English dictionaries, gold and silver standard corpora for biomedical natural language processing related to SARS-CoV-2 and COVID-19

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Abstract
Automated information extraction with natural language processing (NLP) tools is required to gain systematic insights from the large number of COVID-19 publications, reports and social media posts, which far exceed human processing capabilities. A key challenge for NLP is the extensive variation in terminology used to describe medical entities, which was especially pronounced for this newly emergent disease.
Here we present an NLP toolbox comprising very large English dictionaries of synonyms for SARS-CoV-2 (including variant names) and COVID-19, which can be used with dictionary-based NLP tools. We also present a silver standard corpus generated with the dictionaries, and a gold standard corpus, consisting of PubMed abstracts manually annotated for disease, virus, symptom, protein/gene, cell type, chemical and species terms, which can be used to train and evaluate COVID-19-related NLP tools. Code for annotation, which can be used to expand the silver standard corpus or for text mining is also included. This toolbox is freely available on GitHub (on https://github.com/Aitslab/corona) and zenodo (https://doi.org/10.5281/zenodo.6642275).
The toolbox can be used for a variety of text analytics tasks related to the COVID-19 crisis and has already been used to create a COVID-19 knowledge graph, study the variability and evolution of COVID-19-related terminology and develop and benchmark text mining tools.

Keywords
COVID-19, SARS-CoV-2, natural language processing, BioNLP, text mining, linguistics, dictionary, medical informatics, bioinformatics
Introduction

The analysis of various types of text from scientific articles to reports or social media posts can be used to support research on SARS-CoV-2/COVID-19 and public health management of the pandemic. It can also be used for studying the social impact of the crisis or the linguistic development that accompanies it.

One critical step in biomedical natural language processing (BioNLP), as for most types of text analysis, is the identification of relevant keywords and phrases as well as the detection of synonymous expressions. This so-called named entity recognition (NER) and disambiguation can be especially challenging with newly emerging diseases such as COVID-19 because no official name had been defined during the early phases of the outbreak (Masters-Waage, Jha, & Reb, 2020) and because such a large and diverse global community was involved in the writing of COVID-19-related texts. Many authors thus used a wide range of descriptive terms such as “Wuhan seafood market pneumonia” (Santoni & Vergni, 2020).

NER can be performed using dictionaries of keywords or with the help of machine learning models, which are trained on annotated corpora in which keywords have been labelled manually by experts (gold standard) or automatically (silver standard) (Cook & Jensen, 2019). Dictionary and model-based methods can also be combined as the approaches are complimentary. Here, we have developed a toolbox for NER related to SARS-CoV-2 and COVID-19. It includes English dictionaries of synonymous terms as well as an annotated gold and silver standard corpus and an annotation script. A first version was released at an early stage of the pandemic. It was already used to generate COVID-19 knowledge graphs (Peng et al., 2022)) and analyse the variation and evolution of COVID-19 terminology (Leaman & Lu, 2020). We have now expanded the dictionaries with additional terms and added new entity types to the gold standard. The original toolbox and its updated version are available on GitHub (on https://github.com/Aitslab/corona) and zenodo (https://doi.org/10.5281/zenodo.6642275) (Rashed, Ahmed, Frid, & Aits, 2022).

Methods

Generation of SARS-CoV-2 and COVID-19 dictionaries

Synonyms and biomedical identifiers for COVID-19 and SARS-CoV-2 were identified by reviewing a variety of databases and text sources including: NCBI Taxonomy database (Federhen, 2012), Wikidata (https://www.wikidata.org/), the International Classification of Diseases (International Classification of Diseases, v10, https://icd.who.int/browse10/2019/en and v11. https://icd.who.int/browse11), Disease Ontology (Schriml et al., 2019), Medical Subject Headings (MeSH, https://www.ncbi.nlm.nih.gov/mesh/), medical literature, twitter feeds, and newspaper websites. Terms from lists on https://github.com/ncbi-nlp/CovidTermVar, created by the Leaman and Lu group, were also added, but excluding terms containing commas, full-stops or colons (e.g. “COVID-19, infection”), spelling error variants (e.g. “CVOID-19”), highly ambiguous (e.g. “CI), non-sensical terms (e.g. “novel coronavirus Coronavirus Disease”) and terms referring to a patient characteristic (e.g. COVID-19 infected), rather than the disease itself. From this manually curated list, plural forms were resolved to singular (e.g. “infections” replaced with “infection”), hyphens stripped, and letters changed to lower case. Ambiguous abbreviations (e.g. NCP - novel coronavirus pneumonia) were removed since they can be detected through abbreviation resolution. Variants for virus names and disease names were generated as follows:

Virus names:
- Adding '2019', '2019novel', '2019new', '2019 novel', '2019 new' as prefixes or 2019 as suffix (only if '19' was not in the virus name)
- interchanging corona virus and coronavirus
- removing virus names containing the same word twice or containing both 'new' and
'novel'
- interchanging Wuhan and Hubei

Disease names:
- interchanging corona virus and coronavirus
- pairing the terms of the virus list with generic terms indicating the disease, e.g. illness, disorder, disease, pneumonia
- interchanging the terms disease, disorder, syndrome, pneumonia, infection
- adding the adjectives acute, severe, and respiratory alone or in combination
- removing disease names containing the same word twice or containing both 'new' and 'novel'

Duplicate dictionary entries as well as automatically generated entries with duplicate or semantically similar words (i.e. containing both “novel” and “new”, both “Hubei” and “Wuhan” or both “corona virus” and “coronavirus”) were removed.

For the SARS-CoV-2 variant name dictionary (Supplemental_file3), variant and clade names were collected on 2022-01-13 from the WHO (https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/), GSAID (Shu & McCauley, 2017) (https://www.gisaid.org/...-aids-in-genomic-epidemiology-of-active-hcov-19-viruses/), Nextstrain (Hadfield et al., 2018) (https://github.com/nextstrain/ncov/blob/master/defaults/clades.tsv) and Pango (https://cov-lineages.org/lineage_list.html).

Production of Corona silver standard corpus
SARS-CoV-2/COVID-19 related studies were identified on PubMed on March 16 2020 with the search term (((COVID-19 OR SARS-CoV-2 OR (Wuhan AND virus) OR 2019-nCoV OR (Wuhan AND pneumonia)) AND English[lang]) AND ("2019/12"[Date - Create] : "2020"[Date - Create])). The 987 detected records were downloaded in text format (even those containing only a heading and no abstract). The text was stripped of hyphens and “/” replaced with blank spaces. Tokenization (chopping up text into individual words/terms), and detection of dictionary terms was performed with spacy (Honnibal, Montani, Van Landeghem, & Boyd, 2020)(https://spacy.io/) and the scispacy (Neumann, King, Beltagy, & Ammar, 2019) model en_core_sci_md-0.2.4, using the spacy lookup module in a capitalization-independent manner. A second tokenization step was performed by splitting the terms matching the dictionaries on blank spaces. Annotations were stored in IOB2 format where the first token of an entity is labelled 'B', subsequent tokens belonging to the entity are labelled 'I', and all other tokens are labelled ‘O’. When matches were found in both dictionaries, the correct one was selected manually. Scripts can be found in Supplemental_file8.

Production of Corona gold standard corpora
Using BioQRator (Kwon, Kim, Shin, & Wilbur, 2013)(http://www.bioqrator.org/), English abstracts related to COVID-19/SARS-CoV-2 and published between Dec 2019 and March 6 2020 were identified on PubMed with the following search query: (((COVID-19 OR SARS-CoV-2 OR (Wuhan AND virus) OR 2019-nCoV OR (Wuhan AND pneumonia)) AND English[lang]) AND ("2019/12"[Date - Create] : "2020"[Date - Create])). From the abstracts loaded into BioQRator without error, 10 were randomly selected and subsequently annotated for the following concepts:
- Virus_SARS-CoV-2: for terms representing SARS-CoV-2, including generic terms when they referred to this specific virus-based on the context (e.g. “the virus”)
- Virus other: for terms representing a specific virus other than SARS-CoV-2 (e.g. MERS, SARS-CoV)
• Virus_family: for terms representing more than one virus (e.g. coronaviruses) or all viruses; for this concept, unique identifiers from the NCBI taxonomy database were also indicated
• Cell: for terms describing specific cell types, e.g. “mast cells”
• Protein: for terms representing specific proteins or genes, but not a protein family (e.g. IL-2 is annotated under this concept, but not protease, IL-1 family members or interleukins); for this concept, unique identifiers from the UniProt database were also indicated
• Disease_COVID-19: for terms representing COVID-19
• Disease_other: for terms representing a disease other than COVID-19 (e.g. Zika virus infection) or general terms for disease (e.g. infection)
• Symptom: for terms representing disease symptoms (e.g. fever, cough). “Pneumonia” was annotated as Disease_other or Symptom depending on the context.
• Species_human: for terms representing humans (e.g. “man”, “patient”)
• Species_other: for terms representing other species, including terms referring to groups of species (e.g. “mammals”)

Abbreviations were annotated independently unless they were nested inside an expression, e.g. in the expression novel coronavirus (2019-nCoV) both “novel coronavirus” and “2019-nCoV” were annotated as Virus_SARS-CoV-2.

The corpus was exported from BioQRator as a csv and BioC xml file and converted to BioC json format (Supplemental_file5-7) using the script of the BioC-JSON tool from the NLM/NCBI BioNLP Research Group (Comeau et al., 2013)(https://github.com/ncbi-nlp/BioC-JSON) with minor changes. Scripts can be found in Supplemental_file8.

Results
Production of SARS-CoV-2 and COVID-19 dictionaries
Synonyms for SARS-CoV-2 (for the virus dictionary) and COVID-19 (for the disease dictionary) were collected by browsing through a variety of biomedical texts and other public text sources such as news reports and social media posts. For completeness, even biomedical identifiers, colloquial and derogatory terms (e.g. “China virus” and “kung flu”) as well as terms which can match other biomedical entities (e.g. “coronavirus”) were included. In contrast, highly ambiguous abbreviations (e.g. “CI”, “CV”) and were excluded as these would result in many false-positive matches. When needed, these could be added easily. Hyphens and capitalization were removed as these add a lot of variation but can be resolved by adequate pre-processing of texts to be analysed with the dictionaries. For similar reasons, plural forms and spelling errors, discoverable by using the dictionaries with incomplete matching techniques, were not taken into account.

The dictionaries were then expanded by artificially generating variations that account for potential differences in spelling (e.g. “coronavirus” and “corona virus”), common pre-fixes (e.g. “2019”) or interchangeably used terms (“infection” and “disease”). Duplicates and non-sensical expressions, which contained the same or similar words twice were excluded. Some of the generated terms are very unlikely to exist but as they would simply be unmatched in text mining procedures there is no large benefit from excluding them. The first version of the dictionaries, published with the first pre-print version of this article, contained 215 virus synonyms (Supplemental_file1) and 12915 disease synonyms, including 9 database identifiers (Supplemental_file2). The current second version, which includes additional terms, contains 807 virus synonyms (Supplemental_file1_v2) and 89901 disease synonyms (Supplemental_file2_v2). The variant dictionary contains 5330 terms (Supplemental_file3).
Production of Corona silver standard corpus and annotation script

To generate the Corona silver standard (computationally annotated) corpus, 987 PubMed records, including abstracts when available, were extracted as text file. After tokenization with spacy, the corpus was annotated in IOB2 format by comparing tokens against the SARS-CoV-2/COVID-19 terms in our dictionaries (Supplemental_file4). Additional versions of the silver standard corpus, including more abstracts and/or other annotations, can be generated by the end user with the provided dictionaries and script (supplemental_file1_v2, Supplemental_file2_v2, Supplemental_file3, Supplemental_file8_v2). The script can also be easily modified to identify COVID-19-related entities in any text or text collection, on which the user wants to perform text mining.

Production of Corona gold standard corpus

To produce a small gold standard corpus for testing NLP tools, 10 randomly selected PubMed abstracts related to SARS-CoV-2/COVID-19 were annotated in BioQRator by a biomedical expert who labelled virus, disease, symptom, and protein/gene terms. BioQRator does not allow for overlapping annotations which was problematic when annotating the expression “respiratory, enteric and systemic infections”. In this case, the words respiratory and enteric were annotated as individual entities of the Disease_other category. In total, the corpus contains 199 annotations across the 11 concepts (Table1). The corpus in its second version is available in BioQRator csv, BioC xml and BioC json format (Supplemental_file5-7).

Table1. Entity counts for the articles in the Corona gold standard corpus

| PMID   | 31896 | 31991 | 31992 | 31996 | 32007 | 643 | 32013 | 32015 | 32020 | 32029 | 32036 | Total |
|--------|-------|-------|-------|-------|-------|-----|-------|-------|-------|-------|-------|-------|
| Cell   | 5     |       |       |       |       |     |       |       |       |       |       | 5     |
| Chemical | 1     |       |       |       |       |     |       |       |       |       |       | 1     |
| Disease_COVID_19 | 3   | 2     | 1     |       | 2     | 6   |       |       |       |       |       | 14    |
| Disease_other | 5   | 3     | 5     | 5     | 3     | 2   | 3     |       |       |       |       | 26    |
| Protein | 8     |       |       |       |       |     |       |       |       |       |       | 14    |
| Symptom | 16    |       |       |       |       |     |       |       |       |       |       | 28    |
| Species_human | 17 | 2     | 5     | 3     |       |     |       |       |       |       |       | 28    |
| Species_other | 1    |       |       |       |       |     |       |       |       |       |       | 7     |
| Virus_family | 1    | 3     | 5     | 3     | 4     |     |       |       |       |       |       | 19    |
| Virus_other | 1     |       |       |       |       |     |       |       |       |       |       | 4     |
| Virus_SARS-CoV-2 | 5 | 4     | 2     | 7     | 6     | 1   | 5     | 5     | 3     | 10    |       | 48    |
| Total   | 55    | 6     | 4     | 10    | 10    | 28  | 24    | 26    | 11    | 25    |       | 199   |

Articles are indicated by PubMed ID (PMID).

Discussion

The ongoing COVID-19 pandemic has resulted in an explosion of texts related to it, which far exceeds the capacity of human readers. To handle this challenge, automated text processing is essential. The presented COVID-19-related NLP toolbox can be applied in a variety of text analytics settings. Recently, it has been used in a framework to generate a comprehensive COVID-19 knowledge graph (Peng et al., 2022). Such knowledge graphs can be an important tool to direct experimental work or support systematic literature review. In addition, our toolbox has been used in a linguistic study on COVID-19 terminology (Leaman & Lu, 2020). Other potential uses include information extraction from electronic health records, social media and news item analysis, chatbots, tools to track misinformation and many other areas where large amounts of COVID-19-related text need to be processed. Our tools can also be combined with other COVID-19-related BioNLP resources which have recently been published (Chen, Allot, & Lu, 2020; Lu Wang et al., 2020) and with powerful subject-agnostic NLP tools such as spacy (Honnibal et al., 2020).

Even though the toolbox is designed for use with the English language, the dictionaries can also
be applied for NLP in other languages because many of the terms for the virus and disease are highly similar across different languages. Small differences between terms can be handled using fuzzy matching approaches.

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Competing Interests
We have no competing interest in connection with this publication.

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The following supplemental files are available for download from GitHub or zenodo
https://github.com/Aitslab/corona/tree/master/manuscript_v2
https://zenodo.org/record/6642275

Supplemental_file1
SARS-CoV-2 dictionary, version 2

Supplemental_file2
COVID-19 dictionary, version 2

Supplemental_file3
SARS-CoV-2 variant dictionary, version 1

Supplemental_file4
Corona silver standard corpus, version 1

Supplemental_file5
Corona gold standard corpus, version 2 in BioC xml format

Supplemental_file6
Corona gold standard corpus, version 2 in BioC json format

Supplemental_file7
Corona gold standard corpus, version 2 in BioQRator csv format

Supplemental_file8
Jupyter notebook with scripts, version 2