

Limited applicability of a COVID-19 specific mortality prediction rule to the intensive care setting

C. Dupuis ¹², E. De Montmollin^{2,3}, M. Neuville ⁴, B. Mourvillier⁵, S. Ruckly² and J. F. Timsit ^{2,3}

ARISING FROM Yan et al. Nature Machine Intelligence https://doi.org/10.1038/s42256-020-0180-7 (2020)

We read the Article by Yan et al. with great interest. The COVID-19 pandemic has established itself as a major burden on healthcare services worldwide. Scores or algorithms to optimize the use of healthcare resources are of paramount importance. Against this background, Yan et al. gathered samples from a cohort of 485 infected patients in the region of Wuhan, China with a high mortality rate of almost 40% and proposed a simple and operable decision rule based on lactic dehydrogenase (LDH), lymphocytes and high-sensitivity C-reactive protein (hs-CRP) to predict the occurrence of death in the following 10 days.

Since March 2020, France has also been confronted with the COVID-19 pandemic. The decision rule of Yan et al. could be used in our patients, but external repeatability would first be required. To validate the generalizability of the rule, we used data from Outcomerea, a French multicentre cohort of intensive care units (ICUs) involved in the management of patients critically ill with COVID-19. Methods for data collection and the quality of the database have been described in detail elsewhere². Since the beginning of the COVID outbreak in France, a range of specific clinical and biological data for patients with COVID have also been recorded prospectively into this database.

We included 178 patients aged over 18 years who were admitted to the ICU from 1 March 2020 to 1 June 2020 with laboratory-confirmed COVID-19. Patients without a measurement of LDH, hs-CRP or lymphocytes during the first three days after ICU admission were excluded. The main characteristics of our cohort are reported in Table 1. Among the 178 patients, fever was the most common initial symptom (80.8%), followed by dyspnoea (74.2%), cough (63%) and fatigue (43.2%). The median time from symptoms onset to ICU admission was 10 days (range 7-12 days) and the median duration between hospital and ICU admission was 2 days (range 1-3 days). They had a median age of 61 years (range 52-69 years), a median Charlson comorbidity index of 1 (range 0-3) and a median sepsis-related organ failure assessment score (SOFA) score of 5 (range 4-8). The median LDH, hs-CRP levels and percentage of lymphocytes were 453 Uil⁻¹ (range 352–603 Uil⁻¹), 166 mg l⁻¹ (range $92.4-223\,\text{mg}\,l^{-1}$) and 9.6% (range 6.2-15%), respectively. The median ICU length of stay was 11 days (range 6-19 days). At days 14 and 28, the mortality rates were 18% and 34.2%. The results presented in Tables 2 and 3 show that the precision and accuracy of the decision rule were extremely low for the prediction of death.

database	is of the Outcomerea

Characteristics ^a	N=178 patients
Age	61 [52; 69]
Sex (Male)	143 (80.4)
Body mass index (kg cm ⁻²)	28.8 [25.6; 32.4]
Comorbidities	
At least one comorbidity	113 (63.4)
Charlson score	1[0;3]
Liver	6 (3.4)
Cardiovascular	50 (28)
Respiratory	23 (13)
Kidney	22 (12.4)
Immunosuppression	27 (15.2)
Symptoms on onset	
Fever	144 (80.8)
Cough	112 (63)
Fatigue	77 (43.2)
Dyspnoea	132 (74.2)
Diarrhoea	33 (18.6)
Chest distress	16 (9)
Anosmia	12 (6.8)
Arthralgia	17 (9.6)
Time from first symptoms to ICU admission (days)	10 [7; 12]
Time from hospital to ICU admission (days)	2 [1; 3]
Laboratory test on admission	
Neutrophils (×10 ⁹ l ⁻¹)	5,950 [4,000; 9,200]
Lymphocytes (×10° l ⁻¹)	800 [580; 1,110]
Lymphocytes (%)	9.6 [6.2; 15]
High-sensitivity CRP (mg l ⁻¹)	165.6 [92.4; 223]
	Continued

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Table 1 | Characteristics of the 178 patients of the Outcomerea database (continued)

Characteristics ^a	N=178 patients
Ferritin (µg l ⁻¹)	1,213 [745; 2,008.8]
D-dimers (µg l ⁻¹)	1,300 [741; 3,706.8]
LDH (Uil-1)	453 [352; 603]
Severity on admission	
T>39°C	68 (38.2)
Simplified Acute Physiology Score II	33.6 [25; 47]
Sepsis-related Organ Failure Assessment score	5 [4; 8]
Norepinephrine on admission	62 (34.8)
Glasgow Coma Scale < 15	37 (20.8)
Invasive mechanical ventilation on admission	83 (46.6)
PaO ₂ /FiO ₂	179.2 [131.6; 243.6]
$PaO_2/FiO_2 < 200$ (ratio of arterial oxygen partial pressure (PaO_2 in mmHg) to fractional inspired oxygen (FiO_2))	157(88%)
Treatments on admission	
Lopinavir/ritonavir	72 (40.4)
Hydroxychloroquine	21 (11.8)
Corticosteroids	69 (38.8)
During ICU stay	
Invasive mechanical ventilation during ICU stay	115 (64.6)
Any nosocomial infection	60 (33.8)
Bacteremia	35 (19.6)
Hospital-acquired and ventilator-associated pneumonia	54 (30.4)
Outcomes	
ICU ventilatory free days	3 [1; 7]
ICU length of stay	11 [6; 19]
ICU death	58 (32.6)
Mortality at day 60	62 (34.8)
^a Data are presented as N (%) or median [interquartile range, IQI	R].

The least bad results were obtained at day 28, with a precision of 37% (positive predictive value) and an accuracy of 43%, but a recall of 93% (negative predictive value). This decision rule lacked specificity in our preselected cohort of critically ill patients, which could compromise its routine use.

These results could be explained by the real specificity of our cohort. Indeed, only ~5% of patients with COVID-19 are admitted to ICU for acute hypoxemic respiratory failure (AHRF)³. Consequently, our ICU population did not include (1) the vast

Table 3 | Performance of the decision rule of Yan et al. on the French Outcomerea dataset

		Precision	Recall	F1 score	Support ^a
Day 7	Survival	1	0.14	0.24	23
	Death	0.06	1	0.11	155
	Accuracy			0.18	178
Day 14	Survival	0.87	0.14	0.24	23
	Death	0.21	0.92	0.35	155
	Accuracy			0.30	178
Day 28	Survival	0.83	0.16	0.27	23
	Death	0.37	0.93	0.53	155
	Accuracy			0.43	178
^a Predicted number of patients.					

majority of pauci-symptomatic patients with very low LDH and hs-CRP serum levels and high lymphocyte counts (these patients have good outcomes) and (2) some of the most severely ill patients with high hs-CRP and LDH serum levels and low lymphocyte counts, who are not admitted to ICU because of therapeutic limitation (these patients have the worst outcomes). Thus, it is not surprising that the predictive rule of Yan et al. was not accurate in our cohort. However, their proposed biomarkers might be interesting for predicting ICU admission and also death for patients admitted to ICU, but with other thresholds. As a result, we believe that different rules should be adapted to different stages of the illness. For example, a decision tree could be rebuilt in the ICU to predict the occurrence of death. Furthermore, death might not be the most appropriate outcome—worsening of the disease could be better. Another decision rule could be built for patients admitted to the emergency room to predict worsening, that is, the occurrence of severe or critical types of COVID (COS-COVID)4. Finally, as already mentioned by Yan et al., we agree that, for the development of more rigorous prediction models, collaboration and sharing of well-documented individual data for COVID-19 are needed. The predictors already identified, such as LDH, hs-CRP and lym-

Reporting Summary

new models5.

Further information on research design is available in the Nature Research Reporting Summary linked to this article.

phocyte counts, should be considered as candidate predictors for

Data availability

The data that support the findings of this study are available in the Supplementary Information. Source data are provided with this paper.

Table 2 Cor	nfusion matrix fo	or the French O	utcomere	a dataset					
		Day 7			Day 14			Day 28	
					True label				
	Survival	Death	All	Survival	Death	All	Survival	Death	All
Predicted labe	el								
Survival	23	0	23	20	3	23	19	4	23
Death	146	9	155	122	33	155	98	57	155
All	169	9	178	142	36	178	117	61	178

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References

- Yan, L. et al. An interpretable mortality prediction model for COVID-19 patients. Nat. Mach. Intell. 2, 283–288 (2020).
- Dupuis, C. et al. Effect of transfusion on mortality and other adverse events among critically ill septic patients: an observational study using a marginal structural Cox model. Crit. Care Med. 45, 1972–1980 (2017).
- 3. Wu, Z. & McGoogan, J. M. Characteristics of and important lessons from the coronavirus disease 2019 (COVID-19) outbreak in China: summary of a report of 72,314 cases from the Chinese Center for Disease Control and Prevention. *JAMA* 323, 1239–1242 (2020).
- Jin, X. et al. Core outcome set for clinical trials on coronavirus disease 2019 (COS-COVID). Engineering https://doi.org/10.1016/j.eng.2020.03.002 (2020).
- Wynants, L. et al. Prediction models for diagnosis and prognosis of Covid-19: systematic review and critical appraisal. BMJ 369, m1328 (2020).

Author contributions

C.D and J.T.conceived and drafted the letter. C.D. and S.R. analysed the data. C.D., E.M., M.N and B.M. collected data.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary information is available for this paper at https://doi.org/10.1038/s42256-020-00252-4.

Correspondence and requests for materials should be addressed to C.D.

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Sample size	102 patients
Data exclusions	No
Replication	No
Randomization	No
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Population characteristics

We analysed 102 cases of confirmed COVID-19 admitted between the 1st march 2020 and 16 April 2020 in one of 3 ICUs participating in the outcomerea database (Bichat university hospital (APHP, France), Foch hospital (Suresnes, France), Clermont Ferrand University hospital (France). Those patients were included only if the had hsCRP, LDH, Lymphocytes measurments on admission and outcome at Day 28. Only complete case analyses were performed. They had a median age of 59 years [range 52-67], a median Charlson comorbidity index of 1 [range 0-2] and a median SOFA score of 1 [range 0-3]. The median LDH and CRP levels and median percentage of lymphocytes were 503 Ui/L [range 367.7-651], 174 mg/L range [86.5-245] and 9% [range 5.3-13.8], respectively. At days 14 and 28, mortality rates were 15% and 32%, respectively.

Recruitment

It is a retrospective analysis of the prospective outcomerea cohort, including most of the patients with COVID-19 admitted in one of its participating ICU. We only included patients from 3 hospitals (Bichat university hospital, APHP - Clermont Ferrand university hospital, Foch hospital (France)), having LDH, hsCRP and lymphocytes recorded on admission and outcome at day 28 available at the time of the analysis.

Ethics oversight

In accordance with French law, the OutcomeReaTM database was declared to the "Commission Nationale de l'Informatique et des Libertés" (number 999262). The objectives of this data collection were approved by the institutional review board (number 5891) of the Clermont-Ferrand University Hospital (Clermont-Ferrand, France).

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Study protocol	Na						
Data collection	Data came from the Outcomerea database, a French prospective cohort						
Outcomes	Outcome at Day 7, 14 and 28 were recorded (death or alive)						
Dual use research							
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Could the accidental, deli in the manuscript, pose a	berate or reckless misuse of agents or technologies generated in the work, or the application of information presented threat to:						
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Nodels & analysis n/a Involved in the study Functional and/or effective connectivity Graph analysis Multivariate modeling or predictive analysis		
Functional and/or effective conn	Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).	
Graph analysis	Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).	

Specify independent variables, features extraction and dimension reduction, model, training and evaluation

Multivariate modeling and predictive analysis

metrics.