**Table2.** Summary of methods used in this study

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Method name** | **Method name in this paper** | **R function name** | **R package name** | **Parameters (default)** |
| Cox | Cox | coxph | survival | NA |
| Cox with backward elimination using AIC | Cox\_bw\_AIC | cph, fastbw | rms | rule="aic", sls=.05,k.aic=2 |
| Cox with backward elimination using p value | Cox\_bw\_p | cph, fastbw | rms | rule="p", sls=.05 |
| Cox with backward elimination using BIC | Cox\_bw\_BIC | cph, fastbw | rms | rule="aic",sls=.05,k.aic = log(as.numeric(table(train$status)[2])) |
| Lasso cox (for clinical datasets) | Lasso\_Cox | penalized | penalized | Lambda1=1, lambda2=0 |
| Ridge cox (for clinical datasets) | Ridge\_Cox | penalized | penalized | Lambda1=0, lambda2=1 |
| Elastic net cox (for clinical datasets) | EN\_Cox | penalized | penalized | Lambda1=1, lambda2=1 |
| Lasso cox (for omics datasets) | Lasso\_Cox | glmnet | glmnet | alpha=1, nfolds = 5,type.measure = "C" |
| Ridge cox (for omics datasets) | Ridge\_Cox | glmnet | glmnet | alpha=0, nfolds = 5,type.measure = "C" |
| Elastic net cox (for omics datasets) | EN\_Cox | glmnet | glmnet | alpha=0.5, nfolds = 5,type.measure = "C" |
| Random survival forest | RSF | rfsrc | RandomSurvivalForest | Default:ntree = 1000,mtry = 10 |
| Multi task logistic regression method | MTLR | mtlr | MTLR | C1=1 |
| DNNSurv (Deep learning survival model) | DNNSurv | multiple functions as in Github codes | DNNSurv | Default: no parameter arguments to be changed by users |
| Boosting cox model | CoxBoost | coxboost | CoxBoost | stepnumber=10, penalty number=100 |
| Cox model with genetic algorithm as feature selection method | Cox (GA) | GenAlg | GenAlgo | n.features=10 (for omics) , n.features=4 (for clinical) , generation\_num=20 |
| Multi task logistic regression model with genetic algorithm as feature selection method | MTLR(GA) | GenAlg | GenAlgo | n.features=10 (for omics) , n.features=4 (for clinical) ,generation\_num=20 |
| Boosting cox model with genetic algorithm as feature selection method | CoxBoost (GA) | GenAlg | GenAlgo | n.features=10 (for omics) , n.features=4 (for clinical) , generation\_num=20 |
| Multi task logistic regression model with ranking based method as feature selection meth | MTLR(DE) | lmFit,eBayes | limma | n.features=10 (for omics) , n.features=4 (for clinical) |
| Boosting cox model with ranking based method as feature selection method | CoxBoost (DE) | lmFit,eBayes | limma | n.features=10 (for omics) , n.features=4 (for clinical) |
| Survival support vector machine | SurvivalSVM | survivalsvm | survivalsvm | Default: sgf.sv = 5, sigf = 7, maxiter = 20, margin = 0.05, bound = 10, eig.tol = 1e-06, conv.tol = 1e-07, posd.tol = 1e-08 |
| DeepSurv (Deep learning survival model) | DeepSurv | deepsurv | survivalmodels | Default: frac = 0.3, activation = "relu",  num\_nodes = c(4L, 8L, 4L, 2L), dropout = 0.1, early\_stopping = TRUE, epochs = 100L,  batch\_size = 32L |
| DeepHit (Deep learning survival model) | DeepHit | deephit | survivalmodels | Default: frac = 0.3, activation = "relu",  num\_nodes = c(4L, 8L, 4L, 2L), dropout = 0.1, early\_stopping = TRUE, epochs = 100L,  batch\_size = 32L |

Data table showing the methods used in this benchmark study. R packages and functions with parameters are listed.