

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

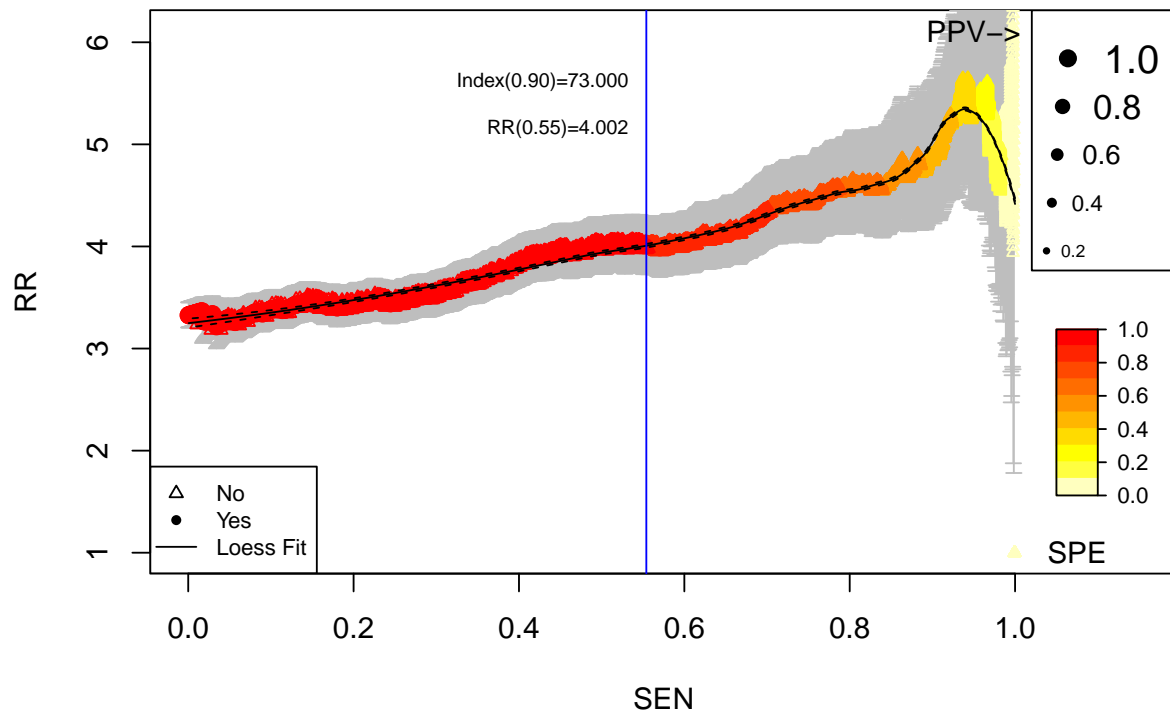
```
convar <- colnames(dataFL)[lapply(apply(dataFL,2,unique),length) > 10]
convar <- convar[convar != "time"]
topvar <- univariate_BinEnsemble(dataFL[,c("status",convar)],"status")
pander::pander(topvar)
```

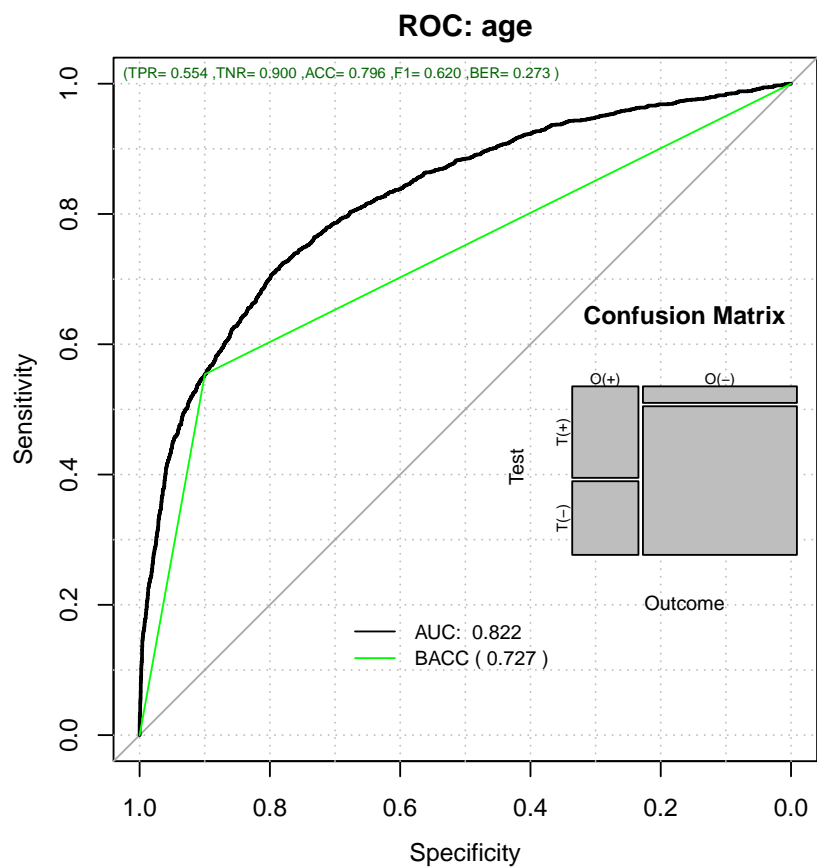
age	kappa	lambda	creatinine
0	0	0	0

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

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

Relative Risk: age





```

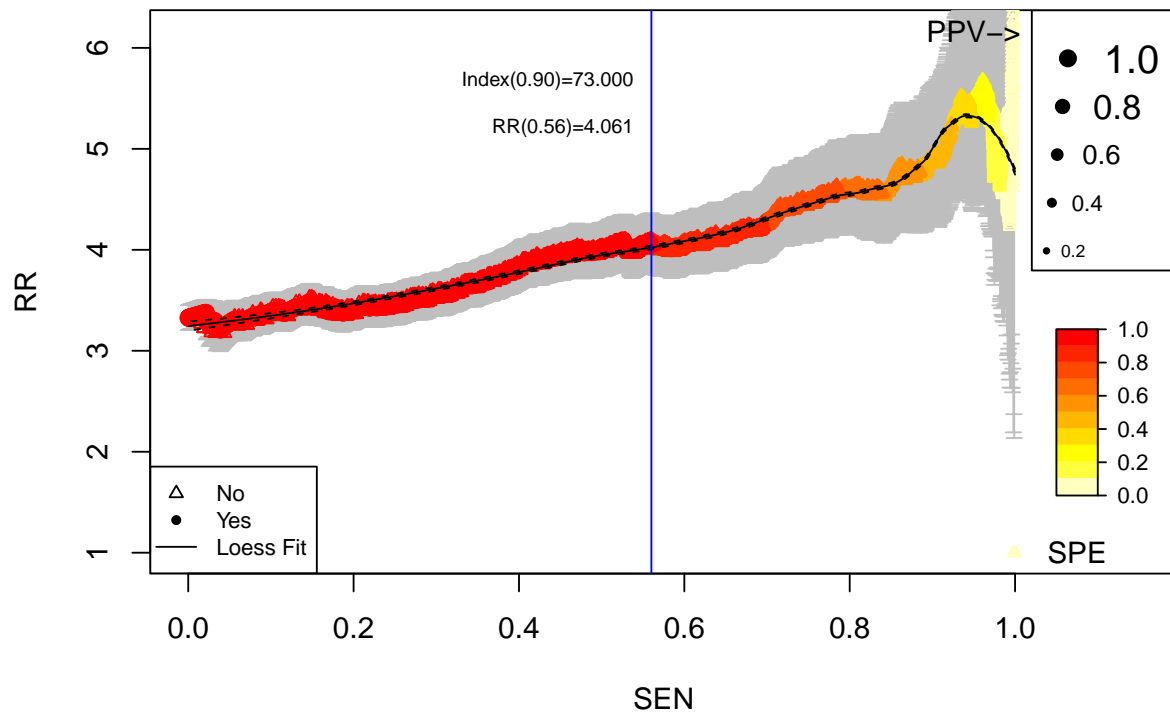
par(op)

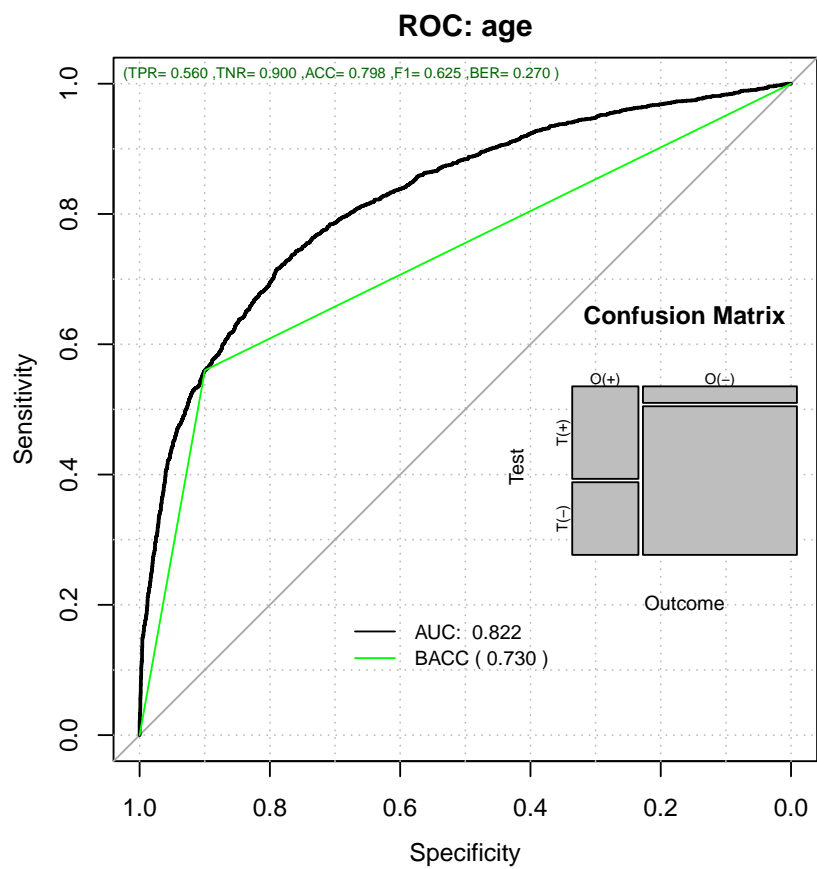
## With Survival Analysis
RRanalysis <- list();
idx <- 1
for (topf in topFive)
{
  RRanalysis[[idx]] <- RRPlot(cbind(dataFL$status,dataFL[,topf]),
                             timetoEvent=dataFL$time,
                             atProb=c(0.90,0.80),
                             title=topf)

  idx <- idx + 1
  par(op)
}

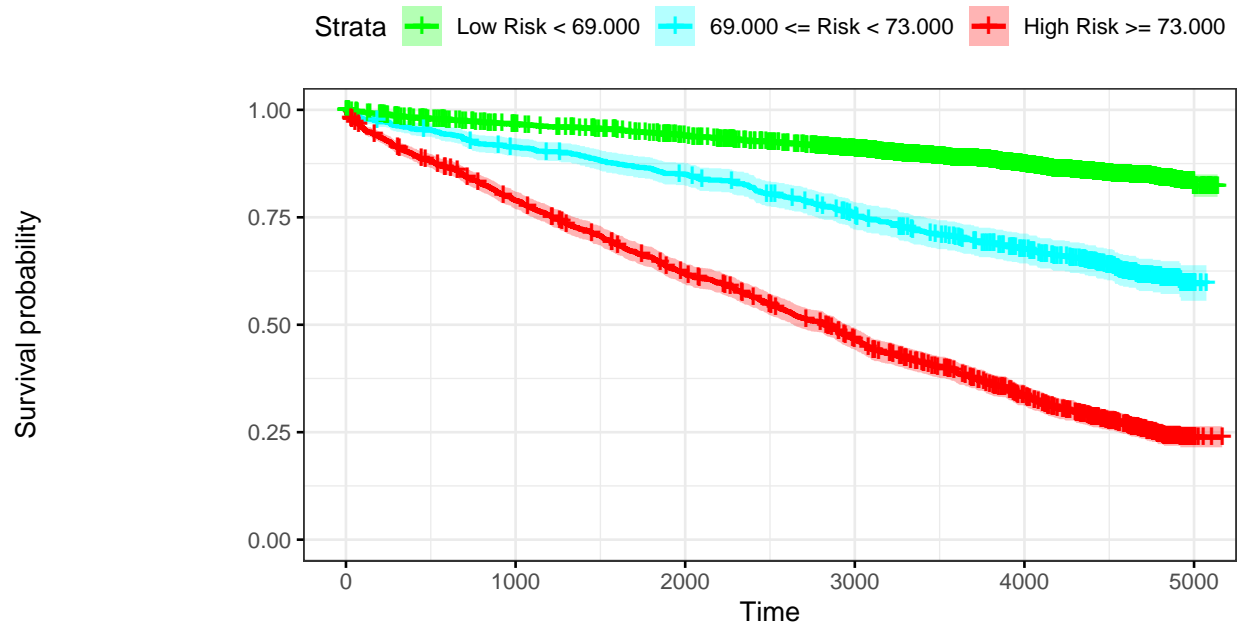
```

Relative Risk: age





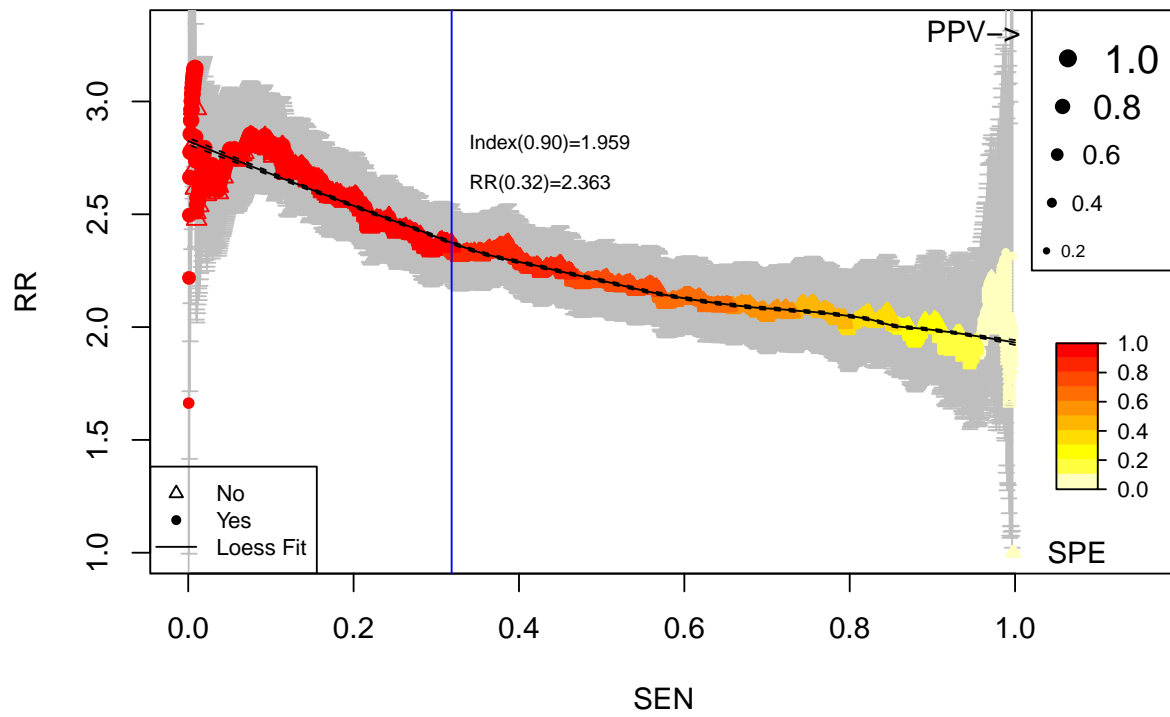
Kaplan–Meier: age

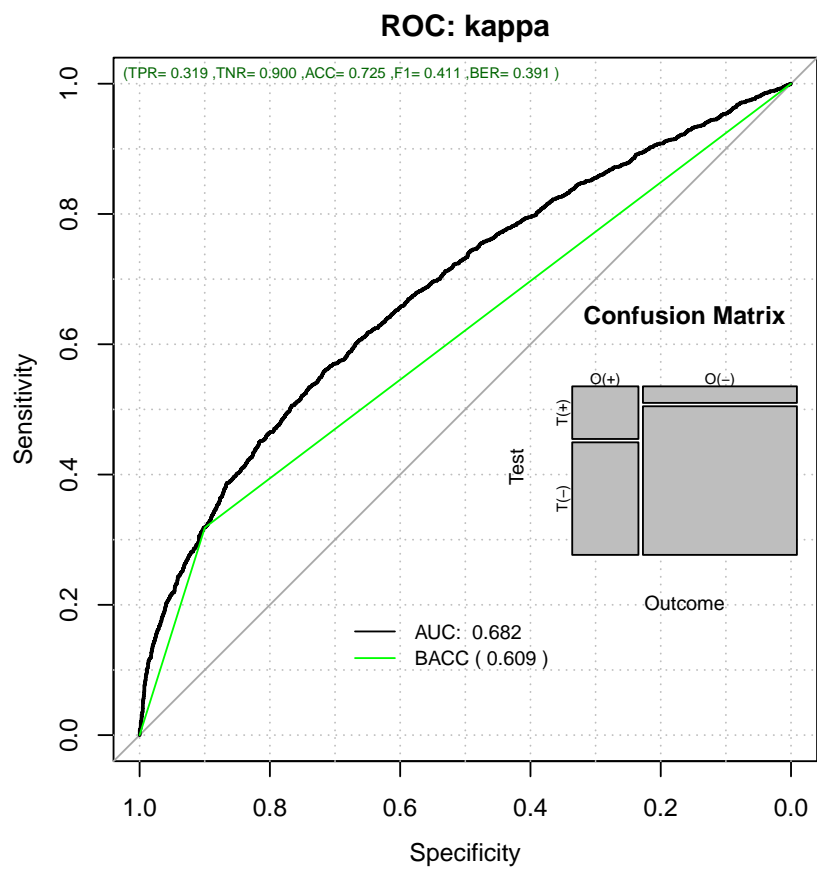


Number at risk

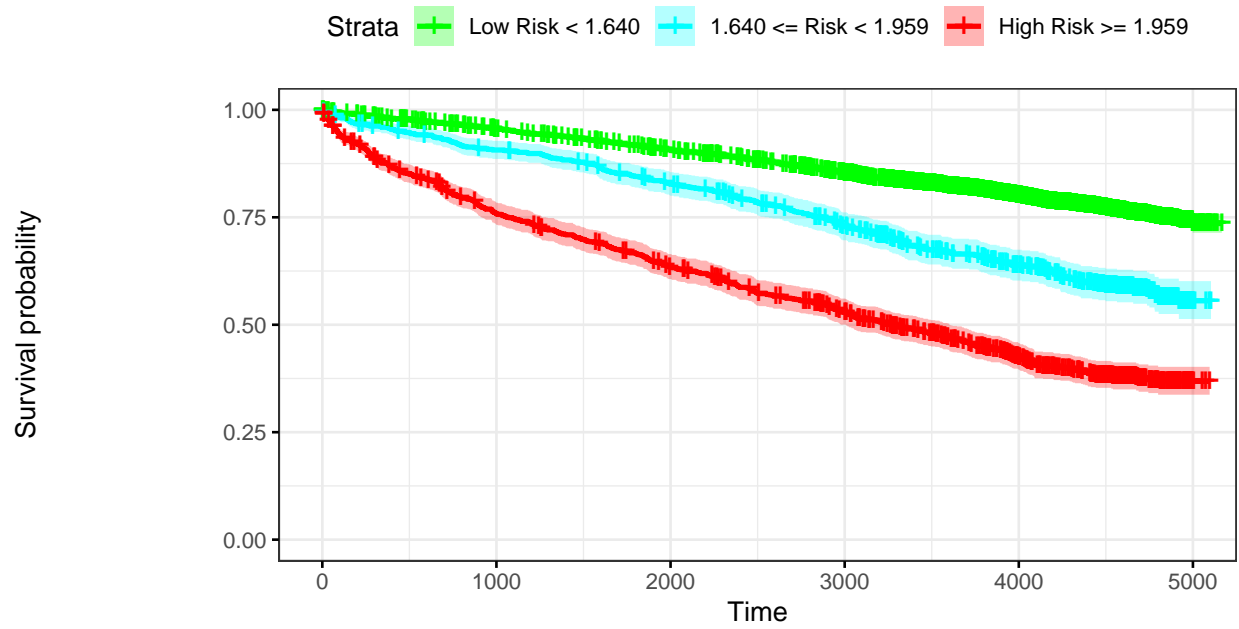
Low Risk < 69.000	4248	4022	3865	3610	2934	55
69.000 <= Risk < 73.000	720	653	604	521	422	16
High Risk >= 73.000	1556	1212	938	684	437	10

Relative Risk: kappa





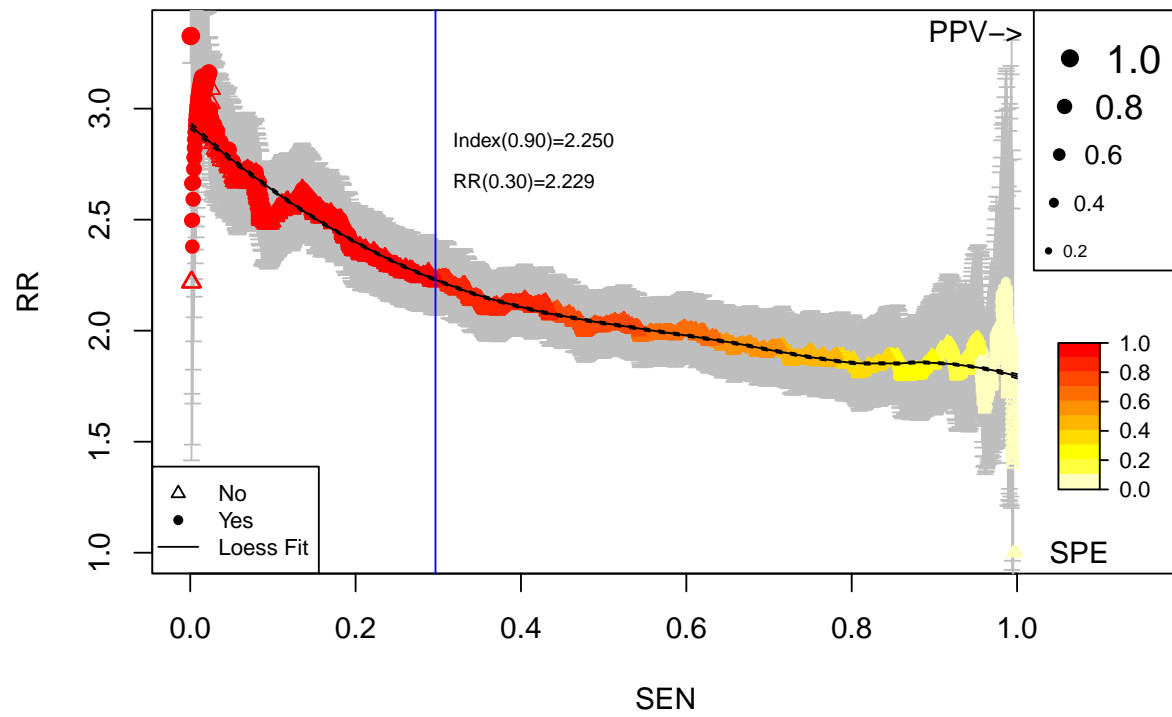
Kaplan–Meier: kappa

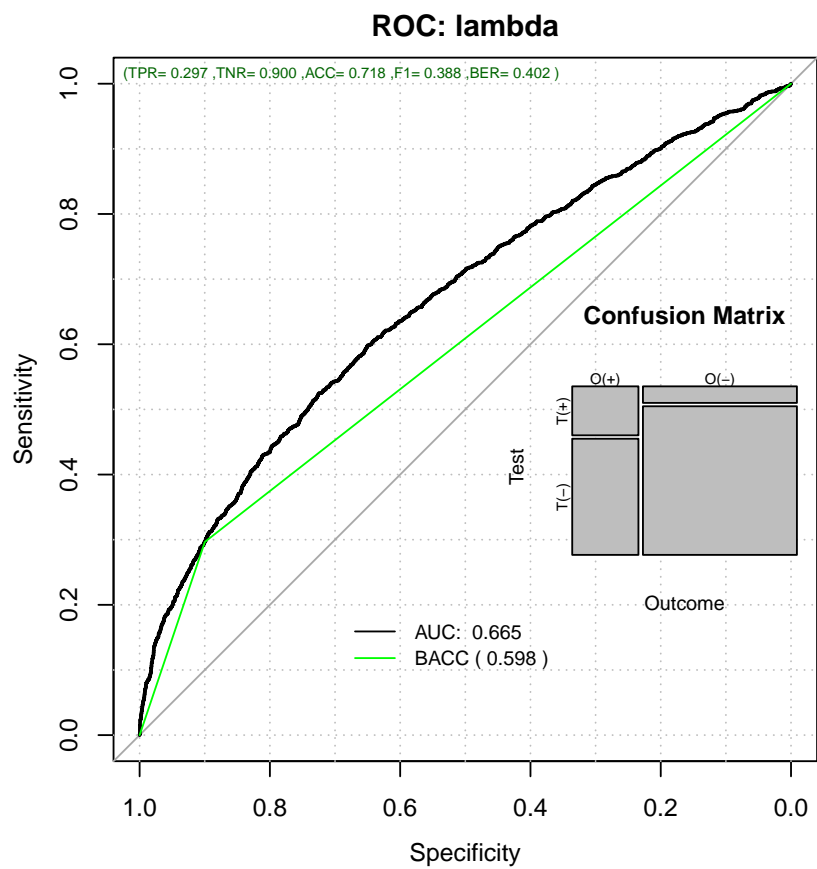


Number at risk

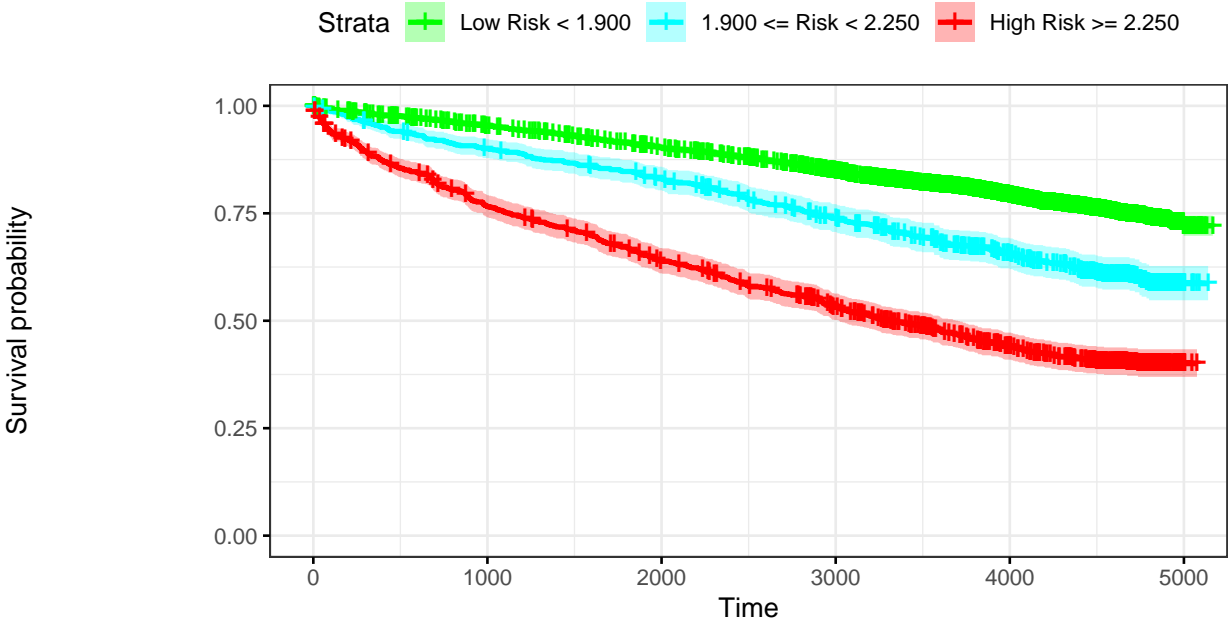
Low Risk < 1.640	4699	4420	4149	3790	3097	70
1.640 <= Risk < 1.959	743	666	599	503	363	6
High Risk >= 1.959	1082	801	659	522	333	5

Relative Risk: lambda





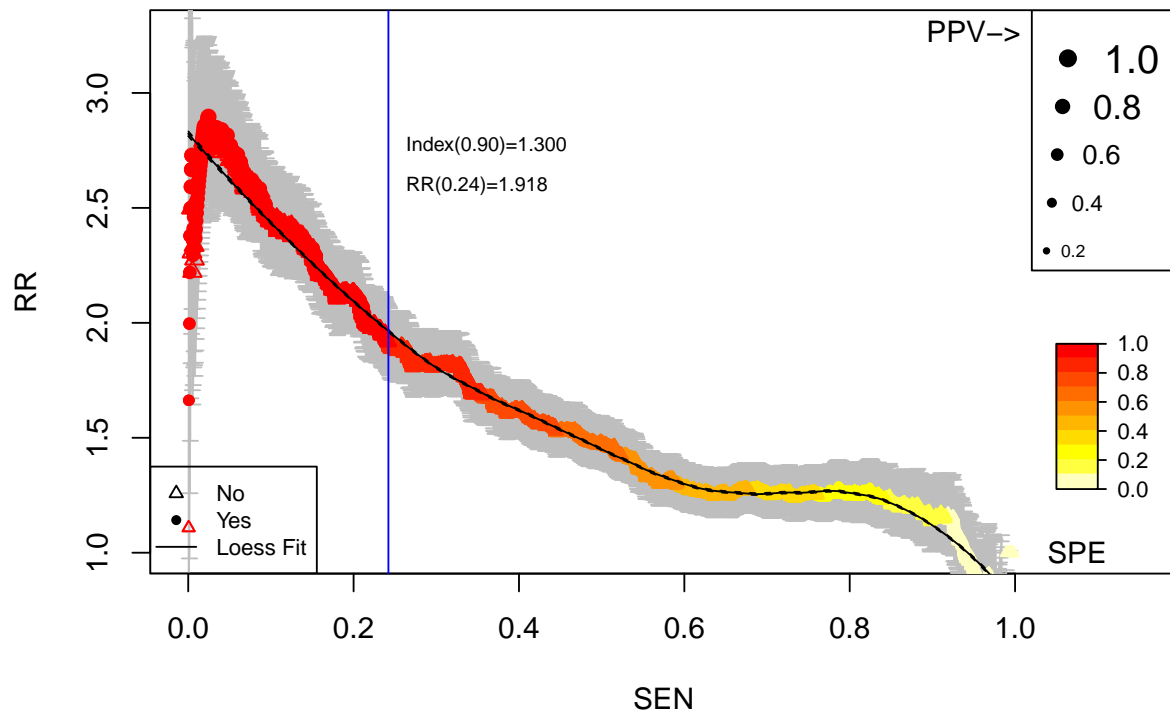
Kaplan–Meier: lambda

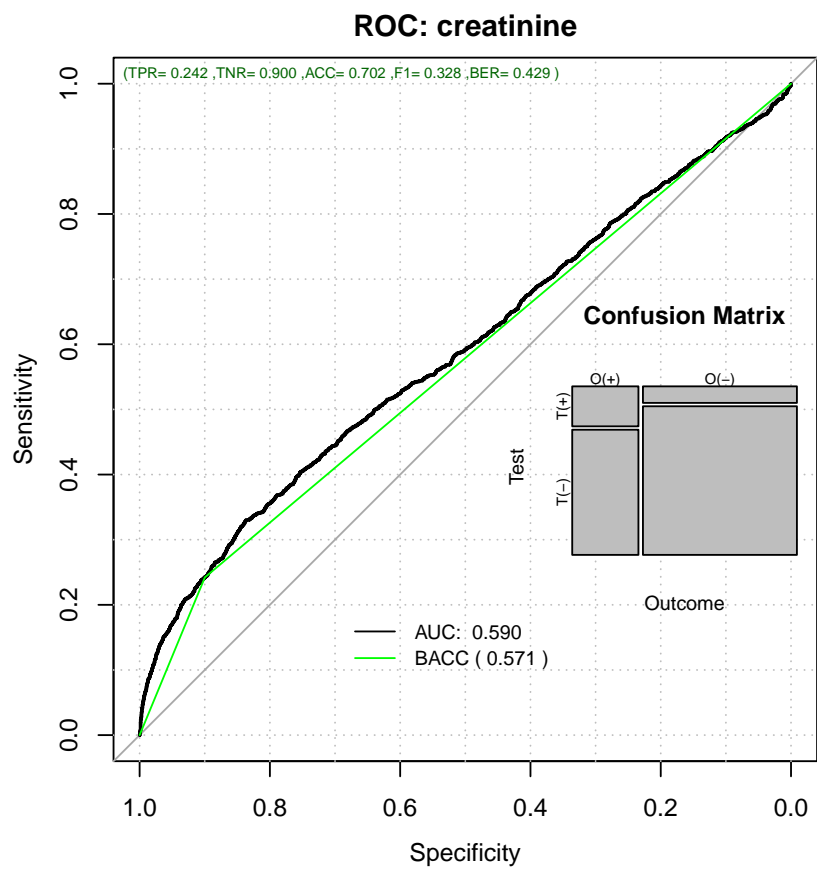


Number at risk

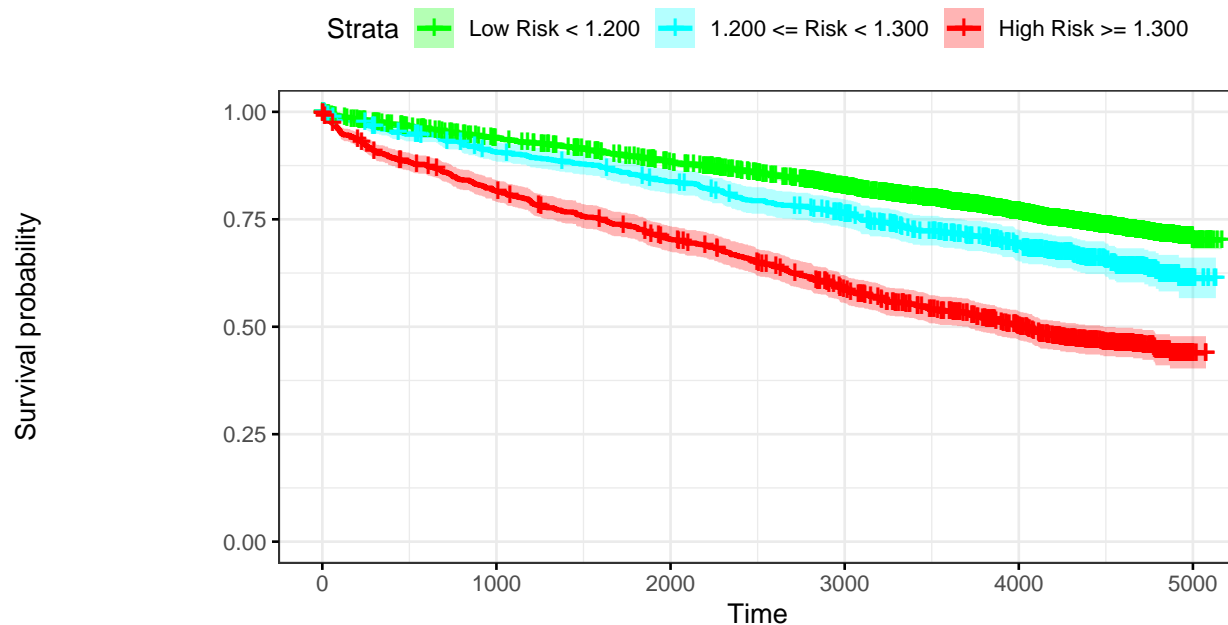
Low Risk < 1.900	4759	4459	4177	3810	3082	62
1.900 <= Risk < 2.250	726	647	590	501	371	11
High Risk >= 2.250	1039	781	640	504	340	8

Relative Risk: creatinine





Kaplan–Meier: creatinine



Number at risk

Low Risk < 1.200	4913	4537	4220	3827	3100	68
1.200 <= Risk < 1.300	679	600	550	483	345	9
High Risk >= 1.300	932	750	637	505	348	4

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

1.2 Reporting the Metrics

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

for (topf in topFive)
{
  CstatCI <- rbind(CstatCI, RRanalysis[[topf]]$c.index$cstatCI)
  RRratios <- rbind(RRratios, 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(RRratios) <- 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	0.590	0.574	0.606

```
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	0.683
lambda	0.657	0.657	0.645	0.670
creatinine	0.586	0.586	0.572	0.600

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

	est	lower	upper
age	4.06	3.79	4.35
kappa	2.36	2.21	2.53
lambda	2.23	2.08	2.39
creatinine	1.92	1.78	2.07

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

age	0.00e+00
kappa	1.07e-176
lambda	1.14e-142
creatinine	6.21e-73

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

	est	lower	upper
age	0.560	0.538	0.582
kappa	0.319	0.298	0.340
lambda	0.297	0.276	0.317
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],RRratios[,1])
colnames(meanMatrix) <- c("ROCAUC","C-Stat","Sen","Spe","RR")
pander::pander(meanMatrix)
```

	ROCAUC	C-Stat	Sen	Spe	RR
age	0.822	0.775	0.560	0.9	4.06
kappa	0.682	0.671	0.319	0.9	2.36
lambda	0.665	0.657	0.297	0.9	2.23
creatinine	0.590	0.586	0.242	0.9	1.92