

# ROC Curve

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5/3/2023

```
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
```

```
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

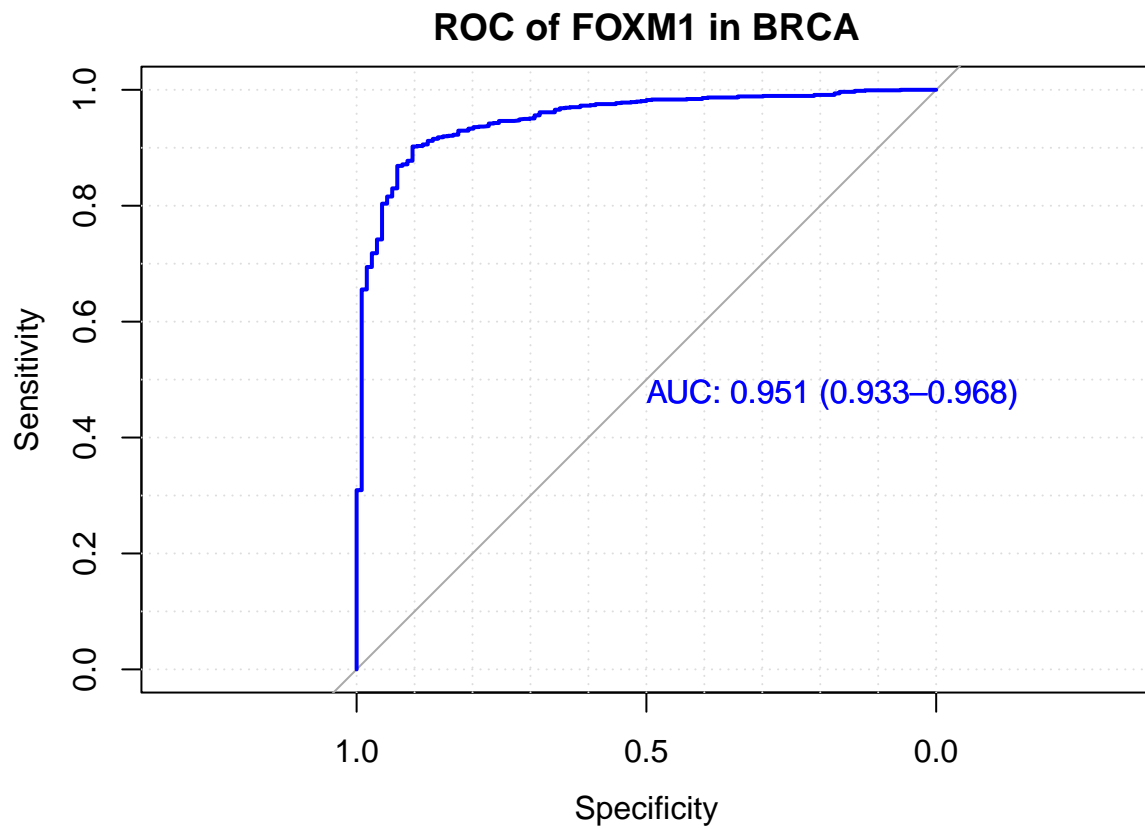
```
##      cov, smooth, var
```

```
setwd('E:/R-Programming-Practices/Data Visualization/ROC Curve')
```

```
data<- data.frame(read.csv('FOXM1 and SOX9.csv'))
```

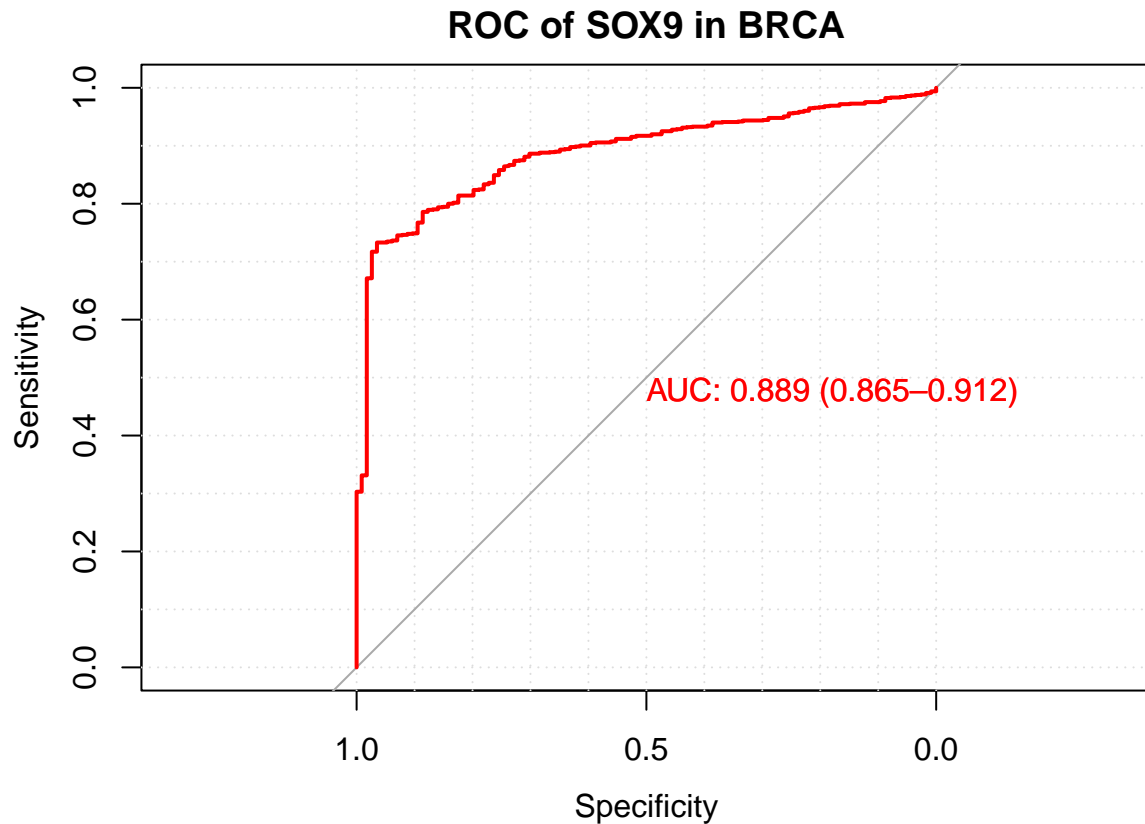
```
rocobj1 <- plot.roc(data$Sample, data$FOXM1, levels=c("Normal", "BRCA"), alpha=0.05, #Alpha specifies C
                  ci=T, print.auc=T, percent=F, grid=T, main="ROC of FOXM1 in BRCA",
                  col= 'blue')
```

```
## Setting direction: controls < cases
```



```
rocobj2 <- plot.roc(data$Sample, data$SOX9, levels=c("Normal", "BRCA"), alpha=0.05, #Alpha specifies CI
  ci=T, print.auc=T, percent=F, grid=T, main="ROC of SOX9 in BRCA",
  col= 'red')
```

```
## Setting direction: controls < cases
```



```
#Check differences between two ROCs
```

```
diff<- roc.test(rocobj1, rocobj2)
```

```
#Combine two ROCs
```

```
roc1<- plot.roc(data$Sample, data$FOX1, levels=c("Normal", "BRCA"), alpha=0.05, #Alpha specifies CI  
               ci=T, print.auc=F, percent=T, grid=T, main="ROC of FOX1 and SOX9 in BRCA",  
               col= 'blue')
```

```
## Setting direction: controls < cases
```

```
Combined_roc<- plot.roc(data$Sample, data$SOX9, levels=c("Normal", "BRCA"), alpha=0.05,  
                       percent=roc1$percent, #Specify percent of previous ROC  
                       add=T, col= 'red')
```

```
## Setting direction: controls < cases
```

```
legend("bottomright", legend=c("FOXm1", "SOX9"), col=c("blue", "red"), lwd=2)
```

