fflchain: RRPlot Demo

Jose Tamez

2023-05-11

Contents

```
library(survival)
library(FRESA.CAD)
```

```
## Loading required package: Rcpp

## Loading required package: stringr

## Loading required package: miscTools

## Loading required package: Hmisc

##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:base':
##
##     format.pval, units

## Loading required package: pROC

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

##
## Attaching package: 'pROC'

## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
#library(corrplot)
#source("~/GitHub/FRESA.CAD/R/RRPlot.R")
op <- par(no.readonly = TRUE)
pander::panderOptions('digits', 3)
pander::panderOptions('keep.trailing.zeros',TRUE)
```

1 RRPLOTS and flchain

```
odata <- flchain
odata$chapter <- NULL
pander::pander(table(odata$death))
```

0	1
5705	2169

```r
rownames(odata) <- c(1:nrow(odata))
data <- as.data.frame(model.matrix(Surv(futime,death)~.,odata))

data$`(Intercept)` <- NULL

dataFL <- as.data.frame(cbind(time=odata[rownames(data),"futime"],
                              status=odata[rownames(data),"death"],
                              data))
pander::pander(table(dataFL$status))
```

0	1
4562	1962

1.1 Exploring Raw Features with RRPlot
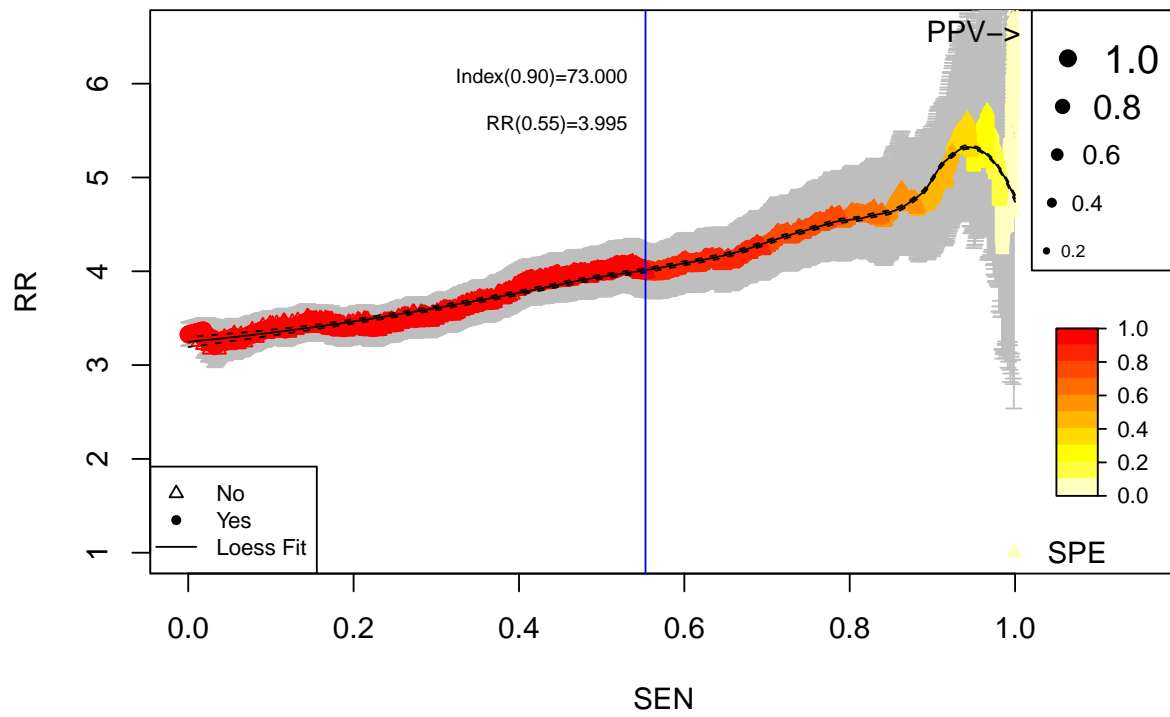
```r
convar <- colnames(dataFL)[lapply(apply(dataFL,2,unique),length) > 10]
convar <- convar[convar != "time"]
topvar <- univariate_BinEnsemble(dataFL[,c("status",convar)],"status")
pander::pander(topvar)
```

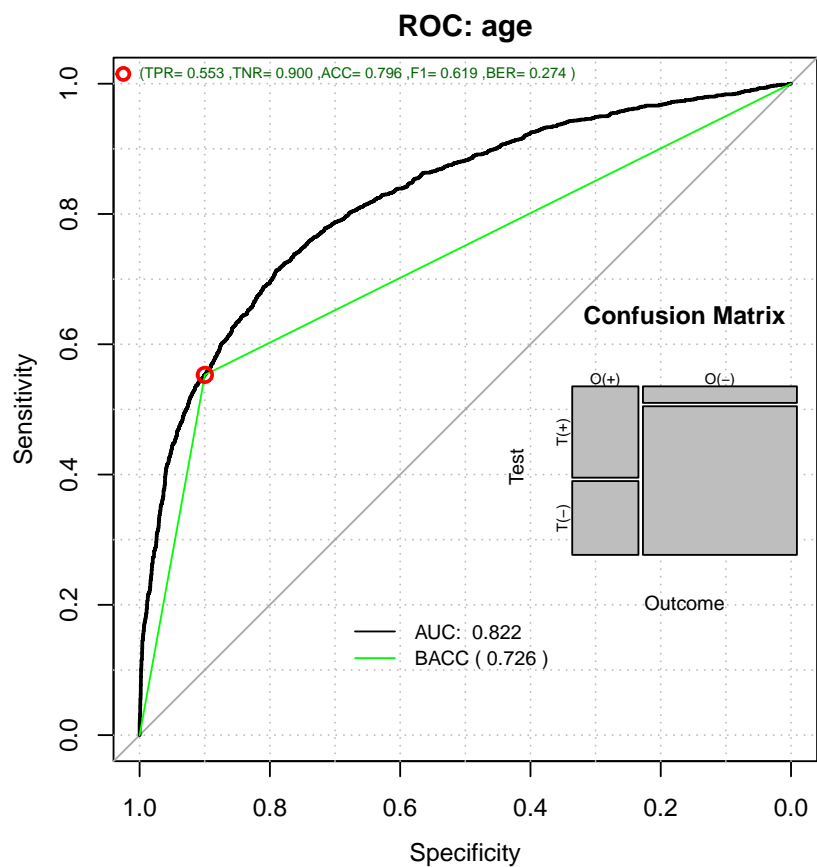| age	kappa	lambda	creatinine
0	0	0	0

```r
topv <- min(5,length(topvar))
topFive <- names(topvar)[1:topv]

topFeature <- RRPlot(cbind(dataFL$status,dataFL[,topFive[1]]),
                 title=topFive[1])
```

Relative Risk: age

ROC: age

(TPR= 0.553 ,TNR= 0.900 ,ACC= 0.796 ,F1= 0.619 ,BER= 0.274)

AUC: 0.822
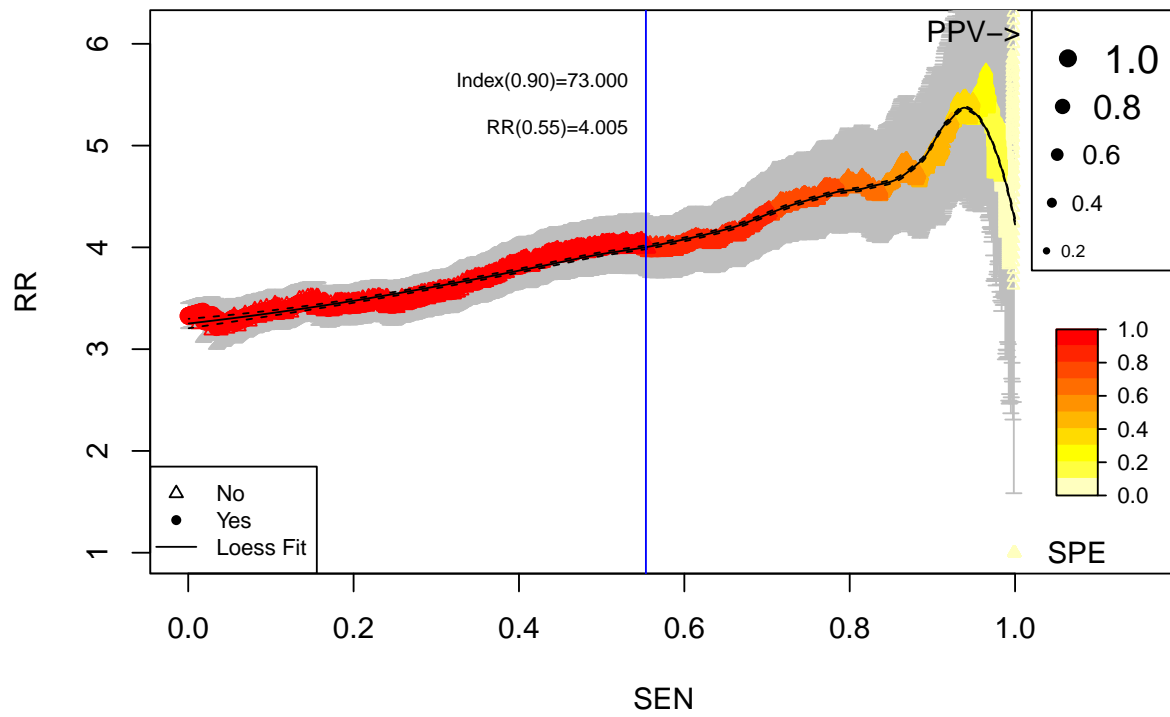BACC (0.726)

Confusion Matrix

```
  par(op)

## With Survival Analysis
RRanalysis <- list();
idx <- 1
for (topf in topFive)
{
  RRanalysis[[idx]] <- RRPlot(cbind(dataFL$status,dataFL[,topf]),
                 timetoEvent=dataFL$time,
                 atProb=c(0.90,0.80),
                 title=topf)
  idx <- idx + 1
  par(op)
}
```

Relative Risk: age

Index(0.90)=73.000

RR(0.55)=4.005

PPV->

- 1.0
- 0.8
- 0.6
- 0.4
- 0.2

1.0
0.8
0.6
0.4
0.2
0.0

△ No
● Yes
— Loess Fit

SPE

RR

SEN

ROC: age

(TPR= 0.554 ,TNR= 0.900 ,ACC= 0.796 ,F1= 0.620 ,BER= 0.273)

AUC: 0.822
BACC (0.727)

Confusion Matrix

O(+) O(−)

Test
T(+)
T(−)

Outcome

Sensitivity

Specificity

6

Kaplan–Meier: age

Strata + Low Risk < 69.000 + 69.000 <= Risk < 73.000 + High Risk >= 73.000
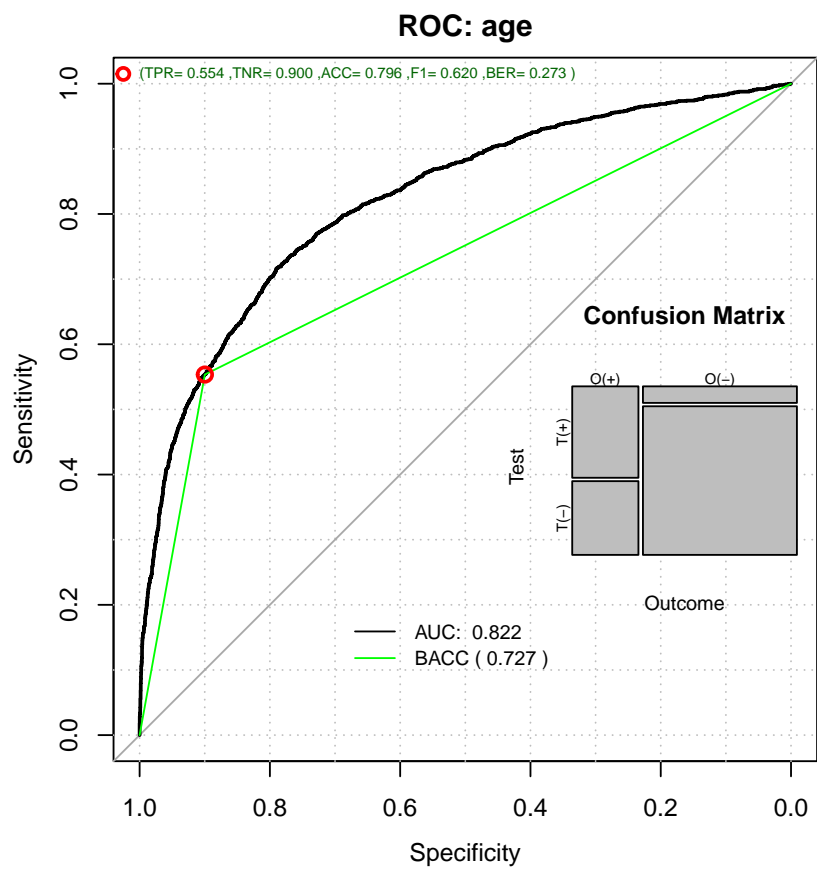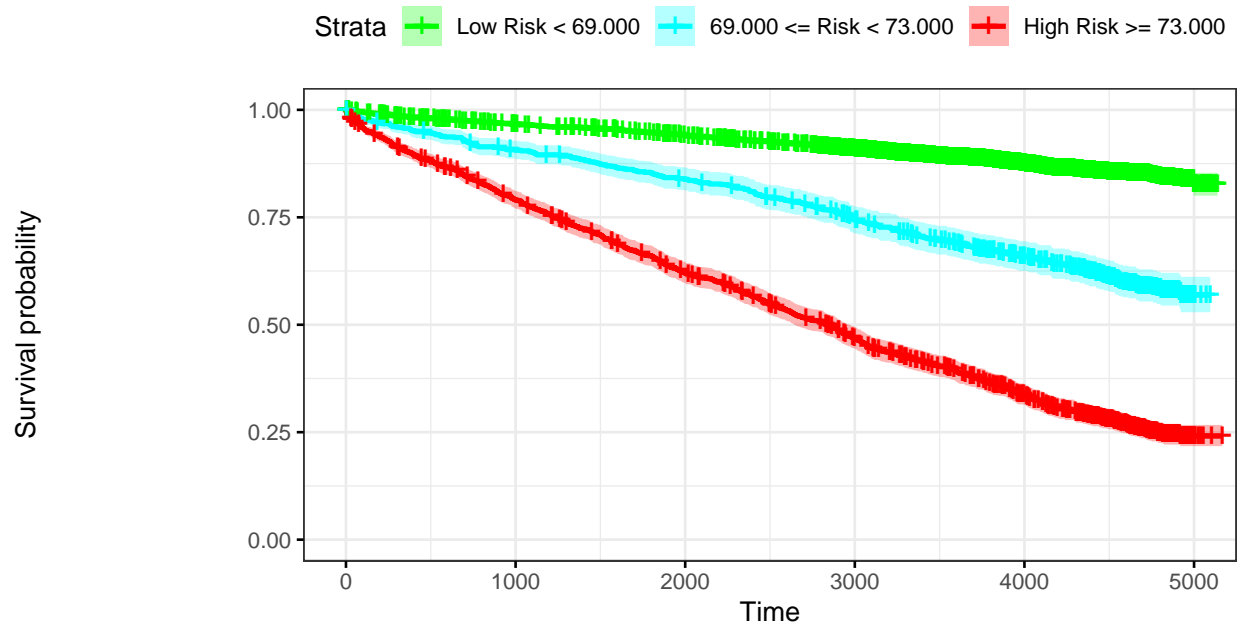
Number at risk

Low Risk < 69.000	4234	4011	3855	3601	2933	53
69.000 <= Risk < 73.000	747	672	618	534	423	17
High Risk >= 73.000	1543	1204	934	680	437	11

Relative Risk: kappa

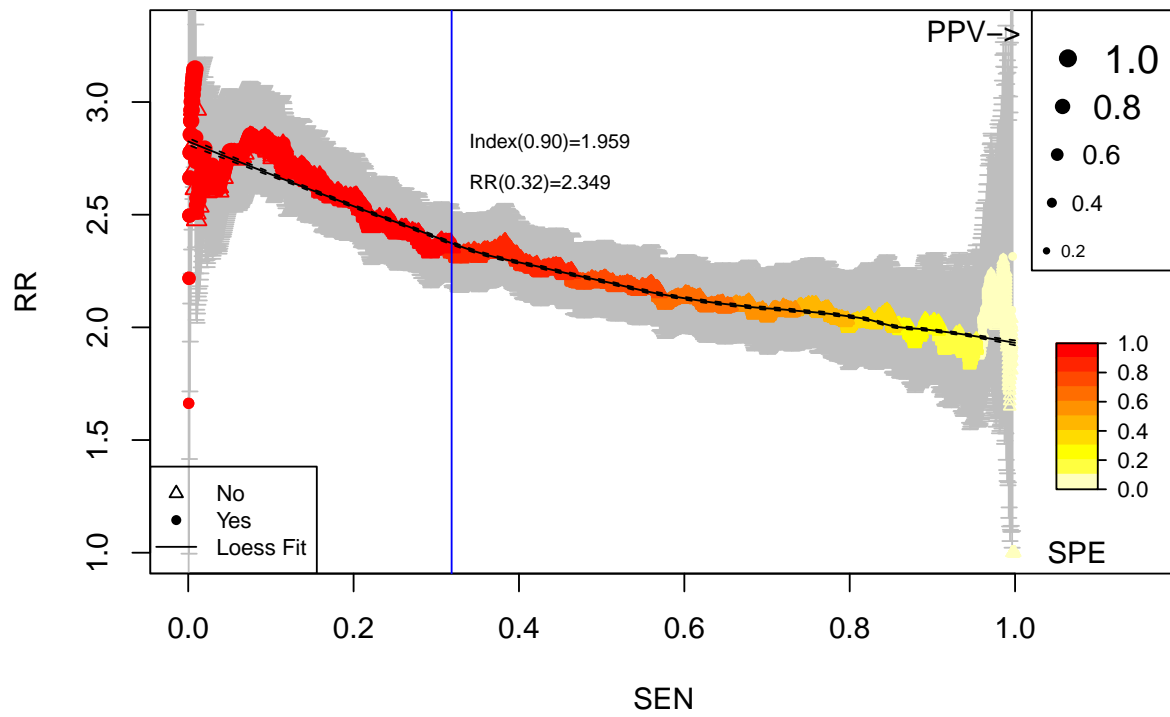Index(0.90)=1.959

RR(0.32)=2.349

PPV−>

SPE

RR

SEN

No
Yes
Loess Fit

ROC: kappa

(TPR= 0.319 ,TNR= 0.900 ,ACC= 0.725 ,F1= 0.411 ,BER= 0.391)

Sensitivity

Specificity

AUC: 0.682
BACC (0.609)

Confusion Matrix

O(+)　　　　O(−)

T(+)

Test

T(−)

Outcome

Kaplan−Meier: kappa

Strata + Low Risk < 1.640 + 1.640 <= Risk < 1.959 + High Risk >= 1.959
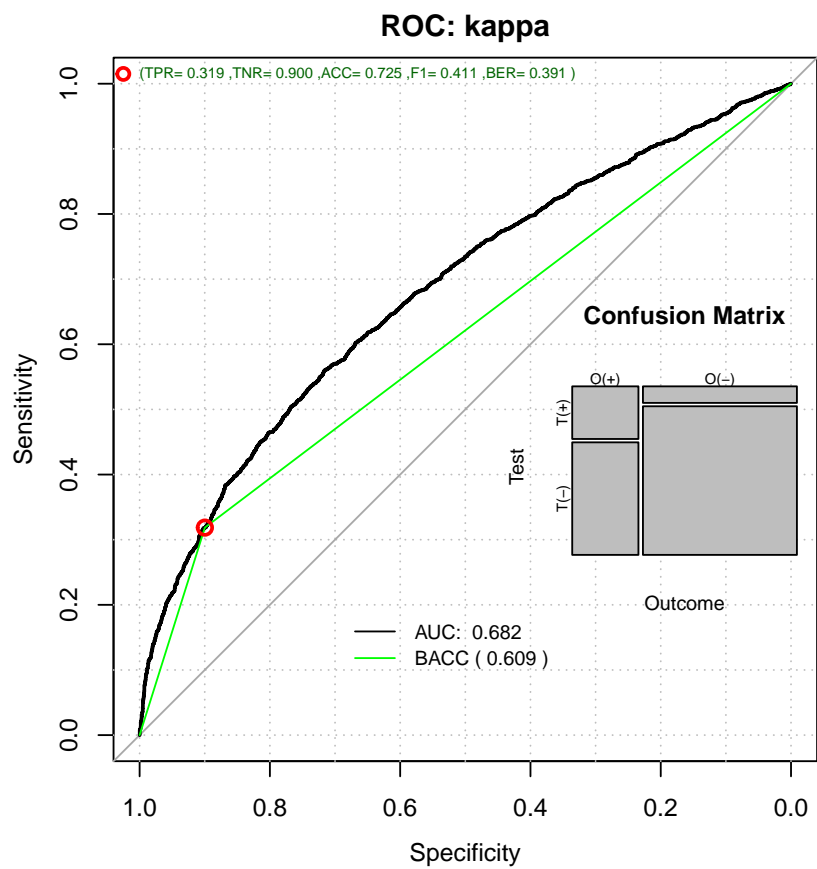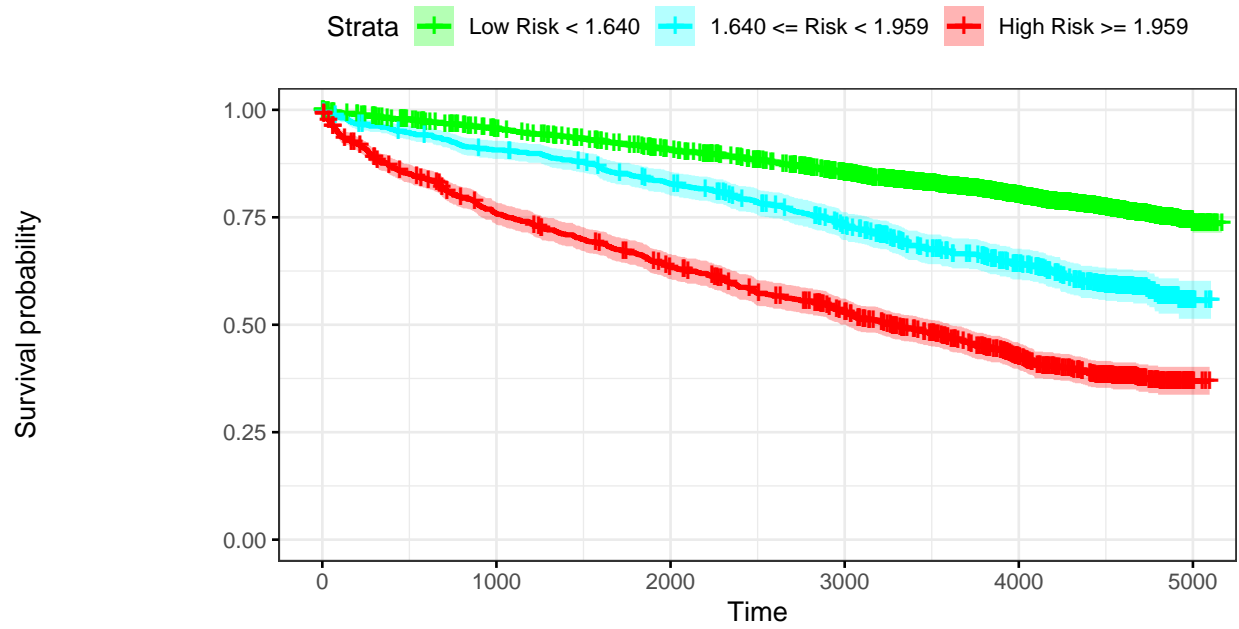
Number at risk

Low Risk < 1.640	4699	4419	4147	3788	3095	70
1.640 <= Risk < 1.959	743	667	601	505	365	6
High Risk >= 1.959	1082	801	659	522	333	5

Relative Risk: lambda
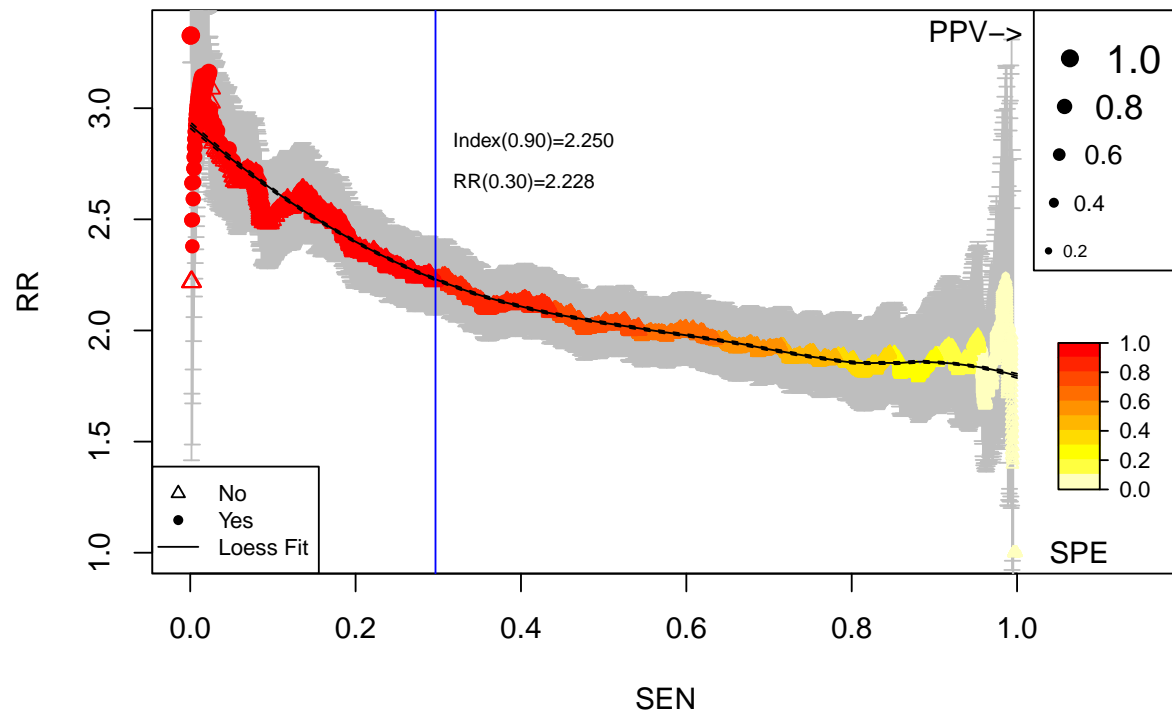
ROC: lambda

(TPR= 0.297 ,TNR= 0.900 ,ACC= 0.718 ,F1= 0.388 ,BER= 0.402)

Sensitivity

Specificity

Confusion Matrix

O(+)   O(−)

T(+)

Test

T(−)

Outcome

AUC: 0.665

BACC (0.598)

Kaplan–Meier: lambda

Strata + Low Risk < 1.900 + 1.900 <= Risk < 2.250 + High Risk >= 2.250
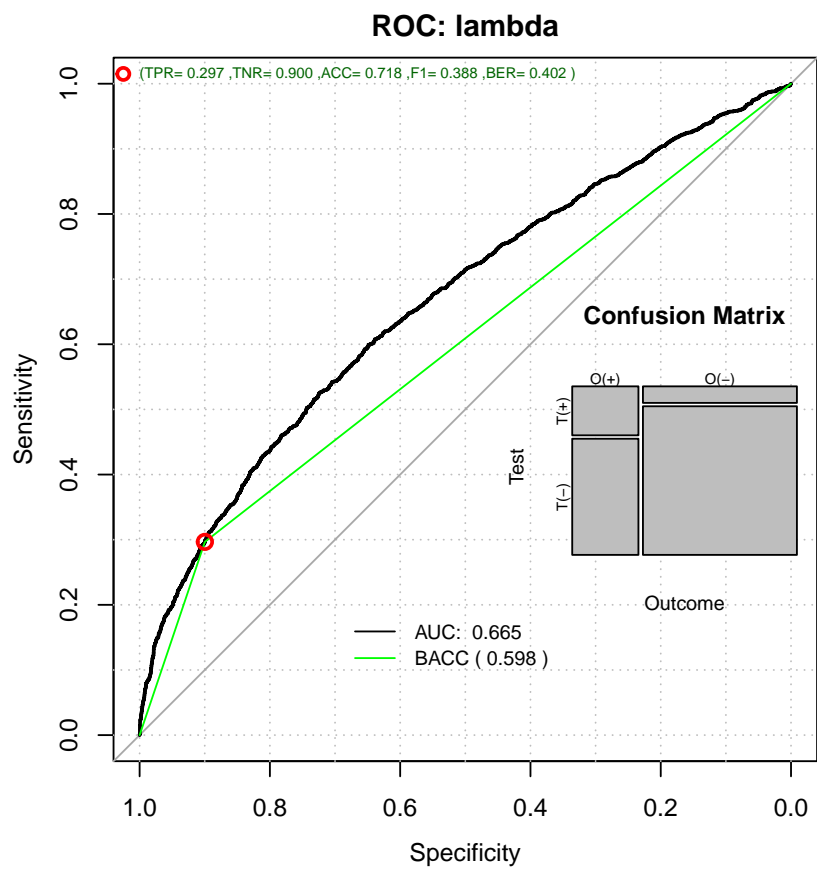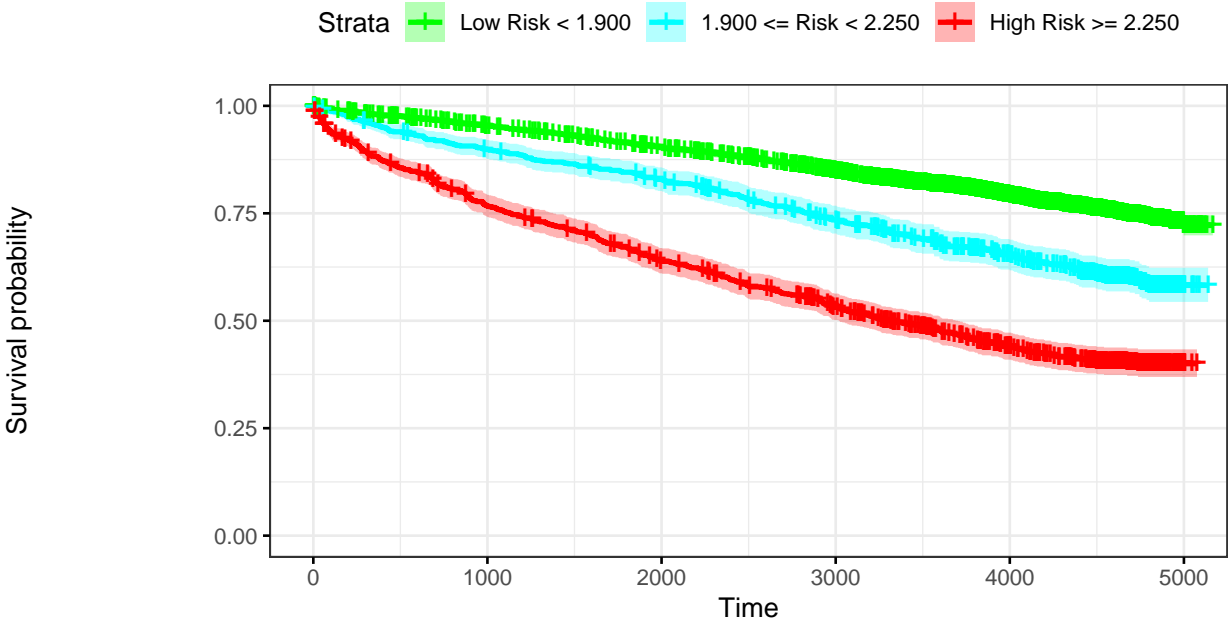
Number at risk

Low Risk < 1.900	4754	4455	4174	3808	3079	62
1.900 <= Risk < 2.250	731	650	593	503	375	11
High Risk >= 2.250	1039	782	640	504	339	8

13

Relative Risk: creatinine

ROC: creatinine

(TPR= 0.244 ,TNR= 0.900 ,ACC= 0.703 ,F1= 0.331 ,BER= 0.428)

Sensitivity

Specificity

AUC: 0.589
BACC (0.572)

Confusion Matrix

O(+)   O(−)

T(+)

Test

T(−)

Outcome
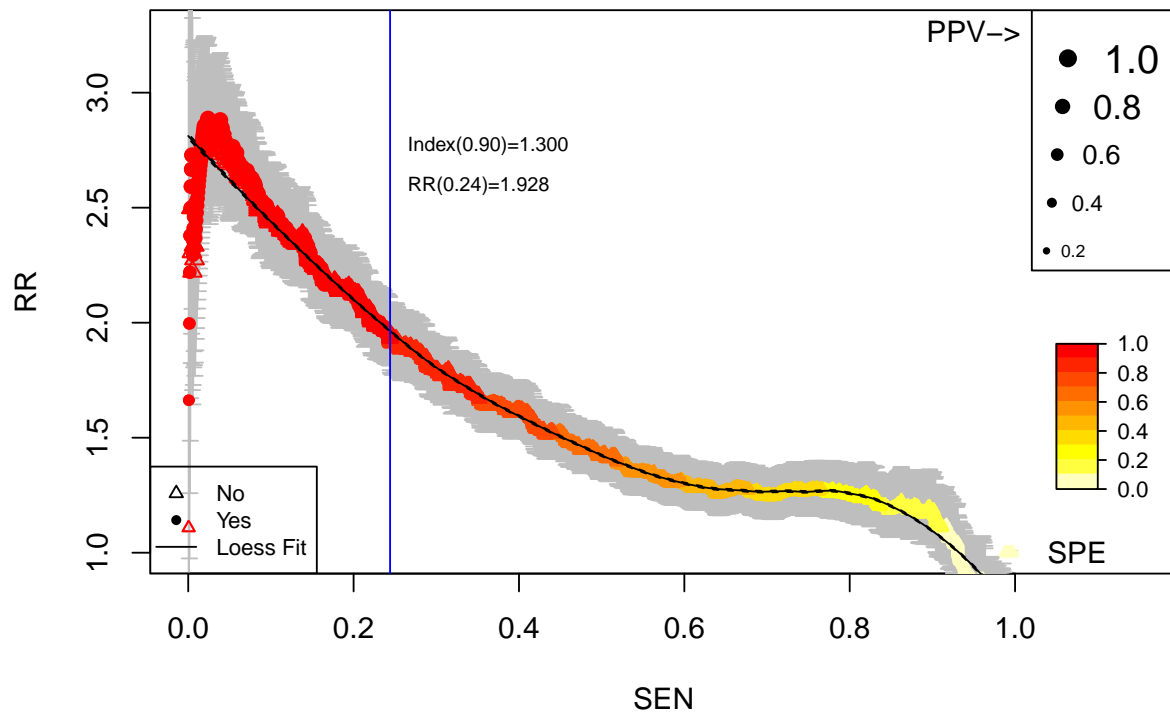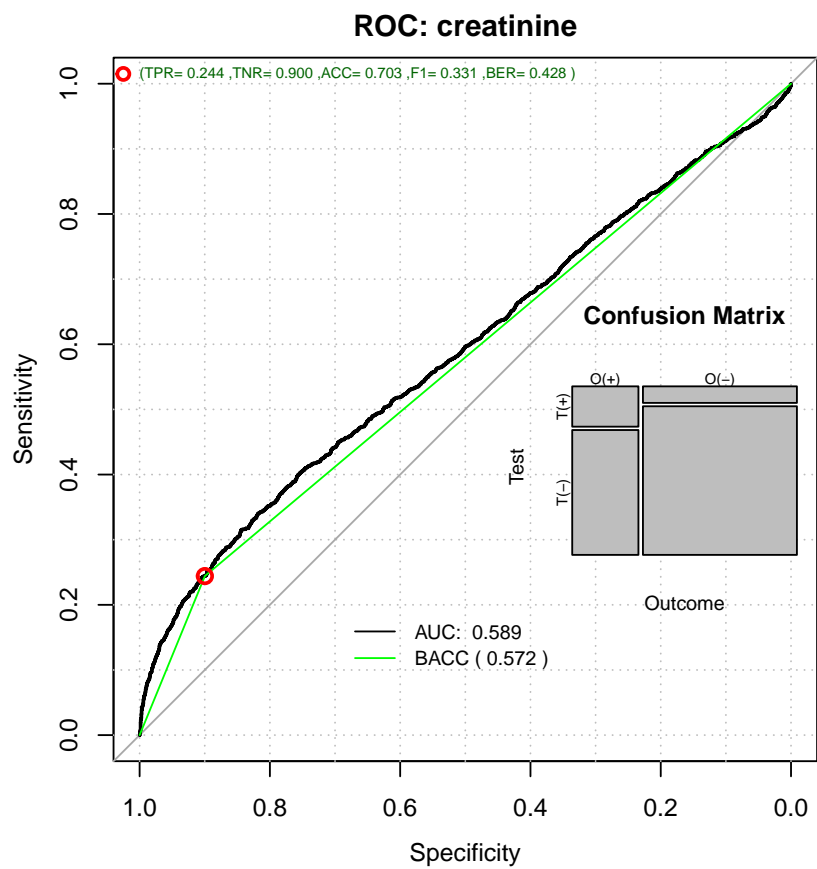
Kaplan–Meier: creatinine

Strata ┼ Low Risk < 1.200 ┼ 1.200 <= Risk < 1.300 ┼ High Risk >= 1.300
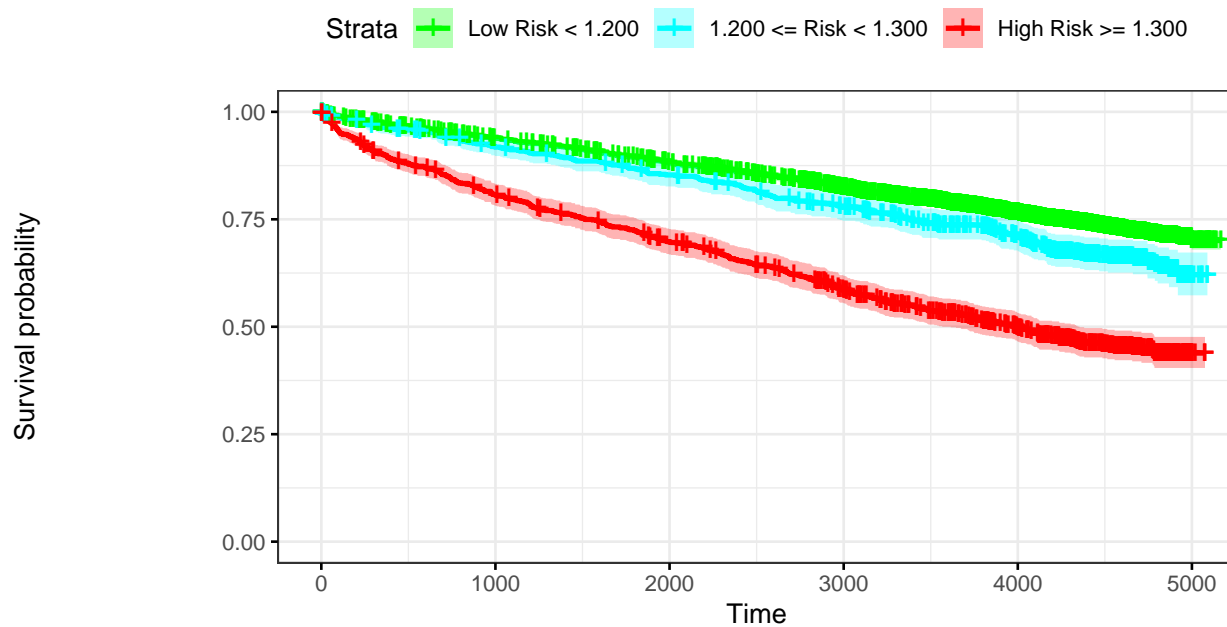
Number at risk

Low Risk < 1.200	4920	4544	4223	3822	3089	70
1.200 <= Risk < 1.300	668	598	551	488	367	6
High Risk >= 1.300	936	745	633	505	337	5

```
names(RRanalysis) <- topFive
```

1.2   Reporting the Metrics

```
pander::pander(t(RRanalysis[[1]]$keyPoints),caption="Threshold values")
```

Table 4: Threshold values

	@:0.9	@:0.8	@MAX_BACC	@MAX_RR	@SPE100
Thr	73.000	69.000	68.000	54.000	50.00000
RR	4.002	4.352	4.450	5.741	1.00000
SEN	0.554	0.702	0.717	0.965	1.00000
SPE	0.900	0.800	0.790	0.232	0.00175
BACC	0.727	0.751	0.753	0.599	0.50088

```
ROCAUC <- NULL
CstatCI <- NULL
RRatios <- NULL
LogRangp <- NULL
Sensitivity <- NULL
Specificity <- NULL

for (topf in topFive)
{
```

16

```
  CstatCI <- rbind(CstatCI,RRanalysis[[topf]]$c.index$cstatCI)
  RRatios <- rbind(RRatios,RRanalysis[[topf]]$RR_atP)
  LogRangp <- rbind(LogRangp,RRanalysis[[topf]]$surdif$pvalue)
  Sensitivity <- rbind(Sensitivity,RRanalysis[[topf]]$ROCAnalysis$sensitivity)
  Specificity <- rbind(Specificity,RRanalysis[[topf]]$ROCAnalysis$specificity)
  ROCAUC <- rbind(ROCAUC,RRanalysis[[topf]]$ROCAnalysis$aucs)
}
rownames(CstatCI) <- topFive
rownames(RRatios) <- topFive
rownames(LogRangp) <- topFive
rownames(Sensitivity) <- topFive
rownames(Specificity) <- topFive
rownames(ROCAUC) <- topFive

pander::pander(ROCAUC)
```

	est	lower	upper
age	0.822	0.811	0.833
kappa	0.682	0.667	0.697
lambda	0.665	0.650	0.680
creatinine	0.589	0.573	0.604

```
pander::pander(CstatCI)
```

	mean.C Index	median	lower	upper
age	0.775	0.775	0.764	0.785
kappa	0.671	0.671	0.658	0.684
lambda	0.657	0.657	0.644	0.670
creatinine	0.585	0.585	0.571	0.598

```
pander::pander(RRatios)
```

	est	lower	upper
age	4.01	3.74	4.29
kappa	2.35	2.19	2.52
lambda	2.23	2.08	2.39
creatinine	1.93	1.79	2.08

```
pander::pander(LogRangp)
```

age	0.00e+00
kappa	1.53e-176
lambda	1.22e-143
creatinine	8.94e-75

```
pander::pander(Sensitivity)
```

	est	lower	upper
age	0.554	0.531	0.576
kappa	0.319	0.298	0.340
lambda	0.297	0.276	0.317
creatinine	0.244	0.225	0.264

```
pander::pander(Specificity)
```

	est	lower	upper
age	0.9	0.891	0.908
kappa	0.9	0.891	0.908
lambda	0.9	0.891	0.908
creatinine	0.9	0.891	0.908

```
meanMatrix <- cbind(ROCAUC[,1],CstatCI[,1],Sensitivity[,1],Specificity[,1],RRatios[,1])
colnames(meanMatrix) <- c("ROCAUC","C-Stat","Sen","Spe","RR")
pander::pander(meanMatrix)
```

	ROCAUC	C-Stat	Sen	Spe	RR
age	0.822	0.775	0.554	0.9	4.01
kappa	0.682	0.671	0.319	0.9	2.35
lambda	0.665	0.657	0.297	0.9	2.23
creatinine	0.589	0.585	0.244	0.9	1.93