

R Script for Survival Analysis and Hazard Ratio Calculation of β -Catenin Activation in Medulloblastoma

The process of survival analysis using R can be summarized as follows:

1.- Data Preparation

Time-to-event data are extracted from published Kaplan-Meier survival curves and compiled into an Excel file, detailing the time (in years), event status, and group classification. The event status is coded as 1 for the presence of an event (e.g., relapse, censored, or death) and 0 for its absence. Group classification is represented as 1 for the presence and 0 for the absence of β catenin nuclear accumulation.

2.- Reading the Data

The Excel file is imported into R using the *read_excel* function, creating a data frame that organizes the extracted time-to-event data.

3.- Creation of Survival Objects

A survival object is generated using the *surv* function, which takes the time and event status variables as inputs. This object forms the foundation for survival analysis.

4.- Survival Curve Fitting and Plotting

The *survfit* function is applied to the survival object to fit survival curves, while the *ggsurvplot* function is used to visualize the survival data.

5.- Hazard Ratio Calculation

To calculate hazard ratios, a Cox proportional hazards model is applied to the dataset using the *coxph* function. This model estimates the hazard ratio for β -catenin localization, adjusting for relevant covariates where applicable.