Supplementary materials R

Description: Related Computerized Programs for Nomogram With R

APPENDIX

Related Computerized Programs for Nomogram With R

For Nomogram

```
library(survival)
library(rms)
data(package="survival")
dd<-datadist(Ytraindata)
options(datadist="dd")
f<-cph(Surv(Ytraindata$RFS02,Ytraindata$RE)~age6001+FIGO01+myo+LVSI+histotype+ER5+Ki6740+P5301+IIFPF,data=Ytraindata,x=TRUE,y=TRUE,surv=TRUE)
survival<-Survival(f)
survival1<-function(x)survival(12,x)
survival2<-function(x)survival(36,x)
survival3<-function(x)survival(60,x)
nom<-nomogram(f,fun=list(survival1,survival2,survival3),fun.at = c(0.05,seq(0.1,0.9,by=0.1),0.95),funlabel = c('1 year RFS','3 year RFS','5 year RFS'))
plot(nom)
```

For Computing the C-Index and 95% CI in Training cohort and Validation cohort

```
library(survival)
library(rms)
fit<-coxph(Surv(RFS02,RE)~age6001+FIGO01+myo+LVSI+histotype+ER5+Ki6740+P5301+IIFPF,data = Ytraindata)
survConcordance(Surv(Ytraindata$RFS02,Ytraindata$RE)~predict(fit,Ytraindata))
survConcordance(Surv(Ytestdata$RFS02,Ytestdata$RE)~predict(fit,Ytestdata))
```

For Calibration Curve for Training Cohort

```
library(survival)
library(rms)
f1<-cph(Surv(Ytraindata$RFS02,Ytraindata$RE,type = "right")~age6001+FIGO01+myo+LVSI+histotype+ER5+Ki6740+P5301+IIFPF,data = Ytraindata,x=TRUE,y=TRUE,surv=TRUE,time.inc = 1*12)
cal=calibrate(f1,cmethod = 'KM',method = "boot",u=1*12,m=180,B=1000)
plot(cal,lwd=1,lty=1,errbar.col=c(rgb(0,0,0,maxColorValue = 255)),xlim = c(0.8,1),ylim = c(0.7,1),xlab ="Nomogram Predicted Survival",ylab="Actual Survival",col=c(rgb(255,0,0,maxColorValue =255)))
abline(0,1,lty = 3,lwd = 2,col = c(rgb(0,118,192,maxColorValue=255)))
lines(cal[,c('mean.predicted','KM')], type = 'b',lwd = 2, col = c(rgb(192,98,83,maxColorValue = 255)),pch = 16)
```

For predictions of the validation cohort

```
library(survival)
library(rms)
f<-cph(Surv(RFS02,RE)~age6001+FIGO01+myo+LVSI+histotype+ER5+Ki6740+P5301+IIFPF,data = Ytraindata)
fp<-predict(f,newdata = Ytestdata)
predictions<-predict(f,newdata = Ytestdata)
predictions
```

For Calibration Curve for Validation Cohort

```
f2<-cph(Surv(Ytestdata$RFS02,Ytestdata$RE,type = "right")~predictions,x=T,y=T,surv=T, time.inc =1*12)
validate(f2,method = "boot",B=1000,dxy=T,u=1*12)
cal<-calibrate(f2,cmethod = 'KM',method = "boot",u=1*12,m=100,B=1000)
plot(cal,lwd=1,lty=1,errbar.col=c(rgb(0,0,0,maxColorValue = 255)),xlim = c(0.8,1),ylim = c(0.7,1),xlab ="Nomogram Predicted Survival",ylab="Actual
```

```
Survival",col=c(rgb(255,0,0,maxColorValue =255)))
abline(0,1,lty = 3,lwd = 2,col = c(rgb(0,118,192,maxColorValue=255)))
lines(cal[,c('mean.predicted','KM')], type = 'b',lwd = 2, col = c(rgb(192,98,83,maxColorValue = 255)),pch = 16)
```

For Computing the C-Index and 95% CI For Different Models

Model A

```
library(survival)
library(rms)
fit1<-coxph(Surv(RFS02,RE)~age6001+FIGO01+LVSI+histotype,data = Ytraindata)
survConcordance(Surv(Ytraindata$RFS02,Ytraindata$RE)~predict(fit1,Ytraindata))

survConcordance(Surv(Ytestdata$RFS02,Ytestdata$RE)~predict(fit1,Ytestdata))
```

Model B

```
library(survival)
library(rms)
fit2<-coxph(Surv(RFS02,RE)~Ki67+ER+PR+P53,data = Ytraindata)
survConcordance(Surv(Ytraindata$RFS02,Ytraindata$RE)~predict(fit2,Ytraindata))

survConcordance(Surv(Ytestdata$RFS02,Ytestdata$RE)~predict(fit2,Ytestdata))
```

Model C

```
library(survival)
library(rms)
fit3<-coxph(Surv(RFS02,RE)~age6001+Cer+histotype,data = Ytraindata)
survConcordance(Surv(Ytraindata$RFS02,Ytraindata$RE)~predict(fit3,Ytraindata))

survConcordance(Surv(Ytestdata$RFS02,Ytestdata$RE)~predict(fit3,Ytestdata))
```

Model D

```
library(survival)
library(rms)
fit4<-coxph(Surv(RFS02,RE)~Cer+myo+histotype+ER+Ki67+P5301,data =
Ytraindata)
survConcordance(Surv(Ytraindata$RFS02,Ytraindata$RE)~predict(fit4,Ytraindata))

survConcordance(Surv(Ytestdata$RFS02,Ytestdata$RE)~predict(fit4,Ytestdata))
```

Supplementary table 1

Description: Recurrence characteristics and follow-up in two cohorts.

Variable	Training cohort N =775	%	Validation cohort N = 491	%	P value*
Recurrence	106		60		0.454
Death	75		42		0.501
Death of recurrence	70		38		
Death of other disease	5		4		
Sites of relapsed					0.869
Vaginal stump	6	5.7	4	6.7	
Central pelvic region	31	29.2	18	30.0	
Lymph nodes (upper para-aortic)	9	8.5	8	13.3	
Peritoneal metastases	24	22.6	12	20.0	
Metastasis to other organs	36	34.0	18	30.0	
RFS (months)					0.984
Mean (±SD)	18.93 (±10.70)		18.90 (±10.48)		
Median (range)	17.00 (6-50)		17.00 (6-48)		
Follow-up (months)					0.875
Mean (±SD)	37.48 (±21.91)		36.93(±20.78)		
Median (range)	32.00(7-84)		32.00(7-84)		

Abbreviations: RFS, recurrence-free survival; *, the comparison of the parameters between the training cohort and the validation cohort.