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**Bayesian survival analysis: comparison of survival probability of hormone receptor status for breast cancer data**

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**Abstract:** Survival analysis is a family of statistical procedures for data analysis for which the outcome variable of interest is time until an event occurs. The Cox model is the most widely used survival model in health sciences, but it is not the only model, parametric models in which the distribution of the event is specified in terms of unknown parameters. Over the last few years, there has been increased interest shown in the application of survival analysis based on Bayesian methodology. In this article, we consider Bayesian survival analysis to compare survival probability of hormone receptor status for breast cancer based on lognormal distribution estimated survival function. The Bayesian approach is implemented using WinBugs.

**Keywords:** Bayesian survival analysis; survival function; hormone receptor status; breast cancer.

**Reference** to this paper should be made as follows: Avci, E. (2017) 'Bayesian survival analysis: comparison of survival probability of hormone receptor status for breast cancer data', *Int. J. Data Analysis Techniques and Strategies*, Vol. 9, No. 1, pp.63-74.

**Biographical notes:** Esin Avci is an Assistant Professor specialising in Statistics. She held previous faculty positions at Sinop University as a Research Assistant. Her areas of interest and expertise are in Bayesian survival analysis; and in generalised statistical methods involving count data that contain data dispersion.

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**1 Introduction**

Survival analysis deals with analysis of time duration to until one or more events happen. The Cox proportional hazards (PHs) model is popular model for analysing survival data because it is not based on any assumptions concerning the nature or shape of the underlying survival distribution. The utility of this model stems from the fact that few assumption are needed to determine hazard ratios based on the coefficients. The coefficient is easily interpreted and clinically meaningful (Hosmer and Lemeshow, 1989). There are parametric survival models for which the restrictive assumption of hazards is not required. A parametric survival model is one in which survival time is assumed to follow a known distribution. Exponential, Weibull, lognormal, log-logistic and

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## Original Article

### Prognostic and therapeutic implications of lysyl oxidase and cyclooxygenase 2 expressions in epithelial ovarian carcinoma

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## Abstract

**Background:** New prognostic and predictive biomarkers for better choice and improving the current therapies for ovarian cancer are greatly needed. This study aimed to investigate the prognostic and therapeutic importance of lysyl oxidase (LOX) and cyclooxygenase 2 (COX2) expressions in epithelial ovarian carcinoma.

**Methods:** We performed immunohistochemical analysis on formalin-fixed paraffin sections of epithelial ovarian tumors. The association between their expressions in epithelial ovarian carcinoma (EOC) with the survival as well as response to chemotherapy was analyzed.

**Results:** The frequency of the nuclear expression of LOX and cytoplasmic expression of COX2 was significantly higher in malignant tumors than in benign and borderline tumors. Also, there were statistically significant relationships between pathological grades and both LOX and COX2 positivity in EOC being at the higher end for poorly differentiated tumors. Both LOX and COX2 expressions were also correlated significantly with higher tumor stage. Overexpression of either LOX or COX2 in EOC was significantly associated with poor survival. Moreover, LOX and COX2 positive expressions in EOC were associated with poor response to chemotherapy.

**Conclusions:** The increased expressions of LOX and COX2 in EOC are associated with several adverse clinicopathologic parameters, including reduced survival and chemotherapy resistance thus suggesting a role for such biomarkers in disease progression.

**Keywords:** cancer, cyclooxygenase 2, lysyl oxidase, ovary, prognosis

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RESEARCH

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# A simple chest CT score for assessing the severity of pulmonary involvement in COVID-19

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## Abstract

**Background:** A major role of CT in COVID-19 pneumonia is to assess disease severity and progress. In this study, we aimed to assess the validity, reliability, and survival outcomes of simple chest computed tomography (CT) score in the evaluation of the severity of lung involvement in coronavirus disease 2019 (COVID-19) compared with the current chest CT score.

**Results:** This retrospective analysis included 213 patients (121 men and 92 women; mean age, 46±15.6 years; range, 1–85 years). The ROC curve was used to compare the validity of both scores. Interreader agreement (IRA) for both scores was calculated using Cohen's kappa statistic. The survival analysis of both scores was investigated using the Kaplan–Meier survival analysis. The simple score showed a comparable validity with the current score (AUC = 0.89 and 0.90, respectively;  $p = 0.61$ ). The ROC analysis demonstrated that a simple score of  $> 3$  and a current score of  $> 12$  were potential predictors of death with sensitivity values of 81.8% and 86.4% and specificity values of 96.3% and 93.7%, respectively. The simple score showed a higher IRA compared with the current score ( $k = 0.645$  and  $0.458$ , respectively). Both scores were comparable for predicting survival outcomes.

**Conclusion:** The simple score was non-inferior for predicting survival outcome, compared with the current chest CT score. Furthermore, we suggest that the simple score should be used as it is simpler and more consistent.

**Keywords:** Protein corona, Pneumonia, viral, Tomography, X-ray computed, Validation study, Reproducibility of results

## Background

Since the outbreak and the global spread of acute respiratory syndrome in Wuhan, China, in late December 2019 [1], the World Health Organization has announced coronavirus disease 2019 (COVID-19) as a pandemic in March 2020 [2]. COVID-19 continues spreading all over the world, reaching 215 countries with greater than 115 million cases and 2.5 million deaths as of March 2, 2021 [3], which represents a significant challenge to international health agencies [4]. As of now, the world is facing a second-wave outbreak of COVID-19 [5] that urges us to refine our management plans.

The severity of COVID-19 in patients at risk should be classified to prioritize medical resources in hospitals, especially when resources and medical staff are limited [6]. Several studies have developed severity scoring systems that evaluate the percentage of pulmonary involvement in COVID-19 [7–10]. The computed tomography (CT) severity score (CT-SS) was developed by Yang et al. [7]. The score is an adaptation of a method previously used during the severe acute respiratory syndrome epidemic in 2005 [11]. The 18 segments of both lungs were divided into 20 regions in this score. Then, the lung opacities were subjectively assessed on chest CT in all of the 20 lung regions. Each region was given 0, 1, or 2 points based on the parenchymal opacification involved: 0%, 1–50%, or 51–100%, respectively. The overall

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Characteristic	Joint model	
	longitudinal sub-model	survival sub-model
Age, years	-0.09 (-0.16, -0.02)	-0.02 (-0.03, -0.02)
Sex	0.43 (-1.37, 2.22)	-0.10 (-0.21, 0.02)
Interview	-1.04 (-2.91, 0.82)	-0.20 (-0.32, -0.09)
African-American	6.83 (5.03, 8.68)	0.27 (0.16, 0.38)
ICED (2)	-3.61 (-5.77, -1.45)	-0.31 (-0.46, -0.17)
ICED (3)	-5.61 (-7.62, -3.20)	-0.46 (-0.60, -0.31)
Duration, years	0.07 (-0.13, 0.26)	-0.01 (-0.03, -0.00)
Serum albumin, mg/dl	7.63 (5.08, 10.27)	0.79 (0.62, 0.96)
BWT	-0.01 (-0.18, 0.15)	0.03 (0.02, 0.04)
Sleeping pill	-7.61 (-9.60, -5.62)	-0.11 (-0.23, 0.01)
Time, years	-1.57 (-1.94, -1.21)	-
Plus group	0.79 (-0.92, 2.49)	0.02 (-0.08, 0.13)
Ki/K <sub>0</sub> group	0.34 (-1.37, 2.05)	0.06 (-0.04, 0.17)
Model association <sup>a</sup>	-	0.01 (0.01, 0.02)

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Ibrahim is Associate Professor of Biostatistics at the Harvard School of Public Health and Dana-Farber Cancer Institute; Ming-Hui Chen is Associate Professor of Mathematical Science at Worcester Polytechnic Institute; Debajyoti Sinha is Associate Professor of Biostatistics at the Medical University of South Carolina. doi: The book offers a quite up-to-date view of Bayesian Statistics and accounts extensively for Monte Carlo-based sampling methods and for the various methods of prior elicitation, suitable to cope with non-parametric as well as with semi-parametric models. (Fabio Spizzichino, *Statistics in Medicine*, Vol. The authors provide a collection of theoretical and applied problems in the exercises at the end of each chapter. 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