

Language Models for Genomics Information Retrieval

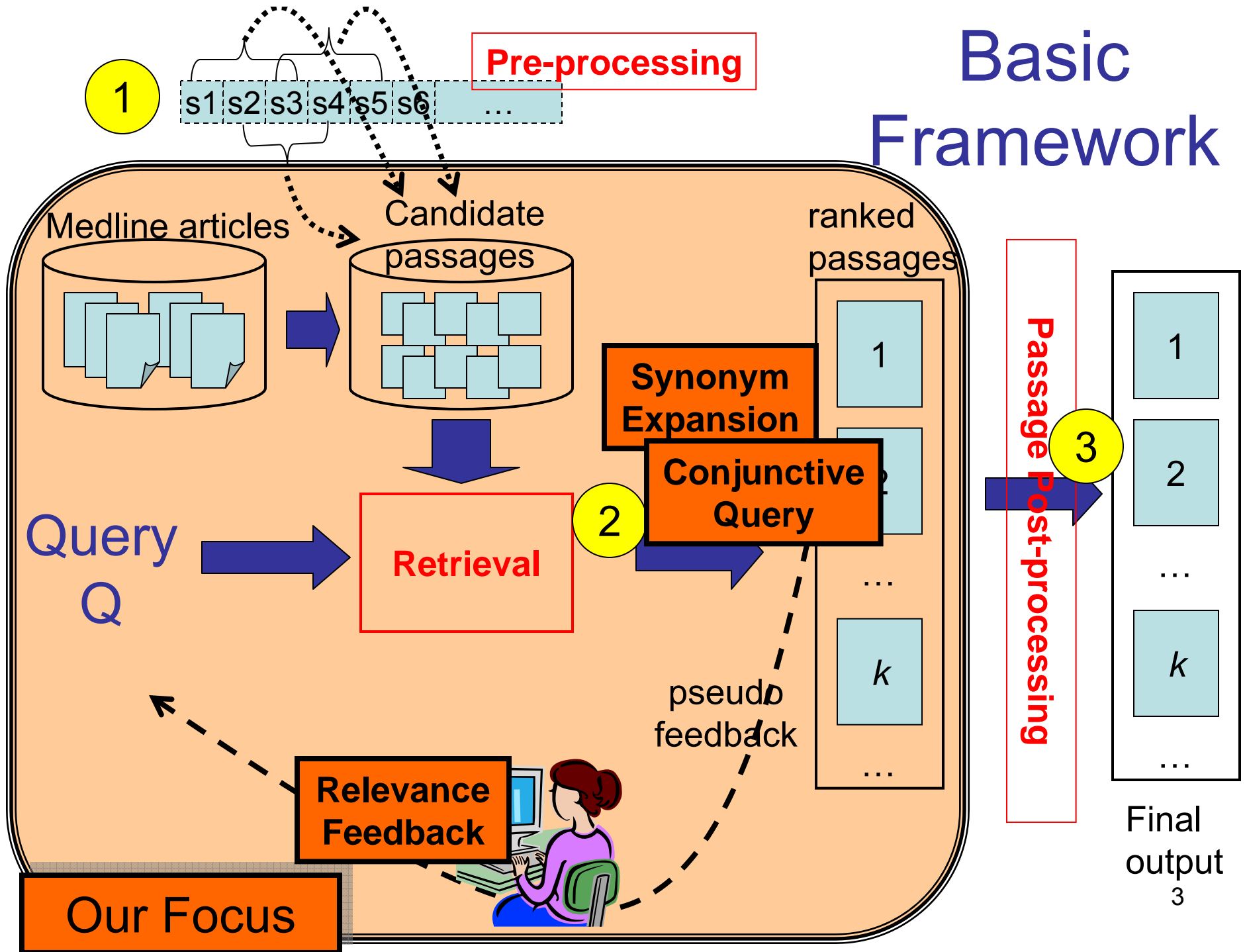
UIUC at TREC 2007 Genomics Track

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Goal of Participation

- Apply language models to genomics retrieval
- Extend standard language models for
 - gene synonym expansion
 - conjunctive query interpretation
- Experiment with relevance feedback

Basic Framework



Gene Synonym Expansion

“What [MOLECULAR FUNCTIONS] is **LITAF** involved in?”

Synonyms:

Ips-induced tn factor

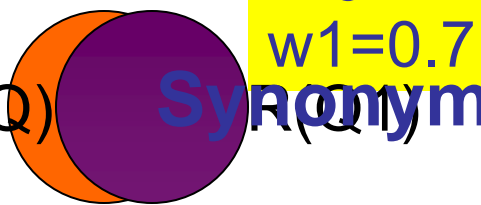
tbx 1

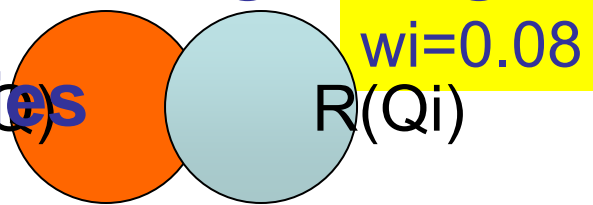


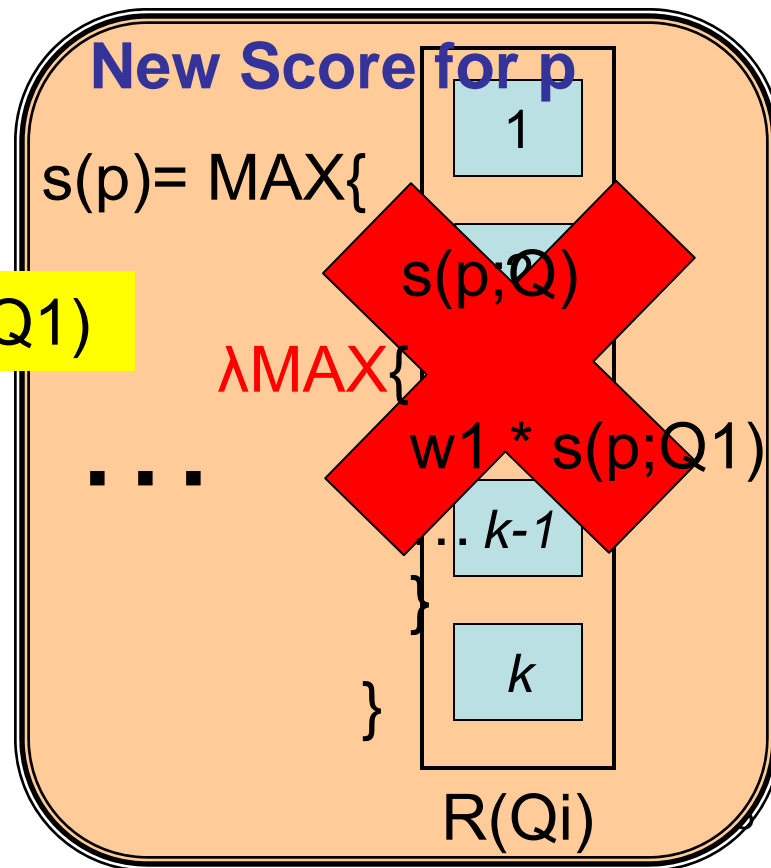
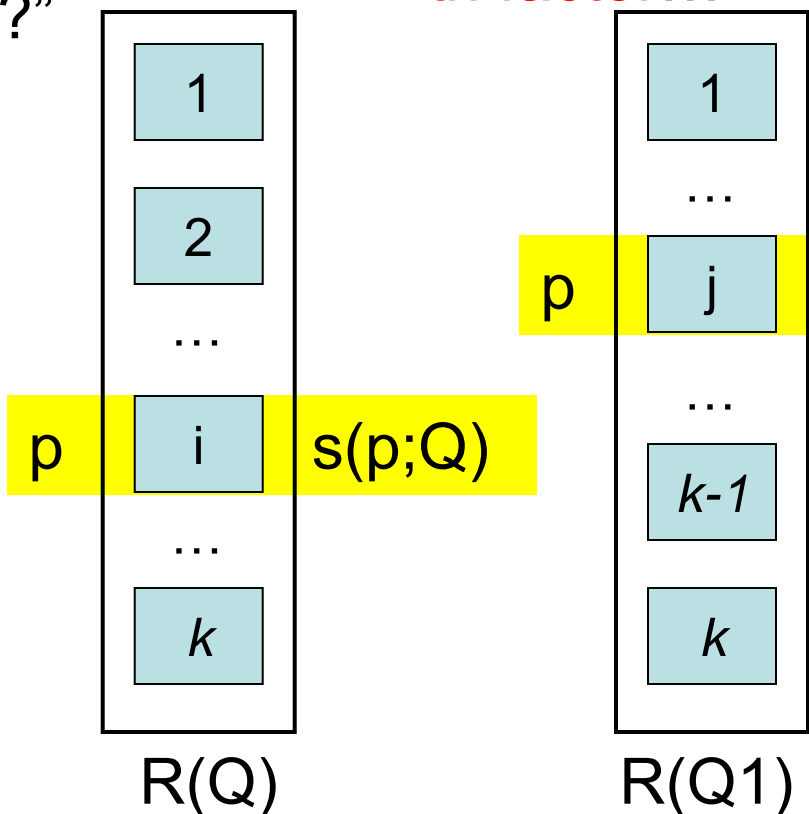
How to distinguish good synonyms from bad ones?
How to assign weights?

Overlap-Based Synonym Weighting

Q= "What
[MOLECULAR
FUNCTIONS] is
LITAF involved
in?"

$R(Q)$  $w_1=0.7$
Synonym Queries
Q1= "... **lps-induced**
tn factor ..."

$R(Q)$  $w_i=0.08$
Qi= "... **tbx 1** ..."



Conjunctive Query Interpretation

“What [MOLECULAR FUNCTIONS] is
LITAF involved in?”

p1 = “**LITAF** ...involve ... **LITAF**... involved
... **LITAF** ...”

Missing “Molecular Function”

p2 = “... **LITAF** ... involve ... molecular
function ...”

Match all query terms



KL-Divergence Retrieval Model

Query

molecular	0.25
functions	0.25
LITAF	0.25
involved	0.25

Q

Query LM

θ_Q

Document LM

θ_D

$$D(\theta_Q || \theta_D)$$

$$= \sum_{w \in V} p(w | \theta_Q) \log \frac{p(w | \theta_Q)}{p(w | \theta_D)}$$

Passage

p

the	0.120
for	0.085
involve	0.068
LITAF	0.052
function	0.034
molecular	0.034
...	...

Background



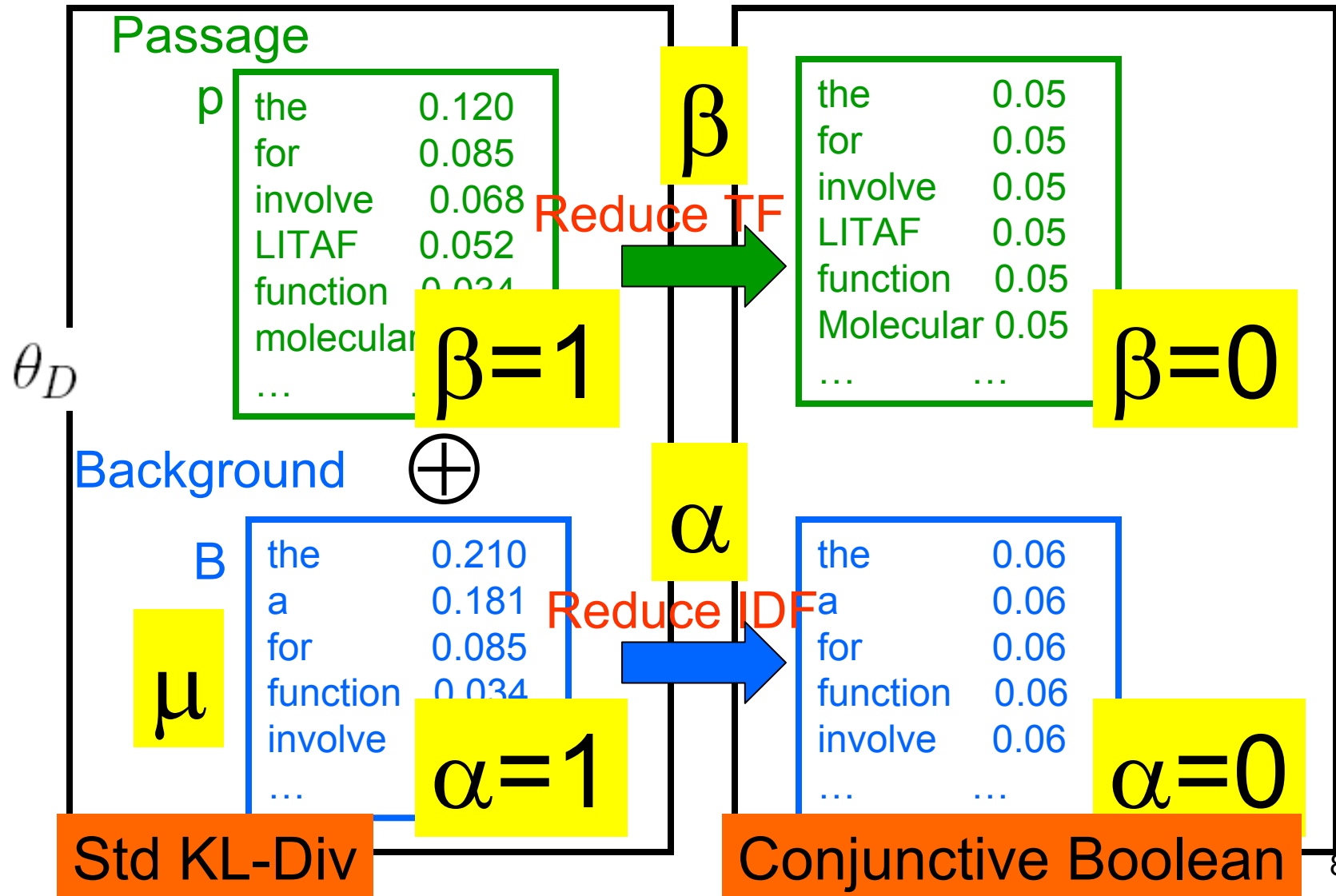
B

the	0.210
a	0.181
for	0.085
function	0.034
involve	0.028

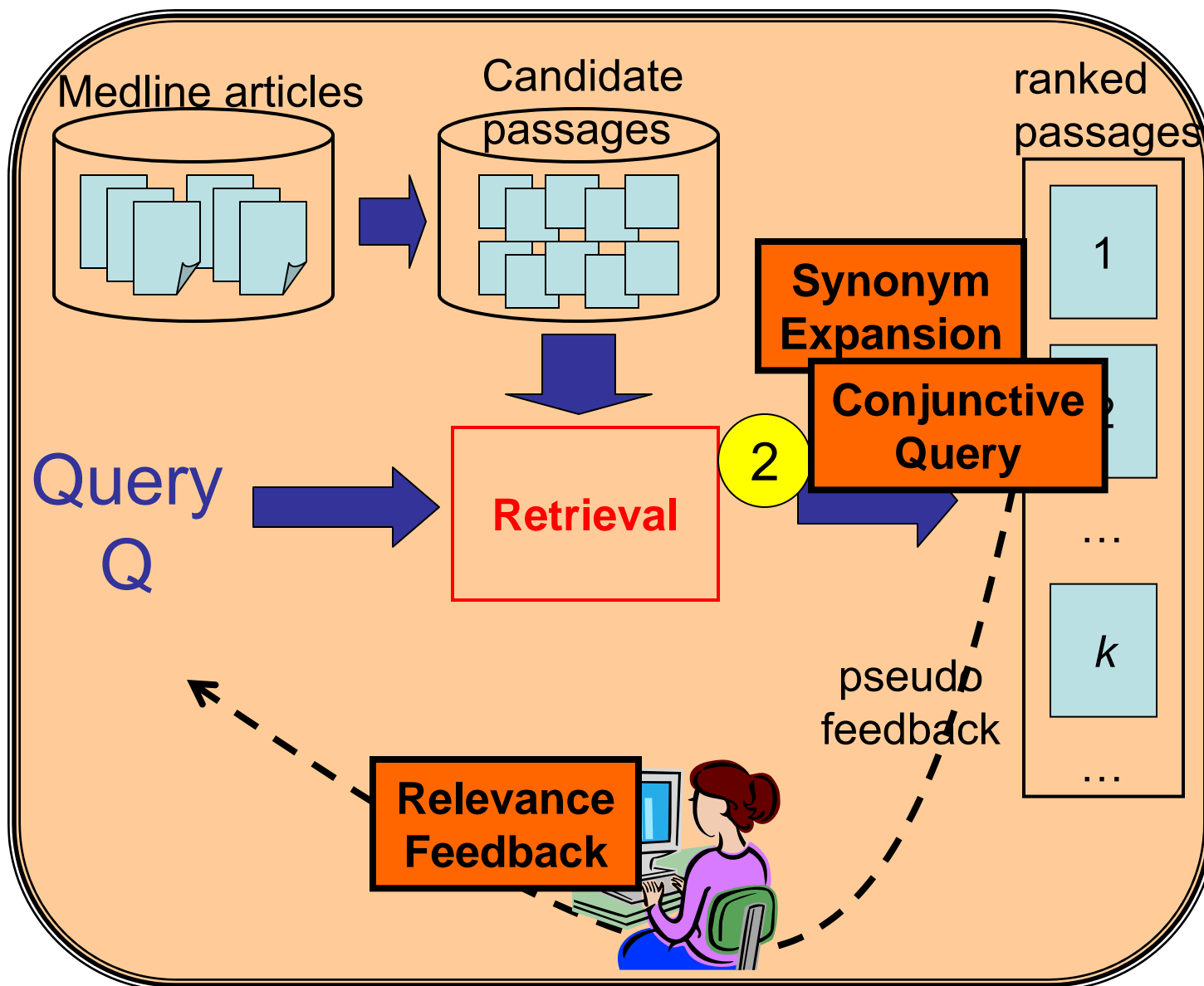
μ

Dirichlet Smoothing

Conjunctive Scoring in LM



Experiments



Gene Synonym Expansion

Method		DocMAP	Psg2MAP
No expansion	Baseline1	0.1777	0.0391
Gene Synonym Expansion	UIUCsyn	0.1926	0.0392

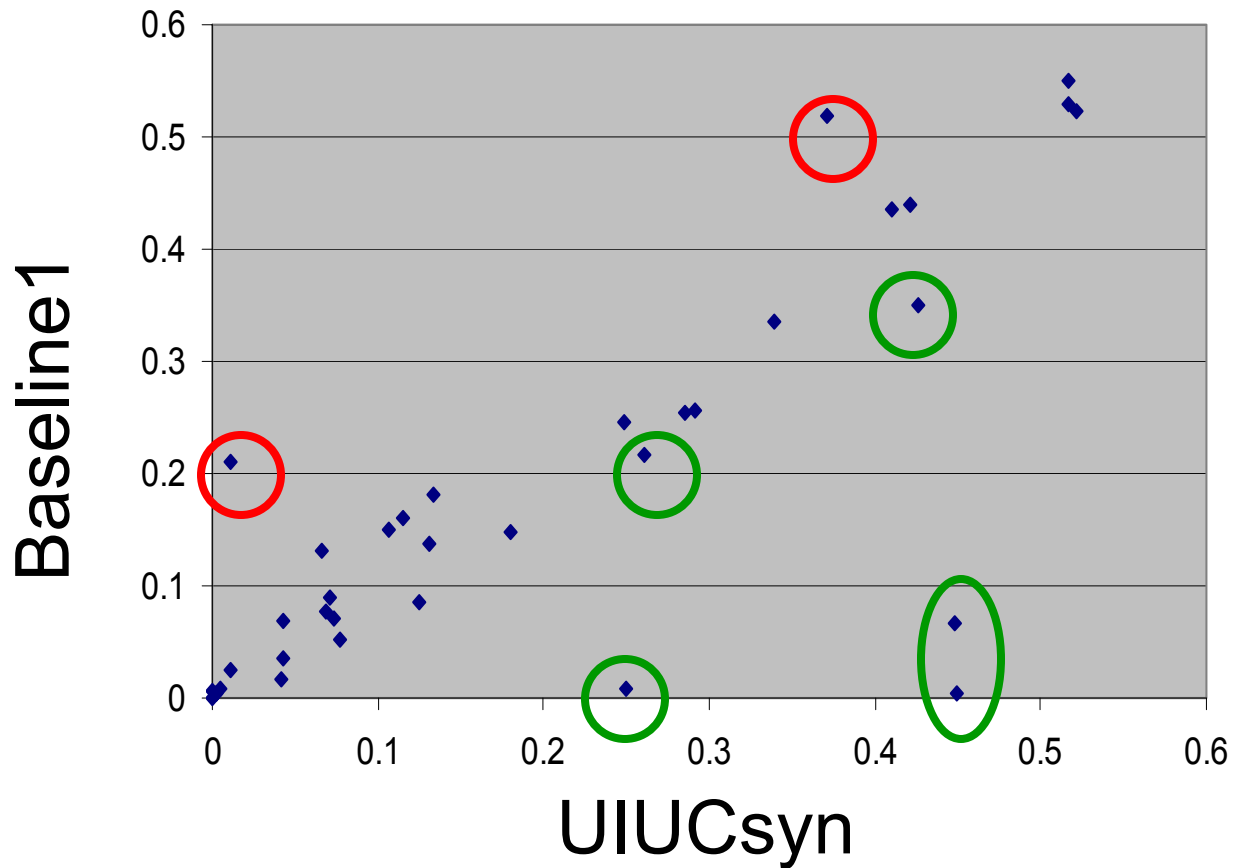
Gene Synonym Expansion

Method		DocMAP	Psg2MAP
No expansion	Baseline1	0.1777	0.0391
Gene Synonym Expansion	UIUCsyn	0.1926	0.0392
Improvement over Baseline1		+8.38%	

Gene Synonym Expansion

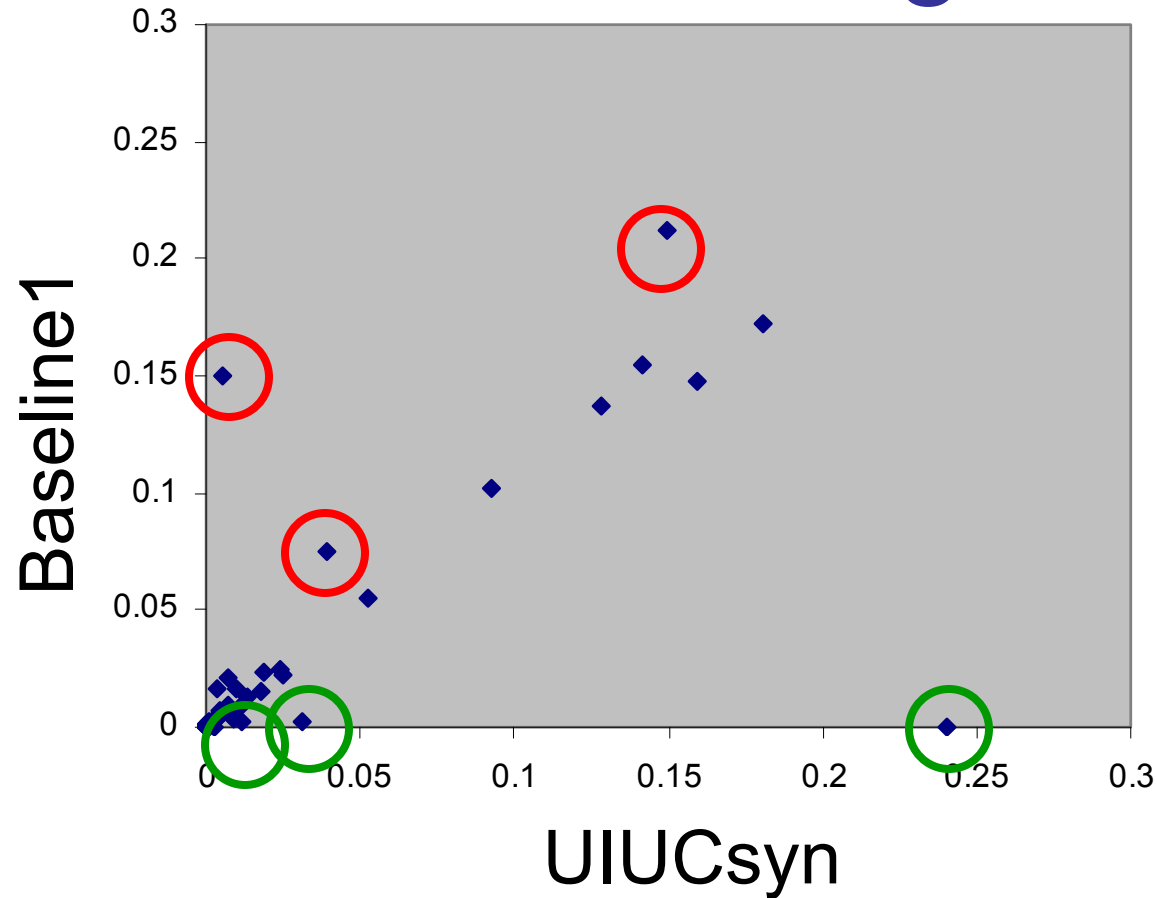
Method		DocMAP	Psg2MAP
No expansion	Baseline1	0.1777	0.0391
Gene Synonym Expansion	UIUCsyn	0.1926	0.0392
Improvement over Baseline1			≈0

Scatter Plot of DocMAP



UIUCsyn **improves** DocMAP on many topics
UIUCsyn **decreases** DocMAP on a few topics

Scatter Plot of Psg2MAP



UIUCsyn **improves** Psg2MAP on some topics

UIUCsyn **decreases** Psg2MAP on some topics

Conjunctive Query Interpretation

Method		DocMAP	Psg2MAP
Std KL-Div.+fb	Baseline2	0.1918	0.0422
Official run	UIUCconj	0.1495	0.0296
Strict Conj. Boolean	UIUCconj2	0.1688	0.0351
Partly discount IDF	UIUCconj3	0.1932	0.0424
Partly discount TF	UIUCconj4	0.1931	0.0423

KL-Divergence Retrieval Model

Query

molecular	0.25
functions	0.25
LITAF	0.25
involved	0.25

Q

Query LM

θ_Q

Document LM

θ_D

$$D(\theta_Q || \theta_D)$$

$$= \sum_{w \in V} p(w | \theta_Q) \log \frac{p(w | \theta_Q)}{p(w | \theta_D)}$$

Passage

p

the	0.120
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involve	0.068
LITAF	0.052
function	0.034
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...	...

Background

\oplus

B

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a	0.181
for	0.085
function	0.034
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μ

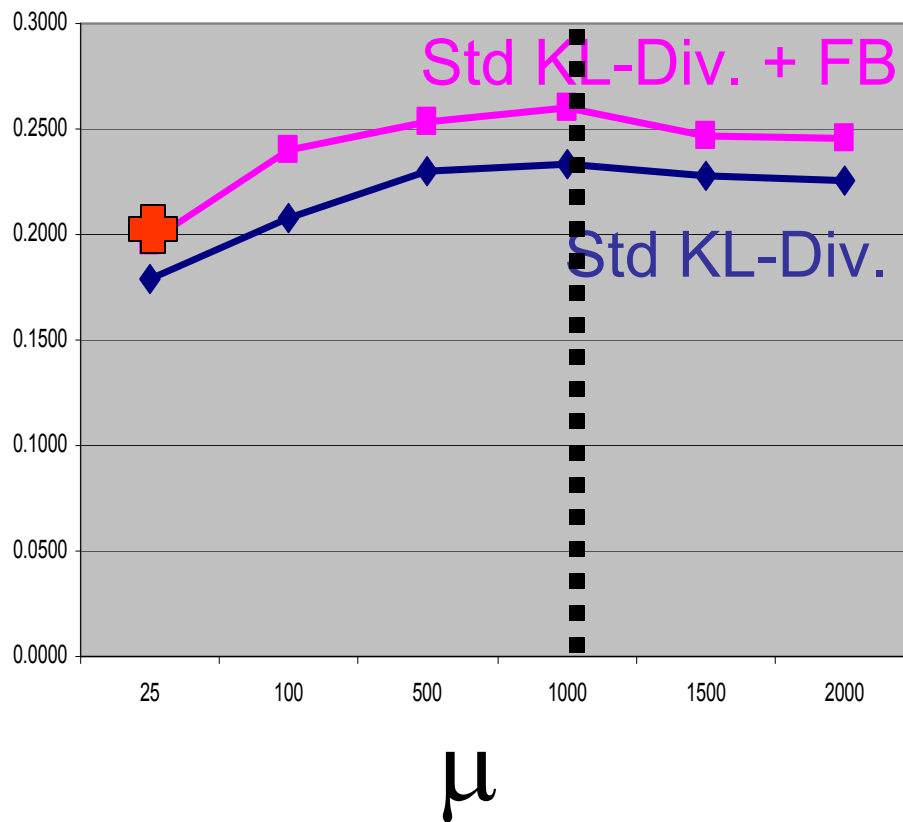
Dirichlet Smoothing

μ - Dirichlet Smoothing

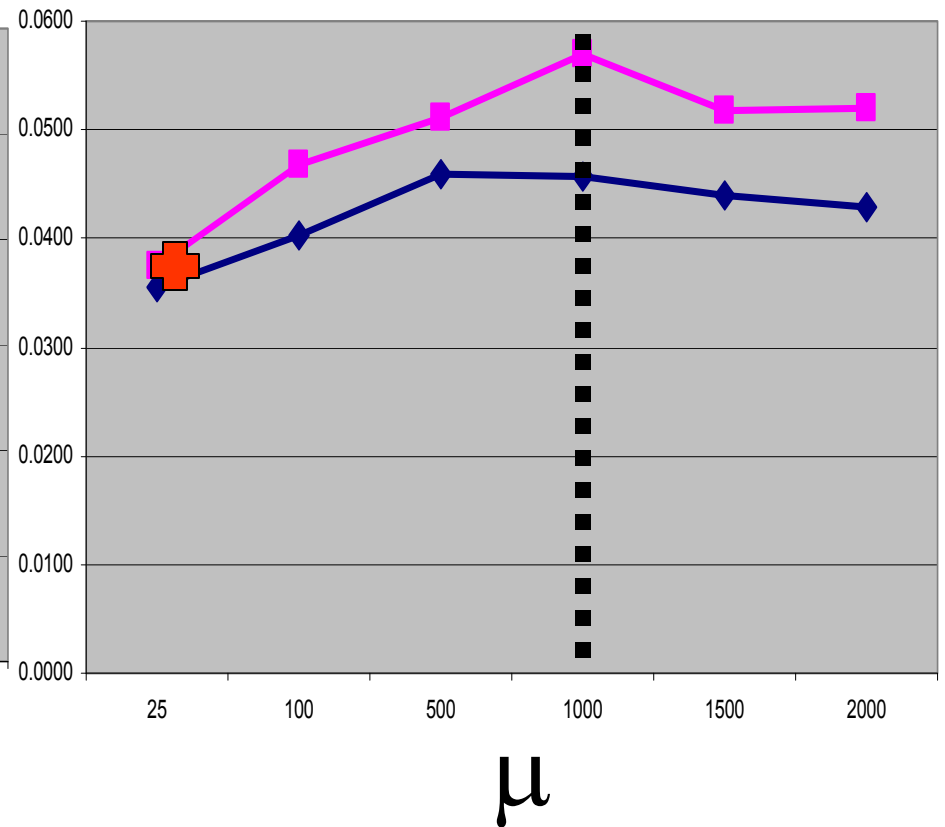


Performance of our best official run

DocMAP



Psg2MAP



Conjunctive Scoring over Optimum μ

Optimum: $\mu=1000$

Method		DocMAP	Psg2MAP
Std KL-Div.+fb	Baseline2	0.2598	0.0570
Partly discount IDF	UIUCconj3	0.2660	0.0680
Improvement		+2.4%	19.3%

Relevance Feedback

Method		DocMAP	Psg2MAP
No Feedback	Baseline1	0.1777	0.0391
Pseudo Feedback	Baseline2	0.1918	0.0422
Relevance Feedback	UIUCrelfb	0.1940	0.0364

Both feedback methods **improve** DocMAP,
but **NOT** necessarily Psg2MAP

Conclusions and Future Work

- Standard KL-Div. retrieval methods are effective but also sensitive to Dirichlet smoothing μ
- **Conjunctive scoring** improves performance based on optimum μ
- **Synonym expansion** and **User relevance feedback** tend to improve DocMAP but not Psg2MAP
- Future work
 - Automatically set optimum Dirichlet smoothing
 - More aggressive synonym expansion

Questions?