7.6 ( <sup>†</sup> +5.6)	8.3 (+15.3)	7.9 (+9.7)	8.5 (+18.1)
fly	Gen	19.2	20.7 (+7.8)	21.1 (+9.9)	21.1 (+9.9)	21.0 (+9.4)

Except these<sup>†</sup>, all improvements are statistically significant at  $p < 0.05$  using paired t-test

# Summary

