

Comments on “Frailty As a Significant Predictor of COVID-19 Among Vaccinated Older Adults”

Elahesh Sanjari¹, Hadi Raeisi Shahraki²

¹Shahrekord University of Medical Sciences, Student Research Committee, Shahrekord, Iran

²Shahrekord University of Medical Sciences Faculty of Health, Department of Epidemiology and Biostatistics, Shahrekord, Iran

Dear Editor,

Recently, Hafizoğlu et al. (1) published a paper that showed that frailty is a significant predictor of coronavirus disease-2019 (COVID-19) among vaccinated older adults. Although their study makes a valuable contribution, taking into account some methodological issues to avoid misinterpretation of the study's results is necessary.

Violation of the Proportionality of Hazards (PH) Assumption

The PH in the Cox regression is a critical assumption, which means that the hazard of variables is independent of time. The PH violation leads to unreliable and biased estimates (2). The displayed Kaplan-Meier curves indicate a dramatic violation of the PH assumption due to the crossed curves for the seropositive and age clinical frailty scale (CFS) scores. Therefore, using the Cox regression leads to unreliable estimates.

A Very Low Infection Rate

The Cox regression model was implemented to assess the hazard of COVID-19 infection when the total number of infected participants was lower than 20%. Thus, the event did not occur for most patients, and the nature of the data shows a plateau survival curve, which may be the expected infection rate in the general population. In this situation, Cox regression is no longer applicable, and the cure model must be used. In addition, cure models have more advantages than Cox regression models in terms of both assumptions and applications.

The Lower P-value and Largest Hazard Ratio Doesn't Necessarily Indicate the Strongest Association

Comparing regular hazard ratios to assess the strongest predictor is not true because the types of units and scales differ dramatically among variables. Instead, the authors must use the standardized hazard ratios extracted from the standardized coefficients.

Lack of Prediction Capability Assessment

To demonstrate that high CFS scores among vaccinated older adults should be considered an easy-to-assess, high-risk marker for predicting breakthrough COVID-19 infection, the prediction accuracy of factors must be determined using receiver operating characteristic analysis or other appropriate indices.

In conclusion, the performed statistical analysis by Hafizoğlu et al. (1) may not be appropriate, and the findings must be interpreted with caution.

Keywords: Aging, aging biology, frailty, geriatrics, healthy aging

Ethics

Authorship Contributions

Surgical and Medical Practices: E.S., H.R.S., Concept: E.S., H.R.S., Design: E.S., H.R.S., Data Collection or Processing: E.S., H.R.S., Analysis or Interpretation: E.S., H.R.S., Literature Search: E.S., H.R.S., Writing: E.S., H.R.S.

Address for Correspondence: Hadi Raeisi Shahraki, Shahrekord University of Medical Sciences Faculty of Health, Department of Epidemiology and Biostatistics, Shahrekord, Iran

Phone: +98 383 333 56 53 **E-mail:** raeisi.shahraki_hadi@yahoo.com **ORCID:** orcid.org/0000-0003-3071-5587

Received: 03.03.2024 **Accepted:** 20.05.2024

Cite this article as: Sanjari E, Raeisi Shahraki H. Comments on "Frailty As a Significant Predictor of COVID-19 Among Vaccinated Older Adults". Eur J Geriatr Gerontol. 2024;6(2):163-164



Conflict of Interest: No conflict of interest was declared by the authors.

Financial Disclosure: The authors declared that this study received no financial support.

References

1. Hafizoğlu M, Okyar Baş A, Sertçelik A, Akbıyık F, Oytun Güner M, Şahiner Z, Ceylan S, Balcı C, Doğu BB, Cankurtaran M, Çakır B, Ünal S, Gülhan Halil M. Frailty As a Significant Predictor of COVID-19 Among Vaccinated Older Adults. *Eur J Geriatr Gerontol.* 2024;6:146-152.
2. Zeng Z, Gao Y, Li J, Zhang G, Sun S, Wu Q, Gong Y, Xie C. Violations of proportional hazard assumption in Cox regression model of transcriptomic data in TCGA pan-cancer cohorts. *Comput Struct Biotechnol J.* 2022;20:496-507.