

Internal Report

Deliverable D3.1a: Refined vocabulary for cross-context knowledge discovery in plant immune signalling

National Institute of Biology

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Abstract: To improve vocabulary for cross-context knowledge discovery in plant immune signalling, we have identified several steps where the vocabulary should be improved. Three important steps were chosen, namely searching query to retrieve the articles from open access databases, top keywords in OntoGen and SVM keywords in Ontogen. For each separate step, we performed several cycles of refining, often including manually curated corrections.

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Introduction

It is known that plants have the circadian rhythm, which means that some of their genes are differently expressed in the morning, at noon and in the evening. We have noticed that plants react differently to the infection with the pathogen if they are infected in different parts of the rhythm. We can conclude that genetic networks that are important for the defence of plants against pathogens are differently expressed in the different parts of the day. We focused on knowledge discovery by combining knowledge from two different domains (plant defence and circadian rhythm) to get new insights and derive new conclusions. Our cross-domain literature mining methodology includes three complementary text mining tools: literature (text) preparation and extraction tool, clustering and topic ontology creation tool OntoGen and a cross-domain bridging terms exploration tool CrossBee. Using OntoGen we try to identify outlier documents while CrossBee allows bridging concepts exploration and identification.

Data preparation

We have developed a web application which allows for search, preprocessing, extraction and download of PubMed Central (PMC) free-text articles. PMC archives ~4.7 million articles of which more than 2 million have free full-text available for download. Moreover, the majority of the free full-text collection is released under the open access licence (OAC). NCBI provides an API which allows searching and downloading full texts of articles. However, API query rates are limited to allow uninterrupted access to NCBI website and web tools. Therefore, NCBI also makes their free full-text articles collection available as a set of large archives of compressed XML documents.

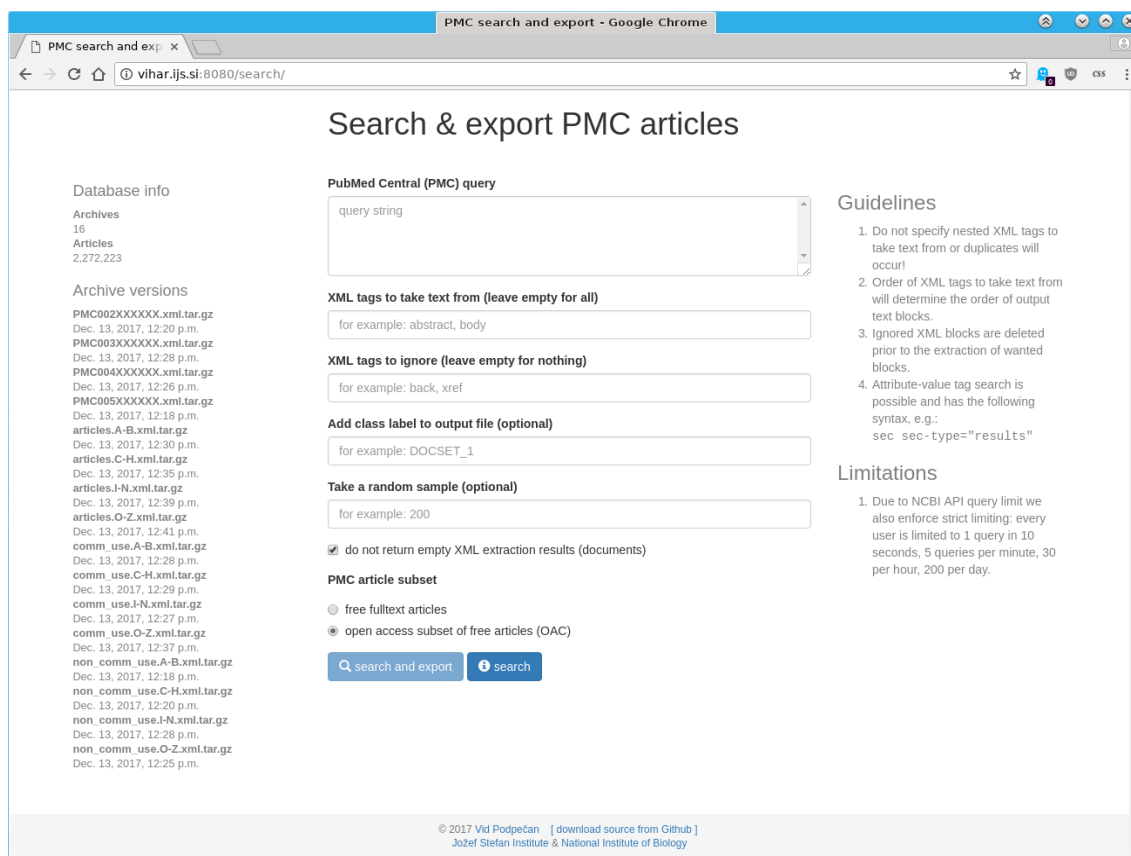


Figure 1: A screenshot of the web application for search, extraction and download of free full-text articles from PMC.

To allow search and text mining on the complete free full-text document collection we have constructed a database which contains all available free full-text documents extracted from the compressed archives of XML files. On top of that, we provide a web application which offers PMC search, XML extraction and preprocessing, random sampling and export in the widely used *Indoc* format which can be read by OntoGen and CrossBee. Figure 1 shows a screenshot of the application in a browser window. The complete code of the web application is available under the MIT licence on GitHub: <https://github.com/vpodpecan/pmcutils>

Results

Queries to retrieve the articles from open access databases for several different domains that could be combined with plant immune signalling domain were prepared. An example of a query is shown in Figure 2.

- D1: (Arabidopsis OR Oryza OR Solanum OR Nicotiana OR maize OR cotton) AND ("defence" OR "defense" OR "immune" OR "hypersensitive" OR "hypersensitivity" OR "resistance" OR "susceptible" OR "susceptibility" OR "pathogen" OR "virus") NOT (cigarette OR smoking OR carcinoma OR cancer OR insulin OR diabetes OR "Parkinson's" OR mice OR rodents OR zebrafish OR teenagers)
- D2: (circadian) AND (rhythm OR clock)

Figure 2: An example of a query to retrieve the articles from open access databases.

Retrieved articles were processed Ontogen. On the basis of top keywords in OntoGen, the queries were refined. Several cycles of refining the queries were performed.

On the basis of SVM keywords obtained in OntoGen, the list of stop words was produced. Several cycles of refining the stop words were performed. An example of a stop words list is shown in Figure 3.

- fig
- figure
- table
- result
- mm
- al.
- cca
- cca.
- sequencing
- gene
- expression
- example
- use
- source
- method
- approach
- percentage
- al
- patients
- mice
- genes
- proteins
- mirnas
- rna
- transcriptional
- snp

- qtl
- genome
- cell
- root
- strains
- mutant

Figure 3: An example of a stop words list for OntoGen.