

Name:	Ben Busby
Affiliation:	National Center for Biotechnology Information, Bethesda, MD
Email:	busbybr@ncbi.nlm.nih.gov
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PubRunner: A framework to update biomedical text mining analysis with the latest publications

Kishore R. Anekalla¹ J.P. Courneya², Nicolas Fiorini³, Jake Lever⁴, Michael Muchow⁵ and Ben Busby⁶

¹Northwestern University, Chicago, IL, USA ²Health Sciences and Human Services Library, University of Maryland, Baltimore, MD ³National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD ⁴Canada's Michael Smith Genome Sciences Centre, University of British Columbia, Vancouver, BC, Canada ⁵National Institute of Standards and Technology, Gaithersburg, MD ⁶National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD

Abstract

Biomedical text mining offers the possibility of extracting large amounts of knowledge from the millions of published articles. These technologies are becoming essential as knowledge is spread across larger numbers of journals and subject domains. However this extracted knowledge is only valuable if it is based on the latest publications and not kept static. Unfortunately many text mining resources are static and after publication these resources are not maintained. The community needs a method to make it easy to keep these analysis up to date. We present PubRunner, a framework that downloads the latest publications from PubMed, runs whichever text mining tools are needed and uploads the data to a publicly available location. We hope to encourage researchers in our community to use this framework to keep text mining results up-to-date so that they are truly valuable to biologists, and extend this service to other corpora used for NLP.

Introduction

All biology researchers face the substantial challenge of keeping abreast of all appropriate research in their field. This problem is exacerbated by the fact that the number of publications in Pubmed, the largest indexed collection of biomedical abstracts, is increasing at an exponential rate¹. Text mining tools can be used to help researchers in several ways, including extracting knowledge (such as miRNA regulation data²), suggesting potential hypothesis (the FACTA+ system³) or assisting in improved PubMed search⁴. However text mining tools are only useful if they provide results with the latest papers. Unfortunately some text mining results are static and never updated. The most common reason is that projects are never revisited once published and the technical costs to keep them updated are too high. This necessitates the development of a framework to make updating results easier. Our approach, PubRunner, manages the updates from PubMed, execution of text mining tools and uploads of data to publicly available locations such as FTPs or Zenodo data hosting. We hope this initiative will encourage more sharing of tools and up-to-date data in the biomedical text mining community.

Approach

PubRunner consists of four main components shown in Figure 1. The first component manages the download of Pubmed abstracts from the NCBI FTP website. This intelligently checks for new Pubmed files and only downloads what is required. The second component manages the execution of text mining tools on the downloaded Pubmed data. It checks for appropriate exit status. The third component moves the resulting output data to a publicly available space such as a public FTP or Zenodo permanent hosting location. The fourth component then updates the main PubRunner website with information about what tools have been executed and where the data can be found.

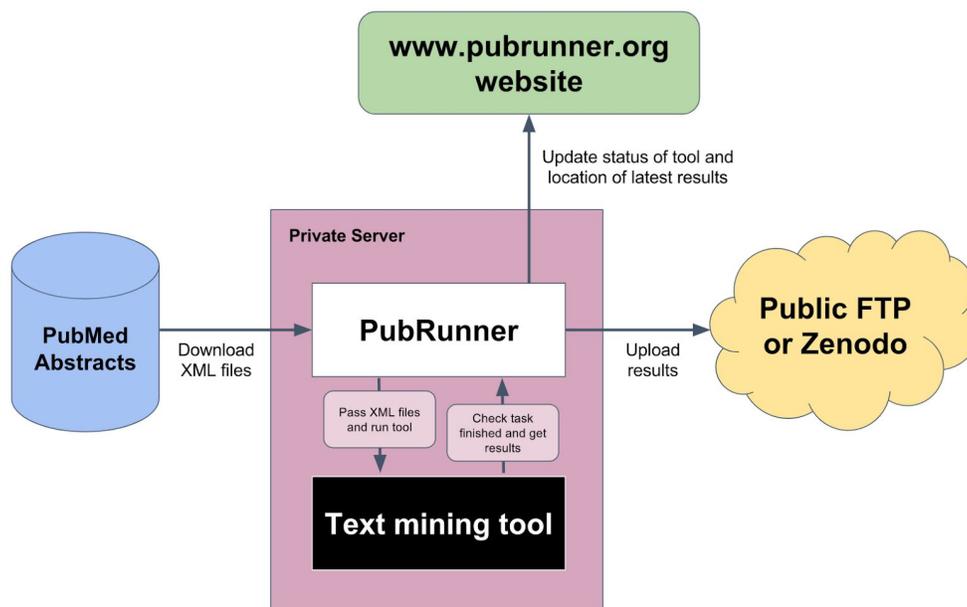


Figure 1. Main workflow of PubRunner

The PubRunner framework was tested with several different tools. Three tools were developed as test cases and these tools calculate basic word counts on the abstracts. The main tool tested was word2vec⁵ which is a very popular program for calculating word vector representations and is commonly used in text mining analysis. PubRunner is currently run monthly on these four text mining tools and we plan to expand the framework and add more tools.

Conclusion

The text mining community has built a wealth of valuable tools that can extract valuable knowledge for biologists and build useful data for other text mining researchers. However the output of these tools, as presented by the original authors, is often out-dated. PubRunner is the first step towards solving this problem and allowing biologists and text mining researchers to use the latest data in their work.

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