

Evaluation System for Information Retrieval in Biomedical Field

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1 Introduction

Information Retrieval (IR) technology has grown rapidly accompanied by the development of the advanced computational power. More information is being stored as electro-magnetic forms, and anyone can access to it with a PC beyond time and space [1].

Biomedical field is no exception as you know well. Thanks to IR (i.e., PubMed search), you can easily get literature information related to your research area from the vast amount of data which is otherwise intractable [2]. Thus, the aim of IR is to alleviate the cost for you to find your most wanted information.

When developing an IR system, you need to evaluate it, but it is time consuming and needs people having thorough knowledge in the area the IR system focuses on. Usually, filed experts evaluate the system by using it in a practical situation. In this situation, you need to provide them with a comprehensive user interface to efficiently and effectively collect the data [1]. To meet this demand, we developed an IR evaluation system which satisfies both system developers and experts.

2 System

Our system consists of several CGI (Common Gateway Interface) scripts and provides a web-based user interface which mediates a user and an IR system. The system is mainly composed of two parts: system launcher and system evaluator.

The system launcher more focuses on a specific IR system and launches the retrieval as an external process. In our case, we developed an IR system for TREC conference¹. In the conference, participants need to develop an IR system which takes a LocusLink ID, and retrieves papers related to the gene. Therefore, a user inputs a LocusLink ID and the system launches the IR system by feeding it with the input data.

After retrieving papers, the user can see the result by the order of score. At this point, the user can select papers to be shown in the following session (see Figure 1). Then, the system evaluator is launched (see Figure 2). For each paper, the system shows a PMID, a LLID, matched queries, the title, and the abstract with a couple of check boxes for evaluation. A user can review each retrieved paper by checking those boxes. As for title and abstract, text is split by the sentence, and each sentence has some boxes for a user to check or put data in. Therefore, in addition to evaluating system performance, a user can provide other related information such as a sentence which contains a gene name or words which describe a substance involved in an interaction with the gene.

¹Text REtrieval Conference (Genome track), <http://trec.nist.gov/>

