imi_mug at TREC 2017 Precision Medicine Track

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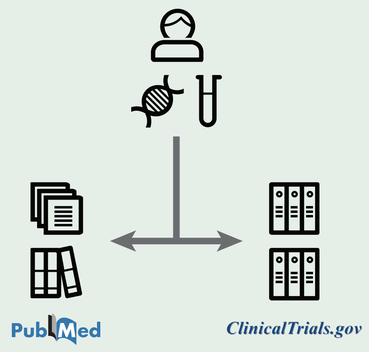
Introduction

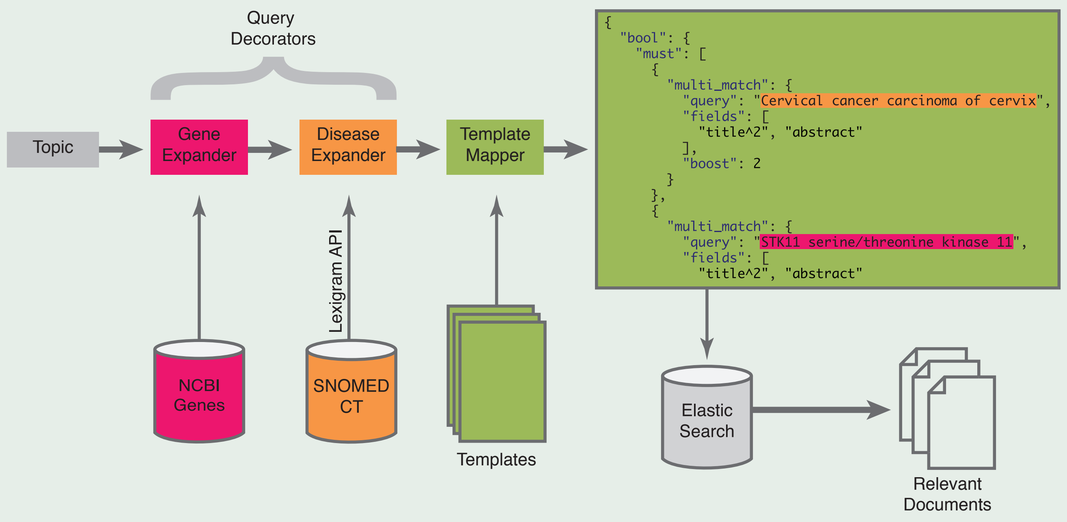
- 30 input topics: cancer patients
- Challenge: find relevant documents from two collections
  - Biomedical articles: Pubmed abstracts @ Jan 17 + ASCO/AACR proceedings
  - Clinical trials: ClinicalTrials.gov @ Apr 17

```
<topic number="15">
  <disease>Cervical cancer</disease>
  <gene>STK11</gene>
  <demographic>26-year-old female</demographic>
  <other>None</other>
</topic>
```



Infrastructure and Framework

- Elasticsearch 5.4.0 as search engine backend
- Open-source framework available on GitHub under the MIT License
  - Based on modular blocks: query templates and query decorators
- Reference standard built for the biomedical articles subtask
  - 739 topic-document pairs
  - Three annotators: two medical doctors, one computer scientist
  - 46 topics annotated by at least two annotators



Strategies and Resources

- Usage of `must` and `should` clauses in Elasticsearch
- Boosting of ASCO and AACR documents
  - Enabled for every submitted run
- Query expansion: diseases
  - Based on the Lexigram API [1]
  - Uses SNOMED CT, MeSH and ICD classification systems
- Query expansion: genes
  - Based on the NCBI Homo Sapiens Gene List [2]
  - Only expansion with the column `description` improved results
- Keyword boosting: positive and negative
  - N-grams extracted from the examples provided (Extra Topics)
  - Manual inspection of results during reference standard creation
  - Previous medical knowledge
- Positive keyword boosting: common chemotherapy suffixes
  - Extracted from the code L section of the ATC classification system

Positive boosters			Negative boosters	
surgery	resistance	-mab	transcript	probes
therapy	recurrence	-nib	paraffin	detection
treatment	targets	-cin	tumorigenesis	screening
prognosis	malignancy	-one	embedded	
prognostic	study	-ate	formalin	
survival	therapeutical	-mus	fish	
patient	outcome	-lin	tissue	

Table: Final list of positive and negative keyword boosters.

Some References

[1] Lexigram Inc. Lexigram HTTP API Documentation. https://docs.lexigram.io, 2017.

[2] National Center for Biotechnology Information (NCBI). NCBI Gene Lists. ftp://ftp.ncbi.nih.gov/gene/DATA/GENE_INFO, 2017.

Biomedical Articles: Submitted Runs

Strategy	mugpubboost	mugpubshould	mugpubbase	mugpubdiseas	mugpubgene
Matching disease + gene on MeSH and text fields	must	should	must	must	must
Keyword boosting: chemotherapy suffixes	Y	Y		Y	Y
Keyword boosting: positive	Y	Y	Y	Y	Y
Keyword boosting: negative	Y	Y		Y	Y
Query expansion: diseases				Y	
Query expansion: genes					Y
infNDCG	0.4088	0.2864	0.4031	0.3596	0.3016
P@10	0.6172	0.4483	0.6138	0.4759	0.4552
R-Prec	0.2735	0.1887	0.2743	0.2393	0.2065

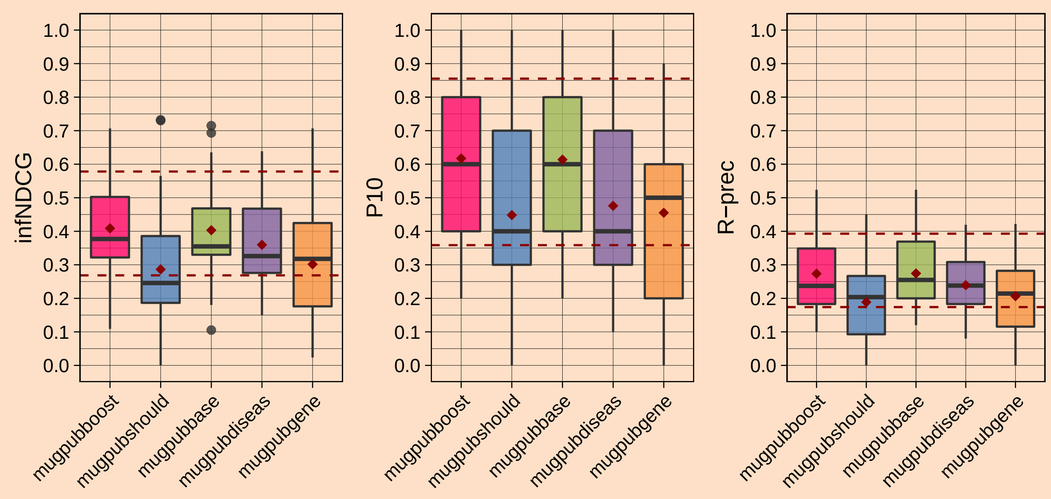


Figure: Boxplots comparing different runs to the overall best and median results.

Clinical Trials: Submitted Runs

Strategy	mugctboost	mugctdisease	mugctbase	mugctgene	mugctmust
Matching disease + gene on title and inclusion criteria	must	must	should	must	should
Matching age + sex on metadata	must	must	must	must	should
Comorbidities should not match exclusion criteria	Y	Y		Y	Y
Keyword boosting: positive	Y	Y		Y	
Query expansion: diseases		Y			
Query expansion: genes				Y	
P@5	0.2500	0.0929	0.3000	0.2357	0.2929
P@10	0.2286	0.0679	0.2643	0.2321	0.2536
P@15	0.1952	0.0738	0.2262	0.2119	0.2143

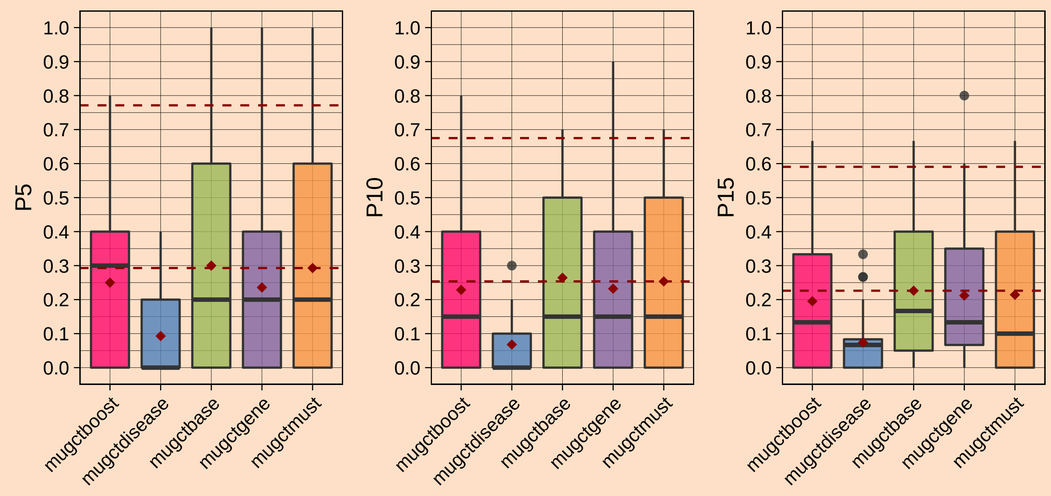


Figure: Boxplots comparing different runs to the overall best and median results.

Limitations and Future Work

- Improve recall
  - Synonym, hypo-, and hypernym list based on MeSH
  - Tiered indexes
  - Pseudo-relevance feedback
- Explore other ranking strategies
  - Use decay functions to push down older documents
  - Restrict to MeSH major topics
  - Debug Elasticsearch's `english` analyzer
  - Disable field-length normalization (aka BM15)

Acknowledgements

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Source code available at `https://goo.gl/axTw5J`.