Data and text mining

BeCAS: biomedical concept recognition services and visualization

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ABSTRACT

Summary: The continuous growth of the biomedical scientific literature has been motivating the development of text-mining tools able to efficiently process all this information. Although numerous domain-specific solutions are available, there is no web-based concept-recognition system that combines the ability to select multiple concept types to annotate, to reference external databases and to automatically annotate nested and intercepted concepts. BeCAS, the Biomedical Concept Annotation System, is an API for biomedical concept identification and a web-based tool that addresses these limitations. MEDLINE abstracts or free text can be annotated directly in the web interface, where identified concepts are enriched with links to reference databases. Using its customizable widget, it can also be used to augment external web pages with concept highlighting features. Furthermore, all text-processing and annotation features are made available through an HTTP REST API, allowing integration in any text-processing pipeline.

Availability: BeCAS is freely available for non-commercial use at http://bioinformatics.ua.pt/becas.

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1 INTRODUCTION

Exponential growth of the biomedical literature during the past decades has prompted the development of automatic techniques and systems to ease the task of finding relevant information in unstructured documents (Lu, 2011). However, the offer of no-installation, no-maintenance and online modular solutions for concept annotation that can be easily integrated in any text-processing pipeline is still scarce. Whatizit (Rebholz-Schuhmann et al., 2008), for instance, offers dictionary-based annotation of documents with a large set of vocabularies and is available both through a web service and a web page. Yet, annotation of concepts from different types is only possible by repeating the annotation process several times and combining the results generated by different pipelines. iHOP (Hoffmann and Valencia, 2004) is a web application offering programmatic access to pre-annotated abstracts from MEDLINE. It is a protein-centric system and does not allow the annotation of external documents submitted by the user. Another solution focused on genes, proteins and small-molecules is Reflect (Pafilis et al., 2009), a web service that annotates these concepts on web pages and provides, through pop-ups, additional information such as synonyms, database identifiers and related literature. Cocoa is a multiple concept annotator with an online interface and an HTTP API (http://npjoint.com). It annotates entities in user submitted text, but it is limited to named entities and does not provide concept identifiers or external references.

BeCAS exposes its functionalities through three interfaces: an HTTP REST API, a widget embeddable in web pages and an interactive web application. It provides annotations both for user-supplied texts

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and for MEDLINE abstracts, which are automatically fetched from PubMed.

3.1 Exploring annotations on a web interface

BeCAS web interface was built with a strong focus on usability. Specific entity types can be highlighted or muted in real-time by using simple toggle controls, and nested and intersected annotations are also easily identified by the colour-coding scheme used. An info-box with links to external databases is displayed by placing the mouse over highlighted entities, and users can explore this same information, grouped by concept type, through the concept tree (Fig. 1). Annotated text can be exported in several formats such as JSON and A1. Users and other websites can link to annotated PubMed publications by using direct links (e.g. http://bioinformatics.ua.pt/becas/pmid/22957306).

Concept highlighting with external references can easily be integrated in any website through the use of the BeCAS Javascript widget. Host pages only need to include a <script> tag linking to the plugin and a few configuration parameters. Every feature implemented in the main web interface is exposed by the widget, apart from the concept tree.

3.2 Processing text and MEDLINE publications

Text can be annotated programmatically using one of BeCAS HTTP REST endpoints. Clients should make HTTP POST requests to one of the endpoints with a JSON encoded payload, specifying the text to annotate, the desired output format and types of entities that should be annotated. Because of inherent representation constraints, the available output formats support different levels of granularity in the results. CoNLL format is the most comprehensive, providing sentence splitting, tokenization, lemmatization, POS tagging, chunking and identification of isolated, nested and intersected concepts. JSON format includes sentence splitting and concept identification. IeXML formatted results contain the same information as JSON, but nested and intersected annotations are limited to a depth of one level, with deeper annotations resolved to the largest

4 CONCLUSION

BeCAS provides three distinct user interfaces for biomedical concept identification, presenting state-of-the-art performance, as evaluated on various corpora. It currently recognizes and annotates 1.2 million concepts and enriches them with 1.6 million external references to 30 online resources. The REST API is suitable for integration in custom text-processing pipelines, whereas the widget can be easily integrated in any web page. Finally, users can also use BeCAS annotation services as a stand-alone web application. In the future, we plan to add support for more entity types and continue to improve annotation performance, with focus on concept disambiguation.

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