

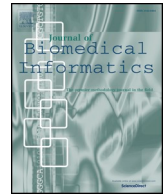


Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Journal of Biomedical Informatics

journal homepage: www.elsevier.com/locate/yjbin

Call for Papers

Special Issue on Novel Informatics Approaches to COVID-19 Research

Due date for submissions: October 15, 2020

Hua Xu^a, David Buckeridge^b, Fei Wang (Guest Editors)^c^a School of Biomedical Informatics, The University of Texas Health Science Center at Houston, Houston, TX USA^b Department of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, Quebec, Canada^c Department of Population Health Sciences, Cornell University, New York, NY USA

The outbreak of the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) started in December 2019 and it was declared a pandemic by the World Health Organization (WHO) on March 11th 2020 [1]. As of May 27th, over 5 million cases and 355,000 deaths have been reported worldwide [2]. In addition to the human health burden, the COVID-19 pandemic has disrupted the global economy and daily life on an unprecedented scale.

Researchers worldwide have acted quickly to combat the pandemic of COVID-19, working from different perspectives such as omics, imaging, clinical, and population health research, to understand the etiology and to identify effective treatment and prevention strategies. Informatics methods and tools have played an important role in research about the COVID-19 pandemic. For example, using virus genomes collected across the world, researchers were able to reconstruct the early evolutionary paths of COVID-19 by genetic network analysis, providing insights to virus transmission patterns [3]. In a clinical context, researchers have developed novel approaches to predict infection with SARS-Cov-2 accurately using lung CT scans and other clinical data [4]. At a population scale, researchers have used Bayesian methods to integrate continental-scale data on mobility and mortality to infer the time-varying reproductive rate and the true number of people infected [5].

This Special Issue aims to highlight the development of novel informatics approaches to collect, integrate, harmonize, and analyze all types of data relevant to COVID-19 in order to accelerate knowledge acquisition and scientific discoveries in COVID-19 research, thus informing better decision making in clinical practice and health policies.

Investigators are encouraged to submit clear and detailed descriptions of their novel methodological results. Topics of interest include, but are not limited to, the following:

- COVID-19 related data processing technologies such as data collection and normalization.

- Novel visualization technologies for COVID-19 outbreak [6].
- Data integration (e.g., linking different types of data) and data sharing (e.g., FAIR principles) for COVID-19 related datasets
- Bioinformatics approaches for sequence analysis of COVID-19, or any omics analysis
- Literature mining to better understand COVID-19 characteristics (e.g., risk factors, incubation time, susceptibility, etc.)
- Computational approaches for drug and vaccine development for COVID-19
- Imaging informatics approaches¹ (e.g., chest X-ray and CT) for diagnoses or prognoses of COVID-19
- Clinical informatics for observational studies using electronic health records, e.g., to support treatment and outcome studies [7]
- Deep learning for predictive modeling of outcomes such as death, ICU admission, intubation, etc.
- Deep phenotyping of COVID-19
- Epidemic monitoring and prediction of transmission by linking multiple sources of data and application of statistical and machine learning methods
- Mobile technologies for monitoring and intervention of COVID-19 transmission
- Informatics approaches to address disparities, fairness and ethical issues of COVID-19 related research
- Methods for determining fake news related to COVID-19 and their influence on public opinion and health policy
- Methods for comparing different predictive models for COVID-19 transmission and evaluating their correctness [8]
- Impact of cultural differences, government policies, geography, genetics, living conditions on human behavior and disease transmission patterns
- Informatics strategies to support public health control activities such as contact tracing and epidemic detection.
- Global tracking of COVID-19 control measures and impacts through

E-mail addresses: hua.xu@uth.tmc.edu (H. Xu), david.buckeridge@mcgill.ca (D. Buckeridge), few2001@med.cornell.edu (F. Wang).

¹ According to JBI, one reason for returning papers without review is that a paper does not deal with the core informatics notions of information and knowledge management. We are looking for novel imaging informatics methods focusing on information/knowledge processing and management. Papers that focus on new numerical methods only (e.g., segmentation algorithms) or papers that apply standard methods (e.g., CNN) to COVID-19 tasks are out of the scope of this special issue.

<https://doi.org/10.1016/j.jbi.2020.103485>

the application of machine learning and other methods to online media and social media.

1. Peer Review Process

All submitted papers must be original and will go through a rigorous peer-review process with at least two reviewers. Papers previously published in conference proceedings will not be considered. JBI's editorial policy will be strictly followed by special issue reviewers. Note in particular that JBI emphasizes the publication of papers that introduce innovative and generalizable methods of interest to the informatics community. Specific applications can be described to motivate the methodology being introduced, but papers that focus solely on a specific application are not suitable for JBI.

2. Submissions

Authors must submit their papers via the online Elsevier Editorial System (EES) at <http://ees.elsevier.com/jbi> by **October 15, 2020**. Authors should select "Informatics in COVID-19 Research" as their submission category and note in a cover letter that their submission is for the "Special Issue on Novel Informatics Approaches to COVID-19 Research." If the manuscript is not intended as an original research paper, the cover letter should also specify if it is, rather, a *Methodological Review, Commentary, or Special Communication*. Authors should make sure to place their work in the context of human-focused biomedical research or health care, and to review carefully the relevant literature.

JBI's editorial policy, and the types of articles that the journal publishes, are outlined under *Aims and Scope* on the journal home page at <https://www.journals.elsevier.com/journal-of-biomedical-informatics> (click on "Read more" for full details). All submissions should follow the guidelines for authors at <https://www.elsevier.com/journals/journal-of-biomedical-informatics/1532-0464/guide-for-authors>, including format and manuscript structure. If the authors speak a first language other than English, editorial assistance by a native English speaker is highly recommended prior to submission. Open-source software code and data should ideally be made available through Internet resources that are enduring. JBI is an

international journal and generalizable contributions from throughout the world are highly encouraged.

Authors will have the opportunity to select whether their accepted paper will be published in JBI or in JBI-X – the new open-access mirror journal of JBI (<https://www.sciencedirect.com/journal/journal-of-biomedical-informatics-x>). For this Special Issue, the publication fee of \$2300 will be waived, if authors of accepted articles select to publish in JBI-X.

JBI and JBI-X recognize that authors want their accepted papers published as soon as possible. Therefore it is JBI and JBI-X policy to publish accepted special issue papers in a regular issue of the journal upon acceptance. The full special issue is then compiled when the last paper has been accepted (see the collection of virtual special issues at <https://www.sciencedirect.com/journal/journal-of-biomedical-informatics/special-issues>). Special issues contain a mix of papers from JBI and JBI-X, depending on the publication preference of the authors.

3. Questions Regarding the Special Issue

Please direct any questions regarding the special issue to Dr. Hua Xu (hua.xu@uth.tmc.edu).

References

- [1] Situation Summary | CDC. <https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/summary.html> (accessed 29 March, 2020).
- [2] Johns Hopkins Coronavirus Resource Center. <https://coronavirus.jhu.edu/map.html> (accessed 27 May, 2020).
- [3] P. Forster, et al., Phylogenetic network analysis of SARS-CoV-2 genomes, *Proc. Natl. Acad. Sci. USA* (2020).
- [4] X. Mei, H.-C. Lee, K.-y. Diao, M. Huang, B. Lin, C. Liu, Z. Xie, et al., "Artificial intelligence-enabled rapid diagnosis of patients with COVID-19.", *Nat. Med.* (2020) 1–5.
- [5] Report 23 - State-level tracking of COVID-19 in the United States. <https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/report-23-united-states/> (accessed 29 May, 2020).
- [6] Lauren N. Carroll, et al., "Visualization and analytics tools for infectious disease epidemiology: A systematic review.", *J. Biomed. Inform.* 51 (2014) 287–298.
- [7] Gregory F. Cooper, et al., "A method for detecting and characterizing outbreaks of infectious disease from clinical reports.", *J. Biomed. Inform.* 53 (2015) 15–26.
- [8] Yirong Chen, et al., "The utility of LASSO-based models for real time forecasts of endemic infectious diseases: A cross country comparison.", *J. Biomed. Inform.* 81 (2018) 16–30.