

```

library(dplyr)
library(pROC)
library(ggplot2)
library(survival)
library(regplot)
library(rms)
library(ggsci)
library(survminer)
library(timeROC)
#devtools::install_github('yikeshu0611/ggDCA')
library(ggDCA)
library(limma)

inputFile="exp.txt"
hub="hub.txt"
rt=read.table(inputFile, header=T, sep="\t", check.names=F)
rt=as.matrix(rt)
rownames(rt)=rt[,1]
exp=rt[,2:ncol(rt)]
dimnames=list(rownames(exp),colnames(exp))
data=matrix(as.numeric(as.matrix(exp)),nrow=nrow(exp),dimnames=dimnames)
data=avereps(data)
data=t(data)
sample=read.table("sample.txt",sep="\t",header=F,check.names=F)
colnames(sample)=c("ID","Type")
data=data[sample$ID,]
aSAH1=data[,read.table(hub, header=F, sep="\t", check.names=F)[,1]]
aSAH=cbind(sample,aSAH1)
aflist=roc(Type~CEBPA+CXCL2+FOXO1+JUN, data = aSAH)
g3 <- ggroc(aflist, size = 1.2,alpha=.6,)
g5=g3+ggsci::scale_color_lancet()
dd <- datadist(aSAH)
options(datadist="dd")
fit <- lrm(formula = Type ~ CEBPA+CXCL2+FOXO1+JUN, data =aSAH)
print(fit)
coef=as.data.frame(fit$coefficients)[-1,,drop=F]
coefout=cbind(ID=rownames(coef),coef)
write.table(coefout,file="coefficients.txt",sep="\t",quote=F,row.names = F)
plot(regplot(fit,plots=c("density","boxes"), observation=T, title="Prediction Nomogram",
clickable=T, points=TRUE,droplines=TRUE))
nomoscore=predict(fit, data=t(aSAH))
aSAH$nomoscore=nomoscore
write.table(aSAH,file="nomoscore.txt",sep="\t",quote=F,row.names = F)

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```

library(pROC)
library(ggplot2)
afcol="green"
hub="hub.txt"
exp=read.table("exp.txt",sep = "\t",header = F,check.names = F)
exp=t(exp)
colnames(exp)=exp[1,]
exp=exp[2:nrow(exp),]
colnames(exp)[1]="ID"
cli=read.table("sample.txt",sep = "\t",header = F,check.names = F)
cli[,2]=ifelse(cli[,2]==C,0,1)
colnames(cli)=c("ID","P")
af=merge(cli,exp,by = "ID")
af[,3:ncol(af)]=lapply(af[,3:ncol(af)],as.numeric)
genes=read.table(hub,sep = " ",header = F,check.names = F)[,1]
genes=intersect(colnames(af),genes)
nomoscore=(read.table("nomoscore.txt",sep = "\t",header = T,check.names = F)[rownames(af),,], "nomoscore")
af$nomoscore=as.numeric(nomoscore)
for (i in c(genes,"nomoscore")) {
  for (j in c("P")) {
    afroc=roc(af[,j],af[,i])
    print(paste0(auc(afroc),"_",i,"_",j))
    pdf(file=paste0(i,"_",j,".pdf"), width=6, height=6)
    plot(afroc, print.auc=TRUE, auc.polygon=TRUE,axes=FALSE, grid.col=c("green", "red"),
    max.auc.polygon=TRUE, auc.polygon.col=afcol, print.thres=F,main=i)
    dev.off()
  }
}

```