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Editorial



Federica Napolitani

Editor in Chief

Istituto Superiore di Sanità, Rome, Italy

Contact: federica.napolitani@iss.it

Dear EAHIL members,

It is with the utmost pleasure that I present this June's *JEAHIL* theme-issue "Evidence surveillance during the pandemic using automation and crowdsourcing", edited by James Thomas, Director of the EPPI-Centre's Reviews Facility for the Department of Health, England, UCL Institute of Education, University College London. We are so grateful for having him on board and accepting *JEAHIL's* invite to gather articles on the complex, current, and ever evolving topic of Artificial Intelligence and its impact on EAHIL's areas of interest.

Do you recall the supercomputer HAL9000's artificial eye in Stanley Kubrik's 1968 masterpiece "2001 : Space Odyssey"? The mere concept that HAL (the computer) could comprehend and process the human language, even through lip reading, and interact and dialogue with astronauts by using a human voice was something that, at the time, was pure science fiction. And yet, natural language processing, robotics, space exploration, machine-learning techniques, web crawling technologies, and automation are becoming the realities of our time. I am also very aware that I do not possess the knowledge necessary to fully comprehend the mechanics of such technologies, and therefore I am grateful to the authors of this June's edition for introducing me to the many AI applications within our society and within the workplace.

Following these papers, you will be able to read the Letter from our President Lotta Haglund, the news from US MLA by Carol Lefebvre and the column on Publications and new products by Letizia Sampaolo. I also invite you to read the updates on *JEAHIL* online usage by Rebecca Wojturska who shares with us some wonderful usage statistics referring to 2020 and announces the new indexing of the Journal in different databases, such as AGORA, CAB Abstracts and Global Health databases, the European Reference Index for the Humanities and the Social Sciences (ERIH PLUS), Hinari, JournalTOCs, Norwegian Register for Scientific Journals, and Researcher. A big thank you goes to Rebecca and to all the members of the Editorial Board: Petra Wallgren Björk, Gerhard Bissels, Fiona Brown, Katri Larmo, Letizia Sampaolo and Michelle Wake!

The Table in the following page shows the themes of *JEAHIL* future issues.

If you would like to contribute, please contact the editors or myself. Also, please inform us if you wish to see some specific topics covered in these pages.

Future JEAHIL issues

Issue	Theme	Deadline
2021		
3 (September)	EAHIL Virtual Workshop 2021, Istanbul, Turkey	5 August
4 (December)	Infodemics and libraries* edited by Katri Larmo and Michelle Wake	5 November
2022		
1 (March)	No-theme issue	5 February

* *Provisional title*

Wish you the best for the summer holidays

Federica

MONOGRAPHIC SECTION

Evidence surveillance during the pandemic using
automation and crowdsourcing

Edited by

James Thomas

UCL Institute of Education, University College London, London, UK
james.thomas@ucl.ac.uk



Evidence surveillance during the COVID-19 pandemic using automation and crowdsourcing

James Thomas

UCL Institute of Education, University College London, London, UK
james.thomas@ucl.ac.uk

The COVID-19 pandemic has generated a heightened appreciation of the importance of research to inform decisions. It has also highlighted major flaws in the way that findings from research can be utilised, with one article describing *how COVID broke the evidence pipeline*.¹ Over the past year, tens of thousands of empirical research and systematic review articles have been published on different aspects of COVID-19, many of which report findings that could ostensibly inform decisions about policy, practice, or future research commissioning. However, keeping track and making sense of this vast, heterogeneous, and fast-moving evidence base has tested the limits and capacity of current evidence surveillance systems, tools and workflows. One of the sessions at the 6th meeting of the International Collaboration for the Automation of Systematic Reviews (ICASR) in April 2021 featured some of the projects that have been addressing this problem, and five of them are presented as papers in this issue.

An important initiative to address information overload that features in one of the papers in this issue is the COVID-19 Research Dataset (CHORD-19). This was released in early 2020 by US technology companies with the objective of catalysing the computer science community into action to assist in datamining COVID-19 research papers. At the time of its launch, this dataset contained 28,000 research articles, but it has since grown to include nearly 600,000². Researchers have analysed this dataset in many different ways, developing experimental information retrieval and extraction tools, and applications that answer questions and make conceptual linkages between papers. The “TREC-COVID task”, which is the subject of the first paper in this issue, was developed to provide some structure to this experimentation. In this work, a gold standard dataset was created for biomedical researchers to use when developing and evaluating new information retrieval tools. Voorhees and Kanoulas describe the importance of this type of dataset and “task” in assisting the field to agree on common benchmarks for evaluating tool performance. Without such work, it is difficult to compare like-with-like, hampering the advance of the field.

With so many individuals and organisations responding to the pandemic at speed, some coordination of effort was required. The COVID-END initiative³, facilitated by McMaster University, stepped in to fulfil this role, forming seven working groups to assist in planning. COVID-END is particularly concerned about making evidence available to decision-makers, and so the initiative hosts an inventory of “best evidence syntheses” and supports pre-registration of systematic review protocols in the PROSPERO database. However, this has not prevented widespread duplication of effort in pandemic responses, including those of the international evidence synthesis community. A recent paper⁴ reported that hundreds of rapid reviews, systematic reviews and overviews have been published in response to the pandemic with considerable overlap in topic. Many are of poor quality, use unclear methods, and have discordant findings, which undermines the trustworthiness of the synthesised evidence base.

¹ [How COVID broke the evidence pipeline \(nature.com\)](https://doi.org/10.1186/s12916-020-01818-1)

² [CORD-19: The Covid-19 Open Research Dataset \(nih.gov\)](https://www.nih.gov/research-datasets/covid-19-research-dataset) and [CORD-19 Historical Releases \(ai2-semantic-scholar-cord-19.s3-us-west-2.amazonaws.com\)](https://www.semanticscholar.org/collection/cord-19)

³ <https://www.mcmasterforum.org/networks/covid-end>

⁴ <https://ebm.bmj.com/content/early/2021/06/03/bmjebm-2021-111710>

PREFACE

While many of the tools developed by the computer science community using the CHORD-19 dataset have used new natural language processing and machine learning techniques, most of the systematic and rapid reviews on COVID-19 appear to have used conventional manual methods. This may have been a missed opportunity, with a large opportunity cost. The remaining papers in this issue describe four initiatives that have used a combination of human and machine effort to ‘map’ the evidence. The first paper in this section, by Shemilt and colleagues, describes how one living map of COVID-19 research moved from searching conventional databases to find relevant studies (MEDLINE and Embase) to using a single, comprehensive source, based on web crawling technology (Microsoft Academic Graph). They found many more records using MAG and, in conjunction with using machine learning tools, this has made the workflow more efficient. One of the first maps of COVID-19 research to appear early in 2020 was produced by Keenan and colleagues. They used a novel automation tool – a Twitter Bot – to find and disseminate research and overcame bias in conventional English language search sources by collaborating with a team in China. The papers by Hair and Noel-Storr describe the application of crowdsourcing and automation to locate relevant studies. Hair and colleagues undertook significant custom software development to fine-tune a study identification and publication system in R. They also developed a detailed classification tool for coding records in detail based on full text reports. (Most other maps described research based on titles and abstracts alone.) Thanks to the use of automation for study identification, including the use of machine learning, and the coding being done by a crowd, they found this to be a sustainable workflow for keeping up with the evidence. Finally, Noel-Storr and colleagues describe the work of a major pre-existing “crowd” in assisting with pandemic response in Cochrane. Here, the crowd contributed to a range of evidence synthesis workflows, from identifying studies that could be relevant for specific reviews on COVID-19 to helping to maintain the Cochrane COVID-19 Study Register and other, study type specific, datasets. The team also used machine learning for some workflows and found that the pandemic enabled them to further understand the ways that crowdsourcing can contribute to maintaining a surveillance of the evidence base.

The papers thus describe considerable innovation in maintaining databases of research on COVID-19. One other presentation at ICASR featured the Epistemonikos database, which also uses a combination of human and machine effort, to identify research on COVID-19. These databases are not the only activities concerned with identifying and “mapping” COVID-19 research of course. For example, the World Health Organisation maintains its own database, which has evolved over the course of the pandemic. As with the example of systematic review production highlighted above, there appears to be some duplication of effort in tool development and data curation across the various COVID-19 databases of research. While this may have been difficult to avoid in every case, due to the rapidity with which organisations needed to react and the different users and funders they supported, some lessons can still be drawn.

First, while these projects have indeed used novel methods and tools, it is worth observing that they have not been working from CHORD-19 or using the TREC-COVID data for evaluation as outlined by Voorhees and Kanoulas. Thus, even though the field of evidence synthesis has been struggling to cope with the “infodemic”, it does not appear to have taken advantage of the innovation emerging from the information and computer science community; and perhaps one of the key messages of the session at the ICASR meeting was that the evidence synthesis and computer science communities have been engaged in similar, but parallel tasks. The lack of collaboration is striking, and worthy of more detailed examination and reflection. It may be that the evidence synthesis community does not find the tools developed by computer science to be suitable for its work; or it might be simply unaware of the potential of existing tools. Whichever is the case, more collaboration is likely to result in more efficient working practices.

Second, each database contains similar, but different, classification schema for describing the studies they contain. To some extent these reflect different perspectives and organisational objectives. However, it is also

clear that the same records have been examined by multiple different people across the projects, with similar (and in some cases, precisely the same) classifications being applied. Reducing duplication of effort between two or more ongoing database projects is not straightforward, as sharing workflows requires coordination and agreement on classification schema, mutual trust in quality assurance standards, and the ability to integrate data across tools. Work to facilitate better data sharing has therefore been discussed in the COVID-END working groups, and the COVID-19 Knowledge Accelerator project⁵ led by Brian Alper has been working throughout the pandemic to develop standards for the detailed description of COVID-19 evidence.⁶

Third, it is important to bear in mind that, sometimes, the most effective way to avoid duplication of effort is simply to stop and leave the work to others. After being one of the first maps to appear in the early stages of the pandemic, while others were still establishing workflows, this is the decision that Keenan and colleagues made. They could see that other groups had more sustainable production models, and they decided to cease work on their map and to focus their effort elsewhere.

All the work described in these papers has had impact, with the tools and datasets being used globally in response to the pandemic. Some of the lessons learned are already bearing fruit in the various tools and workflows described. Combining human effort and automation has been of demonstrable value in helping us to keep pace with such a huge volume of research; and further reflection on what has worked, and what can be improved, will help the field to continue to innovate in this area.

⁵ <https://confluence.hl7.org/pages/viewpage.action?pageId=97468919>

⁶ <https://www.sciencedirect.com/science/article/pii/S1532046421000149?via%3Dihub>

TREC-COVID: building a pandemic retrieval test collection

Ellen Voorhees (a) and Evangelos Kanoulas (b)

(a) National Institute of Standards and Technology, Gaithersburg, Maryland, USA

(b) University of Amsterdam, Amsterdam, The Netherlands

Abstract

Assessing how good is a search engine has been an active area of development for more than three decades. During the COVID-19 pandemic however the rate of change in what people are interested in, and the available information online has introduced further challenges for search. TREC-COVID introduces a benchmark collection to evaluate search engines and provide the means to improve them under the special circumstances of a pandemic.

Key words: COVID-19; search engine; benchmarking; systematic review; automation.

Introduction

One of the first steps to conduct a systematic review is to search and find all the articles published on the question of interest. Currently researchers in the field of evidence-based medicine depend on medical keywords and Boolean logic for their searches and manually inspect all the resulting articles. This manual process has become unsustainable due to the vast, increasing amount of medical scientific literature. Automation calls for the use of modern search technology that goes beyond keywords, allowing searches to identify and prioritize only the most promising fraction of articles for researchers to examine (1).

But how good is modern search technology at finding articles in biomedical repositories? Can it be trusted for the important task of evidence synthesis? Does it lead to unbiased reviews? Is it better than the current methodology used in the field? Can it speed up the synthesis of evidence? Could it be better? These are important measurement questions because we cannot build better search systems if we do not know how good current systems are.

The Text REtrieval Conference (TREC)

The US National Institute of Standards and Technology (NIST) develops the infrastructure necessary to evaluate the quality of search engines. The work is done through a project called the Text REtrieval Conference

(TREC) (2). The first TREC was held in 1992, which means TREC started before web search engines even existed. In fact, the first search engines were library systems that dated back to the 1960s. The researchers of that era were the first to grapple with basic questions of search engine performance: what it means for a search result to be “good” or for one result to be better than another, and whether people agree on the relative quality of different search results. Evaluating search engine effectiveness is hard in part because people don’t agree surprisingly often, and while it is easy to tell when returned information is not on-topic, it is very difficult to know if a system has not returned something you would want to see. Think about it: If you as a user of a search system knew all of the information that should have been returned, you wouldn’t have searched!

As a way of investigating these questions, a British librarian named Cyril Cleverdon developed a measurement device called a “test collection” (3). A test collection contains a set of documents, a sample set of questions that can be answered by information in the documents, and an answer key that says which documents have information for which questions. For example, the initial test collection that Cleverdon built contained a set of 1,400 abstracts of scientific journal articles and 225 questions that library patrons had asked in the past. Cleverdon enlisted graduate students to go through the abstracts and indicate which articles

Address for correspondence: Evangelos Kanoulas, P.O. Box 94323, 1090 GH Amsterdam, The Netherlands.
E-mail: e.kanoulas@uva.nl.

should have been given to the researcher who had asked that particular question. Once you have a test collection, you can score the quality of a search engine result by comparing how closely the search result matches the ideal result of returning all relevant documents and no nonrelevant documents.

In the '70s and '80s, several more test collections were created and shared among research groups. But there was a problem. To create the answer key for each question, some human had to look at all the documents to determine the relevant set. This necessarily limited the size of the test collections that could be built. To build a large test collection, you need to avoid having a human look at every document in the collection for a question while still finding the set of relevant documents for that question. It turns out that if you assemble a broad cross-section of different types of search engines and look at only the top-ranking documents from each system, you find the vast majority of relevant documents and look at a very tiny percentage of the total number of documents. TREC was the first to implement this so-called pooling strategy, and by doing so it built a sound test collection that was 100 times bigger than the other test collections that existed at the time. No single organization could produce a collection of comparable quality because it would lack the diversity of search results that are necessary.

TREC-COVID

TREC has gone on to standardize evaluation methodology and to build dozens of collections for a variety of different types of search problems. Then in March 2020 TREC launched [TREC-COVID](#), an effort to build a test collection for search during a pandemic.

Why was a pandemic test collection needed? While test collections based on scientific articles already existed, the information needs during a pandemic are different. The biggest difference is the rate of change: Over the course of a pandemic, the scientific questions of interest change and the literature explodes. The variability in the quality of the literature increases, too, since time pressures mean a much smaller percentage of the articles are subject to full peer review. By capturing snapshots of this progression during the early part of the COVID pandemic, TREC-COVID created data that search systems can use to train for future biomedical crises.

TREC-COVID was structured as a series of rounds, with each round using a later version of the coronavirus scientific literature dataset called CORD-19 and an expanding set of queries (4, 5). The queries are based on biomedical researchers' real questions from harvested logs of medical library search systems. TREC-COVID participants used their own systems to search CORD-19 for each query to create search results they submitted to NIST. Once all the results were in, NIST used the submissions to select a set of articles that were judged for relevance by humans with medical expertise. Those judgments were then used to score the participants' submissions, while the set of relevant articles is a human-curated answer for the original question.

TREC-COVID resulted in a collection of 50 queries, and a total of 69,381 judgments. The test collection was used to evaluate hundreds of participating search engines and many different technologies, some of which have been deployed as online open access tools. Quality control tests of the collection itself demonstrate that having a set of diverse, high-quality search engines did indeed enable an effective collection to be built (6). TREC-COVID also confirmed the research hypothesis that hybrid search approaches in which systems incorporate users' feedback regarding the quality of previous search results retrieve relevant articles more quickly than fully automatic approaches. Whether the quality of the developed search technology is sufficient for automating systematic reviews remains an open question; however, TREC-COVID provides the means to study and further improve search under the special circumstances of a pandemic.

Acknowledgements

This paper originates from a presentation at the International Collaboration for the Automation of Systematic Reviews (ICASR) meeting held in April 2021.

*Submitted on invitation.
Accepted on 7 June 2021.*

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Using automation to produce a “living map” of the COVID-19 research literature

Ian Shemilt (a)*, Anneliese Arno (a)*, James Thomas (a)*, Theo Lorenc (b), Claire C Khouja (b), Gary Raine (b), Katy Sutcliffe (a), Preethy D’Souza (a), Kath Wright (b), Amanda Sowden (b)
 (a) EPPI-Centre, UCL Social Research Institute, University College London, London, UK
 (b) Centre for Reviews and Dissemination, Alcuin College, University of York, York

* Joint first authors

Abstract

The COVID-19 pandemic has disrupted life worldwide and presented unique challenges in the health evidence synthesis space. The urgent nature of the pandemic required extreme rapidity for keeping track of research, and this presented a unique opportunity for long-proposed automation systems to be deployed and evaluated. We compared the use of novel automation technologies with conventional manual screening; and Microsoft Academic Graph (MAG) with the MEDLINE and Embase databases locating the emerging research evidence. We found that a new workflow involving machine learning to identify relevant research in MAG achieved a much higher recall with lower manual effort than using conventional approaches.

Key words: *evidence synthesis; literature mapping; COVID-19; automation; machine learning.*

Introduction

The COVID-19 pandemic disrupted life worldwide, and also presented unique challenges in the health evidence synthesis space. As previous papers have observed, COVID-19 evidence has been published at an unprecedented rate: by June 2020, the United States National Institute of Health (NIH) had indexed more than 28,000 articles (1). A thorough, though non-systematic and non-exhaustive, list compiled by the NIHR Policy Research Programme Reviews Facility identified more than 250 COVID-19 maps, auto-searches, and databases as of 19th June 2020 (2). The urgent nature of the pandemic required extreme rapidity for keeping track of research, and this presented a unique opportunity for long-proposed automation systems to be deployed and evaluated.

Observing the range of different semi-automation approaches being adopted across many databases, we initially proposed to conduct an analysis of the strengths and weaknesses of each technology. However, despite appearing similar, many tools had quite different objectives, and so in order to provide a robust evaluation,

we decided to conduct a formal cost-effectiveness analysis, where the costs and effects of adopting specific automation tools could be assessed in detail. We selected the COVID-19 living evidence map (3), produced by the Reviews Facility as a case study (illustrated in Figure 1).

About the “living map”

The NIHR Policy Research Programme Reviews Facility¹ is a collaboration between the EPPI Centre at University College London, the Centre for Reviews and Dissemination at the University of York, and the Public Health, Environments and Society at the London School of Hygiene and Tropical Medicine. The facility uses the methods of evidence synthesis to inform policy development and implementation.

In February 2020, a few weeks after the WHO declared a global pandemic, it became clear that there was a need to keep on top of the emerging research evidence. After discussion with DHSC and the office of the Chief Medical Officer, the first evidence map was published in mid-March.

¹ <https://eppi.ioe.ac.uk/cms/Default.aspx?tabid=73>

Address for correspondence: James Thomas, UCL Institute of Education, University College, London, 20 Bedford Way, London WC1H 0AL, UK. E-mail: james.thomas@ucl.ac.uk.

Searches were run on the MEDLINE and Embase database platforms each week (to begin with) and, out of the 1,049 records found in the first search after duplicates had been removed, 271 met the inclusion criteria. Records were assigned to one of eleven descriptive categories, which captured the key characteristic of the record (for example “treatment development” and “transmission”).

The workflow was established as a mostly manual process. Records were downloaded in the form of text files and imported into EndNote. Deduplication took place in EndNote before the records were uploaded into EPPI-Reviewer (4) and the deduplication process run again. Records were then manually screened and assigned to the aforementioned categories with difficult to assign records discussed within the team. The map itself was published using the “EPPI-Mapper” application (5), which is a self-contained HTML5 application, containing the data and the code necessary to produce an interactive visualisation (Figure 1).

By the beginning of June 2020, the scale of both the pandemic, and the work involved in maintaining the map, was becoming apparent. After an initial peak in the first search (which was effectively “catching up” on publications up until that point), search yields steadily

rose from a few hundred each week to between two and three thousand records per week (Figure 2). Following developments in search strategies for COVID-19 literature, the search itself developed over this period too, but it seems likely that most of the increase was simply due to the volume of research being produced.

The map itself had been accessed more than 10,000 times by this point, and the team was receiving frequent requests for copies of the data. This prompted development of the mapping software to enable users to download all, or subsets, of the data in RIS format. This new feature proved popular and accessible; very few requests for data were received after it was deployed in September 2020. The challenge of addressing the increasing workload of screening the records was addressed in several ways.

First, as the time required for deduplication across tens of thousands of records was increasing every week, eventually taking more than a day of work in EndNote, we adopted a new deduplication algorithm in EPPI-Reviewer (which had been co-incidentally under development and was not implemented simply for this project). This has proved to be both more accurate and efficient than the original de-duplication method.

Second, we evaluated options for the semi-automation of the workflow, and the searching of a single source of

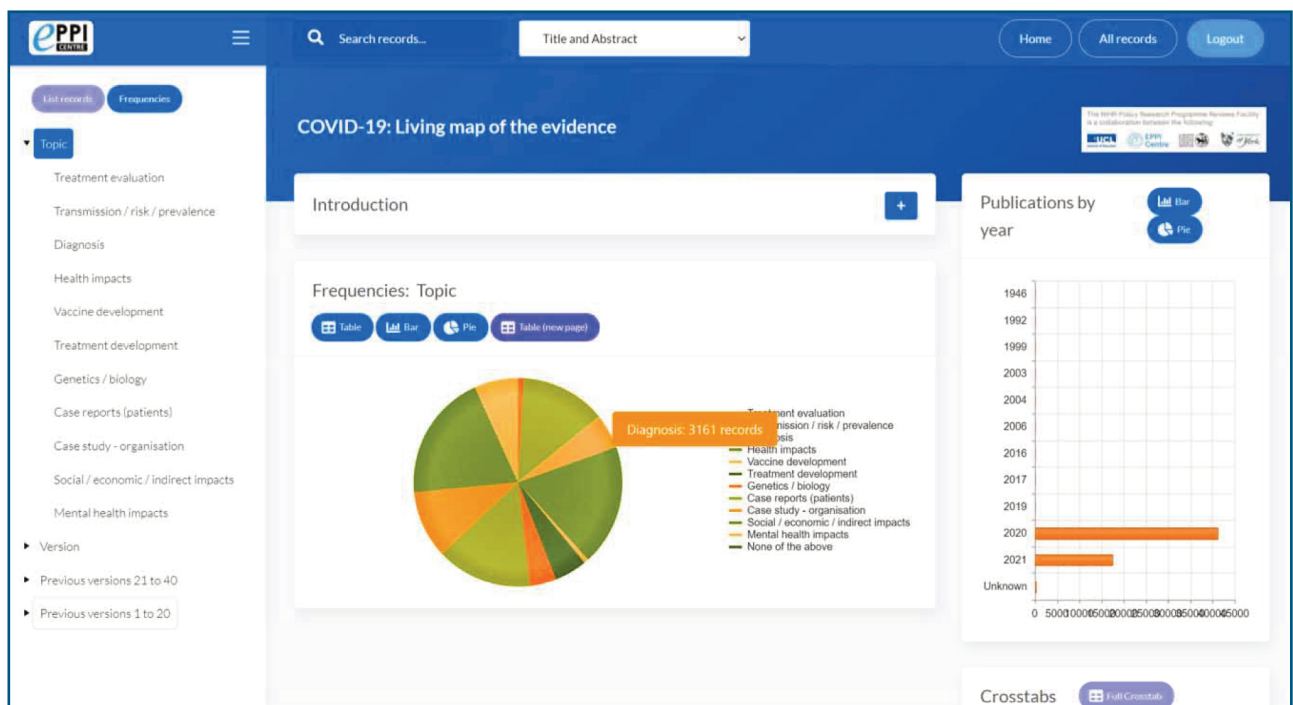


Fig. 1. Living COVID-19 evidence map.

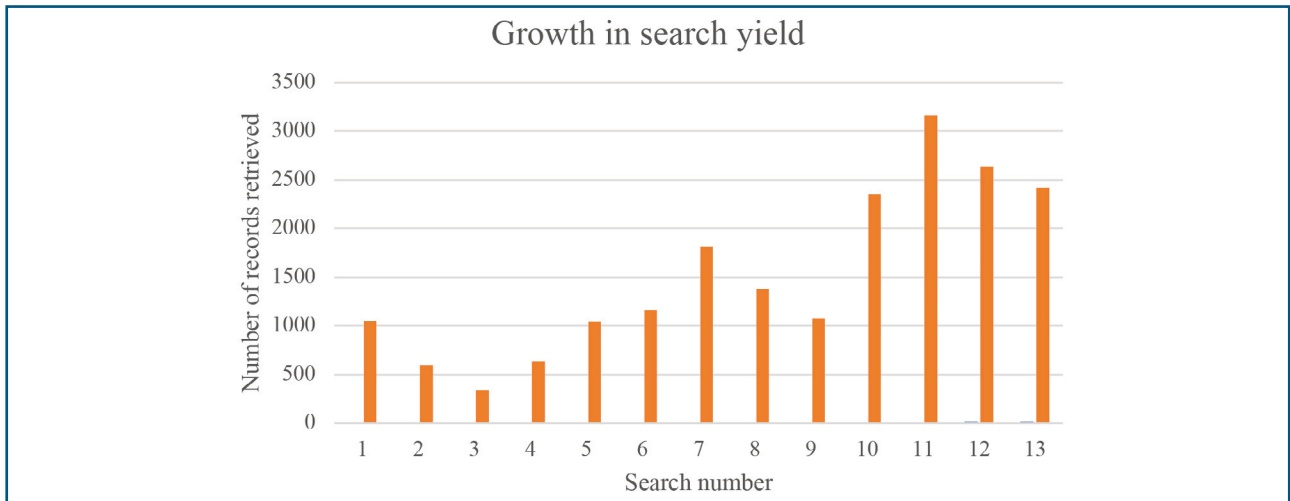


Fig. 2. *The growth in the number of records retrieved in searches 1-13.*

bibliographic records (Microsoft Academic Graph (6)), as opposed to the combination of MEDLINE and Embase.

Methods

Objective

Our objective was to investigate the acceptability, efficiency, and effectiveness of using semi-automated, versus manual, study identification methods to identify eligible study reports for our living map of COVID-19 research; and of using Microsoft Academic Graph as a single source for identification of research.

Acceptability

Adopting the use of semi-automation requires clarity about the process within which it will be introduced. In this case, it was agreed that recall was a key issue: was the team aiming to achieve 100% recall, or was a lower percentage acceptable? If a lower percentage was acceptable, what figure was this? Resource was also an important issue: what was the maximum resource that could be devoted to the task, (this was regardless of whether this was sufficient to assess all records)? These questions informed the adoption decisions made about semi-automation.

Efficiency

Three options for increasing efficiency were evaluated and rolled out in the live workflow:

1. the use of a machine-learning classifier to automatically exclude irrelevant records;

2. the use of the above classifier PLUS prioritised screening with a fixed weekly screening target;
3. the use of Microsoft Academic Graph as a single source of records.

Use of a machine-learning classifier

EPPI-Reviewer contains a feature that uses logistic regression to distinguish between two classes of records (relevant or irrelevant). The classifier requires “training data”, i.e. examples of the two classes of records, from which to learn. In this use case, we had thousands of examples of relevant and irrelevant records from which to build the classifier. When built, the classifier can be applied to unseen records, returning a probability score that the record is, or is not, the class of interest. This score can be used to “calibrate” the classifier when used in practice, to determine a pre-specified level of recall. There is usually a trade-off to be made between precision and recall, where higher levels of recall are associated with lower levels of precision. Team deliberations (see “acceptability”, above) determined the level of recall that was used in practice.

Use of a machine-learning classifier, plus prioritised screening with a fixed screening target

Prioritised (or “priority”) screening uses a machine-learning model to rank the records according to their likely relevance. It uses the same model as described above to score records according to relevance, but the key addition here is that the records are then screened

in order of relevance, and so those records most likely to be included are found at the top of the list. As screeners begin to record their decisions, the priority screening mode observes these decisions and periodically updates the order of the record list such that studies more likely to be included according to previous decisions are now listed towards the top. When using such a workflow, the question for reviewers is whether they should screen the whole list, or whether they should stop after assessing a given proportion, or fixed number. In our use case, a fixed screening target was adopted.

Microsoft Academic Graph as a single source of records

The final change to the workflow was a switch to using Microsoft Academic Graph (MAG) instead of the more conventional sources of MEDLINE and Embase. MAG is an open-access dataset comprising more than 250 million bibliographic records in a network graph map, constructed with the aim of creating a comprehensive single source for citation information. In the “MAG-enabled” workflows, a novel machine-learning recommender model automatically searches each update of the MAG dataset and imports the resulting records into EPPI-Reviewer. The rationale for using this source was to eliminate the need for manual searching of MEDLINE/Embase, and to reduce duplicate checking to a minimum. The team first evaluated the recall of MAG compared with MEDLINE/Embase, by checking whether all the records retrieved by the conventional searches for June 2020, were present in MAG. The “reverse” recall was also checked to see how many papers published during this period (according to MAG) were present in MEDLINE/Embase.

Results

Acceptability

The team discussed the trade-offs involved in maximising recall when using machine learning to increase precision and reduce unnecessary manual work. An issue of concern was performance for each inclusion category – does the classifier or MAG perform especially well for some categories, while not as well for others? There was a similar concern regarding study designs retrieved using semi-automation – might semi-automation perform well for randomised controlled trials (RCTs) for example, but less well for cohort studies? The team decided that a recall of 95% would be acceptable when using the binary

machine-learning classifier. The team also decided that the maximum resource available each week was sufficient to screen 1,500 records, so the “fixed screening target” was set at this level.

Efficiency

During the first 19 weeks of operation, the team screened 34,193 records retrieved from MEDLINE/Embase at an average precision of 36%. This fully manual period is used as a baseline.

Use of a machine-learning classifier

The machine-learning classifier, calibrated to achieve 95% recall, was used during weeks 20-29 to automatically eliminate records that were unlikely to be relevant. During this period, 19,891 records were screened from MEDLINE/Embase with an average precision of 61%.

Use of a machine-learning classifier, plus prioritised screening with a fixed screening target

The use of prioritised screening was introduced during weeks 30-34, along with a fixed screening target of 1,500 records per week. During this period 7,685 records were screened from searches of MEDLINE/Embase with an average precision of 79%.

Microsoft Academic Graph as a single source of records

Figure 3 shows the number of unique records found in each source during our evaluation period and the overlap between them. We found that while MAG had a 99% recall overall, MEDLINE/Embase only had a recall of up to 83% due to the large number of additional records found in MAG that were not in our conventional searches.

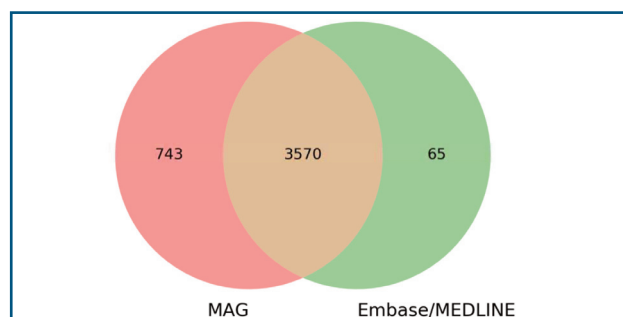


Fig. 3. Number of records found in each source.

We, therefore, moved over to use MAG as a single source from weeks 35 onwards, maintaining the use of the machine-learning classifier, prioritised screening, and the fixed screening target. During this period, 32,100 records were screened at an average precision of 69%.

Discussion

This analysis showed that the semi-automated MAG-enabled workflow achieved a higher recall and higher precision than the fully manual workflow and the workflow using the machine-learning classifier alone. It did not achieve the levels of precision obtained using the same automation tools used in the MEDLINE/Embase workflow. However, as it has a higher “baseline” recall (99% compared with 83% for MEDLINE/Embase) and has other efficiencies linked to removing the need to carry out manual searches and deduplicate results, the MAG-enabled workflow was more efficient than the other options. In addition, MAG appears to be more language-inclusive in its study identification, potentially improving our ability to identify non-English-language studies (i.e. we observed, but did not systematically assess, more non-English language records appearing in the workflow when evaluating the possibility of switching to using MAG as a single source of records).

Conclusions

Using MAG in the maintenance of a COVID-19 living evidence map resulted in a higher recall compared with manual searches of MEDLINE and Embase. When combined with other automation tools, namely a binary machine-learning classifier and active learning screening prioritisation, use of MAG had a higher recall and a lower cost, making it more effective and more efficient.

Acknowledgements

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A rapid response to the COVID-19 outbreak: the meta-evidence project

Ciara Keenan (a), Chris Noone (b), Karen McConnell (c), Samantha H Cheng (d)

(a) Campbell UK & Ireland, Queen's University, Belfast, United Kingdom

(b) School of Psychology, NUI Galway, Ireland

(c) School of Nursing and Midwifery, Queen's University Belfast, United Kingdom

(d) Center for Biodiversity and Conservation, American Museum of Natural History, New York, NY, USA

Abstract

Early in the pandemic, as scientific reports and preliminary research on both clinical and public health aspects of COVID-19 were rapidly generated, we recognised the need for a dynamic, interactive tool that could capture and collate emerging evidence sources to inform research and decision-making efforts. In particular, we observed that numerous similar research efforts across the globe were happening in parallel - prompting an urgent need to connect research teams with each other and maximize research efficiency. Our colleagues in China provided daily translations of emerging evidence to aid networking between research groups working across the world. Here we describe how the meta-evidence project met daily and ongoing challenges and what was learned as a result. We describe the benefit of finding ways to instead work with better resourced teams and promote collective and open efforts to synthesise the evidence, which in the end, outweighed the considerable costs.

Key words: COVID-19; systematic review; infodemic; evidence-based practice; technology.

Background

On 11 March 2020, the WHO declared the SARS-CoV-2 outbreak a global pandemic and as of 29 April 2021, there have been 147,443,848 confirmed cases and 3,117,542 deaths (European Centre for Disease Prevention and Control figures). As the global spread of COVID-19 continues to grow, disease control and prevention will be challenging, and this requires collaborative solutions and cooperative spirit from all groups. There has been a tremendous response from the scientific community to generate timely and responsive research, which has translated to an exponential growth in COVID-19 related research literature (*Figure 1*). It is estimated that there are at least 129,570 COVID-19-related publications to date (1). While this wealth of research is a potential boon for addressing both multi-dimensional aspects of the pandemic, from clinic to social, the reliability and rigor of these papers is quite variable. In fact, a study conducted two months after the pandemic was declared found that most of the papers being published had a shorter time to publication and were of lower methodological quality than matched control studies on other clinical studies from

the same journals (2). Moreover, many papers are quite similar in topic - for example, as of the 30 April 2021, there are approximately 5,590 health systematic reviews on COVID-19 (L.OVE platform, Epistemonikos foundation) with many on the same topic. One research team identified 25 systematic reviews reporting on 17 primary studies, all answering the same question of interest (3). This overlap and duplications signal that much of the race to research COVID-19 has resulted in "research waste" (4) and that research efforts could be combined to produce more rigorous and/or comprehensive insights.

The role of evidence synthesis and semi-automated text-mining bots

The rapidly evolving landscape of knowledge with respect to viral biology, disease presentation, clinical outcomes, social and economic impacts, and potential treatments and prevention required and continues to require a rapid, dynamic approach to synthesize emerging information to inform on-the-ground decisions. Evidence syntheses (including systematic reviews, evidence and gap maps, scoping reviews, and

Address for correspondence: Ciara Keenan, Campbell UK & Ireland, Queen's University, University Road Belfast, Northern Ireland BT7 1NN United Kingdom. E-mail: c.keenan@qub.ac.uk

A rapid response to the COVID-19 outbreak

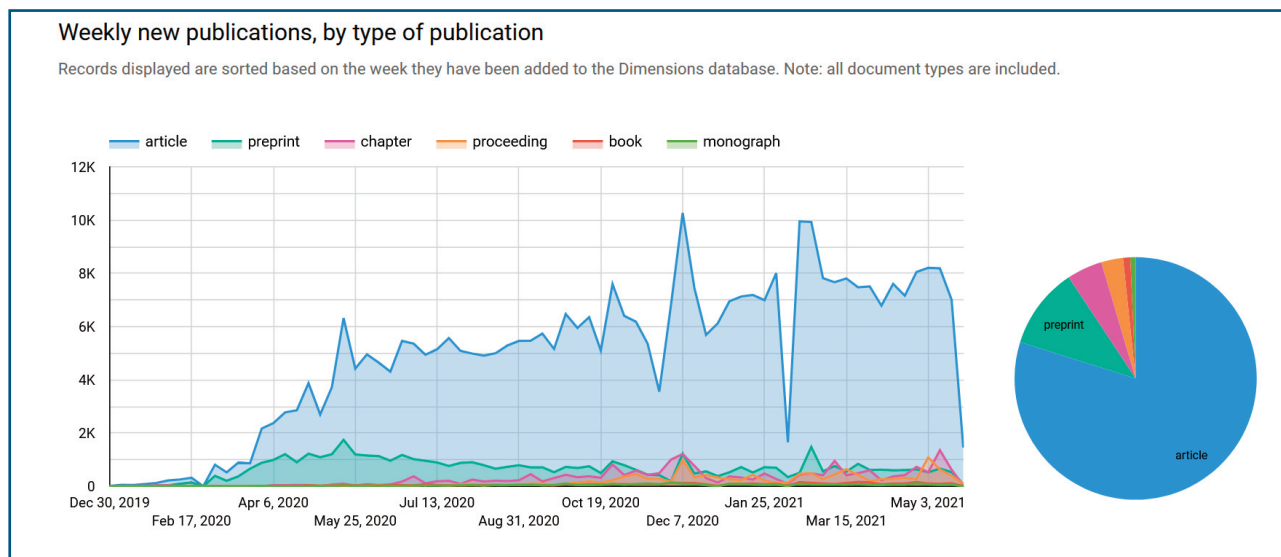


Fig. 1. This automatically generated report is based on Dimensions data and was retrieved from <https://reports.dimensions.ai/covid-19/> on 28 May 2021 to depict weekly new publications on COVID-19, by type of publication.

meta-analysis) are critical tools for collating and synthesising insights from the broad evidence base using transparent and reproducible methods.

The information-poor and high-risk context of the COVID-19 pandemic requires rapid approaches for evidence synthesis (5) to provide and communicate reliable summaries of emerging evidence and inform and update clinical guidelines and public health recommendations.

Over this past year, while many syntheses (including systematic reviews) have been conducted, the pace of knowledge production means that these reviews become rapidly outdated and lose both relevancy and accuracy (5). Dr Gabriel Rada, co-founder of Epistemonikos, describes reviewers missing relevant studies and outlines an unpublished analysis which found 95% of reviews about drug treatments in COVID-19 were out of date due to rapid publication of new clinical trial data (6). In addition, the rapid production of reviews to keep up with the pace of publications has resulted in the production of reviews with lower methodological quality - thus reliability - which is further exacerbated by the acceleration of the publication process, often skipping or rushing the peer review process (7).

We developed the COVID-19 twitter bot ([www.twitter.com/@COVID_Evidence](https://twitter.com/COVID_Evidence)) to harness, in real-time, the emerge of COVID-19 research. The bot, which has

now been active for over a year, produces a diverse range of real-time research and commissioned reports directly onto a twitter feed using the RSS sources from a range of science and medical databases. The COVID-19 Twitter Bot was one of the first sources to emerge with a focus on real-time acquisition and collation of research findings about COVID-19.

This bot created by an evidence synthesis expert and a consultant kidney physician was capable of persistently posting relevant content without requiring sustained human involvement past its creation.

Building a collaborative “living” atlas of COVID-19 research

Building and launching the COVID-19 Twitter Bot allowed our group to collate significant bibliographies of emerging research on COVID-19. Given growing limitations on resources under economic impacts from the pandemic, we saw a need for a living atlas that could aid networking between research groups working across the world. Having this knowledge could help future research efforts be more targeted towards existing gaps, reduce inefficiency and duplication, and foster collaboration. We built an interactive, visual database of COVID-19 research that featured an interactive geographical map that reflected emerging evidence sources (e.g. articles and resources) collated from the automated aggregating Twitter feed, and supplemented by

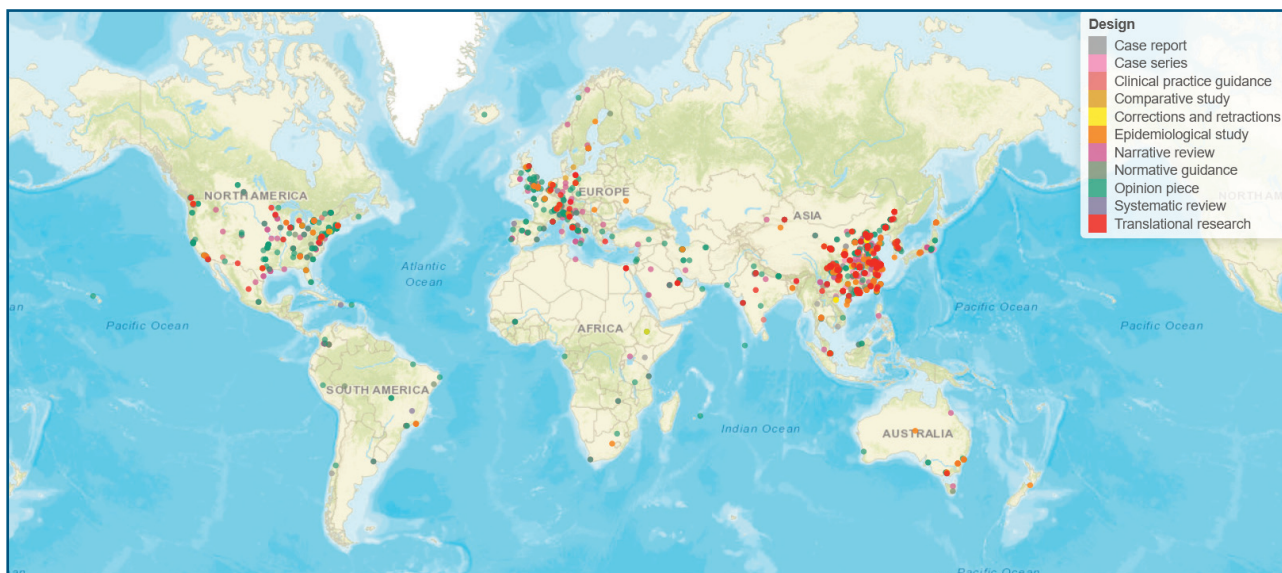


Fig. 2. A screenshot of the interactive geographical map built using EviAtlas (8).

sources such as the WHO database (Figure 2). We named this endeavor the meta-evidence project. The interactive geographic map was powered by EviAtlas, an open access platform for visualizing synthesis data (8). In particular, at the time we were building the map, the literature being captured by the bot was primarily in English and limited to geographies with users present on Twitter. Thus, there were significant gaps in coverage, particularly research emerging from China, who at that stage, had more lived experience of the virus and disease than the rest of the world. Dr Howard White, CEO of the Campbell Collaboration collaborated with Professor Kehu Yang, Director of Lanzhou University's Evidence Based Medicine Centre in China to compile and translate evidence from sources in Chinese to expand the map's coverage. This work was made possible given the generous *pro bono* effort from Professor Yang and a team of seven researchers.

Challenges

The meta-evidence project responded rapidly to the global spread of COVID-19 at a time when rumours and conjecture were also spreading through social and mainstream media, this pace was met with various and significant challenges.

First, the "living" atlas was dependent on the resources of volunteers who were building the atlas in their spare time. This effort was borne from a tweet asking for help and

pulled in medical professionals, data scientists and evidence synthesis experts from all disciplines, globally, and highlighted a true sense of community contribution. However, this meant that volunteers were working on the map in their "spare" time, typically after long workdays and during a time when spare time was already being eaten due to closures of schools and daycare facilities. Also, we learned of much-better resourced groups like the EPPI-Centre, COVID-NMA and the Norwegian Institute of Public Health who were, and still are working hard to avoid out-of-date research by producing living maps of Evidence.

Second, we noted that publishers had relaxed some of their strict guidelines. This meant that many studies had been widely published without sufficient peer review. We felt that it is important to incorporate an assessment of quality so that readers can understand which studies are likely to be reliable. However, this was something we simply did not have the people power to do.

Third, pandemics such as COVID-19 require expedited data and research findings to help understand the situation and potential treatment and vaccines. Rarely though does a pandemic affect all sectors of society and the research community on such a global scale. Due to the impact of COVID-19 across all sectors of society, the research was and still is being produced in large volumes across all disciplines which made it difficult to categorise. This difficulty meant that it was difficult to continue map-

ping the research on the atlas in a meaningful and useful way for individual disciplines.

Finally, after conversations with key people in leading organisations including Cochrane, Campbell, EPPI-Centre, Evidence Aid, Evidence synthesis Ireland, it became clear that this work had been overtaken by other teams with dedicated resources. One of the most influential conversations had in this time was with Professor Mike Clarke, founder of Evidence Aid and expert in the human response to humanitarian disasters. After speaking with Prof Clarke, we realised that our effort, although commendable and extremely useful at the early stage, was also adding to research waste and our time might be better spent supporting others who could sustain the effort required.

One of the key lessons we draw from the meta-evidence project (and hindsight afforded to us over a year after the pandemic started) is the importance of early and meaningful stakeholder engagement when creating research priorities. Stakeholder engagement was simply something we did not consider, and possibly may have ignored due to limited time and resources and the increased pressure to provide information, fast.

However, Cochrane's Question prioritization process and the Core Outcome Measures in Effectiveness Trials (COMET) initiative (9) demonstrates that engaging with multiple stakeholders including researchers, clinicians, patients, funders and policy makers is possible and will likely provide useful and meaningful research findings.

Conclusions

Combinations of evidence synthesis, information retrieval, and medical expertise allowed the team to carefully curate specific and useful RSS feeds which directly fed to an automated twitter bot. This was a good way of finding and presenting much needed evidence quickly and early in the pandemic at a time where rumours and conjecture were spreading throughout social media and causing panic.

We were able to recognise (through the bot and early mapping exercise) that there was important and potentially life-saving research being produced from all corners of the world, particularly China, and we recognise the need to engage with researchers in China to allow us to effectively map and better represent the global evidence.

In conclusion, the meta-evidence project was extremely useful in the early stages of the project as a place to produce, in real time, the emerging global evidence,

and also to visually present it. The decision to halt some parts of the project was a pragmatic one. A decision that allowed us to collaborate and support those groups who are still working tirelessly today.

of this research.

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Authors' contribution statement

Ciara Keenan: conceptualization, writing - original draft; Samantha H Cheng: writing - original draft; Chris Noone: writing - original draft; Karen McConnell: writing - original draft.

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Building a Systematic Online Living Evidence Summary of COVID-19 Research

The CAMARADES COVID-SOLES Group*

Centre for Clinical Brain Sciences, University of Edinburgh, Edinburgh, UK
Kaitlyn.Hair@ed.ac.uk

*The members of the CAMARADES COVID-SOLES Group are reported before the References

Abstract

Throughout the global coronavirus pandemic, we have seen an unprecedented volume of COVID-19 research publications. This vast body of evidence continues to grow, making it difficult for research users to keep up with the pace of evolving research findings. To enable the synthesis of this evidence for timely use by researchers, policymakers, and other stakeholders, we developed an automated workflow to collect, categorise, and visualise the evidence from primary COVID-19 research studies. We trained a crowd of volunteer reviewers to annotate studies by relevance to COVID-19, study objectives, and methodological approaches. Using these human decisions, we are training machine learning classifiers and applying text-mining tools to continually categorise the findings and evaluate the quality of COVID-19 evidence.

Key words: COVID-19; evidence synthesis; machine learning; web application; database.

Background

The COVID-19 pandemic continues to present a major challenge for health services and society worldwide. Since the emergence of the SARS-CoV-2 virus, the research community has shown an extraordinary response to the pandemic. This volume of information and rate of publication makes it exceedingly challenging for research stakeholders (including researchers, funders, and policymakers) to efficiently identify studies relevant to their interests, evaluate the quality of those studies, and utilise their findings for health benefit (1). This “infodemic”, along with the dissemination of unsubstantiated claims in both lay and social media, risks fuelling a growing distrust in science and highlights the need for an accessible resource to support public understanding of, and access to, research findings.

Evidence is incremental, and new experimental findings offer the greatest value when considered in the context of other studies that have addressed the same or related research questions in different settings. Systematic reviews capture, summarise, and critically appraise the available evidence relevant to a pre-specified research question. They are considered the most effective method of reaching a rigorous understanding of the literature, and informing decision-making (2). Unfortunately, the

time taken to perform traditional systematic reviews means that the findings are often outdated by the time of dissemination. The urgent need for evidence-based treatments for COVID-19 infection combined with a rapidly accumulating COVID-19 literature has made this an even greater challenge. Automation technologies (e.g. machine learning and text-mining) can be used to reduce the time and resources required. For example, we can train a machine to classify research as relevant or not relevant to our research question, or to extract structured information from publications, at greatly reduced human effort (3-5). Such technologies facilitate the development of “Living” systematic reviews, in which new evidence is incorporated into the review as and when it becomes available (6, 7). Further, by incorporating crowdsourcing approaches to recruit and train external reviewers, a much larger team can work together to extract information from publications at a faster pace.

Building upon existing living review methodologies, we have developed and integrated a series of automation tools and methodologies for the continual collection, categorisation, and quality assessment of COVID-19 evidence from primary research studies. We have built a Systematic Online Living Evidence Summary (SOLES) of all primary research relevant to COVID-

Address for correspondence: Kaitlyn Hair, the CAMARADES COVID-SOLES Group, Centre for Clinical Brain Sciences, University of Edinburgh, Edinburgh BioQuarter, 49 Little France Crescent, Edinburgh, EH16 4SB, UK.
E-mail: Kaitlyn.Hair@ed.ac.uk

19; an interactive web application, which allows users to interact with a visual summary of the curated information, interrogate the dataset, and download relevant citations filtered by study characteristic of interest. This resource is intended for use by all stakeholders in COVID-19 research, including researchers working within the field or performing rapid or systematic reviews of COVID-19 literature.

METHODS

Identifying new research papers

To retrieve up-to-date research reports we retrieve citations weekly from PubMed (National Library of Medicine), Web of Science (all available databases: Web of Science Core Collection, BIOSIS Citation Index, Current Contents Connect, Data Citation Index, Derwent Innovations Index, KCI-Korean Journal Database, MEDLINE, Russian Science Citation Index, SciELO Citation Index, Zoological Record), EMBASE (OVID), and the World Health Organisation's COVID-19 database (8). Our search terms are described in our study protocol and have been updated over time to address changes in COVID-19 research terminology (9). To identify new research from PubMed programmatically, we use the pubmedTools R package (10) developed within our group to access the Entrez application programming interface, while other

records are obtained through manual searching of the platforms/databases outlined above .

Duplicate removal

To maintain a database of unique citations, we identify and remove duplicate citations (bibliographic duplicates of work published in the same journal at the same time by the same authors) identified across different databases using an automated, R-based tool developed within our research group, the automated systematic search de-duplicator (11).

Retrieving full text publications

We retrieve full-text publications using custom R code (12) to access full-text portable document formats (PDFs) where we have institutional access (University of Edinburgh). The extraction code uses digital object identifiers (DOIs) to retrieve PDF links through Cross-Ref, PubMed Central, and doi.org, then downloads the PDF file using the retrieved link.

Crowdsourced study annotation

To adequately capture the broad spectrum of primary COVID-19 research, we developed a schema (Figure 1) to classify research by type, objective, methods, and patient population/ sample type, based on previously proposed definitions (13). Using these classifications, we

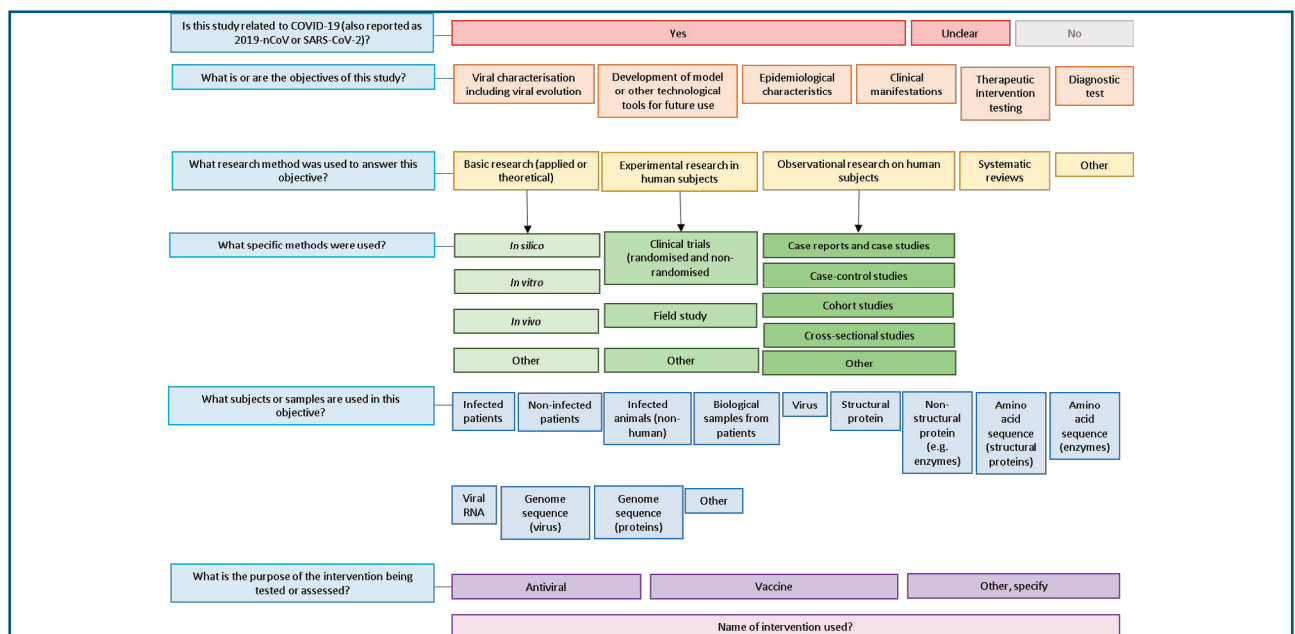


Fig. 1. Research classification schema for primary COVID-19 studies. Arrows indicate a tree-like structure where reviews can only add subsequent annotations based on the previous annotation.

designed a project on the Systematic Review Facility (SyRF; <http://syrf.org.uk/>), a widely used and freely available online platform developed within our research group (14). SyRF facilitates the conduct of large, collaborative systematic review projects and allows users to design structured annotation forms with custom questions. Once the project plan had been finalised, three independent researchers within our group annotated a test batch of 16 research papers. Through discussion, we arrived at a consensus on how each paper should be annotated. These annotations became our “gold-standard” annotated dataset used to train a crowdsourced team of human reviewers.

To recruit a team of reviewers to annotate COVID-19 research, we advertised the project via our social media profiles, existing contacts, and university research networks. Trainee reviewers were required to annotate a minimum of eight papers which were then checked against the gold-standard annotations. Once complete, we provided feedback and either asked trainees to complete more training papers or allowed them to continue as a reviewer on the main project. To ensure quality, each article is annotated by two independent reviewers. To keep reviewers up to date, fortnightly progress reports are sent out via email. Reports are generated programmatically with R code which interacts with SyRF and published online on the RPub server as a living RMarkdown document (15).

Integration with the Systematic Review Facility

Subsets from our dataset of unique COVID-19 records are selected based on the date they are retrieved, with older records uploaded first. Custom R scripts are scheduled (using the CronR package) to periodically interact with SyRF to obtain information on the number of reviewers working on the project, the number of studies annotated, and the annotations themselves. This allows us to keep an up-to-date record of progress.

Reconciliation of annotations

For each paper, annotations from two independent reviewers are compared using a custom R script. If reviewers agree on whether the paper describes primary research relevant to COVID-19, this study is immediately classified as “included” or “excluded” – irrespective of whether they agree on all classifications. If reviewers do agree across all classifications, the study is classed as “reconciled” and those classifications are final. If there are dis-

agreements on one or more annotations, the paper is passed to a senior reviewer who will reconcile the disagreements before submitting a final set of classifications.

Machine-assisted classification of primary studies

We used the “included” or “excluded” decisions from reconciled annotations to train a machine learning algorithm hosted by collaborators at The Evidence for Policy and Practice Information and Co-ordinating Centre (EPPI-Centre), University College London. The algorithm uses natural language processing to identify features within the Title and Abstract of citations. We aimed to train it to automatically classify non-annotated studies as either “primary COVID-19 research” or “other” research.

Web application and dataset availability

We built a user interface to access our entire COVID-19 dataset via an R Shiny web application. The application allows users to visualise the annotated evidence, search the citation database (using regular expressions), and download relevant citations. The COVID-SOLES application is freely available online (16).

RESULTS

COVID-SOLES citation database

At the time of writing (May 2021) we have identified a total of 812,261 potentially relevant citations since our COVID-19 searches began in March 2020. The distribution of records retrieved from each database is shown in Figure 2. We obtained the highest number of records from the WHO COVID-19 database (N= 246,299) and the lowest number from PubMed (N=129,973).

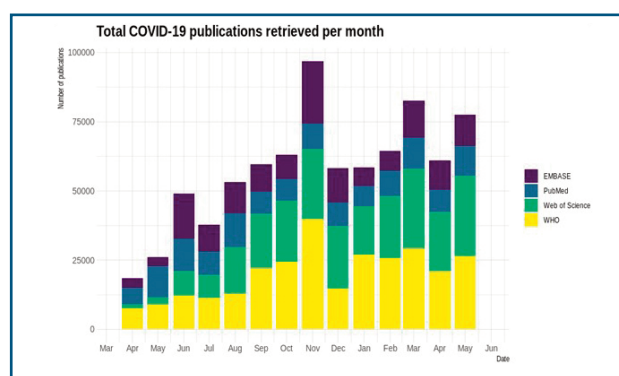


Fig. 2. Total COVID-19 citations retrieved from each database per month.

Following extensive de-duplication 349,726 unique citations have been identified. Over time, the number of unique publications retrieved per month has increased, with a brief levelling off period over the new year. In May 2021, we identified 50,095 publications, the largest monthly publication count yet.

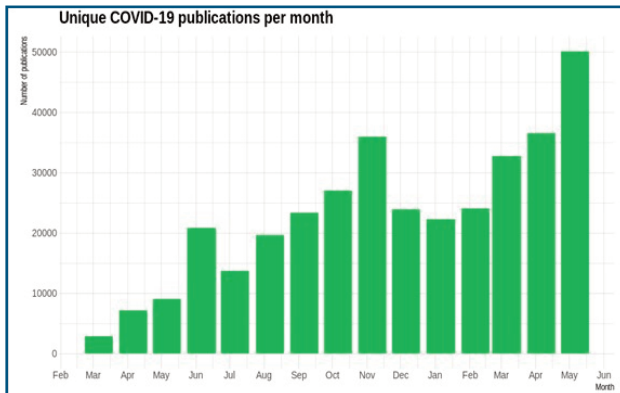


Fig. 3. COVID-19 citations retrieved per month. Bars indicate unique citations retrieved across databases following the removal of duplicates.

Crowdsourced annotation

We have recruited 88 trainee reviewers of which 78 have completed training and are able to annotate COVID-19 publications. The median number of papers annotated by each reviewer was 99 (interquartile range: 70.75 – 173.75). Two reviewers were particularly active, annotating 1,874 and 6,597 publications, respectively.

Machine classification of COVID-19 research

From a total of 226,417 citations in our dataset which had abstracts, 3,405 had been classified by humans as “primary COVID-19 research” (N=1312) or “other” (N=2093). This dataset was randomly split into a training set, validation set, and test set. We used a pre-set sensitivity threshold of at least >95% to ensure we captured the majority of relevant publications. On the test set (N=681), the classifier performed at a sensitivity (percentage of citations correctly included) of 95.2%, a specificity (percentage of citations correctly excluded) of 76.6%, and precision (percentage of correctly included citations from all included citations) of 71.9%. To date, the number of fully annotated primary studies is too low to train classifiers to identify specific objectives or study methodologies (N=1,174). A summary of the primary studies annotated by objective and methodology is shown in Figure 4. Due to our chronological approach to annotating studies, this summary reflects COVID-19 research conducted early in the pandemic, in March and April 2020.

Use of Web application

Since we developed the COVID-SOLES application, it has been accessed over 1,700 times by users from 45 countries.

LIMITATIONS AND FUTURE WORK

Optimising citation retrieval

Some retrieved citations lack useful meta-data, such as

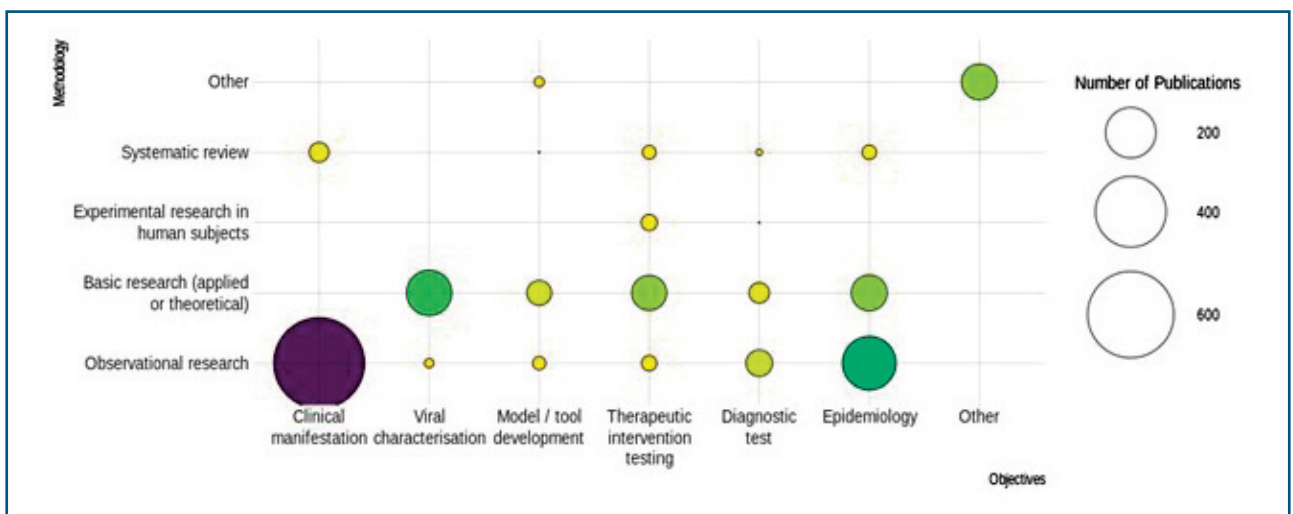


Fig. 4. COVID-SOLES database citations annotated by objective and methodology (N=1,174). Darker colours and larger bubble sizes indicate a higher number of publications.

DOI. This may be, in part, due to the uniquely challenging pace of COVID-19 research and our continual searching to retrieve newly published research. In some cases, we may be retrieving publications before they are fully indexed in biomedical databases. *Figure 5* indicates the percentage of unique citations retrieved from each database that lacks digital object identifiers (DOIs). Of unique records retrieved from the WHO COVID-19 database and Web of Science, 33.5% and 21.3% of citations are missing DOIs, respectively. To remedy this, we are now employing the *rcrossref* R package (17) to programmatically query the CrossRef database using titles and to identify the corresponding DOI information. Furthermore, we are refining our deduplication code to set a preference for retaining PubMed records over other databases, as 95.8% of citations we receive from PubMed have DOIs.

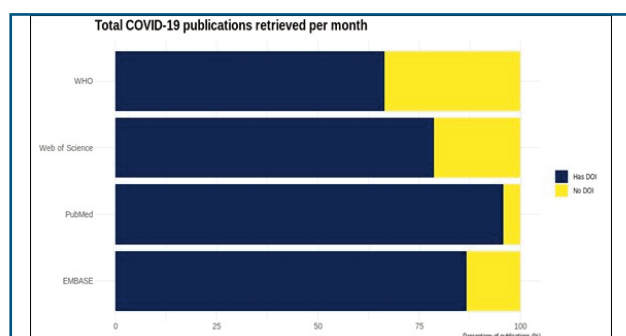


Fig. 5. DOI status across databases searched to obtain COVID-19 citations.

Supplementing our study type annotations

A major limitation is that we are not yet able to classify research automatically. The ability to do this as new research emerges would provide us with insights into research trends over time and identify gaps where more research may be needed. To obtain more study type annotations to drive automatic study type detection, we aim to recruit more volunteers by launching a new campaign across social media and other research networks. We are also exploring the possibility of exploiting annotation data from other openly available systematic evidence summaries of the COVID-19 literature and from published systematic reviews with accessible data. Past reviews have focused primarily on the clinical literature, so we will aim to make use of the existing data to classify human research and focus our crowd towards areas where there has been comparatively less attention e.g. *in vivo* research and *in vitro* research.

Improving our user interface

At present, some elements of the R Shiny user interface load slowly and it does not support full text searching of PDFs or Boolean searching of our database. We are currently building a new web interface to support these functionalities and sustain the growing COVID-SOLES database going forward.

Conclusion

We have developed a living workflow to synthesise COVID-19 research which enables research users to make rapid use of the currently available evidence. The SOLES workflow is sustainable, requiring minimal human effort to maintain – except the efforts of crowd-sourced volunteers – and is transferrable to other research areas. We will continue to improve upon this workflow, enable more automated categorisation tools, and upgrade the user interface to enable features most useful to the evidence synthesis community.

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Members of The COVID-SOLES Group (authorship)

Project administration: Emily Sena (University of Edinburgh). **Study design:** Gillian Currie, Zsanett Bahor, Emily Sena, Malcolm Macleod, Emma Wilson, Kaitlyn Hair. **Software and architecture:** Kaitlyn Hair, Emma Wilson, Chris Sena, Can Ayder, Jing Liao, Ezgi Tanriver Ayder. **Annotation:** Joly Ghanawi, Anthony Tsang, Anne Collins, Malcolm Macleod, Alice Carstairs, Sarah Antar, Katie Drax, Kleber Neves, Thomas Ottavi, Yoke Yue Chow, David Henry, Cigdem Selli, Mariam Fofana, Martina Rudnicki, Brendan Gabriel, Esther J. Pearl, Simran S. Kapoor, Julija Baginskaite, Santosh Shevade, Alexandria Chung, Marianna Antonia Przybylska, David E. Henshall, Karina Lôbo Hajdu, Sarah McCann, Catherine Sutherland, Tiago Lubiana Alves, Rachel Blacow, Rebecca J. Hood, Nadia Soliman, Alison Harris, Stephanie L. Swift, Torsten Rackoll, Nathalie Percie du Sert, Fergal Waldron, Magnus Macleod, Ruth Moulson, Juin W. Low, Kristiina Rannikmae, Kirsten Miller, Alexandra Bannach-Brown, Fiona Kerr, Harry L. Hebert, Sarah Gregory, Isaac William Shaw,

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Crowdsourcing and COVID-19: a case study of Cochrane Crowd

Anna Noel-Storr (a, b, c), Gordon Dooley (d), Robin Featherstone (e), Susanna Wisniewski (f), Ian Shemilt (g), James Thomas (g), Gerald Gartlehner (h, i), Barbara Nußbaumer-Steit (h, j), Christopher Mavergames (f)

(a) Radcliffe Department of Medicine, Cochrane Dementia and Cognitive Improvement Group, Oxford University, Oxford, UK

(b) Cochrane People Services Department, Cochrane, London, UK

(c) Henley Business School, Reading University, Reading, Berkshire, UK

(d) Metaxis Ltd, Oxford, UK

(e) Cochrane Editorial and Methods Department, Cochrane, London, UK

(f) Cochrane ITS Department, Cochrane, London, UK

(g) EPPI-Centre, UCL Social Research Institute, University College London, London, UK

(h) Department for Evidence-based Medicine and Evaluation, Danube University Krems, Krems an der Donau, Austria

(i) RTI International, Research Triangle Park, NC, USA

(j) Department of Family Medicine, Care and Public Health Research Institute, Maastricht University, Maastricht, The Netherlands

Abstract

Cochrane has used crowdsourcing effectively to identify health evidence since 2014. To date, over 175,000 trials have been identified for Cochrane's Central Register of Controlled Trials via Cochrane Crowd (<https://crowd.cochrane.org>), Cochrane's citizen science platform, engaging a Crowd of over 20,000 people from 166 countries. The COVID-19 pandemic presented the evidence synthesis community with the enormous challenge of keeping up with the exponential output of COVID-19 research. This case study will detail the new tasks we developed to aid the production of COVID-19 rapid reviews and supply the Cochrane COVID-19 study register. The pandemic initially looked set to disrupt the Crowd team's plans for 2020 but has in fact served to further our understanding of the potential role crowdsourcing can play in the health evidence ecosystem.

Key words: *crowdsourcing; COVID-19; systematic review; evidence-based health care.*

Introduction

Crowdsourcing in health research has become increasingly popular over the last decade (1). Cochrane, an international network that produces systematic reviews, has been harnessing a type of crowdsourcing called “human intelligence tasking” since 2014 (2, 3). Human intelligence tasking involves filtering or classifying large amounts of data or information via an online community. In May 2016, Cochrane launched Cochrane Crowd (<https://crowd.cochrane.org>), its citizen science platform, with its first crowdsourcing task: the identification of reports of randomised controlled trials (RCTs) from Embase. Other tasks followed soon after and new tasks are in development and rolling out on an ongoing basis. Our evaluations of the Crowd's performance in terms of accuracy demonstrated that a crowdsourcing approach to identifying RCTs was both

robust and efficient (2). By early 2020, over 20,000 contributors had signed up to Cochrane Crowd from 166 countries and generated over 5 million individual classifications, helping to identify around 175,000 reports of randomised trials.

2020 looked to be a busy year, but we did not anticipate how large an impact the COVID-19 pandemic would have on Cochrane Crowd. We had launched a new version of the Crowd platform in early March 2020 and work was about to begin on a new PICO extraction task as part of Cochrane's trial surveillance initiative. Initially, the pandemic was hugely disruptive to the latter planned work, with our efforts immediately re-focused to help.

One of the main challenges presented by the pandemic was the corresponding infodemic. According to the World Health Organization: “[A]n infodemic is too

Address for correspondence: Anna Noel-Storr, Room 4401c, Level 4, John Radcliffe Hospital, Oxford, OX3 9DU, UK; anna.noel-storr@rdm.ox.ac.uk

much information including false or misleading information in digital and physical environments during a disease outbreak. It causes confusion and risk-taking behaviors that can harm health. It also leads to mistrust in health authorities and undermines the public health response. An infodemic can intensify or lengthen outbreaks when people are unsure about what they need to do to protect their health and the health of people around them” (4).

The dramatic increase in COVID-19 research production and publication throughout 2020 and 2021 has created significant information retrieval challenges, both from the sheer volume of research and in the nature of the research output. One example was the so-called “preprint rush,” with both demand for, and availability of, preprints soaring during 2020 (5, 6). Cochrane was able to adapt existing skills and systems for the organisation of COVID-19 research to assist with review production.

Cochrane prioritised resources and developed initiatives to respond to the pandemic, including a programme of work to produce rapid reviews and the production of special collections of existing relevant health evidence on topics such as infection control and prevention measures and remote care through telehealth (7).

Another major undertaking within the network was the development of a curated register of COVID-19 studies, the Cochrane COVID-19 Study Register (CCSR)

(<https://covid-19.cochrane.org>) (8). The CCSR is a continuously updated open access repository of COVID-19 human studies that have been identified from a range of sources and tagged by study type, study design and study aim. Related reports about the same study are linked together to create a “study based” register. The register went live in April 2020 and within twelve months over 57,000 COVID-19 studies had been identified and described.

Cochrane Crowd was uniquely placed to help in the response as our thriving community of contributors were eager to support Cochrane’s response to the pandemic. This case study will detail four main areas of work undertaken by Cochrane Crowd during the first twelve months of the pandemic: 1) COVID Quest – a new Cochrane Crowd task; 2) direct review input and methodological research; 3) weekly screening challenges; 4) a COVID-19 machine learning classifier.

COVID Quest

We developed a new crowdsourced task: COVID Quest. In COVID Quest the Crowd identify COVID-related studies based on assessing title-abstract records (Figure 1). Unlike most Cochrane Crowd tasks, it is a “multi-question” task – made up of a series of questions about the record.

COVID Quest tasks contributors with identifying a range of different study types and study designs, which

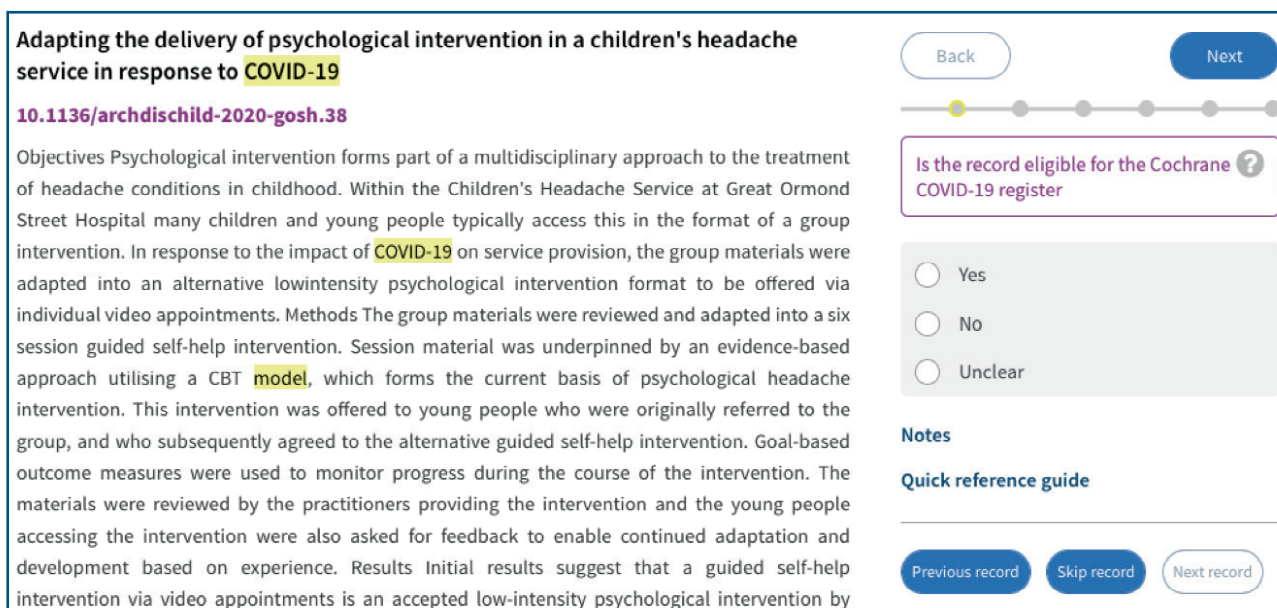


Fig. 1. Screen capture of Cochrane Crowd’s COVID-19 task: COVID Quest.

is another key difference with this task compared to other mainstream tasks on Cochrane Crowd, which relate to identification or description of randomised controlled trials. This is crucial because in a pandemic, a range of study types are needed to answer urgent questions regarding treatment, diagnostics, health services, mental health and the larger societal impact. Controlled vocabularies are used for each question within the task. Anyone can join, though completion of a brief training module is mandatory.

We launched the task in June 2020 after a rapid development and testing phase, and to date (June 2021) the Crowd have amassed around 60,000 assessments helping to identify and describe thousands of studies for the CCSR. We have evaluated Crowd accuracy against a gold standard dataset made up of 2000 records assessed by Cochrane information specialists working on the register. Within this set, 566 records were eligible for the CCSR. The Crowd correctly identified 558 as eligible giving a Crowd sensitivity of 98.5%. The Crowd achieved similarly high levels of sensitivity across the study type (whether the study described was an observational, interventional, qualitative, or mathematical modelling study) and the specific study design used (RCT, cohort study/case control, case report, cross-section etc.) components of COVID Quest: 98.2% and 97.6% respectively. In addition, around 85% of records assessed had matching classifications under our agreement algorithm, with only 15% requiring resolution by an “expert” after discordant classifications between Crowd contributors.

COVID Quest forms part of a study identification

workflow that is largely based on processes that Cochrane’s Centralised Search Service already had in place for identifying studies for the Cochrane Central Register of Controlled Trials (CENTRAL) (9) (Figure 2). Having some of the foundations and technical infrastructure in place facilitated rapid implementation of this end-to-end process.

Review input

As already described, Cochrane undertook a programme of COVID-related, rapidly produced reviews. This work presented an opportunity to test the Crowd’s ability to identify studies for reviews in a time-sensitive context. Four reviews were used in this methodological work: Quarantine alone or in combination with other public health measures to control COVID-19 (10); Barriers and facilitators to healthcare workers’ adherence with infection prevention and control (IPC) guidelines for respiratory infectious diseases (11); Universal screening for Severe Acute Respiratory Syndrome Coronavirus 2 (12); and Convalescent plasma or hyperimmune immunoglobulin for people with COVID-19 (13). We created a corresponding crowdsourced task for each of these reviews in Cochrane Crowd. Crowd contributors were tasked with assessing the search results and making one of two possible classifications on each title-abstract record: *Possibly relevant* or *Not relevant*.

As with COVID Quest, these new crowd tasks marked a departure from Crowd tasks focussed on identifying RCTs. This collection of rapidly produced reviews covered a wide range of eligible study types and designs including mathematical modelling studies, observational studies, interventional studies, and qualitative and mixed study designs. The Crowd had to become familiar with both the topic of the review and study types eligible for the review. They were also only given 48 hours to complete each task. The Crowd performed well, comfortably completing the screening task for three of the four reviews within 48 hours (one review took just over 48 hours to complete). Crowd accuracy levels were high, ranging from 90%-100% recall across the four reviews. This methodological work furthered our understanding of crowdsourcing capabilities in topic-based screening tasks under tight time constraints. The Crowd also inputted directly into the update of the rapid review on quarantine measures, where 65 Crowd contributors screened the 5000 results re-

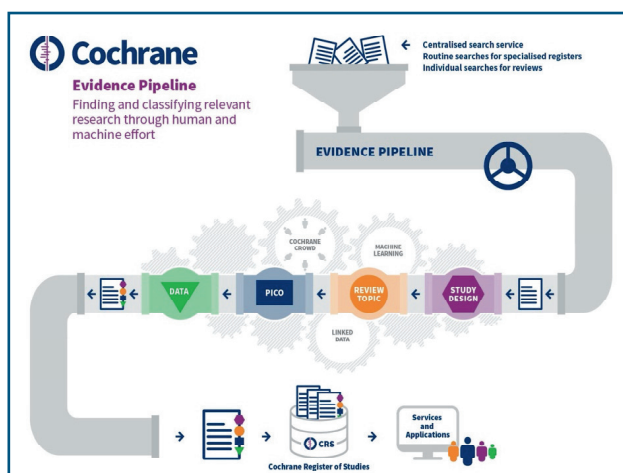


Fig. 2. Cochrane’s Evidence Pipeline vision.

trieved from the update search in 22 hours (<https://www.cochrane.org/news/cochrane-crowd-does-it-again-rapid-study-identification-cochrane-rapid-review>).

Weekly screening challenges

From April 2020, we started a series of weekly 3-hour Crowd challenges. Each week we select a task and encourage as many as possible to get online and join in. During the early days of the pandemic, when most of us were in strict lockdown with many not able to work, this felt like a suitable community engagement activity that enabled us to keep some of our “business as usual” tasks going. We have now completed over 50 weekly challenges and in that time, screened approximately 100,000 records mostly from the RCT Identification task.

COVID-19 machine learning classifier

The final area of Crowd input is related to the development of a machine learning classifier for COVID-19 studies. In July 2020 members of the CCSR team and the COVID EPPI-Centre Map team, based at University College London, set up a series of meetings with the aim of sharing best practice and reducing duplication of effort across the two initiatives. One area of focus was on strategies to reduce study identification screening burden. The EPPI-Centre Map team had already developed a binary machine learning classifier that worked to reduce screening workload as well as to help prioritise screening. Given the differing scope regarding studies eligible for the CCSR and the EPPI-Centre COVID Map, we decided that a new binary machine learning classifier should be developed specifically for the CCSR workflow. We therefore used high quality training data generated by both the core Cochrane register team and Cochrane Crowd to train, calibrate and evaluate a COVID-19 study classifier. We followed the same stages of training, calibration and validation as we had done for the development of the Cochrane RCT classifier (14). The result is a classifier that helps to accurately identify records that are not eligible for the CCSR. We have been using this classifier since February 2021, reducing screening burden by between 20-25%.

Conclusion

COVID-19 presented us with major information retrieval challenges, but also provided important oppor-

tunities for research and development on methods, processes, and tools. Our experiences have highlighted the benefit of focussed and collaborative working. Development, testing and full implementation of Cochrane Crowd’s most complex task to date took eight weeks instead of the more usual 12-24 months. We were able to use and adapt existing systems (such as the Cochrane Crowd platform), processes, for example Cochrane’s Centralised Search Service, and expertise across information and data science disciplines. The Cochrane Crowd community itself played an invaluable role in enabling us to keep-up, advancing our expectations of crowdsourced capability in evidence synthesis. We are now working on extending the Crowd’s role to include PICO extraction of both COVID-19 studies as well as studies in other health care areas. This will, we hope, significantly improve search precision, and support accurate surveillance of the evidence as it emerges.

In its early days, the pandemic appeared to be highly disruptive to “business as usual”, but in hindsight it has accelerated our work and our understanding of the value of human and machine input in the production of health research. Sharing an overarching mission to help during a global health crisis, organisations at different levels of the evidence ecosystem pulled together to make the emerging evidence base FAIR (findable, accessible, interoperable, and reusable). Duplication of effort still occurred and enormous challenges remain as the deluge of information around COVID-19 shows little sign of abating, but for the Cochrane Crowd team, the experience and the learning of the last twelve months has been important and lasting.

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On behalf of the Marmara University Rectorate and International Program Committee & the Local Organizing Committee, it is a great pleasure for us welcoming you to the EAHIL2021 Virtual Workshop in Istanbul. EAHIL 2021 Virtual Workshop will take place between the 5th - 8th of July 2021 on <https://eahil.digicon.ist> virtual platform. We look forward to having a dynamic meeting with you in the virtual exhibition area to increase the interaction in the workshop!

The main theme of the virtual workshop is "Crossing the Bridge: New Challenges, New Opportunities" The Bridge is connecting Europe and Asia and it's a symbol of Istanbul. The idea of a bridge crossing the Bosphorus dates back to antiquity and it's a link between the continents. Let's meet where the continents meet!

EAHIL 2021 Virtual Workshop will have an exceptional keynote speakers. On the 6th of July, Prof. Dr. Messoud Efendiyev from Marmara University and on 7th of July Prof. Dr. Rümeyza Kazancıoğlu from Bezmialem Vakıf University will be with us. The workshop program includes 2 Continuing Education Courses (CEC), 7 Interactive Workshops, and 25+ online oral presentations. At the same time, 16 poster works will be exhibited in the online exhibition and workshop hall. Exhibition area we will be able to hold interactive business meetings with publishers, meeting with medical library association experts all around the World at the Virtual Coffee Breaks.

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Assoc. Prof Güssün GÜNEŞ,
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gussun.gunes@marmara.edu.tr or eahil2021@marmara.edu.tr

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Letter from the President



Lotta Haglund

Swedish School of Sport and Health Sciences, GIH
Stockholm, Sweden
Contact: lotta.haglund@gih.se

Dear EAHIL Colleagues,

When this letter is published in the June issue of *JEAHIL*, summer will have arrived, and in the northern part of my country, you can see the midnight sun. We're only a few weeks from our next event, which we're all looking forward to. The EAHIL 2021 workshop, hosted virtually by the Marmara University in Istanbul, Turkey, will be the second EAHIL event organised as an online meeting. It promises to be successful, with exciting keynote speakers, presentations and posters, as well as CECs and interactive sessions. Our Turkish colleagues have worked very hard to organise an exciting program and some fun social events. I hope to see you all on-screen in July!

Even though we're still in the middle of the pandemic, we now see more initiatives for the “restart” of our societies. Some of these initiatives include libraries, like the Italian National Recovery and Resilience Plan, which describes investments in digital strategy and platforms for cultural heritage, the removal of physical and cognitive barriers in museums, libraries, and archives to enable wider access to and participation in culture, and improving energy efficiency in cinemas, theatres, and museums. In Sweden, the Library Association arranges an annual conference, this year with the theme “Restart”. The European Union has a plan for “the new generation EU,” which includes digital initiatives. Initiatives like these inspire hope for the future, and I will make sure to keep a lookout for opportunities for funding new development in my library.

Recently the EAHIL Board has been made aware of two changes in connection to the EAHIL events. The first one is a direct consequence of the pandemic; the Czech manufacturer of the crystal trophies awarded the winners of best poster/best oral presentation at EAHIL events since 2008, is no longer able to provide the same services. It has been incorporated into a larger company with a different line of products. I want to extend the gratitude of the EAHIL Board to Helena Bouzková and Ondřej Horsák for their longstanding help in providing us with the beautiful trophies and the EAHIL awards for outstanding medical librarianship or contributions to the field or special services and dedication to EAHIL.

The other change affects the EAHIL-EBSCO scholarships. One of the aims of EAHIL is “the training, education and mobility of health librarians and information officers in Europe”, and for many years the Association has been able to offer a varying number of scholarships to attend the year's event. For 2021 we have been able to offer two scholarships, jointly sponsored by EBSCO. In March, we were informed that EBSCO will pause their financial support for the scholarship from 2022. We want to thank EBSCO for their support and hope we'll be able to work together in the future

Since my previous letter, the EAHIL Executive Board has met twice, in late February, for our scheduled winter meeting and in March for an update with the organisers of the future EAHIL events. Planning for both the 2022 Conference in Rotterdam and the 2023 Workshop in Trondheim is well underway, and in preparation for next year's event, we can look forward to a call for papers for Rotterdam later this year.

Previously, as a Board member, and now in my new role as President, one of my aims has been to encourage dialogue between the EAHIL Board, the Council and all members. Dialogue needs transparency since it's difficult to have views and comments when you don't know what's being discussed in different fora. Consequently, short reports in relation to every Board meeting will be published on the web site blog. We're also discussing the possibility of replacing this column published in *JEAHIL* with more frequent blog posts, to disseminate more current news from the association.

The next Board meeting will be the pre-conference meeting on 5 July. Please let me know if there are any items that you feel should be added to our agenda for discussion. The Board strongly encourages your input, comments & feedback, either by e-mail to the official EAHIL inbox (EAHIL-SECR@LIST.ECOMPASS.NL) or during EAHIL events using the available "feedback to the Board" arrangement, e.g. flipchart, Padlet etc.

JEAHIL online usage



Rebecca Wojturska

Open Access Publishing Officer
University of Edinburgh, Edinburgh, UK

Rebecca.Wojturska@ed.ac.uk

2020 saw another year of great website and article usage for *JEAHIL*, so I thought I would share the statistics!

The journal homepage views went from 11,797 in 2019 to 17,228 views in 2020, the table-of-content views for issues went from 13,439 in 2019 to 18,138 in 2020, and the abstract page (or article landing page) views went from 36,806 in 2019 to 70,934 in 2020 – almost double! Most importantly, the article views (including browser and computer downloads), increased from 17,407 in 2019 to 27,819 in 2020, which is absolutely fantastic!

The top 10 articles (*Table 1*) are different from last year, with plenty of new entries from 2020 issues. This is great as we can see the new content is being eagerly sought and the consistent use of back content highlights the continued relevance of all the journals research. We can also see that the most used issue (*Table 2*) is still Vol 11 No 3 (2015) – a very popular issue indeed.

Also, Google Analytics tells us that the amount of unique users on the *JEAHIL* website increased from 3,866 in 2019 to 4,997 in 2020 – more great news! We can also see that most people came from the US, followed by Sweden, and then the UK (*Figure 1*).

The library has also been submitting *JEAHIL* to various abstractors and indexers, and are pleased to confirm there is one new indexing arrangement to date: the journal is now indexed in CAB Abstracts and Global Health databases!

It's wonderful to see that the pandemic hasn't negatively impacted the journal's usage and hopefully *JEAHIL* continues to go from strength to strength.

The library has also been submitting *JEAHIL* to various abstractors and indexers, and are pleased to confirm there is many new indexing arrangements to date: AGORA, CAB Abstracts and Global Health databases, the European Reference Index for the Humanities and the Social Sciences (ERIH PLUS), Hinari, JournalTOCs, Norwegian Register for Scientific Journals, and Researcher. The journal policies are also now listed in Sherpa Romeo. These databases join the Directory of Open Access Journals (DOAJ), which *JEAHIL* is already indexed in.

Rank	Article title	Author(s)	Issue	Count
1	Open access: how to ensure systematic searching?	Julian Hirt, Thomas Nordhausen	Vol 16 No 1 (2020)	302
2	The Medical Library at Umeå University during the coronavirus pandemic	Karina Sjogren	Vol 16 No 3 (2020)	287
3	Medical students prefer print textbooks for studying but value the e-books' search function and availability	Sabine D. Klein	Vol 16 No 1 (2020)	285
4	Remembering Laura Shane Godbolt	Suzanne Bakker	Vol 15 No 4 (2019)	283
5	Serving library users during a pandemic: the case of Karlstad University Library, Sweden	Jakob Harnesk, Marie-Louise	Vol 16 No 3 (2020)	250
6	Hunting for the library value	Karen Johanne Buset, Ghislaine Declève, Tuulevi	Vol 15 No 1 (2019)	232
7	Qualitative research methods: interviewing as a way of learning and knowing	Johanna Rivano Eckerdal	Vol 12 No 1 (2016)	230
8	Pivotal in a pandemic: an interview with Ian Roberts, head of the WHO libraries	Ray Phillips	Vol 16 No 3 (2020)	229
9	Surrounded by science: The Researchers' Gallery at Malmö University Library	Annsophie Olsson, Lotti Dorthé	Vol 16 No 2 (2020)	194
10	Artificial Intelligence (AI) – What is it and what does it do?	Tiina Heino	Vol 16 No 1 (2020)	191

Table 1. JEAHIL top 10 article downloads 2020.

Rank	Issue	Count
1	Vol 11 No 3 (2015)	2271
2	Vol 12 No 1 (2016)	2218
3	Vol 16 No 2 (2020)	2005
4	Vol 15 No 4 (2019)	1642
5	Vol 16 No 3 (2020)	1616

Table 2. JEAHIL top 5 issues 2020.

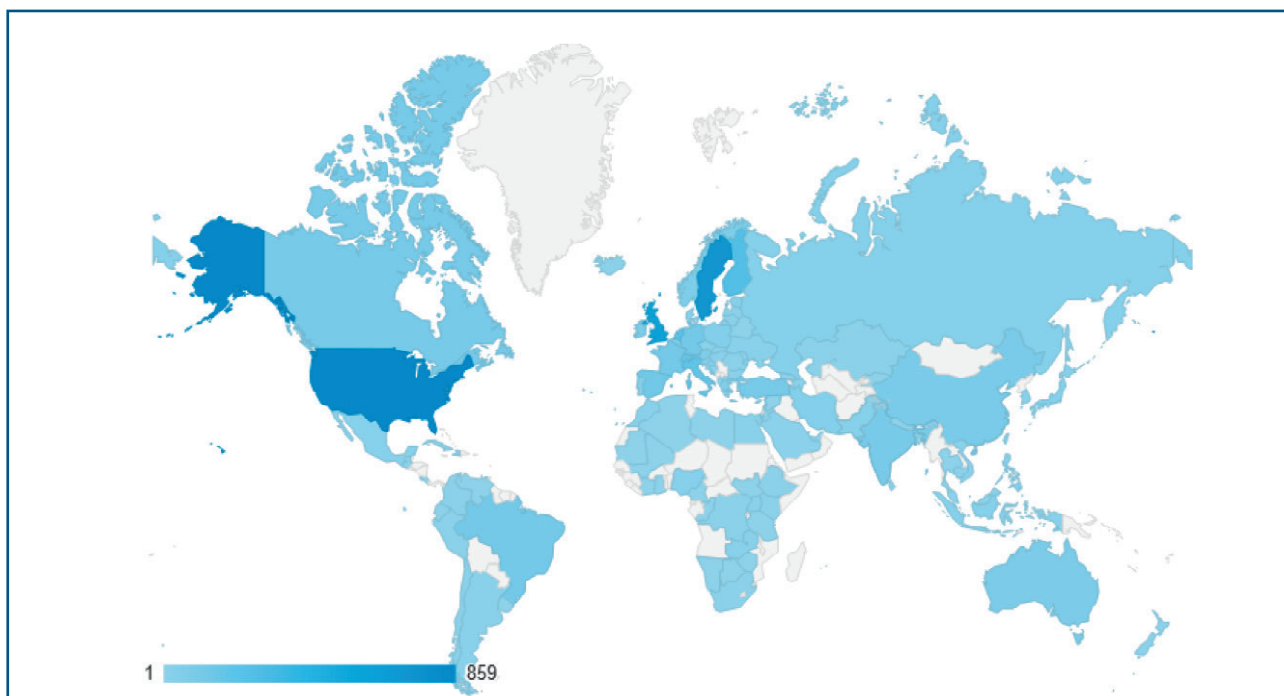


Fig. 1. Google Analytics Users by Country 2020.

US Medical Library Association report for EAHIL



Carol Lefebvre

MLA Representative to EAHIL
Independent Information Consultant
Lefebvre Associates Ltd, Oxford, UK
Contact: Carol@LefebvreAssociates.org



Report on MLA '21 vConference

As some of you may remember, MLA '21 was due to be held in Washington DC again this year. The first MLA meeting that I ever attended (in 1995) had been held in Washington DC, so I was looking forward to a return visit but the global pandemic saw to it that that did not happen. Instead of an in-person event, MLA '21 was held as a virtual conference (or vConference) again this year, as it had been last year.

I hope that some of you were able to attend the vConference remotely this year. You may have had conference funds in your budgets that you had been unable to spend on attending conferences in person this year and the ability to watch the sessions immediately after they had taken place went a long way towards solving any issues around time differences between Europe and the US.

The meeting, which was spread over 3 weeks from 10-27 May, was a great success with c. 1,200 registrants (more than the most recent in-person annual meeting) from at least 12 countries. There were three major keynote presentations, the John P. McGovern Award Lecture delivered by Damon Tweedy, the Joseph Leiter NLM/MLA Lecture delivered by Mitzi Baum and the Janet Doe Lecture delivered by Sandra G. Franklin. In addition, there was the usual NLM Update. Damon Tweedy, author of the *New York Times* bestseller "Black Man in a White Coat", selected by *Time* magazine as one of the top 10 non-fiction books of 2015, has published articles about race and medicine in the *Journal of the American Medical Association* and other medical journals. His columns and op-eds have appeared in *The New York Times*, *The Washington Post* and various other news publications, focussing on the impact of race on the medical profession at all levels. He is a graduate of Duke University School of Medicine and Yale Law School and completed both his medical internship and psychiatry residency at Duke Hospital. He is currently an associate professor of psychiatry at Duke University School of Medicine and a staff psychiatrist at the Durham Veteran Affairs Health Care System. He spoke about his experiences growing up as a black American, from his school days through his experiences at medical school, to his present position as a practising physician. Here are some quotations from his presentation:

"Not everything that is faced can be changed but nothing can be changed until it is faced". (James Baldwin).

"The need to move away from the notion that 'being black is bad for your health'".

"We should all think about our sphere of influence, because everyone has one".

News from us MLA

“If I cannot do great things, I can do small things in a great way” (Martin Luther King Jr).

The other keynotes are still on my To Do list, as they all only took place a couple of days before the deadline for this article.

With respect to the contributed programme, c. 100 papers and c. 50 “Lightning Talks” were presented, which could be viewed as videos / slidecasts online, listening to the presenters in your own time and interacting with attendees and presenters in virtual sessions and through “chat”. Additionally, there were c. 100 posters (with over 10,000 poster views), which could also be viewed online with presenter / audience interaction as above.

This year there were again c. 20 Immersion sessions, described as follows. “They are intended to: provide an in-depth perspective on areas of interest to MLA members. They are your chance to design and offer the programming that you want to see. Immersion sessions should strive for excellent engagement and can vary in format from a panel of invited speakers to a single invited speaker, a facilitated book discussion, as well as less-conventional sessions like an 'unconference' or flipped session. The only type of programming excluded from immersion sessions are paper presentations”. These were an innovation in the 2019 MLA programme.

Presentations remain open to meeting delegates exclusively for one year after the event and thereafter, from 1 June 2022, they are available for 3 years to all MLA members.

The Exhibition again was fully virtual this year with c. 40 exhibitors and sponsors. Delegates were able to view the exhibit booths (there were 12,000 booth views), set up appointments with the exhibitors and participate in or watch on “catch-up” the c. 20 Exhibitor Solution Showcase presentations, with live Q&A, which were attended by 1,500 delegates.

Networking events, of which there were 17, were also fully virtual this year, with over 1,000 attendees taking part.

Continuing Education courses, which would normally be held during the two days prior to the conference, were held throughout the year instead, including instructor-led courses, self-paced courses and webinars.
<https://www.mlanet.org/p/cm/ld/fid=412>

The MLA '21 Blog, as usual, provided coverage of a range of topics including programme sessions, plenary sessions, exhibition, activity and virtual social events, before, during and after the meeting.
<https://www.mlanet.org/p/bl/et/blogid=155>

Additionally, attendees and others were able to follow the meeting on Twitter with the MLA '21 hashtag #mlanet21 and follow MLA more generally on Facebook at: <https://www.facebook.com/MedicalLibraryAssn>

Future MLA annual meetings - dates for your diary:

New Orleans, Louisiana 2-7 May 2022 (with some virtual content)

vConference and Exhibits (subject to change) May 2023

Portland, Oregon 18-21 May 2024

Membership of MLA

MLA offers International Membership to individuals at a reduced rate. This category applies if you work or have worked in a health- or health-information-related environment and live outside the US or Canada. The current annual subscription rate for International Membership is 150 US dollars (or 25 US dollars if you are from a HINARI-eligible Group A or Group B country).

<https://www.mlanet.org/join>

News and publications from MLA

The latest issue of the *Journal of the Medical Library Association (JMLA)* (Volume 109 (1) Jan 2021) is now available (open access) at:

<https://www.ncbi.nlm.nih.gov/pmc/journals/93/latest/>

Open access to back issues of the *JMLA* (and its predecessors back to 1898) is available from:

<https://www.ncbi.nlm.nih.gov/pmc/journals/93/>

Preprints of articles from the forthcoming issue of the *JMLA* are no longer available. *JMLA* does, however, encourage self-archiving at any point in the manuscript preparation or peer review process:

<http://jmla.mlanet.org/ojs/jmla/article/view/877>

MLAConnect is MLA's members-only e-mail newsletter and is circulated weekly. The online version now displays all articles to which members have access, including from blogs of MLA sections and is updated continually. Most articles are restricted to MLA members and / or to members of specific MLA sections. For the most complete display of articles, you need to login with your username and password.



Publications and new products

Letizia Sampaolo

Istituto Superiore di Sanità, Rome, Italy

letizia.sampaolo@iss.it

Dear friends,

I grew up in a musical family and started singing at a very young age. In fact, we all loved singing and playing so much that our parents made us kids took up piano lessons very early. Thank our parents, we also grew up listening to a variety of different music, even though country music stood out to us.

Today I'd like to tell you the story about my father, born on the 22nd May 1927 and no longer with us, because of difficulties in health care caused last year by covid-19.

He lived in a small village in central Italy. Despite the world war, he made up his studies and became a scientist in chemistry and toxicology. After getting married to his tender and very young fiancée, he moved to Rome and together started a family with five children and, later on, 13 grandchildren and 12 great-grandchildren. Throughout his life, he devoted himself to studying, writing books and essays, acting as an Italian representative at the European Union, and teaching at the university, which he did even after he retired and until he could. Music was one of his greatest loves in life; he loved playing his harmonica and make music together, which we pleasantly did nearly until the end, making us feel united.

He lived his last years with dementia and reached the point he only knew us as some people passing by and even did not know us by our names. What was stunning, though, was that we could still connect through singing and playing music. No book, no tale, nor therapy could give us our father or grandfather back like music did, instead.

Today, the number of people affected by Alzheimer's disease is growing bigger and bigger, and I am sure anyone of you could tell about a case among his/her relatives or friends. Though, I believe sharing experiences is crucial and can give support to the families affected.

New Alzheimer's drug aducanumab is creating new hopes – by the way, read the [interesting post](#) published on The Conversation blog last June 11th – although further research is still needed. However, Alzheimer's disease awareness is rising in many countries, and many websites collecting stakeholders and families' experiences exist. For example, in New Zealand, the [Alzheimer New Zealand](#) website “represents people living with dementia at a national level by raising awareness of dementia, providing information and resources, advocating for high-quality services, and promoting research about prevention, treatment, cure and care”. Through their excellent Strategic Framework and work, they want to move towards a world without dementia. Besides receiving support and advice, people can share [one's own story](#), explore new possibilities, and be involved through this website. So please, surf it and enjoy the stories told.

JOURNAL ISSUES

Health Information and Libraries Journal: Contents of June 2021 (38:2)

Editorial

- **Supporting, enabling, and empowering**

Maria J Grant

PUBLICATIONS AND NEW PRODUCTS

Review

- **Personal, technical and organisational factors affect whether physicians seek answers to clinical questions during patient care: a literature review**
Azra Daei, Mohammad Reza Soleymani, Hasan Ashrafi-Rizi, Roya Kelishadi and Ali Zargham Boroujeni

Original Articles

- **A clinical librarian in a hospital critical care unit may generate a positive return on investment (ROI)**
Ned Hartfiel, Girendra Sadera, Victoria Treadway, Catherine Lawrence and Rhiannon Tudor Edwards
- **Performance evaluation of three semantic expansions to query PubMed**
Clément Massonnaud, Romain Lelong, Gaetan Kerdelhué, Émeline Lejeune, Julien Grosjean, Nicolas Griffon, Stefan Darmoni
- **Application of bibliometrics in medicine: a historical bibliometrics analysis**
Peter Kokol, Helena Blažun Vošner and Jernej Završnik

Regular Features

- ***Dissertations into Practice***
Delivering eye health education to deprived communities in India through a social media-based innovation.
Chandrani Maitra and Jenny Rowley
- ***International Perspectives and Initiatives***
An exploration of how fake news is taking over social media and putting public health at risk.
Salman Bin Naeem
- ***Teaching and Learning in Action***
Health literacy: the role of NHS Library and Knowledge Services
Joanne Naughton, Kerry Booth, Paula Elliott, Morag Evans, Maria Simoes and Suzanne Wilson

FROM THE WEB

- **PatientView and myhealthapps.net**

PatientView is a UK-based research, publishing, and consultancy group, born out of a belief that the patients' views should be considered in all-important healthcare decisions. It was formed in response to the powerful new global patient movement. PatientView organisation acts worldwide to connect with the health Non-Governmental Organisations comprising the patient movement. Patient organisations are in an excellent position to provide valued insights since they are the only stakeholder to interact across every facet of the healthcare system. In addition, they hold resilient views about the experiences and needs of patients with whom they are familiar, their country's healthcare policies, and systems and technologies' values (digital and mobile).

Myhealthapps.net, brought to us by PatientView, brings together the world's favourite healthcare apps – tried and tested by people, to find trusted apps and support people or someone people care for. Each app is classified to make it easier for users to find ones relevant to them. [Check here](#) to learn more about their methodology and how apps are classified.



- **Even ancient queens and kings sometimes have to move**

Last April 3rd, Middle East BBC news showed how Egyptian mummies passed through Cairo in ancient rulers' parade. It was a luxurious vision that saw 22 mummies - 18 kings and four queens - transported from the existing Egyptian Museum to their new resting place 5km away. They were conveyed in chronological order of their reigns - from the 17th Dynasty ruler, Seqenenre Taa II, to Ramses IX, who reigned in the 12th Century BC. In BBC's words, "each mummy was carried on a decorated vehicle fitted with special shock-absorbers and surrounded by a motorcade, including replica horse-drawn war chariots". The main attractions were King Ramses II, who ruled for 67 years and is remembered for signing the first known peace treaty, and Queen Hatshepsut, who became monarch even though at her time women did not become pharaohs. Read the [BBC's captivating post](#) and watch the 18 kings and four queens stunning parade.

SOME INTERESTING FORTHCOMING EVENTS:

ICML+AHILA 2021

June 21-25, 2021, Pretoria, South Africa

Info: <https://icml2021.org/>

July 5-8, 2021, Istanbul, Turkey

EAHIL 2021 Online Workshop

Info: <https://etkinlik.marmara.edu.tr/eahil2021>

... and we hope, many more to come!

Please feel free to contact me (letizia.sampaolo@iss.it) if you have any further suggestion about events you would like to promote.

Special Issue: Shane Godbolt

Health Information & Libraries Journal

Read the Issue > bit.ly/35kqAMg



This **special issue** of **HILJ** has been published to celebrate the life and work of Shane Godbolt. The issue not only records the astonishing achievements of a unique medical health librarian, but also records the development of medical/health care librarianship, and the contributions of many of those who were involved with her in these developments, over half a century.

About the Journal: Published by the Health Libraries Group in conjunction with Wiley, HILJ aims to promote debate about new health information developments with an emphasis on communicating evidence-based information both in the management and support of healthcare services.

Find out more about HILJ at:
onlinelibrary.wiley.com/journal/14711842

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Editorial Board

CHIEF EDITOR: Federica Napolitani Cheyne

Scientific Communication Unit, Istituto Superiore di Sanità,
Viale Regina Elena 299, I-00161 Roma, Italy

- Tel: +39 06 4990 2945
- E-mail: federica.napolitani@iss.it

Petra Wallgren Björk

Karolinska Institutet University Library, 171 77 Stockholm

- Tel: +46852484483
- E-mail: petra.bjork@ki.se

Gerhard Bissels

HTW Chur, University of Applied Sciences
Ringstrasse 34, 7004 Chur, Switzerland

- Tel. +41 81 286 38 02
- E-mail: gerhard.bissels@htwchur.ch

Fiona Brown

The Lady Smith of Kelvin Veterinary Library, Royal (Dick)
School of Veterinary Studies, University of Edinburgh, Easter
Bush, Midlothian

- EH25 9RG, Scotland, UK
- Tel: +44 131 650 6176
- E-mail: F.Brown@ed.ac.uk

Katri Larmo

Terkko - Meilahti Campus Library, P. O. Box 61
(Haartmaninkatu 4) 00014 University of Helsinki, Finland

- Tel: +358 2941 26629
- E-mail: katri.larmo@helsinki.fi

Letizia Sampaolo

CNAPS, Istituto Superiore di Sanità
Viale Regina Elena 299, I-00161 Roma, Italy

- Tel: +39 06 4990 4323
- E-mail: letizia.sampaolo@iss.it

Michelle Wake

UCL School of Pharmacy, 29-39 Brunswick Square,
London WC1N 1AX, United Kingdom

- Tel: + 44 (0)20 77535833
- E-mail: m.wake@ucl.ac.uk

Whilst the Editorial Board endeavours to obtain items of interest, the facts and opinions expressed in these are the responsibility of the authors concerned and do not necessarily reflect the policies and opinions of the Association.

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Instructions to Authors

Instructions to Authors are available online at www.eahil.eu. For further information please contact Federica Napolitani, Chief Editor of JEAHIL federica.napolitani@iss.it

Editorial layout and pagination: **De Vittoria srl**, Rome, Italy

EAHIL Executive Board (2021-2022)

- President** **Lotta Haglund**
The Swedish School of Sport and Health Sciences, Library, Box 5626, SE-114 86 Stockholm, Sweden
• Tel: +46 8 120 537 00
• E-mail: lotta.haglund@gih.se
- Past President** **Maurella Della Seta**
formerly, Istituto Superiore di Sanità
Viale Regina Elena 299, I-00161 Roma, Italy
• E-mail: maurella.dellaseta@gmail.com
- Vice President** **Tiina Heino**
Meilahti Campus Library Terkko
Helsinki University Library
University of Helsinki
PO Box 61, FI-00014 Helsinki, Finland
• Tel. +358 50 4485626
• E-mail: tiina.m.heino@helsinki.fi
- Treasurer** **Witold Kozakiewicz**
Information and Library Centre
Medical University of Lodz
Muszynskiego 2
90-151 Lodz, Poland
• Tel: +48 42 272 54 01
• E-mail: witold.kozakiewicz@umed.lodz.pl
- Deputy Treasurer** **Aoife Lawton**
Health Service Executive Ireland
Dr. Steevens' Library, Dr. Steevens' Hospital,
Dublin 8, IRELAND.
• Tel: 0876831498
• E-mail: Aoife.lawton@hse.ie
- Board Member** **Alicia Fátima Gómez Sánchez**
TU Wien Bibliothek
Resselgasse 4, A-1040 Wien, Austria
• T +43 1 58801-44101
• E-mail: alicia.gomez@tuwien.ac.at
- Board Member** **Francesca Gualtieri**
Rottapharm Biotech s.r.l., via Valosa di Sopra 9
20900 Monza, Italy
• Tel: +39 9066091
• E-mail: francesca.gualtieri@rottapharmbiotech.com
- Co-opted Board Member** **Astrid Kilvik**
NTNU University Library, The Medicine and Health Library
Olav Kyrres gt 10, NO-7006 Trondheim, Norway
• Tel: 004773412177
• E-mail: astrid.kilvik@ntnu.no
- Co-opted Board Member** **Petra Wallgren Björk**
Karolinska Institutet University Library, 171 77 Stockholm
• Tel: +46852484483
• E-mail: petra.bjork@ki.se
- Administrative Liaison** **Marion Heymans**
Zuyderland Medical Center
Dr H. van der Hoffplein 1, 6162 BG Sittard-Geleen | Henri Dunantstraat 5
6419 PC Heerlen, The Netherlands
• Tel 0031 88 4596006
• Mob. 0031 6 13073056
• E-mail: m.heymans@zuyderland.nl
- JEAHIL Editor** **Federica Napolitani Cheyne** (Observer)
Scientific Communication Unit,
Istituto Superiore di Sanità
• Tel: +39 06 4990 2945
• E-mail: federica.napolitani@iss.it
- EAHIL Secretariat:** NL-3600 BJ Maarssen,
The Netherlands.
• E-mail: eahil-secr@list.ecompass.nl

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