Precision Medicine Track

Summary
Precision medicine focuses on developing new treatments based on an individual's genetic, environmental, and lifestyle profile. The vast literature available for precision medicine makes it difficult to find the most appropriate treatment for the clinician's current patient thereby creating a problem for clinicians. The ability to quickly locate relevant information for a current patient using information retrieval (IR) is thus important.

Task
The 2019 Precision Medicine track focuses on the case of providing clinical decision support to cancer patients with genetic variations that might impact the choice of treatment. The track uses synthetic patients developed by precision oncologists. Participants are challenged with retrieving relevant scientific literature articles discussing potential treatments, as well as potential clinical trials for each patient.

Data
There are two target document collections: scientific abstracts and clinical trials. Both XML and TXT versions are available for both sets. XML is the official collection and has the complete information for each abstract/trial but the TXT versions may not have all the information. MEDLINE 2019 baseline is used for the scientific abstracts. The 2019 baseline is a snapshot of PubMed abstracts(ftp://ftp.ncbi.nlm.nih.gov/pubmed/baseline/). May-2019 snapshot of ClinicalTrials.gov is used for the clinical trial descriptions.
The topics consist of the disease, genetic variants, and demographic information about the patients.

Evaluation of Runs
The evaluation follows standard TREC evaluation procedures for ad hoc retrieval tasks. Participants can submit a maximum of five automatic or manual runs for each corpus (scientific abstracts and clinical trials), each consisting of a ranked list of up to one thousand IDs (PMIDs for MEDLINE abstracts and NCT IDs for trials), plus the optional specific treatments for just the literature abstracts. The highest-ranked results for each topic are pooled and judged by physicians trained in medical informatics. Assessors are instructed to judge abstracts and clinical trials according to each of the three topic dimensions: disease, gene, demographic. Each of the dimension corresponds to different categories.

1. Disease: Exact, More General, More Specific, Not Disease
2. Gene: Exact, Missing Gene, Missing Variant, Different Variant
3. Demographic: Matches, Excludes, Not Discussed

4. Other: Matches, Excludes, Not Discussed

An abstract/trial result is evaluated according to all four of the categories. In order to calculate a relevance score (i.e., what is used for metrics like P@10, infNDCG), the human-assigned categories are automatically converted to a relevance score.

Approach to the Task

As the related information and knowledge are to be retrieved, it is required to expand the query. Query terms especially disease and gene information can be expanded. After that BM25 can be used for retrieval.