```
FpAUC index: FITTED PARTIAL AREA UNDER THE ROC CURVE
#
     FOR HIGH SENSITIVITY INTERVAL (TPR0, 1)
#
#
     The FpaucHS function computes the FpAUC index
#
#
 Notation:
#
   xsample
           = Gold standard
#
   ysample = test scores
#
   lower.sen = tpr0 (the minimum sensitivity required)#
# CHECK THE GOLD STANDARD
   The 1st is the negative group
   The 2nd is the positive group
CheckGoldStandard <- function(xsample, positive=NULL) {</pre>
 xs=NULL; xs.levels=NULL;
 xs <- as.factor(xsample)</pre>
 xs.levels <- levels(xs)</pre>
 if (length(xs.levels) !=2 ) {
   stop("Error in the Gold Standard: it must be binary")
 if (!is.null(positive)) {
   if (!any(xs.levels == positive)) {
     stop("Error in Gold Standard: positive case must be one of the levels")
 } else {
   positive <- xs.levels[2]</pre>
 if (xs.levels[2] != positive) {
   xs <- relevel(xs, ref=positive)</pre>
 xs <- (xs == positive)*1
 return(xs)}
# POINTS OF THE ROC CURVE
  ROCpoints function calculates the coordinates (FPR, TPR)
ROCpoints <- function(xsample, ysample) {</pre>
 fpr.p=NULL; sen.p=NULL; xy.roc=NULL; x.p=NULL; y.p=NULL; pts=NULL;
 x.p <- xsample[which(is.na(xsample)==FALSE & is.na(ysample)==FALSE)]</pre>
 y.p <- ysample[which(is.na(xsample)==FALSE & is.na(ysample)==FALSE)]</pre>
 x.p <- CheckGoldStandard(x.p)</pre>
 pts <- sort(y.p)</pre>
 pts <- append(pts[-length(pts)]+diff(pts)/2, min(y.p)-1, 0)</pre>
 pts <- append(pts, max(y.p)+1, length(pts))</pre>
 for (i.pt in 1:length(pts)) {
   pre.p <- NULL
   pt=NULL
   pt <- pts[i.pt]</pre>
   pre.p \leftarrow (y.p > pt)*1
   fpr.p[i.pt] \leftarrow sum((pre.p == 1)*(x.p == 0))/sum(x.p == 0)
   sen.p[i.pt] \leftarrow sum((pre.p == 1)*(x.p == 1))/sum(x.p == 1)
 if (is.unsorted(sen.p)) {
   sen.p <- rev(sen.p)</pre>
   fpr.p <- rev(fpr.p)}</pre>
 xy.roc <- cbind(fpr=fpr.p, tpr=sen.p)</pre>
 return(xy.roc)}
# POINTS OF THE PARTIAL ROC CURVE FOR HIGH SENSITIVITY
   pHSpoints function calculates the points in (tpr0, 1)
```

```
pHSpoints <- function(xsample, ysample, lower.sen) {
  pts.roc=NULL; fpr.roc=NULL; sen.roc=NULL; fpr.p=NULL; sen.p=NULL;
ppoints=NULL;
  i.low=NULL; j.low=NULL; lscale=NULL;
  if ((lower.sen >= 1) || (lower.sen<0)) {stop("Error in the prefixed TPR
range")}
  pts.roc <- ROCpoints(xsample, ysample)</pre>
  fpr.roc <- pts.roc[,1]</pre>
  sen.roc <- pts.roc[,2]</pre>
  i.low <- min(which(sen.roc >= lower.sen))
  j.low \leftarrow max(i.low -1, 1)
  fpr.p <- fpr.roc[i.low:length(fpr.roc)]</pre>
  sen.p <- sen.roc[i.low:length(sen.roc)]</pre>
  if ((sen.roc[i.low] > lower.sen) && (i.low>1)) {
    sen.p <- append(sen.p, lower.sen, 0)</pre>
    lscale <- (sen.p[1]-sen.roc[j.low])/(sen.roc[i.low]-sen.roc[j.low])</pre>
    fpr.p <- append(fpr.p, fpr.roc[j.low]+(fpr.roc[i.low]-</pre>
fpr.roc[j.low])*lscale, 0)}
 ppoints=cbind(fprp=fpr.p, tprp=sen.p)
 return(ppoints)}
# PARTIAL AREA UNDER THE ROC CURVE FOR HIGH SENSITIVITY
  paucHS function calculates the pAUC between (tpr0, 1)
paucHS <- function(xsample, ysample, lower.sen) {</pre>
 pts.proc=NULL; fpr.p=NULL; sen.p=NULL; esp.p=NULL; auc.p=NULL;
  pts.proc <- pHSpoints(xsample, ysample, lower.sen)</pre>
  fpr.p <- pts.proc[,1]</pre>
  sen.p <- pts.proc[,2]</pre>
  esp.p <- 1-fpr.p
  auc.p <- sum(diff(sen.p)*apply(cbind(esp.p[-1],esp.p[-length(esp.p)]), 1,</pre>
mean))
  return(auc.p)}
# PARTIAL NEGATIVE LIKELIHOOD RATIO FOR HIGH SENSITIVITY
  pNLR_HS function calculates the NLR between (tpr0, 1)
pNLR_HS <- function(xsample, ysample, lower.sen) {</pre>
  pts.proc=NULL; fpr.p=NULL; sen.p=NULL; pnlr=NULL;
  pts.proc <- pHSpoints(xsample, ysample, lower.sen)</pre>
  fpr.p <- pts.proc[,1]</pre>
  sen.p <- pts.proc[,2]</pre>
  fpr.p <- fpr.p[-length(fpr.p)]</pre>
  sen.p <- sen.p[-length(sen.p)]</pre>
  pnlr <- (1-sen.p)/(1-fpr.p)</pre>
  return(pnlr)}
# PARTIAL ROC CURVE SHAPE FOR HIGH SENSITIVITY
   shapepROC function classifies the ROC curve by its pNLR
shapepROC <- function(xsample, ysample, lower.sen) {</pre>
 nlr.p=NULL; nlr0=NULL; sproc=NULL;
 nlr.p <- pNLR_HS(xsample, ysample, lower.sen)</pre>
  nlr0 <- nlr.p[1]</pre>
  if ((all(nlr.p <= nlr0)) & (is.finite(nlr0))) {</pre>
    sproc <- "BpNLR"
    } else {
      if (all(nlr.p <= 1)) {
        sproc <- "pProp"
        } else {
          sproc <- "other"
  return(sproc)}
```

```
# FITTED PARTIAL AREA INDEX FOR HIGH SENSITIVITY
   FpaucHS function calculates the FpAUC index in (tpr0, 1)
FpaucHS <- function(xsample, ysample, lower.sen) {</pre>
 fpr.p=NULL; sen.p=NULL; pauc.p=NULL; sproc.p=NULL; fpauc.p=NULL;
 fpr.p <- pHSpoints(xsample, ysample, lower.sen)[,1]</pre>
 sen.p <- pHSpoints(xsample, ysample, lower.sen)[,2]</pre>
 pauc.p <- paucHS(xsample, ysample, lower.sen)</pre>
 sproc.p <- shapepROC(xsample, ysample, lower.sen)</pre>
 fpauc.p <- switch(sproc.p,</pre>
                  BpNLR = pauc.p/((1-fpr.p[1])*(1-sen.p[1])),
                  pProp = (pauc.p+(1-sen.p[1])*(sen.p[1]-fpr.p[1]))/
((1+sen.p[1]-2*fpr.p[1])*(1-sen.p[1])),
                  other = (pauc.p+(1-sen.p[1])*(1-fpr.p[1]))/(2*(1-fpr.p[1]))
fpr.p[1])*(1-sen.p[1]))
 return(fpauc.p)}
```