Promoting Ranking Diversity for Biomedical Information Retrieval based on LDA

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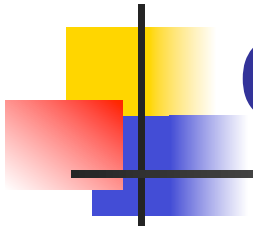
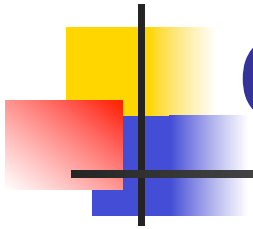


Outline

- Background and Motivation
- Related Work and Contributions
- Reranking Strategies Based on LDA
  - Aspect Discovery and Transformation
  - Reranking with N-size Slide Window
- Experiments
  - Test Collections, Evaluation Measures and Baseline Runs
  - Experimental Results and Analyses
- Conclusion and Future Work



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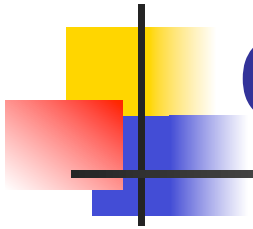
Background and Motivation

- Background
  - Traditional IR models assume that the relevance of a document is independent of the relevance of other documents.

    ⇒ High redundancy and low diversity.
  - Aspect search in biomedical IR
    - In many cases, the desired information of a question (query) asked by biologists is a list of a certain type of entities covering different aspects that are related to the question, such as genes, proteins, diseases, mutations, etc.
    - TREC 2007 Genomics tracks' "aspect retrieval" : to study how a biomedical retrieval system can support a user gather information about the different aspects of a topic.
    - Diversity evaluation: Aspect Mean Average Precision (Aspect MAP).
- Motivation: promoting ranking diversity for biomedical IR



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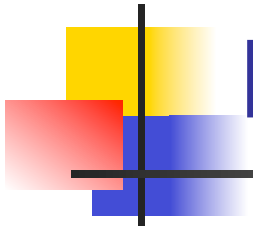


Related Work

- Carbonell *et al.* introduced the maximal marginal relevance (MMR) method, which attempts to maximize relevance while minimizing similarity to higher ranked documents.
- Zhang *et al.* presented four redundancy measures. They modeled relevance and redundancy separately. Since they focused on redundant document filtering, experiments in their study were only conducted on a set of relevant documents.
- Zhai *et al.* validated a subtopic retrieval method based on a risk minimization framework. Their subtopic retrieval method combines the mixture model novelty measure with the query likelihood relevance ranking.

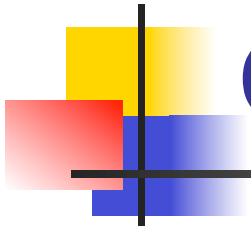
Related Work

- Rianne Kaptein *et al.* employed a top down sliding window to diversify ranked list of retrieved documents and diversity according to some diversity indicators.
- Genomics aspect retrieval conducted by Huang *et al.* demonstrated that the hidden property based re-ranking method can achieve promising and stable performance improvements.
- Yin *et al.* proposed a cost-based re-ranking method to promote ranking diversity. This method concerns with finding the passages that cover more different aspects of a query topic.
- University of Wisconsin re-ranked the passages using a clustering-based approach named GRASSHOPPER to promote ranking diversity.

Related Work

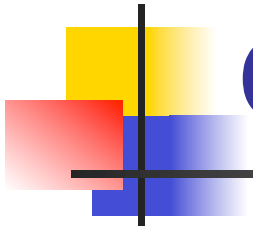
- Consider the aspects of user query and retrieved documents mainly on word level.
- For example, given two retrieved passages:
  - the first one is related to some disease research, in which **kidneys** of white rats are used as experimental materials;
  - the second one is relevant to subject of **kidney** transplantation.
- Two Reasons:
  - Firstly, one or more co-occurrence words in a passage are used to identify the aspect.
  - Secondly, words in a passage are considered as independent to each other.

→ It is insufficient to identify aspect on word level.



Contribution

- Our contribution is three-fold.
  - First, to the best of our knowledge, this is the first study of adopting topic model to biomedical IR.
  - Second, some transformations with topic distribution for retrieved passages are made.
  - Third, two re-ranking algorithms based on "N-size slide window" are proposed, which take both passage novelty and relevance into account.



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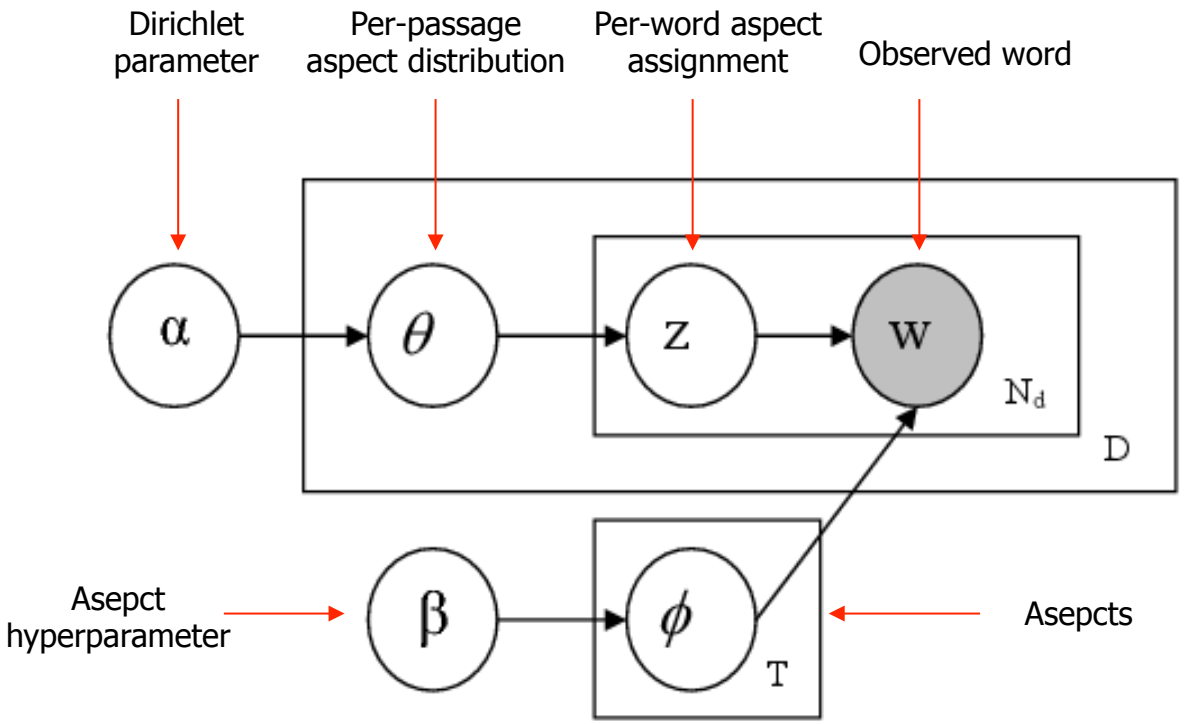
Aspect Discovery



LDA Model

Aspect Distribution Transformation

Aspect distribution matrix

$$\theta = (\theta_1, \theta_2, \cdots, \theta_D)^T$$

$$= \begin{pmatrix} a_{11} & \cdots & a_{1j} & \cdots & a_{1T} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ a_{i1} & \cdots & a_{ij} & \cdots & a_{iT} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ a_{D1} & \cdots & a_{Dj} & \cdots & a_{DT} \end{pmatrix}$$

A new matrix $\Theta = (\Theta_1, \Theta_2, \cdots, \Theta_T)^T$

Measuring the passage importance for each aspect

$$\begin{pmatrix} N_1(a_{11}) & \cdots & N_1(a_{j1}) & \cdots & N_1(a_{D1}) \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ N_i(a_{1i}) & \cdots & N_i(a_{ji}) & \cdots & N_i(a_{Di}) \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ N_T(a_{1T}) & \cdots & N_T(a_{jT}) & \cdots & N_T(a_{DT}) \end{pmatrix}$$

$(1 \le i \le T, 1 \le j \le D)$

$$\mu_i = \frac{\sum_{j=1} \cdots}{D}$$

Re-ranking with N-size Slide Window

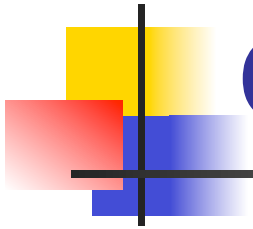
Algorithm 2 rank_NWin_Group Algorithm

1: **Input:** An initial passage ranking R produced for current user query only with respect to relevance, and the size N of the slide window
2: **Output:** A reranked passage list S
3: **Process:**
4: Given top N passages in R, we find a passage $pass_1$ containing the most aspect coverage value using Eq.(5);
5: $R \leftarrow R \setminus \{pass_1\}$;
6: $S \leftarrow \emptyset \cup \{pass_1\}$;
7: Group passages in R into $\lceil R.length/N \rceil$ groups;
8: **for** each group i **do**
9: **for** each passage j in group$i$ **do**
10: $distance\_R_j = 0$;
11: **for** each passage k in S **do**
12: $distance\_R_j = distance\_R_j + Distance(R_j, S_k)$;
13: **end for**
14: $distance\_R_j = distance\_R_j / S.length$;
15: **end for**
16: Rank passages in group i according to $distance_R$ in a descend order.
17: $R \leftarrow R \setminus \{pass\ in\ group\ i\}$;
18: $S \leftarrow S \cup \{pass\ in\ group\ i\}$;
19: **end for**
20: return S.

$$MaxAspCoverg = \arg\max_{q \in [1,N]} \sum_{t=1}^{T} N_t(a_{tq})$$

$$Distance(i,j) = \sqrt{\sum_{t=1}^{T} \left(N_t(a_{ti}) - N_t(a_{tj})\right)^2} \quad (i \neq j)$$

$$Distance(i,j)^* = \sqrt{\sum_{t=1}^{T} \mu_t \left(N_t(a_{ti}) - N_t(a_{tj})\right)^2} \quad (i \neq j)$$



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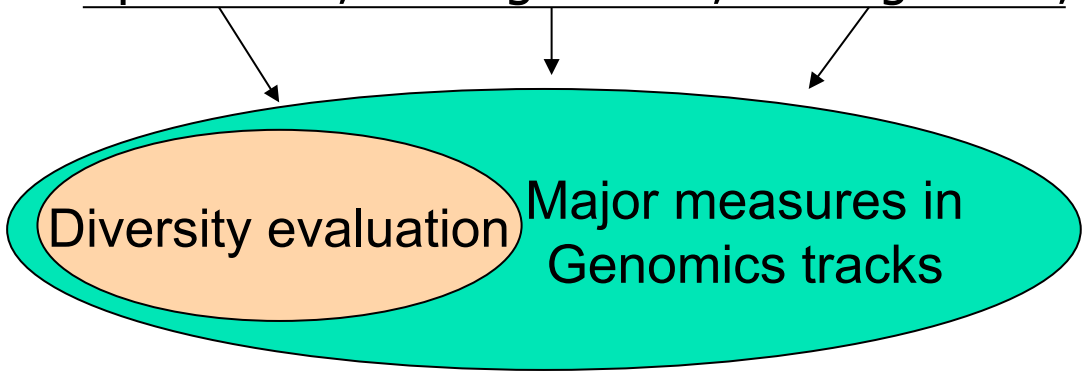
Test Collection and Evaluation Measures

- TREC 2007 Genomics Track Collections
  - Full-text biomedical literature corpus.
  - 36 topics from the 2007 Genomics track;
  - Topics are in the form of questions asking for lists of specific entities that cover different portions of full answers to the topics.
- Evaluations Measures
  - Aspect MAP; Passage2 MAP; Passage MAP; Document MAP



IR Baseline Runs

- NLMinter
  - It achieved the highest Aspect MAP, Passage2 MAP and Document MAP in 2007 Genomics track.
- UniNE2
  - Its performance was above average among all results reported in 2007 Genomics track.

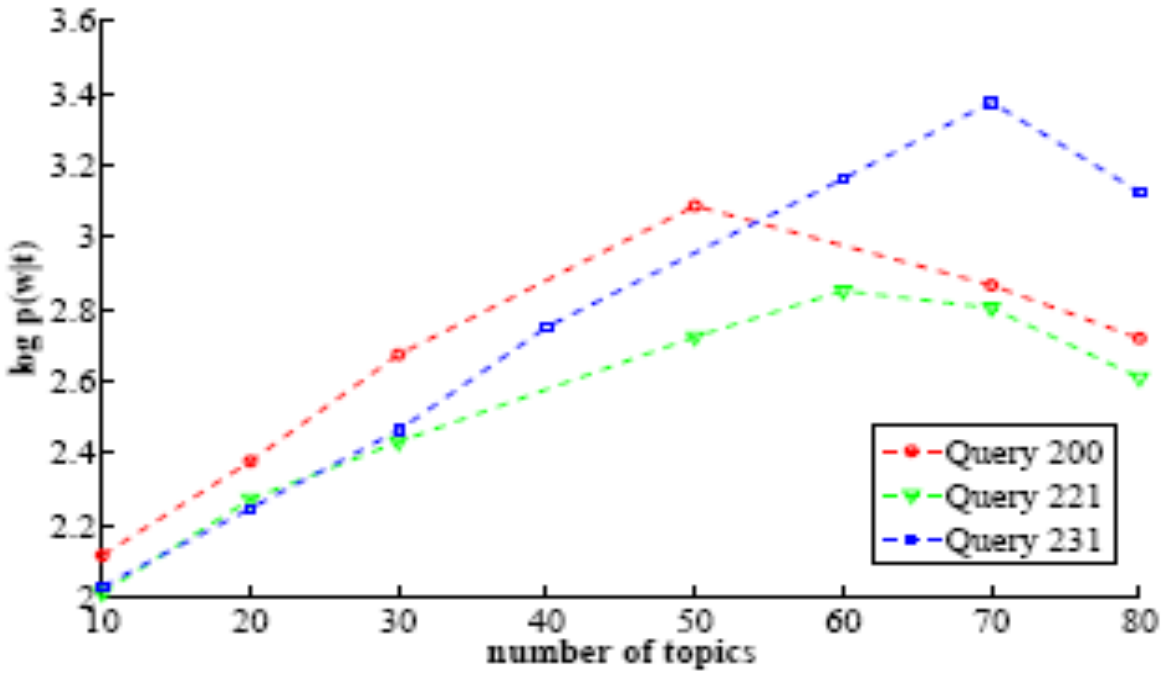
Experimental Results

NLMinter model				
MAP	Aspect	Passage2	Passage	Document
NLMinter	0.23068962	0.07335484	0.05971977	0.20962491
$rank\_NWin$	0.2438342 (+5.70%)	0.07368625 (+0.45%)	0.05868155 (-1.74%)	0.20790886 (-0.82%)
$rank\_NWin^*$	0.24426998 (+5.89%)	0.07372402 (+0.50%)	0.05849706 (-2.05%)	0.20744464 (-1.04%)
$rank\_NWin\_Group$	0.24908569 (+7.97%)	0.07792334 (+6.23%)	0.06151813 (+3.01%)	0.20976964 (+0.07%)
$rank\_NWin\_Group^*$	**0.24910669 (+7.98%)**	0.07793161 (+6.24%)	0.06152586 (+3.02%)	0.20977025 (+0.07%)

UniNE2 model				
MAP	Aspect	Passage2	Passage	Document
UniNE2	0.09880169	0.01777397	0.05236709	0.13771527
$rank\_NWin$	0.1052544 (+6.53%)	0.01946295 (+9.50%)	0.05459447 (+4.25%)	0.13969831 (+1.44%)
$rank\_NWin^*$	0.1052544 (+6.53%)	0.01946007 (+9.49%)	0.05459788 (+4.26%)	0.13964510 (+1.40%)
$rank\_NWin\_Group$	**0.10554020 (+6.82%)**	0.01902429 (+7.03%)	0.05490502 (+4.85%)	0.14035642 (+1.92%)
$rank\_NWin\_Group^*$	0.10549095 (+6.77%)	0.01902427 (+7.03%)	0.05490508 (+4.85%)	0.14035350 (+1.92%)

Results Analysis

- Impact of Parameter β
- Impact of Parameter α and T



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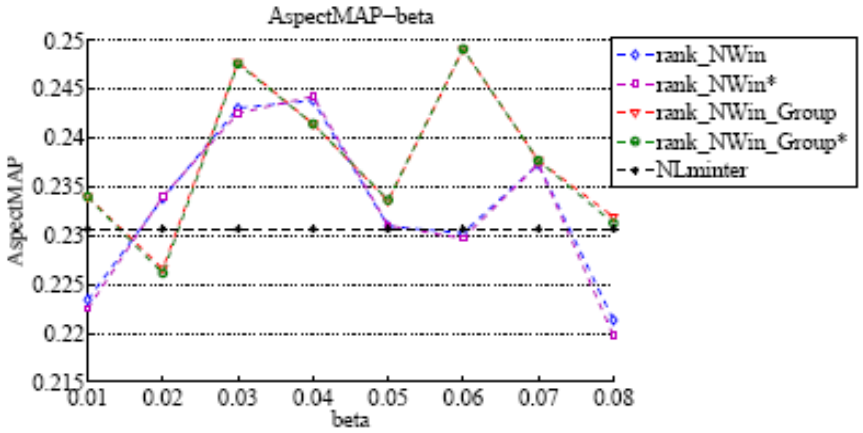
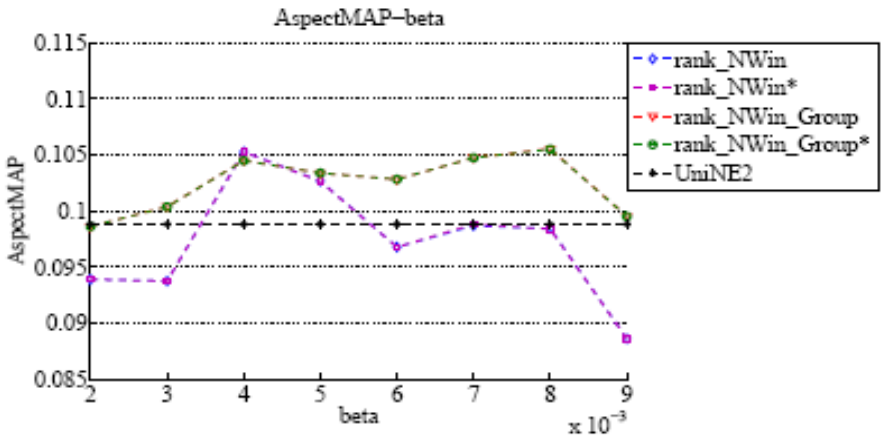
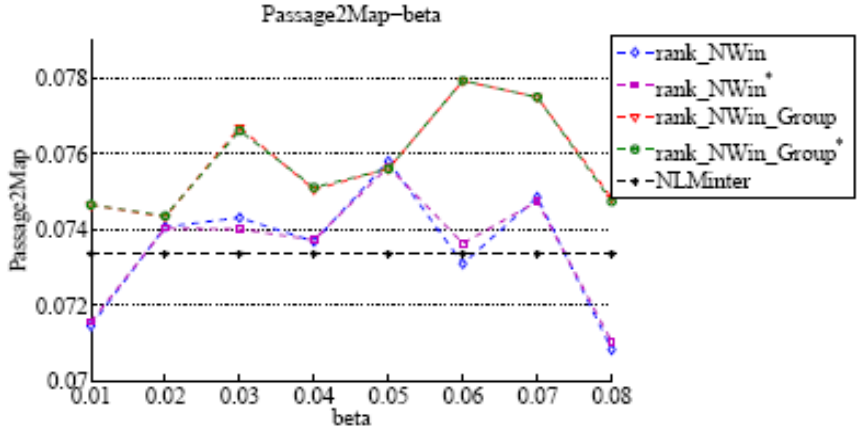


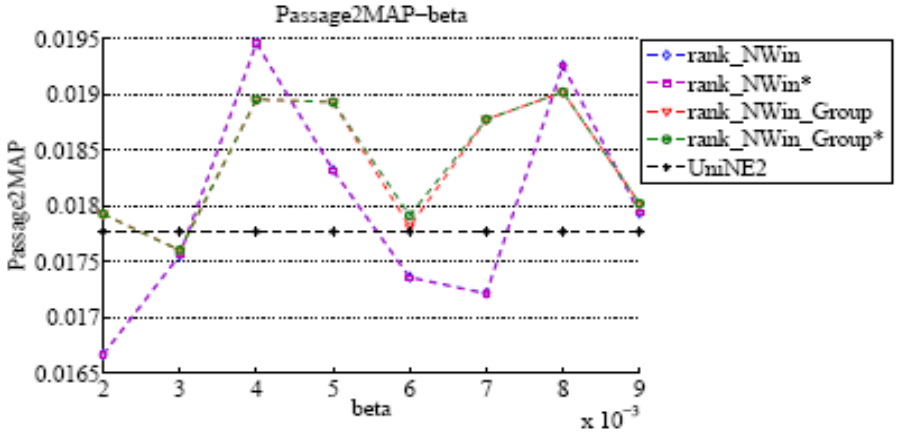
(a) Aspect MAP for NLMinter Run



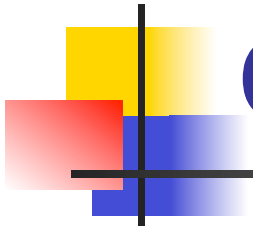
(b) Aspect MAP for UniNE2 Run



(c) Passage2 MAP for NLMinter Run



(d) Passage2 MAP for UniNE2 Run



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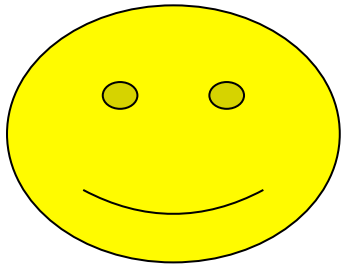
Conclusion and Future Work

- We propose an approach which employs LDA to promoting ranking diversity for biomedical IR.
  - The first study of adopting topic model to biomedical IR.
  - Transformations with topic distribution for retrieved passages are made.
  - Two re-ranking algorithms based on "N-size slide window" are proposed.
- We intend to extend this work by exploring both more complex models and more sophisticated algorithms.
- We also plan to further improve our approach to solve the diversification in the other application fields, such as SNS, recommendation system, etc.

Thank you!



Questions?

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