R running of Nomogram for Resected SCLC

This is the R running report of nomogram development and validation of the cohort using R software. (The IASLC validation was conducted by the biostatisticians using the same methods.) Text in blue represents the codes and text in blue represents the corresponding output.

1.R code for nomogram:

```
library(rms)
library(foreign)
library(survival)
setwd("C:/R work")

dev<-read.csv("dev.csv")
head(dev)
      id Sex Age T N Surgery LNR Chemotherapy follow death
1   1   1   2 1 1       1   1            2      46     1
2   3   2   2 2 2       1   2            1      20     1
3   4   2   2 3 2       3   2            1      17     1
4   5   2   3 1 1       1   1            2      10     1
5   6   1   2 3 1       1   1            1     103     1
6   7   2   2 2 3       2   2            1      20     1
str(dev)
'data.frame':    1052 obs. of   10 variables:
 $ id          : int   1 3 4 5 6 7 8 9 10 11 ...
 $ Sex         : int   1 2 2 2 1 2 1 2 2 2 ...
 $ Age         : int   2 2 2 3 2 2 3 1 3 3 ...
 $ T           : int   1 2 3 1 3 2 3 3 2 2 ...
 $ N           : int   1 2 2 1 1 3 1 3 1 1 ...
 $ Surgery     : int   1 1 3 1 1 2 2 2 1 1 ...
 $ LNR         : int   1 2 2 1 1 2 3 2 1 1 ...
 $ Chemotherapy: int   2 1 1 2 1 1 1 1 2 1 ...
 $ follow      : int   46 20 17 10 103 20 33 28 31 42 ...
 $ death       : int   1 1 1 1 1 1 1 1 1 1 ...
dev$Age<-factor(dev$Age,labels=c('<=60','60-70','>70'))
dev$Sex<-factor(dev$Sex,labels=c('Female','Male'))
dev$Surgery<-factor(dev$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
dev$T<-factor(dev$T,labels=c('T1','T2','T3-T4'))
dev$N<-factor(dev$N,labels=c('N0','N1','N2'))
dev$LNR<-factor(dev$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
dev$Chemotherapy<-factor(dev$Chemotherapy,labels=c('Yes','No/Unknown'))

str(dev)
'data.frame':    1052 obs. of   10 variables:
 $ id          : int   1 3 4 5 6 7 8 9 10 11 ...
 $ Sex         : Factor w/ 2 levels "Female","Male": 1 2 2 2 1 2 1 2 2 2 ...
```

```
 $ Age          : Factor w/ 3 levels "<=60","60-70",..: 2 2 2 3 2 2 3 1 3 3 ...
 $ T            : int   1 2 3 1 3 2 3 3 2 2 ...
 $ N            : Factor w/ 3 levels "N0","N1","N2": 1 2 2 1 1 3 1 3 1 1 ...
 $ Surgery      : Factor w/ 3 levels "Lobectomy","Sublobar Ectomy",..: 1 1 3 1 1 2 2 2 1 1 ...
 $ LNR          : Factor w/ 3 levels "<=0.01",">0.01",..: 1 2 2 1 1 2 3 2 1 1 ...
 $ Chemotherapy: Factor w/ 2 levels "Yes","No/Unknown": 2 1 1 2 1 1 1 1 2 1 ...
 $ follow       : int   46 20 17 10 103 20 33 28 31 42 ...
 $ death        : int   1 1 1 1 1 1 1 1 1 1 ...
```

```
y<-Surv(dev$follow,dev$death==1,type="right")
mod<-coxph(y~Age + Sex + Surgery + T + N + LNR + Chemotherapy, data=dev)
temp <- cox.zph(mod,transform="rank",global=F)
temp
```

	rho	chisq	p
Age60-70	-0.03277	0.7162	3.97e-01
Age>70	-0.02537	0.4176	5.18e-01
SexMale	0.00537	0.0190	8.90e-01
SurgerySublobar Ectomy	0.01548	0.1736	6.77e-01
SurgeryPneumonectomy	-0.02646	0.4635	4.96e-01
T	-0.08378	4.8307	2.80e-02
NN1	-0.03090	0.6058	4.36e-01
NN2	-0.05470	1.9656	1.61e-01
LNR>0.01	0.01310	0.1104	7.40e-01
LNRNo Lymph Node Detected	-0.01071	0.0829	7.73e-01
ChemotherapyNo/Unknown	-0.24712	40.1353	2.37e-10

```
ddist <- datadist(dev)
options(datadist='ddist')

units(dev$follow) <- "Month"

fcox <- cph(Surv(follow,death) ~ Age + Sex + Surgery + T + N + LNR +
Chemotherapy,surv=T,x=T, y=T,data=dev)

surv <- Survival(fcox)
nom <- nomogram(fcox, fun=list(function(x) surv(12, x),
                               function(x) surv(36, x),
                               function(x) surv(60, x)),
              funlabel=c("1-years Survival Probability",
                         "3-years Survival Probability",
                         "5-years Survival Probability"),lp=F)
plot(nom)
```

```
surv <- Survival(fcox)
nom <- nomogram(fcox, fun=list(function(x) surv(12, x),
                               function(x) surv(36, x),
                               function(x) surv(60, x)),
              funlabel=c("1-years Survival Probability",
                         "3-years Survival Probability",
                         "5-years Survival Probability"),lp=F)
plot(nom,col.grid=c("red","green","blue"))
```

2.R code for ROC curve:

```
library(rms)
library(foreign)
library(survival)

setwd("C:/R work")
source("stdca.R")
dev<-read.csv("dev.csv")
head(dev)
str(dev)

dev$Age<-factor(dev$Age,labels=c('<=60','60-70','>70'))
dev$Sex<-factor(dev$Sex,labels=c('Female','Male'))
dev$Surgery<-factor(dev$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
dev$T<-factor(dev$T,labels=c('T1','T2','T3-T4'))
dev$N<-factor(dev$N,labels=c('N0','N1','N2'))
dev$LNR<-factor(dev$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
dev$Chemotherapy<-factor(dev$Chemotherapy,labels=c('Yes','No/Unknown'))

str(dev)

library(survivalROC)
nobs<-NROW(dev)
cutoff1<-12
cutoff2<-36
Cutoff3<-60

Srv=Surv(dev$follow,dev$death)

coxmod=coxph(Srv ~   Age + Sex + Surgery + T + N + LNR + Chemotherapy,data=dev)

summary(coxmod)
Call:
coxph(formula = Srv ~ Age + Sex + Surgery + T + N + LNR + Chemotherapy,
    data = dev)
```

n= 1052, number of events= 650

	coef	exp(coef)	se(coef)	z	Pr(>|z|)	
Age60-70	0.42254	1.52584	0.10529	4.013	5.99e-05	***
Age>70	0.71858	2.05152	0.10546	6.814	9.50e-12	***
SexMale	0.19270	1.21252	0.07943	2.426	0.015272	*
SurgerySublobectomy	0.37066	1.44869	0.09719	3.814	0.000137	***
SurgeryPneumonectomy	0.45003	1.56836	0.19603	2.296	0.021688	*
TT2	0.22629	1.25394	0.09228	2.452	0.014196	*
TT3-T4	0.70473	2.02330	0.10704	6.584	4.59e-11	***
NN1	0.42896	1.53566	0.18466	2.323	0.020182	*
NN2	0.46019	1.58438	0.16449	2.798	0.005148	**
LNR>0.01	0.27311	1.31404	0.17979	1.519	0.128752	
LNRNo Lymph Node Resected	0.43604	1.54657	0.13237	3.294	0.000987	***
ChemotherapyNo/Unknown	0.42872	1.53529	0.08883	4.826	1.39e-06	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

	exp(coef)	exp(-coef)	lower .95	upper .95
Age60-70	1.526	0.6554	1.2413	1.876
Age>70	2.052	0.4874	1.6684	2.523
SexMale	1.213	0.8247	1.0377	1.417
SurgerySublobectomy	1.449	0.6903	1.1974	1.753
SurgeryPneumonectomy	1.568	0.6376	1.0680	2.303
TT2	1.254	0.7975	1.0465	1.503
TT3-T4	2.023	0.4942	1.6404	2.496
NN1	1.536	0.6512	1.0693	2.205
NN2	1.584	0.6312	1.1477	2.187
LNR>0.01	1.314	0.7610	0.9238	1.869
LNRNo Lymph Node Resected	1.547	0.6466	1.1932	2.005
ChemotherapyNo/Unknown	1.535	0.6513	1.2900	1.827

Concordance= 0.669   (se = 0.012)
Likelihood ratio test= 212.1   on 12 df,   p=<2e-16
Wald test   = 208.2   on 12 df,   p=<2e-16
Score (logrank) test = 217.1   on 12 df,   p=<2e-16

Sexn<- as.numeric(dev$Sex)
dev$sexpoint<- ifelse(Sexn==1,0,0.19270)

Agen<- as.numeric(dev$Age)
dev$agepoint<- ifelse(Agen==1,0,ifelse(Agen==2,0.42254,0.71858))

```r
Surgeryn<- as.numeric(dev$Surgery)
dev$surgerypoint<- ifelse(Surgeryn==1,0,ifelse(Surgeryn==2,0.37066,0.45003))

Tn<- as.numeric(dev$T)
dev$tpoint<- ifelse(Tn==1,0,ifelse(Tn==2,0.22629,0.70473))

Nn<- as.numeric(dev$N)
dev$npoint<- ifelse(Nn==1,0,ifelse(Nn==2,0.42896,0.46019))

LNRn<- as.numeric(dev$LNR)
dev$lnrpoint<- ifelse(LNRn==1,0,ifelse(LNRn==2,0.27311,0.43604))

Chemotherapyn<- as.numeric(dev$Chemotherapy)
dev$chemotherapypoint<- ifelse(Chemotherapyn==1,0,0.42872)

dev$PI<-dev$points<-rowSums(dev[,c("agepoint","sexpoint","surgerypoint","lnrpoint","tpoint","n
point","chemotherapypoint")])

data<-dev[which(dev$death!="NA"),]

write.csv(dev, "devnew.csv")

SROC= survivalROC(Stime = data$follow, status = data$death, marker = data$PI, predict.time
=cutoff1, method= "KM" )
cut.op= SROC$cut.values[which.max(SROC$TP-SROC$FP)]
cut.op
[1] 1.68211
plot(SROC$FP,SROC$TP, type="l", xlim=c(0,1), ylim=c(0,1),
     xlab = paste( "FP","\n", "AUC = ",round(SROC$AUC,3)),
     ylab = "TP", col="red")
abline(0,1)
legend("bottomright",c("One Year Survival Probability PI"),col="red",lty=c(1,1))

SROC= survivalROC(Stime = data$follow, status = data$death, marker = data$PI, predict.time
=cutoff2, method= "KM" )
cut.op= SROC$cut.values[which.max(SROC$TP-SROC$FP)]
cut.op
[1] 1.1521
plot(SROC$FP,SROC$TP, type="l", xlim=c(0,1), ylim=c(0,1),
     xlab = paste( "FP","\n", "AUC = ",round(SROC$AUC,3)),
     ylab = "TP", col="red")
abline(0,1)
legend("bottomright",c("Three Year Survival Probability PI "),col="red",lty=c(1,1))
```

```r
SROC= survivalROC(Stime = data$follow, status = data$death, marker = data$PI, predict.time
=cutoff3, method= "KM" )
cut.op= SROC$cut.values[which.max(SROC$TP-SROC$FP)]
cut.op
```
[1] 1.43803
```r
plot(SROC$FP,SROC$TP, type="l", xlim=c(0,1), ylim=c(0,1),
     xlab = paste( "FP","\n", "AUC = ",round(SROC$AUC,3)),
     ylab = "TP", col="red")
abline(0,1)
legend("bottomright",c("Five Year Survival Probability PI "),col="red",lty=c(1,1))


library(rms)
library(foreign)
library(survival)

setwd("C:/R work")
source("stdca.R")
vad<-read.csv("vad.csv")
head(vad)
str(vad)

vad$Age<-factor(vad$Age,labels=c('<=60','60-70','>70'))
vad$Sex<-factor(vad$Sex,labels=c('Female','Male'))
vad$Surgery<-factor(vad$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
vad$T<-factor(vad$T,labels=c('T1','T2','T3-T4'))
vad$N<-factor(vad$N,labels=c('N0','N1','N2'))
vad$LNR<-factor(vad$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
vad$Chemotherapy<-factor(vad$Chemotherapy,labels=c('Yes','No/Unknown'))

str(vad)

library(survivalROC)
nobs<-NROW(vad)
cutoff1<-12
cutoff2<-36
Cutoff3<-60

Srv=Surv(vad$follow,vad$death)

coxmod=coxph(Srv ~   Age + Sex + Surgery + T + N + LNR + Chemotherapy,data=vad)

Sexn<- as.numeric(vad$Sex)
vad$sexpoint<- ifelse(Sexn==1,0,0.19270)
```

```
Agen<- as.numeric(vad$Age)
vad$agepoint<- ifelse(Agen==1,0,ifelse(Agen==2,0.42254,0.71858))

Surgeryn<- as.numeric(vad$Surgery)
vad$surgerypoint<- ifelse(Surgeryn==1,0,ifelse(Surgeryn==2,0.37066,0.45003))

Tn<- as.numeric(vad$T)
vad$tpoint<- ifelse(Tn==1,0,ifelse(Tn==2,0.22629,0.70473))

Nn<- as.numeric(vad$N)
vad$npoint<- ifelse(Nn==1,0,ifelse(Nn==2,0.42896,0.46019))

LNRn<- as.numeric(vad$LNR)
vad$lnrpoint<- ifelse(LNRn==1,0,ifelse(LNRn==2,0.27311,0.43604))

Chemotherapyn<- as.numeric(vad$Chemotherapy)
vad$chemotherapypoint<- ifelse(Chemotherapyn==1,0,0.42872)

vad$PI<-vad$points<-rowSums(vad[,c("agepoint","sexpoint","surgerypoint","lnrpoint","tpoint","n
point","chemotherapypoint")])

data<-vad[which(vad$death!="NA"),]

write.csv(vad, "vadnew.csv")

SROC= survivalROC(Stime = data$follow, status = data$death, marker = data$PI, predict.time
=cutoff1, method= "KM" )
cut.op= SROC$cut.values[which.max(SROC$TP-SROC$FP)]
cut.op
[1] 1.7835
plot(SROC$FP,SROC$TP, type="l", xlim=c(0,1), ylim=c(0,1),
     xlab = paste( "FP","\n", "AUC = ",round(SROC$AUC,3)),
     ylab = "TP", col="red")
abline(0,1)
legend("bottomright",c("One Year Survival Probability PI"),col="red",lty=c(1,1))

SROC= survivalROC(Stime = data$follow, status = data$death, marker = data$PI, predict.time
=cutoff2, method= "KM" )
cut.op= SROC$cut.values[which.max(SROC$TP-SROC$FP)]
cut.op
[1] 1.61335
plot(SROC$FP,SROC$TP, type="l", xlim=c(0,1), ylim=c(0,1),
     xlab = paste( "FP","\n", "AUC = ",round(SROC$AUC,3)),
```

```
     ylab = "TP", col="red")
abline(0,1)
legend("bottomright",c("Three Year Survival Probability PI "),col="red",lty=c(1,1))

SROC= survivalROC(Stime = data$follow, status = data$death, marker = data$PI, predict.time
=cutoff3, method= "KM" )
cut.op= SROC$cut.values[which.max(SROC$TP-SROC$FP)]
cut.op
[1] 1.61335
plot(SROC$FP,SROC$TP, type="l", xlim=c(0,1), ylim=c(0,1),
     xlab = paste( "FP","\n", "AUC = ",round(SROC$AUC,3)),
     ylab = "TP", col="red")
abline(0,1)
legend("bottomright",c("Five Year Survival Probability PI "),col="red",lty=c(1,1))
```

3.R code for calibration plot:

```
library(rms)
library(foreign)
library(survival)
setwd("C:/R  work")

dev<-read.csv("dev.csv")
head(dev)
str(dev)

dev$Age<-factor(dev$Age,labels=c('<=60','60-70','>70'))
dev$Sex<-factor(dev$Sex,labels=c('Female','Male'))
dev$Surgery<-factor(dev$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
dev$T<-factor(dev$T,labels=c('T1','T2','T3-T4'))
dev$N<-factor(dev$N,labels=c('N0','N1','N2'))
dev$LNR<-factor(dev$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
dev$Chemotherapy<-factor(dev$Chemotherapy,labels=c('Yes','No/Unknown'))

str(dev)

ddist <- datadist(dev)
options(datadist='ddist')

units(dev$follow) <- "Month"
fcox <- cph(Surv(follow,death) ~ Age + Sex + Surgery + T + N + LNR + Chemotherapy,surv
=T,x=T, y=T,data=dev)

fcox1 <- cph(Surv(follow,death) ~Age + Sex + Surgery + T + N + LNR + Chemotherapy,surv
=T,x=T, y=T,time.inc = 12,data=dev)
```

```
cal1 <- calibrate(fcox1, cmethod="KM", method="boot", u=12, m=250, B=1000)

plot(cal1,col=c("red"))

fcox2 <- cph(Surv(follow,death) ~Age + Sex + Surgery + T + N + LNR + Chemotherapy,surv
=T,x=T, y=T,time.inc = 36,data=dev)

cal2 <- calibrate(fcox2, cmethod="KM", method="boot", u=36, m=250, B=1000)

plot(cal2,col=c("blue"))

fcox2 <- cph(Surv(follow,death) ~Age + Sex + Surgery + T + N + LNR + Chemotherapy,surv
=T,x=T, y=T,time.inc = 60,data=dev)

cal2 <- calibrate(fcox2, cmethod="KM", method="boot", u=60, m=250, B=1000)

plot(cal2,col=c("green"))


vad<-read.csv("vad.csv")

vad$Age<-factor(vad$Age,labels=c('<=60','60-70','>70'))
vad$Sex<-factor(vad$Sex,labels=c('Female','Male'))
vad$Surgery<-factor(vad$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
vad$T<-factor(vad$T,labels=c('T1','T2','T3-T4'))
vad$N<-factor(vad$N,labels=c('N0','N1','N2'))
vad$LNR<-factor(vad$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
vad$Chemotherapy<-factor(vad$Chemotherapy,labels=c('Yes','No/Unknown'))

str(vad)

ddist <- datadist(vad)
options(datadist='ddist')

units(vad$follow) <- "Month"

fcox <- cph(Surv(follow,death) ~ Age + Sex + Surgery + T + N + LNR + Chemotherapy,sur
v=T,x=T, y=T,data=vad)

fvad1 <- cph(Surv(follow, death) ~predict(fcox, newdata=vad), x=T, y=T, surv=T, data=vad,
time.inc=12)
cfvad1 <- calibrate(fvad1, cmethod="KM", method="boot", u=12, m=26, B=1000)
plot(cfvad1,col=c("red"))
```

```
fvad2 <- cph(Surv(follow, death) ~predict(fcox, newdata=vad), x=T, y=T, surv=T, data=vad,
time.inc=36)
cfvad2 <- calibrate(fvad2, cmethod="KM", method="boot", u=36, m=26, B=1000)
plot(cfvad2,col=c("blue"))

fvad2 <- cph(Surv(follow, death) ~predict(fcox, newdata=vad), x=T, y=T, surv=T, data=vad,
time.inc=60)
cfvad2 <- calibrate(fvad2, cmethod="KM", method="boot", u=60, m=26, B=1000)
plot(cfvad2,col=c("green"))
```

4. R code for DCA curve:

```
library(rms)
library(foreign)
library(survival)
setwd("C:/R work")
dev<-read.csv("dev.csv")
head(dev)
str(dev)

dev$Age<-factor(dev$Age,labels=c('<=60','61-70','>70'))
dev$Sex<-factor(dev$Sex,labels=c('Female','Male'))
dev$Surgery<-factor(dev$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
dev$T<-factor(dev$T,labels=c('T1','T2','T3-T4'))
dev$N<-factor(dev$N,labels=c('N0','N1','N2'))
dev$LNR<-factor(dev$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
dev$Chemotherapy<-factor(dev$Chemotherapy,labels=c('Yes','No/Unknown'))

str(dev)

ddist <- datadist(dev)
options(datadist='ddist')
units(dev$os) <- "Month"

y<-Surv(dev$os,dev$ status ==1,type="right")
mod1<-coxph(y~ Age + Sex + Surgery + T + N + LNR + Chemotherapy, data=dev)
summary(mod1)

fcox1 <- cph(Surv(os, status) ~ Age + Sex + Surgery + T + N + LNR + Chemotherapy,surv=T,x=T,
y=T,data=dev)
med    <- Quantile(fcox1)
nom.sur1 <- nomogram(fcox1, fun=function(x) med(lp=x), funlabel="Median Survival
Time",lp=F)
plot(nom.sur1)
```

```
surv <- Survival(fcox1)
nom1 <- nomogram(fcox1, fun=list(function(x) surv(12, x),
                                 function(x) surv(36, x),
                                 function(x) surv(60, x)),
                 funlabel=c("1-years Survival Probability",
                            "3-years Survival Probability",
                            "5-years Survival Probability"),lp=F)
plot(nom1)

library(nomogramEx)
nomogramEx(nomo=nom1, np=3, digit=7)
```

$RESULT
[1] "The equation of each variable as follows:"

[[2]]
```
        Age
1     0.00000
2    58.80252
3   100.00000
```

[[3]]
```
        Sex
4     0.00000
5    26.81631
```

[[4]]
```
    Surgery
6    0.00000
7   51.58236
8   62.62947
```

[[5]]
```
          T
9      0.00000
10    31.49101
11    98.07385
```

[[6]]
```
          N
12     0.00000
13    59.69837
14    64.04490
```

[[7]]
```
        LNR
15   0.00000
16  38.00325
17  60.68040
```

[[8]]
```
    Chemotherapy
18       0.00000
19      59.66232
```

[[9]]
[1] "1-years Survival Probability = 0 * points ^3 + -6.5e-06 * points ^2 + 0.0004805 * points + 0.8956765"

[[10]]
[1] "3-years Survival Probability = 0 * points ^3 + -8.3e-06 * points ^2 + -0.0009098 * points + 0.8024442"

[[11]]
[1] "5-years Survival Probability = 0 * points ^3 + -8.9e-06 * points ^2 + -0.0012152 * points + 0.7362696"

```
dev$Agepoint<- ifelse(dev$Age=="<=60",0,ifelse(dev$Age=="61-70", 58.80252,100))
dev$Surgerypoint<- ifelse(dev$Surgery=="Lobectomy",0,ifelse(dev$Surgery=="Sublobectomy",
  51.58236,62.62947))
dev$Sexpoint<- ifelse(dev$Sex=="Female",0, 26.81631)
dev$Tpoint<- ifelse(dev$T=="T1",0,ifelse(dev$T=="T2", 31.49101,98.07385))
dev$Npoint<- ifelse(dev$N=="N0",0,ifelse(dev$N=="N1", 59.69837,64.04490))
dev$LNRpoint<- ifelse(dev$LNR=="<=0.01",0,ifelse(dev$LNR==">0.01", 38.00325,60.68040))
dev$Chemotherapypoint<- ifelse(dev$Chemotherapy=="Yes",0, 59.66232)
dev$points1 <- dev$Agepoint + dev$Surgerypoint + dev$Sexpoint + dev$Tpoint + dev$Npoint + dev$LNRpoint + dev$Chemotherapypoint
```

```
dev$one.years.Survival.Probabilitynew1 = c(summary(survfit(mod1,newdata=dev),times=12)$surv)

dev$one.years.death.Probabilitynew1 =1- dev$one.years.Survival.Probabilitynew1

dev$three.years.Survival.Probabilitynew1 = c(summary(survfit(mod1,newdata=dev),times=36)$surv)

dev$three.years.death.Probabilitynew1 =1- dev$three.years.Survival.Probabilitynew1
```

```
dev$five.years.Survival.Probabilitynew1 = c(summary(survfit(mod1,newdata=dev),times=60)$surv)

dev$five.years.death.Probabilitynew1 =1- dev$five.years.Survival.Probabilitynew1


y<-Surv(dev$os,dev$ status ==1,type="right")
mod2<-coxph(y~ T + N , data=dev)
summary(mod2)

fcox2 <- cph(Surv(os, status) ~T+N,surv=T,x=T, y=T,data=dev)
med   <- Quantile(fcox2)

nom.sur2 <- nomogram(fcox2, fun=function(x) med(lp=x), funlabel="Median Survival Time",
lp=F)
plot(nom.sur2)

surv <- Survival(fcox2)
nom2 <- nomogram(fcox2, fun=list(function(x) surv(12, x),
                                 function(x) surv(36, x),
                                 function(x) surv(60, x)),
                 funlabel=c("1-years Survival Probability",
                            "3-years Survival Probability",
                            "5-years Survival Probability"),lp=F)
plot(nom2)

library(nomogramEx)
nomogramEx(nomo=nom2, np=3, digit=2)
$RESULT
[1] "The equation of each variable as follows:"

[[2]]
   T
1 0
2 0
3 0

[[3]]
     N
4    0
5    0
6 100

[[4]]
```

[1] "1-years Survival Probability = 0 * points ^3 + 0 * points ^2 + 0 * points + 0.89"

[[5]]
[1] "3-years Survival Probability = 0 * points ^3 + 0 * points ^2 + 0 * points + 0.71"

[[6]]
[1] "5-years Survival Probability = 0 * points ^3 + 0 * points ^2 + 0 * points + 0.65"

```
dev$Tpoint<- ifelse(dev$T=="T1",0,ifelse(dev$T=="T2", 0,0))
dev$Npoint<- ifelse(dev$N=="N0",0,ifelse(dev$N=="N1", 0,100))
dev$points2 <- dev$Tpoint + dev$Npoint
```

```
dev$one.years.Survival.Probabilitynew2 = c(summary(survfit(mod2,newdata=dev),times=12)$surv)

dev$one.years.death.Probabilitynew2 =1- dev$one.years.Survival.Probabilitynew2

dev$three.years.Survival.Probabilitynew2 = c(summary(survfit(mod2,newdata=dev),times=36)$surv)

dev$three.years.death.Probabilitynew2 =1- dev$three.years.Survival.Probabilitynew2

dev$five.years.Survival.Probabilitynew2 = c(summary(survfit(mod2,newdata=dev),times=60)$surv)

dev$five.years.death.Probabilitynew2 =1- dev$five.years.Survival.Probabilitynew2
```

```
source("stdca.R")

stdca(data=dev,outcome="status",ttoutcome="os",timepoint=12,
predictors=c("one.years.death.Probabilitynew1",
"one.years.death.Probabilitynew2") ,smooth=TRUE ,probability=c("TRUE", "TRUE"))
stdca(data=dev,outcome="status",ttoutcome="os",timepoint=36,
predictors=c("three.years.death.Probabilitynew1",
"three.years.death.Probabilitynew2") ,smooth=TRUE ,probability=c("TRUE", "TRUE"))
stdca(data=dev,outcome="status",ttoutcome="os",timepoint=60,
predictors=c("five.years.death.Probabilitynew1",
"five.years.death.Probabilitynew2") ,smooth=TRUE ,probability=c("TRUE", "TRUE"))

stdca(data=dev,outcome="status",ttoutcome="os",timepoint=12,             predictors=c("points1",
"points2") ,smooth=TRUE ,probability=c("FALSE", "FALSE"))
```

5.R code for K-M curve and logrank test

```
library(rms)
library(foreign)
library(survival)
library(nricens)
setwd("C:/R work")
devnew<-read.csv("devnew.csv")
head(devnew)
str(devnew)
library("survival")
fit <- survfit(Surv(follow,death)
~ PI, data = devnew)
class(fit)
library("survminer")
ggsurvplot(fit, data = devnew)

ggsurvplot(fit, data = devnew, fun = "event")
ggsurvplot(fit, data = devnew, fun = "cumhaz")

ggsurvplot(fit, data = devnew, conf.int = TRUE, pval = TRUE, fun = "pct", risk.table = TRUE,
size = 1, linetype = "strata", palette = c("#E7B800", "#2E9FDF"), legend = "bottom",legend.title =
"PI",legend.labs = c("high risk","low risk"))

library(rms)
library(foreign)
library(survival)
library(nricens)
setwd("C:/R work")
vadnew<-read.csv("vadnew.csv")
head(vadnew)
str(vadnew)
library("survival")
fit <- survfit(Surv(follow,death)
~ PI, data = vadnew)
class(fit)
library("survminer")
ggsurvplot(fit, data = vadnew)

ggsurvplot(fit, data = vadnew, fun = "event")
ggsurvplot(fit, data = vadnew, fun = "cumhaz")

ggsurvplot(fit, data = vadnew, conf.int = TRUE, pval = TRUE, fun = "pct", risk.table = TRUE,
size = 1, linetype = "strata", palette = c("#E7B800", "#2E9FDF"), legend = "bottom",legend.title =
"PI",legend.labs = c("high risk","low risk"))
```

6.R code for IDI

```
library(rms)
library(foreign)
library(survival)
library(nricens)

setwd("C:/R work")

dev<-read.csv("dev.csv")
head(dev)
str(dev)

dev$Age<-factor(dev$Age,labels=c('<=60','60-70','>70'))
dev$Sex<-factor(dev$Sex,labels=c('Female','Male'))
dev$Surgery<-factor(dev$Surgery,labels=c('Lobectomy','Sublobectomy','Pneumonectomy'))
dev$T<-factor(dev$T,labels=c('T1','T2','T3-T4'))
dev$N<-factor(dev$N,labels=c('N0','N1','N2'))
dev$LNR<-factor(dev$LNR,labels=c('<=0.01','>0.01','No Lymph Node Resected'))
dev$Chemotherapy<-factor(dev$Chemotherapy,labels=c('Yes','No/Unknown'))

str(dev)

mstd=coxph(Surv(dev$follow,dev$death==1)~T + N,x=TRUE,data=dev)

mnew=coxph(Surv(dev$follow,dev$death==1)~   Age + Sex + Surgery + T + N + LNR +
Chemotherapy,x=TRUE,data=dev)

Srv=Surv(dev$follow,dev$death)

dev$oldone.years.Survival.Probability                    =                    c(1-
(summary(survfit(mstd,newdata=dev),times=12)$surv))
dev$newone.years.Survival.Probability                    =                    c(1-
(summary(survfit(mnew,newdata=dev),times=12)$surv))

devevent<-dev[dev$death==1,]
devnonevent<-dev[dev$death==0,]

IDIevent<-               devevent$newone.years.Survival.Probability                -
devevent$oldone.years.Survival.Probability
IDInonevent<-            devnonevent$newone.years.Survival.Probability             -
devnonevent$oldone.years.Survival.Probability

mean(IDIevent)
[1]   0.02302352
mean(IDInonevent)
```

[1] -0.02718314
IDI= mean(IDIevent)- mean(IDInonevent)
IDI
[1] 0.05020666
SEevent = sd(IDIevent)/sqrt(length(IDIevent))
SEnonevnt = sd(IDInonevent)/sqrt(length(IDInonevent))

Z = IDI/sqrt(SEevent*SEevent + SEnonevnt*SEnonevnt)
Z
[1] 9.204749
P= 1- pnorm(Z)
P
[1] 0
dev$oldthree.years.Survival.Probability   =   c(1-
(summary(survfit(mstd,newdata=dev),times=36)$surv))
dev$newthree.years.Survival.Probability   =   c(1-
(summary(survfit(mnew,newdata=dev),times=36)$surv))

devevent<-dev[dev$death==1,]
devnonevent<-dev[dev$death==0,]

IDIevent<-   devevent$newthree.years.Survival.Probability   -
devevent$oldthree.years.Survival.Probability
IDInonevent<-   devnonevent$newthree.years.Survival.Probability   -
devnonevent$oldthree.years.Survival.Probability

mean(IDIevent)
[1] 0.0292221
mean(IDInonevent)
[1] -0.05058821
IDI= mean(IDIevent)- mean(IDInonevent)
IDI
[1] 0.07981032
SEevent = sd(IDIevent)/sqrt(length(IDIevent))
SEnonevnt = sd(IDInonevent)/sqrt(length(IDInonevent))

Z = IDI/sqrt(SEevent*SEevent + SEnonevnt*SEnonevnt)
Z
[1] 8.894716
P= 1- pnorm(Z)
P
[1] 0
dev$oldfive.years.Survival.Probability   =   c(1-
(summary(survfit(mstd,newdata=dev),times=60)$surv))

```
dev$newfive.years.Survival.Probability                =                c(1-
(summary(survfit(mnew,newdata=dev),times=60)$surv))

devevent<-dev[dev$death==1,]
devnonevent<-dev[dev$death==0,]

IDIevent<-              devevent$newfive.years.Survival.Probability           -
devevent$oldfive.years.Survival.Probability
IDInonevent<-            devnonevent$newfive.years.Survival.Probability          -
devnonevent$oldfive.years.Survival.Probability

mean(IDIevent)
[2] 0.02560333
mean(IDInonevent)
[2] -0.05282392
IDI= mean(IDIevent)- mean(IDInonevent)
IDI
[2] 0.07842724
SEevent = sd(IDIevent)/sqrt(length(IDIevent))
SEnonevnt = sd(IDInonevent)/sqrt(length(IDInonevent))

Z = IDI/sqrt(SEevent*SEevent + SEnonevnt*SEnonevnt )
Z
[2] 8.604544
P= 1- pnorm(Z)
P
[1] 0
```

Year	IDI	p value
One-year	0.050	< 0.001
Three-year	0.080	< 0.001
Five-year	0.078	< 0.001