The crucial codes are as follows:

library(tableone)

library(plyr)

library(survival)

library(survminer)

library(MatchIt)

library(ggDCA)

library(dcurves)

library(foreign)

library(tidyr)

library(dplyr)

library(rms)

library(pec)

library(prodlim)

#######################

vars <- c("Age","Race","Surgery","Marital", "Radiation","Chemotherapy","brainMeta","liverMeta",

 "lungMeta","Grade", "Gleason","PSA", "TStage","N")

catvars <- c("Age","Race","Surgery","Marital", "Radiation","Chemotherapy","brainMeta","liverMeta",

 "lungMeta","Grade", "Gleason","PSA", "TStage","N")

tableone <- CreateTableOne(vars = vars,factorVars = catvars,strata="cohort",data = data)

table1 <- print(tableone, contdigits=3,pDigits =4,showAllLevels = TRUE, quote = FALSE, noSpace = TRUE, printToggle = FALSE)

write.csv(table1,"table1.csv")

tableall<- CreateTableOne(vars = vars,factorVars = catvars,data = data)

table0 <- print(tableall, contdigits=3,pDigits =4,showAllLevels = TRUE, quote = FALSE, noSpace = TRUE, printToggle = FALSE)

########Univariate COX regression#####################

y<- Surv(time = aa$Survival,event = aa$CSS==0)

Uni\_cox\_model<- function(x){

 FML <- as.formula(paste0 ("y~",x))

 cox<- coxph(FML,data=aa)

 cox1<-summary(cox)

 HR <- round(cox1$coefficients[,2],2)

 PValue <- round(cox1$coefficients[,5],3)

 CI5 <-round(cox1$conf.int[,3],2)

 CI95 <-round(cox1$conf.int[,4],2)

 Uni\_cox\_model<- data.frame(

 names <-rownames(cox1$conf.int),

 'HR' = HR,

 'CI5' = CI5,

 'CI95' = CI95,

 'P' = PValue)

 return(Uni\_cox\_model)

}

names(aa)

variable.names<- colnames(aa)[c(1,3:4,12:18,20:21,24:26)];variable.names

Uni\_cox <- lapply(variable.names, Uni\_cox\_model)

Uni\_cox<- ldply(Uni\_cox, data.frame)

Uni\_cox$HR.CI95<-paste0(Uni\_cox$HR," (",Uni\_cox$CI5,'-',Uni\_cox$CI95,")");Uni\_cox

write.csv(Uni\_cox)

yos<- Surv(time = aa$Survival,event = aa$OS==0)

Uni\_cox\_modelos<- function(x){

 FMLos <- as.formula(paste0 ("yos~",x))

 coxos<- coxph(FMLos,data=aa)

 cox1os<-summary(coxos)

 HR <- round(cox1os$coefficients[,2],2)

 PValue <- round(cox1os$coefficients[,5],3)

 CI5 <-round(cox1os$conf.int[,3],2)

 CI95 <-round(cox1os$conf.int[,4],2)

 Uni\_cox\_modelos<- data.frame(

 names <-rownames(cox1os$conf.int),

 'HR' = HR,

 'CI5' = CI5,

 'CI95' = CI95,

 'P' = PValue)

 return(Uni\_cox\_modelos)

}

variable.names<- colnames(aa)[c(1,3:4,12:18,20:21,24:26)];variable.names

Uni\_coxos <- lapply(variable.names, Uni\_cox\_modelos)

Uni\_coxos<- ldply(Uni\_coxos, data.frame)

Uni\_coxos$HR.CI95<-paste0(Uni\_coxos$HR," (",Uni\_coxos$CI5,'-',Uni\_coxos$CI95,")");Uni\_coxos

write.csv(Uni\_coxos)

#######Multivariate COX regression#######

mul\_cox<-coxph(Surv(time = aa$Survival,event = aa$CSS==0)~ Age+Race+Marital+Surgery+Radiation+Chemotherapy+Grade+Gleason+PSA+TStage+N+liverMeta+lungMeta+brainMeta,data=aa)

summary(mul\_cox)

coxcss1<-summary(mul\_cox)

coxcss1$coefficients

coxcss1$conf.int

mul\_HR<- round(coxcss1$coefficients[,2],2)

mul\_PValue<- round(coxcss1$coefficients[,5],4)

mul\_CI1<-round(coxcss1$conf.int[,3],2)

mul\_CI2<-round(coxcss1$conf.int[,4],2)

mul\_CI95<-paste(mul\_CI1,'-',mul\_CI2)

mul\_coxcss1 <- data.frame("HR" =mul\_HR,

 "CI95" =mul\_CI95,

 "P"=mul\_PValue);mul\_coxcss1

mul\_cox3<-coxph(Surv(time = aa$Survival,event = aa$OS==0)~ Age+Race+Marital+Surgery+Grade+Gleason+Radiation+Chemotherapy+PSA+TStage+N+liverMeta+lungMeta+brainMeta,data=aa)

summary(mul\_cox3)

coxos<-summary(mul\_cox3)

coxos$coefficients

coxos$conf.int

mul\_HR<- round(coxos$coefficients[,2],2)

mul\_PValue<- round(coxos$coefficients[,5],4)

mul\_CI1<-round(coxos$conf.int[,3],2)

mul\_CI2<-round(coxos$conf.int[,4],2)

mul\_CI95<-paste(mul\_CI1,'-',mul\_CI2)

mul\_coxos <- data.frame("HR" =mul\_HR,

 "CI95" =mul\_CI95,

 "P"=mul\_PValue);mul\_coxos

####K-M survival curves using age, surgery and chemotherapy for examples#######

kmcssage<-survfit(Surv(time = aa$Survival,event =aa$CSS==0)~Age,data=aa)

summary(kmcssage)

summary(kmcssage,time=c(36,60))

ggsurvplot(kmcssage,

 pval=TRUE,

 pval.coord = c(0, 0.4),

 xlab="Survival Months",

 ylab="Cancer Specific Survival",

 legend= "left",

 break.x.by=12,

 xlim=c(0,96),

 pval.size =5,

 risk.table=TRUE,

 risk.table.height = 0.25,

 palette="lancet",

 title="CSS (n=5,120)",

 legend.labs=c("＞81yrs","≤73yrs","74-81yrs"),

 legend.title="Age",

 surv.median.line = "hv")

kmosage<-survfit(Surv(time = aa$Survival,event =aa$OS==0)~Age,data=aa)

summary(kmosage)

summary(kmosage,time=c(36,60))

ggsurvplot(kmosage,

 pval=TRUE,

 pval.coord = c(0, 0.4),

 xlab="Survival Months",

 ylab="Overall Survival",

 legend= "left",

 break.x.by=12,

 xlim=c(0,96),

 pval.size =5,

 risk.table=TRUE,

 risk.table.height = 0.25,

 palette="lancet",

 title="OS (n=5,120)",

 legend.labs=c("＞81yrs","≤73yrs","74-81yrs"),

 legend.title="Age",

 surv.median.line = "hv")

kmcss1<-survfit(Surv(time = aa$Survival,event =aa$CSS==0)~Surgery,data=aa)

summary(kmcss1)

summary(kmcss1,time=c(36,60))

ggsurvplot(kmcss1,

 pval=TRUE,

 pval.coord = c(0, 0.4),

 xlab="Survival Months",

 ylab="Cancer Specific Survival",

 legend= "left",

 break.x.by=12,

 xlim=c(0,96),

 pval.size =5,

 risk.table=TRUE,

 risk.table.height = 0.25,

 palette="lancet",

 title="CSS (n=5,120)",

 legend.labs=c("No","Local Surgery","Radical Surgery"),

 legend.title="Surgery",

 surv.median.line = "hv")

kmos1<-survfit(Surv(time = aa$Survival,event =aa$OS==0)~Surgery,data=aa)

summary(kmos1)

summary(kmos1,time=c(36,60))

ggsurvplot(kmos1,

 pval=TRUE,

 pval.coord = c(0, 0.4),

 xlab="Survival Months",

 ylab="Overall Survival",

 legend= "left",

 break.x.by=12,

 xlim=c(0,96),

 pval.size =5,

 risk.table=TRUE,

 risk.table.height = 0.25,

 palette="lancet",

 title="OS (n=5,120)",

 legend.labs=c("No","Local Surgery","Radical Surgery"),

 legend.title="Surgery",

 surv.median.line = "hv")

kmcssct<-survfit(Surv(time = aa$Survival,event =aa$CSS==0)~Chemotherapy,data=aa)

summary(kmcssct)

summary(kmcssct,time=c(36,60))

ggsurvplot(kmcssct,

 pval=TRUE,

 pval.coord = c(0, 0.4),

 xlab="Survival Months",

 ylab="cancer-Specific Survival",

 legend= "left",

 break.x.by=12,

 xlim=c(0,96),

 pval.size =5,

 risk.table=TRUE,

 risk.table.height = 0.25,

 palette="lancet",

 title="CSS (n=5,120)",

 legend.labs=c("No/Unknown","Yes"),

 legend.title="Chemotherapy",

 surv.median.line = "hv")

kmos2<-survfit(Surv(time = aa$Survival,event =aa$OS==0)~Chemotherapy,data=aa)

summary(kmos2)

summary(kmos2,time=c(36,60))

ggsurvplot(kmos2,

 pval=TRUE,

 pval.coord = c(0, 0.4),

 xlab="Survival Months",

 ylab="Overall Survival",

 legend= "left",

 break.x.by=12,

 xlim=c(0,96),

 pval.size =5,

 risk.table=TRUE,

 risk.table.height = 0.25,

 palette="lancet",

 title="OS (n=5,120)",

 legend.labs=c("No/Unknown","Yes"),

 legend.title="Chemotherapy",

 surv.median.line = "hv")

########PSM screens matching participants, taking Chemothrapy stratification as example####################

vars <- c("Age","Race","Surgery","Marital", "Radiation","Chemotherapy","brainMeta","liverMeta","lungMeta","Grade", "Gleason","PSA", "TStage","N")

catvars <- c("Age","Race","Surgery","Marital", "Radiation","Chemotherapy","brainMeta","liverMeta",

 "lungMeta","Grade", "Gleason","PSA", "TStage","N")

tabletwo <- CreateTableOne(vars = vars,factorVars = catvars,strata="Chemotherapy",data = aa)

table2 <- print(tabletwo, contdigits=3,pDigits =4,showAllLevels = TRUE,

 quote = FALSE, noSpace = TRUE, printToggle = FALSE)

tableall2<- CreateTableOne(vars = vars,factorVars = catvars,data = aa)

table00 <- print(tableall2, contdigits=3,pDigits =4,showAllLevels = TRUE, quote = FALSE,

 noSpace = TRUE, printToggle = FALSE)

aa$Chemotherapy <- as.factor(aa$Chemotherapy)

m.out <- matchit(Chemotherapy ~ Age + Surgery + Marital+liverMeta+lungMeta +Gleason+N+Grade,

 method = "nearest", ratio =1, data = aa,

 distance = "logit", replace = FALSE)

summary(m.out)

aamatched<- match.data(m.out)

library(tableone)

vars <- c("Age","Race","Surgery","Marital", "Radiation","Chemotherapy","brainMeta","liverMeta",

 "lungMeta","Grade", "Gleason","PSA", "TStage","N")

catvars <-

c("Age","Race","Surgery","Marital", "Radiation","Chemotherapy","brainMeta","liverMeta",

 "lungMeta","Grade", "Gleason","PSA", "TStage","N")

table3 <- CreateTableOne(vars = vars,factorVars = catvars,strata="Chemotherapy",

 addOverall = TRUE, data = aamatched)

tablematched <- print(table3, showAllLevels = TRUE, quote = FALSE, noSpace = TRUE, printToggle = FALSE)

mm=aamatched

ym<- Surv(time = mm$Survival,event = mm$CSS==0)

Uni\_coxm<- function(x){

 FMLm <- as.formula(paste0 ("ym~",x))

 coxm<- coxph(FMLm,data=mm)

 cox1m<-summary(coxm)

 HR <- round(cox1m$coefficients[,2],2)

 PValue <- round(cox1m$coefficients[,5],3)

 CI5 <-round(cox1m$conf.int[,3],2)

 CI95 <-round(cox1m$conf.int[,4],2)

 Uni\_coxm<- data.frame(

 names <-rownames(cox1m$conf.int),

 'HR' = HR,

 'CI5' = CI5,

 'CI95' = CI95,

 'P' = PValue)

 return(Uni\_coxm)

}

variable.names<- colnames(mm)[c(1,3:4,12:18,20:21,24:26)];variable.names

library(plyr)

Uni\_coxpsm <- lapply(variable.names, Uni\_coxm)

Uni\_coxpsm<- ldply(Uni\_coxpsm, data.frame)

Uni\_coxpsm$HR.CI95<-paste0(Uni\_coxpsm$HR," (",Uni\_coxpsm$CI5,'-',Uni\_coxpsm$CI95,")");Uni\_coxpsm

library(survival)

ymos<- Surv(time = mm$Survival,event = mm$OS==0)

Uni\_coxmos<- function(x){

 FMLmos <- as.formula(paste0 ("ymos~",x))

 coxmos<- coxph(FMLmos,data=mm)

 cox2<-summary(coxmos)

 HR <- round(cox2$coefficients[,2],2)

 PValue <- round(cox2$coefficients[,5],3)

 CI5 <-round(cox2$conf.int[,3],2)

 CI95 <-round(cox2$conf.int[,4],2)

 Uni\_coxmos<- data.frame(

 names <-rownames(cox2$conf.int),

 'HR' = HR,

 'CI5' = CI5,

 'CI95' = CI95,

 'P' = PValue)

 return(Uni\_coxmos)

}

Uni\_coxpsmos <- lapply(variable.names, Uni\_coxmos)

Uni\_coxpsmos<- ldply(Uni\_coxpsmos, data.frame)

Uni\_coxpsmos$HR.CI95<-paste0(Uni\_coxpsmos$HR," (",Uni\_coxpsmos$CI5,'-',Uni\_coxpsmos$CI95,")");Uni\_coxpsmos

###Multivariate COX regression after PSM(chemotherapy stratification)#####

mul\_coxm<-coxph(Surv(time = mm$Survival,event = mm$CSS==0)~ Age+Race+Marital+Surgery+Radiation+Chemotherapy+Grade+Gleason+PSA+TStage+N+liverMeta+lungMeta+brainMeta,

data=mm)

summary(mul\_coxm)

coxcssm<-summary(mul\_coxm)

coxcssm$coefficients

coxcssm$conf.int

mul\_HR<- round(coxcssm$coefficients[,2],2)

mul\_PValue<- round(coxcssm$coefficients[,5],4)

mul\_CI1<-round(coxcssm$conf.int[,3],2)

mul\_CI2<-round(coxcssm$conf.int[,4],2)

mul\_CI95<-paste(mul\_CI1,'-',mul\_CI2)

mul\_coxcssm <- data.frame("HR" =mul\_HR,

 "CI95" =mul\_CI95,

 "P"=mul\_PValue);mul\_coxm

mul\_coxmos<-coxph(Surv(time = mm$Survival,event = mm$OS==0)~ Age+Race+Marital+Surgery+Radiation+Chemotherapy+Grade+Gleason+PSA+TStage+N+liverMeta+lungMeta+brainMeta,data=mm)

summary(mul\_coxmos)

coxcssm2<-summary(mul\_coxmos)

coxcssm2$coefficients

coxcssm2$conf.int

mul\_HR<- round(coxcssm2$coefficients[,2],2)

mul\_PValue<- round(coxcssm2$coefficients[,5],4)

mul\_CI1<-round(coxcssm2$conf.int[,3],2)

mul\_CI2<-round(coxcssm2$conf.int[,4],2)

mul\_CI95<-paste(mul\_CI1,'-',mul\_CI2)

mul\_coxcssm2 <- data.frame("HR" =mul\_HR,

 "CI95" =mul\_CI95,

 "P"=mul\_PValue);mul\_coxmos

###Nomogram、Calibration Curve######

nomo<-datadist(aa)

options(datadist='nomo')

nomo0 <- cph(Surv(time = aa$Survival,event =aa$CSS==0)~Age+Race+Marital+Surgery+Chemotherapy+Grade+Gleason+PSA+

 TStage+liverMeta+lungMeta,

 x=T,y=T,

 data=aa,

 surv=T,

 time.inc = 12\*3);nomo0

Cindex0 <- rcorrcens(Surv(as.numeric(aa$Survival),aa$CSS==0)~predict(nomo0))

surv <- Survival(nomo0)

surv1 <- function(x)surv(12\*3,lp=x)

surv2 <- function(x)surv(12\*5,lp=x)

nomo1<-nomogram(nomo0,

 fun=list(surv1,surv2),

 funlabel=c('3-year Cancer-Spefic Survival',

 '5-year Cancer-Specific Survival'),

 lp =F,

 maxscale=100,

 fun.at=c("0.99","0.95",'0.9','0.8',

 '0.7','0.6','0.5','0.4',

 '0.3','0.2','0.1')

);plot(nomo1,col.grid = gray(c(0.8,0.95)), xfrac = 0.35,cex.var = 1,cex.axis=0.8, tcl=-0.3,lmgp=0.3)

nomoos <- cph(Surv(time = aa$Survival,event =aa$OS==0)~Age+Race+Marital+Grade+Gleason+PSA+Surgery+

 Chemotherapy+TStage+liverMeta+lungMeta+brainMeta,

 x=T,y=T,

 data=aa,

 surv=T,

 time.inc = 12\*3);nomoos

Cindexos <- rcorrcens(Surv(as.numeric(aa$Survival),aa$OS==0)~predict(nomoos))

survos <- Survival(nomoos)

survos1 <- function(x)survos(12\*3,lp=x)

survos2 <- function(x)survos(12\*5,lp=x)

nomo2<-nomogram(nomoos,

 fun=list(survos1,survos2),

 funlabel=c('3-year Overall Survival',

 '5-year Overall Survival'),

 lp =F,

 maxscale=100,

 fun.at=c("0.99","0.95",'0.9','0.8',

 '0.7','0.6','0.5','0.4',

 '0.3','0.2','0.1')

);plot(nomo2,col.grid = gray(c(0.8,0.95)), xfrac = 0.35,cex.var = 1,cex.axis=0.8, tcl=-0.3,lmgp=0.3)

p <- calibrate(nomo0,

 cmethod='KM',

 method='boot',

 u=12\*3,

 m=1700,

 B=1000)

plot(p,

 add=F,

 conf.int=T,

 subtitles = F,

 cex.subtitles=0.8,

 lwd=2,

 lty=1,

 errbar.col="blue",

 xlim=c(0.1,0.8),

 ylim=c(0.1,0.8),

 xlab="Nomogram Predicted 3-year Cancer-Specific Survival in Training Cohort",

 ylab="Actual 3-year Survival",

 col="blue")

p <- calibrate(nomoos,

 cmethod='KM',

 method='boot',

 u=12\*3,

 m=1700,

 B=1000)

plot(p,

 add=F,

 conf.int=T,

 subtitles = F,

 cex.subtitles=0.8,

 lwd=2,

 lty=1,

 errbar.col="blue",

 xlim=c(0.1,0.8),

 ylim=c(0.1,0.8),

 xlab="Nomogram Predicted 3-year Overall Survival in Training Cohort",

 ylab="Actual 3-year Survival",

 col="blue")

#####Decision Curve##############

f1 <- coxph(Surv(Survival, CSS==0) ~Age+Race+Marital+Gleason+PSA+Surgery+Grade+Chemotherapy+TStage+liverMeta+lungMeta,

 data = aa)

aa$Nomogram= c(1- (summary(survfit(f1, aa), times=36)$surv))

dca(Surv(Survival, CSS==0)~Nomogram,

 data = aa,

 time = 36,

 thresholds = 1:100/ 100) %>%

 standardized\_net\_benefit() %>%

 plot(smooth = T)

f2 <- coxph(Surv(Survival, CSS==0) ~Age+Race+Marital+Gleason+PSA+Surgery+Grade+Chemotherapy+TStage+liverMeta+lungMeta,

 data = aa)

aa$Nomogram= c(1- (summary(survfit(f2, aa), times=60)$surv))

dca(Surv(Survival, CSS==0)~Nomogram,

 data = aa,

 time = 60,

 thresholds = 1:100/ 100) %>%

 standardized\_net\_benefit() %>%

 plot(smooth = T)

f3 <- coxph(Surv(Survival, OS==0) ~Age+Race+Marital+Gleason+PSA+Surgery+Grade+Chemotherapy+

 TStage+liverMeta+lungMeta+brainMeta,

 data = aa)

aa$Nomogram= c(1- (summary(survfit(f3, aa), times=36)$surv))

dca(Surv(Survival, OS==0)~Nomogram,

 data = aa,

 time = 36,

 thresholds = 1:100/ 100) %>%

 standardized\_net\_benefit() %>%

 plot(smooth = T)

f4 <- coxph(Surv(Survival, OS==0) ~Age+Race+Marital+Gleason+PSA+Surgery+Grade+Chemotherapy+

 TStage+liverMeta+lungMeta+brainMeta,

 data = aa)

aa$Nomogram= c(1- (summary(survfit(f4, aa), times=60)$surv))

dca(Surv(Survival, OS==0)~Nomogram,

 data = aa,

 time = 60,

 thresholds = 1:100/ 100) %>%

 standardized\_net\_benefit() %>%

 plot(smooth = T)