# InfoLabPM at TREC 2018 Precision Medicine Track

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## ABSTRACT

This paper reports the participation of the InfoLab at the TREC Precision Medicine Track 2018. InfoLab is an informal group that brings together researchers with interest in the information area and is located at Faculty of Engineering of University of Porto. The experiments made in this participation include query expansion approaches for the disease and gene concepts. The expansion of the disease terms was done using Unified Medical Language System (UMLS). UMLS is a repository that provides the mapping between a large number of vocabularies. The gene terms were expanded using Ensembl. Ensembl provides a genome browser that maps genes to their synonyms. An additional layer was developed on top of Terrier to provide the execution of a large batch of experiments. Multiple runs were evaluated in order to measure the influence of each expansion approach.

## 1 INTRODUCTION

When comes to cancer treatment, Precision Medicine initiative is important, it enables researchers and clinicians work together to develop more efficient ways of treatment, it takes into account genetic, environmental and lifestyle factors when identifying the best approach for a given patient.

The goal of the Precision Medicine track is to provide useful information, related to the medical condition of the patient. The automatization of this process is of great importance. With a large amount of information available, using automatic methodologies, this information can be processed and become useful to assist medical professionals in their tasks.

The documents retrieved in this task are either biomedical articles or clinical trials. Clinical trials are studies which are used to test if a new treatment performs well in terms of safety and efficacy on a patient. Our approach to this problem was to expand the query with synonyms of the initial terms. The variation of the term's weights was also taken into consideration. In this paper are also described the techniques used for indexing and query expansion for both collections.

## 2 DATA STRUCTURE

The biomedical articles are made available in both XML and TXT formats. The documents include information about the title, abstract and MESH headings for XML documents. The TXT files contain the title and the background sections.

The XML documents related to the clinical trials include the descriptions and the criteria, that is, the gender and age range for each trial.

The topics provided contained synthesized information about the patients from which the queries are generated. These files hold information about fields for the disease, gene, and demographics, the later containing information about the age and gender. This year the field 'other' was not included. Example of a topic:

```
<topic number="1">
        <disease>melanoma</disease>
        <gene>BRAF (V600E)</gene>
        <demographic>
        64-year-old male
    </demographic>
</topic>
```

## 3 INDEXING

The selected search engine was Terrier [4], with support to query expansion.

Since we wanted to index the fields of the clinical trials, the documents were pre-processed to a TREC file format with 'brief title', 'brief summary', 'detailed description', 'criteria', 'gender' and 'ages' as the fields. When generating the 'gender' field, the term 'all' was expanded to 'Female Male', to later make use of Terrier's ability to query a term from fields. This way, for the query 'gender:Female' all documents originally with the term 'all' and 'Female' are retrieved. The same procedure was applied to the field 'ages'. It was expanded to contain each individual age in the age range. For instance, if the minimum age was '14' and the maximum '35', the expanded result was '14 15 16 ... 33 34 35'. We needed to do so because Terrier does not support the syntax for searching a numerical range. With this approach for the query 'ages:32' all the documents which contained 32 in the field ages are retrieved.

Biomedical articles and clinical trials were indexed removing stop words and the terms were stemmed using the Porter Stemmer [5] algorithm provided by Terrier. The fields 'gender' and 'ages' were indexed for later filtering when retrieving the trials. Since there was a need to index these fields, the class *BlockSinglePassIndexer* was used.

## 4 QUERY EXPANSION

As aforementioned, the topics were composed of 'disease', 'gene' and 'demographics'. Since the diseases and the genes can be represented in multiple ways, both were expanded. To expand the disease field, the UMLS [1] services were used. UMLS Rest API provides a way to retrieve the best matching Concept Unique Identifier (CUI). A concept is a unique identifier that represents a single meaning which contains all the atoms that express this meaning. An atom is the smallest unit of naming a source. In order to retrieve information through the Rest API, the first step is to retrieve the best matching CUI for a specific term. From the list of CUIs, the first one was selected as the CUI for the disease. With this CUI it is possible to retrieve all the related concepts or only the default preferred atom.

The querying language of Terrier provides a way to search for multiple terms in the same phrase, the syntax for that is the following: *"term1 term2"*. It also supports the notion of synonyms, for the query *{term1 term2}*, *term1* and *term2* are considered the same. Unfortunately, Terrier does not support the use of both constructs in conjunction. To that end, only the default preferred atom was used. Without the ability to organize multiple definitions as synonyms, the runs obtain a considerable lower performance due to the increasing number of definitions to match. As an example, for the disease "pancreatic cancer", the default preferred atom is "pancreatic carcinoma".

Ensembl [2] Rest API was used in order to expand the gene information by retrieving synonyms. Similarly to the UMLS Rest API, in order to find the synonyms of a gene, the ID for a specific gene is retrieved. To retrieve the most relevant ID, a call to the API was performed, sending the gene retrieved from the patient data. The result is in form of a list of matching IDs, ordered by relevance, for the gene in question, the most relevant was chosen. With this ID the synonyms can be obtained. As an example, for the gene *EGFR* the synonyms returned were *ERBB* and *ERBB1*.

Both services were cached to provide a more fluid workflow, enabling multiple experiments to be made.

The age included in the demographic field were also expanded to the terms proposed by Kastner et al.[3] mentioned in Table 1. This expansion was not performed for the clinical trials due to the fact that the age was already specified by the age field.

Terrier's querying language provides a way to fine tune queries providing different weights to terms. To double the weight of *term1*, the following syntax is used *term1^2.00*. We used this weighting scheme to assign more importance to the original terms than to the expanded terms, we also experimented the use of the same weights for both terms. The querying expansion included only expanding the disease, genes or both.

Table 2 describes the runs. The runs were the same for both the biomedical articles and clinical trials collections. The table contains information about the parameters used, which terms were expanded, their weights and the terms added. Furthermore, the baseline to which results are compared is also presented. The baseline uses MB25 as matching model without any expansions or weighting to the query.

The name of a run has the following nomenclature *<collection>-<matching_model>-(<term><weight>)*-<terms-added>*. The *<collection>* indicates if the run was related to clinical trials (ctl) or biomedical articles (bma), the *<matching_model>* indicates the matching model used (BB2 or BM25). The *<term>* indicates the weighted term or if the term was expanded, it can assume values of Ge (Gene expanded), De (Disease Expanded), D (Disease), G (Gene), A (Age) or g (Gender). The *<weight>* is the numeric value of the term's weight. Lastly, *<terms-added>* indicates the terms added to every run, human, neoplasm (neo) or animal. The run 'BB2-human-neo' had terms added namely *human* and *neoplasm*. Since all the topics were cancer-related, these terms were used as an attempt to favor documents related to humans and cancer diseases. Similarly, the run 'BB2-GeDeD2G2-animal' had the term *animal^-1* added as an attempt to penalize documents in which the keyword animal occurs.

**Table 1: Terms proposed by Kastner et al.[3]**

| Term | Range |
|---|---|
| Fetus | Fetus |
| Newborn | Birth to 1 month |
| Infant | > 1 month to < 24 months |
| Preschool | 2 years to < 6 years |
| Child | 6 years to < 13 years |
| Adolescent | 13 years to < 19 years |
| Adult | 19 years to < 45 years |
| Middle age | 45 years to < 65 years |
| Aged | 65 years to < 80 years |
| Aged 80 | ≥ 80 years |

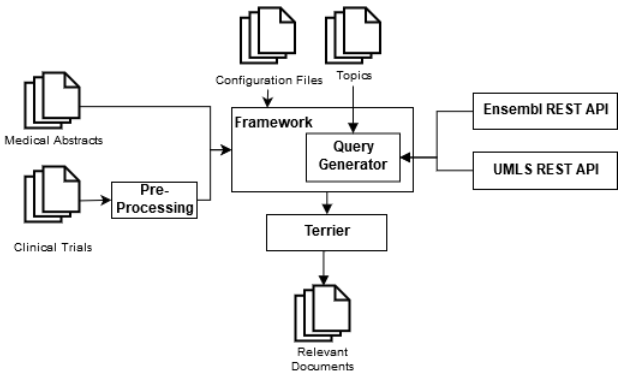


**Figure 1: Framework Architecture.**

## 5 FRAMEWORK

Figure 1 depicts, at a higher level, the process to retrieve relevant documents. Through configurations files, it is possible to define which field is going to be expanded (disease, genes or age as stated previously), manually set the weight of each original term as well as the translated terms. The addition of custom terms, selection of the matching model and merging different result sets are other possible actions. Table 3 contains a description of all the commands used to create the configuration files. Runs that are merged are MergeA, MergeB, MergeC, MergeD, MergeE, MergeF, and MergeG. These merges were done interleaving the results from the involved runs. Table 2 contains information about the merged runs. The results from both files are mixed taking 15 results, ordered by relevance, from each file and joining the results by relevance.

This layer facilitated the evaluation and adjustment of multiple runs, 47 runs were evaluated and compared. The used weight models were BB2 and Okapi BM25.

## 6 RESULTS

The runs were evaluated using the *qrels* file from the previous year, processed to a *csv* format and later compared. The results can be seen at Table 4 and Table 5.

For both tasks, from all the weight models used, BB2 performed better overall. The expanded queries performed relatively worse when comparing to the nonexpanded ones. Also, queries, where the disease was not weighted, performed better.

For the clinical trials, the results which weighted more the gene in relation to the other terms seem to perform better overall. Also, the queries without expansion of the disease term had a better result when compared to the expanded version.

Table 6 contains the results for the submitted runs.

### 6.1 Submitted Runs

From the runs obtained (Table 4 and Table 5) the best runs were selected.

For the biomedical articles, four runs were submitted, being 'minfolabBA', 'minfolabBC', 'minfolabBD' and 'minfolabTH', that maps to 'BB2', 'BB2-De', 'BB2-GeDe' and 'BB2-human-neo' respectively. All these results had BB2 as the matching model. Details of these runs are described in Table 2. The weight of each term remained the same for these runs. Our additional runs had multiple weight for the disease, genes and their respective translations, however, the submitted runs had better results.

The submitted clinical trials consisted of three runs, 'BB2-G2', 'BB2-DeG2', 'BM25-G2', submitted as 'tinfolabBF', 'tinfolabBK', and 'tinfolabF' respectively. Unfortunately, one run could not be sent due to some topics missing in the results file.

## 7 CONCLUSIONS

We submitted seven automatic runs, four runs for the biomedical articles and 3 for the clinical trials. The development of a small interpreter to automate the process wasn't a time-consuming task. Furthermore, it contributed to the evaluation of a large batch of experiment and to quickly fine-tuning the generated queries. While evaluating locally, the queries without the expansion of the original terms, achieved better results when compared with the same queries in which terms were expanded. As expected, the same behavior occurred with the submitted runs. In the case of the clinical trials, the queries where the genes were boosted performed better in comparison to the other runs.

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**Table 2: Parameters used for each run.**
**Numeric values represent the weight associated with each term. Terms not included are represented by missing values.**

| Run | Matching Model | Expanded Gene | Expanded Disease | Disease | Gene | Age | Gender | Added Terms |
|---|---|---|---|---|---|---|---|---|
| Baseline | BM25 | | | 1 | 1 | 1 | 1 | |
| BB2 | BB2 | | | 1 | 1 | 1 | 1 | |
| BB2-Ge | BB2 | 1 | | 1 | 1 | 1 | 1 | |
| BB2-De | BB2 | | 1 | 1 | 1 | 1 | 1 | |
| BB2-GeDe | BB2 | 1 | 1 | 1 | 1 | 1 | 1 | |
| BB2-D2 | BB2 | | | 2 | 1 | 1 | 1 | |
| BB2-G2 | BB2 | | | 1 | 2 | 1 | 1 | |
| BB2-D2G2 | BB2 | | | 2 | 2 | 1 | 1 | |
| BB2-DeD3 | BB2 | | 1 | 3 | 1 | 1 | 1 | |
| BB2-GeD2 | BB2 | 1 | | 2 | 1 | 1 | 1 | |
| BB2-GeG2 | BB2 | 1 | | 1 | 2 | 1 | 1 | |
| BB2-DeG2 | BB2 | | 1 | 1 | 2 | 1 | 1 | |
| BB2-GeDeD2G2-animal | BB2 | 1 | 1 | 2 | 2 | 1 | 1 | animalˆ-1 |
| BM25-Ge | BM25 | 1 | | 1 | 1 | 1 | 1 | |
| BM25-De | BM25 | | 1 | 1 | 1 | 1 | 1 | |
| BM25-GeDe | BM25 | 1 | 1 | 1 | 1 | 1 | 1 | |
| BM25-D2 | BM25 | | | 2 | 1 | 1 | 1 | |
| BM25-G2 | BM25 | | | 1 | 2 | 1 | 1 | |
| BM25-D2G2 | BM25 | | | 2 | 2 | 1 | 1 | |
| BM25-DeD2 | BM25 | | 1 | 2 | 1 | 1 | 1 | |
| BM25-GeD2 | BM25 | 1 | | 2 | 1 | 1 | 1 | |
| BM25-GeG2 | BM25 | 1 | | 1 | 2 | 1 | 1 | |
| BM25-DeG2 | BM25 | | 1 | 1 | 2 | 1 | 1 | |
| BM25-GeDeD2G2-animal | BM25 | 1 | 1 | 2 | 2 | 1 | 1 | animalˆ-1 |
| BB2-GeDe | BB2 | 1 | 1 | 1 | 1 | 1 | 1 | |
| BB2-GeDe0.2 | BB2 | 1 | 0.2 | 1 | 1 | 1 | 1 | |
| BB2-Ge0.2De | BB2 | 0.2 | 1 | 1 | 1 | 1 | 1 | |
| BB2-Ge0.2De0.2 | BB2 | 0.2 | 0.2 | 1 | 1 | 1 | 1 | |
| BB2-D2-human | BB2 | | | 2 | 1 | 1 | 1 | human |
| BB2-GE0.2De0.2-human | BB2 | | | 1 | 1 | 1 | 1 | |
| BB2-Ge0.2De0.2-human-neo | BB2 | 0.2 | 0.2 | 1 | 1 | 1 | 1 | human neo |
| BB2-human-neo | BB2 | | | 1 | 1 | 1 | 1 | human neo |
| BB2-Ge0.2De0.2-neo | BB2 | 0.2 | 0.2 | 1 | 1 | 1 | 1 | neo |
| BB2-D2G2-neo | BB2 | | | 2 | 2 | 1 | 1 | neo |
| BB2-Ge0.2De0.2D2G1.5-human-neo | BB2 | 0.2 | 0.2 | 2 | 1.5 | 1 | 1 | human neo |
| BB2-Ge0.2D2G1.5-human-neo | BB2 | 0.2 | | 2 | 1.5 | 1 | 1 | human neo |
| BB2-De0.2D2G1.5-human-ne | BB2 | | 0.2 | 2 | 1.5 | 1 | 1 | human |
| BB2-Ge0.3De0.3D2G1.5-human-neo | BB2 | 0.3 | 0.3 | 2 | 1.5 | 1 | 1 | human neo |
| BB2-De0.3D2G1.5A0g0-human-neo | BB2 | | 0.3 | 2 | 1.5 | | | human neo |
| BB2-Ge0.3De0.3D2G1.5A0g0 | BB2 | 0.3 | 0.3 | 2 | 1.5 | | | |
| MergeA | Merged runs BB2-GeDe and BB2-Ge0.2De0.2-human-neo | | | | | | | |
| MergeB | Merged runs BM25-GeDe and BM25-D2 | | | | | | | |
| MergeC | Merged runs BM25-Ge0.2[4] and BM25-D2 | | | | | | | |
| MergeD | Merged runs BM25-DeD2 and BM25-GeDe | | | | | | | |
| MergeE | Merged runs BM25-DeD2 and BM25-GeG2 | | | | | | | |
| MergeF | Merged runs BM25-D2 and BM25-G2 | | | | | | | |
| MergeG | Merged runs BM25-DeD2G2 and BM25-G2 | | | | | | | |

**Table 3: Commands used.**

| Command | Arguments | Description |
|---|---|---|
| **xml.tags** | *<DOC_TAG>* *<ID_TAG>* *<TERMS>* *<USE_UTF>* | Directly sets the properties used by Terrier: *<XML_DOCTAG>* *<XLM_IDTAG>* *<XML_TERMS>* *<XML_USE_UTF>*. |
| | **Usage** | *xml.tags PubmedArticle PMID ArticleTitle,AbstractText false* |
| **index.(xml/txt)** | *<DOC_PATH>* *<COLLEC-TION_NAME>* | Index the documents at the *<DOC_PATH>* and associate them with the collection name *<COLLECTION_NAME>*. |
| | **Usage** | *index.xml medline_folder medlinexml* |
| **query.params** | *<Disease>* *<Genes>* *<Gender>* *<Age>* | Numerical inputs. Sets the weight of each original term. |
| | **Usage** | *query.params 100 100 100 100* |
| **query.params. translations** | *<Disease>* *<Genes>* | Numerical inputs. Sets the weight of each translated term. |
| | **Usage** | *query.params.translations 010 020* |
| **query.translate** | *<Disease>* *<Genes>* *<Gender>* *<Age>* | Boolean inputs. Defines what fields to translate. |
| | **Usage** | *query.translate true true false true* |
| **query.append** | *<expression>* | Appends the *<expression>* to the original query |
| | **Usage** | *query.append human^2 neoplasms* |
| **matching.model** | *<Model>* | Sets the matching model to use. |
| | **Usage** | *matching.model BB2* |
| **search.topics** | *<COLLECTIONS>* *<TOPICS>* *<RUNID>* *<trials>* | Queries a set of topics through the collections. The results are stored in a file with name of *<RUNID>* |
| | **Usage** | *search.topics trials2018 topics2018.xml runName true* |

**Table 4: Results of runs from biomedical articles. Submitted runs and best results in bold.**

| Run | Rprec | P@5 | P@10 | P@15 | P@20 |
|---|---|---|---|---|---|
| bma-Baseline | 0.1064 | 0.3200 | 0.3267 | 0.3111 | 0.2950 |
| **bma-BB2** | **0.1230** | 0.3600 | **0.3567** | **0.3289** | **0.3200** |
| bma-BB2-Ge | 0.0882 | 0.2600 | 0.2767 | 0.2733 | 0.2550 |
| **bma-BB2-De** | 0.1209 | **0.3733** | 0.3433 | 0.3178 | 0.2917 |
| **bma-BB2-GeDe** | 0.1089 | **0.3733** | 0.3200 | 0.2978 | 0.2750 |
| bma-BB2-D2 | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-G2 | 0.1209 | 0.3133 | 0.3233 | 0.3111 | 0.2917 |
| bma-BB2-D2G2 | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-DeD2 | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-GeD2 | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-GeG2 | 0.0832 | 0.2733 | 0.2767 | 0.2467 | 0.2333 |
| bma-BB2-DeG2 | 0.1220 | 0.3000 | 0.2800 | 0.2867 | 0.2750 |
| bma-BB2-GeDeD2G2-animal | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BM25-Ge | 0.0944 | 0.2667 | 0.2967 | 0.2733 | 0.2550 |
| bma-BM25-De | 0.1019 | 0.3467 | 0.2933 | 0.2733 | 0.2650 |
| bma-BM25-GeDe | 0.1042 | 0.3200 | 0.2733 | 0.2844 | 0.2683 |
| bma-BM25-D2 | 0.0096 | 0.0267 | 0.0167 | 0.0133 | 0.0100 |
| bma-BM25-G2 | 0.1016 | 0.3000 | 0.3033 | 0.2778 | 0.2667 |
| bma-BM25-D2G2 | 0.0096 | 0.0267 | 0.0167 | 0.0133 | 0.0100 |
| bma-BM25-DeD2 | 0.0096 | 0.0267 | 0.0167 | 0.0133 | 0.0100 |
| bma-BM25-GeD2 | 0.0096 | 0.0267 | 0.0167 | 0.0133 | 0.0100 |
| bma-BM25-GeG2 | 0.0861 | 0.2600 | 0.2833 | 0.2400 | 0.2350 |
| bma-BM25-DeG2 | 0.1016 | 0.2933 | 0.2567 | 0.2533 | 0.2433 |
| bma-BM25-GeDeD2G2-animal | 0.0096 | 0.0267 | 0.0167 | 0.0133 | 0.0100 |
| bma-BB2-GeDe | 0.1089 | **0.3733** | 0.3200 | 0.2978 | 0.2750 |
| bma-BB2-GeDe0.2 | 0.0072 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-Ge0.2De | 0.1115 | 0.3600 | 0.3200 | 0.2956 | 0.2700 |
| bma-BB2-Ge0.2De0.2 | 0.0072 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-D2-human | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-GE0.2De0.2-human | 0.0072 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-Ge0.2De0.2-human-neo | 0.0072 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| **bma-BB2-human-neo** | 0.1129 | 0.3533 | 0.3267 | 0.3244 | 0.3067 |
| bma-BB2-Ge0.2De0.2-neo | 0.0072 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-D2G2-neo | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-Ge0.2De0.2D2G1.5-human-neo | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-Ge0.2D2G1.5-human-neo | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-De0.2D2G1.5-human-neo | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-Ge0.3De0.3D2G1.5-human-neo | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-De0.3D2G1.5A0g0-human-neo | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-BB2-Ge0.3De0.3D2G1.5A0g0 | 0.0093 | 0.0267 | 0.0167 | 0.0111 | 0.0117 |
| bma-MergeA | 0.0625 | 0.2933 | 0.2767 | 0.2244 | 0.2067 |
| bma-MergeB | 0.0062 | 0.0231 | 0.0154 | 0.0154 | 0.0154 |
| bma-MergeC | 0.0469 | 0.2600 | 0.2300 | 0.2067 | 0.1733 |
| bma-MergeD | 0.0062 | 0.0231 | 0.0154 | 0.0154 | 0.0154 |
| bma-MergeE | 0.0267 | 0.1067 | 0.1233 | 0.1356 | 0.1200 |
| bma-MergeF | 0.0204 | 0.0733 | 0.0967 | 0.0978 | 0.0917 |
| bma-MergeG | 0.0187 | 0.0933 | 0.1000 | 0.0978 | 0.0900 |

**Table 5: Results of runs from clinical trials. Submitted runs and best results in bold.**

| Run | Rprec | P@5 | P@10 | P@15 | P@20 |
|---|---|---|---|---|---|
| clt-Baseline | 0.2070 | 0.3360 | 0.3080 | 0.2773 | 0.2640 |
| clt-BB2 | 0.2237 | 0.3440 | 0.3200 | 0.2960 | 0.2600 |
| clt-BB2-Ge | 0.1869 | 0.2316 | 0.2316 | 0.2386 | 0.2132 |
| clt-BB2-De | 0.1810 | 0.3520 | 0.3000 | 0.2640 | 0.2300 |
| clt-BB2-GeDe | 0.2121 | 0.3368 | 0.2895 | 0.2386 | 0.2211 |
| clt-BB2-D2 | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| **clt-BB2-G2** | **0.2524** | 0.4067 | **0.3667** | **0.3311** | 0.2900 |
| clt-BB2-D2G2 | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-DeD2 | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-GeD2 | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-GeG2 | 0.1768 | 0.2421 | 0.2368 | 0.2526 | 0.2289 |
| **clt-BB2-DeG2** | 0.2151 | **0.4200** | 0.3333 | 0.2867 | 0.2650 |
| clt-BB2-GeDeD2G2-animal | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BM25-Ge | 0.1793 | 0.2737 | 0.2474 | 0.2386 | 0.2289 |
| clt-BM25-De | 0.1601 | 0.3360 | 0.2600 | 0.2320 | 0.2100 |
| clt-BM25-GeDe | 0.1700 | 0.3474 | 0.2789 | 0.2281 | 0.2053 |
| clt-BM25-D2 | 0.0262 | 0.0267 | 0.0500 | 0.0378 | 0.0350 |
| **clt-BM25-G2** | 0.2400 | 0.3867 | 0.3467 | 0.3156 | **0.2917** |
| clt-BM25-D2G2 | 0.0262 | 0.0267 | 0.0500 | 0.0378 | 0.0350 |
| clt-BM25-DeD2 | 0.0262 | 0.0267 | 0.0500 | 0.0378 | 0.0350 |
| clt-BM25-GeD2 | 0.0262 | 0.0267 | 0.0500 | 0.0378 | 0.0350 |
| clt-BM25-GeG2 | 0.1828 | 0.2947 | 0.2789 | 0.2386 | 0.2132 |
| clt-BM25-DeG2 | 0.1860 | 0.3733 | 0.2933 | 0.2689 | 0.2400 |
| clt-BM25-GeDeD2G2-animal | 0.0262 | 0.0267 | 0.0500 | 0.0378 | 0.0350 |
| clt-BB2-GeDe | 0.2121 | 0.3368 | 0.2895 | 0.2386 | 0.2211 |
| clt-BB2-GeDe0.2 | 0.0199 | 0.0200 | 0.0300 | 0.0267 | 0.0317 |
| clt-BB2-Ge0.2De | 0.2121 | 0.3579 | 0.2947 | 0.2421 | 0.2184 |
| clt-BB2-Ge0.2De0.2 | 0.0199 | 0.0200 | 0.0300 | 0.0267 | 0.0317 |
| clt-BB2-D2-human | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-GE0.2De0.2-human | 0.0199 | 0.0200 | 0.0300 | 0.0267 | 0.0317 |
| clt-BB2-Ge0.2De0.2-human-neo | 0.0199 | 0.0200 | 0.0300 | 0.0267 | 0.0317 |
| clt-BB2-human-neo | 0.1609 | 0.3067 | 0.2633 | 0.2467 | 0.2317 |
| clt-BB2-Ge0.2De0.2-neo | 0.0199 | 0.0200 | 0.0300 | 0.0267 | 0.0317 |
| clt-BB2-D2G2-neo | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-Ge0.2De0.2D2G1.5-human-neo | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-Ge0.2D2G1.5-human-neo | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-De0.2D2G1.5-human-neo | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-Ge0.3De0.3D2G1.5-human-neo | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-De0.3D2G1.5A0g0-human-neo | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-BB2-Ge0.3De0.3D2G1.5A0g0 | 0.0262 | 0.0467 | 0.0467 | 0.0333 | 0.0333 |
| clt-MergeA | 0.0991 | 0.2667 | 0.2400 | 0.2156 | 0.1767 |
| clt-MergeB | 0.0279 | 0.0471 | 0.0588 | 0.0431 | 0.0412 |
| clt-MergeC | 0.1297 | 0.1793 | 0.1690 | 0.1770 | 0.1517 |
| clt-MergeD | 0.0279 | 0.0471 | 0.0588 | 0.0431 | 0.0412 |
| clt-MergeE | 0.1478 | 0.2867 | 0.2700 | 0.2422 | 0.2050 |
| clt-MergeF | 0.0883 | 0.1643 | 0.1679 | 0.1333 | 0.1196 |
| clt-MergeG | 0.1069 | 0.1714 | 0.1750 | 0.1595 | 0.1357 |

**Table 6: Results of runs from 2018. Best results in bold.**

| Run | Rprec | P@5 | P@10 | P@15 | P@20 |
|---|---|---|---|---|---|
| **Medical Abstracts** | | | | | |
| **bma-BB2** | **0.1848** | **0.5440** | **0.5020** | **0.4613** | **0.4400** |
| **bma-BB2-De** | 0.1763 | 0.5040 | 0.4740 | 0.4467 | **0.4400** |
| bma-BB2-GeDe | 0.1651 | 0.4760 | 0.4500 | 0.4200 | 0.4060 |
| bma-BB2-human-neo | 0.1622 | 0.4920 | 0.4680 | 0.4493 | 0.4370 |
| **Clinical Trials** | | | | | |
| **clt-BB2-G2** | **0.3199** | **0.5680** | **0.5260** | **0.4893** | **0.4650** |
| clt-BB2-DeG2 | 0.2857 | 0.5560 | 0.4960 | 0.4733 | 0.4420 |
| clt-BM25-G2 | 0.3014 | 0.5600 | 0.5020 | 0.4733 | 0.4470 |