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#install.packages("survivalROC")
#if(!require("ggsci")) BiocManager::install("ggsci",update=F,ask = F)
#if(!require("timeROC")) BiocManager::install("timeROC",update=F,ask = F)

bioROC=function(riskFile=null,cliFile=null,outFile=null,year){
  risk=read.table(riskFile,header=T,sep="\t",check.names=F,row.names=1)
  cli=read.table(cliFile,sep="\t",check.names=F,header=T,row.names=1)
  sameSample=intersect(row.names(cli),row.names(risk))
  risk=risk[sameSample,]
  cli=cli[sameSample,]
  rt=cbind(futime=risk[,1],fustat=risk[,2],cli,riskScore=risk[,ncol(risk)-1])

  rt=rt[,c(grep("futime",colnames(rt)),
           grep("fustat",colnames(rt)),
           grep("riskScore",colnames(rt)),
           grep("IPI",colnames(rt)))]
  rt$id=row.names(rt)

  cox<- coxph(Surv(futime,fustat) ~ IPI,data =rt)
  score=predict(cox,type="risk",newdata=rt)
  score=cbind(id=rt$id,IPI=as.numeric(score))
  rt=rt[,~grep("IPI",colnames(rt))]
  rt=merge(rt,score,by="id")
  rt[,ncol(rt)]=as.numeric(rt[,ncol(rt)])

  cox<- coxph(Surv(futime,fustat) ~riskScore+IPI,data =rt)
  score=predict(cox,type="risk",newdata=rt)
  score=cbind(id=rt$id,Mergeed_score=as.numeric(score))
  rt=merge(rt,score,by="id")
  rt[,ncol(rt)]=as.numeric(rt[,ncol(rt)])

  rownames(rt)=rt$id
  rt=rt[,~grep("id",colnames(rt))]

  rocCol=jcopal
  colnames(rt)[grep("riskScore",colnames(rt))]="Risk score"

  for (k in 1:length(year)) {
    aucText=c()
    pdf(file=outFile[k],width=6.5,height=6.5)
    par(oma=c(0.5,1,0,1),font.lab=1.5,font.axis=1.5)
  }
}

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ROC<- timeROC(T=rt$futime,
              delta=rt$fustat,
              marker=rt$Mergeed_score,
              cause=1,
              weighting="marginal",
              times=c(1,3,5),
              iid=TRUE)
plot(ROC$FP[k], ROC$TP[k], type="", xlim=c(0,1), ylim=c(0,1),col="#ED0000B2",
     xlab="False positive rate", ylab="True positive rate",
     lwd = 5,lty=1, cex.main=1.3, cex.lab=1.2, cex.axis=1.2, font=1.2)
abline(0,1)
confint=confint(ROC, level = 0.95)$CI_AUC
key=paste(as.numeric(round(ROC$AUC[k],3)),(" ",confint[k,1],"-",confint[k,2],"),",sep="")
aucText=c(aucText,paste("Merged score", " ",key," ",sep=""))

j=0
for(i in colnames(rt[,3:(ncol(rt)-1)])){
  ROC_cli<- timeROC(T=rt$futime,
                    delta=rt$fustat,
                    marker=rt[,i],
                    cause=1,
                    weighting="marginal",
                    times=c(1,3,5),
                    iid=TRUE)

  j=j+1
  lines(ROC_cli$FP[k], ROC_cli$TP[k], type="l", xlim=c(0,1),
        ylim=c(0,1),col=rocCol[j],
        xlab="False positive rate", ylab="True positive rate",
        lwd = 5,lty=1, cex.main=1.3, cex.lab=1.2, cex.axis=1.2, font=1.2)
  confint=confint(ROC_cli, level = 0.95)$CI_AUC

  key=paste(as.numeric(round(ROC_cli$AUC[k],3)),(" ",confint[k,1],"-",confint[k,2],"),",sep="")
  P=compare(ROC_cli,ROC, adjusted = TRUE)

  pvalue=ifelse(P$p_values_AUC[2,k]>=0.001,round(P$p_values_AUC[2,k],3),"<0.001")
  aucText=c(aucText,paste(i, " ",key," ",pvalue,sep=""))
}

legend("bottomright", c(paste(" ",paste0(year[k],"-year
AUC(95%CI)"), " ", "P-value",sep=""),
  aucText),
  col=c("white","#ED0000B2",rocCol),bty='n', lty=1, lwd=4.5, cex=0.95)
dev.off()
}

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}  
bioROC(riskFile="tcgaRisk.txt",cliFile="result-10846.txt",outFile=c("tcgaROC1(nomogram).pdf","tc  
gaROC3(nomogram).pdf","tcgaROC5(nomogram).pdf"),year=c(1,3,5))  
bioROC(riskFile="geoRisk-4732.txt",cliFile="result-4732.txt",outFile=c("geoROC1(nomogram).pdf"  
,"geoROC3(nomogram).pdf","geoROC5(nomogram).pdf"),year=c(1,3,5))
```