https://doi.org/10.1038/s42256-020-0206-1



Reply to: Clinical interpretation of an interpretable prognostic model for patients with COVID-19

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REPLYING TO D. Giacobbe Nature Machine Intelligence https://doi.org/10.1038/s42256-020-0207-0 (2020)

The article¹ by Giacobbe is very interesting and relevant. They suggest a new research direction regarding the hypothesis that severe bacterial superinfections are a major cause of death in patients with COVID-19. We would be open to exploring this hypothesis with the proposed machine learning approaches², provided that new data becomes available. The new data would need to confirm the existence of bacterial superinfections and quantify the type and severity of the infection. We could then test the impact of bacterial superinfections on COVID-19 mortality and determine how this additional information could improve predictions of patient outcomes. We also agree that ongoing collaboration and discussion between clinicians and machine learning modellers would drive advances in this field.

Received: 27 May 2020; Accepted: 24 June 2020; Published online: 12 August 2020

References

 Giacobbe, D. Clinical interpretation of an interpretable prognostic model for patients with COVID-19. Nat. Mach. Intell. https://doi.org/10.1038/ s42256-020-0207-0 (2020) Yan, L., Zhang, H. & Goncalves, J. et al. An interpretable mortality prediction model for COVID-19 patients. *Nat. Mach. Intell.* 2, 283–288 (2020)

Author contributions

All authors drafted the manuscript, provided critical review of the manuscript and approved the final draft for publication.

Competing interests

The authors declare no competing interests.

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