

```

library(survival)
library(rms)
library(pec)
library(dplyr)
library(ggDCA)
library(ggplot2)
library(foreign)
library(regplot)
library(DynNom)
library(timeROC)
setwd("D://Rdata")
data<-read.csv("all1.csv")
names(data)
str(data)
data$Sex <- factor(data$Sex,levels=c(1,2),labels=c("Male","Female"))
data$Race <- factor(data$Race,levels=c(1,2,3,4),labels=c("White", "Black", "Asian or Pacific Islander", "American
Indian/Alaska Native"))
data$Marital_status <- factor(data$Marital_status,levels=c(0,1,2),labels=c("Single", "Married",
"Divorced/Widowed/Separated"))
data$ICD_O_3 <-
factor(data$ICD_O_3,levels=c(9180.3,9181.3,9182.3,9183.3,9184.3,9185.3,9186.3,9187.3,9192.3,9193.3,9194.3),labels
=c("Osteosarcoma, NOS", "Chondroblastic osteosarcoma", "Fibroblastic osteosarcoma", "Telangiectatic
osteosarcoma", "Osteosarcoma in Paget disease of bone", "Small cell osteosarcoma", "Central osteosarcoma",
"Intraosseous well differentiated osteosarcoma", "Parosteal osteosarcoma", "Periosteal osteosarcoma", "High grade
surface osteosarcoma"))
data$Primary_Site <- factor(data$Primary_Site,levels=c(1,2,3),labels=c("Extremities", "Pelvis/Spine", "Skull/Mandible
and others"))
data$Grade <- factor(data$Grade,levels=c(1,2,3),labels=c("Grade I/II", "Grade III/IV", "Unknown"))
data$Laterality <- factor(data$Laterality,levels=c(0,1,2),labels=c("Not a paired site (axial)", "Left - origin of
primary", "Right - origin of primary"))
data$AJCC_stage <- factor(data$AJCC_stage,levels=c(1,2,3,4),labels=c("I", "II", "III", "IV"))
data$AJCC_T <- factor(data$AJCC_T,levels=c(1,2,3),labels=c("T1", "T2", "T3"))
data$AJCC_N <- factor(data$AJCC_N,levels=c(0,1),labels=c("N0", "N1"))
data$AJCC_M <- factor(data$AJCC_M,levels=c(0,1),labels=c("M0", "M1"))
data$Surgery_code <- factor(data$Surgery_code,levels=c(1,2,3,4,5),labels=c("Local or partial resection", "Radical
resection with limb salvage", "Amputation", "Forequarter/hindquarter/hemipelvectomy", "Surgery, NOS"))
data$Radiation <- factor(data$Radiation,levels=c(0,1),labels=c("None/unknown", "Yes"))
data$Chemotherapy <- factor(data$Chemotherapy,levels=c(0,1),labels=c("No/Unknown", "Yes"))
data.1<-data[1:1057, c(1:22)]
data.2<-data[1058:2114, c(1:22)]
data.3<-data[2115:2179, c(1:22)]

#The following is the nomogram code for OS
res.cox <- coxph(Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1)
summary(res.cox)
coxph(formula = Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1)
dd<-datadist(data)
options(datadist="dd")
f=cph(Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1,x=TRUE,y=T

```

```

RUE,surv=TRUE)
survival<-Survival(f)
survival1<-function(x)survival(12,x)
survival3<-function(x)survival(36,x)
survival5<-function(x)survival(60,x)
Nom<-nomogram(f,fun = list(survival1,survival3,survival5),fun.at =c(0.05,seq(0.1,0.9,by=0.1),0.95),lp=FALSE,funlabel
=c("1 year OS","3 year OS","5 year OS"))
plot(Nom)

```

#The following is the c-index code for OS

```

sum.surv <-
summary(coxph(Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data =data.1))
c_index <-sum.surv$concordance
c_index

```

#The following is the calibration curves code for OS, using training set

```

rccens(Surv(Survival_months,OS) ~ predict(f), data = data.1)
fcox <- psm(Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,x=T,
y=T,data=data.1,dist='lognormal')
cal1 <- calibrate(fcox, cmethod='KM', method="boot",u=12,m=260,B=1000)
par(mar=c(8,5,3,2),cex = 1.0)
plot(cal1,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram
-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))
cal3 <- calibrate(fcox, cmethod='KM', method="boot",u=36,m=260,B=1000)
par(mar=c(8,5,3,2),cex = 1.0)
plot(cal3,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram
-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))
cal5 <- calibrate(fcox, cmethod='KM', method="boot",u=60,m=260,B=1000)
par(mar=c(8,5,3,2),cex = 1.0)
plot(cal5,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram
-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))

```

#The following is the c-index code and calibration curves code for OS, using intervalidate set

```

fiv <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.2), x=T, y=T, surv=T, data=data.2)
validate(fiv, method="boot", B=1000, dxy=T)
rccens(Surv(Survival_months,OS) ~ predict(f, newdata=data.2), data = data.2)
fiv1 <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.2), x=T, y=T, surv=T, data=data.2, time.inc=12)
caliv1 <- calibrate(fiv1, cmethod="KM", method="boot", u=12, m=260, B=1000)
plot(caliv1,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogra
m-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))
fiv3 <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.2), x=T, y=T, surv=T, data=data.2, time.inc=36)
caliv3 <- calibrate(fiv3, cmethod="KM", method="boot", u=36, m=260, B=1000)
plot(caliv3,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogra
m-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))
fiv5 <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.2), x=T, y=T, surv=T, data=data.2, time.inc=60)
caliv5 <- calibrate(fiv5, cmethod="KM", method="boot", u=60, m=260, B=1000)
plot(caliv5,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogra
m-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))

```

```

#The following is the c-index code and calibration curves code for OS, using extevaldate set
fev <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.3), x=T, y=T, surv=T, data=data.3)
validate(fev, method="boot", B=1000, dxy=T)
rccrcens(Surv(Survival_months,OS) ~ predict(f, newdata=data.3), data = data.3)
fev1 <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.3), x=T, y=T, surv=T, data=data.3, time.inc=12)
calev1 <- calibrate(fev1, cmethod="KM", method="boot", u=12, m=16, B=1000)
plot(calev1,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))
fev3 <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.3), x=T, y=T, surv=T, data=data.3, time.inc=36)
calev3 <- calibrate(fev3, cmethod="KM", method="boot", u=36, m=16, B=1000)
plot(calev3,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))
fev5 <- cph(Surv(Survival_months,OS) ~ predict(f, newdata=data.3), x=T, y=T, surv=T, data=data.3, time.inc=60)
calev5 <- calibrate(fev5, cmethod="KM", method="boot", u=60, m=16, B=1000)
plot(calev5,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of OS",ylab="Observed OS",col=c(rgb(192,98,83,maxColorValue=255)))

```

#The following is the nomogram code for CSS

```

res.coxA <-
coxph(Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1)
summary(res.coxA)
coxph(formula = Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1)
dd<- datadist(data)
options(datadist="dd")
fA=cph(Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1,x=TRUE,y=TRUE,surv=TRUE)
survivalA<-Survival(fA)
survivalA1<-function(x)survivalA(12,x)
survivalA3<-function(x)survivalA(36,x)
survivalA5<-function(x)survivalA(60,x)
NomA<-nomogram(fA,fun = list(survivalA1,survivalA3,survivalA5),fun.at=c(0.05,seq(0.1,0.9,by=0.1),0.95),lp=FALSE,funlabel = c("1 year CSS","3 year CSS","5 year CSS"))
plot(NomA)

```

#The following is the c-index code for CSS

```

sum.survA <-
summary(coxph(Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data =data.1))
c_index <-sum.survA$concordance
c_index

```

#The following is the calibration curves code for CSS, using training set

```

rccrcens(Surv(Survival_months,CSS) ~ predict(fA), data = data.1)
fcoxA <- psm(Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,x=T,y=T,data=data.1,dist='lognormal')
calA1 <- calibrate(fcoxA, cmethod='KM', method="boot",u=12,m=260,B=1000)
par(mar=c(8,5,3,2),cex = 1.0)
plot(calA1,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))
calA3 <- calibrate(fcoxA, cmethod='KM', method="boot",u=36,m=260,B=1000)

```

```

par(mar=c(8,5,3,2),cex = 1.0)
plot(calA3,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))
calA5 <- calibrate(fcoxA, cmethod='KM', method="boot",u=60,m=260,B=1000)
par(mar=c(8,5,3,2),cex = 1.0)
plot(calA5,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))

```

```

#The following is the c-index code and calibration curves code for CSS, using intervalidate set
fivA <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.2), x=T, y=T, surv=T, data=data.2)
validate(fivA, method="boot", B=1000, dxy=T)
rccorrcens(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.2), data = data.2)
fivA1 <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.2), x=T, y=T, surv=T, data=data.2, time.inc=12)
calivA1 <- calibrate(fivA1, cmethod="KM", method="boot", u=12, m=260, B=1000)
plot(calivA1,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))
fivA3 <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.2), x=T, y=T, surv=T, data=data.2, time.inc=36)
calivA3 <- calibrate(fivA3, cmethod="KM", method="boot", u=36, m=260, B=1000)
plot(calivA3,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))
fivA5 <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.2), x=T, y=T, surv=T, data=data.2, time.inc=60)
calivA5 <- calibrate(fivA5, cmethod="KM", method="boot", u=60, m=260, B=1000)
plot(calivA5,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))

```

```

#The following is the c-index code and calibration curves code for CSS, using extervalidate set
fevA <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.3), x=T, y=T, surv=T, data=data.3)
validate(fevA, method="boot", B=1000, dxy=T)
rccorrcens(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.3), data = data.3)
fevA1 <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.3), x=T, y=T, surv=T, data=data.3, time.inc=12)
calevA1 <- calibrate(fevA1, cmethod="KM", method="boot", u=12, m=16, B=1000)
plot(calevA1,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))
fevA3 <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.3), x=T, y=T, surv=T, data=data.3, time.inc=36)
calevA3 <- calibrate(fevA3, cmethod="KM", method="boot", u=36, m=16, B=1000)
plot(calevA3,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))
fevA5 <- cph(Surv(Survival_months,CSS) ~ predict(fA, newdata=data.3), x=T, y=T, surv=T, data=data.3, time.inc=60)
calevA5 <- calibrate(fevA5, cmethod="KM", method="boot", u=60, m=16, B=1000)
plot(calevA5,lwd=2,lty=1,errbar.col=c(rgb(0,118,192,maxColorValue=255)),xlim=c(0,1.0),ylim=c(0,1.0),xlab="Nomogram-Predicted Probability of CSS",ylab="Observed CSS",col=c(rgb(192,98,83,maxColorValue=255)))

```

```

#The following is the DCA curves code for CSS and OS
m1<-cph(Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension, data.1)
d_train_OS<-dca(m1,times=c(12,36,60))
m2<-cph(Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension, data.1)
d_train_CSS<-dca(m2,times=c(12,36,60))
ggplot(d_train_OS)
ggplot(d_train_CSS)

```

```

d_iv_OS<-dca(m1,new.data=data.2,times=c(12,36,60))
d_iv_CSS<-dca(m2,new.data=data.2,times=c(12,36,60))
ggplot(d_iv_OS)
ggplot(d_iv_CSS)
d_ev_OS<-dca(m1,new.data=data.3,times=c(12,36,60))
d_ev_CSS<-dca(m2,new.data=data.3,times=c(12,36,60))
ggplot(d_ev_OS)
ggplot(d_ev_CSS)

#The following is the tdROC code to compare AJCC-Stage and nomogram
data=data.1
f=cph(Surv(Survival_months,OS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1,x=TRUE,y=T
RUE,surv=TRUE)
pred_f_training<-predict(f,data.1,type="lp")
data_table<-data.frame(time=data.1[,"Survival_months"],status=data.1[,"OS"],score=pred_f_training)
time_roc_res1 <- timeROC(T = data_table$time, delta = data_table$status, marker = data_table$score, cause = 1,
weighting="marginal", times = c(12, 36, 60), ROC = TRUE, iid = TRUE)
time_ROC_df1 <- data.frame( TP_1year = time_roc_res1$TP[ 1], FP_1year = time_roc_res1$FP[ 1], TP_3year =
time_roc_res1$TP[ 2], FP_3year = time_roc_res1$FP[ 2], TP_5year = time_roc_res1$TP[ 3], FP_5year =
time_roc_res1$FP[ 3] )
time_roc_res1$AUC
confint(time_roc_res1, level = 0.95)$CI_AUC
time_ROC_df1 <- data.frame(
TP_1year = time_roc_res1$TP[ 1],
FP_1year = time_roc_res1$FP[ 1],
TP_3year = time_roc_res1$TP[ 2],
FP_3year = time_roc_res1$FP[ 2],
TP_5year = time_roc_res1$TP[ 3],
FP_5year = time_roc_res1$FP[ 3]
)
ggplot(data = time_ROC_df1) +
geom_line(aes(x = FP_1year, y = TP_1year), size = 1, color = "#BC3C29FF") +
geom_line(aes(x = FP_3year, y = TP_3year), size = 1, color = "#0072B5FF") +
geom_line(aes(x = FP_5year, y = TP_5year), size = 1, color = "#E18727FF") +
geom_abline(slope = 1, intercept = 0, color = "grey", size = 1, linetype = 2) +
theme_bw() +annotate("text",x = 0.75, y = 0.25, size = 4.5,label = paste0("AUC at 1 years = ", sprintf("%.3f",
time_roc_res1$AUC[[1]])), color = "#BC3C29FF") +annotate("text",x = 0.75, y = 0.15, size = 4.5,label = paste0("AUC
at 3 years = ", sprintf("%.3f", time_roc_res1$AUC[[2]])), color = "#0072B5FF" ) +annotate("text",x = 0.75, y = 0.05, size
= 4.5,
label = paste0("AUC at 5 years = ", sprintf("%.3f", time_roc_res1$AUC[[3]])), color = "#E18727FF") +
labs(x = "False positive rate", y = "True positive rate") +theme(axis.text = element_text(face = "bold", size = 11, color
= "black"),axis.title.x = element_text(face = "bold", size = 14, color = "black", margin = margin(c(15, 0, 0,
0))),axis.title.y = element_text(face = "bold", size = 14, color = "black", margin = margin(c(0, 15, 0, 0))))
f_AJCC=cph(Surv(Survival_months,OS)~AJCC_stage,data=data.1,x=TRUE,y=TRUE,surv=TRUE)
pred_AJCC_training<-predict(f_AJCC,data.1,type="lp")
data_table<-data.frame(time=data.1[,"Survival_months"],status=data.1[,"OS"],score=pred_AJCC_training)
time_roc_res2 <- timeROC(T = data_table$time, delta = data_table$status, marker = data_table$score, cause = 1,
weighting="marginal", times = c(12, 36, 60), ROC = TRUE, iid = TRUE)
time_ROC_df2 <- data.frame( TP_1year = time_roc_res2$TP[ 1], FP_1year = time_roc_res2$FP[ 1], TP_3year

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= time_roc_res2$TP[, 2],   FP_3year = time_roc_res2$FP[, 2],   TP_5year = time_roc_res2$TP[, 3],   FP_5year =
time_roc_res2$FP[, 3] )
time_roc_res2$AUC
confint(time_roc_res2, level = 0.95)$CI_AUC
time_ROC_df1 <- data.frame(
  TP_1year = time_roc_res2$TP[, 1],
  FP_1year = time_roc_res2$FP[, 1],
  TP_3year = time_roc_res2$TP[, 2],
  FP_3year = time_roc_res2$FP[, 2],
  TP_5year = time_roc_res2$TP[, 3],
  FP_5year = time_roc_res2$FP[, 3]
)
ggplot(data = time_ROC_df2) +
  geom_line(aes(x = FP_1year, y = TP_1year), size = 1, color = "#BC3C29FF") +
  geom_line(aes(x = FP_3year, y = TP_3year), size = 1, color = "#0072B5FF") +
  geom_line(aes(x = FP_5year, y = TP_5year), size = 1, color = "#E18727FF") +
  geom_abline(slope = 1, intercept = 0, color = "grey", size = 1, linetype = 2) +
  theme_bw() + annotate("text", x = 0.75, y = 0.25, size = 4.5, label = paste0("AUC at 1 years = ", sprintf("%.3f",
time_roc_res2$AUC[[1]])), color = "#BC3C29FF") + annotate("text", x = 0.75, y = 0.15, size = 4.5, label = paste0("AUC
at 3 years = ", sprintf("%.3f", time_roc_res2$AUC[[2]])), color = "#0072B5FF") + annotate("text", x = 0.75, y = 0.05, size
= 4.5, label = paste0("AUC at 5 years = ", sprintf("%.3f", time_roc_res2$AUC[[3]])), color = "#E18727FF") +
  labs(x = "False positive rate", y = "True positive rate") + theme(axis.text = element_text(face = "bold", size = 11,
color = "black"), axis.title.x = element_text(face = "bold", size = 14, color = "black", margin = margin(c(15, 0, 0, 0))),
axis.title.y = element_text(face = "bold", size = 14, color = "black", margin = margin(c(0, 15, 0, 0))))
  compare(time_roc_res1, time_roc_res2, adjusted = TRUE)
data=data.1
fA=cph(Surv(Survival_months,CSS)~Age+ICD_O_3+AJCC_N+AJCC_M+Tumor_size+Extension,data=data.1,x=TRUE,y
=TRUE,surv=TRUE)
pred_fA_training<-predict(fA,data.1,type="lp")
data_tableA<-data.frame(time=data.1[,"Survival_months"],status=data.1[,"CSS"],score=pred_fA_training)
time_roc_resA1 <- timeROC(T = data_tableA$time, delta = data_tableA$status, marker = data_tableA$score, cause
= 1, weighting="marginal", times = c(12, 36, 60), ROC = TRUE, iid = TRUE)
time_ROC_dfa1 <- data.frame( TP_1year = time_roc_resA1$TP[, 1],   FP_1year = time_roc_resA1$FP[, 1],
TP_3year = time_roc_resA1$TP[, 2],   FP_3year = time_roc_resA1$FP[, 2],   TP_5year = time_roc_resA1$TP[, 3],
FP_5year = time_roc_resA1$FP[, 3] )
time_roc_resA1$AUC
confint(time_roc_resA1, level = 0.95)$CI_AUC
time_ROC_dfa1 <- data.frame(
  TP_1year = time_roc_resA1$TP[, 1],
  FP_1year = time_roc_resA1$FP[, 1],
  TP_3year = time_roc_resA1$TP[, 2],
  FP_3year = time_roc_resA1$FP[, 2],
  TP_5year = time_roc_resA1$TP[, 3],
  FP_5year = time_roc_resA1$FP[, 3]
)
ggplot(data = time_ROC_dfa1) +
  geom_line(aes(x = FP_1year, y = TP_1year), size = 1, color = "#BC3C29FF") +
  geom_line(aes(x = FP_3year, y = TP_3year), size = 1, color = "#0072B5FF") +
  geom_line(aes(x = FP_5year, y = TP_5year), size = 1, color = "#E18727FF") +

```

```

geom_abline(slope = 1, intercept = 0, color = "grey", size = 1, linetype = 2) +
theme_bw() +annotate("text",x = 0.75, y = 0.25, size = 4.5,label = paste0("AUC at 1 years = ", sprintf("%.3f",
time_roc_resA1$AUC[[1]])), color = "#BC3C29FF") +annotate("text",x = 0.75, y = 0.15, size = 4.5,
label = paste0("AUC at 3 years = ", sprintf("%.3f", time_roc_resA1$AUC[[2]])), color = "#0072B5FF") +annotate("text",x
= 0.75, y = 0.05, size = 4.5,label = paste0("AUC at 5 years = ", sprintf("%.3f", time_roc_resA1$AUC[[3]])), color =
"#E18727FF" ) +
labs(x = "False positive rate", y = "True positive rate") +theme(axis.text = element_text(face = "bold", size = 11, color
= "black"),axis.title.x = element_text(face = "bold", size = 14, color = "black", margin = margin(c(15, 0, 0,
0))),axis.title.y = element_text(face = "bold", size = 14, color = "black", margin = margin(c(0, 15, 0, 0))))
fA_AJCC=cph(Surv(Survival_months,CSS)~AJCC_stage,data=data.1,x=TRUE,y=TRUE,surv=TRUE)
pred_AJCC_training<-predict(fA_AJCC,data.1,type="lp")
data_table<-data.frame(time=data.1["Survival_months"],status=data.1["CSS"],score=pred_AJCC_training)
time_roc_resA2 <- timeROC(T = data_table$time, delta = data_table$status, marker = data_table$score, cause = 1,
weighting="marginal", times = c(12, 36, 60), ROC = TRUE, iid = TRUE)
time_ROC_dfA2 <- data.frame( TP_1year = time_roc_resA2$TP[ 1], FP_1year = time_roc_resA2$FP[ 1],
TP_3year = time_roc_resA2$TP[ 2], FP_3year = time_roc_resA2$FP[ 2], TP_5year = time_roc_resA2$TP[ 3],
FP_5year = time_roc_resA2$FP[ 3] )
time_roc_resA2$AUC
confint(time_roc_resA2, level = 0.95)$CI_AUC
time_ROC_dfA2 <- data.frame(
TP_1year = time_roc_resA2$TP[ 1],
FP_1year = time_roc_resA2$FP[ 1],
TP_3year = time_roc_resA2$TP[ 2],
FP_3year = time_roc_resA2$FP[ 2],
TP_5year = time_roc_resA2$TP[ 3],
FP_5year = time_roc_resA2$FP[ 3])
ggplot(data = time_ROC_dfA2) +
geom_line(aes(x = FP_1year, y = TP_1year), size = 1, color = "#BC3C29FF") +
geom_line(aes(x = FP_3year, y = TP_3year), size = 1, color = "#0072B5FF") +
geom_line(aes(x = FP_5year, y = TP_5year), size = 1, color = "#E18727FF") +
geom_abline(slope = 1, intercept = 0, color = "grey", size = 1, linetype = 2) +
theme_bw() +annotate("text", x = 0.75, y = 0.25, size = 4.5, label = paste0("AUC at 1 years = ", sprintf("%.3f",
time_roc_resA2$AUC[[1]])), color = "#BC3C29FF" ) +annotate("text", x = 0.75, y = 0.15, size = 4.5, label =
paste0("AUC at 3 years = ", sprintf("%.3f", time_roc_resA2$AUC[[2]])), color = "#0072B5FF" ) +annotate("text", x =
0.75, y = 0.05, size = 4.5,label = paste0("AUC at 5 years = ", sprintf("%.3f", time_roc_resA2$AUC[[3]])), color =
"#E18727FF" ) +
labs(x = "False positive rate", y = "True positive rate") + theme( axis.text = element_text(face = "bold", size = 11,
color = "black"),axis.title.x = element_text(face = "bold", size = 14, color = "black", margin = margin(c(15, 0, 0, 0))),
axis.title.y = element_text(face = "bold", size = 14, color = "black", margin = margin(c(0, 15, 0, 0))))
compare(time_roc_resA1, time_roc_resA2, adjusted = TRUE)

```

#The following is the dynamic and online nomogram code

```

regplot(f,
plots = c("density", "no plot"),
observation=data[17,],
failtime = c(12, 36, 60), prfail = TRUE )
DynNom(f, data)
DNbuilder(f)
regplot(fA,

```

```
plots = c("density", "no plot"),  
observation=data[17,],  
failtime = c(12, 36, 60), prfail = TRUE )  
DynNom(fA, data)  
DNbuilder(fA)
```