Extras

SURVIVAL ANALAYSIS

GBSG2 Data set

The GBSG2 (German Breast Cancer Study Group) data set:

- horTh: hormonal therapy, a factor at two levels (yes and no).
- age: age of the patients in years.
- menostat: menopausal status, a factor at two levels pre (premenopausal) and post (postmenopausal).
- tsize: tumor size (in mm).
- tgrade: tumor grade, a ordered factor at levels I < II < III.
- pnodes: number of positive nodes.
- progrec: progesterone receptor (in fmol).
- estrec: estrogen receptor (in fmol).
- time: recurrence free survival time (in days).
- cens: censoring indicator (0- censored, 1- event).

LASSO

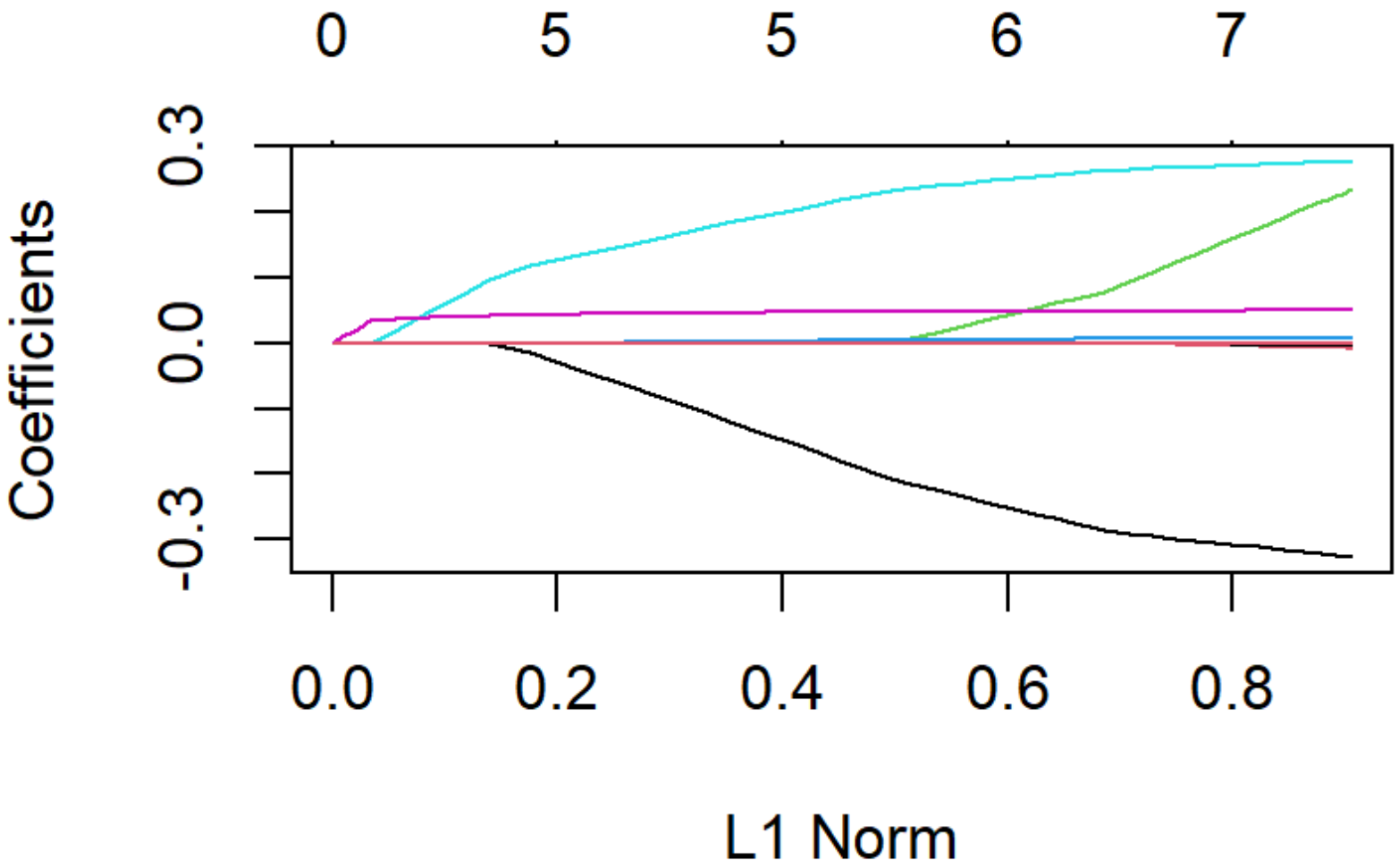
Lasso

The glmnet package in R can be used to perform LASSO (and Ridge) regression for Survival data

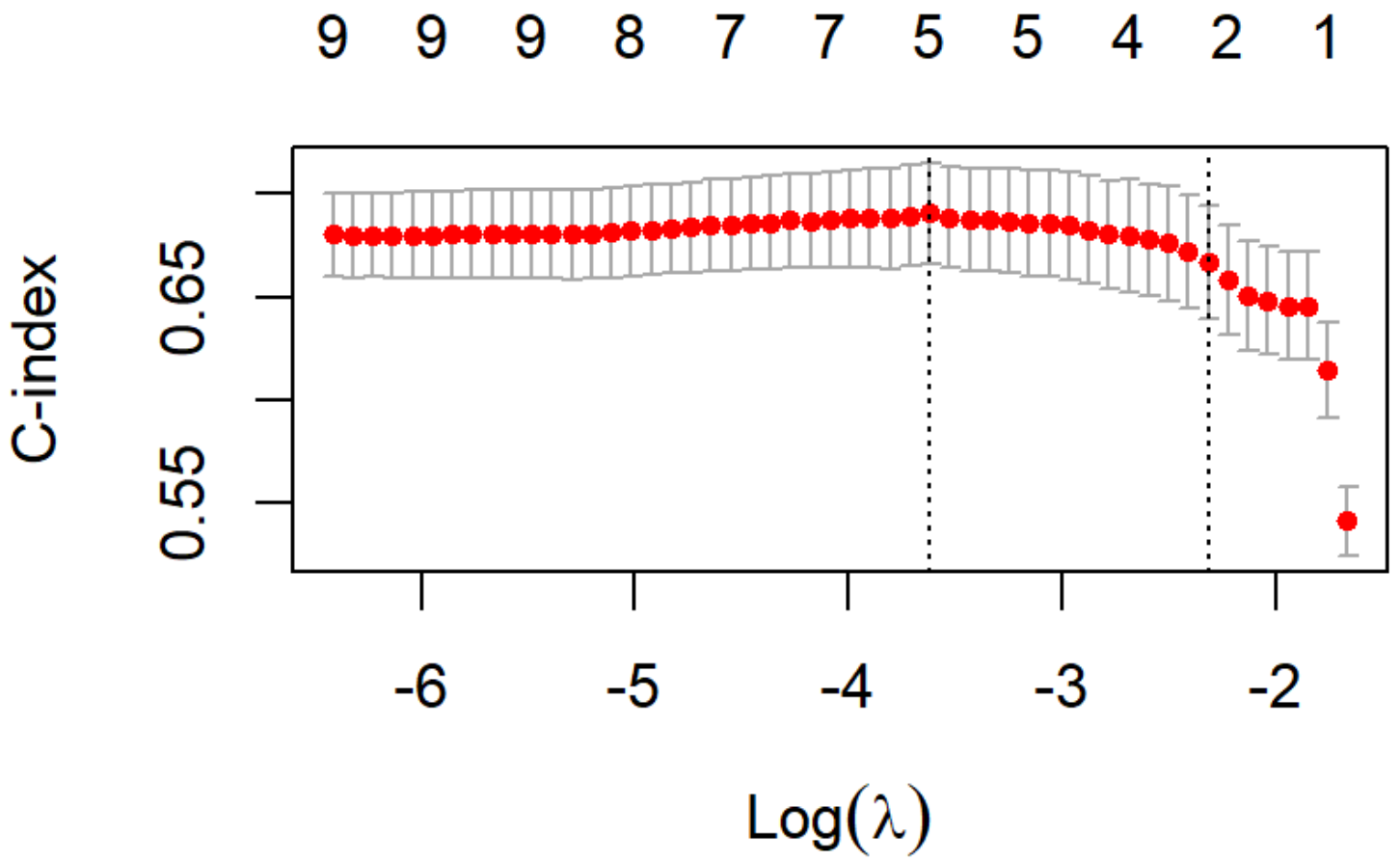
- Underlying model is Cox PH

All the functionalities that you have done previously, you are able to implement here

```
library(glmnet)
x=GBSG2 %>% select(horTh,age,menostat,tsize,
tgrade, pnodes, progrec, estrec)
y=Surv(time=GBSG2$time,event=GBSG2$cens)
model1<-glmnet(x,y,family="cox")
plot(model1)
```


0
5
5
6
7
Coefficients
0.3
0.0
-0.3
0.0
0.2
0.4
0.6
0.8
L1 Norm

```
x1<-as.matrix(x1) # had to dummy code!!
set.seed(1287)
cvfit <- cv.glmnet(x1, y, family = "cox", type.measure = "C")
plot(cvfit)
```



Using Lambda information....

From previous slide, we have that log(0.02673542) = -3.621766

Now we can pull of coef for this lambda value…

coef(model1,s=0.03)

horTh	-0.176785737
age	.
menostat	.
tsize	0.004002226
tgrade	0.216889004
pnodes	0.047722334
progrec	-0.001325963
estrec	.

Can also do repeated events and stratified analysis, see https://glmnet.stanford.edu/articles/Coxnet.html.

Decision Trees

Creating the conditional tree

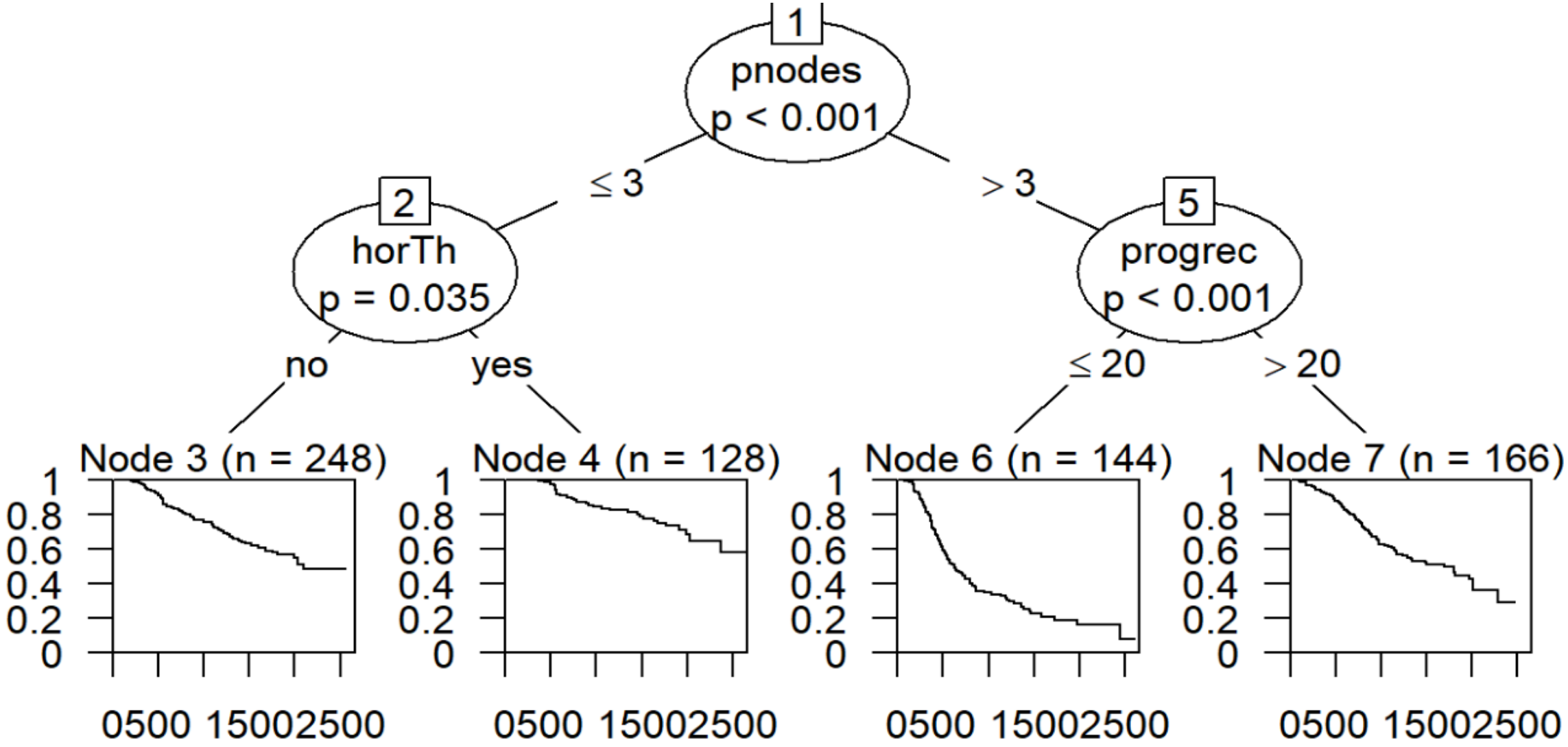
Splitting criteria is based on adjusted p-values from Logrank test (binary splits)

```
tree.surv<- ctree(Surv(time,cens) ~ . ,data=GBSG2)
tree.surv
```

Model formula:

```
Surv(time, cens) ~ horTh + age + menostat + tsize + tgrade +
    pnodes + progrec + estrec
```

Fitted party:
[1] root
| [2] pnodes <= 3
| | [3] horTh in no: 2093.000 (n = 248)
| | [4] horTh in yes: Inf (n = 128)
| [5] pnodes > 3
| | [6] progrec <= 20: 624.000 (n = 144)
| | [7] progrec > 20: 1701.000 (n = 166)


1
pnodes
p < 0.001
≤ 3
> 3
2
horTh
p = 0.035
5
progrec
p < 0.001
no
yes
≤ 20
> 20
Node 3 (n = 248)
Node 4 (n = 128)
Node 6 (n = 144)
Node 7 (n = 166)
1
0.8
0.6
0.4
0.2
0
0500 15002500

```
predict(tree.surv, newdata = GBSG2[1:2,], type = "node")
1 2
3 7
predict(tree.surv, newdata = GBSG2[1:2,], type = "response")
  1    2
2093 1701
```

Predicting median survival time

Nice reference: https://cran.r-project.org/web/packages/partykit/vignettes/ctree.pdf

Random Forest

Packages

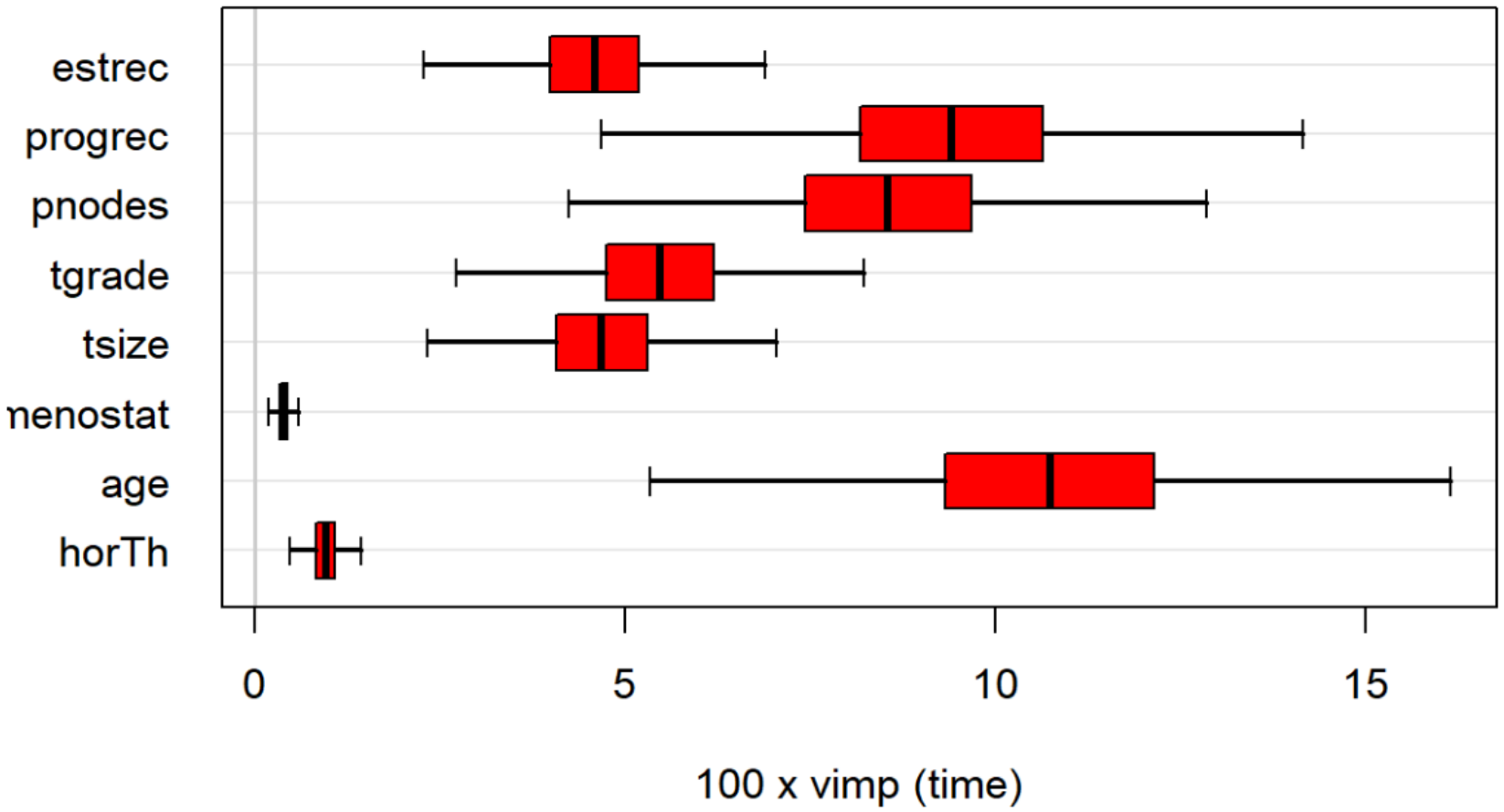
```
library(randomForestSRC)

library(ggRandomForests)
```

Creating the forest of trees

```
surv.rf <- rfsrc(Surv(time,cens) ~ . ,data=GBSG2,importance = TRUE,splitrule="logrankscore")
print(surv.rf$importance)
```

horTh	age	menostat
0.009596967	0.107318858	0.003980492
tsize	tgrade	pnodes
0.046818500	0.054757864	0.085496537
progrec	estrec	
0.094066472	0.045879145	

Variable importance



Survival curves for first two people in data

Good reference: https://www.randomforestsrc.org/articles/survival.html