R代码

#install.packages("rms")

#install.packages("pROC")

#install.packages("rmda")

#install.packages("riskRegression")

library(rms)

library(pROC)

library(rmda)

library(readr)

library(riskRegression)

library(glue)

library(foreign)

library(survival)

mydata1<- BPD5\_31\_25

mydata$chorioamnionitis<- factor(mydata$chorioamnionitis)

mydata$NEC<- factor(mydata$NEC)

mydata$sepsis<-factor(mydata$sepsis)

dd=datadist(mydata)

option<-options(datadist="dd")

formula<-as.formula(sepsis ~Invasive\_ventilator\_duration+CRIBII+chorioamnionitis+NEC)

model<-lrm(formula,

data=mydata1,

x= T,

y=T)

model

save(model,file = '/Users/hmoye/Desktop/sepis/model\_data.Rdata')

OR <-exp(model$coefficients)

OR

library(nomogramFormula)

Nomogram\_1<-nomogram(model,

fun = function(x)1/(1+exp(-x)),

lp=F,

fun.at = c(0.1,0.3,0.5,0.7,0.9),

funlabel = "Risk")

plot(Nomogram\_1)

model\_ROC<-glm(formula,data = mydata1,family = binomial())

mydata1$predvalues<-predict(model\_ROC,type = "response")

ROC<-roc(mydata1$sepsis,mydata1$predvalues)

auc(ROC)

ci(auc(ROC))

#校准曲线

cal1<-calibrate(model,method = "boot",B=1000)

plot(cal1,xlim=c(0,1.0),ylim=c(0,1.0))

library(ggDCA)

library(ggplot2)

mydata2<-BPD5\_31

DCA\_training<decision\_curve(sepsis~Invasive\_ventilator\_duration+CRIBII+chorioamnionitis+NEC,

data=mydata2,

#,policy = "opt-in"

study.design='cohort',

thresholds=seq(0,1, by=0.05), bootstraps=1000)

# DCA绘图

plot\_decision\_curve(DCA\_training,

curve.names=c('Nomogram model'),

cost.benefit.axis=FALSE,

col=c("red","#E69F00","#009E73","#D55E33","#CC79A7"),

confidence.intervals=FALSE,

standardize=FALSE,

legend.position=c("topright"))

# CIC绘图

plot\_clinical\_impact(DCA\_training,population.size=1000,

cost.benefit.axis=T,

n.cost.benefits=8,

col=c('red','blue'),

confidence.intervals=F)

library(rms)

#加载R语言中的rms包

mydata4<- mydata2

f1 <- glm(sepsis ~Invasive\_ventilator\_duration+CRIBII+chorioamnionitis+NEC,

data = mydata4, family = binomial(link = "logit"))

P1 <- predict(f1, type = "response")

val.prob(P1, mydata4$sepsis)