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))
```

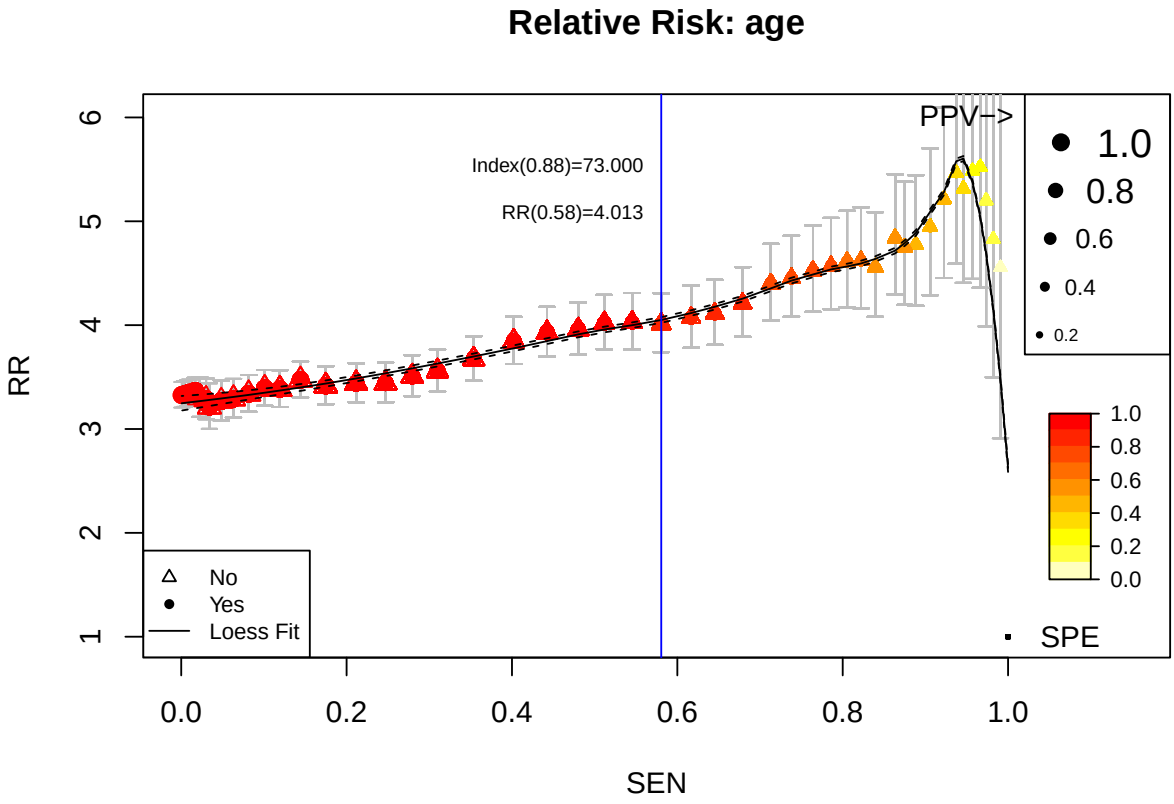
0	1
4562	1962

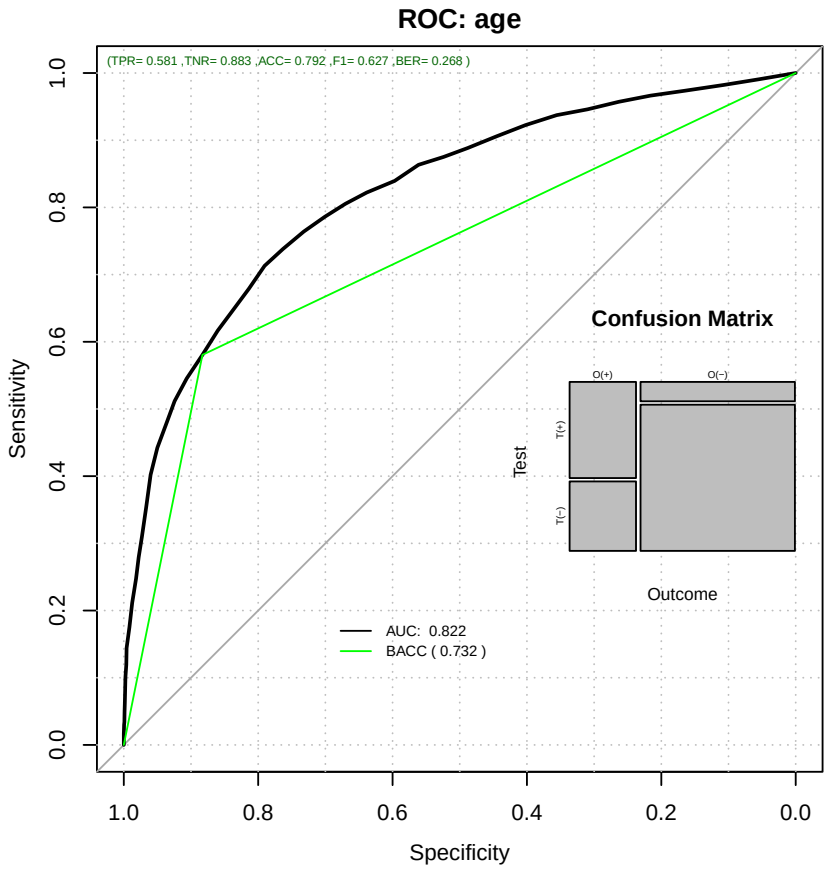
1.1 Exploring Raw Features with RRPlot

```
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)
```

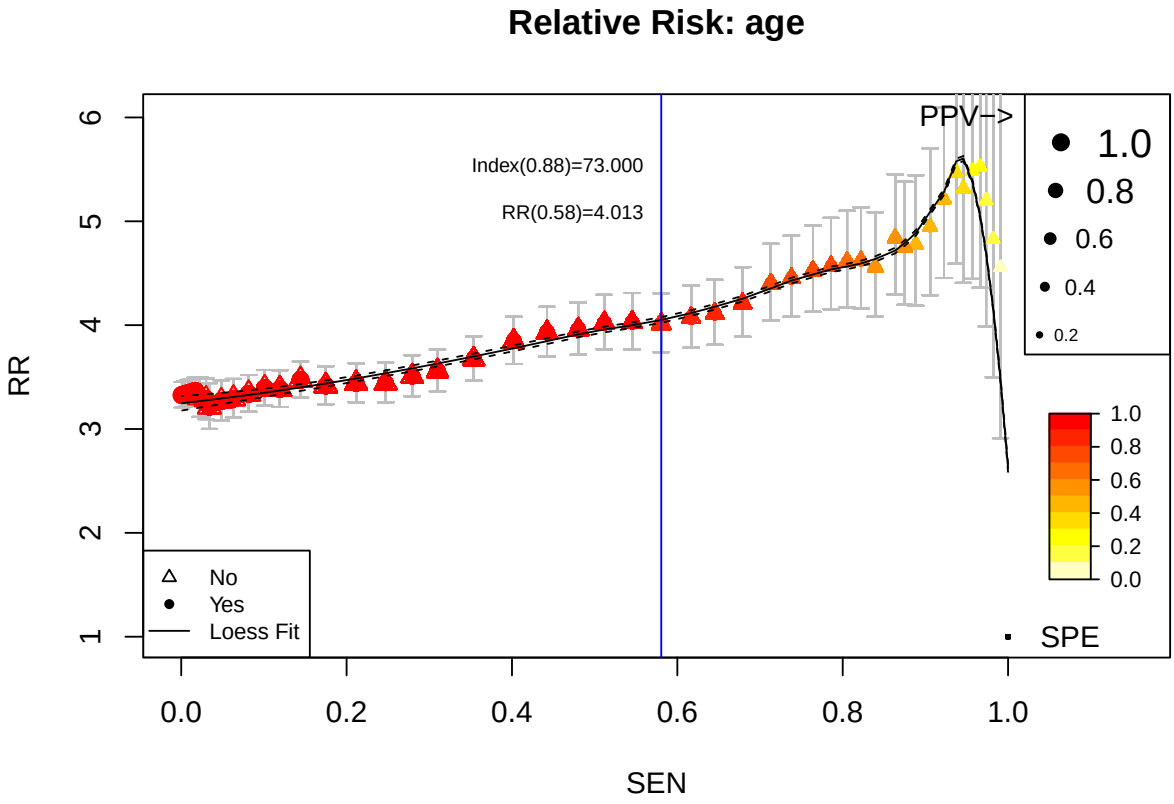
age	kappa	lambda	creatinine
0	0	0	0

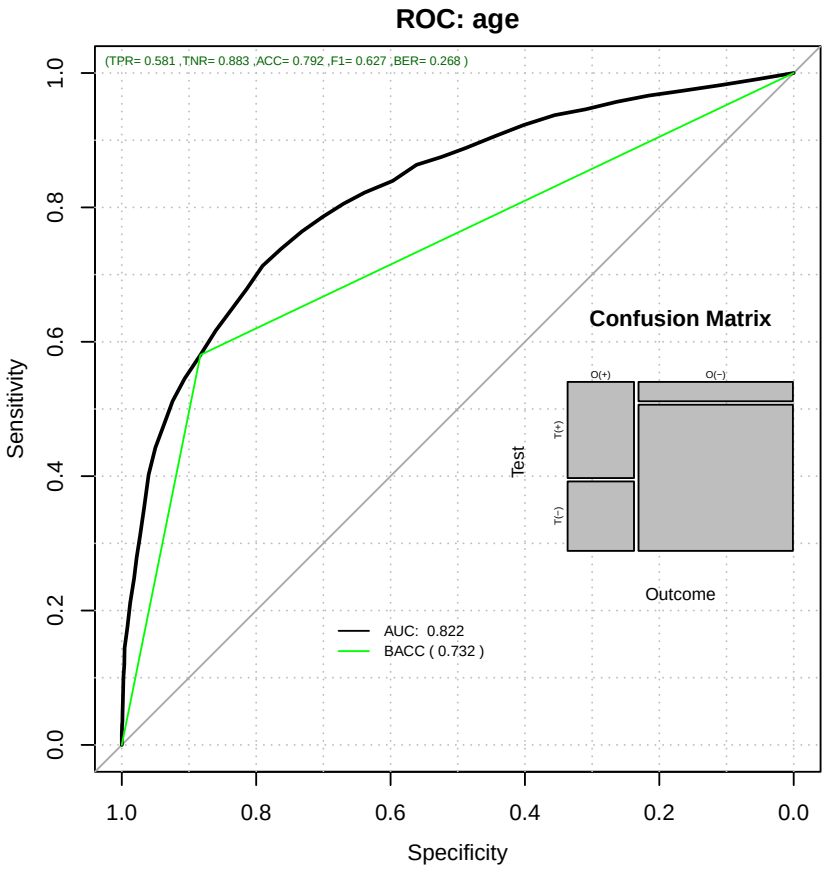
```
topv <- min(5,length(topvar))
topFive <- names(topvar)[1:topv]

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

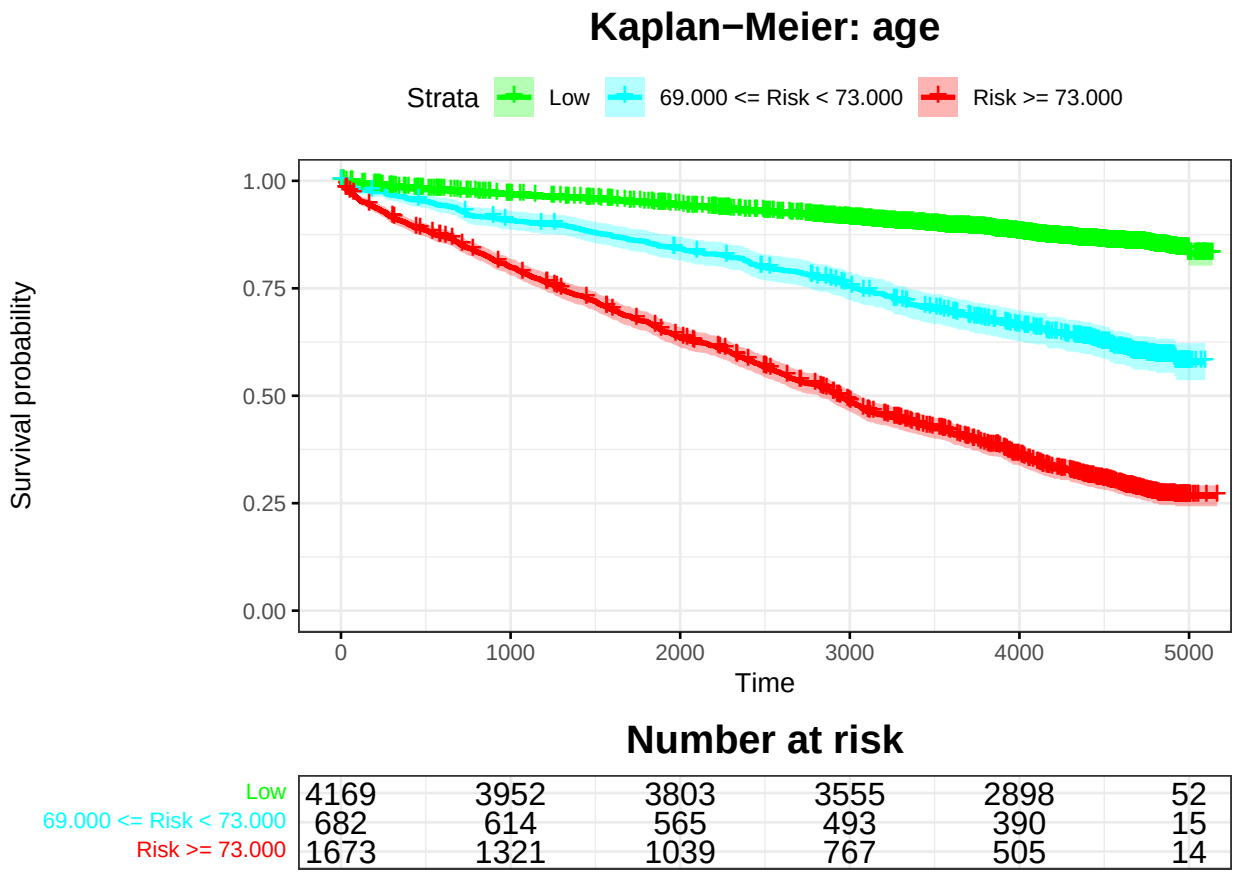

Relative Risk: age
Index(0.88)=73.000
RR(0.58)=4.013
PPV−>
1.0
0.8
0.6
0.4
0.2
1.0
0.8
0.6
0.4
0.2
0.0
No
Yes
Loess Fit
SPE
RR
SEN
1
2
3
4
5
6
0.0
0.2
0.4
0.6
0.8
1.0




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

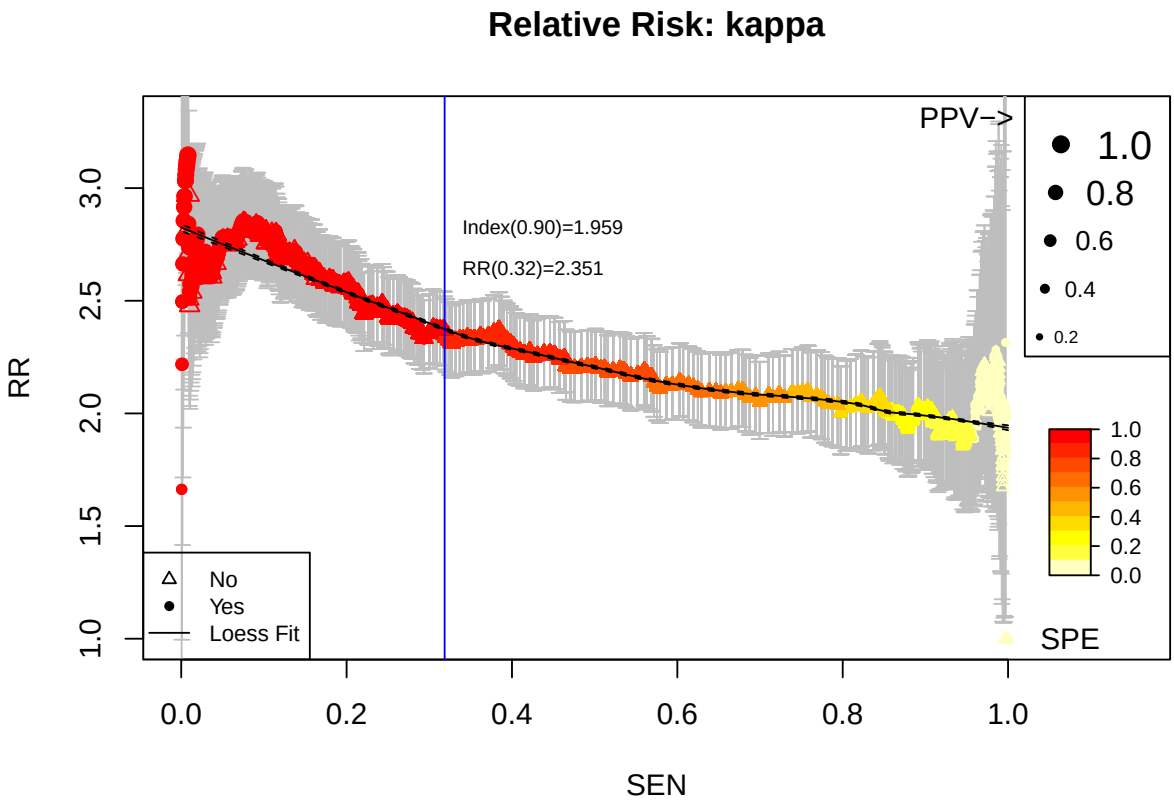

Relative Risk: age
Index(0.88)=73.000
RR(0.58)=4.013
PPV−>
1.0
0.8
0.6
0.4
0.2
1.0
0.8
0.6
0.4
0.2
0.0
No
Yes
Loess Fit
SPE
RR
SEN
1
2
3
4
5
6
0.0
0.2
0.4
0.6
0.8
1.0

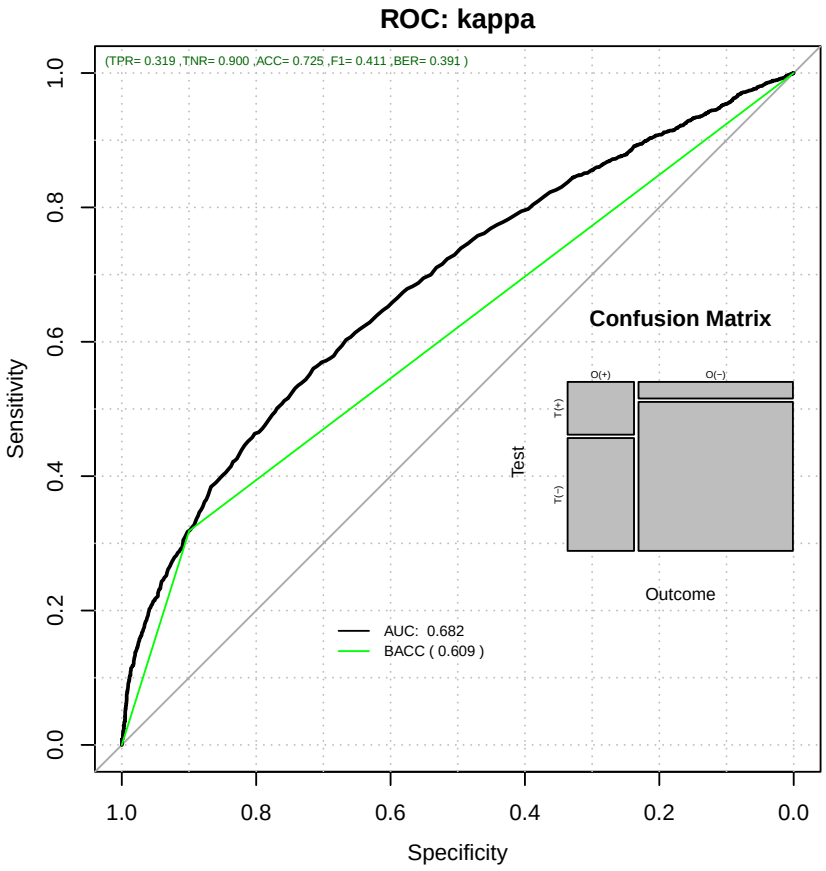

ROC: age
(TPR= 0.581 ,TNR= 0.883 ,ACC= 0.792 ,F1= 0.627 ,BER= 0.268)
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
Specificity
1.0
0.8
0.6
0.4
0.2
0.0
AUC: 0.822
BACC (0.732)
Confusion Matrix
O(+)
O(−)
T(+)
T(−)
Test
Outcome

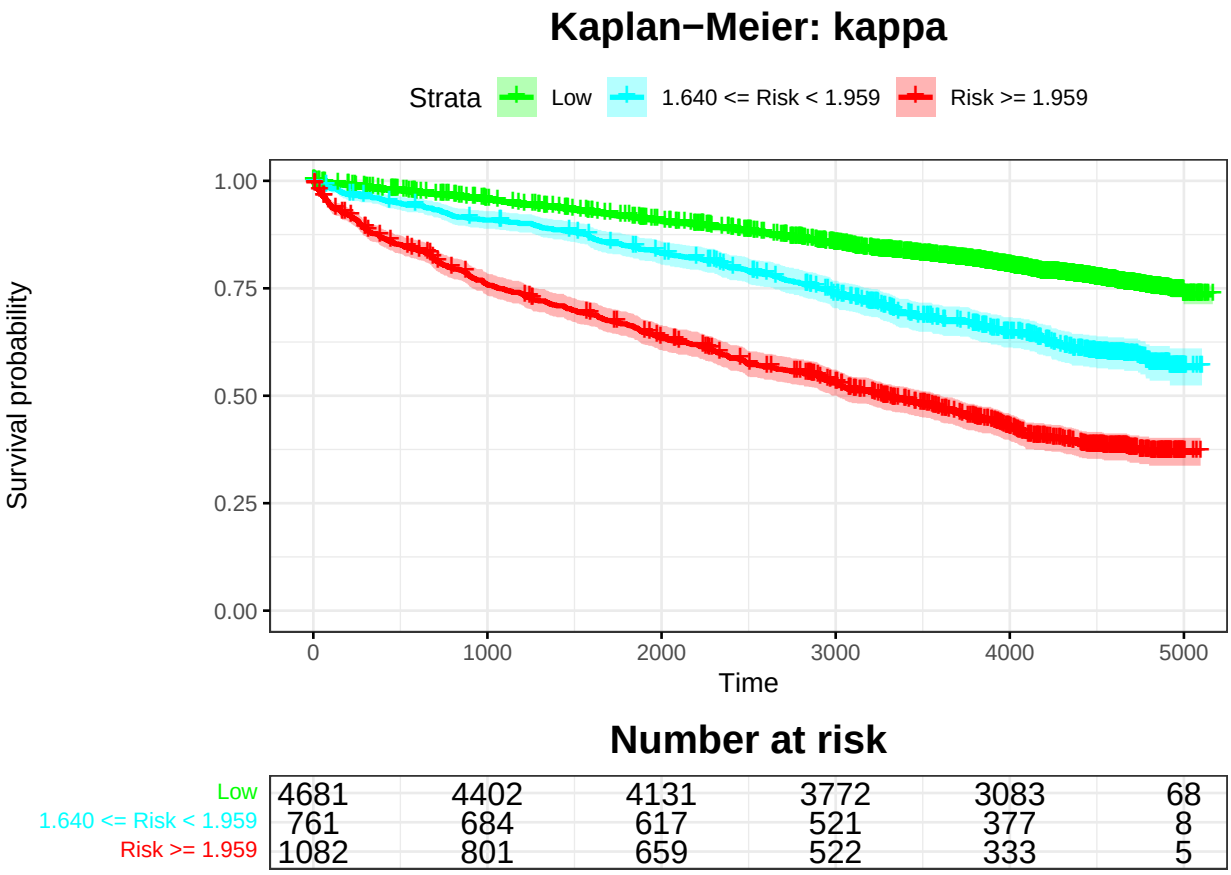


Number at risk

Low	4169	3952	3803	3555	2898	52
69.000 <= Risk < 73.000	682	614	565	493	390	15
Risk >= 73.000	1673	1321	1039	767	505	14

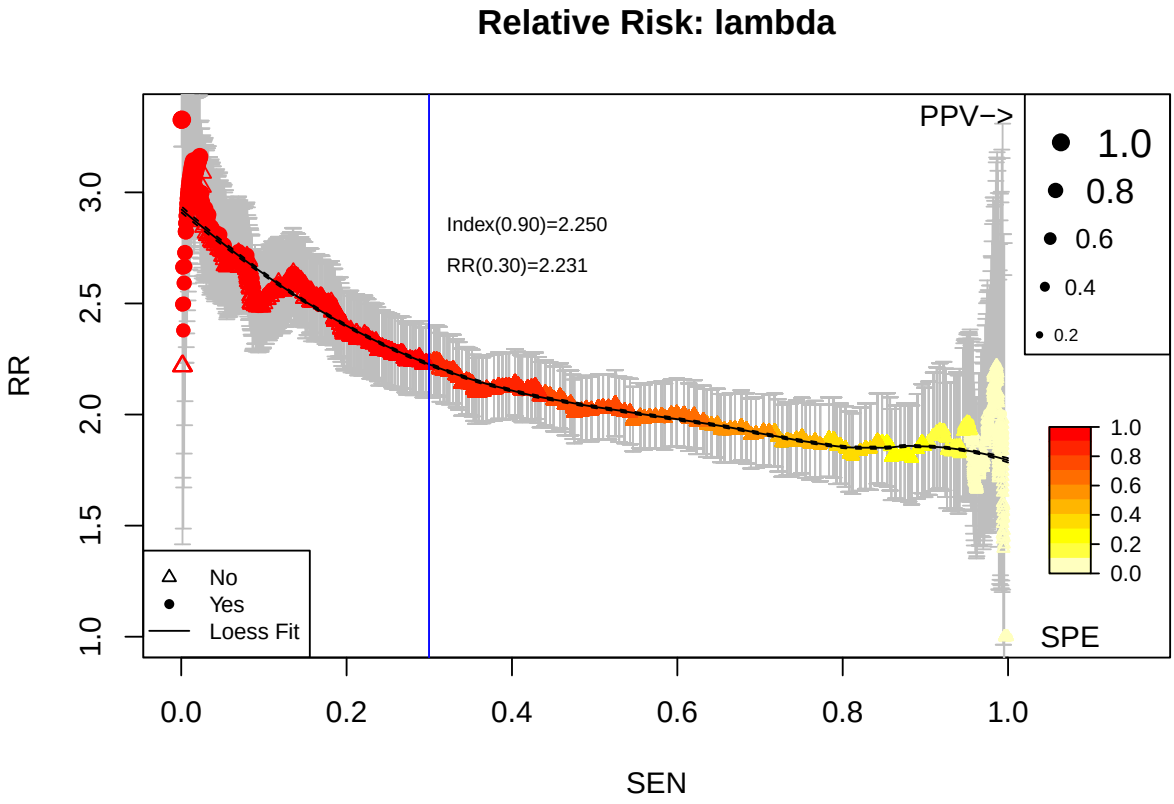

Relative Risk: kappa
PPV–>
1.0
0.8
0.6
0.4
0.2
Index(0.90)=1.959
RR(0.32)=2.351
1.0
0.8
0.6
0.4
0.2
0.0
SPE
No
Yes
Loess Fit
RR
1.0
1.5
2.0
2.5
3.0
0.0
0.2
0.4
0.6
0.8
1.0
SEN

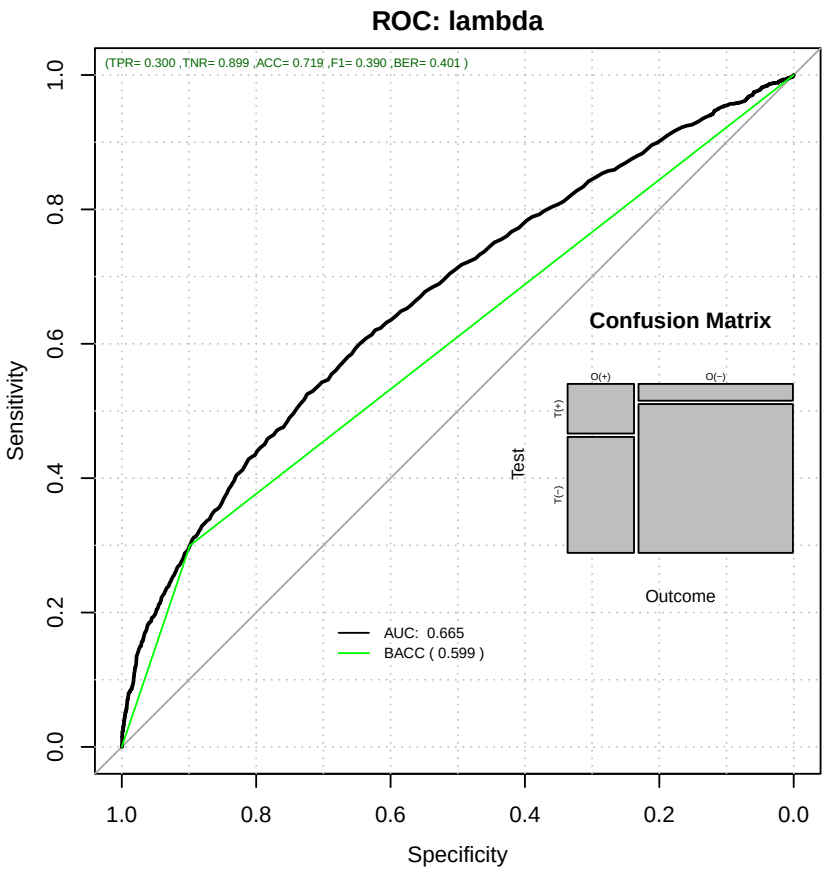

ROC: kappa
(TPR= 0.319 ,TNR= 0.900 ,ACC= 0.725 ,F1= 0.411 ,BER= 0.391)
Sensitivity
Specificity
1.0
0.8
0.6
0.4
0.2
0.0
Confusion Matrix
O(+)
O(−)
T(+)
T(−)
Test
Outcome
AUC: 0.682
BACC (0.609)

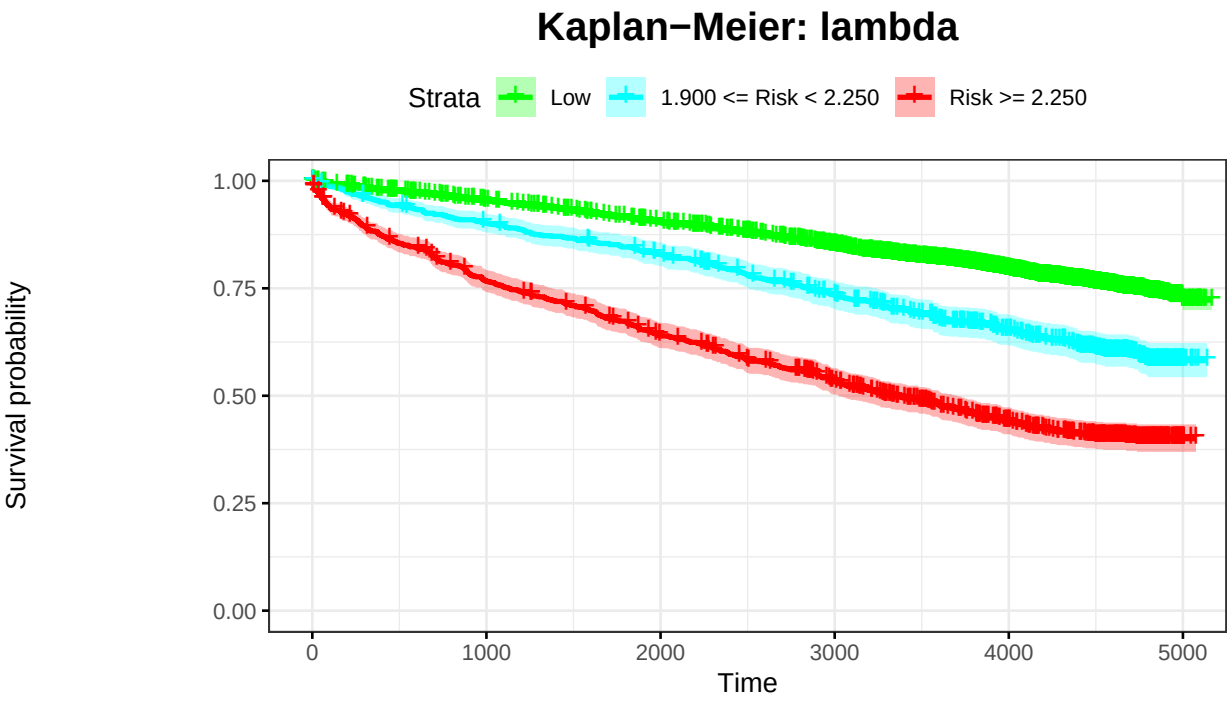


Number at risk

Low	4681	4402	4131	3772	3083	68
1.640 <= Risk < 1.959	761	684	617	521	377	8
Risk >= 1.959	1082	801	659	522	333	5

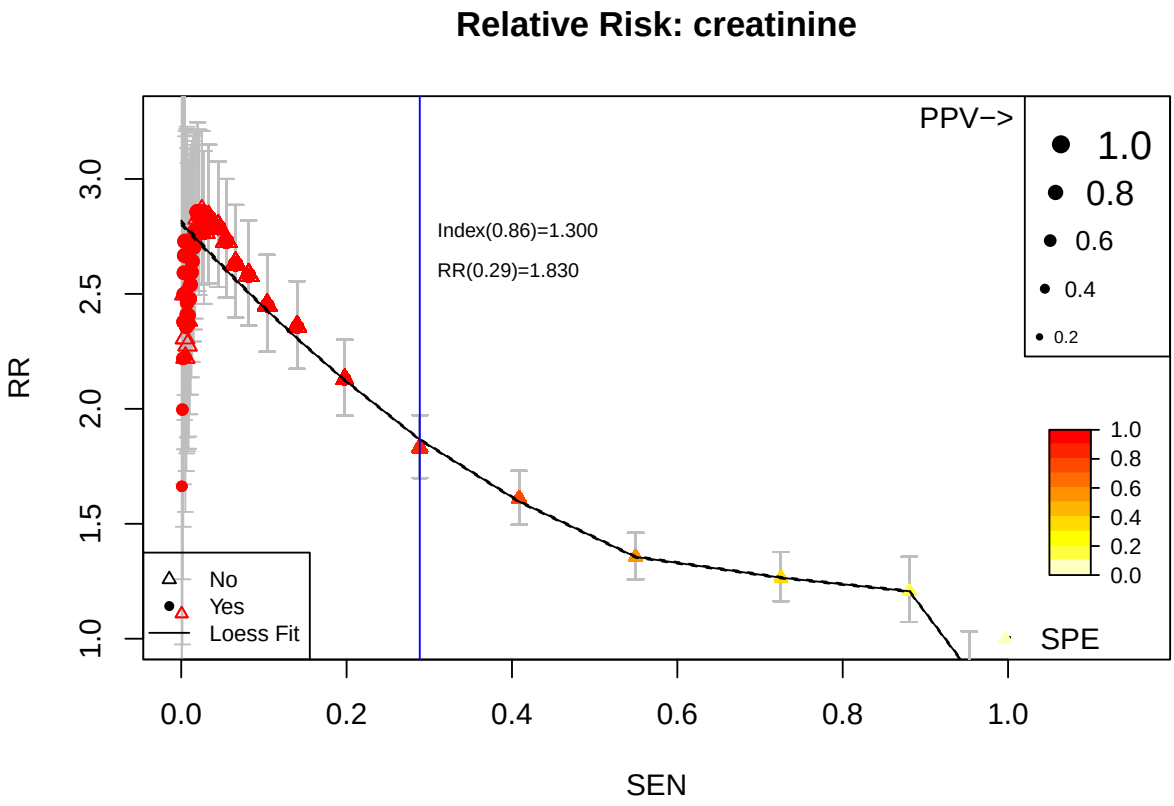

Relative Risk: lambda
PPV−>
1.0
0.8
0.6
0.4
0.2
Index(0.90)=2.250
RR(0.30)=2.231
1.0
0.8
0.6
0.4
0.2
0.0
SPE
No
Yes
Loess Fit
RR
1.0
1.5
2.0
2.5
3.0
0.0
0.2
0.4
0.6
0.8
1.0
SEN

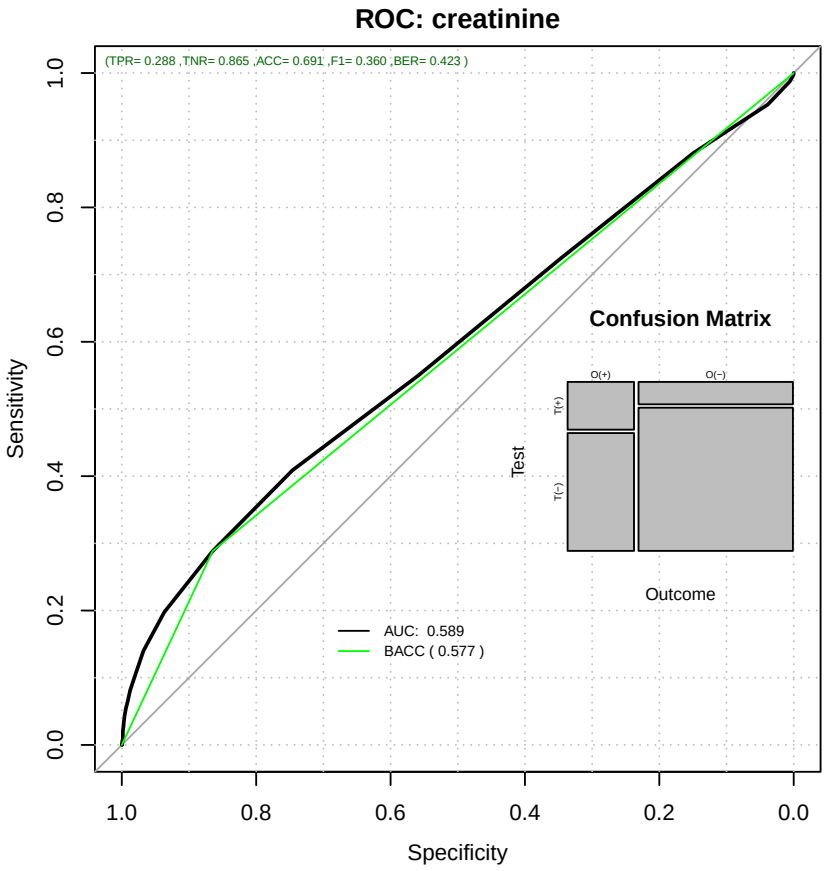

ROC: lambda
(TPR= 0.300 ,TNR= 0.899 ,ACC= 0.719 ,F1= 0.390 ,BER= 0.401)
Sensitivity
Specificity
1.0
0.8
0.6
0.4
0.2
0.0
AUC: 0.665
BACC (0.599)
Confusion Matrix
O(+)
O(−)
T(+)
T(−)
Test
Outcome

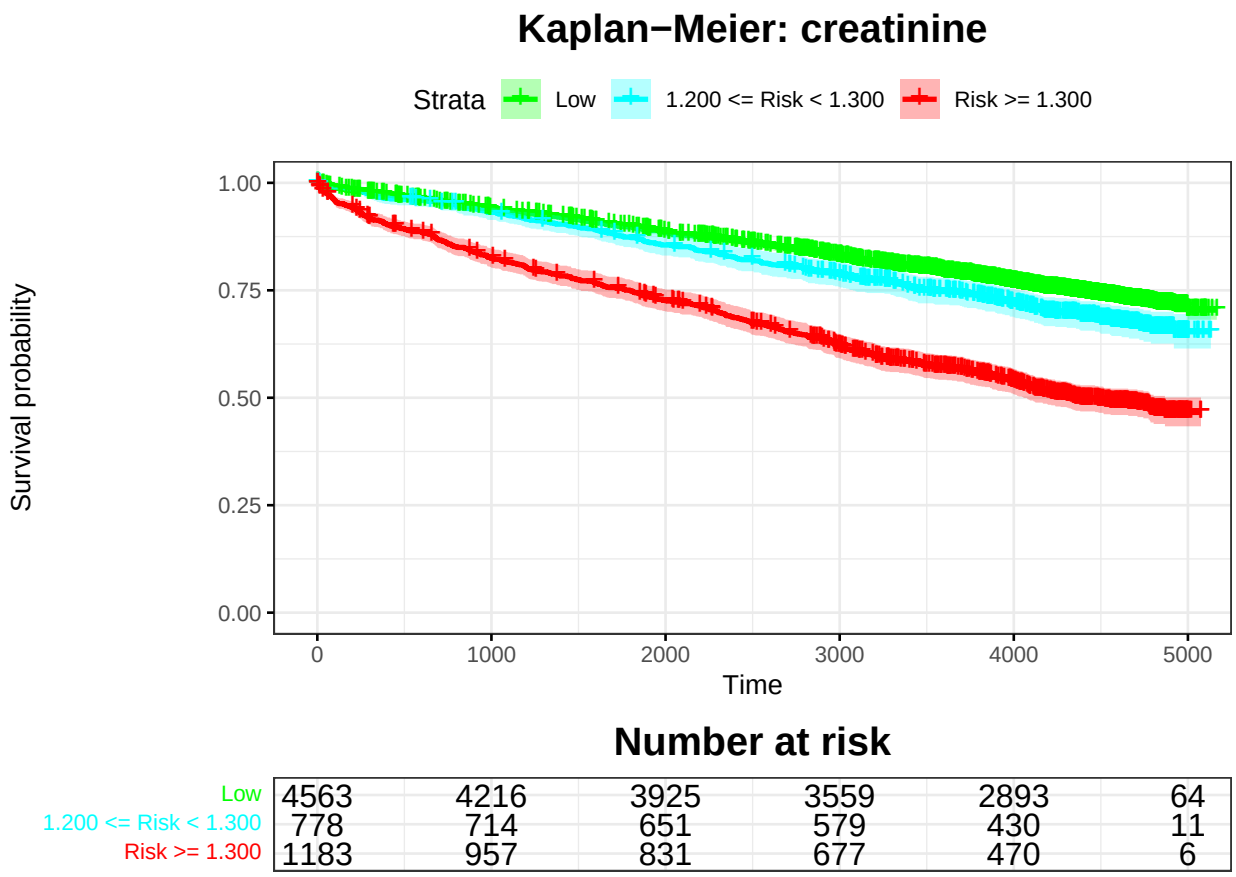


Number at risk

Low	4741	4443	4164	3801	3075	61
1.900 <= Risk < 2.250	733	654	595	504	374	12
Risk >= 2.250	1050	790	648	510	344	8


Relative Risk: creatinine
PPV–>
1.0
0.8
0.6
0.4
0.2
Index(0.86)=1.300
RR(0.29)=1.830
1.0
0.8
0.6
0.4
0.2
0.0
SPE
No
Yes
Loess Fit
RR
1.0
1.5
2.0
2.5
3.0
0.0
0.2
0.4
0.6
0.8
1.0
SEN


ROC: creatinine
(TPR= 0.288 ,TNR= 0.865 ,ACC= 0.691 ,F1= 0.360 ,BER= 0.423)
Sensitivity
1.0
0.8
0.6
0.4
0.2
0.0
Specificity
1.0
0.8
0.6
0.4
0.2
0.0
AUC: 0.589
BACC (0.577)
Confusion Matrix
O(+)
O(−)
T(+)
T(−)
Test
Outcome




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

1.2 Reporting the Metrics

```
CstatCI <- NULL
RRatios <- NULL
LogRangp <- NULL
Sensitvity <- 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$pvalue)
  Sensitvity <- rbind(Sensitvity,RRanalysis[[topf]]$ROCAnalysis$sensitivity)
}
rownames(CstatCI) <- topFive
rownames(RRatios) <- topFive
rownames(LogRangp) <- topFive
rownames(Sensitvity) <- topFive

pander::pander(CstatCI)
```

	mean.C Index	median	lower	upper
age	0.775	0.774	0.763	0.784
kappa	0.671	0.671	0.657	0.683
lambda	0.657	0.657	0.646	0.670
creatinine	0.586	0.586	0.571	0.599

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

	est	lower	upper
age	4.01	3.74	4.31
kappa	2.35	2.19	2.52
lambda	2.23	2.08	2.39
creatinine	1.83	1.70	1.97

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

age	0.00e+00
kappa	4.90e-175
lambda	4.41e-145
creatinine	2.67e-67

```
pander::pander(Sensitvity)
```

	est	lower	upper
age	0.581	0.558	0.602
kappa	0.319	0.298	0.340
lambda	0.300	0.279	0.321
creatinine	0.288	0.269	0.309