variant2literature: full text literature search for genetic variants

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Abstract

Motivation: Whole genome sequencing (WGS) by next-generation sequencing produces millions of variants for an individual. The retrieval of biomedical literature for such a large number of genetic variants remains challenging, because in many cases the variants are only present in figures or tables as images, or in the supplementary documents of which the file formats are diverse.

Results: The proposed tool named variant2literature from the TaiGenomics (Toolkits for AI genomics) resolves the problem by incorporating image processing in text recognition. In addition to the adoption of text retrieval by image processing, the recall rate of finding the literature containing the variants of interest is further improved by employing the skill of variant normalization. Different variant presentations are transformed into chromosome coordinates (standard VCF format) such that false negatives can be largely avoided. variant2literature is available in two ways. First, a web-based interface is provided to search all the PMC literatures. Second, the command-line executable can be downloaded such that the users are free to search all the files in a specified directory locally.

Availability: http://variant2literature.taigenomics.com/

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1 Introduction

Whole-exome sequencing (WES) and whole-genome sequencing (WGS) become more and more popular in diagnosis of diseases and discovery of phenotype-related variants

[1-3]. The annotation of variants involves a critical step that finds literature to explain the potential influence of a discovered variant on protein functions, cell behaviors, organ normality, etc. In this regard, many efforts have been made to improve the search performance [4, 5]. Even though, we observed that the sensitivity of variant queries still has space to increase. For example, when a researcher sends a query in the literature database, it is most likely that the related papers are missing in the result page owing to the fact that the search is not comprehensively performed on the full text of the papers as a well as all the supplementary files. The challenge of this task is that most accessible literatures are released in PDF format. In this study, we used PubMed Central (PMC) database to demonstrate that the adoption of image processing followed by deep learning can largely increase the recall rate of literature search.

In addition to tackle the barrier due to diverse file formats, variant2literature also resolves the format issue of variant queries by translating all types of variant presentations into chromosome-based coordinates. The literature files were preprocessed to record all the variants using chromosome-based coordinates in a local database. Moreover, if a gene has multiple isoforms, a known variant of one particular isoform will be also annotated on the other isoforms with corrected coordinates. Meanwhile, RSID (Rapid Stain Identification Series) is also acceptable. All of these designs were shown to improve the sensitivity of variant query on literature search. Currently, variant2literature accepts documents files in XML, PDF, DOCX, DOC, XLSX, and CSV formats. Both web interface and command-line executable are available now.

2 Materials and methods

When handling PDF files, fasterRCNN [6] was used to detect table regions. Recognition of table structures was performed by in-house rule-based methods. Figure and table captions in PDF were retrieved by PDFFigures 2.0 [7]. variant2lieterature used tmVar [8] (or our LSTM model) to extract variants from paragraphs and tables, and used GNormplus [9] (or our LSTM model) to extract genes from paragraphs and tables. The assignment of variants to genes were implemented by in-house rule-based methods. It is important that variant representations were made consistent by some rules, e.g. checking introns and position ranges. Finally, the variants and the associated genes were normalized into the VCF format [10]. Accordingly, the literature files were indexed by the normalized variants.

variant2literature is available in two ways: web interface and command-line executable. In the web server, query can be made in different ways. Some examples can be found on the web site (http://variant2literature.taigenomics.com/). Meanwhile, uploading a VCF file is acceptable in both web interface and command-line executable.

3 Results and discussions

The disease 'deafness' is used as an example to demonstrate the power of variant2literature. The Deafness Variation Database (DVD) [11] contains 876,135 known variants (v8.1.2017-11-08). There are 10,036 variants being linked to 3,095 papers, constituting 18,410 variant-paper pairs. Among the 3,095 papers, 206 papers can be found in the PMC database, containing 1,026 variant-paper pairs. It is noticed that not all the variant-paper pairs in these 206 papers were curated in the DVD database. In this regard, three domain experts were recruited in this study to identify all the variant-paper pairs present in these 206 papers. Finally, 3,217 pairs were recorded as positive instances, involving 2,277 variants.

After invoking variant2literature on 2,277 variants against the 206 papers, 3,011 pairs were reported as positives, resulting a recall rate of 90.86% and a precision rate of 97.08%. For comparison, we performed the same query of variant set on LitVar [4]. By uploading the 2,277 variants to LitVar, 1,138 pairs were reported as positives, resulting a recall rate of 32.76% and a precision rate of 92.62%.

Table 1. Performance of variant2literature with different settings.

Methods	Variant-paper pairs predicted	Recall	Precision	F1 score
variant2literature (without suppl.)	2,377	72.21%	97.73%	0.83
variant2literature (with suppl.)	2,754	82.69%	96.59%	0.89
variant2literature (with suppl. + table text retrieval)	3,011	90.86%	97.08%	0.94
LitVar	1,138	32.76%	92.62%	0.48

Abbreviation: suppl. stands for supplementary files.

3.1 Limitations

The following limitations of variant2literature should be noticed. First, when a user specifies a query like this: 'Gene_name, A123C', variant2literature cannot tell whether the position 123 is the coordinate of bases on cDNA or residues on proteins. Currently, variant2literautre assumes the number is regarding residue coordinates. Only when the residue information does not match the amino acid sequence of the protein, it switches to the cDNA position instead. Second, there are still some formats of variants remained

unrecognized in the literature, e.g. '104 A [G'. Such limitations will be gradually resolved according to user feedback in the future.

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