

# Sensitivity, specificity and ROC

*PhD Flavio Lichtenstein*

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## Two distributions - t-student test (t.test)

Here we will present 2 distributions and makey them close togheter or far appart. The statistics that measures the distance between two normal distribuitons is t-student.

```
source("c:/colaboracoes/losac/R/support.R")
```

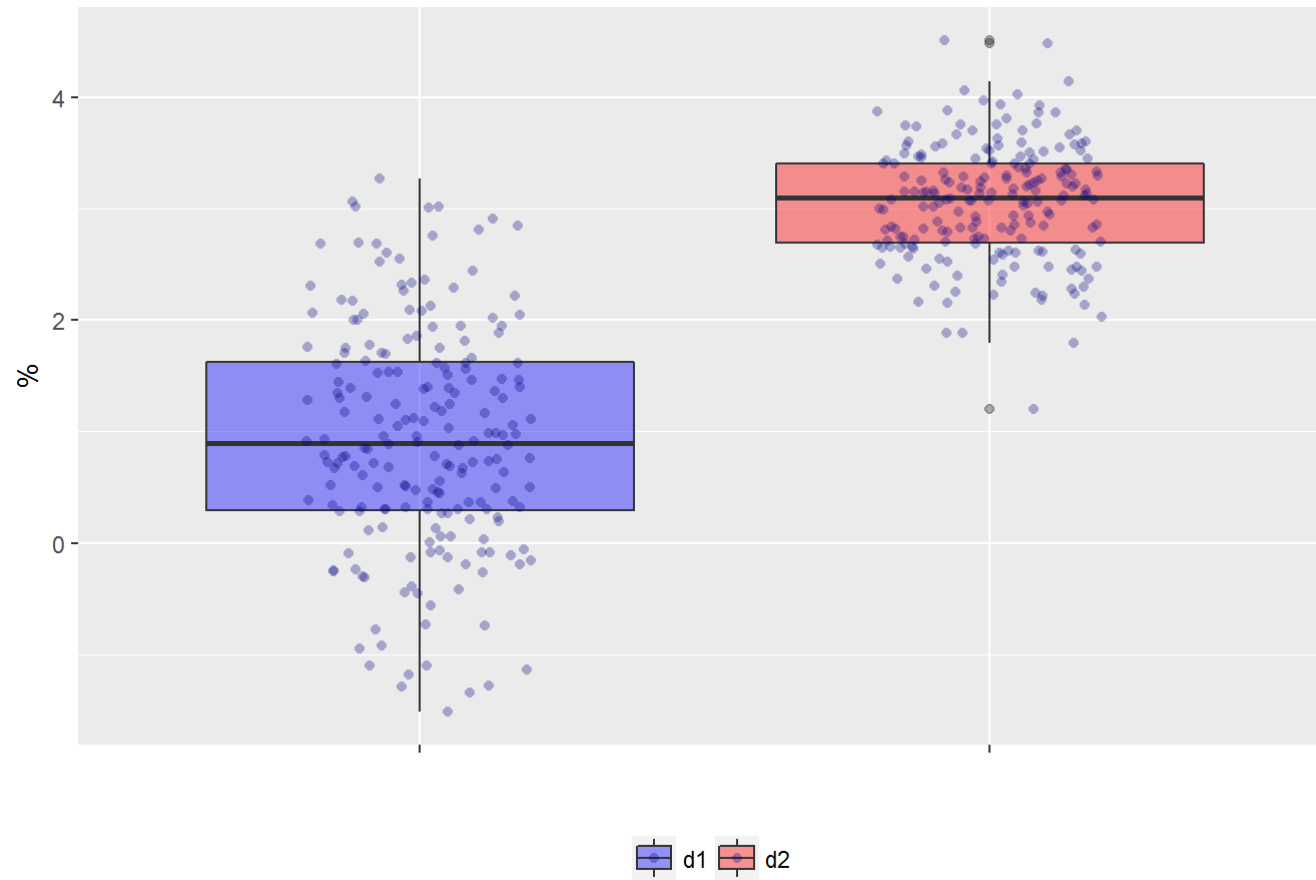
```
d1 = rnorm(200, mean=1, sd=1)
d2 = rnorm(200, mean=3, sd=.5)
```

```
data = data.frame(d1, d2)
options(digits=5)
head(data)
```

```
##      d1      d2
## 1 0.72062 3.0741
## 2 0.98587 2.3686
## 3 1.60485 3.2819
## 4 -0.23900 2.8000
## 5 0.51608 3.5503
## 6 1.17288 3.5979
```

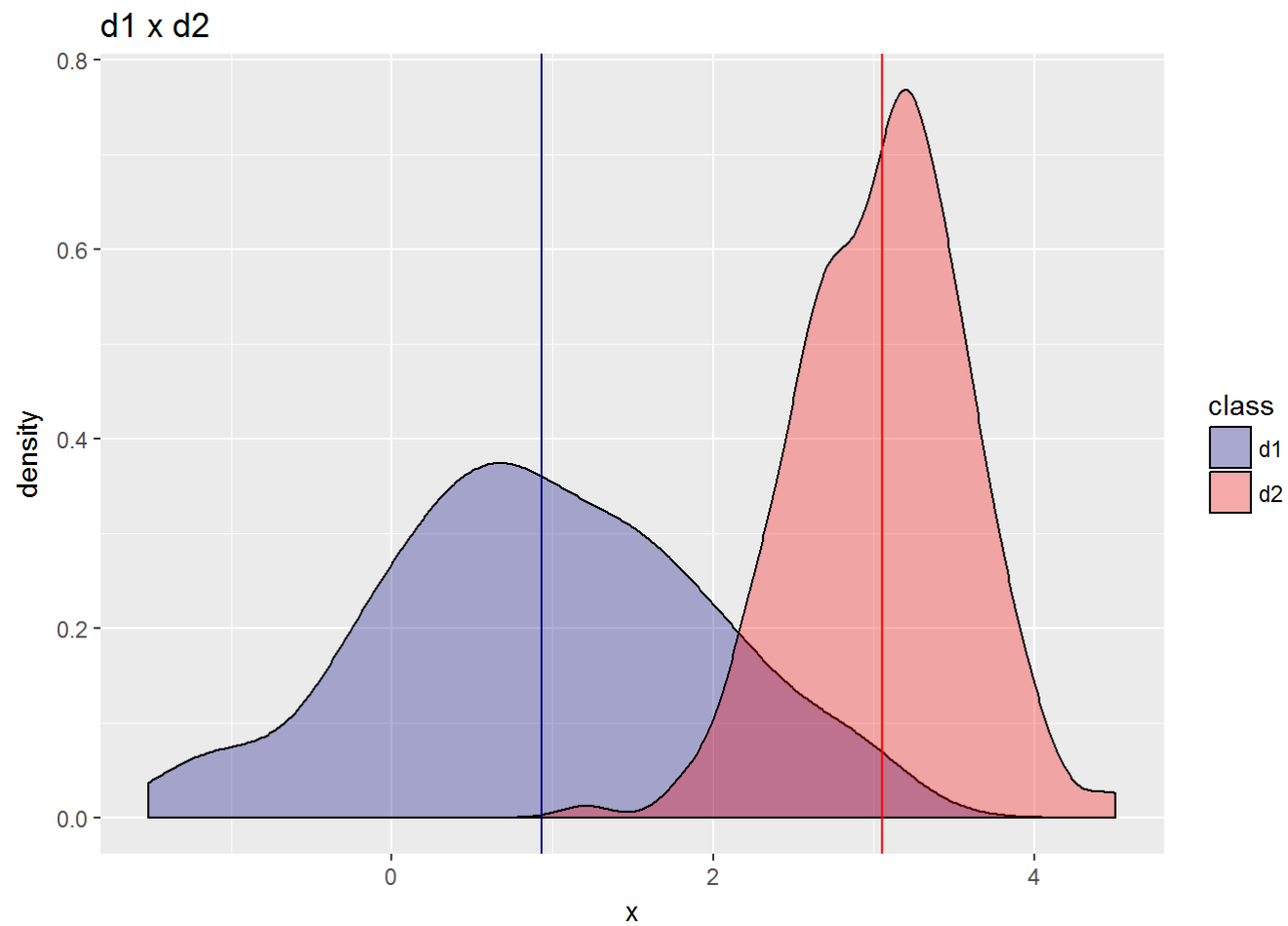
```
my.boxplot(data, classX=c("one","two"), cols=c(1,2), title="normal distribution", ylab="", colors=c("blue", "red"),
is.log=F,ylim=NA)
```

normal distribution



Can we define if the distributions are sufficient far appart?

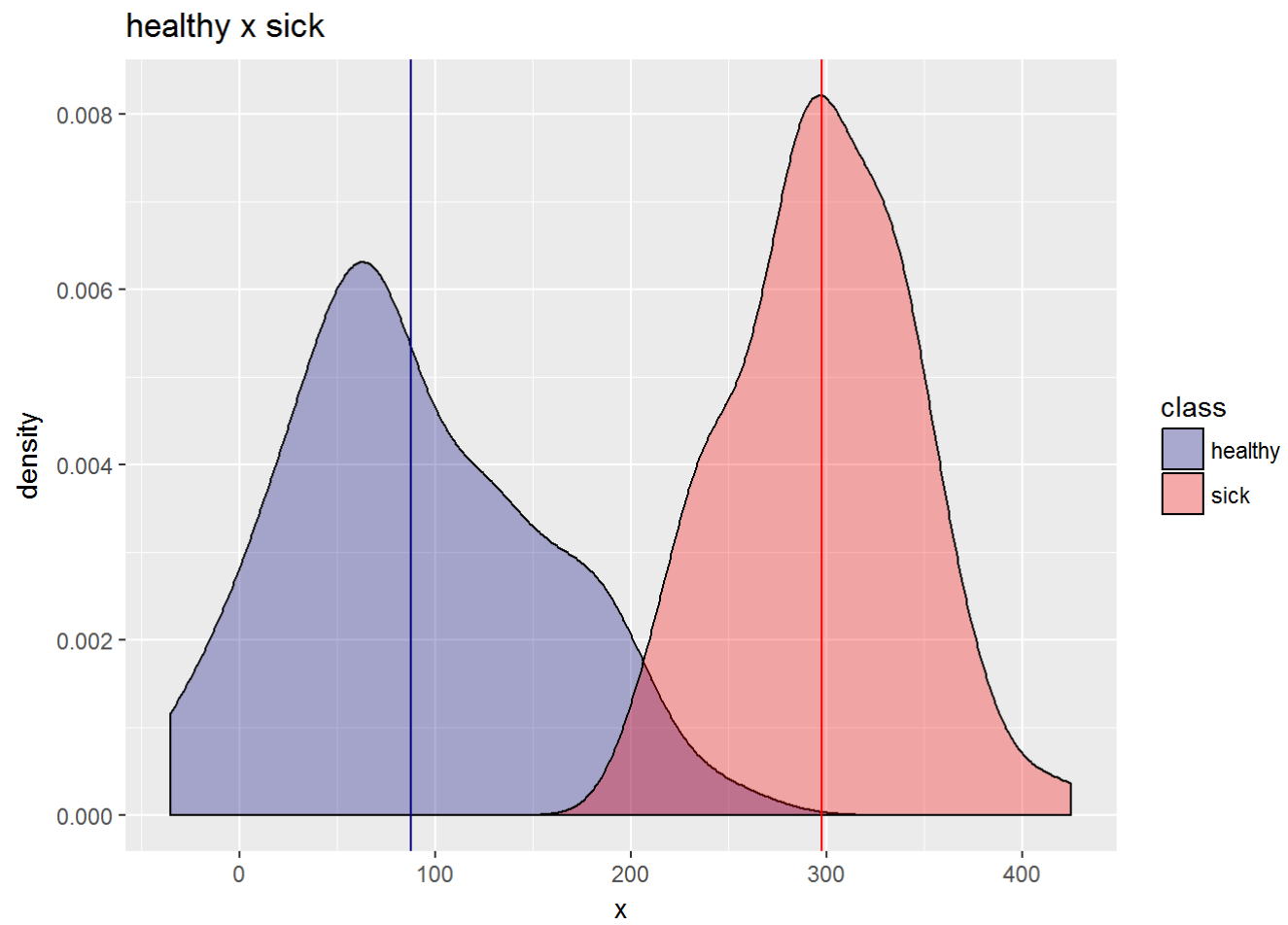
```
print_2densities(d1, d2)
```



```
healthy = rnorm(100, mean=1, sd=.7)
sick     = rnorm(100, mean=3, sd=.5)

healthy = round(healthy*100)
sick    = round(sick*100)

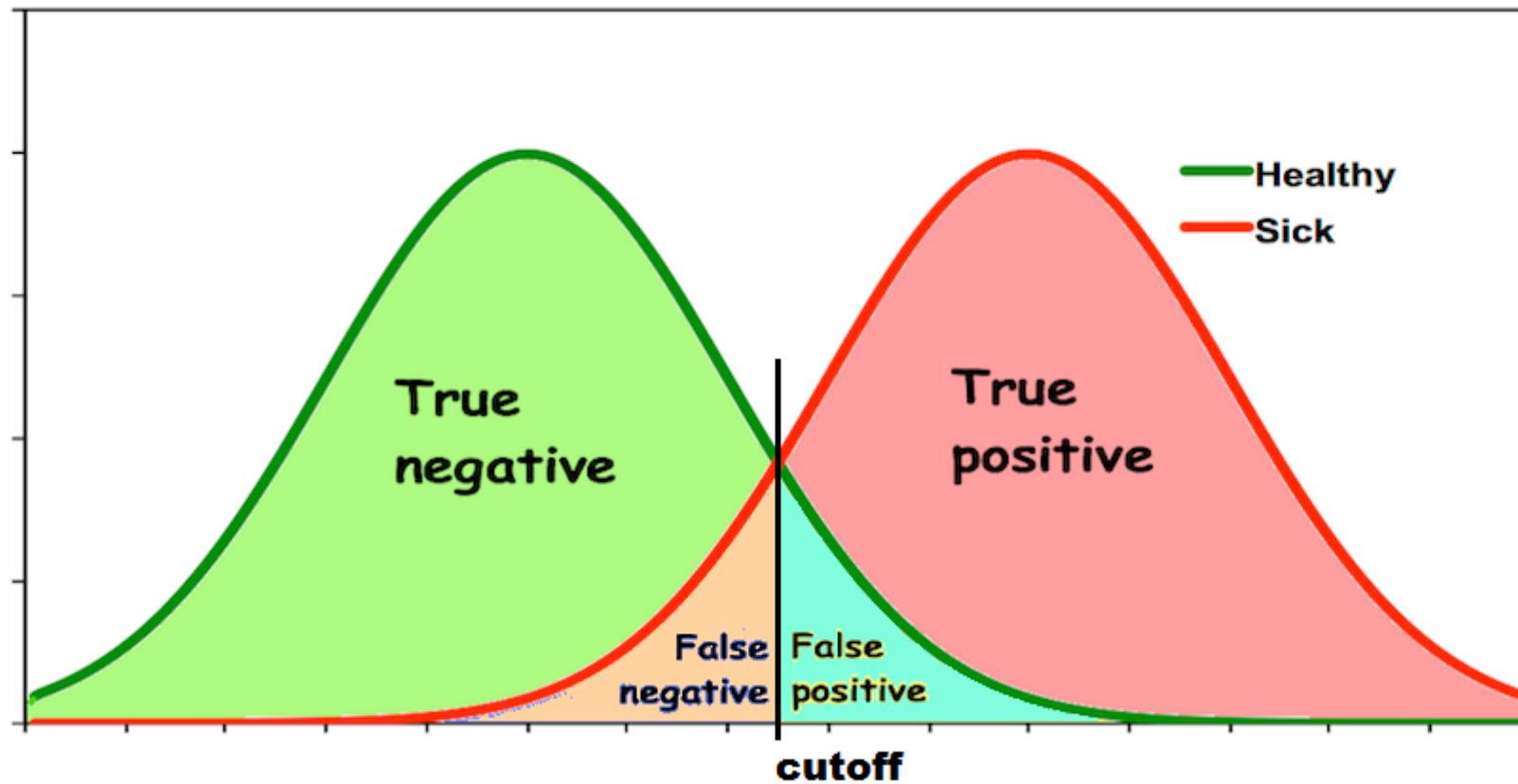
print_2densities(healthy, sick, title="healthy x sick", classes=c("healthy", "sick"))
```



GOLD STANDARD

Classification Outcome

	Sick	Healthy
Test+	True Positives (TP)	False Positives (FP)
Test-	False Negatives (FN)	True Negatives (TN)



Conditional: truth table

[https://en.wikipedia.org/wiki/Confusion\\_matrix](https://en.wikipedia.org/wiki/Confusion_matrix) ([https://en.wikipedia.org/wiki/Confusion\\_matrix](https://en.wikipedia.org/wiki/Confusion_matrix))

## Sensitivity

Sensitivity, recall, hit rate, or true positive rate (TPR)

$$Sensitivity = TPR = \frac{TP}{P} = \frac{TP}{TP + FN}$$

	<b>Sick</b>	<b>Healthy</b>
<b>Test+</b>	True Positives (TP)	False Positives (FP)
<b>Test-</b>	False Negatives (FN)	True Negatives (TN)

Conditional: sensitivity

## Especificity

specificity or true negative rate (TNR)

$$Especificity = TNR = \frac{TN}{N} = \frac{TN}{TN + FP}$$

	<b>Sick</b>	<b>Healthy</b>
<b>Test+</b>	True Positives (TP)	False Positives (FP)
<b>Test-</b>	False Negatives (FN)	True Negatives (TN)

Conditional: specificity

## Precision

precision or positive predictive value (PPV)

$$Precision = PPV = \frac{TP}{TP + FP}$$

	<b>Sick</b>	<b>Healthy</b>
<b>Test+</b>	True Positives (TP)	False Positives (FP)
<b>Test-</b>	False Negatives (FN)	True Negatives (TN)

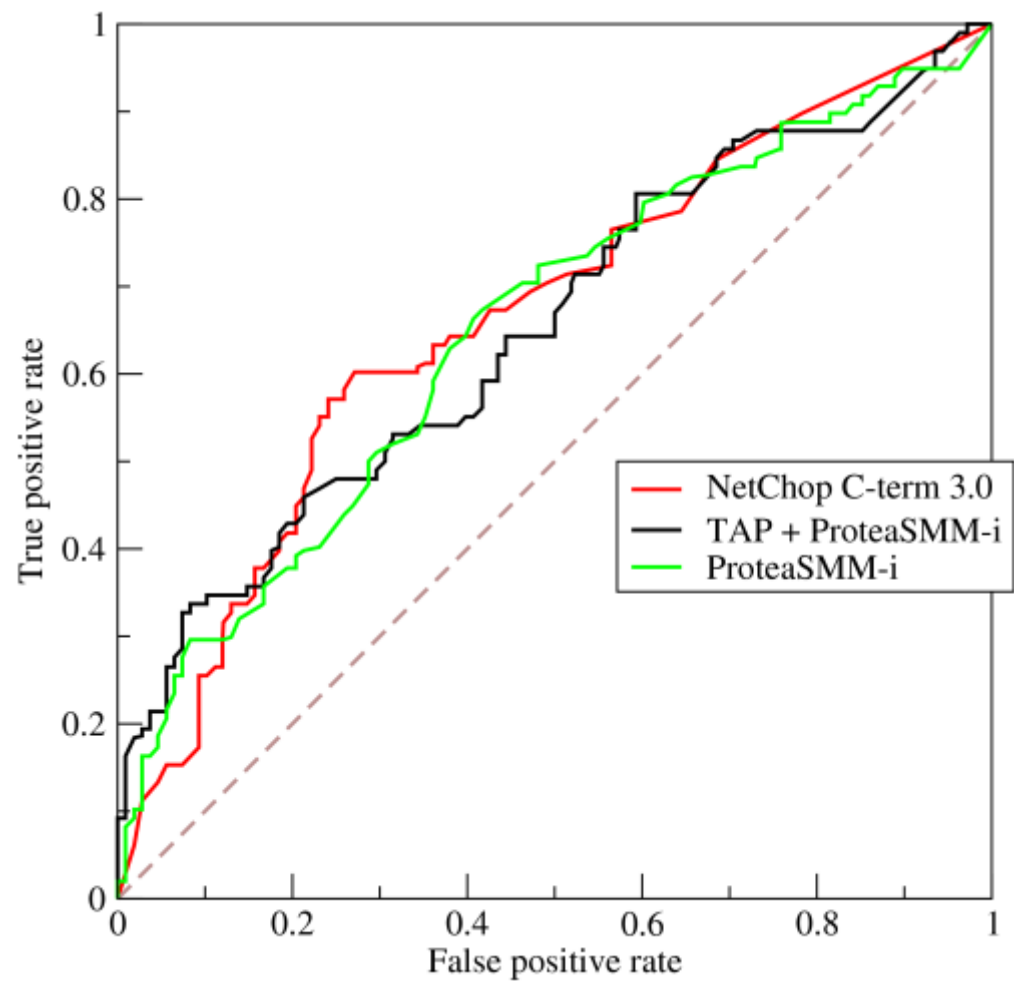


## ROC - Receiver Operating Curve

In statistics, a receiver operating characteristic curve, i.e. ROC curve, is a graphical plot that illustrates the diagnostic ability of a binary classifier system as its discrimination threshold is varied.

The ROC curve is created by plotting the true positive rate (TPR) against the false positive rate (FPR) at various threshold settings. The true-positive rate is also known as sensitivity, recall or probability of detection[1] in machine learning.

[https://en.wikipedia.org/wiki/Receiver\\_operating\\_characteristic](https://en.wikipedia.org/wiki/Receiver_operating_characteristic) ([https://en.wikipedia.org/wiki/Receiver\\_operating\\_characteristic](https://en.wikipedia.org/wiki/Receiver_operating_characteristic))



```
# lista = contingency_table(healthy, sick)
# names(lista)

healthy = rnorm(100, mean=1, sd=.3)
sick    = rnorm(100, mean=2, sd=.3)

lista = doRoc(healthy, sick, "healthy", "sick", "healthy", "sick", xlab="measure", isLog=F, titleAux="")
names(lista)
```

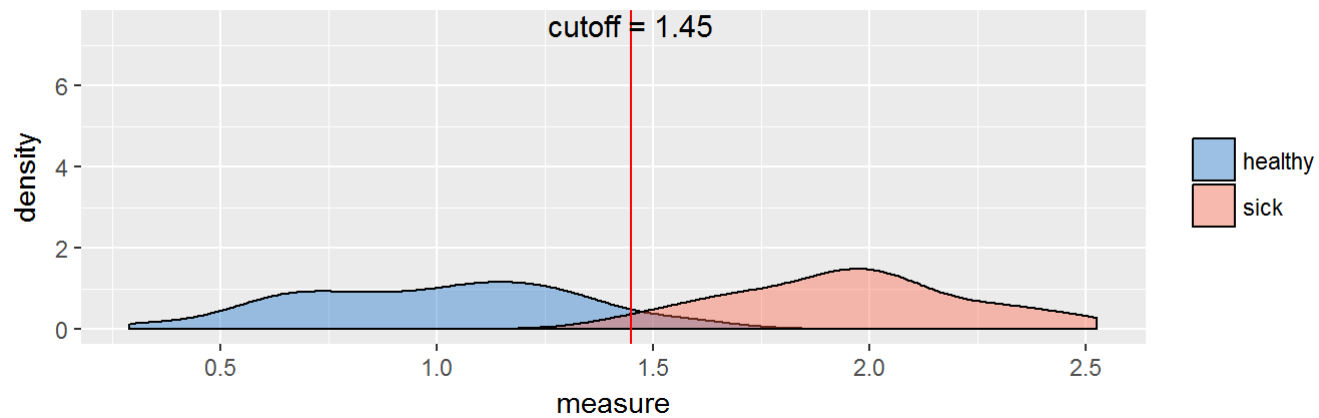
```
## [1] "p1"      "p2"      "best_sens" "best_spec" "cutoff"
```

```
p1 = lista[["p1"]]
```

```
p2 = lista[["p2"]]
```

```
multiplot(p1,p2,layout=matrix(c(1,2),ncol=1, byrow=F))
```

ROC: sick x healthy



best cutoff=1.45, sens=0.97, spec=0.95 (sum=1.92)

