

# flchain: RRPlot Demo

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```
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

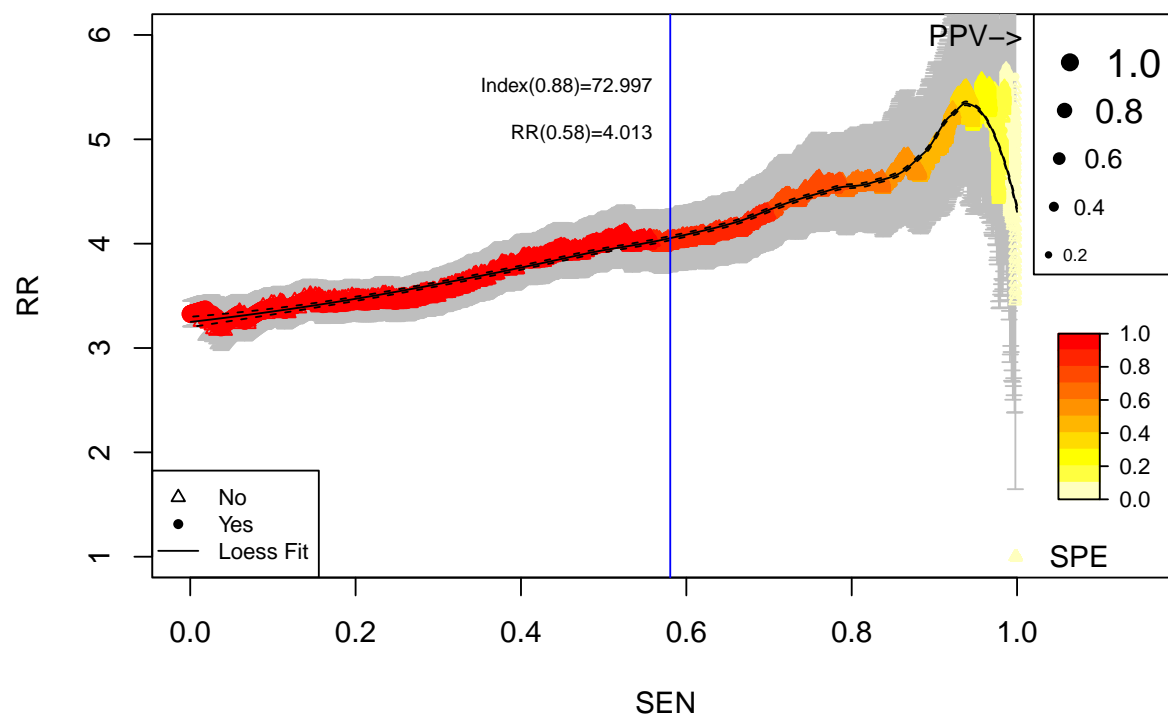
```
convar <- colnames(dataFL)[lapply(apply(dataFL,2,unique),length) > 10]
convar <- convar[convar != "time"]
topvar <- univariate_BinEnsemble(dataFL[,c("status",convar)],"status")
pander::pander(topvar)
```

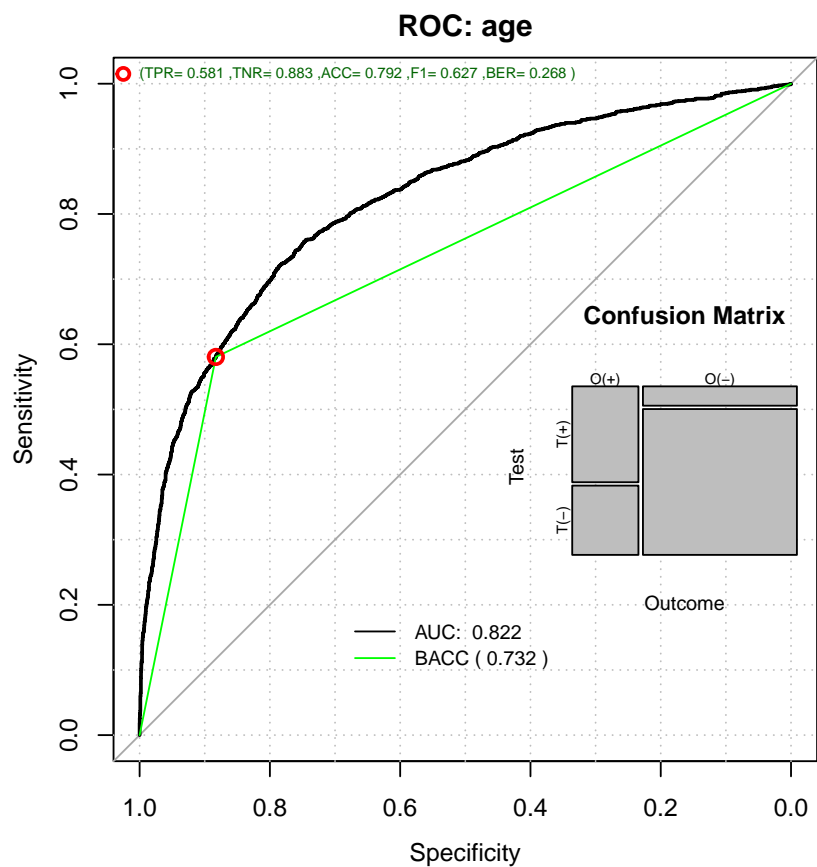
age	kappa	lambda	creatinine
0	0	0	0

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

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

# Relative Risk: age





```

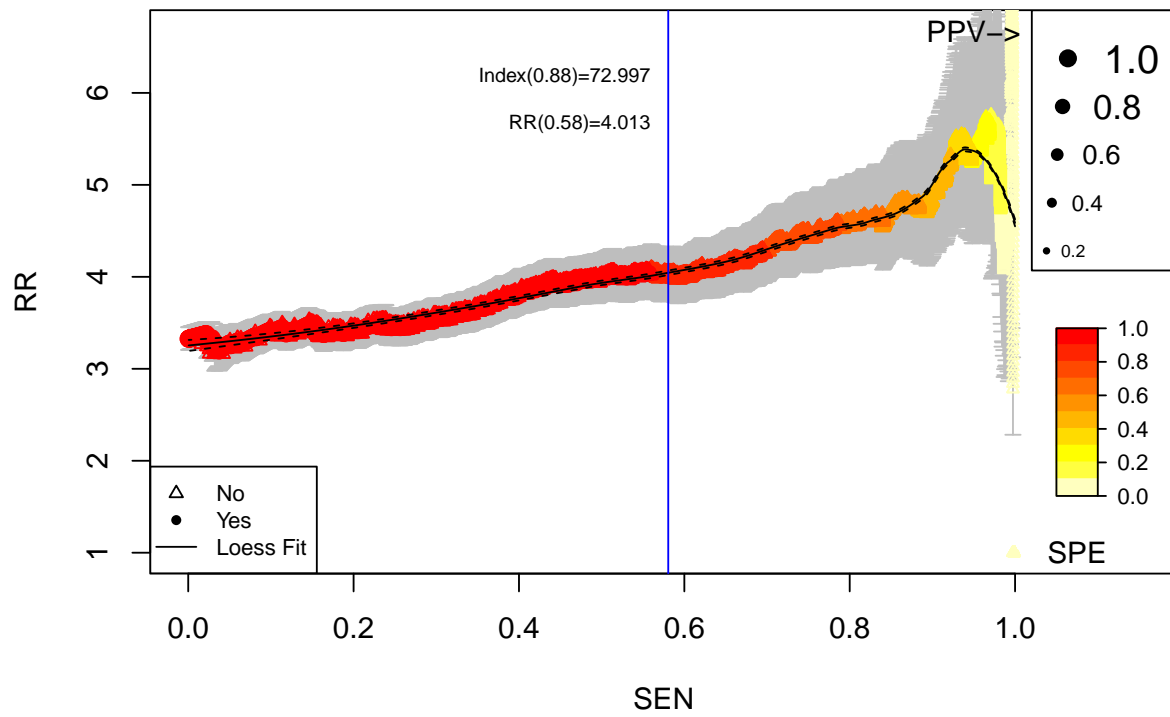
par(op)

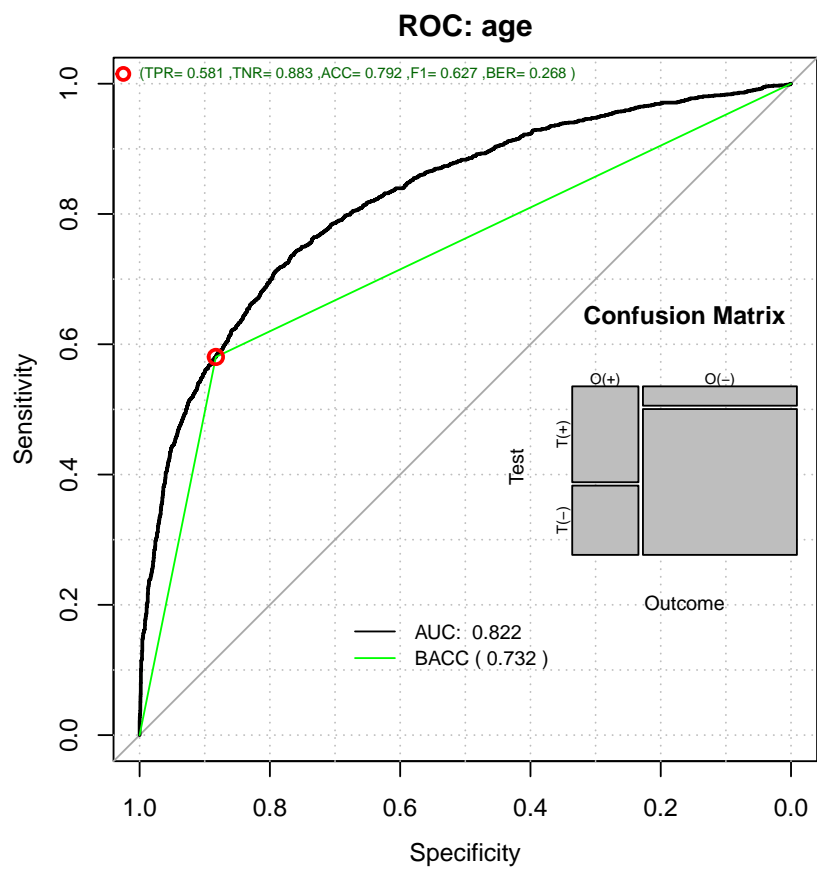
## With Survival Analysis
RRanalysis <- list();
idx <- 1
for (topf in topFive)
{
  RRanalysis[[idx]] <- RRPlot(cbind(dataFL$status,dataFL[,topf]),
                              timetoEvent=dataFL$time,
                              atRate=c(0.90,0.80),
                              title=topf)

  idx <- idx + 1
  par(op)
}

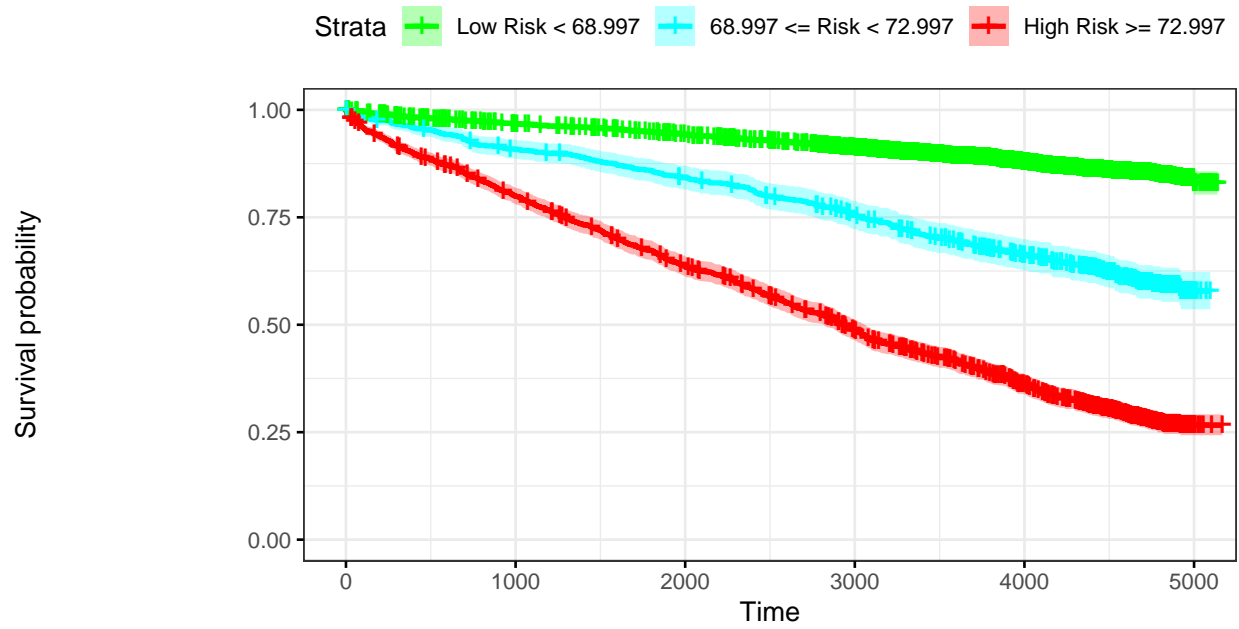
```

# Relative Risk: age





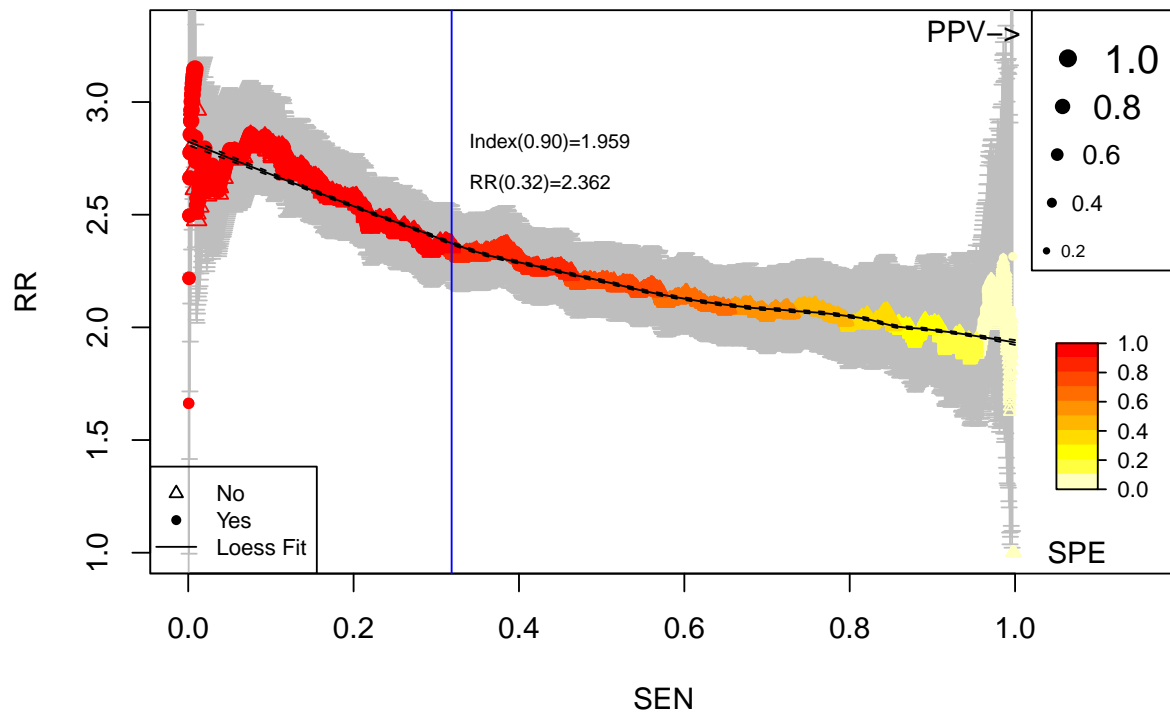
# Kaplan–Meier: age



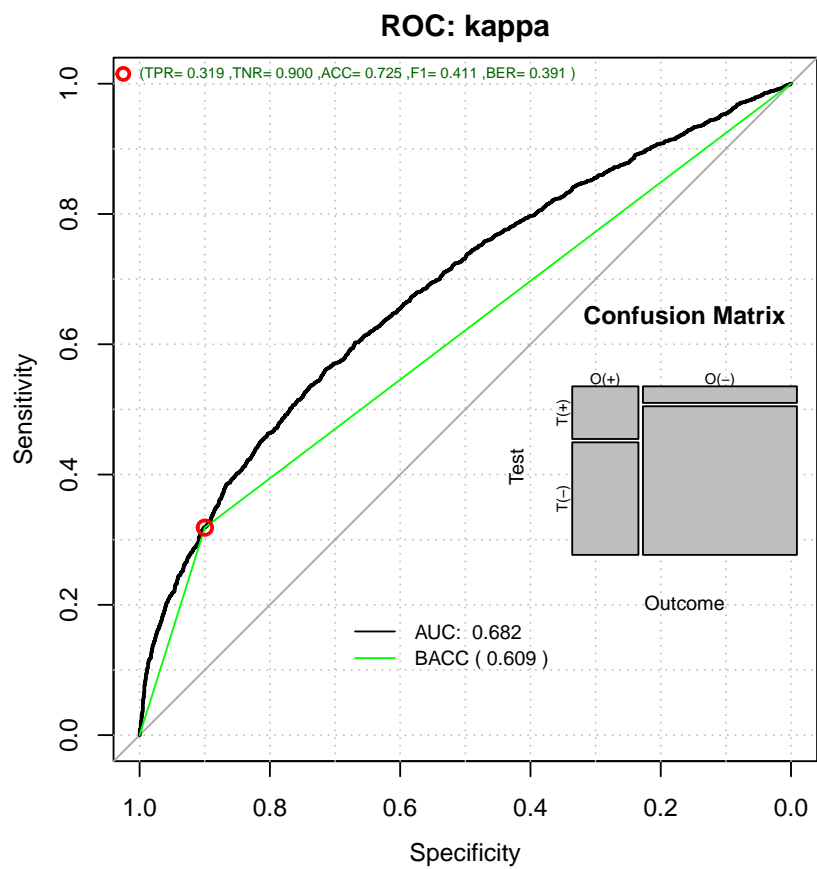
## Number at risk

Low Risk < 68.997	4169	3952	3803	3555	2898	52
68.997 <= Risk < 72.997	682	614	565	493	390	15
High Risk >= 72.997	1673	1321	1039	767	505	14

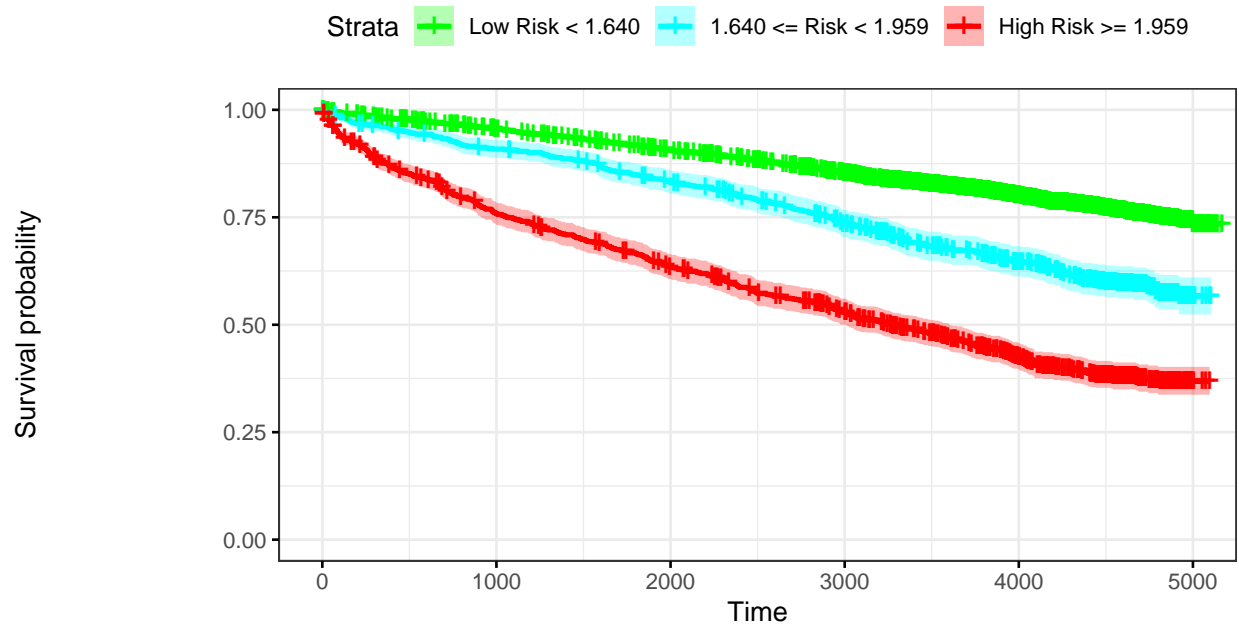
# Relative Risk: kappa







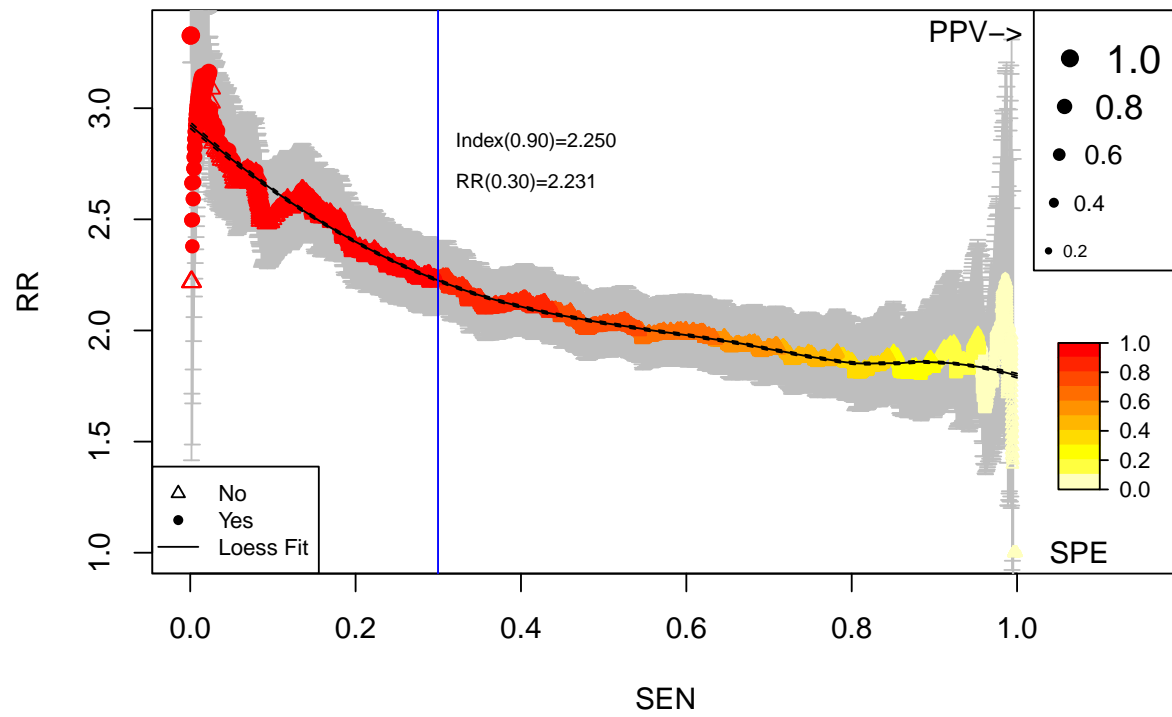
## Kaplan–Meier: kappa

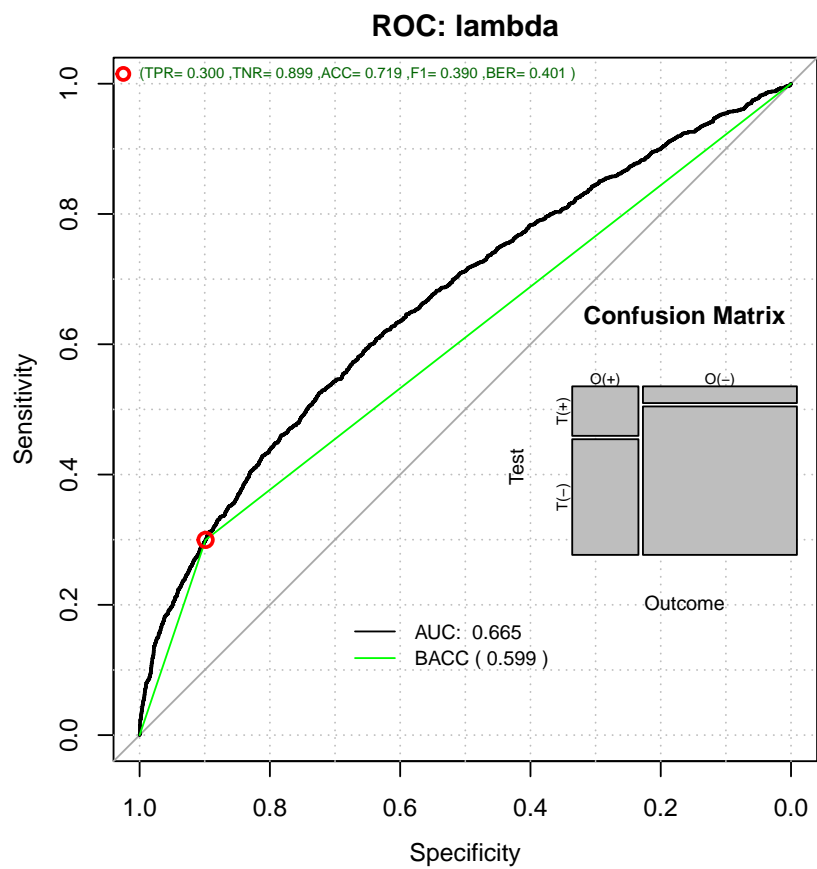


### Number at risk

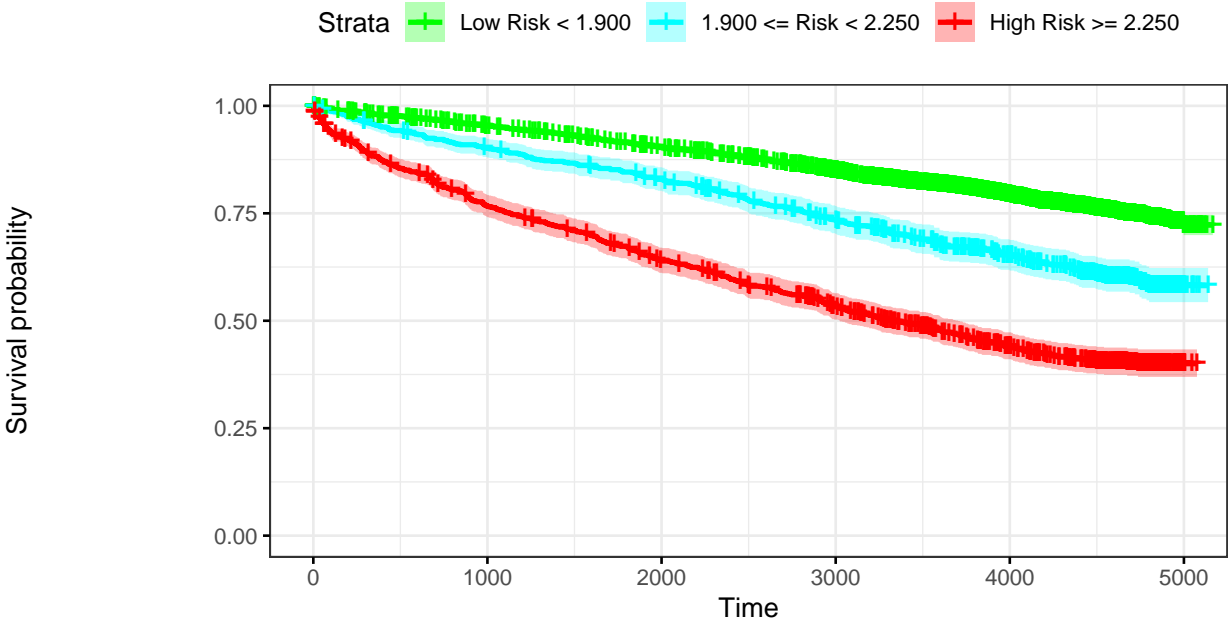
Low Risk < 1.640	4681	4402	4131	3772	3083	68
1.640 <= Risk < 1.959	761	684	617	521	377	8
High Risk >= 1.959	1082	801	659	522	333	5

# Relative Risk: lambda





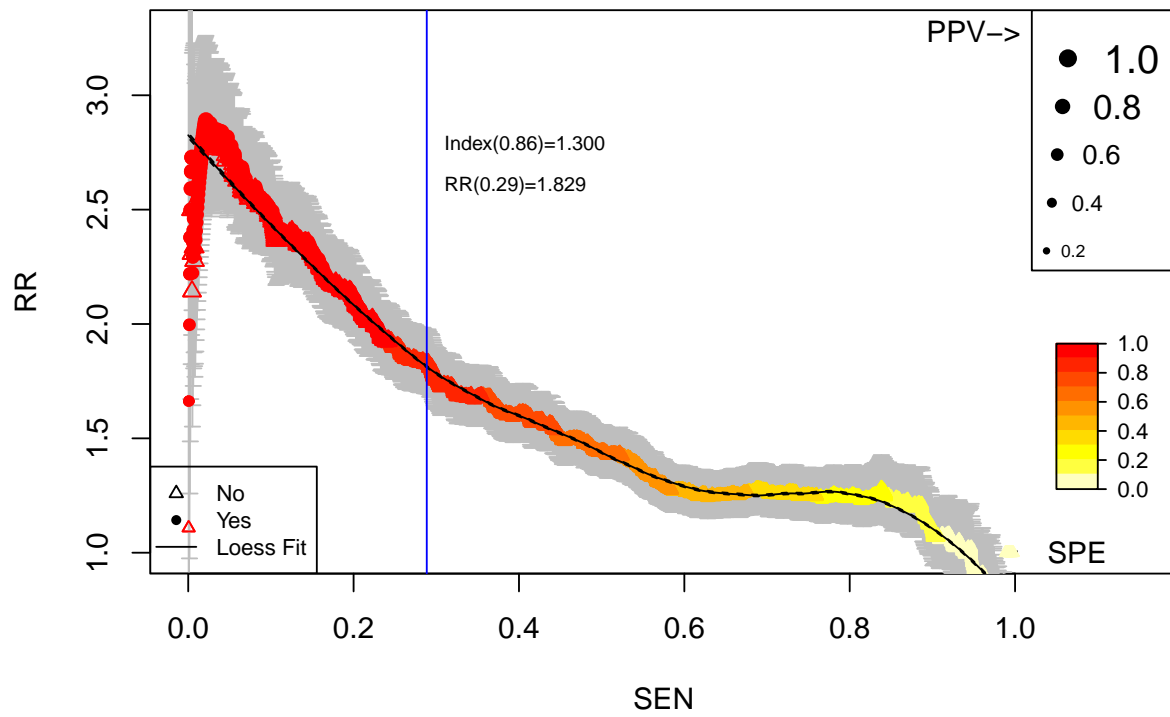
# Kaplan–Meier: lambda

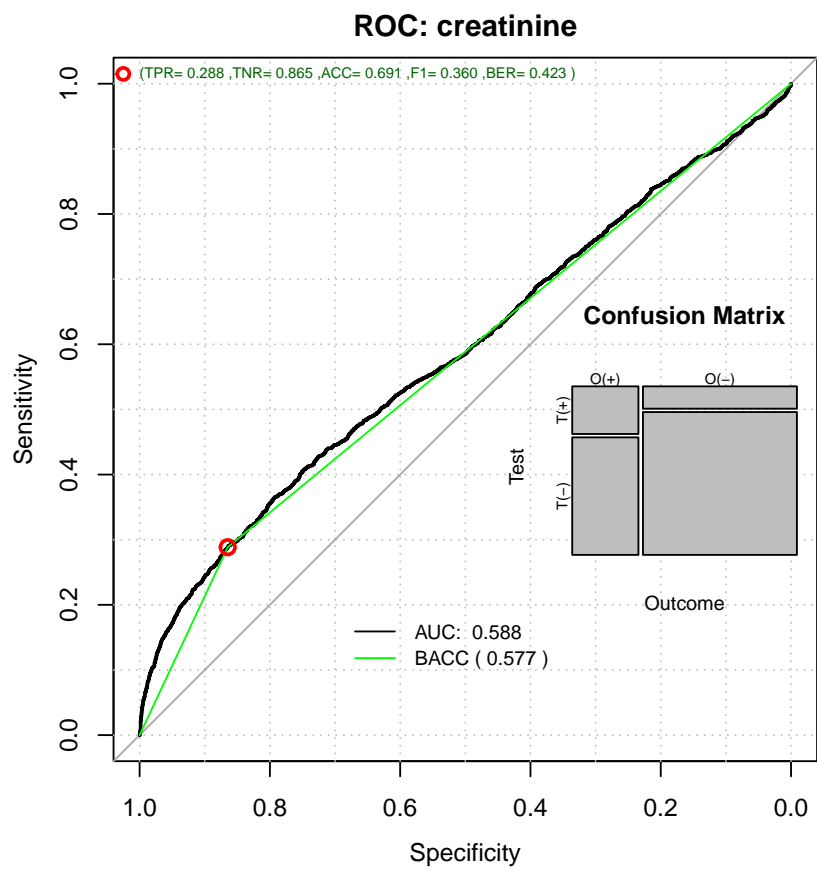


## Number at risk

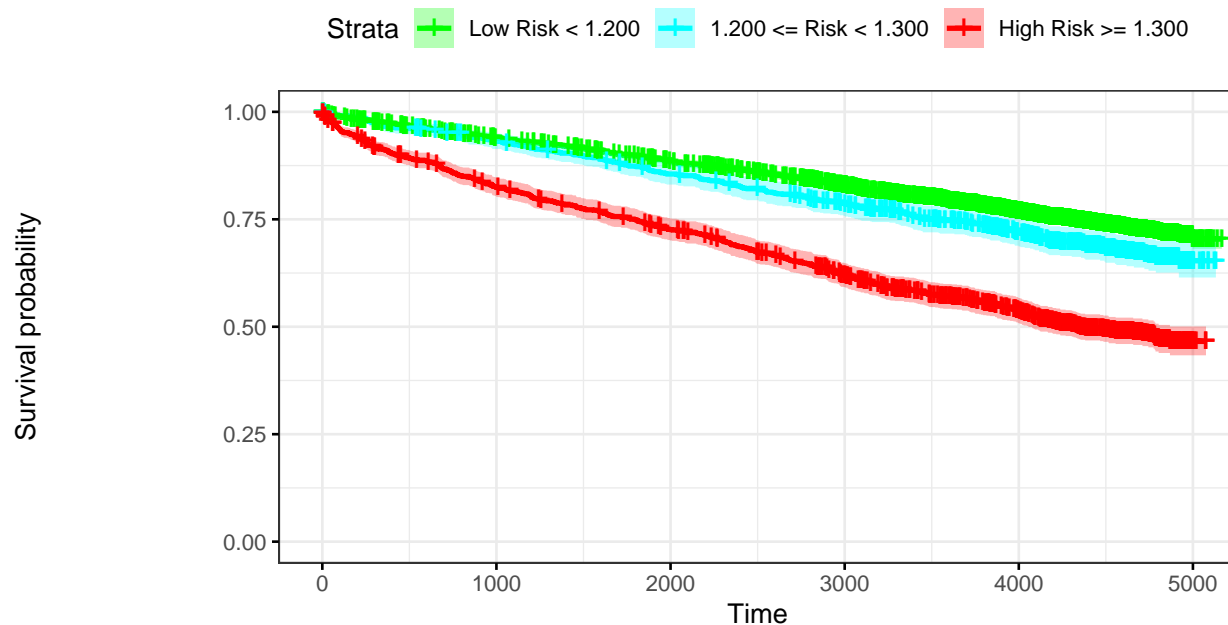
Low Risk < 1.900	4741	4443	4164	3801	3075	61
1.900 <= Risk < 2.250	733	654	595	504	374	12
High Risk >= 2.250	1050	790	648	510	344	8

## Relative Risk: creatinine





## Kaplan–Meier: creatinine



### Number at risk

Low Risk < 1.200	4563	4216	3925	3559	2893	64
1.200 <= Risk < 1.300	778	714	651	579	430	11
High Risk >= 1.300	1183	957	831	677	470	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
<b>Thr</b>	73.000	69.000	69.000	53.000	5.00e+01
<b>RR</b>	4.013	4.399	4.395	5.766	1.00e+00
<b>RR_LCI</b>	3.740	4.045	4.043	4.471	0.00e+00
<b>RR_UCI</b>	4.305	4.783	4.778	7.437	0.00e+00
<b>SEN</b>	0.581	0.713	0.712	0.971	1.00e+00
<b>SPE</b>	0.883	0.790	0.792	0.198	8.77e-04
<b>BACC</b>	0.732	0.752	0.752	0.584	5.00e-01

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



```

for (topf in topFive)
{
  CstatCI <- rbind(CstatCI,RRanalysis[[topf]]$c.index$cstatCI)
  RRs <- rbind(RRs,RRanalysis[[topf]]$RR_atP)
  LogRangp <- rbind(LogRangp,RRanalysis[[topf]]$surdif$pvalue)
  Sensitivity <- rbind(Sensitivity,RRanalysis[[topf]]$ROCAanalysis$sensitivity)
  Specificity <- rbind(Specificity,RRanalysis[[topf]]$ROCAanalysis$specificity)
  ROCAUC <- rbind(ROCAUC,RRanalysis[[topf]]$ROCAanalysis$aucs)
}
rownames(CstatCI) <- topFive
rownames(LogRangp) <- topFive
rownames(Sensitivity) <- topFive
rownames(Specificity) <- topFive
rownames(ROCAUC) <- topFive

pander::pander(ROCAUC)

```

	est	lower	upper
<b>age</b>	0.822	0.811	0.833
<b>kappa</b>	0.682	0.667	0.696
<b>lambda</b>	0.665	0.650	0.680
<b>creatinine</b>	0.588	0.572	0.604

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

	mean.C Index	median	lower	upper
<b>age</b>	0.775	0.775	0.764	0.786
<b>kappa</b>	0.671	0.671	0.658	0.684
<b>lambda</b>	0.657	0.657	0.645	0.670
<b>creatinine</b>	0.584	0.584	0.571	0.597

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

<b>age</b>	0.00e+00
<b>kappa</b>	4.90e-175
<b>lambda</b>	4.41e-145
<b>creatinine</b>	2.67e-67

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

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

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

	est	lower	upper
<b>age</b>	0.883	0.873	0.892
<b>kappa</b>	0.900	0.891	0.908
<b>lambda</b>	0.899	0.890	0.907
<b>creatinine</b>	0.865	0.854	0.875

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

	ROCAUC	C-Stat	Sen	Spe
<b>age</b>	0.822	0.775	0.581	0.883
<b>kappa</b>	0.682	0.671	0.319	0.900
<b>lambda</b>	0.665	0.657	0.300	0.899
<b>creatinine</b>	0.588	0.584	0.288	0.865