fflchain: RRPlot Demo

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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

```
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
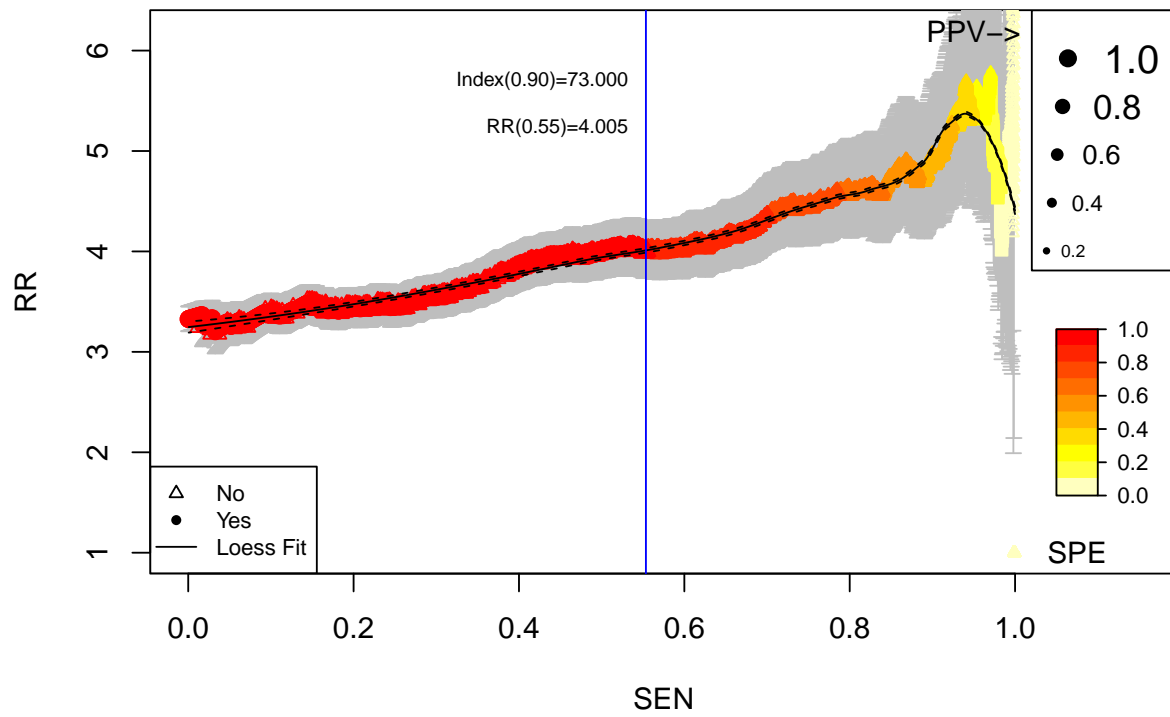
```
convar <- colnames(dataFL)[lapply(apply(dataFL,2,unique),length) > 10]
convar <- convar[convar != "time"]
topvar <- univariate_BinEnsemble(dataFL[,c("status",convar)],"status")
pander::pander(topvar)
```
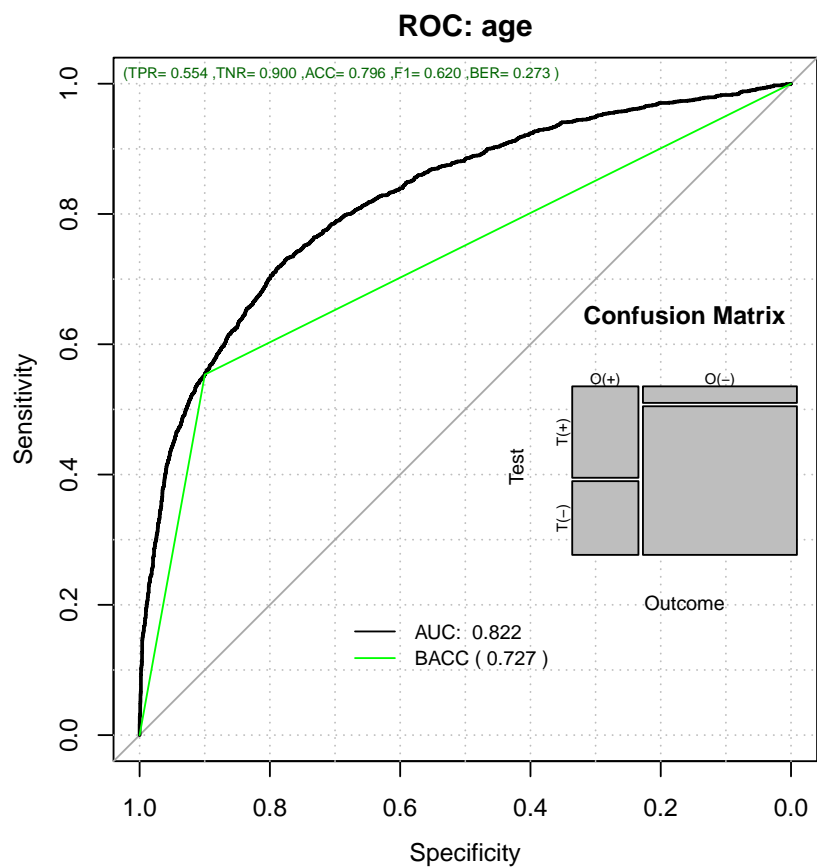
age	kappa	lambda	creatinine
0	0	0	0

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

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

Relative Risk: age

PPV->

SPE

Index(0.90)=73.000

RR(0.55)=4.005

RR

SEN

△ No
● Yes
— Loess Fit

● 1.0
● 0.8
● 0.6
· 0.4
· 0.2

1.0
0.8
0.6
0.4
0.2
0.0

ROC: age

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

Confusion Matrix

AUC: 0.822
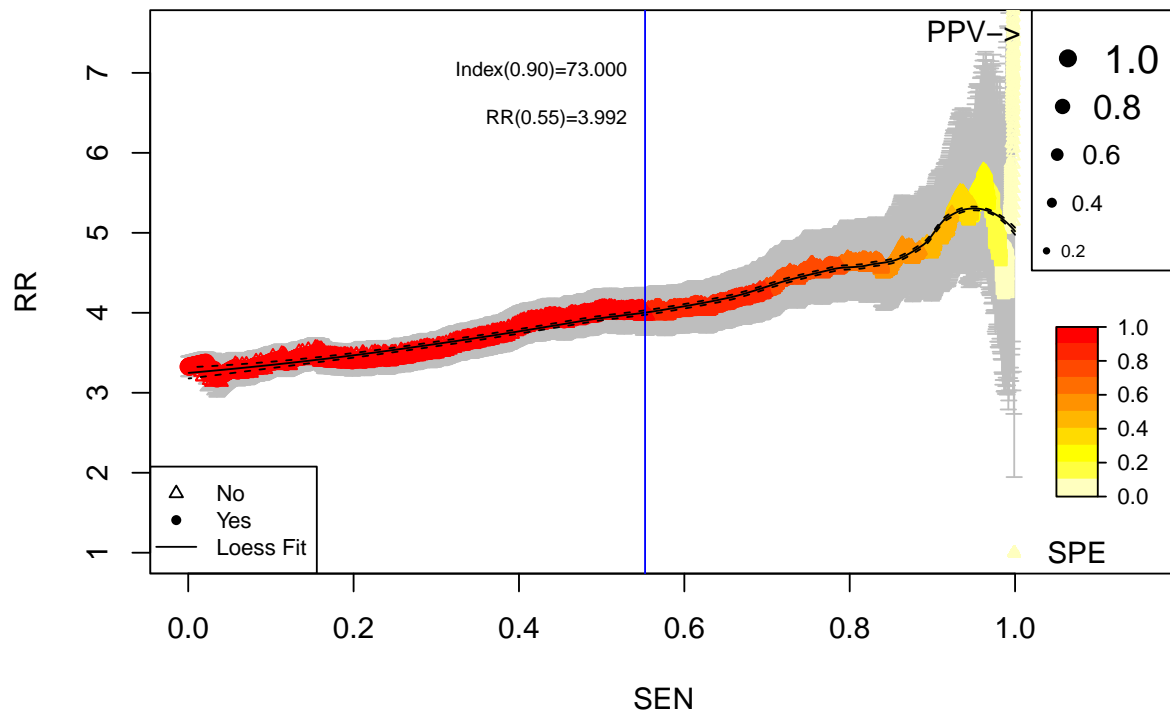BACC (0.727)

Sensitivity

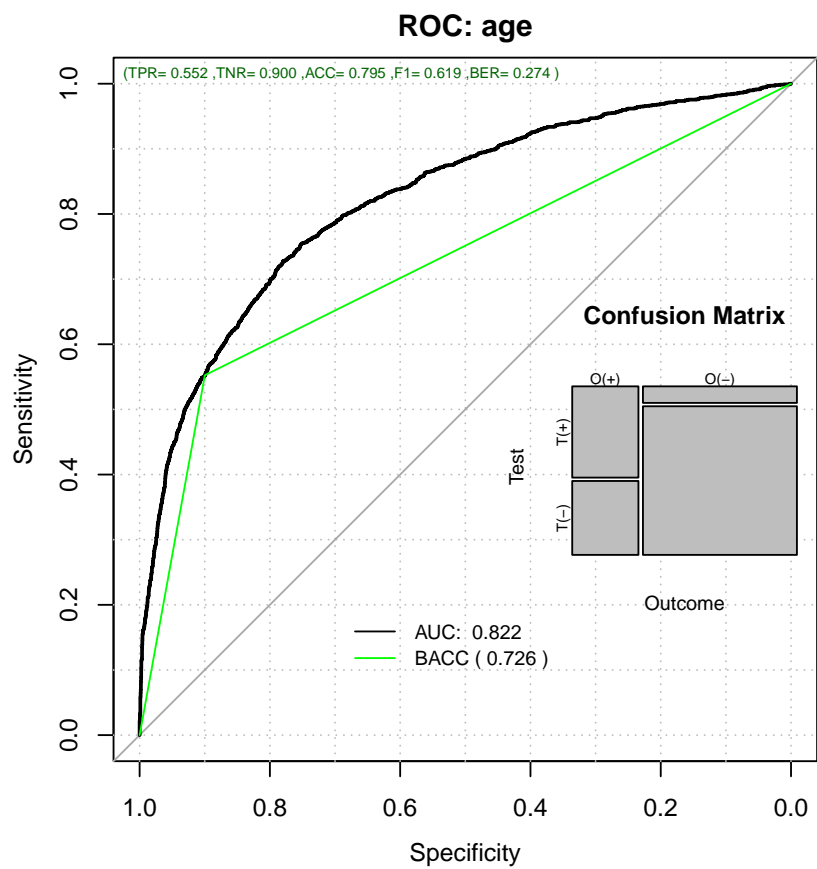Specificity

```
  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)
}
```
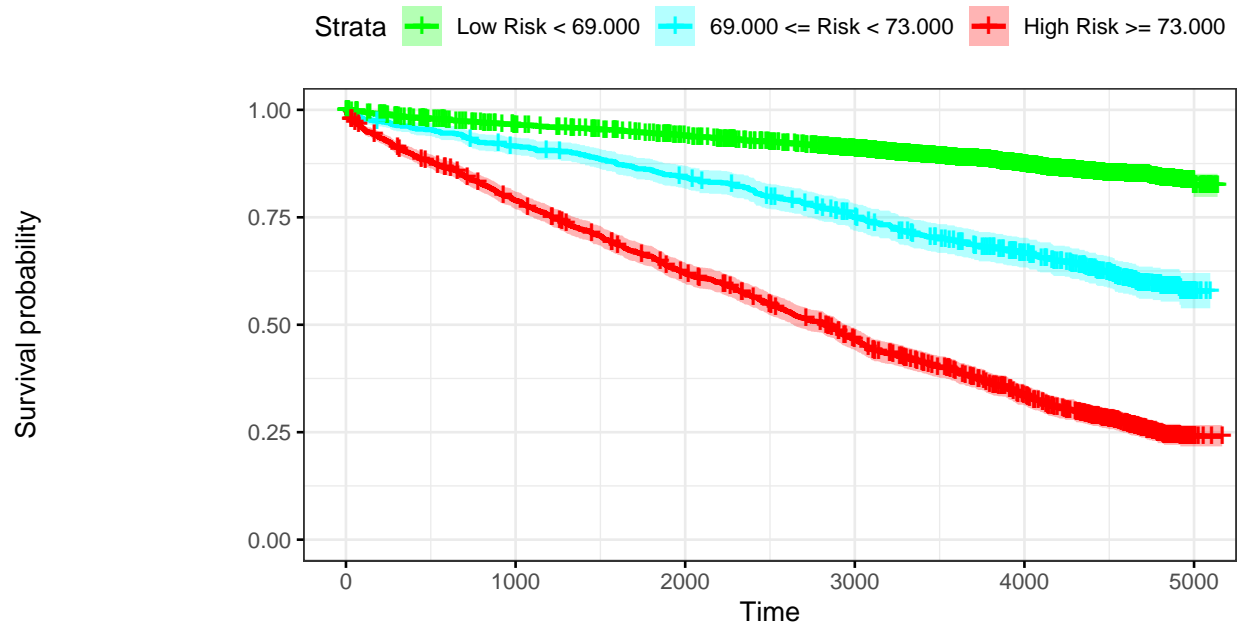
Relative Risk: age

ROC: age

(TPR= 0.552 ,TNR= 0.900 ,ACC= 0.795 ,F1= 0.619 ,BER= 0.274)

Sensitivity

Specificity

Confusion Matrix

O(+) O(−)

T(+)

Test

T(−)

Outcome

AUC: 0.822
BACC (0.726)

Kaplan−Meier: age

Strata ┼ Low Risk < 69.000 ┼ 69.000 <= Risk < 73.000 ┼ High Risk >= 73.000

Number at risk

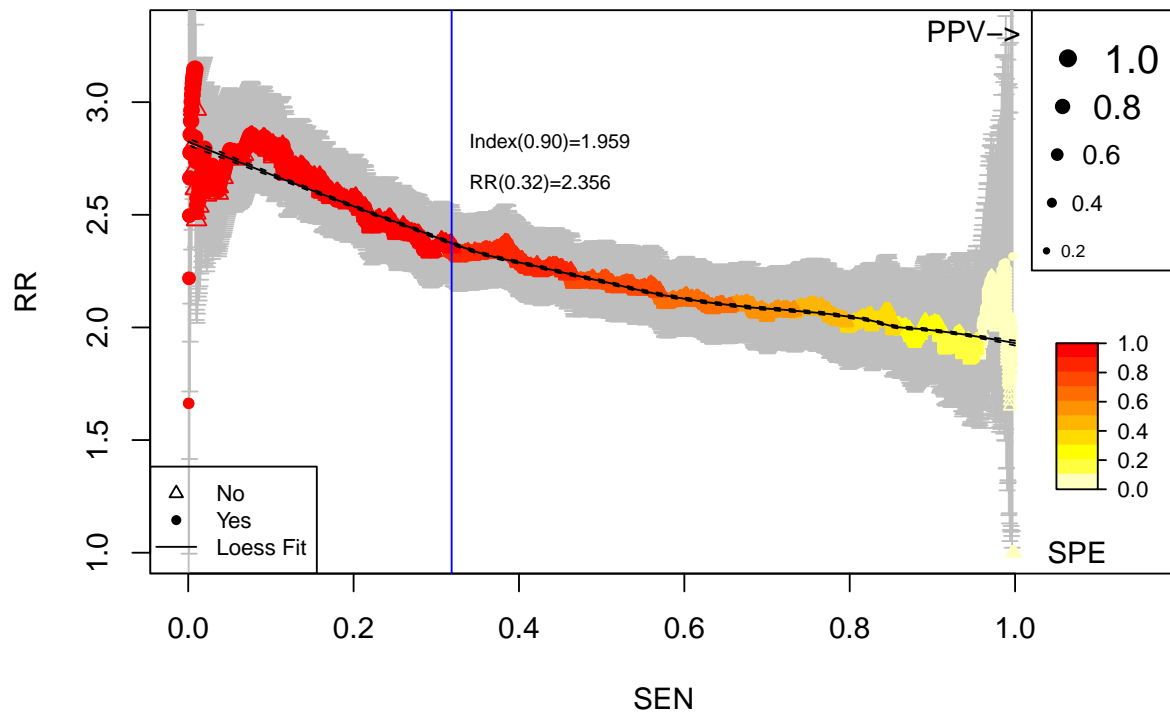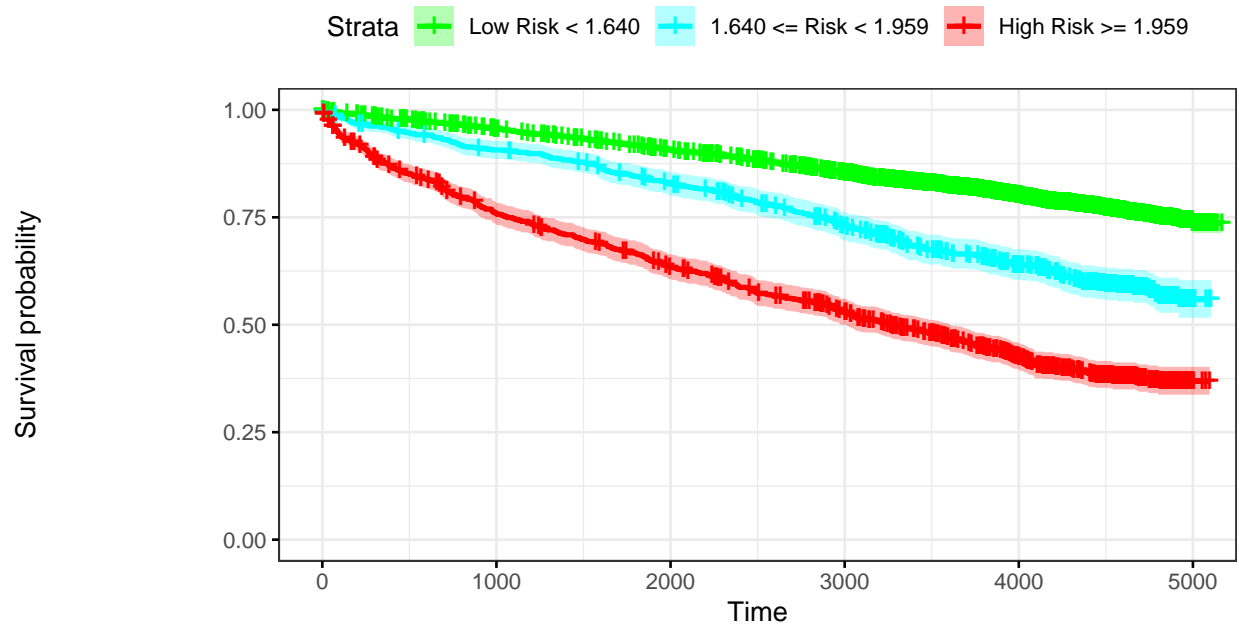|						
Low Risk < 69.000	4244	4014	3860	3607	2935	52
69.000 <= Risk < 73.000	739	673	616	532	424	20
High Risk >= 73.000	1541	1200	931	676	434	9

Relative Risk: kappa

ROC: kappa

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

Sensitivity

Specificity

Confusion Matrix

O(+)   O(−)

T(+)

Test

T(−)

Outcome

AUC: 0.682
BACC (0.609)

9

Kaplan−Meier: kappa

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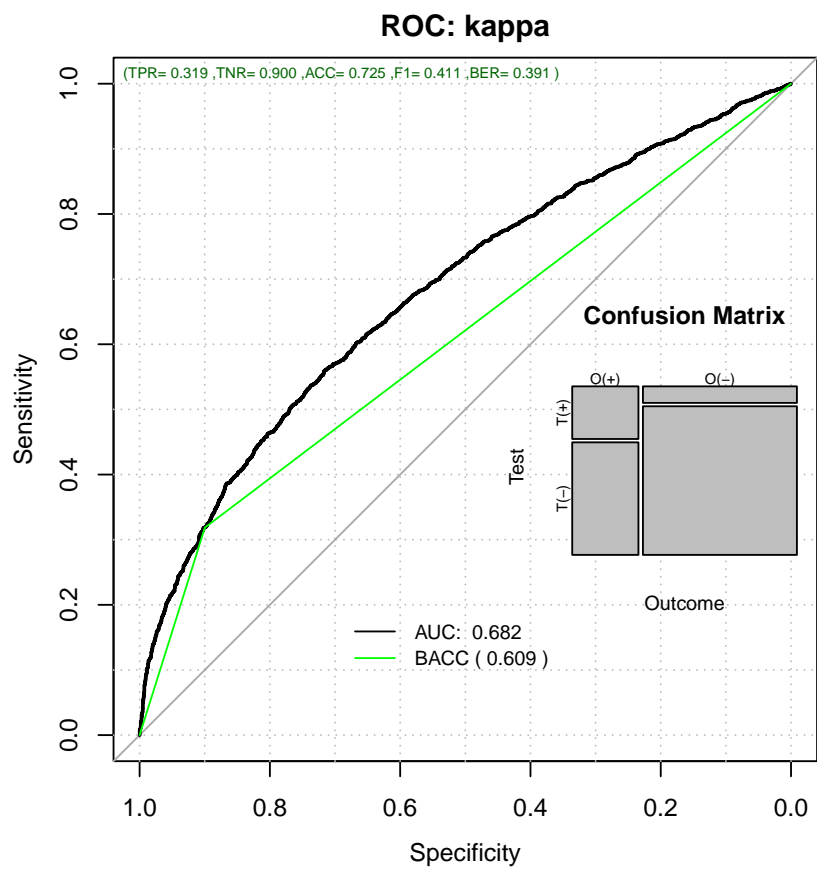
Number at risk

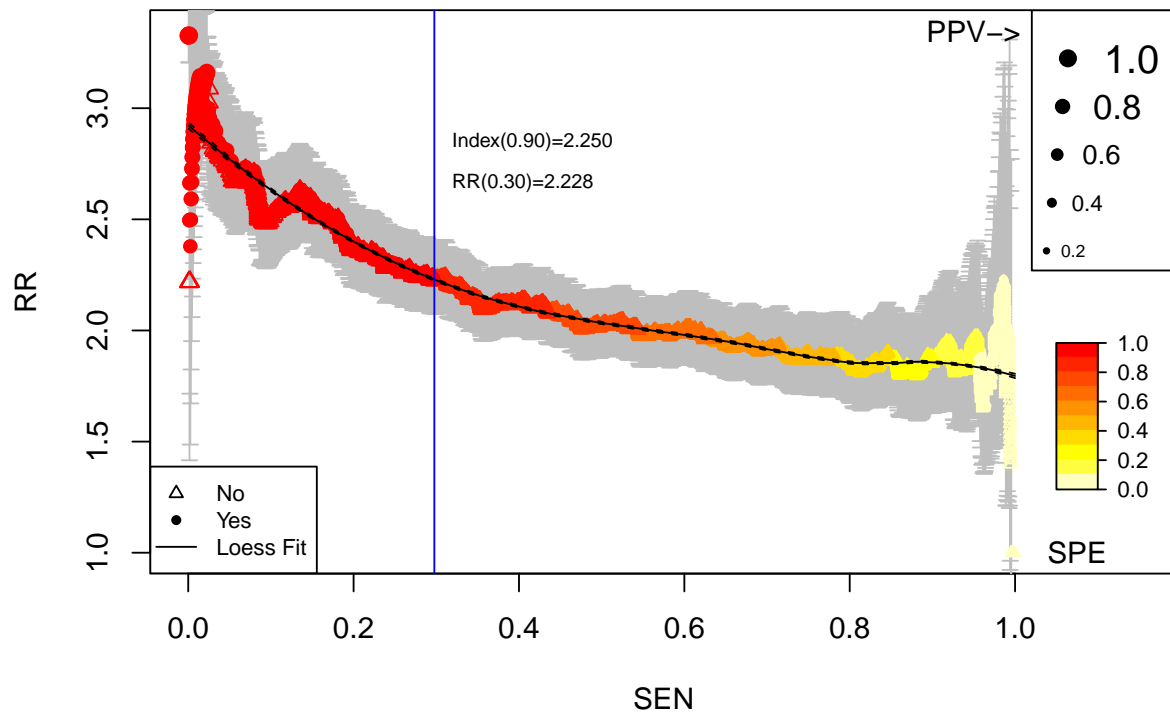|					
Low Risk < 1.640	4700	4420	4149	3790	3094	69
1.640 <= Risk < 1.959	742	666	599	503	366	7
High Risk >= 1.959	1082	801	659	522	333	5

Relative Risk: lambda

ROC: lambda

(TPR= 0.298 ,TNR= 0.900 ,ACC= 0.719 ,F1= 0.389 ,BER= 0.401)

Sensitivity

Specificity

Confusion Matrix

O(+) O(−)

T(+)

Test

T(−)

Outcome

AUC: 0.665
BACC (0.599)

Kaplan–Meier: lambda

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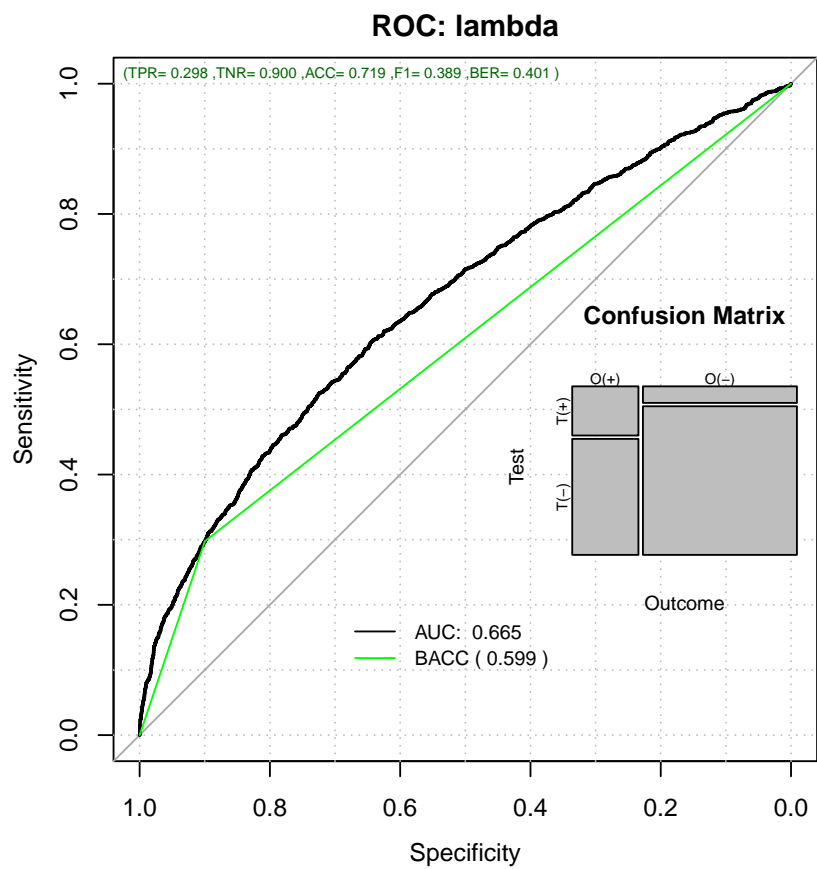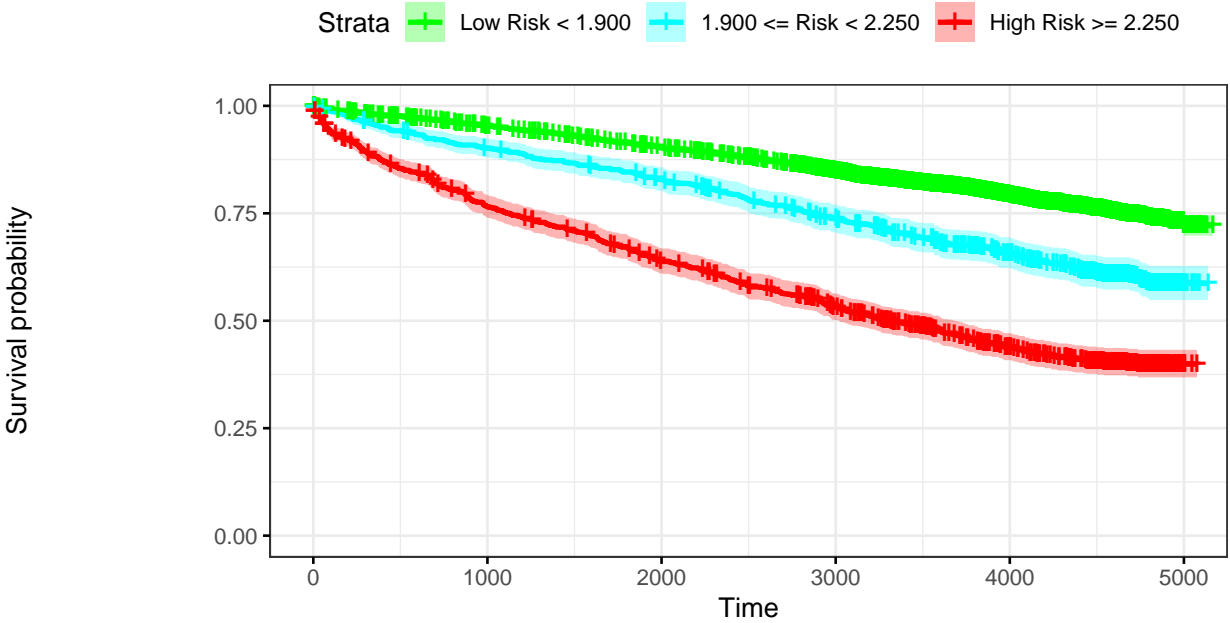
Number at risk

Low Risk < 1.900	4756	4456	4176	3808	3079	61
1.900 <= Risk < 2.250	727	649	590	503	375	13
High Risk >= 2.250	1041	782	641	504	339	7

Relative Risk: creatinine

ROC: creatinine

(TPR= 0.242 ,TNR= 0.900 ,ACC= 0.702 ,F1= 0.328 ,BER= 0.429)

Confusion Matrix

O(+)   O(−)

T(+)

Test

T(−)

Outcome

AUC: 0.591
BACC (0.571)

Sensitivity

Specificity
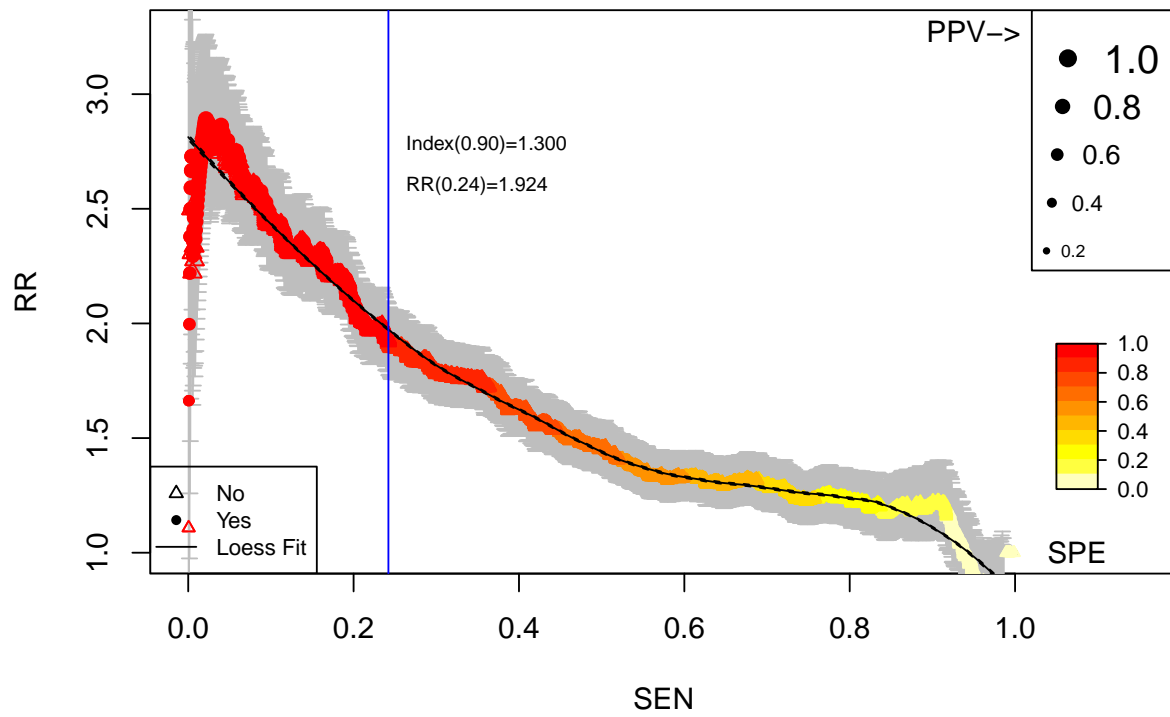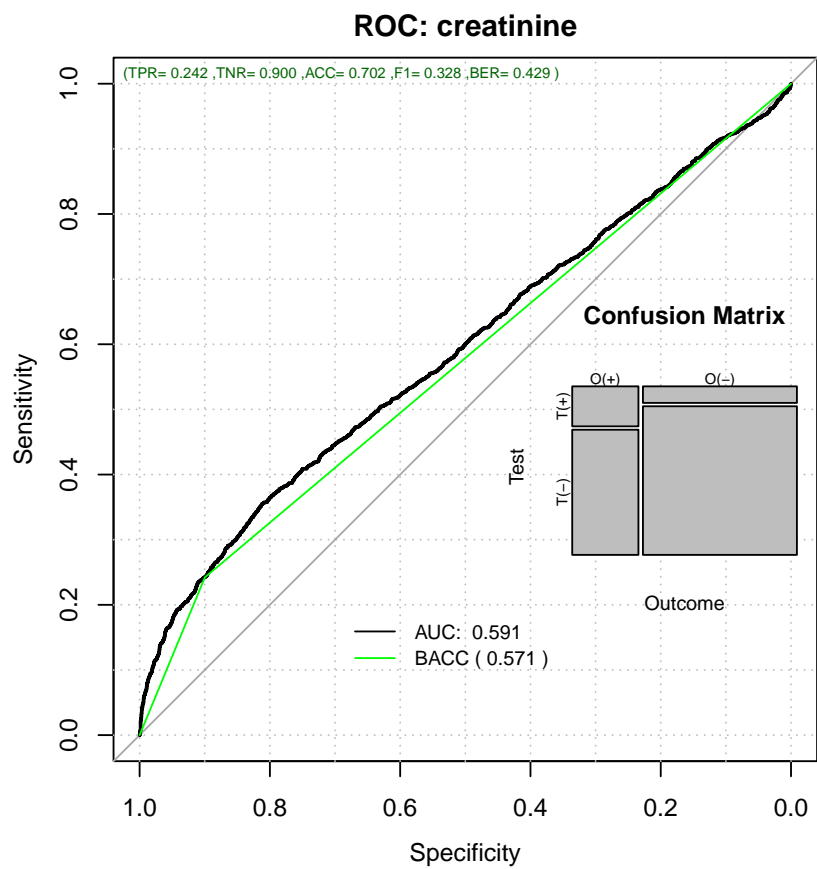
Kaplan–Meier: creatinine

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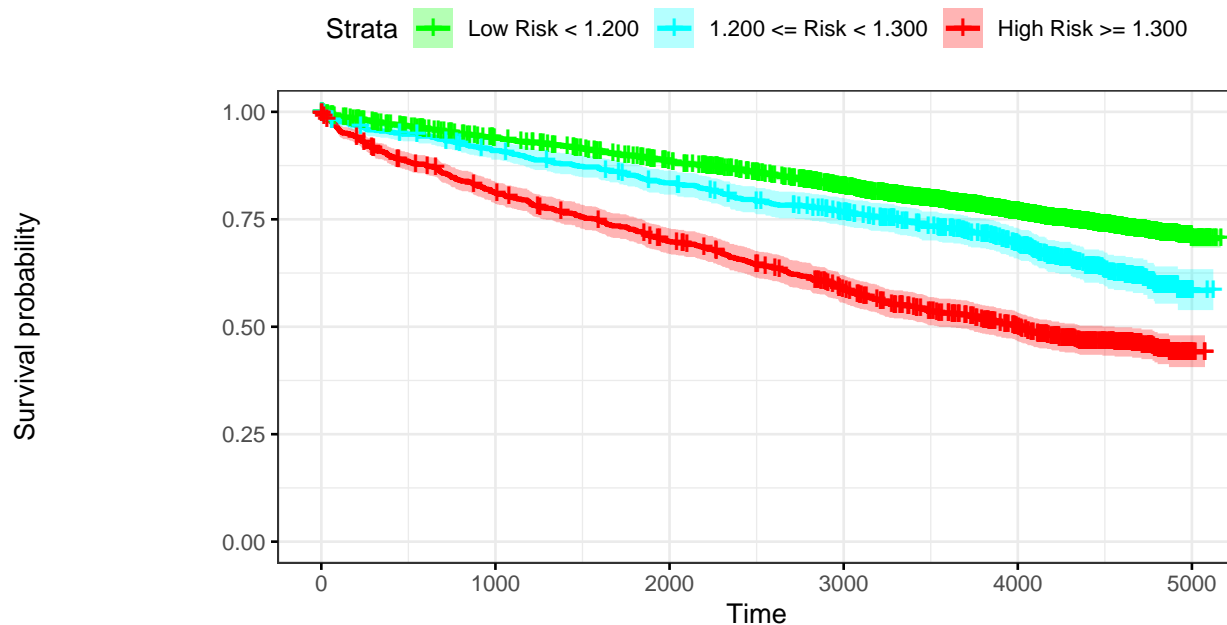
Number at risk

Low Risk < 1.200	4896	4523	4213	3812	3085	72
1.200 <= Risk < 1.300	696	621	564	499	358	3
High Risk >= 1.300	932	743	630	504	350	6

```
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	3.992	4.284	4.496	5.793	1.00000
SEN	0.552	0.697	0.728	0.962	1.00000
SPE	0.900	0.800	0.780	0.251	0.00175
BACC	0.726	0.749	0.754	0.606	0.50088

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


for (topf in topFive)
{
```

```
  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	0.834
kappa	0.682	0.667	0.696
lambda	0.665	0.650	0.680
creatinine	0.591	0.575	0.607

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

	mean.C Index	median	lower	upper
age	0.775	0.774	0.764	0.785
kappa	0.671	0.671	0.658	0.683
lambda	0.657	0.657	0.644	0.670
creatinine	0.587	0.587	0.573	0.601

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

	est	lower	upper
age	3.99	3.73	4.27
kappa	2.36	2.20	2.52
lambda	2.23	2.08	2.39
creatinine	1.92	1.78	2.08

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

age	0.00e+00
kappa	2.64e-176
lambda	4.02e-144
creatinine	5.52e-75

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

	est	lower	upper
age	0.552	0.530	0.575
kappa	0.319	0.298	0.340
lambda	0.298	0.277	0.318
creatinine	0.242	0.223	0.262

```
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	0.552	0.9	3.99
kappa	0.682	0.671	0.319	0.9	2.36
lambda	0.665	0.657	0.298	0.9	2.23
creatinine	0.591	0.587	0.242	0.9	1.92