**Clinical Librarian Service Search Results**

**Request:** In patients who test positive for COVID-19, is there a risk stratification/prognostic indicator that allows mortality to be predicted?

**Summary**

A search of good quality resources has retrieved a small body of literature addressing risk stratification and, primarily, prognostic indicators for mortality and/or severity of disease.

Perhaps the most useful literature retrieved during the search is the brief comparative analysis of clinical risk prediction scores from the Centre for Evidence Based Medicine, (2020).1 A number of individual tools discussed within this analysis are also listed in the results below.2,3,4

A small selection of related literature is also listed below, including a paper, (Hu, et al., 2020)6, *“Comparing rapid scoring systems in mortality prediction of critical* [sic] *ill patients with novel coronavirus disease”.* In this paper, the authors discuss use of the MEWS and REMS scores for predicting mortality.

I hope that I have interpreted your request correctly. Please let me know if you would like me to search further.

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**Feedback**

Once you have read this report, I would appreciate it if you would complete our online literature search feedback form at:

<https://www.smartsurvey.co.uk/s/LiteratureSearchFeedback20202021/>

This relates to this specific search and will help us to monitor and improve our service.

Many Thanks.

Lisa Lawrence

Clinical Librarian

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**Current at:** 18th May 2020.

**Time taken for search:** 3.5 hours.

**Please acknowledge this work in any resulting paper or presentation as:**

Evidence Search: LS50 Risk stratification for C19 mortality. Lisa Lawrence. (18/05/2020). Derby, UK: University Hospitals of Derby & Burton NHS Foundation Trust Library and Knowledge Service.

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**Results**

1. **What prognostic clinical risk prediction scores for COVID-19 are currently available for use in the community setting?**

**Author(s):** Urwin SG, Kandola G, Graziadio S.

**Citation:** Centre for Evidence-Based Medicine, Oxford. April 2020.

**Available at:**

<https://www.cebm.net/covid-19/what-prognostic-clinical-risk-prediction-scores-for-covid-19-are-currently-available-for-use-in-the-community-setting/>

**Source/Database:** Google – CEBM.

1. **COVID-19 Prognostic Tool.**

**Author/Creator:** Mammon B.

**Citation:** QxMD. [Accessed 18/05/2020].

**Available at:** <https://qxmd.com/calculate/calculator_731/covid-19-prognostic-tool>

**Source/Database:** Google - QxMD.

1. **COVID-19 Mortality Risk Calculator.**

**Author/Creator:** Surgisphere.

**Citation:** Surgisphere. [Accessed 18/05/2020].

**Available at:** <https://surgisphere.com/research-tools/mortality.php>

**Source/Database:** Google – Surgisphere.

1. **Predicting Mortality Risk in Patients with Coronavirus or Influenza using Artificial Intelligence.**

**Author/Creator:** Braun H, Patterson D, Molloy A, Davies K.

**Citation:** No citation given. Not peer reviewed. [Accessed 18/05/2020].

**Available at:**

<https://www.i5analytics.com/MortalityRiskinPatientswithCoronavirus.pdf>

**Extract:** *“Overview: About 120,000 people are infected with 2019-nCoV virus and have developed Covid19 at the time of writing (12 th March 2020) [1]. This study researched the mortality risk after admission to hospital for patients with medium to severe symptoms based on length of stay in hospital [2]. The AI that was trained in this paper can be used for health systems to support prioritisation, to inform hospital treatment and to optimise bed management or for people to estimate a level of quarantine based on their medical history. The AI is available online for free on https:\\www.coronavirusrisk.org for individuals accessible with an easy user interface. For processing large population datasets a Webservice endpoint is available from* [*https://www.i5analytics.com/free-healthcare-ai*](https://www.i5analytics.com/free-healthcare-ai)*”.*

**Source/Database:** Google – i5 Analytics.

1. **Coronavirus disease 2019 (COVID-19).**

**Date:** Last updated 18 May 2020.

**Extract:** *“Prognostic scores*

*The APACHE II score was found to be an effective clinical tool to predict hospital mortality in patients with COVID-19, and performed better than SOFA and CURB-65 scores in a small retrospective observational study. An APACHE II score of 17 or more was an early indicator of death and may help provide guidance to make further clinical decisions. Further research is required to confirm these findings, and to validate the use of prognostic scores in patients with COVID-19.*

*New clinical risk scores to predict disease progression and the risk for critical illness in hospitalised patients with COVID-19 have been developed (e.g., COVID-GRAM, CALL score). COVID-GRAM, a web-based calculator to estimate the probability that a patient will develop critical illness (defined as intensive care admission, invasive ventilation, or death) has been validated in a study of nearly 1600 patients in China. It relies on the following 10 variables at admission: chest radiographic abnormality, age, haemoptysis, dyspnoea, unconsciousness, number of comorbidities, cancer history, neutrophil-to-lymphocyte ratio, lactate dehydrogenase, and direct bilirubin. Additional validation studies, especially outside of China, are required”.*

**Source:** BMJ Best Practice.

**Full Text/URL:** <https://bestpractice.bmj.com/topics/en-gb/3000168/prognosis>

1. **Comparing rapid scoring systems in mortality prediction of critical ill patients with novel coronavirus disease.**

**Author(s):** Hu H, Yao N, Qiu Y.

**Citation:** Acad Emerg Med. 2020. Accepted author manuscript. doi: 10.1111/acem.13992

**Available at:** <https://onlinelibrary.wiley.com/doi/abs/10.1111/acem.13992>

**Abstract:** Objectives: Rapid and early severity‐of‐illness assessment appears to be important for critical ill patients with novel coronavirus disease (COVID‐19). This study aimed to evaluate the performance of the rapid scoring system on admission of these patients. Methods: 138 medical records of critical ill patients with COVID‐19 were included in the study. Demographic and clinical characteristics on admission used for calculating Modified Early Warning Score (MEWS) and Rapid Emergency Medicine Score (REMS) and outcomes (survival or death) were collected for each case and extracted for analysis. All patients were divided into two age subgroups (<65 and ≥65years). The receiver operating characteristic curve analyses were performed for overall patients and both subgroups. Results: The median [25%quartile, 75%quartile] of MEWS of survivors versus non‐survivors were 1[1, 2] and 2[1, 3] and that of REMS were 5[2, 6] and 7[6, 10], respectively. In overall analysis, the area under the receiver operating characteristic curve for the REMS in predicting mortality was 0.833 (95% CI: 0.737–0.928), higher than that of MEWS (0.677, 95% CI 0.541–0.813). An optimal cut‐off of REMS (≥6) had a sensitivity of 89.5%, a specificity of 69.8%, a positive predictive value of 39.5%, and a negative predictive value of 96.8%. In the analysis of subgroup of patients aged<65years, the area under the receiver operating characteristic curve for the REMS in predicting mortality was 0.863 (95% CI: 0.743–0.941), higher than that of MEWS (0.603, 95% CI 0.462–0.732). Conclusion: To our knowledge, this study was the first exploration on rapid scoring systems for critical ill patients with COVID‐19. The REMS could provide emergency clinicians with an effective adjunct risk stratification tool for critical ill patients with COVID‐19, especially for the patients aged<65 years. The effectiveness of REMS for screening these patients is attributed to its high negative predictive value.

**Source/Database: WHO global literature on coronavirus disease.**

1. **Prediction models for diagnosis and prognosis of covid-19 infection: systematic review and critical appraisal.**

**Author(s):** Wynants, Laure; Van Calster, Ben; Bonten, Marc M J; Collins, Gary S; Debray, Thomas P A; De Vos, Maarten; Haller, Maria C; Heinze, Georg; Moons, Karel G M; Riley, Richard D; Schuit, Ewoud; Smits, Luc J M; Snell, Kym I E; Steyerberg, Ewout W; Wallisch, Christine; van Smeden, Maarten

**Source:** BMJ (Clinical research ed.); Apr 2020; vol. 369 ; p. m1328

**Publication Type(s):** Research Support, Non-u.s. Gov't Journal Article Systematic Review

**PubMedID:** 32265220

Available at [BMJ (Clinical research ed.)](https://go.openathens.net/redirector/nhs?url=https%3A%2F%2Fwww.bmj.com%2Flookup%2Fdoi%2F10.1136%2Fbmj.m1328) - from BMJ Journals

**Abstract:** OBJECTIVE To review and critically appraise published and preprint reports of prediction models for diagnosing coronavirus disease 2019 (covid-19) in patients with suspected infection, for prognosis of patients with covid-19, and for detecting people in the general population at risk of being admitted to hospital for covid-19 pneumonia. DESIGN Rapid systematic review and critical appraisal. DATA SOURCES PubMed and Embase through Ovid, Arxiv, medRxiv, and bioRxiv up to 24 March 2020. STUDY SELECTION Studies that developed or validated a multivariable covid-19 related prediction model. DATA EXTRACTION At least two authors independently extracted data using the CHARMS (critical appraisal and data extraction for systematic reviews of prediction modelling studies) checklist; risk of bias was assessed using PROBAST (prediction model risk of bias assessment tool). RESULTS 2696 titles were screened, and 27 studies describing 31 prediction models were included. Three models were identified for predicting hospital admission from pneumonia and other events (as proxy outcomes for covid-19 pneumonia) in the general population; 18 diagnostic models for detecting covid-19 infection (13 were machine learning based on computed tomography scans); and 10 prognostic models for predicting mortality risk, progression to severe disease, or length of hospital stay. Only one study used patient data from outside of China. The most reported predictors of presence of covid-19 in patients with suspected disease included age, body temperature, and signs and symptoms. The most reported predictors of severe prognosis in patients with covid-19 included age, sex, features derived from computed tomography scans, C reactive protein, lactic dehydrogenase, and lymphocyte count. C index estimates ranged from 0.73 to 0.81 in prediction models for the general population (reported for all three models), from 0.81 to more than 0.99 in diagnostic models (reported for 13 of the 18 models), and from 0.85 to 0.98 in prognostic models (reported for six of the 10 models). All studies were rated at high risk of bias, mostly because of non-representative selection of control patients, exclusion of patients who had not experienced the event of interest by the end of the study, and high risk of model overfitting. Reporting quality varied substantially between studies. Most reports did not include a description of the study population or intended use of the models, and calibration of predictions was rarely assessed. CONCLUSION Prediction models for covid-19 are quickly entering the academic literature to support medical decision making at a time when they are urgently needed. This review indicates that proposed models are poorly reported, at high risk of bias, and their reported performance is probably optimistic. Immediate sharing of well documented individual participant data from covid-19 studies is needed for collaborative efforts to develop more rigorous prediction models and validate existing ones. The predictors identified in included studies could be considered as candidate predictors for new models. Methodological guidance should be followed because unreliable predictions could cause more harm than benefit in guiding clinical decisions. Finally, studies should adhere to the TRIPOD (transparent reporting of a multivariable prediction model for individual prognosis or diagnosis) reporting guideline. SYSTEMATIC REVIEW REGISTRATION Protocol https://osf.io/ehc47/, registration https://osf.io/wy245.

**Database:** Medline

1. [**Performing risk stratification for COVID-19 when individual level data is not available, the experience of a large healthcare organization**](https://www.medrxiv.org/content/10.1101/2020.04.23.20076976v1)**.**

**Author(s):** Noam Barda, Dan Riesel, Amichay Akriv, Joseph Levi, Uriah Finkel, Gal Yona, Daniel Greenfeld, Shimon Sheiba, Jonathan Somer, Eitan Bachmat, Guy N Rothblum, Uri Shalit, Doron Netzer, Ran Balicer, Noa Dagan.

**Citation: m**edRxiv 2020.04.23.20076976; doi: 10.1101/2020.04.23.20076976

**Available at:** <https://www.medrxiv.org/content/10.1101/2020.04.23.20076976v1>

NB: [This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.](https://www.medrxiv.org/content/what-unrefereed-preprint)

**Abstract:**

With the global coronavirus disease 2019 (COVID-19) pandemic, there is an urgent need for risk stratification tools to support prevention and treatment decisions. The Centers for Disease Control and Prevention (CDC) listed several criteria that define high-risk individuals, but multivariable prediction models may allow for a more accurate and granular risk evaluation. In the early days of the pandemic, when individual level data required for training prediction models was not available, a large healthcare organization developed a prediction model for supporting its COVID-19 policy using a hybrid strategy. The model was constructed on a baseline predictor to rank patients according to their risk for severe respiratory infection or sepsis (trained using over one-million patient records) and was then post-processed to calibrate the predictions to reported COVID-19 case fatality rates. Since its deployment in mid-March, this predictor was integrated into many decision-processes in the organization that involved allocating limited resources. With the accumulation of enough COVID-19 patients, the predictor was validated for its accuracy in predicting COVID-19 mortality among all COVID-19 cases in the organization (3,176, 3.1% death rate). The predictor was found to have good discrimination, with an area under the receiver-operating characteristics curve of 0.942. Calibration was also good, with a marked improvement compared to the calibration of the baseline model when evaluated for the COVID-19 mortality outcome. While the CDC criteria identify 41% of the population as high-risk with a resulting sensitivity of 97%, a 5% absolute risk cutoff by the model tags only 14% to be at high-risk while still achieving a sensitivity of 90%. To summarize, we found that even in the midst of a pandemic, shrouded in epidemiologic "fog of war" and with no individual level data, it was possible to provide a useful predictor with good discrimination and calibration

**Source:** medRxiv.

1. [**Identification and Analysis of Shared Risk Factors in Sepsis and High Mortality Risk COVID-19 Patients**](https://www.medrxiv.org/content/10.1101/2020.05.05.20091918v1)**.**

**Author(s):** Sayoni Das, Krystyna Taylor, Matthew Pearson, James Kozubek, Marcin Pawlowski, Claus Erik Jensen, Zbigniew Skowron, Gert Lykke Møller, Mark Strivens, Steve Gardner.

**Citation:** medRxiv 2020.05.05.20091918; doi: [10.1101/2020.05.05.20091918](https://doi.org/10.1101/2020.05.05.20091918)

Available at: <https://www.medrxiv.org/content/10.1101/2020.05.05.20091918v1>

NB: [This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.](https://www.medrxiv.org/content/what-unrefereed-preprint)

## **Abstract:** BACKGROUND Coronavirus disease 2019 (COVID-19) is a novel coronavirus strain disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The disease is highly transmissible and severe disease including viral sepsis has been reported in up to 16% of hospitalized cases. The admission characteristics associated with increased odds of hospital mortality among confirmed cases of COVID-19 include severe hypoxia, low platelet count, elevated bilirubin, hypoalbuminemia and reduced glomerular filtration rate. These symptoms correlate highly with severe sepsis cases. The diseases also share similar co-morbidity risks including dementia, type 2 diabetes mellitus, coronary heart disease, hypertension and chronic renal failure. Sepsis has been observed in up to 59% of hospitalized COVID-19 patients. It is highly desirable to identify risk factors and novel therapy/drug repurposing avenues for late-stage severe COVID-19 patients. This would enable better protection of at-risk populations and clinical stratification of COVID-19 patients according to their risk for developing life threatening disease. METHODS As there is currently insufficient data available for confirmed COVID-19 patients correlating their genomic profile, disease severity and outcome, co-morbidities and treatments as well as epidemiological risk factors (such as ethnicity, blood group, smoking, BMI etc.), a direct study of the impact of host genomics on disease severity and outcomes is not yet possible. We therefore ran a study on the UK Biobank sepsis cohort as a surrogate to identify sepsis associated signatures and genes, and correlated these with COVID-19 patients. Sepsis is itself a life-threatening inflammatory health condition with a mortality rate of approximately 20%. Like the initial studies for COVID-19 patients, standard genome wide association studies (GWAS) have previously failed to identify more than a handful of genetic variants that predispose individuals to developing sepsis. RESULTS We used a combinatorial association approach to analyze a sepsis population derived from UK Biobank. We identified 70 sepsis risk-associated genes, which provide insights into the disease mechanisms underlying sepsis pathogenesis. Many of these targets can be grouped by common mechanisms of action such as endothelial cell dysfunction, PI3K/mTOR pathway signaling, immune response regulation, aberrant GABA and neurogenic signaling. CONCLUSION This study has identified 70 sepsis related genes, many of them for the first time, that can reasonably be considered to be potentially relevant to severe COVID-19 patients. We have further identified 59 drug repurposing candidates for 13 of these targets that can be used for the development of novel therapeutic strategies to increase the survival rate of patients who develop sepsis and potentially severe COVID-19.

**Source:** medRxiv.

1. **COVID-19 and the role of chronic inflammation in patients with obesity.**

**Author(s):** Chiappetta S, Sharma AM, Bottino V, et al.

**Citation:** Int J Obes. 2020.doi: 10.1038/s41366-020-0597-4

**Available at:** <https://www.nature.com/articles/s41366-020-0597-4.pdf>

**Abstract:** Coronavirus disease 2019 (COVID-19) and the risk of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) poses a particular risk to people living with preexisting conditions that impair immune response or amplify pro-inflammatory response. Low-grade chronic systemic inflammation, common in people with obesity, is associated with the development of atherosclerosis, type 2 diabetes, and hypertension, well known comorbidities that adversely affect the outcomes of patients with COVID-19. Risk stratification based on the Edmonton Obesity Staging System (EOSS), which classifies obesity based on the presence of medical, mental, and/or functional complications rather than on body mass index (BMI), has been shown to be a better predictor of all-cause mortality and it may well be that EOSS stages may better describe the risk of hyperinflammation in patients with COVID-19 infection. Analyzing a group of metabolic ill patients with obesity (EOSS 2 and 3), we found an increased interleukin-6 and linear regression analysis showed a positive correlation with C-reactive protein (CRP) (p = 0.014) and waist-to-hip-ratio (WHR) (p = 0.031). Physicians should be aware of these findings in patients with COVID-19 infection. Early identification of possible hyperinflammation could be fundamental and should guide decision making regarding hospitalization, early respiratory support, and therapy with immunosuppression to improve mortality.

**Source/Database: WHO global literature on coronavirus disease.**

1. **Hypertension in patients with coronavirus disease 2019 (COVID-19): a pooled analysis.**

**Author(s):** Lippi G, Wong J, Henry BM.

**Citation:** Pol Arch Intern Med. 2020. 130(4): 304-309.

**Available at:** <https://www.mp.pl/paim/issue/article/15272>

**Abstract:** Introduction: As the outbreak of coronavirus disease 2019 (COVID-19) was recognized, the clinical predictors of severe or fatal course of the disease should be identified to enable risk stratification and to allocate limited resources optimally. Hypertension has been widely reported to be associated with increased disease severity; however, some studies reported different findings. Objectives: The study aimed to evaluate the association between hypertension and severe and fatal COVID-19. Methods: The Scopus, Medline, and Web of Science databases were searched to identify studies reporting the rate of hypertensive patients in the population diagnosed with severe or nonsevere COVID-19 or in COVID-19 survivors and nonsurvivors. The obtained data were pooled into a meta-analysis to calculate odds ratios (ORs) with 95% CIs. Results: Hypertension was associated with a nearly 2.5-fold increased risk of severe COVID-19 (OR, 2.49; 95% CI, 1.98–3.12; *I*2= 24%), as well as with a similarly significant higher mortality risk (OR, 2.42; 95% CI, 1.51–3.90; *I*2= 0%). In a meta-regression analysis, a correlation was observed between an increase in the mean age of patients with severe COVID-19 and an increased log OR of hypertension and COVID-19 severity (*P* = 0.03). Conclusions: This pooled analysis of the current literature would suggest that hypertension may be associated with an up to 2.5-fold higher risk of severe or fatal COVID-19, especially in older individuals.

**Source/Database: WHO global literature on coronavirus disease.**

1. **Association of Cardiovascular Disease with Coronavirus Disease 2019 (COVID-19) Severity: A Meta-Analysis.**

**Author(s):** Aggarwal G, Cheruiyot I, Aggarwal S, Wong J, Lippi G, Lavie CJ, Henry BM, Sanchis-Gomar F.

**Citation:** Current Problems in Cardiology. 2020. In Press, Corrected Proof. doi: 10.1016/j.cpcardiol.2020.100617

**Available at:**

<https://www.sciencedirect.com/science/article/pii/S0146280620300943?via%3Dihub>

**Abstract:** Observational studies have reported an association between underlying cardiovascular diseases (CVD) and worse prognosis in COVID-19 patients, but this still remains unclear. We conducted a meta-analysis of recent studies that reported the association of CVD with worse prognosis and increased mortality in COVID-19 patients. Literature search through PubMed, the Cochrane Library, and Embase was completed by 2 reviewers from November 1, 2019 to April 20, 2020. Inclusion criteria were observational case-control or cohort studies on COVID-19 patients with a history of CVD included, which reported outcomes of COVID-19 infection severity, clearly outlined the definition of “severe disease” and with sample size >10. Data were abstracted independently by 2 authors. Studies were divided into 2 separate cohorts for analysis: severity (severe vs nonsevere) and mortality (nonsurvivors vs survivors). Data was pooled into a meta-analysis to estimate pooled odds ratio (OR) with 95% confidence interval (95% CI) for each outcome. A total of 18 studies (n = 4858 patients) were included. Sixteen studies were from China, while 2 were from the United States. Pre-existing CVD was associated with a significantly increased risk of a severe form of COVID-19 (OR = 3.14; 95% CI 2.32-4.24; I2 = 0%; Q = 8.68, P= 0.73) and overall risk of COVID-19 all-cause mortality (OR = 11.08; 95% CI: 2.59-47.32; I2 = 55%; P = 0.11). However, this study did not find a significant association between previous history of CVD and mortality in severe COVID-19 disease (OR = 1.72; 95% CI: 0.97-3.06, I2 = 0%, P = 0.46). Pre-existing CVD is associated with worse outcomes among patients with COVID-19. Clinicians and policymakers need to take account of these findings in implementing risk stratification models.

**Source/Database: WHO global literature on coronavirus disease.**

1. **Hematologic, biochemical and immune biomarker abnormalities associated with severe illness and mortality in coronavirus isease 2019 (COVID-19): a meta-analysis.**

**Author(s):** Henry BM, Santos de Oliveira MH, Benoit S, Plebani M, Lippi G.

**Citation:** Clinical Chemistry and Laboratory Medicine. 2020. Ahead of publication. doi: 10.1515/cclm-2020-0369

**Available at:**

<https://www.degruyter.com/view/journals/cclm/ahead-of-print/article-10.1515-cclm-2020-0369/article-10.1515-cclm-2020-0369.xml?tab_body=fullHtml-75008>

**Abstract:** Background As coronavirus disease 2019 (COVID-19) pandemic rages on, there is urgent need for identification of clinical and laboratory predictors for progression towards severe and fatal forms of this illness. In this study we aimed to evaluate the discriminative ability of hematologic, biochemical and immunologic biomarkers in patients with and without the severe or fatal forms of COVID-19. Methods An electronic search in Medline (PubMed interface), Scopus, Web of Science and China National Knowledge Infrastructure (CNKI) was performed, to identify studies reporting on laboratory abnormalities in patients with COVID-19. Studies were divided into two separate cohorts for analysis: severity (severe vs. non-severe and mortality, i.e. non-survivors vs. survivors). Data was pooled into a meta-analysis to estimate weighted mean difference (WMD) with 95% confidence interval (95% CI) for each laboratory parameter. Results A total number of 21 studies was included, totaling 3377 patients and 33 laboratory parameters. While 18 studies (n = 2984) compared laboratory findings between patients with severe and non-severe COVID-19, the other three (n = 393) compared survivors and non-survivors of the disease and were thus analyzed separately. Patients with severe and fatal disease had significantly increased white blood cell (WBC) count, and decreased lymphocyte and platelet counts compared to non-severe disease and survivors. Biomarkers of inflammation, cardiac and muscle injury, liver and kidney function and coagulation measures were also significantly elevated in patients with both severe and fatal COVID-19. Interleukins 6 (IL-6) and 10 (IL-10) and serum ferritin were strong discriminators for severe disease. Conclusions Several biomarkers which may potentially aid in risk stratification models for predicting severe and fatal COVID-19 were identified. In hospitalized patients with respiratory distress, we recommend clinicians closely monitor WBC count, lymphocyte count, platelet count, IL-6 and serum ferritin as markers for potential progression to critical illness.

**Source/Database: WHO global literature on coronavirus disease.**

1. **CT quantification of pneumonia lesions in early days predicts progression to severe illness in a cohort of COVID-19 patients.**

**Author(s):** Liu F, Zhang Q, Huang C, Shi C, Wang L, Shi N, et al.

**Citation:** Theranostics. 2020. 10(12): 5613-5622. doi: 10.7150/thno.45985.

**Available at:** <http://222.thno.org/v10p5613.htm>

**Abstract:** Rationale: Some patients with coronavirus disease 2019 (COVID-19) rapidly develop respiratory failure or even die, underscoring the need for early identification of patients at elevated risk of severe illness. This study aims to quantify pneumonia lesions by computed tomography (CT) in the early days to predict progression to severe illness in a cohort of COVID-19 patients. Methods: This retrospective cohort study included confirmed COVID-19 patients. Three quantitative CT features of pneumonia lesions were automatically calculated using artificial intelligence algorithms, representing the percentages of ground-glass opacity volume (PGV), semi-consolidation volume (PSV), and consolidation volume (PCV) in both lungs. CT features, acute physiology and chronic health evaluation II (APACHE-II) score, neutrophil-to-lymphocyte ratio (NLR), and d-dimer, on day 0 (hospital admission) and day 4, were collected to predict the occurrence of severe illness within a 28-day follow-up using both logistic regression and Cox proportional hazard models. Results: We included 134 patients, of whom 19 (14.2%) developed any severe illness. CT features on day 0 and day 4, as well as their changes from day 0 to day 4, showed predictive capability. Changes in CT features from day 0 to day 4 performed the best in the prediction (area under the receiver operating characteristic curve = 0.93, 95% confidence interval [CI] 0.87~0.99; C-index=0.88, 95% CI 0.81~0.95). The hazard ratios of PGV and PCV were 1.39 (95% CI 1.05~1.84, *P*=0.023) and 1.67 (95% CI 1.17~2.38, *P*=0.005), respectively. CT features, adjusted for age and gender, on day 4 and in terms of changes from day 0 to day 4 outperformed APACHE-II, NLR, and d-dimer. Conclusions: CT quantification of pneumonia lesions can early and non-invasively predict the progression to severe illness, providing a promising prognostic indicator for clinical management of COVID-19.

**Source/Database: WHO global literature on coronavirus disease.**

1. **Prognostic value of NT-proBNP in patients with severe COVID-19.**

**Author(s):** Gao, Lei; Jiang, Dan; Wen, Xue-Song; Cheng, Xiao-Cheng; Sun, Min; He, Bin; You, Lin-Na; Lei, Peng; Tan, Xiao-Wei; Qin, Shu; Cai, Guo-Qiang; Zhang, Dong-Ying

**Source:** Respiratory research; Apr 2020; vol. 21 (no. 1); p. 83

**Publication Type(s):** Journal Article Observational Study

**PubMedID:** 32293449

Available at [Respiratory research](https://respiratory-research.biomedcentral.com/articles/10.1186/s12931-020-01352-w) - from BioMed Central

Available at [Respiratory research](http://europepmc.org/search?query=(DOI:10.1186/s12931-020-01352-w)) - from Europe PubMed Central - Open Access

Available at [Respiratory research](http://search.ebscohost.com/login.aspx?direct=true&scope=site&site=ehost-live&db=mdc&AN=32293449) - from EBSCO (MEDLINE Complete)

Available at [Respiratory research](http://gateway.proquest.com/openurl?ctx_ver=Z39.88-2004&res_id=xri:pqm&req_dat=xri:pqil:pq_clntid=145298&rft_val_fmt=ori/fmt:kev:mtx:journal&genre=article&issn=1465-9921&volume=21&issue=1&spage=83) - from ProQuest (Health Research Premium) - NHS Version

Available at [Respiratory research](https://respiratory-research.biomedcentral.com/track/pdf/10.1186/s12931-020-01352-w) - from Unpaywall

**Abstract:** BACKGROUND The outbreak of coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in China has been declared a public health emergency of international concern. The cardiac injury is a common condition among the hospitalized patients with COVID-19. However, whether N terminal pro B type natriuretic peptide (NT-proBNP) predicted outcome of severe COVID-19 patients was unknown. METHODS The study initially enrolled 102 patients with severe COVID-19 from a continuous sample. After screening out the ineligible cases, 54 patients were analyzed in this study. The primary outcome was in-hospital death defined as the case fatality rate. Research information and following-up data were obtained from their medical records. RESULTS The best cut-off value of NT-proBNP for predicting in-hospital death was 88.64 pg/mL with the sensitivity for 100% and the specificity for 66.67%. Patients with high NT-proBNP values (> 88.64 pg/mL) had a significantly increased risk of death during the days of following-up compared with those with low values (≤88.64 pg/mL). After adjustment for potential risk factors, NT-proBNP was independently correlated with in-hospital death. CONCLUSION NT-proBNP might be an independent risk factor for in-hospital death in patients with severe COVID-19.TRIAL REGISTRATION ClinicalTrials, NCT04292964. Registered 03 March 2020.

**Database:** Medline

1. **Clinical course and risk factors for mortality of adult inpatients with COVID-19 in Wuhan, China: a retrospective cohort study.**

**Author(s):** Zhou, Fei; Yu, Ting; Du, Ronghui; Fan, Guohui; Liu, Ying; Liu, Zhibo; Xiang, Jie; Wang, Yeming; Song, Bin; Gu, Xiaoying; Guan, Lulu; Wei, Yuan; Li, Hui; Wu, Xudong; Xu, Jiuyang; Tu, Shengjin; Zhang, Yi; Chen, Hua; Cao, Bin

**Source:** Lancet (London, England); Mar 2020; vol. 395 (no. 10229); p. 1054-1062

**Publication Type(s):** Journal Article

**PubMedID:** 32171076

Available at [Lancet (London, England)](https://auth.elsevier.com/ShibAuth/institutionLogin?entityID=https://idp.eng.nhs.uk/openathens&appReturnURL=https%3A%2F%2Fwww.clinicalkey.com%2Fcontent%2FplayBy%2Fdoi%2F%3Fv%3D10.1016%2FS0140-6736(20)30566-3) - from ClinicalKey

Available at [Lancet (London, England)](https://doi.org/10.1016/s0140-6736(20)30566-3) - from Unpaywall

**Abstract:** BACKGROUND Since December, 2019, Wuhan, China, has experienced an outbreak of coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Epidemiological and clinical characteristics of patients with COVID-19 have been reported but risk factors for mortality and a detailed clinical course of illness, including viral shedding, have not been well described. METHODS In this retrospective, multicentre cohort study, we included all adult inpatients (≥18 years old) with laboratory-confirmed COVID-19 from Jinyintan Hospital and Wuhan Pulmonary Hospital (Wuhan, China) who had been discharged or had died by Jan 31, 2020. Demographic, clinical, treatment, and laboratory data, including serial samples for viral RNA detection, were extracted from electronic medical records and compared between survivors and non-survivors. We used univariable and multivariable logistic regression methods to explore the risk factors associated with in-hospital death.FINDINGS191 patients (135 from Jinyintan Hospital and 56 from Wuhan Pulmonary Hospital) were included in this study, of whom 137 were discharged and 54 died in hospital. 91 (48%) patients had a comorbidity, with hypertension being the most common (58 [30%] patients), followed by diabetes (36 [19%] patients) and coronary heart disease (15 [8%] patients). Multivariable regression showed increasing odds of in-hospital death associated with older age (odds ratio 1·10, 95% CI 1·03-1·17, per year increase; p=0·0043), higher Sequential Organ Failure Assessment (SOFA) score (5·65, 2·61-12·23; p<0·0001), and d-dimer greater than 1 μg/mL (18·42, 2·64-128·55; p=0·0033) on admission. Median duration of viral shedding was 20·0 days (IQR 17·0-24·0) in survivors, but SARS-CoV-2 was detectable until death in non-survivors. The longest observed duration of viral shedding in survivors was 37 days. INTERPRETATION The potential risk factors of older age, high SOFA score, and d-dimer greater than 1 μg/mL could help clinicians to identify patients with poor prognosis at an early stage. Prolonged viral shedding provides the rationale for a strategy of isolation of infected patients and optimal antiviral interventions in the future. FUNDING Chinese Academy of Medical Sciences Innovation Fund for Medical Sciences; National Science Grant for Distinguished Young Scholars; National Key Research and Development Program of China; The Beijing Science and Technology Project; and Major Projects of National Science and Technology on New Drug Creation and Development.

**Database:** Medline

1. **Risk Factors for Mortality in 244 Older Adults With COVID-19 in Wuhan, China: A Retrospective Study**

**Author(s):** Sun H.; Ning R.; Zhao C.; Meng S.; Tang F.; Tao Y.; Yu C.; Deng X.; Xu D.

**Source:** Journal of the American Geriatrics Society; 2020

**Publication Type(s):** Article

Available at [Journal of the American Geriatrics Society](https://go.openathens.net/redirector/nhs?url=https%3A%2F%2Fonlinelibrary.wiley.com%2Fdoi%2Ffull%2F10.1111%2Fjgs.16533) - from Wiley Online Library Medicine and Nursing Collection 2019 - NHS

**Abstract:** BACKGROUND/OBJECTIVES: Previous studies have reported that older patients may experience worse outcome(s) after infection with severe acute respiratory syndrome coronavirus-2 than younger individuals. This study aimed to identify potential risk factors for mortality in older patients with coronavirus disease 2019 (COVID-19) on admission, which may help identify those with poor prognosis at an early stage. DESIGN: Retrospective case-control. SETTING: Fever ward of Sino-French New City Branch of Tongji Hospital, Wuhan, China. PARTICIPANTS: Patients aged 60 years or older with COVID-19 (n = 244) were included, of whom 123 were discharged and 121 died in hospital. MEASUREMENTS: Data retrieved from electronic medical records regarding symptoms, signs, and laboratory findings on admission, and final outcomes of all older patients with COVID-19, were retrospectively reviewed. Univariate and multivariate logistic regression analyses were used to explore risk factors for death. RESULT(S): Univariate analysis revealed that several clinical characteristics and laboratory variables were significantly different (ie, P <.05) between discharged and deceased patients. Multivariable logistic regression analysis revealed that lymphocyte (LYM) count (odds ratio [OR] = 0.009; 95% confidence interval [CI] = 0.001-0.138; P =.001) and older age (OR = 1.122; 95% CI = 1.007-1.249; P =.037) were independently associated with hospital mortality. White blood cell count was also an important risk factor (P =.052). The area under the receiver operating characteristic curve in the logistic regression model was 0.913. Risk factors for in-hospital death were similar between older men and women. CONCLUSION(S): Older age and lower LYM count on admission were associated with death in hospitalized COVID-19 patients. Stringent monitoring and early intervention are needed to reduce mortality in these patients. Copyright © 2020 The American Geriatrics Society

**Database:** EMBASE

1. **Predictors of mortality for patients with COVID-19 pneumonia caused by SARS-CoV-2: a prospective cohort study**

**Author(s):** Du R.-H.; Yang C.-Q.; Cao T.-Z.; Li M.; Guo G.-Y.; Du J.; Zheng C.-L.; Zhu Q.; Hu M.; Peng P.; Liang L.-R.; Wang W.; Li X.-Y.; Shi H.-Z.

**Source:** The European respiratory journal; May 2020; vol. 55 (no. 5)

**Publication Type(s):** Article

**PubMedID:** 32269088

Available at [The European respiratory journal](https://erj.ersjournals.com/content/erj/early/2020/04/01/13993003.00524-2020.full.pdf) - from Unpaywall

**Abstract:** The aim of this study was to identify factors associated with the death of patients with COVID-19 pneumonia caused by the novel coronavirus SARS-CoV-2.All clinical and laboratory parameters were collected prospectively from a cohort of patients with COVID-19 pneumonia who were hospitalised to Wuhan Pulmonary Hospital (Wuhan City, Hubei Province, China) between 25 December 2019 and 7 February 2020. Univariate and multivariate logistic regression was performed to investigate the relationship between each variable and the risk of death of COVID-19 pneumonia patients.In total, 179 patients with COVID-19 pneumonia (97 male and 82 female) were included in the present prospective study, of whom 21 died. Univariate and multivariate logistic regression analysis revealed that age >=65 years (OR 3.765, 95% CI 1.146-17.394; p=0.023), pre-existing concurrent cardiovascular or cerebrovascular diseases (OR 2.464, 95% CI 0.755-8.044; p=0.007), CD3+CD8+ T-cells <=75 cells.muL-1 (OR 3.982, 95% CI 1.132-14.006; p<0.001) and cardiac troponin I >=0.05 ng.mL-1 (OR 4.077, 95% CI 1.166-14.253; p<0.001) were associated with an increase in risk of mortality from COVID-19 pneumonia. In a sex-, age- and comorbid illness-matched case-control study, CD3+CD8+ T-cells <=75 cells.muL-1 and cardiac troponin I >=0.05 ng.mL-1 remained as predictors for high mortality from COVID-19 pneumonia. We identified four risk factors: age >=65 years, pre-existing concurrent cardiovascular or cerebrovascular diseases, CD3+CD8+ T-cells <=75 cells.muL-1 and cardiac troponin I >=0.05 ng.mL-1 The latter two factors, especially, were predictors for mortality of COVID-19 pneumonia patients. Copyright ©ERS 2020.

**Database:** EMBASE

# Development of a Clinical Decision Support System for Severity Risk Prediction and Triage of COVID-19 Patients at Hospital Admission: an International Multicenter Study

**Author(s):** Guangyao Wu, Pei Yang, Henry C. Woodruff, Xiangang Rao, Julien Guiot, Anne-Noelle Frix, et al.

**Citation:**  medRxiv. doi: https://doi.org/10.1101/2020.05.01.20053413

NB: [This article is a preprint and has not been peer-reviewed [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.](https://www.medrxiv.org/content/what-unrefereed-preprint)

**Available at:** <https://www.medrxiv.org/content/10.1101/2020.05.01.20053413v1>

**Abstract:** IMPORTANCE The outbreak of the coronavirus disease 2019 (COVID-19) has globally strained medical resources and caused significant mortality for severely and critically ill patients. However, the availability of validated nomograms and the machine-learning model to predict severity risk and triage of affected patients is limited. OBJECTIVE To develop and validate nomograms and machine-learning models for severity risk assessment and triage for COVID-19 patients at hospital admission. DESIGN, SETTING, AND PARTICIPANTS A retrospective cohort of 299 consecutively hospitalized COVID-19 patients at The Central Hospital of Wuhan, China, from December 23, 2019, to February 13, 2020, was used to train and validate the models. Six cohorts with 426 patients from eight centers in China, Italy, and Belgium, from February 20, 2020, to March 21, 2020, were used to prospectively validate the models. MAIN OUTCOME AND MEASURES The main outcome was the onset of severe or critical illness during hospitalization. Model performances were quantified using the area under the receiver operating characteristic curve (AUC), accuracy, sensitivity, and specificity. RESULTS Of the 299 hospitalized COVID-19 patients in the retrospective cohort, the median age was 50 years ((interquartile range, 35.5-63.0; range, 20-94 years) and 137 (45.8%) were men. Of the 426 hospitalized COVID-19 patients in the prospective cohorts, the median age was 62.0 years ((interquartile range, 50.0-72.0; range, 19-94 years) and 236 (55.4%) were men. The model was prospectively validated on six cohorts yielding AUCs ranging from 0.816 to 0.976, with accuracies ranging from 70.8% to 93.8%, sensitivities ranging from 83.7% to 100%, and specificities ranging from 41.0% to 95.7%. The cut-off values of the low, medium, and high-risk probabilities were 0.072 and 0.244. The developed online calculators can be found at www.predict19risk.ai. CONCLUSION AND RELEVANCE The machine learning models, nomograms, and online calculators might be useful for the prediction of onset of severe and critical illness among COVID-19 patients and triage at hospital admission. Further prospective research and clinical feedback are necessary to evaluate the clinical usefulness of this model and to determine whether these models can help optimize medical resources and reduce mortality rates compared with current clinical practices.

**Source:** medRxiv.

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**Databases searched:**

* + **Evidence-Based Reviews/Point of Care:** BMJ Best Practice.
  + **Healthcare Databases:** MEDLINE, EMBASE, NICE Evidence.
  + **Other:** Google, Google Scholar, World Health Organization global literature on coronavirus disease, LitCOVID, medRxiv.

**Local Guidance:** Local guidance has not been searched as part of this literature search. However, local guidelines, policies and procedures are available via the red button on the intranet.

**Search Terms:**

|  |  |
| --- | --- |
| ***Subject Headings*** | ***Free Text Words*** |
| Coronavirus Infection | 2019-nCoV |
| Coronavirus Infections | 2019nCoV |
| Mortality | COVID-19 |
| Prognosis | “Corona virus” |
| Risk | Coronavirus |
|  | MERS-CoV |
|  | “Middle East Respiratory Syndrome” |
|  | Mortality |
|  | nCoV |
|  | “novel CoV” |
|  | “novel coronavirus” |
|  | Prognostic indicator |
|  | Prognostic ADJ3 indicator |
|  | Risk stratification |
|  | Risk ADJ3 stratification |
|  | SaO2 |
|  | SARS-CoV |
|  | SARS-CoV-2 |
|  | Sarscov2 |
|  | “Severe Acute Respiratory Syndrome” |

**Search Limits:** English language, 2019-2020.

**Search History:**

**Search Example:**

|  |  |  |  |
| --- | --- | --- | --- |
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| 2 | Medline | exp "CORONAVIRUS INFECTIONS"/ | 12381 |
| 3 | Medline | (1 OR 2) | 29707 |
| 4 | Medline | (risk ADJ3 stratification).ti,ab | 30173 |
| 5 | Medline | exp RISK/ | 1189973 |
| 6 | Medline | (prognostic ADJ3 indicator).ti,ab | 9450 |
| 7 | Medline | exp PROGNOSIS/ | 1640136 |
| 8 | Medline | (4 OR 5 OR 6 OR 7) | 2597769 |
| 9 | Medline | (mortality).ti,ab | 735132 |
| 10 | Medline | exp MORTALITY/ | 376448 |
| 11 | Medline | (9 OR 10) | 978006 |
| 12 | Medline | (3 AND 8 AND 11) | 227 |
| 13 | EMBASE | COVID-19 OR coronavirus OR "Corona virus" OR 2019-nCoV OR SARS-CoV OR MERS-CoV OR "Severe Acute Respiratory Syndrome" OR "Middle East Respiratory Syndrome" OR "novel CoV" OR "novel coronavirus" OR SARS-CoV-2 OR sarscov2 OR 2019nCoV OR (nCOV).ti,ab | 33449 |
| 14 | EMBASE | exp "CORONAVIRUS INFECTION"/ | 13308 |
| 15 | EMBASE | (risk ADJ3 stratification).ti,ab | 52903 |
| 16 | EMBASE | (prognostic ADJ3 indicator).ti,ab | 13113 |
| 17 | EMBASE | exp RISK/ | 2455969 |
| 18 | EMBASE | exp PROGNOSIS/ | 713442 |
| 19 | EMBASE | (15 OR 16 OR 17 OR 18) | 3042916 |
| 20 | EMBASE | (13 OR 14) | 33939 |
| 21 | EMBASE | (19 AND 20) | 3415 |
| 22 | EMBASE | (mortality).ti,ab | 1088448 |
| 23 | EMBASE | exp MORTALITY/ | 1059992 |
| 24 | EMBASE | (22 OR 23) | 1443434 |
| 25 | EMBASE | (21 AND 24) | 819 |
| 26 | EMBASE | 25 [DT 2019-2020] [English language] | 373 |

**Search Date: 18/05/2020**

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