

the joint frailty-copula model を用いた動的予測

: ワイブル分布による長期予測モデルの検討

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【Background】 A clinical prediction model is often based on patient characteristics measured at the time of treatment or diagnosis. However, more data will be observed under treatments and the patient's disease progression may have changed over time. Therefore, dynamic prediction which allows prediction to update using newly observed data is receiving attention. The joint frailty-copula model was originally proposed by Emura et al. (2017) to conduct personalized dynamic prediction. The model features that the baseline hazard is approximated nonparametrically by splines. However, in this type of nonparametric method, long-term prediction exceeding the largest follow-up time cannot be achieved. Therefore, we proposed a parametrically method based on the Weibull model to achieve long-term prediction.

【Purpose】 The present study aimed to develop a prediction formula based on the joint frailty-copula model with the Weibull distribution, which makes it possible to predict long-term prediction and calculate life expectancy.

【Methodology】 We proposed estimating the baseline hazards r_0 (for progression) and λ_0 (for death) using Weibull distribution. We set $r_0(t) = m_1 a_1 t^{m_1-1}$ and $\lambda_0(t) = m_2 a_2 t^{m_2-1}$, where m is shape parameter and a is scale parameter.

In order to evaluate the proposed prediction formula, we defined the prediction error as the Brier score. We conducted Monte-Carlo simulations to compare the performance of the proposed model with the spline model. In addition, we illustrate this model through the meta-analysis of breast cancer data.

【Result】 In some simulation scenarios, the proposed model performed better than the spline model did. Overall, however, the performances between the two models are comparable. In the illustration of breast cancer data, we showed the plot of probability of death and calculated the life expectancy.

【Discussion】 The proposed parametric model based on the Weibull model makes it possible to calculate long-term prediction exceeding the largest follow-up time. Furthermore, it is possible to give clinically understandable indicators by calculating the life expectancy.