**Data and text mining**

**GeoBoost2: a natural language processing pipeline for GenBank metadata enrichment for virus phylogeography**

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**Abstract**

**Summary:** We present GeoBoost2, a natural language-processing pipeline for extracting the location of infected hosts for enriching metadata in nucleotide sequences repositories like National Center of Biotechnology Information’s GenBank for downstream analysis including phylogeography and genomic epidemiology. The increasing number of pathogen sequences requires complementary information extraction methods for focused research, including surveillance within countries and between borders. In this article, we describe the enhancements from our earlier release including improvement in end-to-end extraction performance and speed, availability of a fully functional web-interface and state-of-the-art methods for location extraction using deep learning.

**Availability and implementation:** Application is freely available on the web at https://zodo.asu.edu/geoboost2. Source code, usage examples and annotated data for GeoBoost2 is freely available at https://github.com/ZooPhy/geoboost2.

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**Supplementary information:** Supplementary data are available at *Bioinformatics* online.

1 Introduction

Molecular sequences play a vital role in conducting phylogenetic, phylogeographic and epidemiological studies to understand the dynamic nature of evolution and migration of pathogens across countries and continents. The National Center of Biotechnology Information (NCBI) maintains GenBank (Benson et al., 2018), which is one of the largest comprehensive databases of nucleotide sequences available to the public. As of July 2020, GenBank contains 217 million entries (NCBI, 2020a) with over 3 million viral sequences reported in the latest release notes (NCBI, 2020b). The availability of such a database supports research in various domains of public health, particularly infectious diseases such as Ebola, Zika and most recently SARS-CoV-2 (Dudas et al., 2017; Lai et al., 2020; Pybus et al., 2012). However, the quality of geographic metadata about the location of infected hosts (LOIH) that is readily available at the individual record level may be insufficient for studies conducted at the state/province levels within the country (Scotch et al., 2011; Tahsin et al., 2014). The presence of detailed geographic metadata is crucial not just for epidemiological studies, but also in retrospective genomic studies by the wider scientific community.

Geographic metadata about the infected host is not required when submitting a sequence to GenBank. The database offers a *Features* table which includes both mandatory and optional qualifiers (Benson et al., 2018; INSDC, 2019). Geographic metadata is amongst the optional qualifiers including *lat_lon* for the approximate coordinates, and *country* for named locations. Among the over 3 million viral sequences available (NCBI, 2020b), only about 1% of the records contained the infected host’s coordinates in the *lat_-lon* field and only 26% contained host information more specific than a country in the *country* field. Such unavailability of detailed metadata in GenBank creates barriers for phylogeographic and genomic epidemiology at a local level. Researchers are then required to manually analyze other metadata fields in the record and/or review any associated PubMed articles. If no additional metadata is found, then the researcher might decide to exclude these records from the study altogether, reducing the sample size of the study and potentially introducing bias.

GeoBoost2 provides a framework to automate this manual extraction process where the individual metadata fields are analyzed with the objective of extracting the LOIH from associated records. GeoBoost2 improves over its predecessor GeoBoost (Tahsin et al., 2014).
2016, 2018) in extraction performance by over 35% when evaluated on two corpora using advanced data mining methods on the linked PubMed articles to enrich the geospatial metadata. Overall, GeoBoost2 achieved 90% accuracy in resolving the LOIH in GenBank metadata and 57% accuracy in resolving LOIH extraction from associated PubMed articles. To the best of our knowledge, GeoBoost and GeoBoost2 are the only systems that use natural language-processing (NLP) techniques to extract LOIH from articles cited in GenBank accessions. In Supplementary Information, we describe in detail our methods and evaluation of GeoBoost2. We also provide a screenshot of the current version of the interface (Fig. 1).

GeoBoost2 includes:

1. A state-of-the-art deep-learning NLP algorithm trained on manually annotated geographic location mentions in PubMed Central Open Access articles (Magge et al., 2018, 2019). All geographic location mentions are disambiguated and resolved to a unique identifier in GeoNames (2020a,b), a database containing 12 million locations across the globe.

2. A Python 3.7 framework implementation (replacing a Java-based framework) for continuous improvement with deep-learning and machine-learning methods for information extraction.

3. A Web-based interface with a map view that accepts as input any GenBank accession IDs (not limited to viruses) and provides features to export results. In addition to accepting GenBank accession IDs, the tool can also accept PubMed IDs or raw text captured from an article for mining geographic locations.

4. An application programming interface (API) for use of the results in downstream applications. In addition to mining PubMed articles directly linked in the GenBank accessions, GeoBoost2 also mines geographic locations from additional PubMed articles and their respective Supplementary Information that have cited the GenBank accessions in their studies. All data retrieval functionalities in the tool rely on APIs provided by NCBI, ensuring the latest available information.

Results from GeoBoost2 can be used for Bayesian discrete phylogeography on ZooPhy (Scotch et al., 2010, 2019b, ZooPhy, 2020). Here, the probabilities for potential LOIH generated by GeoBoost2 can be used as sampling uncertainties (Scotch et al., 2019a) for the taxa in phylogeographic studies implemented using BEAST (Suchard et al., 2018).

We plan to extend our information extraction and normalization efforts to additional optional qualifiers such as collection_date, host and isolation_source. We also plan to validate the performance of the tool on other pathogens such as bacteria and parasites.

With the growing concern over emerging and re-emerging pathogens, a publicly available, free tool like GeoBoost2 will facilitate public health surveillance and genomic epidemiology.

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